Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

Term
cytokine-mediated signaling pathway (GO:0019221)
cellular response to cytokine stimulus (GO:0071345)
positive regulation of cytokine production (GO:0001819)
positive regulation of intracellular signal transduction (GO:1902533)
regulation of inflammatory response (GO:0050727)
inflammatory response (GO:0006954)
regulation of apoptotic process (GO:0042981)
regulation of cell population proliferation (GO:0042127)
positive regulation of multicellular organismal process (GO:0051240)
negative regulation of apoptotic process (GO:0043066)
regulation of tumor necrosis factor production (GO:0032680)
positive regulation of gene expression (GO:0010628)
positive regulation of cellular process (GO:0048522)
positive regulation of transcription, DNA-templated (GO:0045893)
positive regulation of macromolecule metabolic process (GO:0010604)
positive regulation of protein phosphorylation (GO:0001934)
regulation of interleukin-6 production (GO:0032675)
positive regulation of MAPK cascade (GO:0043410)
positive regulation of transcription by RNA polymerase II (GO:0045944)
negative regulation of programmed cell death (GO:0043069)
positive regulation of cell population proliferation (GO:0008284)
response to lipopolysaccharide (GO:0032496)
positive regulation of interleukin-6 production (GO:0032755)
positive regulation of tumor necrosis factor superfamily cytokine production (G
regulation of gene expression (GO:0010468)
cellular response to interferon-gamma (GO:0071346)
positive regulation of DNA-binding transcription factor activity (GO:0051091)
positive regulation of tumor necrosis factor production (GO:0032760)
positive regulation of inflammatory response (GO:0050729)
cellular response to tumor necrosis factor (GO:0071356)
positive regulation of lymphocyte proliferation (GO:0050671)
positive regulation of T cell activation (GO:0050870)
positive regulation of response to external stimulus (GO:0032103)
negative regulation of cytokine production (GO:0001818)
positive regulation of peptidyl-tyrosine phosphorylation (GO:0050731)
cellular response to lipopolysaccharide (GO:0071222)
cellular response to oxygen-containing compound (GO:1901701)
regulation of interleukin-8 production (GO:0032677)
positive regulation of defense response (GO:0031349)
positive regulation of chemokine production (GO:0032722)
positive regulation of T cell proliferation (GO:0042102)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

positive regulation of cell migration (GO:0030335)
regulation of ERK1 and ERK2 cascade (GO:0070372)
response to cytokine (GO:0034097)
positive regulation of protein kinase B signaling (GO:0051897)
regulation of angiogenesis (GO:0045765)
regulation of T cell proliferation (GO:0042129)
regulation of protein kinase B signaling (GO:0051896)
positive regulation of cell motility (GO:2000147)
positive regulation of nucleic acid-templated transcription (GO:1903508)
positive regulation of NF-kappaB transcription factor activity (GO:0051092)
positive regulation of interleukin-8 production (GO:0032757)
regulation of cell migration (GO:0030334)
regulation of interferon-gamma production (GO:0032649)
cellular response to molecule of bacterial origin (GO:0071219)
positive regulation of phosphorylation (GO:0042327)
positive regulation of ERK1 and ERK2 cascade (GO:0070374)
positive regulation of signal transduction (GO:0009967)
regulation of interleukin-12 production (GO:0032655)
regulation of interleukin-1 beta production (GO:0032651)
regulation of interleukin-10 production (GO:0032653)
regulation of immune response (GO:0050776)
regulation of cytokine production (GO:0001817)
cellular response to lipid (GO:0071396)
positive regulation of cytosolic calcium ion concentration (GO:0007204)
neutrophil migration (GO:1990266)
tumor necrosis factor-mediated signaling pathway (GO:0033209)
granulocyte chemotaxis (GO:0071621)
calcium-mediated signaling (GO:0019722)
neutrophil chemotaxis (GO:0030593)
negative regulation of cell population proliferation (GO:0008285)
neutrophil mediated immunity (GO:0002446)
negative regulation of cellular process (GO:0048523)
regulation of peptidyl-tyrosine phosphorylation (GO:0050730)
regulation of chemokine production (GO:0032642)
second-messenger-mediated signaling (GO:0019932)
apoptotic process (GO:0006915)
interferon-gamma-mediated signaling pathway (GO:0060333)
regulation of tyrosine phosphorylation of STAT protein (GO:0042509)
neutrophil activation involved in immune response (GO:0002283)
response to molecule of bacterial origin (GO:0002237)
neutrophil degranulation (GO:0043312)
positive regulation of immune response (GO:0050778)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

positive regulation of angiogenesis (GO:0045766)
response to interferon-gamma (GO:0034341)
positive regulation of interleukin-1 production (GO:0032732)
positive regulation of tyrosine phosphorylation of STAT protein (GO:0042531)
positive regulation of protein modification process (GO:0031401)
regulation of protein phosphorylation (GO:0001932)
chemokine-mediated signaling pathway (GO:0070098)
positive regulation of interleukin-1 beta production (GO:0032731)
negative regulation of extrinsic apoptotic signaling pathway (GO:2001237)
positive regulation of phosphatidylinositol 3-kinase signaling (GO:0014068)
positive regulation of apoptotic process (GO:0043065)
cellular response to chemokine (GO:1990869)
regulation of cytokine-mediated signaling pathway (GO:0001959)
regulation of cytosolic calcium ion concentration (GO:0051480)
regulation of NIK/NF-kappaB signaling (GO:1901222)
positive regulation of interferon-gamma production (GO:0032729)
positive regulation of vasculature development (GO:1904018)
regulation of smooth muscle cell proliferation (GO:0048660)
positive regulation of endothelial cell migration (GO:0010595)
response to lipid (GO:0033993)
T cell activation (GO:0042110)
negative regulation of inflammatory response (GO:0050728)
dendritic cell chemotaxis (GO:0002407)
extrinsic apoptotic signaling pathway (GO:0097191)
dendritic cell migration (GO:0036336)
negative regulation of macromolecule metabolic process (GO:0010605)
regulation of response to external stimulus (GO:0032101)
innate immune response (GO:0045087)
regulation of interleukin-17 production (GO:0032660)
response to interleukin-1 (GO:0070555)
positive regulation of NIK/NF-kappaB signaling (GO:1901224)
regulation of MAPK cascade (GO:0043408)
positive regulation of interleukin-12 production (GO:0032735)
positive regulation of programmed cell death (GO:0043068)
positive regulation of leukocyte chemotaxis (GO:0002690)
microglial cell activation (GO:0001774)
regulation of B cell proliferation (GO:0030888)
positive regulation of protein serine/threonine kinase activity (GO:0071902)
regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)
negative regulation of transcription, DNA-templated (GO:0045892)
regulation of extrinsic apoptotic signaling pathway (GO:2001236)
regulation of blood vessel endothelial cell migration (GO:0043535)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

cellular response to oxidative stress (GO:0034599)
antigen receptor-mediated signaling pathway (GO:0050851)
negative regulation of multicellular organismal process (GO:0051241)
positive regulation of neuron death (GO:1901216)
positive regulation of cellular biosynthetic process (GO:0031328)
regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043122)
lymphocyte chemotaxis (GO:0048247)
positive regulation of macromolecule biosynthetic process (GO:0010557)
positive regulation of cellular metabolic process (GO:0031325)
cellular response to organic cyclic compound (GO:0071407)
regulation of programmed cell death (GO:0043067)
regulation of transcription by RNA polymerase II (GO:0006357)
defense response to virus (GO:0051607)
positive regulation of protein kinase activity (GO:0045860)
regulation of neuron death (GO:1901214)
response to tumor necrosis factor (GO:0034612)
myeloid leukocyte differentiation (GO:0002573)
defense response to symbiont (GO:0140546)
positive regulation of type I interferon production (GO:0032481)
negative regulation of tumor necrosis factor superfamily cytokine production (G
positive regulation of blood vessel endothelial cell migration (GO:0043536)
positive regulation of interleukin-10 production (GO:0032733)
regulation of defense response (GO:0031347)
macrophage activation (GO:0042116)
activation of protein kinase activity (GO:0032147)
positive regulation of protein metabolic process (GO:0051247)
regulation of MAP kinase activity (GO:0043405)
MAPK cascade (GO:0000165)
positive regulation of epithelial cell proliferation (GO:0050679)
cellular response to type I interferon (GO:0071357)
type I interferon signaling pathway (GO:0060337)
negative regulation of tumor necrosis factor production (GO:0032720)
positive regulation of smooth muscle cell proliferation (GO:0048661)
response to organic cyclic compound (GO:0014070)
negative regulation of gene expression (GO:0010629)
monocyte chemotaxis (GO:0002548)
cellular response to growth factor stimulus (GO:0071363)
T cell receptor signaling pathway (GO:0050852)
transmembrane receptor protein tyrosine kinase signaling pathway (GO:00071 6
positive regulation of cell differentiation (GO:0045597)
positive regulation of epithelial cell migration (GO:0010634)
positive regulation of endothelial cell proliferation (GO:0001938)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

positive regulation of cysteine-type endopeptidase activity involved in apoptotic
positive regulation of metabolic process (GO:0009893)
positive regulation of mononuclear cell migration (GO:0071677)
toll-like receptor signaling pathway (GO:0002224)
positive regulation of cold-induced thermogenesis (GO:0120162)
cell chemotaxis (GO:0060326)
positive regulation of MAP kinase activity (GO:0043406)
negative regulation of neuron death (GO:1901215)
regulation of neuroinflammatory response (GO:0150077)
regulation of pri-miRNA transcription by RNA polymerase II (GO:1902893)
negative regulation of transcription by RNA polymerase II (GO:0000122)
positive regulation of peptidyl-serine phosphorylation (GO:0033138)
positive regulation of cell death (GO:0010942)
cellular response to chemical stress (GO:0062197)
positive regulation of pri-miRNA transcription by RNA polymerase II (GO:19028
positive regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043123)
B cell activation (GO:0042113)
cellular response to organic substance (GO:0071310)
regulation of interleukin-2 production (GO:0032663)
positive regulation of B cell activation (GO:0050871)
regulation of neuron apoptotic process (GO:0043523)
cellular response to virus (GO:0098586)
regulation of endothelial cell apoptotic process (GO:2000351)
platelet degranulation (GO:0002576)
response to reactive oxygen species (GO:0000302)
lymphocyte migration (GO:0072676)
regulation of nitric oxide biosynthetic process (GO:0045428)
cellular response to interleukin-1 (GO:0071347)
positive regulation of immune effector process (GO:0002699)
regulation of receptor signaling pathway via JAK-STAT (GO:0046425)
negative regulation of signal transduction (GO:0009968)
positive regulation of hydrolase activity (GO:0051345)
regulation of endothelial cell migration (GO:0010594)
positive regulation of transport (GO:0051050)
cellular response to peptide (GO:1901653)
defense response to bacterium (GO:0042742)
regulation of endothelial cell proliferation (GO:0001936)
cellular response to reactive oxygen species (GO:0034614)
negative regulation of extrinsic apoptotic signaling pathway via death domain re
regulation of activated T cell proliferation (GO:0046006)
positive regulation of developmental process (GO:0051094)
positive regulation of B cell proliferation (GO:0030890)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

positive regulation of leukocyte mediated cytotoxicity (GO:0001912)
activation of cysteine-type endopeptidase activity involved in apoptotic process
response to peptide (GO:1901652)
positive regulation of interleukin-17 production (GO:0032740)
positive regulation of apoptotic signaling pathway (GO:2001235)
regulated exocytosis (GO:0045055)
regulation of vascular endothelial growth factor production (GO:0010574)
positive regulation of leukocyte cell-cell adhesion (GO:1903039)
receptor signaling pathway via JAK-STAT (GO:0007259)
lipopolysaccharide-mediated signaling pathway (GO:0031663)
negative regulation of interleukin-10 production (GO:0032693)
negative regulation of apoptotic signaling pathway (GO:2001234)
positive regulation of T cell mediated immunity (GO:0002711)
negative regulation of nucleic acid-templated transcription (GO:1903507)
leukocyte cell-cell adhesion (GO:0007159)
regulation of cell growth (GO:0001558)
negative regulation of cell-cell adhesion (GO:0022408)
negative regulation of response to external stimulus (GO:0032102)
regulation of protein secretion (GO:0050708)
regulation of peptidyl-serine phosphorylation (GO:0033135)
protein phosphorylation (GO:0006468)
I-kappaB kinase/NF-kappaB signaling (GO:0007249)
purinergic nucleotide receptor signaling pathway (GO:0035590)
positive regulation of signaling receptor activity (GO:2000273)
positive regulation of cell adhesion (GO:0045785)
regulation of extrinsic apoptotic signaling pathway via death domain receptors (
positive regulation of production of molecular mediator of immune response (G
negative regulation of cellular macromolecule biosynthetic process (GO:20001
mononuclear cell differentiation (GO:1903131)
negative regulation of secretion by cell (GO:1903531)
regulation of peptidyl-threonine phosphorylation (GO:0010799)
regulation of interferon-beta production (GO:0032648)
response to hydrogen peroxide (GO:0042542)
positive regulation of binding (GO:0051099)
response to amyloid-beta (GO:1904645)
regulation of T cell cytokine production (GO:0002724)
negative regulation of immune response (GO:0050777)
regulation of granulocyte macrophage colony-stimulating factor production (GO
negative regulation of defense response (GO:0031348)
pattern recognition receptor signaling pathway (GO:0002221)
negative regulation of T cell activation (GO:0050868)
positive regulation of kinase activity (GO:0033674)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

negative regulation of angiogenesis (GO:0016525)
regulation of T cell migration (GO:2000404)
cellular response to interleukin-6 (GO:0071354)
regulation of immunoglobulin production (GO:0002637)
protein kinase B signaling (GO:0043491)
negative regulation of cytokine production involved in immune response (GO:0)
positive regulation of granulocyte macrophage colony-stimulating factor product
regulation of nitric-oxide synthase biosynthetic process (GO:0051769)
negative regulation of smooth muscle cell proliferation (GO:0048662)
cellular response to interleukin-12 (GO:0071349)
negative regulation of neuron apoptotic process (GO:0043524)
regulation of cytokine production involved in inflammatory response (GO:19000
negative regulation of interferon-gamma production (GO:0032689)
regulation of T cell mediated cytotoxicity (GO:0001914)
lymphocyte differentiation (GO:0030098)
positive regulation of vascular endothelial growth factor production (GO:001057
cellular response to mechanical stimulus (GO:0071260)
positive regulation of reactive oxygen species metabolic process (GO:2000379)
regulation of nitric-oxide synthase activity (GO:0050999)
regulation of T cell differentiation (GO:0045580)
positive regulation of stress-activated MAPK cascade (GO:0032874)
regulation of fat cell differentiation (GO:0045598)
macrophage differentiation (GO:0030225)
extracellular matrix organization (GO:0030198)
positive regulation of interleukin-2 production (GO:0032743)
NIK/NF-kappaB signaling (GO:0038061)
positive regulation of chemotaxis (GO:0050921)
positive regulation of wound healing (GO:0090303)
interleukin-12-mediated signaling pathway (GO:0035722)
regulation of cysteine-type endopeptidase activity involved in apoptotic process
positive regulation of cytokine-mediated signaling pathway (GO:0001961)
positive regulation of interferon-beta production (GO:0032728)
positive regulation of myeloid leukocyte differentiation (GO:0002763)
regulation of GTPase activity (GO:0043087)
positive regulation of nitric oxide biosynthetic process (GO:0045429)
regulation of tumor necrosis factor-mediated signaling pathway (GO:0010803)
regulation of T cell activation (GO:0050863)
regulation of wound healing (GO:0061041)
negative regulation of cell differentiation (GO:0045596)
positive regulation of receptor signaling pathway via STAT (GO:1904894)
eosinophil chemotaxis (GO:0048245)
eosinophil migration (GO:0072677)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

positive regulation of leukocyte adhesion to vascular endothelial cell (GO:1904 9
positive regulation of calcium ion transport (GO:0051928)
negative regulation of blood vessel morphogenesis (GO:2000181)
regulation of chemokine (C-X-C motif) ligand 2 production (GO:2000341)
positive regulation of monooxygenase activity (GO:0032770)
positive regulation of nitric oxide metabolic process (GO:1904407)
negative regulation of long-term synaptic potentiation (GO:1900272)
adaptive immune response based on somatic recombination of immune recept ɔ
regulation of tissue remodeling (GO:0034103)
positive regulation of T cell differentiation (GO:0045582)
positive regulation of receptor signaling pathway via JAK-STAT (GO:0046427)
lymphocyte proliferation (GO:0046651)
positive regulation of biosynthetic process (GO:0009891)
cellular response to vascular endothelial growth factor stimulus (GO:0035924)
positive regulation of calcium ion transport into cytosol (GO:0010524)
positive regulation of peptidyl-threonine phosphorylation (GO:0010800)
positive regulation of T cell migration (GO:2000406)
receptor signaling pathway via STAT (GO:0097696)
regulation of heterotypic cell-cell adhesion (GO:0034114)
regulation of interferon-alpha production (GO:0032647)
positive regulation of T cell cytokine production (GO:0002726)
interleukin-35-mediated signaling pathway (GO:0070757)
positive regulation of nitric-oxide synthase biosynthetic process (GO:0051770)
regulation of dendritic cell apoptotic process (GO:2000668)
positive regulation of superoxide anion generation (GO:0032930)
extrinsic apoptotic signaling pathway via death domain receptors (GO:0008625
regulation of natural killer cell mediated cytotoxicity (GO:0042269)
cellular response to amyloid-beta (GO:1904646)
negative regulation of T cell proliferation (GO:0042130)
positive regulation of lymphocyte activation (GO:0051251)
receptor-mediated endocytosis (GO:0006898)
positive regulation of response to stimulus (GO:0048584)
negative regulation of intrinsic apoptotic signaling pathway (GO:2001243)
positive regulation of T cell mediated cytotoxicity (GO:0001916)
regulation of cell cycle (GO:0051726)
interleukin-6-mediated signaling pathway (GO:0070102)
T cell migration (GO:0072678)
negative regulation of interleukin-6 production (GO:0032715)
regulation of macrophage derived foam cell differentiation (GO:0010743)
regulation of osteoclast differentiation (GO:0045670)
regulation of DNA binding (GO:0051101)
positive regulation of epithelial to mesenchymal transition (GO:0010718)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

phosphorylation (GO:0016310)
positive regulation of toll-like receptor signaling pathway (GO:0034123)
regulation of blood coagulation (GO:0030193)
interleukin-27-mediated signaling pathway (GO:0070106)
positive regulation of osteoclast differentiation (GO:0045672)
regulation of superoxide anion generation (GO:0032928)
regulation of protein-containing complex assembly (GO:0043254)
negative regulation of epithelial cell apoptotic process (GO:1904036)
positive regulation of JNK cascade (GO:0046330)
positive regulation of intracellular protein transport (GO:0090316)
negative regulation of MAPK cascade (GO:0043409)
regulation of interferon-gamma-mediated signaling pathway (GO:0060334)
regulation of mononuclear cell migration (GO:0071675)
cellular response to interleukin-7 (GO:0098761)
heart trabecula morphogenesis (GO:0061384)
interleukin-7-mediated signaling pathway (GO:0038111)
regulation of lymphocyte proliferation (GO:0050670)
regulation of cell motility (GO:2000145)
negative regulation of leukocyte apoptotic process (GO:2000107)
response to unfolded protein (GO:0006986)
adenylate cyclase-activating G protein-coupled receptor signaling pathway (GO
positive regulation of protein-containing complex assembly (GO:0031334)
negative regulation of dendritic cell apoptotic process (GO:2000669)
positive regulation of activation of Janus kinase activity (GO:0010536)
regulation of calcidiol 1-monooxygenase activity (GO:0060558)
positive regulation of receptor-mediated endocytosis (GO:0048260)
peptidyl-tyrosine phosphorylation (GO:0018108)
dendritic cell differentiation (GO:0097028)
positive regulation of neuron apoptotic process (GO:0043525)
regulation of cytokine production involved in immune response (GO:0002718)
regulation of monooxygenase activity (GO:0032768)
regulation of JNK cascade (GO:0046328)
negative regulation of lymphocyte proliferation (GO:0050672)
activation of NF-kappaB-inducing kinase activity (GO:0007250)
regulation of interleukin-1 production (GO:0032652)
positive regulation of activated T cell proliferation (GO:0042104)
positive regulation of interferon-alpha production (GO:0032727)
phosphatidylinositol 3-kinase signaling (GO:0014065)
positive regulation of DNA binding (GO:0043388)
regulation of amyloid-beta formation (GO:1902003)
positive regulation of extrinsic apoptotic signaling pathway (GO:2001238)
regulation of bone mineralization (GO:0030500)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

positive regulation of cellular component organization (GO:0051130)
regulation of innate immune response (GO:0045088)
regulation of intracellular signal transduction (GO:1902531)
regulation of cell differentiation (GO:0045595)
response to peptide hormone (GO:0043434)
positive regulation of immunoglobulin production (GO:0002639)
enzyme linked receptor protein signaling pathway (GO:0007167)
positive regulation of phosphate metabolic process (GO:0045937)
regulation of macrophage activation (GO:0043030)
negative regulation of NF-kappaB transcription factor activity (GO:0032088)
positive regulation of protein localization to membrane (GO:1905477)
proteolysis (GO:0006508)
T cell differentiation (GO:0030217)
regulation of cell adhesion (GO:0030155)
hemopoiesis (GO:0030097)
negative regulation of chemokine production (GO:0032682)
positive regulation of cytokine production involved in inflammatory response (G
positive regulation of phagocytosis (GO:0050766)
positive regulation of cell-cell adhesion (GO:0022409)
regulation of regulatory T cell differentiation (GO:0045589)
negative regulation of DNA-binding transcription factor activity (GO:0043433)
regulation of viral genome replication (GO:0045069)
positive regulation of protein tyrosine kinase activity (GO:0061098)
regulation of peptide hormone secretion (GO:0090276)
positive regulation of endocytosis (GO:0045807)
steroid metabolic process (GO:0008202)
regulation of type I interferon production (GO:0032479)
growth hormone receptor signaling pathway via JAK-STAT (GO:0060397)
negative regulation of interleukin-12 production (GO:0032695)
negative regulation of neuroinflammatory response (GO:0150079)
negative regulation of T cell mediated immunity (GO:0002710)
response to UV-A (GO:0070141)
cellular defense response (GO:0006968)
regulation of cellular protein metabolic process (GO:0032268)
B cell proliferation (GO:0042100)
positive regulation of lymphocyte chemotaxis (GO:0140131)
regulation of transforming growth factor beta production (GO:0071634)
cellular response to unfolded protein (GO:0034620)
negative regulation of endothelial cell apoptotic process (GO:2000352)
positive regulation of cellular component movement (GO:0051272)
negative regulation of cellular catabolic process (GO:0031330)
cellular response to interleukin-21 (GO:0098757)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

interleukin-21-mediated signaling pathway (GO:0038114)
regulation of activation of Janus kinase activity (GO:0010533)
protein-containing complex assembly (GO:0065003)
negative regulation of interleukin-17 production (GO:0032700)
PERK-mediated unfolded protein response (GO:0036499)
T cell chemotaxis (GO:0010818)
positive regulation of transferase activity (GO:0051347)
positive regulation of epithelial cell apoptotic process (GO:1904037)
regulation of interleukin-4 production (GO:0032673)
positive regulation of cytokine production involved in immune response (GO:00
positive regulation of defense response to virus by host (GO:0002230)
positive regulation of response to wounding (GO:1903036)
regulation of B cell activation (GO:0050864)
positive regulation of cellular catabolic process (GO:0031331)
phosphatidylinositol-mediated signaling (GO:0048015)
regulation of endopeptidase activity (GO:0052548)
positive regulation of macrophage migration (GO:1905523)
positive regulation of monocyte chemotaxis (GO:0090026)
positive regulation of natural killer cell activation (GO:0032816)
positive regulation of GTPase activity (GO:0043547)
positive regulation of protein binding (GO:0032092)
regulation of phagocytosis (GO:0050764)
negative regulation of cell death (GO:0060548)
positive regulation of release of sequestered calcium ion into cytosol (GO:0051
positive regulation of cell growth (GO:0030307)
negative regulation of protein metabolic process (GO:0051248)
regulation of transcription from RNA polymerase II promoter in response to stre
positive regulation of transcription from RNA polymerase II promoter in respons
MyD88-dependent toll-like receptor signaling pathway (GO:0002755)
positive regulation of leukocyte migration (GO:0002687)
extracellular structure organization (GO:0043062)
negative regulation of cell migration (GO:0030336)
negative regulation of intracellular signal transduction (GO:1902532)
cellular component disassembly (GO:0022411)
extracellular matrix disassembly (GO:0022617)
negative regulation of cysteine-type endopeptidase activity (GO:2000117)
cellular response to hydrogen peroxide (GO:0070301)
positive regulation of cellular amide metabolic process (GO:0034250)
protein deubiquitination (GO:0016579)
positive regulation of T-helper 1 type immune response (GO:0002827)
regulation of dendritic cell differentiation (GO:2001198)
epithelial to mesenchymal transition (GO:0001837)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

positive regulation of alpha-beta T cell activation (GO:0046635)
positive regulation of lymphocyte differentiation (GO:0045621)
regulation of protein modification by small protein conjugation or removal (GO:1
maintenance of blood-brain barrier (GO:0035633)
negative regulation of interleukin-1 production (GO:0032692)
positive regulation of lipid metabolic process (GO:0045834)
regulation of amyloid-beta clearance (GO:1900221)
adenylate cyclase-modulating G protein-coupled receptor signaling pathway (G
cellular response to interleukin-9 (GO:0071355)
interleukin-23-mediated signaling pathway (GO:0038155)
interleukin-9-mediated signaling pathway (GO:0038113)
negative regulation of T cell cytokine production (GO:0002725)
positive regulation of smooth muscle cell apoptotic process (GO:0034393)
regulation of cell adhesion molecule production (GO:0060353)
regulation of dendritic cell antigen processing and presentation (GO:0002604)
T-helper 1 type immune response (GO:0042088)
platelet aggregation (GO:0070527)
regulation of defense response to virus by host (GO:0050691)
cellular response to hypoxia (GO:0071456)
regulation of Notch signaling pathway (GO:0008593)
negative regulation of cysteine-type endopeptidase activity involved in apoptoti c
skeletal system development (GO:0001501)
positive regulation of cysteine-type endopeptidase activity (GO:2001056)
regulation of neurogenesis (GO:0050767)
activation of protein kinase B activity (GO:0032148)
positive regulation of locomotion (GO:0040017)
positive regulation of antigen receptor-mediated signaling pathway (GO:005085
positive regulation of immune system process (GO:0002684)
positive regulation of transcription from RNA polymerase II promoter involved in
regulation of monocyte chemotaxis (GO:0090025)
negative regulation of endothelial cell proliferation (GO:0001937)
regulation of vascular associated smooth muscle cell proliferation (GO:190470 5
natural killer cell activation (GO:0030101)
cellular protein modification process (GO:0006464)
negative regulation of metabolic process (GO:0009892)
negative regulation of viral process (GO:0048525)
cell surface receptor signaling pathway involved in heart development (GO:006
protein modification by small protein removal (GO:0070646)
regulation of leukocyte adhesion to vascular endothelial cell (GO:1904994)
regulation of receptor signaling pathway via STAT (GO:1904892)
negative regulation of protein phosphorylation (GO:0001933)
external encapsulating structure organization (GO:0045229)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

negative regulation of growth (GO:0045926)
negative regulation of protein serine/threonine kinase activity (GO:0071901)
superoxide metabolic process (GO:0006801)
glucose homeostasis (GO:0042593)
homotypic cell-cell adhesion (GO:0034109)
regulation of kinase activity (GO:0043549)
negative regulation of endothelial cell migration (GO:0010596)
negative regulation of inflammatory response to antigenic stimulus (GO:000286
intrinsic apoptotic signaling pathway in response to DNA damage (GO:0008630
mesenchymal cell differentiation (GO:0048762)
negative regulation of epithelial cell proliferation (GO:0050680)
positive regulation of secretion by cell (GO:1903532)
cellular response to organonitrogen compound (GO:0071417)
regulation of inflammatory response to antigenic stimulus (GO:0002861)
positive regulation of Notch signaling pathway (GO:0045747)
apoptotic cell clearance (GO:0043277)
endothelial cell migration (GO:0043542)
negative regulation of protein secretion (GO:0050709)
negative regulation of heterotypic cell-cell adhesion (GO:0034115)
regulation of cell-cell adhesion involved in gastrulation (GO:0070587)
regulation of insulin secretion (GO:0050796)
negative regulation of cell adhesion (GO:0007162)
arginine catabolic process (GO:0006527)
positive regulation of chemokine (C-X-C motif) ligand 2 production (GO:200034
regulation of natural killer cell chemotaxis (GO:2000501)
regulation of natural killer cell mediated cytotoxicity directed against tumor cell t
regulation of natural killer cell proliferation (GO:0032817)
pulmonary valve development (GO:0003177)
regulation of multicellular organism growth (GO:0040014)
regulation of production of miRNAs involved in gene silencing by miRNA (GO:1
regulation of vascular endothelial cell proliferation (GO:1905562)
phospholipase C-activating G protein-coupled receptor signaling pathway (GO:
negative regulation of oxidative stress-induced cell death (GO:1903202)
positive regulation of fibroblast proliferation (GO:0048146)
T cell activation involved in immune response (GO:0002286)
regulation of canonical Wnt signaling pathway (GO:0060828)
regulation of fibroblast proliferation (GO:0048145)
ERK1 and ERK2 cascade (GO:0070371)
positive regulation of cholesterol efflux (GO:0010875)
positive regulation of morphogenesis of an epithelium (GO:1905332)
regulation of necroptotic process (GO:0060544)
Fc receptor mediated stimulatory signaling pathway (GO:0002431)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

positive regulation of lymphocyte migration (GO:2000403)
positive regulation of T-helper cell differentiation (GO:0045624)
positive regulation of type 2 immune response (GO:0002830)
regulation of macrophage cytokine production (GO:0010935)
regulation of response to interferon-gamma (GO:0060330)
T-helper cell differentiation (GO:0042093)
vasodilation (GO:0042311)
negative regulation of blood vessel endothelial cell migration (GO:0043537)
regulation of cell adhesion mediated by integrin (GO:0033628)
negative regulation of blood coagulation (GO:0030195)
positive regulation of ossification (GO:0045778)
regulation of transcription, DNA-templated (GO:0006355)
negative regulation of viral genome replication (GO:0045071)
B cell differentiation (GO:0030183)
regulation of signal transduction (GO:0009966)
regulation of release of cytochrome c from mitochondria (GO:0090199)
blood vessel diameter maintenance (GO:0097746)
regulation of epithelial to mesenchymal transition (GO:0010717)
positive regulation of leukocyte activation (GO:0002696)
positive regulation of oxidoreductase activity (GO:0051353)
mammary gland development (GO:0030879)
positive regulation of cellular component biogenesis (GO:0044089)
cellular response to decreased oxygen levels (GO:0036294)
negative regulation of cell growth (GO:0030308)
modulation of chemical synaptic transmission (GO:0050804)
regulation of protein ubiquitination (GO:0031396)
negative regulation of cytokine-mediated signaling pathway (GO:0001960)
peptidyl-cysteine S-nitrosylation (GO:0018119)
positive regulation of CD4-positive, CD25-positive, alpha-beta regulatory T cell
positive regulation of dendritic cell differentiation (GO:2001200)
positive regulation of transcription from RNA polymerase II promoter in respons
regulation of epithelial cell proliferation (GO:0050678)
cellular response to interleukin-2 (GO:0071352)
interleukin-2-mediated signaling pathway (GO:0038110)
positive regulation of interleukin-13 production (GO:0032736)
positive regulation of leukocyte apoptotic process (GO:2000108)
positive regulation of production of miRNAs involved in gene silencing by miRN
positive regulation of transforming growth factor beta production (GO:0071636)
regulation of monocyte chemotactic protein-1 production (GO:0071637)
regulation of T cell mediated immunity (GO:0002709)
negative regulation of protein catabolic process (GO:0042177)
artery morphogenesis (GO:0048844)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

heterotypic cell-cell adhesion (GO:0034113)
acute-phase response (GO:0006953)
integrated stress response signaling (GO:0140467)
macrophage migration (GO:1905517)
negative regulation of blood pressure (GO:0045776)
negative regulation of leukocyte mediated cytotoxicity (GO:0001911)
positive regulation of response to cytokine stimulus (GO:0060760)
regulation of microglial cell activation (GO:1903978)
regulation of T cell chemotaxis (GO:0010819)
vitamin D metabolic process (GO:0042359)
carbohydrate homeostasis (GO:0033500)
wound healing (GO:0042060)
regulation of autophagy (GO:0010506)
regulation of ossification (GO:0030278)
intrinsic apoptotic signaling pathway (GO:0097193)
receptor internalization (GO:0031623)
negative regulation of peptidase activity (GO:0010466)
interleukin-1-mediated signaling pathway (GO:0070498)
nervous system development (GO:0007399)
Fc-epsilon receptor signaling pathway (GO:0038095)
regulation of calcium ion import (GO:0090279)
Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
growth hormone receptor signaling pathway (GO:0060396)
positive regulation of natural killer cell mediated cytotoxicity (GO:0045954)
regulation of acute inflammatory response (GO:0002673)
toll-like receptor 4 signaling pathway (GO:0034142)
positive regulation of phospholipase C activity (GO:0010863)
Fc receptor signaling pathway (GO:0038093)
antigen processing and presentation of exogenous peptide antigen via MHC cl a
leukocyte aggregation (GO:0070486)
positive regulation of cell migration by vascular endothelial growth factor signali
positive regulation of dendritic cell chemotaxis (GO:2000510)
positive regulation of MHC class II biosynthetic process (GO:0045348)
positive regulation of myeloid cell apoptotic process (GO:0033034)
regulation of vascular wound healing (GO:0061043)
ventricular trabecula myocardium morphogenesis (GO:0003222)
Fc-gamma receptor signaling pathway (GO:0038094)
BMP signaling pathway (GO:0030509)
transcription initiation from RNA polymerase II promoter (GO:0006367)
negative regulation of cell development (GO:0010721)
negative regulation of intrinsic apoptotic signaling pathway in response to DNA
negative regulation of natural killer cell mediated cytotoxicity (GO:0045953)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

positive regulation of alpha-beta T cell proliferation (GO:0046641)
positive regulation of endothelial cell apoptotic process (GO:2000353)
positive regulation of myeloid leukocyte cytokine production involved in immune
regulation of interleukin-13 production (GO:0032656)
blood circulation (GO:0008015)
negative regulation of transport (GO:0051051)
antigen processing and presentation of exogenous peptide antigen via MHC cl a
negative regulation of cell motility (GO:2000146)
cellular response to topologically incorrect protein (GO:0035967)
regulation of chemotaxis (GO:0050920)
neuron apoptotic process (GO:0051402)
positive regulation of myeloid leukocyte mediated immunity (GO:0002888)
positive regulation of neuroinflammatory response (GO:0150078)
regulation of MHC class II biosynthetic process (GO:0045346)
regulation of natural killer cell activation (GO:0032814)
transmembrane receptor protein serine/threonine kinase signaling pathway (G)
negative regulation of cellular biosynthetic process (GO:0031327)
response to UV (GO:0009411)
regulation of phosphorylation (GO:0042325)
regulation of protein tyrosine kinase activity (GO:0061097)
cytoplasmic pattern recognition receptor signaling pathway (GO:0002753)
negative regulation of cation channel activity (GO:2001258)
positive regulation of gene silencing by miRNA (GO:2000637)
positive regulation of nuclear division (GO:0051785)
regulation of toll-like receptor signaling pathway (GO:0034121)
negative regulation of transmembrane receptor protein serine/threonine kinase
positive regulation of Wnt signaling pathway (GO:0030177)
positive regulation of ATP metabolic process (GO:1903580)
regulation of cholesterol efflux (GO:0010874)
negative regulation of peptidyl-threonine phosphorylation (GO:0010801)
pharyngeal system development (GO:0060037)
positive regulation of positive chemotaxis (GO:0050927)
regulation of establishment of endothelial barrier (GO:1903140)
negative regulation of biomineral tissue development (GO:0070168)
osteoclast differentiation (GO:0030316)
positive regulation of amyloid precursor protein catabolic process (GO:1902993
positive regulation of granulocyte chemotaxis (GO:0071624)
regulation of lipid storage (GO:0010883)
regulation of macrophage chemotaxis (GO:0010758)
regulation of membrane protein ectodomain proteolysis (GO:0051043)
regulation of response to cytokine stimulus (GO:0060759)
positive regulation of transmembrane receptor protein serine/threonine kinase s

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

positive regulation of growth (GO:0045927)
regulation of protein binding (GO:0043393)
regulation of protein kinase activity (GO:0045859)
negative regulation of cold-induced thermogenesis (GO:0120163)
nucleotide-binding oligomerization domain containing signaling pathway (GO:0
positive regulation of phosphatidylinositol 3-kinase activity (GO:0043552)
regulation of calcium-mediated signaling (GO:0050848)
regulation of extrinsic apoptotic signaling pathway in absence of ligand (GO:20
response to interferon-beta (GO:0035456)
B cell receptor signaling pathway (GO:0050853)
ventricular cardiac muscle tissue morphogenesis (GO:0055010)
cellular response to UV (GO:0034644)
cellular response to interleukin-17 (GO:0097398)
interleukin-17-mediated signaling pathway (GO:0097400)
negative regulation of leukocyte proliferation (GO:0070664)
negative regulation of necroptotic process (GO:0060546)
peptidyl-cysteine modification (GO:0018198)
positive regulation of memory T cell differentiation (GO:0043382)
regulation of complement-dependent cytotoxicity (GO:1903659)
regulation of interleukin-23 production (GO:0032667)
regulation of leukocyte mediated cytotoxicity (GO:0001910)
regulation of smooth muscle cell apoptotic process (GO:0034391)
regulation of T-helper 1 type immune response (GO:0002825)
response to leptin (GO:0044321)
positive regulation of cellular protein metabolic process (GO:0032270)
regulation of cell death (GO:0010941)
cellular response to interleukin-15 (GO:0071350)
interleukin-15-mediated signaling pathway (GO:0035723)
negative regulation of alcohol biosynthetic process (GO:1902931)
negative regulation of macrophage derived foam cell differentiation (GO:00107
negative regulation of myotube differentiation (GO:0010832)
positive regulation of calcium-mediated signaling (GO:0050850)
positive regulation of purine nucleotide biosynthetic process (GO:1900373)
positive regulation of vascular endothelial cell proliferation (GO:1905564)
response to iron ion (GO:0010039)
regulation of cell development (GO:0060284)
response to growth factor (GO:0070848)
antigen processing and presentation of exogenous peptide antigen via MHC cl a
antigen processing and presentation of exogenous peptide antigen (GO:00024
negative regulation of MAP kinase activity (GO:0043407)
negative regulation of extrinsic apoptotic signaling pathway in absence of ligan d
negative regulation of signal transduction in absence of ligand (GO:1901099)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

positive regulation of histone acetylation (GO:0035066)
positive regulation of JUN kinase activity (GO:0043507)
positive regulation of natural killer cell mediated immunity (GO:0002717)
regulation of cysteine-type endopeptidase activity (GO:2000116)
cellular response to lipoteichoic acid (GO:0071223)
negative regulation of CD8-positive, alpha-beta T cell activation (GO:2001186)
positive regulation of antigen processing and presentation (GO:0002579)
positive regulation of dendritic cell antigen processing and presentation (GO:00
positive regulation of fever generation (GO:0031622)
positive regulation of natural killer cell mediated cytotoxicity directed against tu
positive regulation of natural killer cell mediated immune response to tumor cell
positive regulation of receptor binding (GO:1900122)
regulation of T cell activation via T cell receptor contact with antigen bound to M
response to lipoteichoic acid (GO:0070391)
negative regulation of neurogenesis (GO:0050768)
regulation of JUN kinase activity (GO:0043506)
regulation of lipid biosynthetic process (GO:0046890)
regulation of T cell receptor signaling pathway (GO:0050856)
response to exogenous dsRNA (GO:0043330)
leukocyte tethering or rolling (GO:0050901)
positive regulation of amyloid-beta formation (GO:1902004)
positive regulation of interleukin-4 production (GO:0032753)
regulation of oxidative stress-induced intrinsic apoptotic signaling pathway (GO
release of cytochrome c from mitochondria (GO:0001836)
response to interferon-alpha (GO:0035455)
negative regulation of endopeptidase activity (GO:0010951)
positive regulation of Ras protein signal transduction (GO:0046579)
hydrogen peroxide metabolic process (GO:0042743)
negative regulation of wound healing (GO:0061045)
response to metal ion (GO:0010038)
regulation of stress-activated MAPK cascade (GO:0032872)
negative regulation of cellular component organization (GO:0051129)
response to ionizing radiation (GO:0010212)
regulation of macromolecule metabolic process (GO:0060255)
aortic valve development (GO:0003176)
cellular response to heat (GO:0034605)
negative regulation of fat cell differentiation (GO:0045599)
positive regulation of bone mineralization (GO:0030501)
cellular response to catecholamine stimulus (GO:0071870)
positive regulation of carbohydrate metabolic process (GO:0045913)
regulation of cardiac muscle hypertrophy (GO:0010611)
regulation of reactive oxygen species metabolic process (GO:2000377)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

cellular response to DNA damage stimulus (GO:0006974)
cellular response to peptide hormone stimulus (GO:0071375)
long-chain fatty acid biosynthetic process (GO:0042759)
regulation of long-term synaptic potentiation (GO:1900271)
regulation of vasoconstriction (GO:0019229)
response to alcohol (GO:0097305)
TRIF-dependent toll-like receptor signaling pathway (GO:0035666)
regulation of complement activation (GO:0030449)
negative regulation of proteolysis (GO:0045861)
antigen processing and presentation of endogenous peptide antigen (GO:0002
detection of bacterium (GO:0016045)
negative regulation of T cell differentiation (GO:0045581)
positive regulation of leukocyte degranulation (GO:0043302)
positive regulation of regulatory T cell differentiation (GO:0045591)
positive regulation of T cell chemotaxis (GO:0010820)
positive regulation of T cell receptor signaling pathway (GO:0050862)
vascular endothelial growth factor signaling pathway (GO:0038084)
leukocyte adhesion to vascular endothelial cell (GO:0061756)
negative regulation of nervous system development (GO:0051961)
negative regulation of oxidative stress-induced intrinsic apoptotic signaling path
negative regulation of striated muscle cell differentiation (GO:0051154)
positive regulation of neutrophil chemotaxis (GO:0090023)
pyroptosis (GO:0070269)
regulation of insulin-like growth factor receptor signaling pathway (GO:0043567
receptor metabolic process (GO:0043112)
regulation of pathway-restricted SMAD protein phosphorylation (GO:0060393)
cellular response to dopamine (GO:1903351)
I-kappaB phosphorylation (GO:0007252)
negative regulation of extracellular matrix organization (GO:1903054)
negative regulation of hormone secretion (GO:0046888)
positive regulation of T cell apoptotic process (GO:0070234)
positive regulation of tissue remodeling (GO:0034105)
regulation of memory T cell differentiation (GO:0043380)
response to dopamine (GO:1903350)
ERBB signaling pathway (GO:0038127)
positive regulation of fat cell differentiation (GO:0045600)
regulation of epithelial cell migration (GO:0010632)
negative regulation of response to endoplasmic reticulum stress (GO:1903573)
negative regulation of signaling (GO:0023057)
regulation of neutrophil chemotaxis (GO:0090022)
MyD88-independent toll-like receptor signaling pathway (GO:0002756)
negative regulation of response to DNA damage stimulus (GO:2001021)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

triglyceride homeostasis (GO:0070328)
antigen processing and presentation of peptide antigen via MHC class II (GO:0
negative regulation of autophagy (GO:0010507)
regulation of transcription from RNA polymerase II promoter in response to hyp
vascular endothelial growth factor receptor signaling pathway (GO:0048010)
regulation of intrinsic apoptotic signaling pathway (GO:2001242)
regulation of release of sequestered calcium ion into cytosol (GO:0051279)
regulation of apoptotic signaling pathway (GO:2001233)
positive regulation of RNA metabolic process (GO:0051254)
response to endoplasmic reticulum stress (GO:0034976)
negative regulation of lipid storage (GO:0010888)
positive regulation of nitrogen compound metabolic process (GO:0051173)
regulation of programmed necrotic cell death (GO:0062098)
Notch signaling pathway (GO:0007219)
cellular response to ATP (GO:0071318)
cellular response to exogenous dsRNA (GO:0071360)
nitric oxide biosynthetic process (GO:0006809)
positive regulation of acute inflammatory response (GO:0002675)
positive regulation of heterotypic cell-cell adhesion (GO:0034116)
regulation of extracellular matrix disassembly (GO:0010715)
steroid hormone mediated signaling pathway (GO:0043401)
superoxide anion generation (GO:0042554)
T cell proliferation (GO:0042098)
activation of phospholipase C activity (GO:0007202)
positive regulation of glucose transmembrane transport (GO:0010828)
regulation of cell migration involved in sprouting angiogenesis (GO:0090049)
cellular component assembly (GO:0022607)
negative regulation of interleukin-1 beta production (GO:0032691)
positive regulation of protein insertion into mitochondrial membrane involved in
regulation of protein insertion into mitochondrial membrane involved in apoptoti
regulation of cellular component organization (GO:0051128)
positive regulation of macroautophagy (GO:0016239)
regulation of immune effector process (GO:0002697)
positive regulation of canonical Wnt signaling pathway (GO:0090263)
antigen processing and presentation of endogenous peptide antigen via MHC c
antigen processing and presentation of endogenous peptide antigen via MHC c
cellular response to interleukin-18 (GO:0071351)
death-inducing signaling complex assembly (GO:0071550)
glial cell migration (GO:0008347)
interleukin-18-mediated signaling pathway (GO:0035655)
negative regulation of type 2 immune response (GO:0002829)
positive regulation of interleukin-23 production (GO:0032747)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

positive regulation of mast cell activation (GO:0033005)
positive regulation of NK T cell activation (GO:0051135)
regulation of microglial cell migration (GO:1904139)
regulation of prostaglandin biosynthetic process (GO:0031392)
regulation of T-helper 1 cell differentiation (GO:0045625)
sphingosine-1-phosphate receptor signaling pathway (GO:0003376)
regulation of cellular component biogenesis (GO:0044087)
regulation of receptor-mediated endocytosis (GO:0048259)
regulation of viral entry into host cell (GO:0046596)
positive regulation of nucleocytoplasmic transport (GO:0046824)
positive regulation of protein modification by small protein conjugation or remov
negative regulation of response to stimulus (GO:0048585)
protein homooligomerization (GO:0051260)
protein-containing complex subunit organization (GO:0043933)
cellular response to metal ion (GO:0071248)
angiogenesis involved in wound healing (GO:0060055)
axonal transport of mitochondrion (GO:0019896)
cellular response to UV-A (GO:0071492)
induction of positive chemotaxis (GO:0050930)
negative regulation of activated T cell proliferation (GO:0046007)
negative regulation of programmed necrotic cell death (GO:0062099)
negative regulation of T-helper cell differentiation (GO:0045623)
regulation of T cell apoptotic process (GO:0070232)
regulation of T-helper 2 cell cytokine production (GO:2000551)
regulation of humoral immune response (GO:0002920)
antigen processing and presentation of peptide antigen via MHC class I (GO:0)
positive regulation of cholesterol transport (GO:0032376)
kidney development (GO:0001822)
calcium-mediated signaling using intracellular calcium source (GO:0035584)
extrinsic apoptotic signaling pathway in absence of ligand (GO:0097192)
negative regulation of cell communication (GO:0010648)
neurotrophin signaling pathway (GO:0038179)
positive regulation of vascular associated smooth muscle cell proliferation (GO:
positive regulation of pathway-restricted SMAD protein phosphorylation (GO:00
positive regulation of intrinsic apoptotic signaling pathway (GO:2001244)
acute inflammatory response (GO:0002526)
cellular response to cadmium ion (GO:0071276)
positive regulation of erythrocyte differentiation (GO:0045648)
release of sequestered calcium ion into cytosol (GO:0051209)
response to glucocorticoid (GO:0051384)
necroptotic process (GO:0070266)
negative regulation of epithelial cell differentiation (GO:0030857)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

negative regulation of macrophage activation (GO:0043031)
negative regulation of release of cytochrome c from mitochondria (GO:0090201
neutrophil activation (GO:0042119)
nitric oxide metabolic process (GO:0046209)
positive regulation of small molecule metabolic process (GO:0062013)
regulation of blood vessel endothelial cell proliferation involved in sprouting ang
regulation of hormone secretion (GO:0046883)
T cell mediated immunity (GO:0002456)
axon guidance (GO:0007411)
cellular response to BMP stimulus (GO:0071773)
cholesterol homeostasis (GO:0042632)
gland development (GO:0048732)
regulation of G1/S transition of mitotic cell cycle (GO:2000045)
regulation of hematopoietic stem cell differentiation (GO:1902036)
cellular response to lectin (GO:1990858)
stimulatory C-type lectin receptor signaling pathway (GO:0002223)
negative regulation of mitotic cell cycle (GO:0045930)
positive regulation of mitochondrial outer membrane permeabilization involved i
positive regulation of biomineral tissue development (GO:0070169)
peptidyl-tyrosine modification (GO:0018212)
sterol homeostasis (GO:0055092)
antimicrobial humoral immune response mediated by antimicrobial peptide (GO
antigen processing and presentation of exogenous peptide antigen via MHC cl a
response to ketone (GO:1901654)
exogenous drug catabolic process (GO:0042738)
membrane protein intracellular domain proteolysis (GO:0031293)
negative regulation of interleukin-2 production (GO:0032703)
positive regulation of neural precursor cell proliferation (GO:2000179)
positive regulation of neutrophil migration (GO:1902624)
regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling
circulatory system development (GO:0072359)
negative regulation of catabolic process (GO:0009895)
positive regulation of autophagy (GO:0010508)
defense response to Gram-negative bacterium (GO:0050829)
positive regulation of cell cycle G1/S phase transition (GO:1902808)
positive regulation of lipid biosynthetic process (GO:0046889)
regulation of phosphatidylinositol 3-kinase activity (GO:0043551)
renal system development (GO:0072001)
negative regulation of hemostasis (GO:1900047)
positive regulation of leukocyte proliferation (GO:0070665)
negative regulation of amyloid-beta formation (GO:1902430)
positive regulation of macrophage activation (GO:0043032)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

regulation of neuroblast proliferation (GO:1902692)
response to purine-containing compound (GO:0014074)
cell-cell junction organization (GO:0045216)
regulation of actin cytoskeleton organization (GO:0032956)
regulation of stem cell differentiation (GO:2000736)
cellular response to interferon-alpha (GO:0035457)
immunological synapse formation (GO:0001771)
negative regulation of monooxygenase activity (GO:0032769)
positive regulation of cysteine-type endopeptidase activity involved in apoptotic
positive regulation of fibroblast migration (GO:0010763)
positive regulation of glial cell migration (GO:1903977)
positive regulation of leukocyte differentiation (GO:1902107)
regulation of apoptotic cell clearance (GO:2000425)
regulation of Cdc42 protein signal transduction (GO:0032489)
regulation of dendritic cell chemotaxis (GO:2000508)
regulation of epithelial to mesenchymal transition involved in endocardial cushi
regulation of extracellular matrix constituent secretion (GO:0003330)
regulation of lymphocyte apoptotic process (GO:0070228)
regulation of T-helper 2 cell differentiation (GO:0045628)
regulation of toll-like receptor 3 signaling pathway (GO:0034139)
tyrosine phosphorylation of STAT protein (GO:0007260)
regulation of response to biotic stimulus (GO:0002831)
response to cadmium ion (GO:0046686)
innate immune response activating cell surface receptor signaling pathway (GO
DNA-templated transcription, initiation (GO:0006352)
chordate embryonic development (GO:0043009)
regulation of calcium ion transport (GO:0051924)
regulation of osteoblast differentiation (GO:0045667)
drug catabolic process (GO:0042737)
positive regulation of receptor internalization (GO:0002092)
substantia nigra development (GO:0021762)
axonal transport (GO:0098930)
regulation of cardiac muscle contraction (GO:0055117)
regulation of protein import into nucleus (GO:0042306)
protein stabilization (GO:0050821)
regulation of hematopoietic progenitor cell differentiation (GO:1901532)
inositol lipid-mediated signaling (GO:0048017)
positive regulation of lipid kinase activity (GO:0090218)
positive regulation of protein import (GO:1904591)
positive regulation of small GTPase mediated signal transduction (GO:0051057
branching morphogenesis of an epithelial tube (GO:0048754)
cellular response to dsRNA (GO:0071359)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

negative regulation of biosynthetic process (GO:0009890)
nitric oxide mediated signal transduction (GO:0007263)
positive regulation of cell adhesion mediated by integrin (GO:0033630)
positive regulation of glial cell differentiation (GO:0045687)
positive regulation of macrophage derived foam cell differentiation (GO:001074
positive regulation of nitric-oxide synthase activity (GO:0051000)
positive regulation of phosphoprotein phosphatase activity (GO:0032516)
programmed necrotic cell death (GO:0097300)
regulation of B cell differentiation (GO:0045577)
regulation of brown fat cell differentiation (GO:0090335)
positive regulation of myeloid cell differentiation (GO:0045639)
regulation of erythrocyte differentiation (GO:0045646)
regulation of glucose import (GO:0046324)
regulation of p38MAPK cascade (GO:1900744)
regulation of transport (GO:0051049)
epithelium development (GO:0060429)
cellular protein metabolic process (GO:0044267)
lymphocyte activation involved in immune response (GO:0002285)
negative regulation of ossification (GO:0030279)
nucleotide-binding domain, leucine rich repeat containing receptor signaling pat
positive regulation of viral life cycle (GO:1903902)
wound healing, spreading of cells (GO:0044319)
homeostasis of number of cells (GO:0048872)
icosanoid secretion (GO:0032309)
mature B cell differentiation involved in immune response (GO:0002313)
mitochondrion transport along microtubule (GO:0047497)
negative regulation of hydrogen peroxide-induced cell death (GO:1903206)
negative regulation of intrinsic apoptotic signaling pathway in response to DNA
positive regulation of adaptive immune response based on somatic recombinati
positive regulation of cell aging (GO:0090343)
regulation of interleukin-5 production (GO:0032674)
activation of protein kinase C activity (GO:1990051)
cellular response to nicotine (GO:0071316)
chronic inflammatory response (GO:0002544)
coronary artery morphogenesis (GO:0060982)
mature conventional dendritic cell differentiation (GO:0097029)
negative regulation of metallopeptidase activity (GO:1905049)
negative regulation of regulatory T cell differentiation (GO:0045590)
positive regulation of endothelial cell chemotaxis by VEGF-activated vascular e
positive regulation of natural killer cell chemotaxis (GO:2000503)
positive regulation of natural killer cell proliferation (GO:0032819)
positive regulation of prostaglandin biosynthetic process (GO:0031394)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

positive regulation of prostaglandin secretion (GO:0032308)
regulation of endothelial tube morphogenesis (GO:1901509)
regulation of fever generation (GO:0031620)
regulation of hippocampal neuron apoptotic process (GO:0110089)
regulation of mononuclear cell proliferation (GO:0032944)
negative regulation of developmental process (GO:0051093)
negative regulation of phosphorylation (GO:0042326)
regulation of Ras protein signal transduction (GO:0046578)
regulation of insulin receptor signaling pathway (GO:0046626)
cellular nitrogen compound biosynthetic process (GO:0044271)
prostaglandin metabolic process (GO:0006693)
regulation of developmental growth (GO:0048638)
iron ion homeostasis (GO:0055072)
heart development (GO:0007507)
calcium ion transport (GO:0006816)
positive regulation of cell-substrate adhesion (GO:0010811)
negative regulation of cell junction assembly (GO:1901889)
negative regulation of sequestering of calcium ion (GO:0051283)
regulation of myotube differentiation (GO:0010830)
branching involved in ureteric bud morphogenesis (GO:0001658)
cardiac atrium morphogenesis (GO:0003209)
negative regulation of amyloid precursor protein catabolic process (GO:190299
prostaglandin biosynthetic process (GO:0001516)
regulation of collagen biosynthetic process (GO:0032965)
regulation of leukocyte chemotaxis (GO:0002688)
response to ATP (GO:0033198)
ureteric bud morphogenesis (GO:0060675)
anoikis (GO:0043276)
CD40 signaling pathway (GO:0023035)
cellular response to leptin stimulus (GO:0044320)
negative regulation of lipid localization (GO:1905953)
negative regulation of production of molecular mediator of immune response (G
pericardium development (GO:0060039)
positive regulation of B cell differentiation (GO:0045579)
positive regulation of cholesterol esterification (GO:0010873)
positive regulation of macrophage cytokine production (GO:0060907)
positive regulation of protein kinase C signaling (GO:0090037)
regulation of CD8-positive, alpha-beta T cell activation (GO:2001185)
regulation of gap junction assembly (GO:1903596)
regulation of mammary gland epithelial cell proliferation (GO:0033599)
regulation of transmembrane transporter activity (GO:0022898)
regulation of tumor necrosis factor superfamily cytokine production (GO:19035

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

synapse pruning (GO:0098883)
stress-activated MAPK cascade (GO:0051403)
calcium ion homeostasis (GO:0055074)
axonogenesis (GO:0007409)
membrane protein proteolysis (GO:0033619)
negative regulation of cellular metabolic process (GO:0031324)
hematopoietic progenitor cell differentiation (GO:0002244)
regulation of cellular biosynthetic process (GO:0031326)
transcription by RNA polymerase II (GO:0006366)
antiviral innate immune response (GO:0140374)
branching involved in blood vessel morphogenesis (GO:0001569)
cell junction maintenance (GO:0034331)
cellular response to low-density lipoprotein particle stimulus (GO:0071404)
low-density lipoprotein particle remodeling (GO:0034374)
negative regulation of coagulation (GO:0050819)
positive regulation of glycoprotein biosynthetic process (GO:0010560)
positive regulation of macrophage chemotaxis (GO:0010759)
positive regulation of SMAD protein signal transduction (GO:0060391)
regulation of intrinsic apoptotic signaling pathway in response to DNA damage
steroid catabolic process (GO:0006706)
T cell differentiation in thymus (GO:0033077)
post-translational protein modification (GO:0043687)
cell junction organization (GO:0034330)
positive regulation of protein secretion (GO:0050714)
positive regulation of G1/S transition of mitotic cell cycle (GO:1900087)
positive regulation of glucose import (GO:0046326)
negative regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043124)
positive regulation of catalytic activity (GO:0043085)
positive regulation of cation channel activity (GO:2001259)
response to organonitrogen compound (GO:0010243)
cellular response to interferon-beta (GO:0035458)
positive regulation of heart contraction (GO:0045823)
regulation of lymphocyte differentiation (GO:0045619)
regulation of smooth muscle cell migration (GO:0014910)
apoptotic mitochondrial changes (GO:0008637)
regulation of sprouting angiogenesis (GO:1903670)
regulation of nucleic acid-templated transcription (GO:1903506)
protein autophosphorylation (GO:0046777)
blood vessel morphogenesis (GO:0048514)
positive regulation of establishment of protein localization to mitochondrion (GO
positive regulation of synaptic transmission (GO:0050806)
regulation of Rho protein signal transduction (GO:0035023)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

positive regulation of supramolecular fiber organization (GO:1902905)
regulation of cellular macromolecule biosynthetic process (GO:2000112)
cell-cell adhesion via plasma-membrane adhesion molecules (GO:0098742)
regulation of primary metabolic process (GO:0080090)
epithelial cell differentiation (GO:0030855)
epithelial cell migration (GO:0010631)
regulation of mitochondrial membrane potential (GO:0051881)
negative regulation of protein binding (GO:0032091)
arachidonic acid metabolic process (GO:0019369)
positive regulation of cell junction assembly (GO:1901890)
peptide hormone secretion (GO:0030072)
positive regulation of calcium ion transmembrane transport (GO:1904427)
regulation of vasculature development (GO:1901342)
positive regulation of plasma membrane bounded cell projection assembly (GO
negative regulation of mitochondrion organization (GO:0010823)
response to steroid hormone (GO:0048545)
lipoxygenase pathway (GO:0019372)
negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic
neurotrophin TRK receptor signaling pathway (GO:0048011)
positive regulation of endothelial cell chemotaxis (GO:2001028)
prostanoid biosynthetic process (GO:0046457)
regulation of amyloid fibril formation (GO:1905906)
regulation of endothelial cell chemotaxis (GO:2001026)
arginine metabolic process (GO:0006525)
granulocyte activation (GO:0036230)
leptin-mediated signaling pathway (GO:0033210)
negative regulation of cell-cell adhesion mediated by cadherin (GO:2000048)
negative regulation of inclusion body assembly (GO:0090084)
negative regulation of receptor binding (GO:1900121)
negative regulation of transforming growth factor beta production (GO:0071635
negative regulation of voltage-gated calcium channel activity (GO:1901386)
neuron projection maintenance (GO:1990535)
positive regulation by symbiont of entry into host (GO:0075294)
positive regulation of coagulation (GO:0050820)
positive regulation of hemostasis (GO:1900048)
positive regulation of toll-like receptor 4 signaling pathway (GO:0034145)
positive regulation of viral entry into host cell (GO:0046598)
regulation of cell-cell adhesion mediated by integrin (GO:0033632)
regulation of hydrogen peroxide-induced cell death (GO:1903205)
regulation of macrophage migration (GO:1905521)
regulation of podosome assembly (GO:0071801)
regulation of receptor binding (GO:1900120)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

regulation of T-helper 17 cell differentiation (GO:2000319)
regulation of tau-protein kinase activity (GO:1902947)
cell-cell junction assembly (GO:0007043)
positive regulation of cell cycle (GO:0045787)
endocardial cushion development (GO:0003197)
intrinsic apoptotic signaling pathway in response to DNA damage by p53 class
negative regulation of response to wounding (GO:1903035)
positive regulation of glycolytic process (GO:0045821)
positive regulation of phosphatase activity (GO:0010922)
positive regulation of purine nucleotide metabolic process (GO:1900544)
positive regulation of transcription regulatory region DNA binding (GO:2000679
chemical synaptic transmission (GO:0007268)
response to insulin (GO:0032868)
Ras protein signal transduction (GO:0007265)
axo-dendritic transport (GO:0008088)
B cell chemotaxis (GO:0035754)
foam cell differentiation (GO:0090077)
leukocyte chemotaxis involved in inflammatory response (GO:0002232)
macrophage derived foam cell differentiation (GO:0010742)
monoterpenoid metabolic process (GO:0016098)
negative regulation of blood vessel endothelial cell proliferation involved in spro
neutrophil extravasation (GO:0072672)
peptide antigen assembly with MHC protein complex (GO:0002501)
positive regulation of I-kappaB phosphorylation (GO:1903721)
positive regulation of microglial cell migration (GO:1904141)
positive regulation of T-helper 2 cell differentiation (GO:0045630)
positive regulation of toll-like receptor 3 signaling pathway (GO:0034141)
regulation of hepatocyte proliferation (GO:2000345)
regulation of immature T cell proliferation in thymus (GO:0033084)
regulation of immunoglobulin mediated immune response (GO:0002889)
regulation of nitric oxide mediated signal transduction (GO:0010749)
regulation of NK T cell activation (GO:0051133)
regulation of T-helper 17 cell lineage commitment (GO:2000328)
regulation of type 2 immune response (GO:0002828)
regulation of vitamin D biosynthetic process (GO:0060556)
cellular iron ion homeostasis (GO:0006879)
negative regulation of ERK1 and ERK2 cascade (GO:0070373)
regulation of cellular component movement (GO:0051270)
negative regulation of calcium ion transmembrane transporter activity (GO:190 1
positive regulation of protein import into nucleus (GO:0042307)
regulation of reactive oxygen species biosynthetic process (GO:1903426)
ventricular septum morphogenesis (GO:0060412)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

regulation of BMP signaling pathway (GO:0030510)
cellular response to transforming growth factor beta stimulus (GO:0071560)
negative regulation of type I interferon production (GO:0032480)
regulation of cell-cell adhesion (GO:0022407)
regulation of cell-substrate adhesion (GO:0010810)
signal release from synapse (GO:0099643)
positive regulation of protein localization to nucleus (GO:1900182)
regulation of platelet activation (GO:0010543)
glutamine family amino acid catabolic process (GO:0009065)
negative regulation of anoikis (GO:2000811)
negative regulation of immune effector process (GO:0002698)
regulation of ATP biosynthetic process (GO:2001169)
regulation of ceramide biosynthetic process (GO:2000303)
regulation of systemic arterial blood pressure (GO:0003073)
positive regulation of mitotic nuclear division (GO:0045840)
regulation of receptor internalization (GO:0002090)
protein processing (GO:0016485)
intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stre s
negative regulation of myeloid leukocyte differentiation (GO:0002762)
transition metal ion homeostasis (GO:0055076)
myeloid cell differentiation (GO:0030099)
signal transduction in response to DNA damage (GO:0042770)
neurotransmitter secretion (GO:0007269)
positive regulation of osteoblast differentiation (GO:0045669)
B cell mediated immunity (GO:0019724)
hepatocyte growth factor receptor signaling pathway (GO:0048012)
insulin-like growth factor receptor signaling pathway (GO:0048009)
monocyte differentiation (GO:0030224)
negative regulation of lymphocyte migration (GO:2000402)
negative regulation of natural killer cell mediated immunity (GO:0002716)
negative regulation of receptor signaling pathway via STAT (GO:1904893)
negative regulation of steroid biosynthetic process (GO:0010894)
Notch signaling involved in heart development (GO:0061314)
positive regulation of cellular respiration (GO:1901857)
positive regulation of ceramide biosynthetic process (GO:2000304)
positive regulation of macrophage differentiation (GO:0045651)
positive regulation of neuroblast proliferation (GO:0002052)
positive regulation of sphingolipid biosynthetic process (GO:0090154)
positive regulation of transcription from RNA polymerase II promoter in respons
regulation of cysteine-type endopeptidase activity involved in apoptotic signalin
regulation of toll-like receptor 9 signaling pathway (GO:0034163)
response to prostaglandin E (GO:0034695)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

response to sterol (GO:0036314)
T cell homeostasis (GO:0043029)
central nervous system development (GO:0007417)
positive regulation of DNA biosynthetic process (GO:2000573)
regulation of ion transport (GO:0043269)
defense response to Gram-positive bacterium (GO:0050830)
sterol metabolic process (GO:0016125)
phagocytosis, engulfment (GO:0006911)
cardiac muscle tissue development (GO:0048738)
negative regulation of G protein-coupled receptor signaling pathway (GO:0045
regulation of SMAD protein signal transduction (GO:0060390)
regulation of toll-like receptor 4 signaling pathway (GO:0034143)
response to nutrient levels (GO:0031667)
regulation of cellular response to stress (GO:0080135)
transforming growth factor beta receptor signaling pathway (GO:0007179)
positive regulation of endopeptidase activity (GO:0010950)
regulation of striated muscle contraction (GO:0006942)
regulation of type I interferon-mediated signaling pathway (GO:0060338)
negative regulation of intrinsic apoptotic signaling pathway by p53 class mediat
negative regulation of vascular associated smooth muscle cell proliferation (GO
positive regulation of blood coagulation (GO:0030194)
positive regulation of collagen metabolic process (GO:0010714)
positive regulation of cyclin-dependent protein serine/threonine kinase activity (
positive regulation of muscle hypertrophy (GO:0014742)
pulmonary valve morphogenesis (GO:0003184)
regulation of cell killing (GO:0031341)
negative regulation of cellular response to growth factor stimulus (GO:0090288
regulation of protein localization to plasma membrane (GO:1903076)
positive regulation of cellular protein localization (GO:1903829)
protein tetramerization (GO:0051262)
negative regulation of innate immune response (GO:0045824)
positive regulation of cell development (GO:0010720)
positive regulation of signaling (GO:0023056)
regulation of axon extension (GO:0030516)
response to estradiol (GO:0032355)
ventricular septum development (GO:0003281)
regulation of cellular protein localization (GO:1903827)
gland morphogenesis (GO:0022612)
hyperosmotic response (GO:0006972)
negative regulation of acute inflammatory response (GO:0002674)
negative regulation of membrane protein ectodomain proteolysis (GO:0051045)
negative regulation of T-helper 17 type immune response (GO:2000317)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

pericardium morphogenesis (GO:0003344)
pharyngeal arch artery morphogenesis (GO:0061626)
positive regulation of cardiac epithelial to mesenchymal transition (GO:0062043
positive regulation of gliogenesis (GO:0014015)
positive regulation of interleukin-5 production (GO:0032754)
positive regulation of lymphocyte apoptotic process (GO:0070230)
positive regulation of microtubule nucleation (GO:0090063)
positive regulation of oxidative stress-induced cell death (GO:1903209)
positive regulation of podosome assembly (GO:0071803)
positive regulation of T-helper 17 cell differentiation (GO:2000321)
positive regulation of unsaturated fatty acid biosynthetic process (GO:2001280)
regulation of extracellular matrix assembly (GO:1901201)
regulation of I-kappaB phosphorylation (GO:1903719)
regulation of metallopeptidase activity (GO:1905048)
regulation of morphogenesis of an epithelium (GO:1905330)
regulation of NAD(P)H oxidase activity (GO:0033860)
regulation of systemic arterial blood pressure by renin-angiotensin (GO:000308
regulation of T cell mediated immune response to tumor cell (GO:0002840)
regulation of T cell tolerance induction (GO:0002664)
regulation of transforming growth factor beta2 production (GO:0032909)
regulation of vascular associated smooth muscle cell apoptotic process (GO:19
T cell apoptotic process (GO:0070231)
terpenoid metabolic process (GO:0006721)
TRAIL-activated apoptotic signaling pathway (GO:0036462)
vascular wound healing (GO:0061042)
amyloid fibril formation (GO:1990000)
positive regulation of DNA metabolic process (GO:0051054)
positive regulation of neurogenesis (GO:0050769)
negative regulation of peptidyl-tyrosine phosphorylation (GO:0050732)
defense response to fungus (GO:0050832)
positive regulation of p38MAPK cascade (GO:1900745)
response to gamma radiation (GO:0010332)
positive regulation of cell cycle process (GO:0090068)
angiotensin maturation (GO:0002003)
glomerular visceral epithelial cell differentiation (GO:0072112)
macrophage chemotaxis (GO:0048246)
negative regulation of B cell proliferation (GO:0030889)
negative regulation of gene silencing by miRNA (GO:0060965)
negative regulation of production of miRNAs involved in gene silencing by miR N
organic hydroxy compound catabolic process (GO:1901616)
positive regulation of cellular senescence (GO:2000774)
regulation of angiotensin levels in blood (GO:0002002)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

regulation of astrocyte differentiation (GO:0048710)
regulation of B cell apoptotic process (GO:0002902)
regulation of cholesterol esterification (GO:0010872)
regulation of hemopoiesis (GO:1903706)
regulation of oxidative stress-induced cell death (GO:1903201)
positive regulation of protein ubiquitination (GO:0031398)
cellular divalent inorganic cation homeostasis (GO:0072503)
regulation of protein serine/threonine kinase activity (GO:0071900)
regulation of cellular ketone metabolic process (GO:0010565)
cellular response to fibroblast growth factor stimulus (GO:0044344)
negative regulation of mitotic cell cycle phase transition (GO:1901991)
endothelial cell proliferation (GO:0001935)
negative regulation of interleukin-8 production (GO:0032717)
negative regulation of leukocyte cell-cell adhesion (GO:1903038)
negative regulation of lipid catabolic process (GO:0050995)
positive regulation of cardiac muscle hypertrophy (GO:0010613)
positive regulation of cell migration involved in sprouting angiogenesis (GO:009
positive regulation of fatty acid metabolic process (GO:0045923)
positive regulation of peptidyl-serine phosphorylation of STAT protein (GO:003 3
regulation of cartilage development (GO:0061035)
response to axon injury (GO:0048678)
regulation of protein catabolic process (GO:0042176)
mitochondrion organization (GO:0007005)
ERBB2 signaling pathway (GO:0038128)
negative regulation of cell-matrix adhesion (GO:0001953)
G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide sec ɔ
regulation of heart contraction (GO:0008016)
negative regulation of canonical Wnt signaling pathway (GO:0090090)
myelination (GO:0042552)
acylglycerol homeostasis (GO:0055090)
fat-soluble vitamin metabolic process (GO:0006775)
peripheral nervous system development (GO:0007422)
negative regulation of cell-substrate adhesion (GO:0010812)
negative regulation of cellular protein metabolic process (GO:0032269)
regulation of mitotic nuclear division (GO:0007088)
integrin-mediated signaling pathway (GO:0007229)
cellular metal ion homeostasis (GO:0006875)
embryonic organ development (GO:0048568)
peptidyl-serine phosphorylation (GO:0018105)
positive regulation of protein catabolic process (GO:0045732)
regulation of mRNA stability (GO:0043488)
positive regulation of organelle organization (GO:0010638)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

regulation of histone acetylation (GO:0035065)
vasculogenesis (GO:0001570)
diol metabolic process (GO:0034311)
endocardial cushion morphogenesis (GO:0003203)
long-term memory (GO:0007616)
negative regulation of immune system process (GO:0002683)
regulation of cell-cell adhesion mediated by cadherin (GO:2000047)
regulation of epithelial cell differentiation (GO:0030856)
regulation of glucose transmembrane transport (GO:0010827)
regulation of peptidyl-serine phosphorylation of STAT protein (GO:0033139)
ureteric bud development (GO:0001657)
embryonic hemopoiesis (GO:0035162)
lipid oxidation (GO:0034440)
macrophage activation involved in immune response (GO:0002281)
negative regulation of macromolecule biosynthetic process (GO:0010558)
pathway-restricted SMAD protein phosphorylation (GO:0060389)
positive regulation of calcium ion import (GO:0090280)
positive regulation of cellular carbohydrate metabolic process (GO:0010676)
positive regulation of insulin receptor signaling pathway (GO:0046628)
positive regulation of steroid metabolic process (GO:0045940)
positive regulation of transporter activity (GO:0032411)
regulation of homotypic cell-cell adhesion (GO:0034110)
response to interleukin-6 (GO:0070741)
response to muramyl dipeptide (GO:0032495)
response to nitric oxide (GO:0071731)
toll-like receptor 9 signaling pathway (GO:0034162)
cellular response to hormone stimulus (GO:0032870)
cellular calcium ion homeostasis (GO:0006874)
fat cell differentiation (GO:0045444)
positive regulation of mitochondrion organization (GO:0010822)
negative regulation of protein transport (GO:0051224)
negative regulation of signaling receptor activity (GO:2000272)
regulation of biomineral tissue development (GO:0070167)
TOR signaling (GO:0031929)
negative regulation of cellular amide metabolic process (GO:0034249)
cellular response to starvation (GO:0009267)
cellular response to angiotensin (GO:1904385)
coronary vasculature morphogenesis (GO:0060977)
fusion of virus membrane with host plasma membrane (GO:0019064)
integrin activation (GO:0033622)
membrane fusion involved in viral entry into host cell (GO:0039663)
myeloid leukocyte mediated immunity (GO:0002444)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

negative regulation of amyloid-beta clearance (GO:1900222)
negative regulation of macrophage migration (GO:1905522)
negative regulation of microglial cell activation (GO:1903979)
negative regulation of response to reactive oxygen species (GO:1901032)
negative regulation of T cell mediated cytotoxicity (GO:0001915)
negative regulation of T-helper 17 cell differentiation (GO:2000320)
phosphatidylinositol-3-phosphate biosynthetic process (GO:0036092)
positive regulation of CD4-positive, alpha-beta T cell differentiation (GO:00433
positive regulation of homotypic cell-cell adhesion (GO:0034112)
positive regulation of insulin-like growth factor receptor signaling pathway (GO:
positive regulation of isomerase activity (GO:0010912)
positive regulation of monocyte chemotactic protein-1 production (GO:0071639
positive regulation of oligodendrocyte differentiation (GO:0048714)
positive regulation of ryanodine-sensitive calcium-release channel activity (GO:
regulation of alpha-beta T cell proliferation (GO:0046640)
regulation of CD8-positive, alpha-beta T cell proliferation (GO:2000564)
regulation of chemokine-mediated signaling pathway (GO:0070099)
regulation of dendritic spine maintenance (GO:1902950)
regulation of endodeoxyribonuclease activity (GO:0032071)
regulation of nitrogen compound metabolic process (GO:0051171)
regulation of pattern recognition receptor signaling pathway (GO:0062207)
regulation of positive chemotaxis (GO:0050926)
stress-induced premature senescence (GO:0090400)
sulfur amino acid biosynthetic process (GO:0000097)
negative regulation of Wnt signaling pathway (GO:0030178)
cellular transition metal ion homeostasis (GO:0046916)
phosphatidylcholine metabolic process (GO:0046470)
positive regulation of epidermal growth factor receptor signaling pathway (GO:0
regulation of transmembrane transport (GO:0034762)
calcium ion transmembrane import into cytosol (GO:0097553)
regulation of nervous system development (GO:0051960)
cardiac epithelial to mesenchymal transition (GO:0060317)
mesoderm development (GO:0007498)
myeloid cell development (GO:0061515)
negative regulation of viral life cycle (GO:1903901)
positive regulation of cyclin-dependent protein kinase activity (GO:1904031)
regulation of granulocyte chemotaxis (GO:0071622)
regulation of protein kinase A signaling (GO:0010738)
negative regulation of catalytic activity (GO:0043086)
metal ion transport (GO:0030001)
negative regulation of binding (GO:0051100)
positive regulation of protein transport (GO:0051222)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

regulation of cellular response to heat (GO:1900034)
immune response-regulating cell surface receptor signaling pathway (GO:0002
negative regulation of bone mineralization (GO:0030502)
negative regulation of DNA damage response, signal transduction by p53 class
negative regulation of pri-miRNA transcription by RNA polymerase II (GO:1902
negative regulation of secretion (GO:0051048)
negative regulation of smooth muscle cell migration (GO:0014912)
neurotransmitter biosynthetic process (GO:0042136)
positive regulation of cellular response to insulin stimulus (GO:1900078)
positive regulation of cyclase activity (GO:0031281)
positive regulation of glycogen biosynthetic process (GO:0045725)
regulation of cAMP-dependent protein kinase activity (GO:2000479)
regulation of protein kinase C signaling (GO:0090036)
response to chemokine (GO:1990868)
response to estrogen (GO:0043627)
regulation of plasma membrane bounded cell projection assembly (GO:012003
negative regulation of BMP signaling pathway (GO:0030514)
negative regulation of protein-containing complex assembly (GO:0031333)
protein homotetramerization (GO:0051289)
regulation of endocytosis (GO:0030100)
negative regulation of cell cycle (GO:0045786)
protein complex oligomerization (GO:0051259)
cell-matrix adhesion (GO:0007160)
regulation of transforming growth factor beta receptor signaling pathway (GO:0
positive regulation of cell communication (GO:0010647)
positive regulation of cytosolic calcium ion concentration involved in phospholip
regulation of DNA damage response, signal transduction by p53 class mediator
cardiac ventricle morphogenesis (GO:0003208)
intracellular steroid hormone receptor signaling pathway (GO:0030518)
positive regulation of cell division (GO:0051781)
androgen metabolic process (GO:0008209)
hydrogen peroxide catabolic process (GO:0042744)
regulation of anoikis (GO:2000209)
regulation of cardiac muscle cell proliferation (GO:0060043)
regulation of fibroblast migration (GO:0010762)
regulation of lipoprotein lipase activity (GO:0051004)
response to progesterone (GO:0032570)
intrinsic apoptotic signaling pathway by p53 class mediator (GO:0072332)
positive regulation of substrate adhesion-dependent cell spreading (GO:19000 2
regulation of androgen receptor signaling pathway (GO:0060765)
retina homeostasis (GO:0001895)
negative regulation of kinase activity (GO:0033673)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

ATF6-mediated unfolded protein response (GO:0036500)
endothelial cell chemotaxis (GO:0035767)
hepoxilin biosynthetic process (GO:0051122)
hepoxilin metabolic process (GO:0051121)
negative regulation of alpha-beta T cell activation (GO:0046636)
negative regulation of biomineralization (GO:0110150)
negative regulation of leukocyte degranulation (GO:0043301)
negative regulation of protein activation cascade (GO:2000258)
negative regulation of systemic arterial blood pressure (GO:0003085)
positive regulation of ATP biosynthetic process (GO:2001171)
positive regulation of protein kinase A signaling (GO:0010739)
positive regulation of protein polyubiquitination (GO:1902916)
positive regulation of tumor necrosis factor-mediated signaling pathway (GO:19
regulation of actin filament organization (GO:0110053)
regulation of DNA-templated transcription in response to stress (GO:0043620)
regulation of endothelial cell development (GO:1901550)
regulation of endothelial cell differentiation (GO:0045601)
regulation of glial cell proliferation (GO:0060251)
regulation of nephron tubule epithelial cell differentiation (GO:0072182)
response to vitamin (GO:0033273)
response to vitamin D (GO:0033280)
regulation of mRNA catabolic process (GO:0061013)
regulation of cytoskeleton organization (GO:0051493)
cellular response to radiation (GO:0071478)
positive regulation of nervous system development (GO:0051962)
zymogen activation (GO:0031638)
positive regulation of cytoskeleton organization (GO:0051495)
organonitrogen compound catabolic process (GO:1901565)
regulation of lipid metabolic process (GO:0019216)
retinoid metabolic process (GO:0001523)
mammary gland epithelium development (GO:0061180)
myoblast differentiation (GO:0045445)
negative regulation of leukocyte activation (GO:0002695)
negative regulation of protein processing (GO:0010955)
peptidyl-tyrosine autophosphorylation (GO:0038083)
positive regulation of glycogen metabolic process (GO:0070875)
positive regulation of histone H3-K4 methylation (GO:0051571)
positive regulation of lyase activity (GO:0051349)
positive regulation of membrane protein ectodomain proteolysis (GO:0051044)
positive regulation of protein export from nucleus (GO:0046827)
positive regulation of sprouting angiogenesis (GO:1903672)
regulation of lymphocyte activation (GO:0051249)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

regulation of macrophage differentiation (GO:0045649)
regulation of phospholipase C activity (GO:1900274)
regulation of anatomical structure morphogenesis (GO:0022603)
regulation of proteolysis (GO:0030162)
glial cell differentiation (GO:0010001)
negative regulation of transferase activity (GO:0051348)
positive regulation of dephosphorylation (GO:0035306)
regulation of DNA biosynthetic process (GO:2000278)
regulation of protein targeting to membrane (GO:0090313)
regulation of actin cytoskeleton reorganization (GO:2000249)
neurotransmitter transport (GO:0006836)
cellular response to nerve growth factor stimulus (GO:1990090)
negative regulation of B cell activation (GO:0050869)
negative regulation of lymphocyte activation (GO:0051250)
negative regulation of phosphate metabolic process (GO:0045936)
positive regulation of calcium ion transmembrane transporter activity (GO:1901
diterpenoid metabolic process (GO:0016101)
regulation of transcription initiation from RNA polymerase II promoter (GO:0060
regulation of synaptic transmission, glutamatergic (GO:0051966)
response to cAMP (GO:0051591)
morphogenesis of an epithelium (GO:0002009)
plasma membrane invagination (GO:0099024)
BMP signaling pathway involved in heart development (GO:0061312)
C-terminal protein lipidation (GO:0006501)
cardiac endothelial cell differentiation (GO:0003348)
cardiac muscle cell myoblast differentiation (GO:0060379)
cellular response to indole-3-methanol (GO:0071681)
cellular response to testosterone stimulus (GO:0071394)
dopamine biosynthetic process (GO:0042416)
endocardial cell differentiation (GO:0060956)
endodermal cell fate specification (GO:0001714)
establishment of T cell polarity (GO:0001768)
intracellular distribution of mitochondria (GO:0048312)
monocyte extravasation (GO:0035696)
negative regulation of gene silencing by RNA (GO:0060967)
negative regulation of hydrogen peroxide metabolic process (GO:0010727)
negative regulation of leukocyte adhesion to vascular endothelial cell (GO:1904
negative regulation of macrophage cytokine production (GO:0010936)
negative regulation of plasminogen activation (GO:0010757)
negative regulation of posttranscriptional gene silencing (GO:0060149)
negative regulation of smooth muscle contraction (GO:0045986)
negative regulation of T cell migration (GO:2000405)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

negative regulation of vitamin D biosynthetic process (GO:0010957)
neuroinflammatory response (GO:0150076)
p38MAPK cascade (GO:0038066)
positive regulation of amine transport (GO:0051954)
positive regulation of cAMP-dependent protein kinase activity (GO:2000481)
positive regulation of cell fate commitment (GO:0010455)
positive regulation of cell proliferation involved in heart morphogenesis (GO:20 0
positive regulation of glial cell proliferation (GO:0060252)
positive regulation of glycoprotein metabolic process (GO:1903020)
positive regulation of heat generation (GO:0031652)
positive regulation of histone H3-K9 acetylation (GO:2000617)
positive regulation of metallopeptidase activity (GO:1905050)
positive regulation of protein catabolic process in the vacuole (GO:1904352)
positive regulation of T-helper 1 cell cytokine production (GO:2000556)
positive regulation of toll-like receptor 9 signaling pathway (GO:0034165)
positive regulation of vascular associated smooth muscle cell apoptotic process
pulmonary artery morphogenesis (GO:0061156)
receptor-mediated virion attachment to host cell (GO:0046813)
regulation of core promoter binding (GO:1904796)
regulation of glial cell migration (GO:1903975)
regulation of glomerular mesangial cell proliferation (GO:0072124)
regulation of granulocyte colony-stimulating factor production (GO:0071655)
regulation of guanylate cyclase activity (GO:0031282)
regulation of inflammatory response to wounding (GO:0106014)
regulation of integrin biosynthetic process (GO:0045113)
regulation of microglial cell mediated cytotoxicity (GO:1904149)
regulation of neutrophil degranulation (GO:0043313)
regulation of NK T cell proliferation (GO:0051140)
regulation of nucleotide-binding oligomerization domain containing signaling pa
regulation of protein import (GO:1904589)
regulation of respiratory burst involved in inflammatory response (GO:0060264)
regulation of sterol transport (GO:0032371)
regulation of T-helper 1 cell cytokine production (GO:2000554)
response to indole-3-methanol (GO:0071680)
response to prostaglandin (GO:0034694)
salivary gland development (GO:0007431)
salivary gland morphogenesis (GO:0007435)
tight junction organization (GO:0120193)
vitamin D3 metabolic process (GO:0070640)
epidermal growth factor receptor signaling pathway (GO:0007173)
B cell activation involved in immune response (GO:0002312)
cellular response to corticosteroid stimulus (GO:0071384)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

epiboly involved in wound healing (GO:0090505)
mesenchyme development (GO:0060485)
motor neuron axon guidance (GO:0008045)
negative regulation of receptor signaling pathway via JAK-STAT (GO:0046426)
neuron projection organization (GO:0106027)
positive regulation of collagen biosynthetic process (GO:0032967)
positive regulation of isotype switching (GO:0045830)
regulation of cholesterol storage (GO:0010885)
regulation of mast cell degranulation (GO:0043304)
regulation of monocyte differentiation (GO:0045655)
regulation of phosphate metabolic process (GO:0019220)
regulation of systemic arterial blood pressure by hormone (GO:0001990)
response to organophosphorus (GO:0046683)
retrograde axonal transport (GO:0008090)
adherens junction assembly (GO:0034333)
arachidonate transport (GO:1903963)
arachidonic acid secretion (GO:0050482)
cellular response to interleukin-4 (GO:0071353)
cellular response to oxidised low-density lipoprotein particle stimulus (GO:0140
endodermal cell fate commitment (GO:0001711)
endothelial tube morphogenesis (GO:0061154)
endothelium development (GO:0003158)
granulocyte migration (GO:0097530)
immunoglobulin mediated immune response (GO:0016064)
lipoprotein transport (GO:0042953)
mesenchymal to epithelial transition (GO:0060231)
modulation by symbiont of host process (GO:0044003)
morphogenesis of an epithelial sheet (GO:0002011)
myelin maintenance (GO:0043217)
negative regulation of alpha-beta T cell proliferation (GO:0046642)
negative regulation of cell adhesion mediated by integrin (GO:0033629)
negative regulation of cholesterol storage (GO:0010887)
negative regulation of leukocyte migration (GO:0002686)
negative regulation of transcription by competitive promoter binding (GO:00109
negative regulation of transmembrane transport (GO:0034763)
negative regulation of vascular endothelial growth factor signaling pathway (GO
nerve growth factor signaling pathway (GO:0038180)
neuron remodeling (GO:0016322)
phosphatidylcholine catabolic process (GO:0034638)
positive regulation of vascular endothelial growth factor receptor signaling path
positive regulation of vasculogenesis (GO:2001214)
regulation of DNA methylation (GO:0044030)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

regulation of endoplasmic reticulum unfolded protein response (GO:1900101)
regulation of hair cycle (GO:0042634)
regulation of leukocyte tethering or rolling (GO:1903236)
regulation of mast cell activation (GO:0033003)
regulation of microtubule nucleation (GO:0010968)
regulation of RNA polymerase II transcription preinitiation complex assembly (
regulation of T-helper 17 type immune response (GO:2000316)
removal of superoxide radicals (GO:0019430)
response to laminar fluid shear stress (GO:0034616)
UV protection (GO:0009650)
neuron projection development (GO:0031175)
negative regulation of reactive oxygen species metabolic process (GO:200037
positive regulation of protein autophosphorylation (GO:0031954)
regulation of B cell receptor signaling pathway (GO:0050855)
regulation of protein export from nucleus (GO:0046825)
regulation of supramolecular fiber organization (GO:1902903)
cellular response to nutrient levels (GO:0031669)
cellular response to ketone (GO:1901655)
regulation of cell division (GO:0051302)
steroid hormone biosynthetic process (GO:0120178)
icosanoid metabolic process (GO:0006690)
cellular response to ionizing radiation (GO:0071479)
regulation of protein metabolic process (GO:0051246)
cellular response to insulin stimulus (GO:0032869)
cholesterol metabolic process (GO:0008203)
bone development (GO:0060348)
digestive tract development (GO:0048565)
negative regulation of protein kinase B signaling (GO:0051898)
cholesterol efflux (GO:0033344)
negative regulation of lipid metabolic process (GO:0045833)
positive regulation of protein targeting to membrane (GO:0090314)
aortic valve morphogenesis (GO:0003180)
endodermal cell differentiation (GO:0035987)
long-chain fatty acid transport (GO:0015909)
negative regulation of intracellular steroid hormone receptor signaling pathway
positive regulation of lamellipodium organization (GO:1902745)
regulation of NMDA receptor activity (GO:2000310)
mesenchyme morphogenesis (GO:0072132)
mesonephric tubule development (GO:0072164)
negative regulation of viral entry into host cell (GO:0046597)
positive regulation of cardiac muscle tissue growth (GO:0055023)
positive regulation of smooth muscle cell migration (GO:0014911)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

positive regulation of transcription of Notch receptor target (GO:0007221)
regulation of cellular respiration (GO:0043457)
regulation of cholesterol biosynthetic process (GO:0045540)
regulation of stem cell proliferation (GO:0072091)
organelle organization (GO:0006996)
JNK cascade (GO:0007254)
regulation of filopodium assembly (GO:0051489)
positive regulation of cell morphogenesis involved in differentiation (GO:001077
cell-cell junction maintenance (GO:0045217)
cellular response to superoxide (GO:0071451)
central nervous system myelination (GO:0022010)
fatty acid homeostasis (GO:0055089)
isotype switching (GO:0045190)
lipoprotein localization (GO:0044872)
mesonephros development (GO:0001823)
negative regulation of oxidative stress-induced neuron death (GO:1903204)
negative regulation of platelet-derived growth factor receptor signaling pathway
negative regulation of response to cytokine stimulus (GO:0060761)
positive regulation of bone resorption (GO:0045780)
positive regulation of cellular extravasation (GO:0002693)
positive regulation of epidermal growth factor-activated receptor activity (GO:00
positive regulation of lipid localization (GO:1905954)
regulation of biosynthetic process (GO:0009889)
regulation of coagulation (GO:0050818)
regulation of histone H3-K9 acetylation (GO:2000615)
regulation of inclusion body assembly (GO:0090083)
regulation of mitochondrial depolarization (GO:0051900)
regulation of phospholipase activity (GO:0010517)
response to corticosteroid (GO:0031960)
tetrahydrobiopterin metabolic process (GO:0046146)
vasoconstriction (GO:0042310)
positive regulation of proteasomal ubiquitin-dependent protein catabolic proces
protein-DNA complex assembly (GO:0065004)
neuron projection extension (GO:1990138)
positive regulation of histone modification (GO:0031058)
regulation of protein localization to cell surface (GO:2000008)
in utero embryonic development (GO:0001701)
negative regulation of ion transport (GO:0043271)
positive regulation of ERBB signaling pathway (GO:1901186)
positive regulation of release of cytochrome c from mitochondria (GO:0090200)
regulation of cardiac muscle cell action potential (GO:0098901)
regulation of cholesterol transport (GO:0032374)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

regulation of mitochondrial fission (GO:0090140)
response to dsRNA (GO:0043331)
regulation of mitotic cell cycle (GO:0007346)
negative regulation of protein kinase activity (GO:0006469)
cellular response to light stimulus (GO:0071482)
cholesterol transport (GO:0030301)
regulation of cellular amine metabolic process (GO:0033238)
heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules (
phosphatidylinositol phosphate biosynthetic process (GO:0046854)
amyloid precursor protein metabolic process (GO:0042982)
cell migration involved in sprouting angiogenesis (GO:0002042)
cellular response to glucocorticoid stimulus (GO:0071385)
negative regulation of signal transduction by p53 class mediator (GO:1901797)
negative regulation of tumor necrosis factor-mediated signaling pathway (GO:0
positive regulation of cartilage development (GO:0061036)
positive regulation of extracellular matrix organization (GO:1903055)
regulation of adaptive immune response (GO:0002819)
regulation of fatty acid metabolic process (GO:0019217)
regulation of platelet aggregation (GO:0090330)
regulation of protein sumoylation (GO:0033233)
regulation of macroautophagy (GO:0016241)
activation of Janus kinase activity (GO:0042976)
activation of transmembrane receptor protein tyrosine kinase activity (GO:0007
cell junction disassembly (GO:0150146)
cellular hyperosmotic response (GO:0071474)
cellular response to bacterial lipopeptide (GO:0071221)
cellular triglyceride homeostasis (GO:0035356)
detection of virus (GO:0009597)
establishment of lymphocyte polarity (GO:0001767)
glomerulus vasculature development (GO:0072012)
hydrogen peroxide biosynthetic process (GO:0050665)
lymphocyte apoptotic process (GO:0070227)
negative regulation of cellular extravasation (GO:0002692)
negative regulation of cellular response to hypoxia (GO:1900038)
negative regulation of glucocorticoid receptor signaling pathway (GO:2000323)
negative regulation of lipoprotein lipase activity (GO:0051005)
negative regulation of myeloid leukocyte mediated immunity (GO:0002887)
positive regulation of animal organ morphogenesis (GO:0110110)
positive regulation of deacetylase activity (GO:0090045)
positive regulation of extrinsic apoptotic signaling pathway via death domain re
positive regulation of gap junction assembly (GO:1903598)
positive regulation of immune response to tumor cell (GO:0002839)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

positive regulation of kidney development (GO:0090184)
positive regulation of killing of cells of other organism (GO:0051712)
positive regulation of tau-protein kinase activity (GO:1902949)
protection from natural killer cell mediated cytotoxicity (GO:0042270)
regulation of adipose tissue development (GO:1904177)
regulation of blood vessel remodeling (GO:0060312)
regulation of glomerular filtration (GO:0003093)
regulation of glutamate receptor signaling pathway (GO:1900449)
regulation of hyaluronan biosynthetic process (GO:1900125)
regulation of macromolecule biosynthetic process (GO:0010556)
regulation of macrophage apoptotic process (GO:2000109)
regulation of macrophage proliferation (GO:0120040)
regulation of nucleotide-binding oligomerization domain containing 2 signaling p
regulation of T-helper cell differentiation (GO:0045622)
regulation of thymocyte apoptotic process (GO:0070243)
response to peptidoglycan (GO:0032494)
response to testosterone (GO:0033574)
ventricular compact myocardium morphogenesis (GO:0003223)
regulation of DNA-templated transcription, initiation (GO:2000142)
negative regulation of protein modification process (GO:0031400)
fatty acid biosynthetic process (GO:0006633)
positive regulation of protein dephosphorylation (GO:0035307)
regulation of lamellipodium assembly (GO:0010591)
regulation of myoblast differentiation (GO:0045661)
peptidyl-serine modification (GO:0018209)
positive regulation of developmental growth (GO:0048639)
positive regulation of protein localization to cell periphery (GO:1904377)
positive regulation of protein localization to plasma membrane (GO:1903078)
sprouting angiogenesis (GO:0002040)
cellular response to drug (GO:0035690)
chaperone cofactor-dependent protein refolding (GO:0051085)
glial cell development (GO:0021782)
positive regulation of filopodium assembly (GO:0051491)
positive regulation of histone methylation (GO:0031062)
regulation of myelination (GO:0031641)
cellular response to glucose starvation (GO:0042149)
glutathione metabolic process (GO:0006749)
proteasomal protein catabolic process (GO:0010498)
glucose metabolic process (GO:0006006)
negative regulation of supramolecular fiber organization (GO:1902904)
catecholamine biosynthetic process (GO:0042423)
fat-soluble vitamin catabolic process (GO:0042363)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

gas transport (GO:0015669)
homocysteine metabolic process (GO:0050667)
mitochondrion distribution (GO:0048311)
modulation by host of viral process (GO:0044788)
negative regulation of amyloid fibril formation (GO:1905907)
negative regulation of cardiac muscle hypertrophy (GO:0010614)
negative regulation of cellular response to vascular endothelial growth factor sti
negative regulation of fatty acid biosynthetic process (GO:0045717)
negative regulation of leukocyte chemotaxis (GO:0002689)
negative regulation of oxidoreductase activity (GO:0051354)
negative regulation of release of sequestered calcium ion into cytosol (GO:005 1
negative regulation of ryanodine-sensitive calcium-release channel activity (GO
negative regulation of vascular permeability (GO:0043116)
phospholipid efflux (GO:0033700)
positive regulation of pseudopodium assembly (GO:0031274)
positive regulation of T-helper 17 type immune response (GO:2000318)
regulation of axon regeneration (GO:0048679)
regulation of CD4-positive, alpha-beta T cell differentiation (GO:0043370)
regulation of cell communication by electrical coupling involved in cardiac cond
regulation of feeding behavior (GO:0060259)
regulation of leukocyte cell-cell adhesion (GO:1903037)
regulation of plasminogen activation (GO:0010755)
regulation of pseudopodium assembly (GO:0031272)
regulation of ventricular cardiac muscle cell action potential (GO:0098911)
replicative senescence (GO:0090399)
toll-like receptor 3 signaling pathway (GO:0034138)
urogenital system development (GO:0001655)
epidermal cell differentiation (GO:0009913)
atrioventricular valve morphogenesis (GO:0003181)
dopamine metabolic process (GO:0042417)
mitochondrion localization (GO:0051646)
positive regulation of G protein-coupled receptor signaling pathway (GO:00457
regulation of bicellular tight junction assembly (GO:2000810)
regulation of histone H3-K4 methylation (GO:0051569)
regulation of oligodendrocyte differentiation (GO:0048713)
regulation of vascular endothelial growth factor signaling pathway (GO:190074 6
negative regulation of epithelial cell migration (GO:0010633)
regulation of blood circulation (GO:1903522)
regulation of trans-synaptic signaling (GO:0099177)
respiratory system development (GO:0060541)
peptide metabolic process (GO:0006518)
cation transmembrane transport (GO:0098655)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

regulation of actin filament-based process (GO:0032970)
anterograde trans-synaptic signaling (GO:0098916)
negative regulation of insulin receptor signaling pathway (GO:0046627)
regulation of cell junction assembly (GO:1901888)
regulation of epidermal growth factor-activated receptor activity (GO:0007176)
stress-activated protein kinase signaling cascade (GO:0031098)
regulation of cellular amino acid metabolic process (GO:0006521)
regulation of focal adhesion assembly (GO:0051893)
regulation of stress fiber assembly (GO:0051492)
embryonic limb morphogenesis (GO:0030326)
endoderm formation (GO:0001706)
negative regulation of toll-like receptor signaling pathway (GO:0034122)
chromosome organization (GO:0051276)
endoplasmic reticulum calcium ion homeostasis (GO:0032469)
negative regulation of osteoclast differentiation (GO:0045671)
positive regulation of epidermal cell differentiation (GO:0045606)
positive regulation of hormone secretion (GO:0046887)
positive regulation of peptidyl-lysine acetylation (GO:2000758)
negative regulation of protein modification by small protein conjugation or remo
pyruvate metabolic process (GO:0006090)
cellular response to epidermal growth factor stimulus (GO:0071364)
negative regulation of cellular response to insulin stimulus (GO:1900077)
positive regulation of microtubule polymerization (GO:0031116)
regulation of small molecule metabolic process (GO:0062012)
steroid biosynthetic process (GO:0006694)
cardiac right ventricle morphogenesis (GO:0003215)
cellular component maintenance (GO:0043954)
detection of calcium ion (GO:0005513)
entry into host (GO:0044409)
high-density lipoprotein particle assembly (GO:0034380)
negative regulation by host of viral transcription (GO:0043922)
negative regulation of CD4-positive, alpha-beta T cell activation (GO:2000515)
negative regulation of gluconeogenesis (GO:0045721)
negative regulation of reactive oxygen species biosynthetic process (GO:19034
positive regulation of CD4-positive, alpha-beta T cell activation (GO:2000516)
positive regulation of lipid transport (GO:0032370)
pteridine-containing compound metabolic process (GO:0042558)
regulation of antigen receptor-mediated signaling pathway (GO:0050854)
regulation of cell aging (GO:0090342)
regulation of cell communication by electrical coupling (GO:0010649)
regulation of oxidoreductase activity (GO:0051341)
regulation of protein acetylation (GO:1901983)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

regulation of tube diameter (GO:0035296)
relaxation of cardiac muscle (GO:0055119)
response to UV-B (GO:0010224)
vascular process in circulatory system (GO:0003018)
angiotensin-activated signaling pathway (GO:0038166)
axon ensheathment in central nervous system (GO:0032291)
chemical homeostasis within a tissue (GO:0048875)
chylomicron remnant clearance (GO:0034382)
complement activation, alternative pathway (GO:0006957)
gas homeostasis (GO:0033483)
glomerular epithelial cell development (GO:0072310)
glomerular visceral epithelial cell development (GO:0072015)
lymphoid progenitor cell differentiation (GO:0002320)
modulation by symbiont of host defense response (GO:0052031)
negative regulation of interferon-gamma-mediated signaling pathway (GO:0060
negative regulation of low-density lipoprotein receptor activity (GO:1905598)
negative regulation of MyD88-independent toll-like receptor signaling pathway (
negative regulation of protein sumoylation (GO:0033234)
negative regulation of response to interferon-gamma (GO:0060331)
negative regulation of striated muscle tissue development (GO:0045843)
negative regulation of T cell apoptotic process (GO:0070233)
nucleotide-binding oligomerization domain containing 2 signaling pathway (GO:
oxygen transport (GO:0015671)
positive regulation of amyloid-beta clearance (GO:1900223)
positive regulation of catecholamine secretion (GO:0033605)
positive regulation of epithelial tube formation (GO:1905278)
positive regulation of hormone metabolic process (GO:0032352)
positive regulation of humoral immune response (GO:0002922)
positive regulation of membrane depolarization (GO:1904181)
positive regulation of natural killer cell cytokine production (GO:0002729)
positive regulation of striated muscle contraction (GO:0045989)
positive regulation of vesicle fusion (GO:0031340)
regulation of bone remodeling (GO:0046850)
regulation of cortisol biosynthetic process (GO:2000064)
regulation of defense response to bacterium (GO:1900424)
regulation of dopamine metabolic process (GO:0042053)
regulation of endothelial cell chemotaxis to fibroblast growth factor (GO:200054
regulation of glucocorticoid receptor signaling pathway (GO:2000322)
regulation of histone deacetylase activity (GO:1901725)
regulation of lysosomal protein catabolic process (GO:1905165)
regulation of natural killer cell cytokine production (GO:0002727)
regulation of transforming growth factor beta1 production (GO:0032908)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

release of sequestered calcium ion into cytosol by endoplasmic reticulum (GO:
response to host defenses (GO:0052200)
smooth muscle cell migration (GO:0014909)
substrate-dependent cell migration, cell extension (GO:0006930)
surfactant homeostasis (GO:0043129)
synaptic transmission, dopaminergic (GO:0001963)
xenobiotic catabolic process (GO:0042178)
erythrocyte differentiation (GO:0030218)
regulation of telomerase activity (GO:0051972)
phosphate-containing compound metabolic process (GO:0006796)
anterograde axonal transport (GO:0008089)
supramolecular fiber organization (GO:0097435)
establishment of endothelial barrier (GO:0061028)
regulation of fatty acid biosynthetic process (GO:0042304)
regulation of gluconeogenesis (GO:0006111)
regulation of protein localization to nucleus (GO:1900180)
autonomic nervous system development (GO:0048483)
cellular response to steroid hormone stimulus (GO:0071383)
natural killer cell activation involved in immune response (GO:0002323)
sensory perception of pain (GO:0019233)
positive regulation of catabolic process (GO:0009896)
positive regulation of proteolysis (GO:0045862)
regulation of signal transduction by p53 class mediator (GO:1901796)
atrioventricular valve development (GO:0003171)
covalent chromatin modification (GO:0016569)
heart process (GO:0003015)
negative regulation of cell activation (GO:0050866)
negative regulation of cell migration involved in sprouting angiogenesis (GO:00
positive regulation of brown fat cell differentiation (GO:0090336)
positive regulation of glucose metabolic process (GO:0010907)
positive regulation of insulin secretion involved in cellular response to glucose s
positive regulation of protein-containing complex disassembly (GO:0043243)
positive regulation of transmembrane transport (GO:0034764)
regulation of integrin-mediated signaling pathway (GO:2001044)
regulation of response to endoplasmic reticulum stress (GO:1905897)
regulation of sensory perception of pain (GO:0051930)
regulation of trophoblast cell migration (GO:1901163)
regulation of vasculogenesis (GO:2001212)
response to X-ray (GO:0010165)
substrate-dependent cell migration (GO:0006929)
thymus development (GO:0048538)
positive regulation of DNA repair (GO:0045739)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

regulation of Wnt signaling pathway (GO:0030111)
canonical Wnt signaling pathway (GO:0060070)
negative regulation of transforming growth factor beta receptor signaling pathw
regulation of translational initiation (GO:0006446)
autophagosome assembly (GO:0000045)
positive regulation of mitotic cell cycle phase transition (GO:1901992)
negative regulation of Notch signaling pathway (GO:0045746)
phosphatidylcholine acyl-chain remodeling (GO:0036151)
regulation of catecholamine secretion (GO:0050433)
regulation of protein localization to membrane (GO:1905475)
axon development (GO:0061564)
regulation of neuron differentiation (GO:0045664)

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

Overlap	P-value	Adjusted P-value	Old P-value
266/621	1.1628E-158	5.7186E-155	0
192/482	8.3283E-106	2.0479E-102	0
161/335	7.9258E-104	1.2993E-100	0
163/546	9.68975E-68	1.19135E-64	0
99/206	1.37453E-63	1.35198E-60	0
102/230	3.33059E-61	2.72997E-58	0
170/742	2.37218E-52	1.66663E-49	0
171/764	3.84683E-51	2.36484E-48	0
112/345	1.74617E-50	9.54182E-48	0
132/485	1.56976E-49	7.72006E-47	0
68/124	7.06607E-49	3.15918E-46	0
130/482	2.72831E-48	1.11815E-45	0
149/625	4.74691E-48	1.79579E-45	0
211/1183	2.88231E-46	1.01251E-43	0
113/384	4.24654E-46	1.3923E-43	0
110/371	3.10514E-45	9.54443E-43	0
61/110	2.42247E-44	7.00805E-42	0
92/274	6.23219E-43	1.70277E-40	0
174/908	3.54481E-42	9.17546E-40	0
106/381	9.28373E-41	2.1954E-38	0
119/474	9.37444E-41	2.1954E-38	0
68/159	8.78634E-40	1.96415E-37	0
48/76	6.33863E-39	1.35537E-36	0
49/81	2.17948E-38	4.46611E-36	0
183/1079	8.02158E-37	1.57801E-34	0
57/121	2.32028E-36	4.3889E-34	0
80/246	2.73569E-36	4.983E-34	0
46/77	9.32637E-36	1.63811E-33	0
49/89	1.23016E-35	2.08618E-33	0
70/194	3.55418E-35	5.82648E-33	0
45/75	3.99502E-35	6.13985E-33	0
45/75	3.99502E-35	6.13985E-33	0
59/139	1.9442E-34	2.89745E-32	0
67/182	2.43739E-34	3.52561E-32	0
57/134	2.26722E-33	3.18577E-31	0
54/120	3.20711E-33	4.38126E-31	0
88/323	3.48462E-33	4.63172E-31	0
45/81	4.61849E-33	5.9773E-31	0
49/98	5.44824E-33	6.87038E-31	0
37/53	9.72038E-33	1.19512E-30	0
40/66	1.32087E-31	1.58439E-29	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

78/269	1.54747E-31	1.81201E-29	0
73/238	2.49522E-31	2.85383E-29	0
58/150	3.15571E-31	3.52723E-29	0
60/161	3.25332E-31	3.55552E-29	0
67/203	5.36647E-31	5.73745E-29	0
42/76	8.19913E-31	8.57943E-29	0
67/207	2.04142E-30	2.09161E-28	0
69/221	3.34738E-30	3.35967E-28	0
108/511	6.14863E-30	6.04779E-28	0
57/155	2.34204E-29	2.25846E-27	0
37/61	2.38957E-29	2.25998E-27	0
94/408	3.63778E-29	3.37559E-27	0
43/86	4.19116E-29	3.81706E-27	0
49/115	6.70865E-29	5.99875E-27	0
72/253	1.26532E-28	1.11122E-26	0
59/172	1.86588E-28	1.60989E-26	0
71/252	6.04336E-28	5.12435E-26	0
33/51	1.17438E-27	9.78918E-26	0
41/83	1.53296E-27	1.25651E-25	0
32/48	1.75684E-27	1.41641E-25	0
59/179	2.12651E-27	1.6868E-25	0
54/150	2.42407E-27	1.89231E-25	0
65/219	4.2215E-27	3.24396E-25	0
53/147	6.77171E-27	5.12358E-25	0
38/77	1.33247E-25	9.92892E-24	0
46/116	1.38937E-25	1.01984E-23	0
37/73	1.68811E-25	1.2209E-23	0
43/102	2.73078E-25	1.94637E-23	0
36/70	3.91536E-25	2.75082E-23	0
84/379	6.19063E-25	4.2881E-23	0
97/488	7.93314E-25	5.41877E-23	0
105/566	2.65863E-24	1.79112E-22	0
40/92	3.08989E-24	2.05352E-22	0
28/42	3.32982E-24	2.18347E-22	0
39/89	8.09265E-24	5.2368E-22	0
62/231	2.58853E-23	1.6533E-21	0
34/68	2.75269E-23	1.71363E-21	0
34/68	2.75269E-23	1.71363E-21	0
94/485	2.95669E-23	1.81763E-21	0
35/73	3.8202E-23	2.31947E-21	0
93/481	6.11592E-23	3.66806E-21	0
35/75	1.203E-22	7.12814E-21	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

43/116	1.2727E-22	7.45136E-21	0
36/80	1.41156E-22	8.1671E-21	0
32/62	1.4963E-22	8.55674E-21	0
31/59	3.39634E-22	1.91991E-20	0
58/214	4.04876E-22	2.2627E-20	0
65/266	5.85426E-22	3.23497E-20	0
30/56	7.54428E-22	4.07723E-20	0
30/56	7.54428E-22	4.07723E-20	0
35/80	1.74479E-21	9.32703E-20	0
34/77	4.54802E-21	2.40507E-19	0
69/310	8.70728E-21	4.55558E-19	0
30/60	1.05206E-20	5.44637E-19	0
33/74	1.17901E-20	6.03998E-19	0
46/148	1.85196E-20	9.38965E-19	0
34/80	2.04993E-20	1.02873E-18	0
29/57	2.47088E-20	1.22745E-18	0
38/102	3.08541E-20	1.5174E-18	0
27/49	3.14201E-20	1.52301E-18	0
35/86	3.15874E-20	1.52301E-18	0
40/114	4.02397E-20	1.92135E-18	0
36/92	4.41049E-20	2.08565E-18	0
55/212	4.52675E-20	2.12024E-18	0
16/16	5.0119E-20	2.32533E-18	0
32/72	5.14463E-20	2.36461E-18	0
17/18	5.25004E-20	2.39071E-18	0
52/194	9.92569E-20	4.4784E-18	0
42/130	1.66006E-19	7.42196E-18	0
66/302	1.73216E-19	7.67454E-18	0
22/33	2.74243E-19	1.20422E-17	0
34/86	3.28318E-19	1.42891E-17	0
27/53	4.82503E-19	2.08154E-17	0
47/166	5.13172E-19	2.19459E-17	0
22/34	7.31365E-19	3.10074E-17	0
63/286	7.66249E-19	3.22087E-17	0
27/54	9.08057E-19	3.7846E-17	0
18/22	1.09974E-18	4.54496E-17	0
25/46	1.24191E-18	5.06439E-17	0
37/106	1.25632E-18	5.06439E-17	0
37/106	1.25632E-18	5.06439E-17	0
132/948	1.34095E-18	5.3616E-17	0
29/64	1.49041E-18	5.91117E-17	0
27/55	1.67842E-18	6.60359E-17	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

40/125	1.78716E-18	6.97561E-17	0
49/185	1.97107E-18	7.63284E-17	0
53/214	2.04381E-18	7.8527E-17	0
25/47	2.49681E-18	9.51885E-17	0
48/180	3.25273E-18	1.23053E-16	0
54/224	3.57584E-18	1.34244E-16	0
24/44	5.45574E-18	2.03268E-16	0
40/129	6.31274E-18	2.33429E-16	0
36/105	7.20757E-18	2.64529E-16	0
43/150	9.80666E-18	3.57253E-16	0
49/194	1.6685E-17	6.0336E-16	0
236/2206	1.83002E-17	6.56939E-16	0
40/133	2.10995E-17	7.51938E-16	0
43/154	2.89036E-17	1.02265E-15	0
32/86	3.06431E-17	1.07645E-15	0
36/110	4.03637E-17	1.40786E-15	0
29/71	4.7974E-17	1.66152E-15	0
38/124	6.6112E-17	2.2737E-15	0
30/77	6.68364E-17	2.28265E-15	0
24/48	7.83751E-17	2.64006E-15	0
24/48	7.83751E-17	2.64006E-15	0
20/32	7.95836E-17	2.66253E-15	0
31/83	8.45997E-17	2.81122E-15	0
21/36	1.00726E-16	3.32463E-15	0
36/114	1.47934E-16	4.85026E-15	0
36/115	2.02601E-16	6.59863E-15	0
33/97	2.22348E-16	7.19412E-15	0
61/303	2.66091E-16	8.55316E-15	0
37/123	3.33227E-16	1.06416E-14	0
27/65	3.45981E-16	1.07563E-14	0
27/65	3.45981E-16	1.07563E-14	0
23/46	3.46453E-16	1.07563E-14	0
23/46	3.46453E-16	1.07563E-14	0
26/60	3.47755E-16	1.07563E-14	0
63/322	3.64725E-16	1.12107E-14	0
22/42	4.22193E-16	1.28965E-14	0
42/158	4.70794E-16	1.42047E-14	0
42/158	4.70794E-16	1.42047E-14	0
72/404	5.06248E-16	1.51813E-14	0
55/258	5.94227E-16	1.77116E-14	0
32/94	6.19529E-16	1.83545E-14	0
29/77	6.43276E-16	1.89439E-14	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

36/119	6.85908E-16	2.00791E-14	0
35/113	7.67485E-16	2.23343E-14	0
19/31	8.07859E-16	2.33709E-14	0
31/91	1.72597E-15	4.96394E-14	0
32/97	1.74177E-15	4.98024E-14	0
27/69	2.09532E-15	5.92229E-14	0
27/69	2.09532E-15	5.92229E-14	0
32/98	2.43336E-15	6.83842E-14	0
15/19	2.47466E-15	6.91499E-14	0
22/45	2.8211E-15	7.83852E-14	0
99/684	3.0115E-15	8.32054E-14	0
31/93	3.45676E-15	9.49741E-14	0
26/66	5.71713E-15	1.56205E-13	0
32/101	6.44662E-15	1.75163E-13	0
19/34	8.86799E-15	2.39631E-13	0
42/171	9.72477E-15	2.61347E-13	0
29/85	1.33926E-14	3.5796E-13	0
35/123	1.38613E-14	3.68485E-13	0
22/48	1.56514E-14	4.13836E-13	0
23/53	1.7165E-14	4.5143E-13	0
31/98	1.79253E-14	4.68917E-13	0
19/35	1.82648E-14	4.75271E-13	0
21/44	2.24501E-14	5.81103E-13	0
35/125	2.37428E-14	6.11345E-13	0
24/59	2.69786E-14	6.91045E-13	0
20/40	2.99802E-14	7.60013E-13	0
20/40	2.99802E-14	7.60013E-13	0
39/155	3.74816E-14	9.45304E-13	0
18/32	3.8846E-14	9.74717E-13	0
21/45	3.9626E-14	9.89242E-13	0
53/267	4.49687E-14	1.11695E-12	0
38/149	4.99719E-14	1.23498E-12	0
29/89	5.25702E-14	1.2927E-12	0
29/91	1.00798E-13	2.4663E-12	0
23/57	1.14748E-13	2.79372E-12	0
41/176	1.37647E-13	3.33472E-12	0
29/92	1.38509E-13	3.33916E-12	0
24/63	1.53308E-13	3.6779E-12	0
18/34	1.61038E-13	3.82601E-12	0
18/34	1.61038E-13	3.82601E-12	0
41/177	1.68536E-13	3.98491E-12	0
17/30	1.70048E-13	4.00141E-12	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

20/43	1.74332E-13	4.08269E-12	0
27/81	2.08336E-13	4.8559E-12	0
19/39	2.437E-13	5.65338E-12	0
15/23	2.46615E-13	5.69415E-12	0
23/59	2.76097E-13	6.34507E-12	0
41/180	3.06268E-13	7.0057E-12	0
16/27	3.38397E-13	7.70479E-12	0
17/31	3.54624E-13	7.98088E-12	0
17/31	3.54624E-13	7.98088E-12	0
14/20	3.55391E-13	7.98088E-12	0
13/17	3.97215E-13	8.87956E-12	0
26/78	5.80533E-13	1.29188E-11	0
18/36	5.88018E-13	1.30265E-11	0
72/464	7.05543E-13	1.55599E-11	0
16/28	7.4377E-13	1.63297E-11	0
45/217	7.5187E-13	1.64342E-11	0
19/41	7.66958E-13	1.66898E-11	0
32/118	8.03301E-13	1.73775E-11	0
33/125	8.05626E-13	1.73775E-11	0
29/98	8.44305E-13	1.81323E-11	0
75/496	8.75533E-13	1.87212E-11	0
23/62	9.52813E-13	2.02854E-11	0
14/21	1.0047E-12	2.12978E-11	0
18/37	1.07833E-12	2.27606E-11	0
26/80	1.1354E-12	2.38627E-11	0
19/42	1.31873E-12	2.75979E-11	0
18/38	1.92939E-12	4.02065E-11	0
79/547	2.39704E-12	4.97411E-11	0
15/26	3.24985E-12	6.71544E-11	0
18/39	3.3743E-12	6.9145E-11	0
18/39	3.3743E-12	6.9145E-11	0
20/49	3.57426E-12	7.26373E-11	0
20/49	3.57426E-12	7.26373E-11	0
27/90	3.59855E-12	7.28298E-11	0
19/44	3.68687E-12	7.43116E-11	0
13/19	4.02318E-12	8.07591E-11	0
39/178	4.23164E-12	8.45985E-11	0
12/16	4.90684E-12	9.76997E-11	0
26/85	5.49196E-12	1.08909E-10	0
22/61	5.76461E-12	1.13857E-10	0
19/45	6.00853E-12	1.182E-10	0
30/114	9.60833E-12	1.88262E-10	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

26/87	9.94396E-12	1.94065E-10	0
13/20	1.0835E-11	2.10619E-10	0
15/28	1.39804E-11	2.6963E-10	0
15/28	1.39804E-11	2.6963E-10	0
14/24	1.41813E-11	2.72437E-10	0
12/17	1.57303E-11	3.01018E-10	0
11/14	1.67986E-11	3.18978E-10	0
11/14	1.67986E-11	3.18978E-10	0
16/33	2.1159E-11	4.00231E-10	0
19/48	2.37454E-11	4.47433E-10	0
23/71	2.45436E-11	4.60707E-10	0
18/43	2.58913E-11	4.84158E-10	0
15/29	2.72852E-11	5.06372E-10	0
15/29	2.72852E-11	5.06372E-10	0
25/84	2.74663E-11	5.07816E-10	0
14/25	3.03734E-11	5.59462E-10	0
19/49	3.65207E-11	6.67691E-10	0
19/49	3.65207E-11	6.67691E-10	0
17/39	4.22501E-11	7.66187E-10	0
17/39	4.22501E-11	7.66187E-10	0
27/99	4.23756E-11	7.66187E-10	0
24/80	5.66923E-11	1.02129E-09	0
11/15	5.94183E-11	1.06649E-09	0
51/300	5.98835E-11	1.07094E-09	0
14/26	6.20183E-11	1.10509E-09	0
23/74	6.37224E-11	1.13136E-09	0
18/45	6.47681E-11	1.14579E-09	0
17/40	6.92087E-11	1.21996E-09	0
18/46	1.00209E-10	1.7601E-09	0
25/89	1.10441E-10	1.91849E-09	0
16/36	1.10787E-10	1.91849E-09	0
16/36	1.10787E-10	1.91849E-09	0
16/36	1.10787E-10	1.91849E-09	0
38/189	1.19053E-10	2.05439E-09	0
14/27	1.21389E-10	2.08739E-09	0
20/58	1.35774E-10	2.3266E-09	0
18/47	1.52952E-10	2.60283E-09	0
18/47	1.52952E-10	2.60283E-09	0
38/191	1.64447E-10	2.78879E-09	0
15/32	1.66473E-10	2.81345E-09	0
11/16	1.79347E-10	3.0001E-09	0
11/16	1.79347E-10	3.0001E-09	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

11/16	1.79347E-10	3.0001E-09	0
16/37	1.83886E-10	3.06561E-09	0
23/78	2.09261E-10	3.47684E-09	0
10/13	2.12911E-10	3.52558E-09	0
14/28	2.28801E-10	3.76056E-09	0
14/28	2.28801E-10	3.76056E-09	0
8/8	2.29395E-10	3.76056E-09	0
12/20	2.68452E-10	4.37168E-09	0
12/20	2.68452E-10	4.37168E-09	0
17/43	2.74514E-10	4.45565E-09	0
15/33	2.87571E-10	4.65221E-09	0
16/38	2.99221E-10	4.82482E-09	0
17/44	4.21378E-10	6.77235E-09	0
15/34	4.84881E-10	7.74235E-09	0
15/34	4.84881E-10	7.74235E-09	0
13/25	5.40978E-10	8.5001E-09	0
13/25	5.40978E-10	8.5001E-09	0
13/25	5.40978E-10	8.5001E-09	0
13/25	5.40978E-10	8.5001E-09	0
13/25	5.40978E-10	8.5001E-09	0
12/21	5.90649E-10	9.251E-09	0
9/11	6.9921E-10	1.08477E-08	0
9/11	6.9921E-10	1.08477E-08	0
9/11	6.9921E-10	1.08477E-08	0
10/14	7.03208E-10	1.08754E-08	0
14/30	7.36678E-10	1.13218E-08	0
14/30	7.36678E-10	1.13218E-08	0
15/35	7.99546E-10	1.21739E-08	0
15/35	7.99546E-10	1.21739E-08	0
15/35	7.99546E-10	1.21739E-08	0
31/143	8.75236E-10	1.32852E-08	0
17/46	9.53097E-10	1.44226E-08	0
20/64	1.00498E-09	1.5161E-08	0
13/26	1.01995E-09	1.53398E-08	0
48/296	1.12987E-09	1.69411E-08	0
11/18	1.16263E-09	1.73267E-08	0
11/18	1.16263E-09	1.73267E-08	0
14/31	1.26607E-09	1.87546E-08	0
14/31	1.26607E-09	1.87546E-08	0
15/36	1.29152E-09	1.90742E-08	0
17/47	1.40652E-09	2.07104E-08	0
16/42	1.76472E-09	2.59072E-08	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

58/400	1.78809E-09	2.61721E-08	0
13/27	1.85434E-09	2.69812E-08	0
13/27	1.85434E-09	2.69812E-08	0
10/15	1.99082E-09	2.87122E-08	0
10/15	1.99082E-09	2.87122E-08	0
10/15	1.99082E-09	2.87122E-08	0
27/116	2.03756E-09	2.93003E-08	0
15/37	2.04675E-09	2.93466E-08	0
21/73	2.10334E-09	3.00704E-08	0
31/148	2.13033E-09	3.0368E-08	0
24/94	2.1917E-09	3.11526E-08	0
12/23	2.41593E-09	3.41424E-08	0
12/23	2.41593E-09	3.41424E-08	0
11/19	2.60469E-09	3.63917E-08	0
11/19	2.60469E-09	3.63917E-08	0
11/19	2.60469E-09	3.63917E-08	0
11/19	2.60469E-09	3.63917E-08	0
29/133	2.6381E-09	3.66863E-08	0
9/12	2.6407E-09	3.66863E-08	0
17/49	2.95903E-09	4.0993E-08	0
27/118	3.04252E-09	4.19135E-08	0
27/118	3.04252E-09	4.19135E-08	0
7/7	3.68694E-09	5.03677E-08	0
7/7	3.68694E-09	5.03677E-08	0
7/7	3.68694E-09	5.03677E-08	0
16/44	3.9201E-09	5.34046E-08	0
20/69	4.38481E-09	5.95705E-08	0
12/24	4.55644E-09	6.12257E-08	0
12/24	4.55644E-09	6.12257E-08	0
12/24	4.55644E-09	6.12257E-08	0
12/24	4.55644E-09	6.12257E-08	0
25/105	4.86853E-09	6.52072E-08	0
15/39	4.87927E-09	6.52072E-08	0
10/16	5.01001E-09	6.65926E-08	0
10/16	5.01001E-09	6.65926E-08	0
11/20	5.46015E-09	7.21856E-08	0
11/20	5.46015E-09	7.21856E-08	0
14/34	5.56392E-09	7.29305E-08	0
14/34	5.56392E-09	7.29305E-08	0
14/34	5.56392E-09	7.29305E-08	0
13/29	5.57581E-09	7.29305E-08	0
18/57	5.70564E-09	7.44306E-08	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

26/114	6.3914E-09	8.31559E-08	0
19/64	6.86143E-09	8.90357E-08	0
60/437	7.71326E-09	9.98258E-08	0
31/156	8.07362E-09	1.04215E-07	0
17/52	8.35193E-09	1.07526E-07	0
14/35	8.74021E-09	1.12231E-07	0
29/140	9.1209E-09	1.16814E-07	0
13/30	9.27639E-09	1.1819E-07	0
13/30	9.27639E-09	1.1819E-07	0
21/79	1.00648E-08	1.27904E-07	0
24/101	1.02677E-08	1.30145E-07	0
45/287	1.08386E-08	1.37029E-07	0
15/41	1.09318E-08	1.37853E-07	0
28/133	1.12527E-08	1.41537E-07	0
23/94	1.14123E-08	1.43178E-07	0
10/17	1.14826E-08	1.43328E-07	0
10/17	1.14826E-08	1.43328E-07	0
17/53	1.1583E-08	1.44216E-07	0
16/47	1.18265E-08	1.46876E-07	0
12/26	1.44716E-08	1.79273E-07	0
29/143	1.50877E-08	1.86435E-07	0
19/67	1.58744E-08	1.95666E-07	0
15/42	1.60247E-08	1.97024E-07	0
20/74	1.65379E-08	2.02827E-07	0
16/48	1.67141E-08	2.04478E-07	0
24/104	1.89854E-08	2.31688E-07	0
22/89	1.93521E-08	2.35579E-07	0
9/14	2.14239E-08	2.57611E-07	0
9/14	2.14239E-08	2.57611E-07	0
9/14	2.14239E-08	2.57611E-07	0
9/14	2.14239E-08	2.57611E-07	0
9/14	2.14239E-08	2.57611E-07	0
16/49	2.33833E-08	2.79803E-07	0
16/49	2.33833E-08	2.79803E-07	0
13/32	2.39158E-08	2.8548E-07	0
10/18	2.43827E-08	2.89648E-07	0
10/18	2.43827E-08	2.89648E-07	0
12/27	2.45656E-08	2.89721E-07	0
12/27	2.45656E-08	2.89721E-07	0
12/27	2.45656E-08	2.89721E-07	0
19/69	2.69656E-08	3.17266E-07	0
7/8	2.78906E-08	3.2581E-07	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

7/8	2.78906E-08	3.2581E-07	0
7/8	2.78906E-08	3.2581E-07	0
42/267	3.02654E-08	3.52714E-07	0
8/11	3.19219E-08	3.69393E-07	0
8/11	3.19219E-08	3.69393E-07	0
8/11	3.19219E-08	3.69393E-07	0
29/148	3.37122E-08	3.89194E-07	0
11/23	3.69015E-08	4.24023E-07	0
11/23	3.69015E-08	4.24023E-07	0
13/33	3.72041E-08	4.26503E-07	0
12/28	4.05426E-08	4.61548E-07	0
12/28	4.05426E-08	4.61548E-07	0
12/28	4.05426E-08	4.61548E-07	0
28/141	4.28579E-08	4.86779E-07	0
19/71	4.48261E-08	5.06792E-07	0
19/71	4.48261E-08	5.06792E-07	0
10/19	4.8581E-08	5.46731E-07	0
10/19	4.8581E-08	5.46731E-07	0
9/15	5.05741E-08	5.67862E-07	0
36/214	5.13617E-08	5.75392E-07	0
17/58	5.25483E-08	5.86014E-07	0
17/58	5.25483E-08	5.86014E-07	0
22/94	5.61778E-08	6.25074E-07	0
13/34	5.67912E-08	6.30472E-07	0
23/102	5.92065E-08	6.55805E-07	0
16/52	6.05421E-08	6.69092E-07	0
21/87	6.3282E-08	6.97805E-07	0
11/24	6.42709E-08	7.07124E-07	0
12/29	6.52255E-08	7.1443E-07	0
12/29	6.52255E-08	7.1443E-07	0
36/216	6.55458E-08	7.16342E-07	0
28/144	6.87085E-08	7.49243E-07	0
34/198	7.16876E-08	7.79999E-07	0
18/66	7.34918E-08	7.96107E-07	0
18/66	7.34918E-08	7.96107E-07	0
16/53	8.17138E-08	8.83228E-07	0
13/35	8.51853E-08	9.18731E-07	0
20/81	8.65799E-08	9.31729E-07	0
41/267	8.73695E-08	9.38173E-07	0
8/12	9.04855E-08	9.67408E-07	0
8/12	9.04855E-08	9.67408E-07	0
15/47	9.07295E-08	9.67912E-07	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

10/20	9.17026E-08	9.71968E-07	0
10/20	9.17026E-08	9.71968E-07	0
10/20	9.17026E-08	9.71968E-07	0
12/30	1.02525E-07	1.08202E-06	0
12/30	1.02525E-07	1.08202E-06	0
11/25	1.08278E-07	1.14028E-06	0
9/16	1.09158E-07	1.14709E-06	0
30/165	1.1389E-07	1.19427E-06	0
7/9	1.18683E-07	1.22366E-06	0
7/9	1.18683E-07	1.22366E-06	0
7/9	1.18683E-07	1.22366E-06	0
7/9	1.18683E-07	1.22366E-06	0
7/9	1.18683E-07	1.22366E-06	0
7/9	1.18683E-07	1.22366E-06	0
7/9	1.18683E-07	1.22366E-06	0
7/9	1.18683E-07	1.22366E-06	0
13/36	1.25715E-07	1.29074E-06	0
13/36	1.25715E-07	1.29074E-06	0
26/131	1.30527E-07	1.33736E-06	0
20/83	1.33801E-07	1.36805E-06	0
16/55	1.45395E-07	1.48351E-06	0
29/158	1.49369E-07	1.52091E-06	0
17/62	1.54989E-07	1.57162E-06	0
17/62	1.54989E-07	1.57162E-06	0
12/31	1.57766E-07	1.59321E-06	0
12/31	1.57766E-07	1.59321E-06	0
10/21	1.65236E-07	1.65843E-06	0
10/21	1.65236E-07	1.65843E-06	0
10/21	1.65236E-07	1.65843E-06	0
11/26	1.7707E-07	1.77358E-06	0
13/37	1.82739E-07	1.82294E-06	0
13/37	1.82739E-07	1.82294E-06	0
14/43	1.84009E-07	1.83189E-06	0
106/1025	1.85561E-07	1.84362E-06	0
16/56	1.91805E-07	1.90181E-06	0
18/70	1.95979E-07	1.93929E-06	0
9/17	2.19044E-07	2.16317E-06	0
41/276	2.19712E-07	2.16542E-06	0
8/13	2.22299E-07	2.18217E-06	0
8/13	2.22299E-07	2.18217E-06	0
28/152	2.25273E-07	2.20695E-06	0
35/217	2.26825E-07	2.21775E-06	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

25/126	2.27877E-07	2.22289E-06	0
19/78	2.28255E-07	2.22289E-06	0
12/32	2.38078E-07	2.31396E-06	0
20/86	2.49961E-07	2.42467E-06	0
14/44	2.54406E-07	2.46293E-06	0
21/94	2.61037E-07	2.52216E-06	0
13/38	2.61902E-07	2.52556E-06	0
26/136	2.83734E-07	2.73073E-06	0
15/51	3.03674E-07	2.91124E-06	0
15/51	3.03674E-07	2.91124E-06	0
18/72	3.10636E-07	2.96642E-06	0
18/72	3.10636E-07	2.96642E-06	0
22/103	3.14419E-07	2.99673E-06	0
26/137	3.29659E-07	3.13591E-06	0
14/45	3.48132E-07	3.30524E-06	0
12/33	3.52864E-07	3.34371E-06	0
13/39	3.70426E-07	3.49666E-06	0
13/39	3.70426E-07	3.49666E-06	0
7/10	3.74116E-07	3.51798E-06	0
7/10	3.74116E-07	3.51798E-06	0
22/104	3.755E-07	3.52425E-06	0
18/73	3.884E-07	3.63839E-06	0
6/7	3.92379E-07	3.64098E-06	0
6/7	3.92379E-07	3.64098E-06	0
6/7	3.92379E-07	3.64098E-06	0
6/7	3.92379E-07	3.64098E-06	0
6/7	3.92379E-07	3.64098E-06	0
9/18	4.13707E-07	3.81014E-06	0
9/18	4.13707E-07	3.81014E-06	0
9/18	4.13707E-07	3.81014E-06	0
9/18	4.13707E-07	3.81014E-06	0
19/81	4.30311E-07	3.95565E-06	0
11/28	4.38103E-07	4.00482E-06	0
11/28	4.38103E-07	4.00482E-06	0
11/28	4.38103E-07	4.00482E-06	0
38/253	4.55429E-07	4.15548E-06	0
14/46	4.71764E-07	4.29654E-06	0
10/23	4.77489E-07	4.31671E-06	0
10/23	4.77489E-07	4.31671E-06	0
10/23	4.77489E-07	4.31671E-06	0
10/23	4.77489E-07	4.31671E-06	0
18/74	4.835E-07	4.36303E-06	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

8/14	4.90138E-07	4.36684E-06	0
8/14	4.90138E-07	4.36684E-06	0
8/14	4.90138E-07	4.36684E-06	0
8/14	4.90138E-07	4.36684E-06	0
8/14	4.90138E-07	4.36684E-06	0
8/14	4.90138E-07	4.36684E-06	0
8/14	4.90138E-07	4.36684E-06	0
12/34	5.1436E-07	4.5661E-06	0
12/34	5.1436E-07	4.5661E-06	0
13/40	5.17463E-07	4.57712E-06	0
13/40	5.17463E-07	4.57712E-06	0
196/2244	5.36017E-07	4.73273E-06	0
15/54	6.90058E-07	6.0819E-06	0
16/61	6.93953E-07	6.1053E-06	0
32/198	7.05488E-07	6.1957E-06	0
13/41	7.14487E-07	6.26354E-06	0
12/35	7.38279E-07	6.4606E-06	0
18/76	7.39825E-07	6.46152E-06	0
9/19	7.42326E-07	6.46152E-06	0
9/19	7.42326E-07	6.46152E-06	0
10/24	7.72649E-07	6.71358E-06	0
20/92	7.96225E-07	6.90624E-06	0
17/69	8.23739E-07	7.1323E-06	0
24/126	8.63275E-07	7.46149E-06	0
22/109	8.79036E-07	7.5711E-06	0
22/109	8.79036E-07	7.5711E-06	0
15/55	8.94308E-07	7.68917E-06	0
5/5	9.50251E-07	8.11342E-06	0
5/5	9.50251E-07	8.11342E-06	0
5/5	9.50251E-07	8.11342E-06	0
5/5	9.50251E-07	8.11342E-06	0
20/93	9.55392E-07	8.14319E-06	0
7/11	9.72967E-07	8.1761E-06	0
7/11	9.72967E-07	8.1761E-06	0
7/11	9.72967E-07	8.1761E-06	0
7/11	9.72967E-07	8.1761E-06	0
7/11	9.72967E-07	8.1761E-06	0
7/11	9.72967E-07	8.1761E-06	0
7/11	9.72967E-07	8.1761E-06	0
7/11	9.72967E-07	8.1761E-06	0
13/42	9.75761E-07	8.1761E-06	0
11/30	9.92187E-07	8.1761E-06	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

11/30	9.92187E-07	8.1761E-06	0
8/15	9.92503E-07	8.1761E-06	0
8/15	9.92503E-07	8.1761E-06	0
8/15	9.92503E-07	8.1761E-06	0
8/15	9.92503E-07	8.1761E-06	0
8/15	9.92503E-07	8.1761E-06	0
8/15	9.92503E-07	8.1761E-06	0
8/15	9.92503E-07	8.1761E-06	0
8/15	9.92503E-07	8.1761E-06	0
8/15	9.92503E-07	8.1761E-06	0
17/70	1.0251E-06	8.41641E-06	0
17/70	1.0251E-06	8.41641E-06	0
35/231	1.04002E-06	8.52471E-06	0
12/36	1.04456E-06	8.5477E-06	0
21/102	1.10104E-06	8.9949E-06	0
14/49	1.11267E-06	9.06574E-06	0
16/63	1.1134E-06	9.06574E-06	0
20/94	1.14306E-06	9.29182E-06	0
55/447	1.20964E-06	9.81685E-06	0
22/111	1.21524E-06	9.8325E-06	0
10/25	1.21557E-06	9.8325E-06	0
17/71	1.26996E-06	1.02264E-05	0
9/20	1.27466E-06	1.02264E-05	0
9/20	1.27466E-06	1.02264E-05	0
9/20	1.27466E-06	1.02264E-05	0
9/20	1.27466E-06	1.02264E-05	0
13/43	1.31886E-06	1.05637E-05	0
22/112	1.42412E-06	1.13883E-05	0
6/8	1.48587E-06	1.17295E-05	0
6/8	1.48587E-06	1.17295E-05	0
6/8	1.48587E-06	1.17295E-05	0
6/8	1.48587E-06	1.17295E-05	0
6/8	1.48587E-06	1.17295E-05	0
6/8	1.48587E-06	1.17295E-05	0
6/8	1.48587E-06	1.17295E-05	0
6/8	1.48587E-06	1.17295E-05	0
17/72	1.56648E-06	1.2346E-05	0
16/65	1.74895E-06	1.37622E-05	0
25/140	1.79067E-06	1.40679E-05	0
10/26	1.86464E-06	1.45742E-05	0
10/26	1.86464E-06	1.45742E-05	0
8/16	1.87586E-06	1.45742E-05	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

8/16	1.87586E-06	1.45742E-05	0
8/16	1.87586E-06	1.45742E-05	0
8/16	1.87586E-06	1.45742E-05	0
8/16	1.87586E-06	1.45742E-05	0
14/51	1.89329E-06	1.46633E-05	0
14/51	1.89329E-06	1.46633E-05	0
17/73	1.92411E-06	1.48786E-05	0
22/114	1.94328E-06	1.50032E-05	0
11/32	2.08654E-06	1.60588E-05	0
11/32	2.08654E-06	1.60588E-05	0
9/21	2.10674E-06	1.6189E-05	0
7/12	2.20846E-06	1.68652E-05	0
7/12	2.20846E-06	1.68652E-05	0
7/12	2.20846E-06	1.68652E-05	0
7/12	2.20846E-06	1.68652E-05	0
24/133	2.36429E-06	1.80273E-05	0
14/52	2.44263E-06	1.85957E-05	0
20/99	2.68922E-06	2.04414E-05	0
23/125	2.7011E-06	2.05E-05	0
12/39	2.7393E-06	2.07579E-05	0
10/27	2.79566E-06	2.1023E-05	0
10/27	2.79566E-06	2.1023E-05	0
10/27	2.79566E-06	2.1023E-05	0
10/27	2.79566E-06	2.1023E-05	0
10/27	2.79566E-06	2.1023E-05	0
21/108	2.91157E-06	2.18612E-05	0
26/153	2.93861E-06	2.20306E-05	0
11/33	2.95338E-06	2.2074E-05	0
11/33	2.95338E-06	2.2074E-05	0
8/17	3.3486E-06	2.46871E-05	0
8/17	3.3486E-06	2.46871E-05	0
8/17	3.3486E-06	2.46871E-05	0
8/17	3.3486E-06	2.46871E-05	0
9/22	3.36731E-06	2.46871E-05	0
9/22	3.36731E-06	2.46871E-05	0
9/22	3.36731E-06	2.46871E-05	0
9/22	3.36731E-06	2.46871E-05	0
9/22	3.36731E-06	2.46871E-05	0
9/22	3.36731E-06	2.46871E-05	0
9/22	3.36731E-06	2.46871E-05	0
9/22	3.36731E-06	2.46871E-05	0
19/92	3.36824E-06	2.46871E-05	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

17/76	3.48121E-06	2.54771E-05	0
22/118	3.53077E-06	2.58014E-05	0
21/110	3.95392E-06	2.88507E-05	0
13/47	4.01174E-06	2.92292E-05	0
10/28	4.10542E-06	2.96919E-05	0
10/28	4.10542E-06	2.96919E-05	0
10/28	4.10542E-06	2.96919E-05	0
10/28	4.10542E-06	2.96919E-05	0
10/28	4.10542E-06	2.96919E-05	0
11/34	4.11988E-06	2.9709E-05	0
11/34	4.11988E-06	2.9709E-05	0
17/77	4.20984E-06	2.98638E-05	0
6/9	4.22028E-06	2.98638E-05	0
6/9	4.22028E-06	2.98638E-05	0
6/9	4.22028E-06	2.98638E-05	0
6/9	4.22028E-06	2.98638E-05	0
6/9	4.22028E-06	2.98638E-05	0
6/9	4.22028E-06	2.98638E-05	0
6/9	4.22028E-06	2.98638E-05	0
6/9	4.22028E-06	2.98638E-05	0
6/9	4.22028E-06	2.98638E-05	0
6/9	4.22028E-06	2.98638E-05	0
6/9	4.22028E-06	2.98638E-05	0
6/9	4.22028E-06	2.98638E-05	0
20/102	4.35739E-06	3.07456E-05	0
20/102	4.35739E-06	3.07456E-05	0
7/13	4.52567E-06	3.15259E-05	0
7/13	4.52567E-06	3.15259E-05	0
7/13	4.52567E-06	3.15259E-05	0
7/13	4.52567E-06	3.15259E-05	0
7/13	4.52567E-06	3.15259E-05	0
7/13	4.52567E-06	3.15259E-05	0
7/13	4.52567E-06	3.15259E-05	0
7/13	4.52567E-06	3.15259E-05	0
7/13	4.52567E-06	3.15259E-05	0
12/41	4.9234E-06	3.41996E-05	0
12/41	4.9234E-06	3.41996E-05	0
17/78	5.07261E-06	3.51863E-05	0
20/103	5.09352E-06	3.52816E-05	0
13/48	5.1887E-06	3.58395E-05	0
9/23	5.22507E-06	3.58395E-05	0
9/23	5.22507E-06	3.58395E-05	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

9/23	5.22507E-06	3.58395E-05	0
9/23	5.22507E-06	3.58395E-05	0
9/23	5.22507E-06	3.58395E-05	0
9/23	5.22507E-06	3.58395E-05	0
5/6	5.40554E-06	3.65673E-05	0
5/6	5.40554E-06	3.65673E-05	0
5/6	5.40554E-06	3.65673E-05	0
5/6	5.40554E-06	3.65673E-05	0
5/6	5.40554E-06	3.65673E-05	0
5/6	5.40554E-06	3.65673E-05	0
5/6	5.40554E-06	3.65673E-05	0
5/6	5.40554E-06	3.65673E-05	0
5/6	5.40554E-06	3.65673E-05	0
5/6	5.40554E-06	3.65673E-05	0
11/35	5.66979E-06	3.79615E-05	0
11/35	5.66979E-06	3.79615E-05	0
11/35	5.66979E-06	3.79615E-05	0
11/35	5.66979E-06	3.79615E-05	0
11/35	5.66979E-06	3.79615E-05	0
8/18	5.69655E-06	3.79615E-05	0
8/18	5.69655E-06	3.79615E-05	0
8/18	5.69655E-06	3.79615E-05	0
8/18	5.69655E-06	3.79615E-05	0
8/18	5.69655E-06	3.79615E-05	0
8/18	5.69655E-06	3.79615E-05	0
15/63	5.72048E-06	3.8018E-05	0
15/63	5.72048E-06	3.8018E-05	0
10/29	5.91567E-06	3.92093E-05	0
10/29	5.91567E-06	3.92093E-05	0
16/71	6.0549E-06	4.0078E-05	0
13/49	6.66061E-06	4.40281E-05	0
17/80	7.28851E-06	4.81139E-05	0
16/72	7.33731E-06	4.83712E-05	0
30/200	7.36789E-06	4.85077E-05	0
11/36	7.70491E-06	5.04564E-05	0
11/36	7.70491E-06	5.04564E-05	0
11/36	7.70491E-06	5.04564E-05	0
11/36	7.70491E-06	5.04564E-05	0
9/24	7.89655E-06	5.15056E-05	0
9/24	7.89655E-06	5.15056E-05	0
9/24	7.89655E-06	5.15056E-05	0
14/57	7.91686E-06	5.15697E-05	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

44/350	7.9954E-06	5.20124E-05	0
20/106	8.02555E-06	5.21396E-05	0
10/30	8.37744E-06	5.40685E-05	0
10/30	8.37744E-06	5.40685E-05	0
10/30	8.37744E-06	5.40685E-05	0
10/30	8.37744E-06	5.40685E-05	0
10/30	8.37744E-06	5.40685E-05	0
13/50	8.48895E-06	5.45392E-05	0
12/43	8.50905E-06	5.45392E-05	0
7/14	8.56126E-06	5.45392E-05	0
7/14	8.56126E-06	5.45392E-05	0
7/14	8.56126E-06	5.45392E-05	0
7/14	8.56126E-06	5.45392E-05	0
7/14	8.56126E-06	5.45392E-05	0
7/14	8.56126E-06	5.45392E-05	0
7/14	8.56126E-06	5.45392E-05	0
7/14	8.56126E-06	5.45392E-05	0
8/19	9.29965E-06	5.87108E-05	0
8/19	9.29965E-06	5.87108E-05	0
8/19	9.29965E-06	5.87108E-05	0
8/19	9.29965E-06	5.87108E-05	0
8/19	9.29965E-06	5.87108E-05	0
8/19	9.29965E-06	5.87108E-05	0
8/19	9.29965E-06	5.87108E-05	0
14/58	9.84009E-06	6.19636E-05	0
14/58	9.84009E-06	6.19636E-05	0
6/10	9.9896E-06	6.22673E-05	0
6/10	9.9896E-06	6.22673E-05	0
6/10	9.9896E-06	6.22673E-05	0
6/10	9.9896E-06	6.22673E-05	0
6/10	9.9896E-06	6.22673E-05	0
6/10	9.9896E-06	6.22673E-05	0
6/10	9.9896E-06	6.22673E-05	0
6/10	9.9896E-06	6.22673E-05	0
15/66	1.05306E-05	6.55562E-05	0
13/51	1.07454E-05	6.67244E-05	0
13/51	1.07454E-05	6.67244E-05	0
9/25	1.16546E-05	7.19563E-05	0
9/25	1.16546E-05	7.19563E-05	0
9/25	1.16546E-05	7.19563E-05	0
10/31	1.16757E-05	7.19563E-05	0
10/31	1.16757E-05	7.19563E-05	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

10/31	1.16757E-05	7.19563E-05	0
19/100	1.20919E-05	7.44277E-05	0
14/59	1.21652E-05	7.47853E-05	0
16/75	1.27614E-05	7.83525E-05	0
15/67	1.27912E-05	7.84379E-05	0
13/52	1.3513E-05	8.26577E-05	0
13/52	1.3513E-05	8.26577E-05	0
11/38	1.37445E-05	8.39693E-05	0
12/45	1.42006E-05	8.66482E-05	0
20/110	1.42792E-05	8.70198E-05	0
8/20	1.46497E-05	8.89472E-05	0
8/20	1.46497E-05	8.89472E-05	0
8/20	1.46497E-05	8.89472E-05	0
14/60	1.49623E-05	9.07333E-05	0
7/15	1.5184E-05	9.10669E-05	0
7/15	1.5184E-05	9.10669E-05	0
7/15	1.5184E-05	9.10669E-05	0
7/15	1.5184E-05	9.10669E-05	0
7/15	1.5184E-05	9.10669E-05	0
7/15	1.5184E-05	9.10669E-05	0
7/15	1.5184E-05	9.10669E-05	0
7/15	1.5184E-05	9.10669E-05	0
7/15	1.5184E-05	9.10669E-05	0
10/32	1.60345E-05	9.58171E-05	0
10/32	1.60345E-05	9.58171E-05	0
10/32	1.60345E-05	9.58171E-05	0
35/261	1.67607E-05	0.000100035	0
9/26	1.68376E-05	0.000100064	0
9/26	1.68376E-05	0.000100064	0
9/26	1.68376E-05	0.000100064	0
23/139	1.68635E-05	0.000100064	0
13/53	1.68876E-05	0.000100064	0
13/53	1.68876E-05	0.000100064	0
22/130	1.7771E-05	0.000104405	0
5/7	1.79386E-05	0.000104405	0
5/7	1.79386E-05	0.000104405	0
5/7	1.79386E-05	0.000104405	0
5/7	1.79386E-05	0.000104405	0
5/7	1.79386E-05	0.000104405	0
5/7	1.79386E-05	0.000104405	0
5/7	1.79386E-05	0.000104405	0
5/7	1.79386E-05	0.000104405	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

5/7	1.79386E-05	0.000104405	0
5/7	1.79386E-05	0.000104405	0
5/7	1.79386E-05	0.000104405	0
5/7	1.79386E-05	0.000104405	0
5/7	1.79386E-05	0.000104405	0
5/7	1.79386E-05	0.000104405	0
11/39	1.8068E-05	0.000104786	0
11/39	1.8068E-05	0.000104786	0
11/39	1.8068E-05	0.000104786	0
12/46	1.81265E-05	0.000104888	0
16/77	1.81282E-05	0.000104888	0
14/61	1.83117E-05	0.000105825	0
21/121	1.84521E-05	0.000106511	0
20/112	1.88176E-05	0.000108493	0
22/131	2.01163E-05	0.000115845	0
6/11	2.08097E-05	0.000118589	0
6/11	2.08097E-05	0.000118589	0
6/11	2.08097E-05	0.000118589	0
6/11	2.08097E-05	0.000118589	0
6/11	2.08097E-05	0.000118589	0
6/11	2.08097E-05	0.000118589	0
6/11	2.08097E-05	0.000118589	0
6/11	2.08097E-05	0.000118589	0
6/11	2.08097E-05	0.000118589	0
13/54	2.09791E-05	0.000119416	0
10/33	2.17219E-05	0.000123358	0
10/33	2.17219E-05	0.000123358	0
15/70	2.23639E-05	0.000126156	0
8/21	2.23685E-05	0.000126156	0
8/21	2.23685E-05	0.000126156	0
8/21	2.23685E-05	0.000126156	0
8/21	2.23685E-05	0.000126156	0
8/21	2.23685E-05	0.000126156	0
12/47	2.29658E-05	0.000129377	0
11/40	2.35211E-05	0.000132353	0
9/27	2.38587E-05	0.000133489	0
9/27	2.38587E-05	0.000133489	0
9/27	2.38587E-05	0.000133489	0
9/27	2.38587E-05	0.000133489	0
9/27	2.38587E-05	0.000133489	0
7/16	2.55349E-05	0.00014126	0
7/16	2.55349E-05	0.00014126	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

7/16	2.55349E-05	0.00014126	0
7/16	2.55349E-05	0.00014126	0
7/16	2.55349E-05	0.00014126	0
7/16	2.55349E-05	0.00014126	0
7/16	2.55349E-05	0.00014126	0
7/16	2.55349E-05	0.00014126	0
7/16	2.55349E-05	0.00014126	0
7/16	2.55349E-05	0.00014126	0
29/203	2.66659E-05	0.000146894	0
15/71	2.67325E-05	0.000146894	0
15/71	2.67325E-05	0.000146894	0
15/71	2.67325E-05	0.000146894	0
15/71	2.67325E-05	0.000146894	0
15/71	2.67325E-05	0.000146894	0
20/115	2.80654E-05	0.000153875	0
20/115	2.80654E-05	0.000153875	0
12/48	2.88916E-05	0.000158228	0
10/34	2.90562E-05	0.000158952	0
11/41	3.03403E-05	0.000165793	0
13/56	3.18325E-05	0.000173583	0
15/72	3.18365E-05	0.000173583	0
14/64	3.2642E-05	0.000177778	0
18/98	3.27912E-05	0.000178393	0
9/28	3.32155E-05	0.000179372	0
8/22	3.32264E-05	0.000179372	0
8/22	3.32264E-05	0.000179372	0
8/22	3.32264E-05	0.000179372	0
8/22	3.32264E-05	0.000179372	0
8/22	3.32264E-05	0.000179372	0
8/22	3.32264E-05	0.000179372	0
21/126	3.46139E-05	0.000186657	0
12/49	3.61017E-05	0.000194467	0
17/90	3.70906E-05	0.000199575	0
15/73	3.77795E-05	0.00020306	0
10/35	3.84108E-05	0.000205778	0
10/35	3.84108E-05	0.000205778	0
10/35	3.84108E-05	0.000205778	0
13/57	3.88985E-05	0.000208164	0
6/12	3.94111E-05	0.000210449	0
6/12	3.94111E-05	0.000210449	0
7/17	4.10654E-05	0.000218335	0
7/17	4.10654E-05	0.000218335	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

7/17	4.10654E-05	0.000218335	0
7/17	4.10654E-05	0.000218335	0
16/82	4.1192E-05	0.000218771	0
17/91	4.29893E-05	0.000227825	0
17/91	4.29893E-05	0.000227825	0
5/8	4.53602E-05	0.000236315	0
5/8	4.53602E-05	0.000236315	0
5/8	4.53602E-05	0.000236315	0
5/8	4.53602E-05	0.000236315	0
5/8	4.53602E-05	0.000236315	0
5/8	4.53602E-05	0.000236315	0
5/8	4.53602E-05	0.000236315	0
5/8	4.53602E-05	0.000236315	0
5/8	4.53602E-05	0.000236315	0
5/8	4.53602E-05	0.000236315	0
5/8	4.53602E-05	0.000236315	0
5/8	4.53602E-05	0.000236315	0
5/8	4.53602E-05	0.000236315	0
5/8	4.53602E-05	0.000236315	0
5/8	4.53602E-05	0.000236315	0
5/8	4.53602E-05	0.000236315	0
9/29	4.55006E-05	0.000236545	0
9/29	4.55006E-05	0.000236545	0
20/119	4.66406E-05	0.000242216	0
25/168	4.72909E-05	0.000244829	0
13/58	4.72932E-05	0.000244829	0
13/58	4.72932E-05	0.000244829	0
16/83	4.8104E-05	0.000248535	0
8/23	4.81606E-05	0.000248535	0
8/23	4.81606E-05	0.000248535	0
11/43	4.92112E-05	0.000253691	0
10/36	5.02208E-05	0.000258083	0
10/36	5.02208E-05	0.000258083	0
10/36	5.02208E-05	0.000258083	0
26/179	5.12774E-05	0.000263238	0
15/75	5.26555E-05	0.000270031	0
12/51	5.53066E-05	0.000283331	0
9/30	6.14106E-05	0.000313621	0
9/30	6.14106E-05	0.000313621	0
9/30	6.14106E-05	0.000313621	0
11/44	6.19357E-05	0.000315975	0
7/18	6.3573E-05	0.000320669	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

7/18	6.3573E-05	0.000320669	0
7/18	6.3573E-05	0.000320669	0
7/18	6.3573E-05	0.000320669	0
7/18	6.3573E-05	0.000320669	0
7/18	6.3573E-05	0.000320669	0
7/18	6.3573E-05	0.000320669	0
7/18	6.3573E-05	0.000320669	0
7/18	6.3573E-05	0.000320669	0
7/18	6.3573E-05	0.000320669	0
7/18	6.3573E-05	0.000320669	0
10/37	6.49887E-05	0.000326137	0
10/37	6.49887E-05	0.000326137	0
10/37	6.49887E-05	0.000326137	0
10/37	6.49887E-05	0.000326137	0
10/37	6.49887E-05	0.000326137	0
20/122	6.70724E-05	0.000336251	0
47/417	6.72562E-05	0.000336829	0
8/24	6.82928E-05	0.000340288	0
8/24	6.82928E-05	0.000340288	0
8/24	6.82928E-05	0.000340288	0
8/24	6.82928E-05	0.000340288	0
8/24	6.82928E-05	0.000340288	0
6/13	6.93132E-05	0.000342251	0
6/13	6.93132E-05	0.000342251	0
6/13	6.93132E-05	0.000342251	0
6/13	6.93132E-05	0.000342251	0
6/13	6.93132E-05	0.000342251	0
6/13	6.93132E-05	0.000342251	0
6/13	6.93132E-05	0.000342251	0
6/13	6.93132E-05	0.000342251	0
6/13	6.93132E-05	0.000342251	0
4/5	7.23901E-05	0.000351672	0
4/5	7.23901E-05	0.000351672	0
4/5	7.23901E-05	0.000351672	0
4/5	7.23901E-05	0.000351672	0
4/5	7.23901E-05	0.000351672	0
4/5	7.23901E-05	0.000351672	0
4/5	7.23901E-05	0.000351672	0
4/5	7.23901E-05	0.000351672	0
4/5	7.23901E-05	0.000351672	0
4/5	7.23901E-05	0.000351672	0
4/5	7.23901E-05	0.000351672	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

4/5	7.23901E-05	0.000351672	0
4/5	7.23901E-05	0.000351672	0
4/5	7.23901E-05	0.000351672	0
4/5	7.23901E-05	0.000351672	0
4/5	7.23901E-05	0.000351672	0
15/77	7.24367E-05	0.000351672	0
16/86	7.53469E-05	0.00036508	0
16/86	7.53469E-05	0.00036508	0
11/45	7.73795E-05	0.000374559	0
9/31	8.17568E-05	0.000394583	0
9/31	8.17568E-05	0.000394583	0
9/31	8.17568E-05	0.000394583	0
13/61	8.26129E-05	0.000398324	0
24/164	8.70685E-05	0.000419396	0
19/115	9.07471E-05	0.000436687	0
14/70	9.27481E-05	0.00044588	0
8/25	9.49462E-05	0.000452954	0
8/25	9.49462E-05	0.000452954	0
8/25	9.49462E-05	0.000452954	0
7/19	9.52326E-05	0.000452954	0
7/19	9.52326E-05	0.000452954	0
7/19	9.52326E-05	0.000452954	0
7/19	9.52326E-05	0.000452954	0
7/19	9.52326E-05	0.000452954	0
7/19	9.52326E-05	0.000452954	0
7/19	9.52326E-05	0.000452954	0
7/19	9.52326E-05	0.000452954	0
5/9	9.67857E-05	0.000453326	0
5/9	9.67857E-05	0.000453326	0
5/9	9.67857E-05	0.000453326	0
5/9	9.67857E-05	0.000453326	0
5/9	9.67857E-05	0.000453326	0
5/9	9.67857E-05	0.000453326	0
5/9	9.67857E-05	0.000453326	0
5/9	9.67857E-05	0.000453326	0
5/9	9.67857E-05	0.000453326	0
5/9	9.67857E-05	0.000453326	0
5/9	9.67857E-05	0.000453326	0
5/9	9.67857E-05	0.000453326	0
5/9	9.67857E-05	0.000453326	0
5/9	9.67857E-05	0.000453326	0
5/9	9.67857E-05	0.000453326	0
5/9	9.67857E-05	0.000453326	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

5/9	9.67857E-05	0.000453326	0
13/62	9.86133E-05	0.000461446	0
17/97	9.91329E-05	0.000463437	0
31/240	0.00010127	0.00047298	0
10/39	0.000105781	0.000493109	0
10/39	0.000105781	0.000493109	0
9/32	0.000107474	0.000500056	0
9/32	0.000107474	0.000500056	0
38/320	0.000111033	0.000516125	0
6/14	0.000114877	0.000528007	0
6/14	0.000114877	0.000528007	0
6/14	0.000114877	0.000528007	0
6/14	0.000114877	0.000528007	0
6/14	0.000114877	0.000528007	0
6/14	0.000114877	0.000528007	0
6/14	0.000114877	0.000528007	0
6/14	0.000114877	0.000528007	0
6/14	0.000114877	0.000528007	0
6/14	0.000114877	0.000528007	0
6/14	0.000114877	0.000528007	0
6/14	0.000114877	0.000528007	0
40/345	0.000124954	0.000573784	0
14/72	0.000127579	0.000584748	0
14/72	0.000127579	0.000584748	0
8/26	0.000129661	0.000593185	0
8/26	0.000129661	0.000593185	0
10/40	0.000133201	0.00060712	0
10/40	0.000133201	0.00060712	0
10/40	0.000133201	0.00060712	0
10/40	0.000133201	0.00060712	0
7/20	0.000138624	0.000629503	0
7/20	0.000138624	0.000629503	0
7/20	0.000138624	0.000629503	0
7/20	0.000138624	0.000629503	0
9/33	0.000139632	0.000632912	0
9/33	0.000139632	0.000632912	0
47/430	0.000140483	0.000636182	0
23/159	0.000144661	0.000654499	0
12/56	0.000145574	0.000657422	0
12/56	0.000145574	0.000657422	0
14/73	0.000148888	0.000671155	0
14/73	0.000148888	0.000671155	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

16/91	0.000151216	0.000681025	0
50/468	0.000153282	0.000689698	0
24/170	0.000153751	0.000691177	0
20/130	0.00016518	0.000741876	0
17/101	0.000165629	0.000743214	0
10/41	0.000166382	0.000745234	0
10/41	0.000166382	0.000745234	0
14/74	0.000173204	0.000775083	0
12/57	0.000174021	0.000776055	0
12/57	0.000174021	0.000776055	0
8/27	0.00017421	0.000776055	0
8/27	0.00017421	0.000776055	0
8/27	0.00017421	0.000776055	0
15/83	0.000175626	0.000781656	0
9/34	0.000179439	0.00079547	0
9/34	0.000179439	0.00079547	0
6/15	0.00018134	0.00079547	0
6/15	0.00018134	0.00079547	0
6/15	0.00018134	0.00079547	0
6/15	0.00018134	0.00079547	0
6/15	0.00018134	0.00079547	0
6/15	0.00018134	0.00079547	0
6/15	0.00018134	0.00079547	0
5/10	0.000183583	0.00079547	0
5/10	0.000183583	0.00079547	0
5/10	0.000183583	0.00079547	0
5/10	0.000183583	0.00079547	0
5/10	0.000183583	0.00079547	0
5/10	0.000183583	0.00079547	0
5/10	0.000183583	0.00079547	0
5/10	0.000183583	0.00079547	0
5/10	0.000183583	0.00079547	0
5/10	0.000183583	0.00079547	0
5/10	0.000183583	0.00079547	0
5/10	0.000183583	0.00079547	0
5/10	0.000183583	0.00079547	0
5/10	0.000183583	0.00079547	0
5/10	0.000183583	0.00079547	0
5/10	0.000183583	0.00079547	0
5/10	0.000183583	0.00079547	0
5/10	0.000183583	0.00079547	0
5/10	0.000183583	0.00079547	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

5/10	0.000183583	0.00079547	0
5/10	0.000183583	0.00079547	0
13/66	0.000192295	0.000831758	0
13/66	0.000192295	0.000831758	0
7/21	0.000196752	0.000845826	0
7/21	0.000196752	0.000845826	0
7/21	0.000196752	0.000845826	0
7/21	0.000196752	0.000845826	0
7/21	0.000196752	0.000845826	0
7/21	0.000196752	0.000845826	0
7/21	0.000196752	0.000845826	0
36/306	0.00020004	0.00085921	0
15/84	0.000201628	0.000865277	0
21/142	0.000202346	0.000867601	0
4/6	0.000206361	0.000868906	0
4/6	0.000206361	0.000868906	0
4/6	0.000206361	0.000868906	0
4/6	0.000206361	0.000868906	0
4/6	0.000206361	0.000868906	0
4/6	0.000206361	0.000868906	0
4/6	0.000206361	0.000868906	0
4/6	0.000206361	0.000868906	0
4/6	0.000206361	0.000868906	0
4/6	0.000206361	0.000868906	0
4/6	0.000206361	0.000868906	0
4/6	0.000206361	0.000868906	0
4/6	0.000206361	0.000868906	0
4/6	0.000206361	0.000868906	0
4/6	0.000206361	0.000868906	0
4/6	0.000206361	0.000868906	0
4/6	0.000206361	0.000868906	0
4/6	0.000206361	0.000868906	0
4/6	0.000206361	0.000868906	0
4/6	0.000206361	0.000868906	0
12/58	0.000207081	0.000871191	0
11/50	0.000213514	0.000896721	0
11/50	0.000213514	0.000896721	0
8/28	0.000230608	0.000965218	0
8/28	0.000230608	0.000965218	0
8/28	0.000230608	0.000965218	0
8/28	0.000230608	0.000965218	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

14/76	0.000232261	0.000971309	0
18/114	0.000247417	0.001033813	0
10/43	0.00025384	0.001057058	0
10/43	0.00025384	0.001057058	0
10/43	0.00025384	0.001057058	0
10/43	0.00025384	0.001057058	0
13/68	0.000262603	0.001092623	0
7/22	0.000273064	0.001135189	0
6/16	0.000274824	0.001136741	0
6/16	0.000274824	0.001136741	0
6/16	0.000274824	0.001136741	0
6/16	0.000274824	0.001136741	0
6/16	0.000274824	0.001136741	0
6/16	0.000274824	0.001136741	0
9/36	0.000287603	0.001187599	0
9/36	0.000287603	0.001187599	0
17/106	0.000301094	0.001239277	0
8/29	0.000301126	0.001239277	0
8/29	0.000301126	0.001239277	0
8/29	0.000301126	0.001239277	0
11/52	0.000307775	0.001264528	0
11/52	0.000307775	0.001264528	0
10/44	0.000310283	0.001272703	0
10/44	0.000310283	0.001272703	0
5/11	0.000319228	0.001287909	0
5/11	0.000319228	0.001287909	0
5/11	0.000319228	0.001287909	0
5/11	0.000319228	0.001287909	0
5/11	0.000319228	0.001287909	0
5/11	0.000319228	0.001287909	0
5/11	0.000319228	0.001287909	0
5/11	0.000319228	0.001287909	0
5/11	0.000319228	0.001287909	0
5/11	0.000319228	0.001287909	0
5/11	0.000319228	0.001287909	0
5/11	0.000319228	0.001287909	0
5/11	0.000319228	0.001287909	0
5/11	0.000319228	0.001287909	0
5/11	0.000319228	0.001287909	0
5/11	0.000319228	0.001287909	0
5/11	0.000319228	0.001287909	0
5/11	0.000319228	0.001287909	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

5/11	0.000319228	0.001287909	0
5/11	0.000319228	0.001287909	0
32/268	0.000338731	0.001365474	0
12/61	0.000340106	0.001369894	0
14/79	0.000352963	0.001420516	0
13/70	0.000353779	0.001421473	0
13/70	0.000353779	0.001421473	0
9/37	0.000359158	0.001441908	0
11/53	0.000366708	0.001471022	0
7/23	0.00037146	0.001485235	0
7/23	0.00037146	0.001485235	0
7/23	0.00037146	0.001485235	0
7/23	0.00037146	0.001485235	0
18/118	0.00038226	0.001527175	0
15/89	0.000387626	0.001546264	0
8/30	0.000388295	0.001546264	0
8/30	0.000388295	0.001546264	0
8/30	0.000388295	0.001546264	0
6/17	0.00040233	0.001591841	0
6/17	0.00040233	0.001591841	0
6/17	0.00040233	0.001591841	0
6/17	0.00040233	0.001591841	0
6/17	0.00040233	0.001591841	0
6/17	0.00040233	0.001591841	0
6/17	0.00040233	0.001591841	0
6/17	0.00040233	0.001591841	0
14/80	0.000403602	0.00159431	0
14/80	0.000403602	0.00159431	0
13/71	0.000408651	0.001611666	0
13/71	0.000408651	0.001611666	0
9/38	0.000444772	0.001745722	0
9/38	0.000444772	0.001745722	0
9/38	0.000444772	0.001745722	0
9/38	0.000444772	0.001745722	0
9/38	0.000444772	0.001745722	0
9/38	0.000444772	0.001745722	0
10/46	0.000454834	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
4/7	0.000457593	0.001752679	0
12/63	0.000464145	0.001775012	0
12/63	0.000464145	0.001775012	0
13/72	0.000470583	0.001798233	0
8/31	0.000494918	0.001889756	0
7/24	0.000496294	0.001890606	0
7/24	0.000496294	0.001890606	0
7/24	0.000496294	0.001890606	0
16/101	0.000515823	0.001954765	0
5/12	0.000519098	0.001954765	0
5/12	0.000519098	0.001954765	0
5/12	0.000519098	0.001954765	0
5/12	0.000519098	0.001954765	0
5/12	0.000519098	0.001954765	0
5/12	0.000519098	0.001954765	0
5/12	0.000519098	0.001954765	0
5/12	0.000519098	0.001954765	0
5/12	0.000519098	0.001954765	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

5/12	0.000519098	0.001954765	0
5/12	0.000519098	0.001954765	0
5/12	0.000519098	0.001954765	0
5/12	0.000519098	0.001954765	0
5/12	0.000519098	0.001954765	0
14/82	0.000523669	0.001967542	0
17/111	0.000523691	0.001967542	0
17/111	0.000523691	0.001967542	0
12/64	0.000539229	0.002024373	0
15/92	0.000558355	0.002092978	0
15/92	0.000558355	0.002092978	0
6/18	0.000571709	0.002126827	0
6/18	0.000571709	0.002126827	0
6/18	0.000571709	0.002126827	0
6/18	0.000571709	0.002126827	0
6/18	0.000571709	0.002126827	0
6/18	0.000571709	0.002126827	0
6/18	0.000571709	0.002126827	0
6/18	0.000571709	0.002126827	0
6/18	0.000571709	0.002126827	0
6/18	0.000571709	0.002126827	0
16/102	0.000576932	0.002144635	0
23/175	0.000592701	0.002201587	0
8/32	0.000624066	0.00231358	0
8/32	0.000624066	0.00231358	0
12/65	0.000624262	0.00231358	0
15/93	0.000627935	0.00232544	0
22/165	0.000633931	0.002345879	0
10/48	0.00065128	0.002406883	0
7/25	0.000652374	0.002406883	0
7/25	0.000652374	0.002406883	0
7/25	0.000652374	0.002406883	0
9/40	0.000666452	0.002456979	0
15/94	0.00070476	0.002596263	0
11/57	0.000705723	0.00259725	0
13/75	0.000706085	0.00259725	0
16/104	0.000717901	0.002638743	0
12/66	0.000720255	0.002645417	0
21/156	0.000734114	0.002694308	0
14/85	0.000759959	0.002787085	0
20/146	0.000777581	0.002848731	0
8/33	0.000779086	0.002848731	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

8/33	0.000779086	0.002848731	0
8/33	0.000779086	0.002848731	0
6/19	0.000791622	0.002874694	0
6/19	0.000791622	0.002874694	0
6/19	0.000791622	0.002874694	0
6/19	0.000791622	0.002874694	0
6/19	0.000791622	0.002874694	0
6/19	0.000791622	0.002874694	0
6/19	0.000791622	0.002874694	0
6/19	0.000791622	0.002874694	0
6/19	0.000791622	0.002874694	0
5/13	0.000800215	0.002874694	0
5/13	0.000800215	0.002874694	0
5/13	0.000800215	0.002874694	0
5/13	0.000800215	0.002874694	0
5/13	0.000800215	0.002874694	0
5/13	0.000800215	0.002874694	0
5/13	0.000800215	0.002874694	0
5/13	0.000800215	0.002874694	0
5/13	0.000800215	0.002874694	0
5/13	0.000800215	0.002874694	0
5/13	0.000800215	0.002874694	0
5/13	0.000800215	0.002874694	0
5/13	0.000800215	0.002874694	0
5/13	0.000800215	0.002874694	0
5/13	0.000800215	0.002874694	0
13/76	0.000803858	0.002885674	0
19/136	0.000817205	0.002931446	0
11/58	0.000822427	0.002945882	0
11/58	0.000822427	0.002945882	0
7/26	0.000844953	0.003017778	0
7/26	0.000844953	0.003017778	0
7/26	0.000844953	0.003017778	0
7/26	0.000844953	0.003017778	0
14/86	0.000856444	0.003036063	0
21/158	0.000868007	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
4/8	0.000869828	0.003036063	0
24/191	0.000872875	0.00304454	0
15/96	0.000882558	0.003076129	0
13/77	0.00091275	0.003179109	0
8/34	0.000963593	0.00335145	0
8/34	0.000963593	0.00335145	0
9/42	0.000970964	0.003372318	0
9/42	0.000970964	0.003372318	0
6/20	0.00107148	0.00370312	0
6/20	0.00107148	0.00370312	0
6/20	0.00107148	0.00370312	0
6/20	0.00107148	0.00370312	0
6/20	0.00107148	0.00370312	0
6/20	0.00107148	0.00370312	0
6/20	0.00107148	0.00370312	0
7/27	0.001079714	0.003726774	0
14/88	0.001080598	0.003726774	0
14/88	0.001080598	0.003726774	0
12/69	0.001085127	0.003739774	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

13/79	0.001167819	0.004021944	0
5/14	0.00118096	0.004029456	0
5/14	0.00118096	0.004029456	0
5/14	0.00118096	0.004029456	0
5/14	0.00118096	0.004029456	0
5/14	0.00118096	0.004029456	0
5/14	0.00118096	0.004029456	0
5/14	0.00118096	0.004029456	0
5/14	0.00118096	0.004029456	0
5/14	0.00118096	0.004029456	0
5/14	0.00118096	0.004029456	0
5/14	0.00118096	0.004029456	0
5/14	0.00118096	0.004029456	0
5/14	0.00118096	0.004029456	0
5/14	0.00118096	0.004029456	0
8/35	0.001181471	0.004029456	0
12/70	0.001236442	0.004214012	0
10/52	0.001255079	0.004268657	0
10/52	0.001255079	0.004268657	0
10/52	0.001255079	0.004268657	0
11/61	0.001272073	0.004323465	0
13/80	0.001316101	0.004470016	0
14/90	0.001352023	0.004587667	0
15/100	0.001353539	0.004587667	0
15/100	0.001353539	0.004587667	0
7/28	0.001362751	0.00460936	0
7/28	0.001362751	0.00460936	0
7/28	0.001362751	0.00460936	0
9/44	0.001379495	0.004656388	0
9/44	0.001379495	0.004656388	0
9/44	0.001379495	0.004656388	0
6/21	0.001421373	0.004774804	0
6/21	0.001421373	0.004774804	0
6/21	0.001421373	0.004774804	0
6/21	0.001421373	0.004774804	0
6/21	0.001421373	0.004774804	0
6/21	0.001421373	0.004774804	0
6/21	0.001421373	0.004774804	0
8/36	0.001436863	0.004813687	0
8/36	0.001436863	0.004813687	0
8/36	0.001436863	0.004813687	0
8/36	0.001436863	0.004813687	0
11/62	0.001460585	0.004889827	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

4/9	0.001488265	0.004912273	0
4/9	0.001488265	0.004912273	0
4/9	0.001488265	0.004912273	0
4/9	0.001488265	0.004912273	0
4/9	0.001488265	0.004912273	0
4/9	0.001488265	0.004912273	0
4/9	0.001488265	0.004912273	0
4/9	0.001488265	0.004912273	0
4/9	0.001488265	0.004912273	0
4/9	0.001488265	0.004912273	0
4/9	0.001488265	0.004912273	0
4/9	0.001488265	0.004912273	0
4/9	0.001488265	0.004912273	0
4/9	0.001488265	0.004912273	0
4/9	0.001488265	0.004912273	0
4/9	0.001488265	0.004912273	0
4/9	0.001488265	0.004912273	0
4/9	0.001488265	0.004912273	0
4/9	0.001488265	0.004912273	0
4/9	0.001488265	0.004912273	0
17/122	0.001545714	0.005098472	0
16/112	0.001611814	0.005312938	0
9/45	0.001630163	0.005362636	0
9/45	0.001630163	0.005362636	0
9/45	0.001630163	0.005362636	0
13/82	0.001659832	0.005456585	0
11/63	0.001671371	0.005463341	0
14/92	0.00167817	0.005463341	0
14/92	0.00167817	0.005463341	0
5/15	0.001680772	0.005463341	0
5/15	0.001680772	0.005463341	0
5/15	0.001680772	0.005463341	0
5/15	0.001680772	0.005463341	0
5/15	0.001680772	0.005463341	0
5/15	0.001680772	0.005463341	0
5/15	0.001680772	0.005463341	0
5/15	0.001680772	0.005463341	0
5/15	0.001680772	0.005463341	0
5/15	0.001680772	0.005463341	0
5/15	0.001680772	0.005463341	0
5/15	0.001680772	0.005463341	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

5/15	0.001680772	0.005463341	0
5/15	0.001680772	0.005463341	0
17/123	0.001691486	0.005494535	0
10/54	0.001695052	0.005502149	0
7/29	0.001700542	0.005502149	0
7/29	0.001700542	0.005502149	0
7/29	0.001700542	0.005502149	0
7/29	0.001700542	0.005502149	0
7/29	0.001700542	0.005502149	0
8/37	0.001734162	0.005607238	0
12/73	0.001798478	0.005811377	0
6/22	0.001851991	0.005964697	0
6/22	0.001851991	0.005964697	0
6/22	0.001851991	0.005964697	0
6/22	0.001851991	0.005964697	0
6/22	0.001851991	0.005964697	0
11/64	0.001906344	0.006131721	0
11/64	0.001906344	0.006131721	0
9/46	0.001916055	0.006158926	0
8/38	0.002078	0.006675118	0
7/30	0.002099923	0.00673674	0
7/30	0.002099923	0.00673674	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
3/5	0.002218847	0.006854454	0
9/47	0.002240593	0.006917286	0
5/16	0.002319841	0.007041242	0
5/16	0.002319841	0.007041242	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

5/16	0.002319841	0.007041242	0
5/16	0.002319841	0.007041242	0
5/16	0.002319841	0.007041242	0
5/16	0.002319841	0.007041242	0
5/16	0.002319841	0.007041242	0
5/16	0.002319841	0.007041242	0
5/16	0.002319841	0.007041242	0
5/16	0.002319841	0.007041242	0
5/16	0.002319841	0.007041242	0
5/16	0.002319841	0.007041242	0
5/16	0.002319841	0.007041242	0
5/16	0.002319841	0.007041242	0
5/16	0.002319841	0.007041242	0
5/16	0.002319841	0.007041242	0
5/16	0.002319841	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
4/10	0.002358057	0.007041242	0
21/171	0.00236159	0.007047511	0
6/23	0.002374533	0.007064704	0
6/23	0.002374533	0.007064704	0
6/23	0.002374533	0.007064704	0
6/23	0.002374533	0.007064704	0
6/23	0.002374533	0.007064704	0
11/66	0.002456961	0.007305524	0
8/39	0.002473235	0.007349469	0
12/76	0.00255492	0.007587619	0
7/31	0.002568051	0.007622013	0
10/57	0.002581177	0.007656349	0
9/48	0.002607359	0.007724693	0
9/48	0.002607359	0.007724693	0
17/129	0.002830333	0.008380239	0
12/77	0.002858091	0.008457334	0
8/40	0.002924933	0.00863953	0
8/40	0.002924933	0.00863953	0
8/40	0.002924933	0.00863953	0
6/24	0.003000615	0.008847138	0
6/24	0.003000615	0.008847138	0
6/24	0.003000615	0.008847138	0
7/32	0.003112369	0.009113664	0
7/32	0.003112369	0.009113664	0
7/32	0.003112369	0.009113664	0
7/32	0.003112369	0.009113664	0
7/32	0.003112369	0.009113664	0
7/32	0.003112369	0.009113664	0
5/17	0.003118808	0.009113664	0
5/17	0.003118808	0.009113664	0
5/17	0.003118808	0.009113664	0
5/17	0.003118808	0.009113664	0
5/17	0.003118808	0.009113664	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

5/17	0.003118808	0.009113664	0
5/17	0.003118808	0.009113664	0
5/17	0.003118808	0.009113664	0
5/17	0.003118808	0.009113664	0
41/420	0.00318855	0.009311929	0
8/41	0.003438349	0.010029537	0
8/41	0.003438349	0.010029537	0
9/50	0.003482628	0.010132541	0
4/11	0.003523108	0.010132541	0
4/11	0.003523108	0.010132541	0
4/11	0.003523108	0.010132541	0
4/11	0.003523108	0.010132541	0
4/11	0.003523108	0.010132541	0
4/11	0.003523108	0.010132541	0
4/11	0.003523108	0.010132541	0
4/11	0.003523108	0.010132541	0
4/11	0.003523108	0.010132541	0
4/11	0.003523108	0.010132541	0
4/11	0.003523108	0.010132541	0
4/11	0.003523108	0.010132541	0
4/11	0.003523108	0.010132541	0
4/11	0.003523108	0.010132541	0
4/11	0.003523108	0.010132541	0
4/11	0.003523108	0.010132541	0
4/11	0.003523108	0.010132541	0
4/11	0.003523108	0.010132541	0
4/11	0.003523108	0.010132541	0
4/11	0.003523108	0.010132541	0
4/11	0.003523108	0.010132541	0
4/11	0.003523108	0.010132541	0
4/11	0.003523108	0.010132541	0
4/11	0.003523108	0.010132541	0
12/79	0.003551939	0.010209489	0
18/143	0.003581539	0.010288556	0
7/33	0.003740562	0.010681358	0
7/33	0.003740562	0.010681358	0
7/33	0.003740562	0.010681358	0
6/25	0.003742168	0.010681358	0
6/25	0.003742168	0.010681358	0
6/25	0.003742168	0.010681358	0
6/25	0.003742168	0.010681358	0
6/25	0.003742168	0.010681358	0
6/25	0.003742168	0.010681358	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

6/25	0.003742168	0.010681358	0
6/25	0.003742168	0.010681358	0
21/178	0.00382239	0.010904011	0
13/90	0.003856698	0.010995501	0
11/70	0.003942505	0.011233627	0
9/51	0.003998999	0.011381409	0
9/51	0.003998999	0.011381409	0
8/42	0.004018911	0.011424858	0
8/42	0.004018911	0.011424858	0
5/18	0.004098464	0.011577396	0
5/18	0.004098464	0.011577396	0
5/18	0.004098464	0.011577396	0
5/18	0.004098464	0.011577396	0
5/18	0.004098464	0.011577396	0
5/18	0.004098464	0.011577396	0
5/18	0.004098464	0.011577396	0
5/18	0.004098464	0.011577396	0
5/18	0.004098464	0.011577396	0
5/18	0.004098464	0.011577396	0
15/112	0.004175045	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
3/6	0.004231344	0.011684306	0
10/61	0.004300887	0.011869676	0
12/81	0.004375508	0.012068842	0
11/71	0.004407751	0.012150963	0
7/34	0.004460519	0.012275788	0
7/34	0.004460519	0.012275788	0
7/34	0.004460519	0.012275788	0
20/169	0.004526536	0.012450505	0
9/52	0.004573309	0.012551078	0
9/52	0.004573309	0.012551078	0
9/52	0.004573309	0.012551078	0
9/52	0.004573309	0.012551078	0
6/26	0.004611335	0.012613205	0
6/26	0.004611335	0.012613205	0
6/26	0.004611335	0.012613205	0
6/26	0.004611335	0.012613205	0
6/26	0.004611335	0.012613205	0
6/26	0.004611335	0.012613205	0
8/43	0.004672197	0.012765481	0
8/43	0.004672197	0.012765481	0
23/205	0.00477968	0.013051898	0
10/62	0.0048471	0.013228657	0
11/72	0.004915573	0.013408091	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
4/12	0.005025119	0.01348992	0
9/53	0.00520978	0.013978014	0
5/19	0.005279483	0.014075031	0
5/19	0.005279483	0.014075031	0
5/19	0.005279483	0.014075031	0
5/19	0.005279483	0.014075031	0
5/19	0.005279483	0.014075031	0
5/19	0.005279483	0.014075031	0
5/19	0.005279483	0.014075031	0
5/19	0.005279483	0.014075031	0
7/35	0.005280283	0.014075031	0
7/35	0.005280283	0.014075031	0
7/35	0.005280283	0.014075031	0
7/35	0.005280283	0.014075031	0
12/83	0.005345279	0.014240566	0
8/44	0.005403911	0.014388972	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

11/73	0.005468607	0.014553361	0
26/244	0.005609588	0.014916885	0
6/27	0.005620372	0.014916885	0
6/27	0.005620372	0.014916885	0
6/27	0.005620372	0.014916885	0
6/27	0.005620372	0.014916885	0
9/54	0.005912727	0.015675899	0
9/54	0.005912727	0.015675899	0
11/74	0.006069549	0.016082996	0
7/36	0.006208007	0.016423336	0
7/36	0.006208007	0.016423336	0
7/36	0.006208007	0.016423336	0
14/106	0.00626904	0.016575882	0
5/20	0.006682155	0.017613508	0
5/20	0.006682155	0.017613508	0
5/20	0.006682155	0.017613508	0
5/20	0.006682155	0.017613508	0
5/20	0.006682155	0.017613508	0
9/55	0.006686543	0.017613508	0
9/55	0.006686543	0.017613508	0
6/28	0.006781544	0.017825565	0
6/28	0.006781544	0.017825565	0
6/28	0.006781544	0.017825565	0
6/28	0.006781544	0.017825565	0
10/65	0.006817179	0.017909661	0
4/13	0.00690286	0.01792017	0
4/13	0.00690286	0.01792017	0
4/13	0.00690286	0.01792017	0
4/13	0.00690286	0.01792017	0
4/13	0.00690286	0.01792017	0
4/13	0.00690286	0.01792017	0
4/13	0.00690286	0.01792017	0
4/13	0.00690286	0.01792017	0
4/13	0.00690286	0.01792017	0
4/13	0.00690286	0.01792017	0
4/13	0.00690286	0.01792017	0
4/13	0.00690286	0.01792017	0
4/13	0.00690286	0.01792017	0
4/13	0.00690286	0.01792017	0
4/13	0.00690286	0.01792017	0
4/13	0.00690286	0.01792017	0
4/13	0.00690286	0.01792017	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

4/13	0.00690286	0.01792017	0
4/13	0.00690286	0.01792017	0
4/13	0.00690286	0.01792017	0
4/13	0.00690286	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
3/7	0.007061669	0.01792017	0
8/46	0.007125924	0.018064584	0
8/46	0.007125924	0.018064584	0
23/212	0.007147399	0.018109691	0
7/37	0.007251907	0.018365026	0
34/351	0.007634094	0.01932294	0
6/29	0.008107026	0.020488362	0
6/29	0.008107026	0.020488362	0
6/29	0.008107026	0.020488362	0
8/47	0.008128045	0.020530932	0
5/21	0.008326153	0.020988222	0
5/21	0.008326153	0.020988222	0
5/21	0.008326153	0.020988222	0
5/21	0.008326153	0.020988222	0
10/67	0.008441215	0.021267364	0
9/57	0.008464656	0.021315503	0
18/156	0.008836685	0.02224095	0
4/14	0.009191627	0.022923135	0
4/14	0.009191627	0.022923135	0
4/14	0.009191627	0.022923135	0
4/14	0.009191627	0.022923135	0
4/14	0.009191627	0.022923135	0
4/14	0.009191627	0.022923135	0
4/14	0.009191627	0.022923135	0
4/14	0.009191627	0.022923135	0
4/14	0.009191627	0.022923135	0
4/14	0.009191627	0.022923135	0
4/14	0.009191627	0.022923135	0
4/14	0.009191627	0.022923135	0
4/14	0.009191627	0.022923135	0
4/14	0.009191627	0.022923135	0
4/14	0.009191627	0.022923135	0
4/14	0.009191627	0.022923135	0
4/14	0.009191627	0.022923135	0
4/14	0.009191627	0.022923135	0
8/48	0.009232184	0.023012611	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

14/111	0.009351335	0.023276602	0
10/68	0.009357024	0.023276602	0
10/68	0.009357024	0.023276602	0
10/68	0.009357024	0.023276602	0
9/58	0.009477998	0.02355371	0
9/58	0.009477998	0.02355371	0
6/30	0.009608805	0.023830611	0
6/30	0.009608805	0.023830611	0
6/30	0.009608805	0.023830611	0
6/30	0.009608805	0.023830611	0
11/79	0.009890698	0.024505015	0
11/79	0.009890698	0.024505015	0

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

Old Adjusted P-value	Odds Ratio	Combined Score
0	13.99243297	5088.454801
0	11.54025593	2792.215279
0	15.76808499	3743.323233
0	7.184135501	1108.546003
0	14.9724007	2167.176413
0	12.91436847	1798.384452
0	4.997460911	594.0512477
0	4.84772344	562.7459842
0	7.814218481	895.2893311
0	6.147415109	690.820381
0	19.1873566	2127.328421
0	6.060969305	663.7997897
0	5.190480639	565.5889756
0	3.710575934	389.092187
0	6.770517319	707.3349645
0	6.828989829	699.8572047
0	19.56268222	1964.659783
0	8.097943472	786.9697352
0	3.965260753	378.4567375
0	6.219115522	573.2639216
0	5.446886976	502.0286894
0	11.78549599	1059.872079
0	26.67759173	2346.40505
0	23.84393199	2067.725484
0	3.414153416	283.762283
0	13.93746074	1143.587819
0	7.647875876	626.259171
0	23.04987284	1859.207766
0	19.06699251	1532.668468
0	8.902720494	706.1847557
0	23.28233831	1844.087585
0	23.28233831	1844.087585
0	11.55066065	896.5974074
0	9.169198002	709.6681174
0	11.57632317	870.1546242
0	12.77033493	955.4756796
0	5.96122281	445.5236033
0	19.39572968	1444.113718
0	15.55740433	1155.759794
0	35.68374176	2630.28725
0	23.78580957	1691.215076

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	6.460920448	458.3604153
0	6.979636775	491.8254265
0	9.859196764	692.4204943
0	9.301443998	652.9656635
0	7.74462813	539.8003334
0	19.12202598	1324.69958
0	7.521736245	514.2152668
0	7.142182073	484.7354425
0	4.301439987	289.3205485
0	9.085452774	598.9488972
0	23.77900192	1567.12786
0	4.769885879	312.3492692
0	15.48509934	1011.827216
0	11.53969394	748.5980699
0	6.264771625	402.4305159
0	8.163004098	521.1967909
0	6.172525517	386.8532985
0	28.1938971	1748.276888
0	15.09222747	931.833347
0	30.73502871	1893.470866
0	7.683941555	471.9116934
0	8.765507519	537.1884338
0	6.61765511	401.8875869
0	8.779836962	529.0470264
0	15.02906547	860.8286884
0	10.18653231	583.0341032
0	15.84250869	903.6728165
0	11.27609721	637.7765078
0	16.30936819	916.5819195
0	4.502740621	250.9899211
0	3.946522049	219.0066329
0	3.634711701	197.3075277
0	11.87638951	642.9153777
0	30.63777596	1656.251327
0	12.0340099	639.861375
0	5.732827049	298.1549803
0	15.37797864	798.8380093
0	15.37797864	798.8380093
0	3.814548163	197.8811574
0	14.17254588	731.5748498
0	3.80048475	194.389328
0	13.46247944	679.4789726

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	9.10673138	459.1225132
0	12.5959596	633.7301696
0	16.37976483	823.1466889
0	16.98919789	839.8469587
0	5.794452683	285.4258283
0	5.057427869	247.2561469
0	17.69325269	860.5304846
0	17.69325269	860.5304846
0	11.96345029	571.82486
0	12.15348455	569.2643071
0	4.483054953	207.0728791
0	15.33087633	705.234839
0	12.36260964	567.2833722
0	6.978781222	317.0841037
0	11.35904398	514.9497085
0	15.86710895	716.3543751
0	9.146099547	410.8886803
0	18.77707219	843.2189702
0	10.55259933	473.8278512
0	8.33575111	372.2699229
0	9.89047619	440.7959301
0	5.44575336	242.5631001
0	299984	13331254.98
0	12.27826087	545.3235864
0	258.2787682	11465.8899
0	5.682928262	248.6654796
0	7.366738101	318.5544415
0	4.369083888	188.7433313
0	30.49308381	1303.282717
0	10.04516149	427.525139
0	15.88489819	669.95033
0	6.111351517	257.3714801
0	27.95050176	1167.195464
0	4.40555782	183.7680623
0	15.29575163	635.4310929
0	68.41240876	2828.953051
0	18.18534918	749.7798515
0	8.251080391	340.0959076
0	8.251080391	340.0959076
0	2.592427588	106.6865794
0	12.68894085	520.849036
0	14.74868697	603.6442386

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	7.252732307	296.3894512
0	5.579163404	227.4510929
0	5.107705389	208.0456039
0	17.35781551	703.5385948
0	5.627446535	226.600598
0	4.930296329	198.0614971
0	18.31687042	728.0931103
0	6.925282291	274.2686157
0	8.021470746	316.6186757
0	6.201692765	242.8798067
0	5.230340238	202.0586105
0	1.980367583	76.32260863
0	6.626000018	254.4203874
0	5.976925601	227.6166575
0	9.08820223	345.5709378
0	7.477477477	282.2643195
0	10.57016211	397.1830561
0	6.798385705	253.275097
0	9.776778713	364.1291192
0	15.2607987	565.9471058
0	15.2607987	565.9471058
0	25.36826428	940.3945417
0	9.136302018	338.1217599
0	21.32325203	785.4234084
0	7.092497626	258.5198792
0	7.002344116	253.0317463
0	7.910060037	285.0966676
0	3.92015765	140.5874187
0	6.614028198	235.7087986
0	10.86164861	386.6762981
0	10.86164861	386.6762981
0	15.24918567	542.8524634
0	15.24918567	542.8524634
0	11.68283313	415.8508359
0	3.785831286	134.5764102
0	16.76314076	593.4331224
0	5.580174553	196.9361453
0	5.580174553	196.9361453
0	3.3876575	119.3116197
0	4.20131967	147.2952049
0	7.912143746	277.0640667
0	9.245925396	323.4220758

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	6.663453815	232.659746
0	6.889813175	239.789008
0	24.0802895	836.8416769
0	7.914740437	269.0456543
0	7.545756295	256.4340452
0	9.825105042	332.0794198
0	9.825105042	332.0794198
0	7.431028911	250.0504466
0	56.87196602	1912.756276
0	14.57430927	488.2633871
0	2.66832265	89.21893894
0	7.658606557	255.0196795
0	9.92722449	325.5663917
0	7.106799348	232.2162305
0	19.26114719	623.219997
0	5.014330506	161.7828607
0	7.921688684	253.0510393
0	6.103609076	194.7641916
0	12.89059273	409.7689676
0	11.6866721	370.4196403
0	7.085172498	224.2638851
0	18.05636161	571.1913509
0	13.90053022	436.8586498
0	5.967333699	187.204201
0	10.45840028	326.7594697
0	15.21445979	473.7514916
0	15.21445979	473.7514916
0	5.168764937	159.7919916
0	19.53597497	603.2547234
0	13.32063008	411.0652024
0	3.831756198	117.760633
0	5.260162058	161.1046412
0	7.391993999	226.0222486
0	7.152777045	214.0515316
0	10.30956601	307.184191
0	4.672017141	138.3575013
0	7.038864209	208.4055674
0	9.383737697	276.8796234
0	17.09215328	503.4858916
0	17.09215328	503.4858916
0	4.637414925	136.3939067
0	19.85488094	583.7870616

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	13.22784587	388.6052058
0	7.636846405	222.993059
0	14.44200487	419.4368167
0	28.42991505	825.3473329
0	9.735771806	281.539291
0	4.536595517	130.7188948
0	22.06904674	633.702915
0	18.43569113	528.5091797
0	18.43569113	528.5091797
0	35.3546214	1013.459932
0	49.20941034	1405.140184
0	7.631428571	215.0142038
0	15.19140308	427.8205801
0	2.859791245	80.0164122
0	20.22887989	564.9328319
0	4.030067685	112.5042286
0	13.12769333	366.2146538
0	5.696777763	158.6555269
0	5.494404583	153.0035478
0	6.424725444	178.6090549
0	2.776431238	77.08468173
0	8.985425541	248.710806
0	30.30234438	837.1427222
0	14.39108721	396.5551928
0	7.347996977	202.0996022
0	12.55625353	343.4682101
0	13.67080292	368.7537646
0	2.633016467	70.45106
0	20.67299206	546.85052
0	13.01911714	343.8978211
0	13.01911714	343.8978211
0	10.48768873	276.4267672
0	10.48768873	276.4267672
0	6.542717087	172.4038086
0	11.55051948	304.0817884
0	32.80277329	860.710303
0	4.308177221	112.824401
0	45.3874092	1181.905914
0	6.723486683	174.3247894
0	8.587761574	222.245123
0	11.10567557	286.9466785
0	5.45951796	138.4991824

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	6.502348612	164.7308607
0	28.1151627	709.8583674
0	17.49066468	437.1505524
0	17.49066468	437.1505524
0	21.20824576	529.7627775
0	36.30799031	903.1769475
0	55.43172043	1375.245864
0	55.43172043	1375.245864
0	14.2753989	350.874388
0	9.955217197	243.5407691
0	7.297146444	178.2734515
0	10.93372263	266.5325868
0	16.24046463	395.044048
0	16.24046463	395.044048
0	6.459617884	157.0853945
0	19.27919453	466.8930204
0	9.622862554	231.2676144
0	9.622862554	231.2676144
0	11.72679387	280.1227817
0	11.72679387	280.1227817
0	5.722120098	136.6696879
0	6.529165211	154.0450966
0	41.57157258	978.8616897
0	3.157630522	74.32626312
0	17.67165185	415.3472938
0	6.866800792	161.2083444
0	10.12273587	237.4814895
0	11.2163343	262.3937483
0	9.760688217	224.7277893
0	5.953367149	136.4900918
0	12.13214575	278.1101273
0	12.13214575	278.1101273
0	12.13214575	278.1101273
0	3.858443026	88.17103972
0	16.31142342	372.422708
0	7.99991449	181.7583087
0	9.423609363	212.9820286
0	9.423609363	212.9820286
0	3.807596355	85.77918009
0	13.37235865	301.0945278
0	33.25548387	746.3095418
0	33.25548387	746.3095418

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	33.25548387	746.3095418
0	11.5538076	258.998269
0	6.366034942	141.8826136
0	50.35186677	1121.343392
0	15.14551334	336.2026737
0	15.14551334	336.2026737
0	149992	3329158.54
0	22.68886199	500.0250663
0	22.68886199	500.0250663
0	9.9205523	218.4110516
0	12.62877562	277.4485443
0	11.02804564	241.8432486
0	9.552614203	206.2169617
0	11.96346449	256.5818411
0	11.96346449	256.5818411
0	16.39613624	349.8548823
0	16.39613624	349.8548823
0	16.39613624	349.8548823
0	16.39613624	349.8548823
0	16.39613624	349.8548823
0	20.16680118	428.5404697
0	67.92391304	1431.908731
0	67.92391304	1431.908731
0	67.92391304	1431.908731
0	37.76188558	795.8456553
0	13.25090946	278.6516514
0	13.25090946	278.6516514
0	11.36468447	238.0557905
0	11.36468447	238.0557905
0	11.36468447	238.0557905
0	4.228242096	88.18644761
0	8.892863131	184.7163714
0	6.906801566	143.0971681
0	15.13408724	313.3287844
0	2.976590781	61.32123831
0	23.75138249	488.6272586
0	23.75138249	488.6272586
0	12.47077845	255.4932166
0	12.47077845	255.4932166
0	10.82293111	221.5177203
0	8.595975149	175.2044362
0	9.329430084	188.0371958

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	2.616642893	52.70472779
0	14.05233095	282.5324637
0	14.05233095	282.5324637
0	30.20789686	605.206719
0	30.20789686	605.206719
0	30.20789686	605.206719
0	4.624917383	92.55160096
0	10.33042807	206.681029
0	6.138789869	122.6514209
0	4.046462099	80.79566001
0	5.219420189	104.067868
0	16.49834911	327.3467255
0	16.49834911	327.3467255
0	20.78135081	410.7631739
0	20.78135081	410.7631739
0	20.78135081	410.7631739
0	20.78135081	410.7631739
0	4.254571635	84.04143867
0	45.28019324	894.3844809
0	8.057865681	158.2436142
0	4.522786037	88.69445048
0	4.522786037	88.69445048
0	131243	2548538.088
0	131243	2548538.088
0	131243	2548538.088
0	8.662116831	167.6738819
0	6.200368043	119.3268219
0	15.12267958	290.4571221
0	15.12267958	290.4571221
0	15.12267958	290.4571221
0	15.12267958	290.4571221
0	4.758615416	91.08215559
0	9.468547735	181.2116216
0	25.17190438	481.0810843
0	25.17190438	481.0810843
0	18.47132616	351.4315507
0	18.47132616	351.4315507
0	10.59846403	201.4446193
0	10.59846403	201.4446193
0	10.59846403	201.4446193
0	12.29447698	233.6544161
0	7.003556055	132.9401763

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	4.500797774	84.92245544
0	6.41010101	120.4929113
0	2.455017405	45.86052268
0	3.785862295	70.54826918
0	7.366010651	137.0134932
0	10.09323632	187.2833423
0	3.984768729	73.76881611
0	11.57065476	214.0084399
0	11.57065476	214.0084399
0	5.501976451	101.3146004
0	4.743149271	87.24675629
0	2.853552486	52.3345794
0	8.739264376	160.2046054
0	4.065194876	74.40385984
0	4.927214754	90.11173743
0	21.57476689	394.439284
0	21.57476689	394.439284
0	7.161016568	130.8584556
0	7.822593705	142.78519
0	12.96091318	233.9584409
0	3.879281879	69.86349104
0	6.008505817	107.9040823
0	8.415138439	151.0444514
0	5.624755544	100.7821743
0	7.577732794	135.694555
0	4.564547677	81.15580904
0	4.991365386	88.64895977
0	27.16521739	479.7040113
0	27.16521739	479.7040113
0	27.16521739	479.7040113
0	27.16521739	479.7040113
0	27.16521739	479.7040113
0	7.347711937	129.1084283
0	7.347711937	129.1084283
0	10.35158575	181.6571466
0	18.87691378	330.9007861
0	18.87691378	330.9007861
0	12.09620662	211.9487546
0	12.09620662	211.9487546
0	12.09620662	211.9487546
0	5.767548701	100.5208914
0	105.4951768	1835.085937

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	105.4951768	1835.085937
0	105.4951768	1835.085937
0	2.860060656	49.5169712
0	40.21668008	694.1388563
0	40.21668008	694.1388563
0	40.21668008	694.1388563
0	3.715289717	63.92306807
0	13.85127688	237.0647782
0	13.85127688	237.0647782
0	9.833481422	168.2198556
0	11.33958838	193.0101289
0	11.33958838	193.0101289
0	11.33958838	193.0101289
0	3.775772618	64.05739729
0	5.545126748	93.82618567
0	5.545126748	93.82618567
0	16.77858358	282.5519047
0	16.77858358	282.5519047
0	22.63647343	380.2888174
0	3.091302538	51.88557322
0	6.286041823	105.3637029
0	6.286041823	105.3637029
0	4.643499684	77.52203568
0	9.364720363	156.2399156
0	4.426359626	73.66451474
0	6.734322987	111.9239564
0	4.833000739	80.11019794
0	12.78511166	211.7234828
0	10.67198405	176.5724129
0	10.67198405	176.5724129
0	3.056625514	50.55816704
0	3.677531226	60.65496608
0	3.165971902	52.0832387
0	5.687652068	93.42589886
0	5.687652068	93.42589886
0	6.55196411	106.9283334
0	8.938573946	145.5060117
0	4.977427388	80.94390806
0	2.777163022	45.13756275
0	30.16090105	489.1517938
0	30.16090105	489.1517938
0	7.09837682	115.1029047

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	15.09991942	244.6898998
0	15.09991942	244.6898998
0	15.09991942	244.6898998
0	10.07855798	162.1958011
0	10.07855798	162.1958011
0	11.87125576	190.3979317
0	19.40165631	311.0177399
0	3.387751388	54.16347464
0	52.74477492	841.1107462
0	52.74477492	841.1107462
0	52.74477492	841.1107462
0	52.74477492	841.1107462
0	52.74477492	841.1107462
0	52.74477492	841.1107462
0	52.74477492	841.1107462
0	52.74477492	841.1107462
0	8.54948374	135.8448913
0	8.54948374	135.8448913
0	3.768660836	59.73962769
0	4.818898044	76.26828243
0	6.215301568	97.8525359
0	3.425443104	53.83716004
0	5.726057987	89.78407753
0	5.726057987	89.78407753
0	9.547597808	149.5359191
0	9.547597808	149.5359191
0	13.72646693	214.3509924
0	13.72646693	214.3509924
0	13.72646693	214.3509924
0	11.07924731	172.2459831
0	8.192817717	127.1132555
0	8.192817717	127.1132555
0	7.305773144	113.2999945
0	1.796123563	27.83970154
0	6.059595142	93.72247094
0	5.249017406	81.07241877
0	16.97554348	260.3028956
0	2.669505891	40.92605884
0	24.12743363	369.61397
0	24.12743363	369.61397
0	3.438794081	52.63402491
0	2.936329706	44.92316109

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	3.764960509	57.58303619
0	4.885400616	74.71146485
0	9.069733656	138.3195082
0	4.599118726	69.91562739
0	7.061870116	107.2297934
0	4.367925159	66.21164156
0	7.864684976	119.1916265
0	3.596393321	54.21644917
0	6.308319849	94.67092617
0	6.308319849	94.67092617
0	5.054068667	75.73342002
0	5.054068667	75.73342002
0	4.125566304	61.77020454
0	3.56380217	53.19048286
0	6.833702767	101.6218383
0	8.637380376	128.3271476
0	7.561793215	111.9796534
0	7.561793215	111.9796534
0	35.16130761	520.3416186
0	35.16130761	520.3416186
0	4.075036218	60.29019436
0	4.961911082	73.24390683
0	90.35180723	1332.782848
0	90.35180723	1332.782848
0	90.35180723	1332.782848
0	90.35180723	1332.782848
0	90.35180723	1332.782848
0	15.08856683	221.7733676
0	15.08856683	221.7733676
0	15.08856683	221.7733676
0	15.08856683	221.7733676
0	4.648264034	68.13777394
0	9.774762808	143.1104554
0	9.774762808	143.1104554
0	9.774762808	143.1104554
0	2.700557909	39.4336152
0	6.619795877	96.4291595
0	11.61346309	169.030755
0	11.61346309	169.030755
0	11.61346309	169.030755
0	11.61346309	169.030755
0	4.873044838	70.86486777

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	20.10512202	292.0988672
0	20.10512202	292.0988672
0	20.10512202	292.0988672
0	20.10512202	292.0988672
0	20.10512202	292.0988672
0	20.10512202	292.0988672
0	20.10512202	292.0988672
0	8.244331939	119.380754
0	8.244331939	119.380754
0	7.281337881	105.3924783
0	7.281337881	105.3924783
0	1.515012219	21.87541426
0	5.822130943	82.59560766
0	5.384867296	76.3620544
0	2.9386916	41.62473323
0	7.02091507	99.35789509
0	7.885461628	111.334389
0	4.704505412	66.4128048
0	13.57898551	191.6467116
0	13.57898551	191.6467116
0	10.78335444	151.7589072
0	4.214504919	59.18591016
0	4.953387982	69.39405529
0	3.575818591	49.92748304
0	3.839809957	53.54399965
0	3.839809957	53.54399965
0	5.676274272	79.05469691
0	93745	1299918.798
0	93745	1299918.798
0	93745	1299918.798
0	93745	1299918.798
0	4.156549414	57.6145302
0	26.36957395	365.0317988
0	26.36957395	365.0317988
0	26.36957395	365.0317988
0	26.36957395	365.0317988
0	26.36957395	365.0317988
0	26.36957395	365.0317988
0	26.36957395	365.0317988
0	26.36957395	365.0317988
0	6.778452454	93.8141073
0	8.744906621	120.8839378

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	8.744906621	120.8839378
0	17.23204229	238.1991349
0	17.23204229	238.1991349
0	17.23204229	238.1991349
0	17.23204229	238.1991349
0	17.23204229	238.1991349
0	17.23204229	238.1991349
0	17.23204229	238.1991349
0	17.23204229	238.1991349
0	17.23204229	238.1991349
0	4.8596679	67.01833473
0	4.8596679	67.01833473
0	2.724535949	37.53394116
0	7.556497175	104.0674018
0	3.934838904	53.98304848
0	6.051414713	82.95734492
0	5.155172711	70.66757783
0	4.100160274	56.09759081
0	2.153511279	29.34199446
0	3.753119829	51.11964003
0	10.06392694	137.0736974
0	4.769418933	64.75214936
0	12.34387352	167.5413084
0	12.34387352	167.5413084
0	12.34387352	167.5413084
0	12.34387352	167.5413084
0	6.552154012	88.70794243
0	3.7112196	49.96027027
0	45.17349398	606.2062325
0	45.17349398	606.2062325
0	45.17349398	606.2062325
0	45.17349398	606.2062325
0	45.17349398	606.2062325
0	45.17349398	606.2062325
0	45.17349398	606.2062325
0	45.17349398	606.2062325
0	4.682451746	62.58884352
0	4.944228704	65.54313363
0	3.304135045	43.72336023
0	9.434427881	124.4631679
0	9.434427881	124.4631679
0	15.0772325	198.8150692

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	15.0772325	198.8150692
0	15.0772325	198.8150692
0	15.0772325	198.8150692
0	15.0772325	198.8150692
0	5.723699447	75.42229899
0	5.723699447	75.42229899
0	4.59859053	60.52226879
0	3.630151767	47.74060877
0	7.911213518	103.4787165
0	7.911213518	103.4787165
0	11.31461353	147.8861839
0	21.09453376	274.7186655
0	21.09453376	274.7186655
0	21.09453376	274.7186655
0	21.09453376	274.7186655
0	3.344922725	43.33358209
0	5.572777943	72.01386401
0	3.839628171	49.2480599
0	3.424035575	43.90247724
0	6.715810241	86.01481894
0	8.878987534	113.5395526
0	8.878987534	113.5395526
0	8.878987534	113.5395526
0	8.878987534	113.5395526
0	8.878987534	113.5395526
0	3.662293244	46.68258493
0	3.112145268	39.64117669
0	7.551209677	96.14623343
0	7.551209677	96.14623343
0	13.40126933	168.9493607
0	13.40126933	168.9493607
0	13.40126933	168.9493607
0	13.40126933	168.9493607
0	10.44370123	131.6052121
0	10.44370123	131.6052121
0	10.44370123	131.6052121
0	10.44370123	131.6052121
0	10.44370123	131.6052121
0	10.44370123	131.6052121
0	10.44370123	131.6052121
0	10.44370123	131.6052121
0	3.945516812	49.71792808

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	4.364063401	54.84811377
0	3.47814958	43.66467359
0	3.579610852	44.53323777
0	5.780076974	71.82488905
0	8.385262781	104.0041107
0	8.385262781	104.0041107
0	8.385262781	104.0041107
0	8.385262781	104.0041107
0	8.385262781	104.0041107
0	7.222510519	89.55686994
0	7.222510519	89.55686994
0	4.291099406	53.11559752
0	30.11405622	372.6797859
0	30.11405622	372.6797859
0	30.11405622	372.6797859
0	30.11405622	372.6797859
0	30.11405622	372.6797859
0	30.11405622	372.6797859
0	30.11405622	372.6797859
0	30.11405622	372.6797859
0	30.11405622	372.6797859
0	30.11405622	372.6797859
0	30.11405622	372.6797859
0	30.11405622	372.6797859
0	3.698559569	45.65367377
0	3.698559569	45.65367377
0	17.5778403	216.3084025
0	17.5778403	216.3084025
0	17.5778403	216.3084025
0	17.5778403	216.3084025
0	17.5778403	216.3084025
0	17.5778403	216.3084025
0	17.5778403	216.3084025
0	17.5778403	216.3084025
0	17.5778403	216.3084025
0	6.251982967	76.40867454
0	6.251982967	76.40867454
0	4.220527672	51.4552139
0	3.653802864	44.53087421
0	5.614631895	68.32461078
0	9.697204969	117.93781
0	9.697204969	117.93781

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	9.697204969	117.93781
0	9.697204969	117.93781
0	9.697204969	117.93781
0	9.697204969	117.93781
0	75.23274478	912.4292305
0	75.23274478	912.4292305
0	75.23274478	912.4292305
0	75.23274478	912.4292305
0	75.23274478	912.4292305
0	75.23274478	912.4292305
0	75.23274478	912.4292305
0	75.23274478	912.4292305
0	75.23274478	912.4292305
0	75.23274478	912.4292305
0	6.921202957	83.61061188
0	6.921202957	83.61061188
0	6.921202957	83.61061188
0	6.921202957	83.61061188
0	6.921202957	83.61061188
0	12.06049879	145.6383668
0	12.06049879	145.6383668
0	12.06049879	145.6383668
0	12.06049879	145.6383668
0	12.06049879	145.6383668
0	12.06049879	145.6383668
0	4.728205906	57.07633841
0	4.728205906	57.07633841
0	7.943509055	95.62321151
0	7.943509055	95.62321151
0	4.403444976	52.90582082
0	5.458378209	65.06004403
0	4.086105323	48.33540541
0	4.324580682	51.12752035
0	2.685214626	31.73488606
0	6.644	78.2241515
0	6.644	78.2241515
0	6.644	78.2241515
0	6.644	78.2241515
0	9.050241546	106.3320482
0	9.050241546	106.3320482
0	9.050241546	106.3320482
0	4.923464496	57.83355262

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	2.197128948	25.78692112
0	3.52577787	41.36753081
0	7.545930701	88.21169418
0	7.545930701	88.21169418
0	7.545930701	88.21169418
0	7.545930701	88.21169418
0	7.545930701	88.21169418
0	5.310570668	62.01018264
0	5.848004374	68.27182608
0	15.0659164	175.7930817
0	15.0659164	175.7930817
0	15.0659164	175.7930817
0	15.0659164	175.7930817
0	15.0659164	175.7930817
0	15.0659164	175.7930817
0	15.0659164	175.7930817
0	15.0659164	175.7930817
0	10.96350472	127.0180504
0	10.96350472	127.0180504
0	10.96350472	127.0180504
0	10.96350472	127.0180504
0	10.96350472	127.0180504
0	10.96350472	127.0180504
0	10.96350472	127.0180504
0	4.811310355	55.46981732
0	4.811310355	55.46981732
0	22.58433735	260.0352841
0	22.58433735	260.0352841
0	22.58433735	260.0352841
0	22.58433735	260.0352841
0	22.58433735	260.0352841
0	22.58433735	260.0352841
0	22.58433735	260.0352841
0	22.58433735	260.0352841
0	4.449362269	50.99515435
0	5.170542471	59.15635958
0	5.170542471	59.15635958
0	8.484148551	96.37828065
0	8.484148551	96.37828065
0	8.484148551	96.37828065
0	7.186216953	81.62105432
0	7.186216953	81.62105432

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	7.186216953	81.62105432
0	3.554312971	40.2454079
0	4.704140843	53.23645382
0	4.104027997	46.24865406
0	4.363564227	49.16319515
0	5.037695207	56.48193574
0	5.037695207	56.48193574
0	6.151194743	68.86185202
0	5.492992883	61.31403658
0	3.368354545	37.57975031
0	10.04934299	111.860149
0	10.04934299	111.860149
0	10.04934299	111.860149
0	4.601630874	51.12400402
0	13.18197347	146.2575439
0	13.18197347	146.2575439
0	13.18197347	146.2575439
0	13.18197347	146.2575439
0	13.18197347	146.2575439
0	13.18197347	146.2575439
0	13.18197347	146.2575439
0	13.18197347	146.2575439
0	13.18197347	146.2575439
0	6.859204454	75.73090415
0	6.859204454	75.73090415
0	6.859204454	75.73090415
0	2.359051147	25.94124129
0	7.984654731	87.76647994
0	7.984654731	87.76647994
0	7.984654731	87.76647994
0	3.008529428	33.06482042
0	4.911490307	53.97203658
0	4.911490307	53.97203658
0	3.089699545	33.79494925
0	37.61436597	411.0706261
0	37.61436597	411.0706261
0	37.61436597	411.0706261
0	37.61436597	411.0706261
0	37.61436597	411.0706261
0	37.61436597	411.0706261
0	37.61436597	411.0706261
0	37.61436597	411.0706261

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	37.61436597	411.0706261
0	37.61436597	411.0706261
0	37.61436597	411.0706261
0	37.61436597	411.0706261
0	37.61436597	411.0706261
0	37.61436597	411.0706261
0	5.931192396	64.77674993
0	5.931192396	64.77674993
0	5.931192396	64.77674993
0	5.331149409	58.20622014
0	3.969044933	43.33419125
0	4.503483032	49.12386784
0	3.18397561	34.70639349
0	3.294776251	35.84953831
0	3.061189451	33.10364403
0	18.06650602	194.7585914
0	18.06650602	194.7585914
0	18.06650602	194.7585914
0	18.06650602	194.7585914
0	18.06650602	194.7585914
0	18.06650602	194.7585914
0	18.06650602	194.7585914
0	18.06650602	194.7585914
0	18.06650602	194.7585914
0	4.791441743	51.61332841
0	6.560627825	70.44269876
0	6.560627825	70.44269876
0	4.124889673	44.16957027
0	9.275821524	99.32416424
0	9.275821524	99.32416424
0	9.275821524	99.32416424
0	9.275821524	99.32416424
0	9.275821524	99.32416424
0	5.178554134	55.31473921
0	5.726362625	61.0293485
0	7.540660225	80.2579816
0	7.540660225	80.2579816
0	7.540660225	80.2579816
0	7.540660225	80.2579816
0	7.540660225	80.2579816
0	11.71668453	123.9094032
0	11.71668453	123.9094032

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	11.71668453	123.9094032
0	11.71668453	123.9094032
0	11.71668453	123.9094032
0	11.71668453	123.9094032
0	11.71668453	123.9094032
0	11.71668453	123.9094032
0	11.71668453	123.9094032
0	11.71668453	123.9094032
0	2.533415166	26.68224093
0	4.051014216	42.65569036
0	4.051014216	42.65569036
0	4.051014216	42.65569036
0	4.051014216	42.65569036
0	4.051014216	42.65569036
0	3.190217624	33.43658074
0	3.190217624	33.43658074
0	5.034436373	52.61972678
0	6.286932581	65.67505917
0	5.535188172	57.58274245
0	4.568095578	47.30273656
0	3.979730881	41.20970848
0	4.232594988	43.72233316
0	3.406751825	35.17590871
0	7.143401983	73.66627892
0	8.612803126	88.81664685
0	8.612803126	88.81664685
0	8.612803126	88.81664685
0	8.612803126	88.81664685
0	8.612803126	88.81664685
0	8.612803126	88.81664685
0	3.031544715	31.1377654
0	4.898108763	50.10359175
0	3.524477698	35.95723903
0	3.910905591	39.82766031
0	6.035132957	61.36023945
0	6.035132957	61.36023945
0	6.035132957	61.36023945
0	4.464036569	45.33030432
0	15.05461847	152.6758519
0	15.05461847	152.6758519
0	10.54445338	106.5026242
0	10.54445338	106.5026242

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	10.54445338	106.5026242
0	10.54445338	106.5026242
0	3.667378236	37.03049741
0	3.476663454	34.95631777
0	3.476663454	34.95631777
0	25.07490637	250.7709935
0	25.07490637	250.7709935
0	25.07490637	250.7709935
0	25.07490637	250.7709935
0	25.07490637	250.7709935
0	25.07490637	250.7709935
0	25.07490637	250.7709935
0	25.07490637	250.7709935
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0	25.07490637	250.7709935
0	25.07490637	250.7709935
0	25.07490637	250.7709935
0	25.07490637	250.7709935
0	25.07490637	250.7709935
0	25.07490637	250.7709935
0	25.07490637	250.7709935
0	6.785869565	67.84366807
0	6.785869565	67.84366807
0	3.060663499	30.52411737
0	2.653178795	26.42351861
0	4.364602405	43.46770414
0	4.364602405	43.46770414
0	3.612447882	35.91547779
0	8.038187182	79.90737269
0	8.038187182	79.90737269
0	5.188684476	51.46857968
0	5.802702535	57.44142532
0	5.802702535	57.44142532
0	5.802702535	57.44142532
0	2.579677204	25.48272411
0	3.78013754	37.24092814
0	4.646427019	45.54715125
0	6.462387854	62.67177199
0	6.462387854	62.67177199
0	6.462387854	62.67177199
0	5.031182796	48.74921228
0	9.585355159	92.6263766

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	9.585355159	92.6263766
0	9.585355159	92.6263766
0	9.585355159	92.6263766
0	9.585355159	92.6263766
0	9.585355159	92.6263766
0	9.585355159	92.6263766
0	9.585355159	92.6263766
0	9.585355159	92.6263766
0	9.585355159	92.6263766
0	9.585355159	92.6263766
0	9.585355159	92.6263766
0	5.587489181	53.8706458
0	5.587489181	53.8706458
0	5.587489181	53.8706458
0	5.587489181	53.8706458
0	5.587489181	53.8706458
0	2.970166133	28.54251602
0	1.939061237	18.62856278
0	7.53539823	72.27733054
0	7.53539823	72.27733054
0	7.53539823	72.27733054
0	7.53539823	72.27733054
0	7.53539823	72.27733054
0	12.90327022	123.5730113
0	12.90327022	123.5730113
0	12.90327022	123.5730113
0	12.90327022	123.5730113
0	12.90327022	123.5730113
0	12.90327022	123.5730113
0	12.90327022	123.5730113
0	12.90327022	123.5730113
0	12.90327022	123.5730113
0	60.13793103	573.3213849
0	60.13793103	573.3213849
0	60.13793103	573.3213849
0	60.13793103	573.3213849
0	60.13793103	573.3213849
0	60.13793103	573.3213849
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0	60.13793103	573.3213849
0	60.13793103	573.3213849
0	60.13793103	573.3213849
0	60.13793103	573.3213849

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	60.13793103	573.3213849
0	60.13793103	573.3213849
0	60.13793103	573.3213849
0	60.13793103	573.3213849
0	60.13793103	573.3213849
0	3.657806138	34.8691242
0	3.457073453	32.81940747
0	3.457073453	32.81940747
0	4.88294592	46.22581722
0	6.16831357	58.05469419
0	6.16831357	58.05469419
0	6.16831357	58.05469419
0	4.091158454	38.46239104
0	2.599930143	24.30626689
0	2.99654187	27.89011467
0	3.777890057	35.08006494
0	7.09176092	65.68531144
0	7.09176092	65.68531144
0	7.09176092	65.68531144
0	8.786106645	81.35221341
0	8.786106645	81.35221341
0	8.786106645	81.35221341
0	8.786106645	81.35221341
0	8.786106645	81.35221341
0	8.786106645	81.35221341
0	8.786106645	81.35221341
0	8.786106645	81.35221341
0	18.80517657	173.8164582
0	18.80517657	173.8164582
0	18.80517657	173.8164582
0	18.80517657	173.8164582
0	18.80517657	173.8164582
0	18.80517657	173.8164582
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0	18.80517657	173.8164582
0	18.80517657	173.8164582
0	18.80517657	173.8164582
0	18.80517657	173.8164582

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	18.80517657	173.8164582
0	4.007451123	36.96594987
0	3.21488047	29.63813995
0	2.254059142	20.73219665
0	5.201589375	47.61608188
0	5.201589375	47.61608188
0	5.899810964	53.91399186
0	5.899810964	53.91399186
0	2.051492987	18.68024394
0	11.28975904	102.4166779
0	11.28975904	102.4166779
0	11.28975904	102.4166779
0	11.28975904	102.4166779
0	11.28975904	102.4166779
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0	11.28975904	102.4166779
0	11.28975904	102.4166779
0	11.28975904	102.4166779
0	11.28975904	102.4166779
0	1.997427949	17.9520165
0	3.64722772	32.70386272
0	3.64722772	32.70386272
0	6.697416644	59.94579678
0	6.697416644	59.94579678
0	5.027934461	44.86753639
0	5.027934461	44.86753639
0	5.027934461	44.86753639
0	5.027934461	44.86753639
0	8.109819441	72.04558704
0	8.109819441	72.04558704
0	8.109819441	72.04558704
0	8.109819441	72.04558704
0	5.653683575	50.18493056
0	5.653683575	50.18493056
0	1.871919537	16.60472532
0	2.563344271	22.66283644
0	4.117323355	36.37583517
0	4.117323355	36.37583517
0	3.585218476	31.59408511
0	3.585218476	31.59408511

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	3.225738192	28.37617996
0	1.825731348	16.03582162
0	2.492279867	21.88265407
0	2.752972454	23.97419626
0	3.061134908	26.64950959
0	4.865483091	42.33566095
0	4.865483091	42.33566095
0	3.525276206	30.53256476
0	4.025612053	34.84704607
0	4.025612053	34.84704607
0	6.344582292	54.91393935
0	6.344582292	54.91393935
0	6.344582292	54.91393935
0	3.333987721	28.82950106
0	5.427246377	46.81365645
0	5.427246377	46.81365645
0	10.03480589	86.45120881
0	10.03480589	86.45120881
0	10.03480589	86.45120881
0	10.03480589	86.45120881
0	10.03480589	86.45120881
0	10.03480589	86.45120881
0	10.03480589	86.45120881
0	15.04333868	129.4155282
0	15.04333868	129.4155282
0	15.04333868	129.4155282
0	15.04333868	129.4155282
0	15.04333868	129.4155282
0	15.04333868	129.4155282
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0	15.04333868	129.4155282
0	15.04333868	129.4155282
0	15.04333868	129.4155282
0	15.04333868	129.4155282
0	15.04333868	129.4155282

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	15.04333868	129.4155282
0	15.04333868	129.4155282
0	3.704209467	31.69498669
0	3.704209467	31.69498669
0	7.530144695	64.25900254
0	7.530144695	64.25900254
0	7.530144695	64.25900254
0	7.530144695	64.25900254
0	7.530144695	64.25900254
0	7.530144695	64.25900254
0	7.530144695	64.25900254
0	2.0278738	17.27138886
0	3.285493176	27.95654221
0	2.628421689	22.35612264
0	30.06736167	255.1481539
0	30.06736167	255.1481539
0	30.06736167	255.1481539
0	30.06736167	255.1481539
0	30.06736167	255.1481539
0	30.06736167	255.1481539
0	30.06736167	255.1481539
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0	30.06736167	255.1481539
0	30.06736167	255.1481539
0	30.06736167	255.1481539
0	30.06736167	255.1481539
0	30.06736167	255.1481539
0	30.06736167	255.1481539
0	30.06736167	255.1481539
0	3.937888199	33.40275438
0	4.255789909	35.96912855
0	4.255789909	35.96912855
0	6.027031376	50.47512648
0	6.027031376	50.47512648
0	6.027031376	50.47512648
0	6.027031376	50.47512648

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	3.411192531	28.54366166
0	2.836526764	23.55575105
0	4.570116963	37.83511182
0	4.570116963	37.83511182
0	4.570116963	37.83511182
0	4.570116963	37.83511182
0	3.569129094	29.42699868
0	7.027759914	57.66842499
0	9.030843373	74.04730717
0	9.030843373	74.04730717
0	9.030843373	74.04730717
0	9.030843373	74.04730717
0	9.030843373	74.04730717
0	9.030843373	74.04730717
0	5.024691358	40.97098243
0	5.024691358	40.97098243
0	2.888387085	23.4192966
0	5.739723403	46.53757942
0	5.739723403	46.53757942
0	5.739723403	46.53757942
0	4.047757671	32.7307361
0	4.047757671	32.7307361
0	4.435464758	35.82980109
0	4.435464758	35.82980109
0	12.53544676	100.9054108
0	12.53544676	100.9054108
0	12.53544676	100.9054108
0	12.53544676	100.9054108
0	12.53544676	100.9054108
0	12.53544676	100.9054108
0	12.53544676	100.9054108
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0	12.53544676	100.9054108
0	12.53544676	100.9054108
0	12.53544676	100.9054108
0	12.53544676	100.9054108
0	12.53544676	100.9054108
0	12.53544676	100.9054108

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	12.53544676	100.9054108
0	12.53544676	100.9054108
0	2.059259465	16.45411036
0	3.69620003	29.51879176
0	3.25323052	25.86041109
0	3.443528045	27.36516429
0	3.443528045	27.36516429
0	4.844979296	38.42915979
0	3.951171275	31.25749197
0	6.588173232	52.03385524
0	6.588173232	52.03385524
0	6.588173232	52.03385524
0	6.588173232	52.03385524
0	2.722481752	21.42432686
0	3.062680399	24.05879121
0	5.478534338	43.02701009
0	5.478534338	43.02701009
0	5.478534338	43.02701009
0	8.209419496	64.18319937
0	8.209419496	64.18319937
0	8.209419496	64.18319937
0	8.209419496	64.18319937
0	8.209419496	64.18319937
0	8.209419496	64.18319937
0	8.209419496	64.18319937
0	8.209419496	64.18319937
0	3.203767669	25.03770355
0	3.203767669	25.03770355
0	3.383975823	26.40397313
0	3.383975823	26.40397313
0	4.677661169	36.10194827
0	4.677661169	36.10194827
0	4.677661169	36.10194827
0	4.677661169	36.10194827
0	4.677661169	36.10194827
0	4.677661169	36.10194827
0	4.188602382	32.23371481
0	20.04383855	154.1277261
0	20.04383855	154.1277261
0	20.04383855	154.1277261
0	20.04383855	154.1277261
0	20.04383855	154.1277261

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	20.04383855	154.1277261
0	20.04383855	154.1277261
0	20.04383855	154.1277261
0	20.04383855	154.1277261
0	20.04383855	154.1277261
0	20.04383855	154.1277261
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0	20.04383855	154.1277261
0	20.04383855	154.1277261
0	20.04383855	154.1277261
0	20.04383855	154.1277261
0	20.04383855	154.1277261
0	20.04383855	154.1277261
0	3.550871196	27.25404968
0	3.550871196	27.25404968
0	3.326442321	25.48566718
0	5.240057365	39.88270029
0	6.200302629	47.17402674
0	6.200302629	47.17402674
0	6.200302629	47.17402674
0	2.844715408	21.53377549
0	10.74409539	81.26208739
0	10.74409539	81.26208739
0	10.74409539	81.26208739
0	10.74409539	81.26208739
0	10.74409539	81.26208739
0	10.74409539	81.26208739
0	10.74409539	81.26208739
0	10.74409539	81.26208739
0	10.74409539	81.26208739

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	10.74409539	81.26208739
0	10.74409539	81.26208739
0	10.74409539	81.26208739
0	10.74409539	81.26208739
0	10.74409539	81.26208739
0	3.109206334	23.48896607
0	2.73401669	20.65442556
0	2.73401669	20.65442556
0	3.482398957	26.20634024
0	2.94288236	22.04370882
0	2.94288236	22.04370882
0	7.524899598	56.18752425
0	7.524899598	56.18752425
0	7.524899598	56.18752425
0	7.524899598	56.18752425
0	7.524899598	56.18752425
0	7.524899598	56.18752425
0	7.524899598	56.18752425
0	7.524899598	56.18752425
0	7.524899598	56.18752425
0	7.524899598	56.18752425
0	2.811486677	20.96746617
0	2.291547017	17.02807645
0	5.021453473	37.05458229
0	5.021453473	37.05458229
0	3.416510576	25.21022778
0	2.904997511	21.41876182
0	2.329098078	17.15047757
0	3.967725518	29.10950157
0	5.85552876	42.94967356
0	5.85552876	42.94967356
0	5.85552876	42.94967356
0	4.37540907	31.99974192
0	2.868071771	20.81546923
0	3.606819776	26.17212186
0	3.164977331	22.9643654
0	2.74729481	19.88815802
0	3.353062506	24.26244281
0	2.354074074	16.98899058
0	2.977353206	21.3840817
0	2.401325545	17.19186352
0	4.820337892	34.50103605

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	4.820337892	34.50103605
0	4.820337892	34.50103605
0	6.945690454	49.60213447
0	6.945690454	49.60213447
0	6.945690454	49.60213447
0	6.945690454	49.60213447
0	6.945690454	49.60213447
0	6.945690454	49.60213447
0	6.945690454	49.60213447
0	6.945690454	49.60213447
0	6.945690454	49.60213447
0	9.400581862	67.0320747
0	9.400581862	67.0320747
0	9.400581862	67.0320747
0	9.400581862	67.0320747
0	9.400581862	67.0320747
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0	9.400581862	67.0320747
0	9.400581862	67.0320747
0	9.400581862	67.0320747
0	3.114572916	22.19472072
0	2.455932956	17.46075233
0	3.529890185	25.07369524
0	3.529890185	25.07369524
0	5.547046878	39.2521749
0	5.547046878	39.2521749
0	5.547046878	39.2521749
0	5.547046878	39.2521749
0	2.935843888	20.73504926
0	2.319458786	16.3505857
0	15.03207698	105.9342848
0	15.03207698	105.9342848
0	15.03207698	105.9342848
0	15.03207698	105.9342848
0	15.03207698	105.9342848
0	15.03207698	105.9342848

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	15.03207698	105.9342848
0	15.03207698	105.9342848
0	15.03207698	105.9342848
0	15.03207698	105.9342848
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0	15.03207698	105.9342848
0	15.03207698	105.9342848
0	15.03207698	105.9342848
0	2.176419777	15.33008645
0	2.796955532	19.67011139
0	3.065743639	21.45728995
0	4.634692741	32.18720681
0	4.634692741	32.18720681
0	4.109793588	28.5105458
0	4.109793588	28.5105458
0	6.449225473	44.10440927
0	6.449225473	44.10440927
0	6.449225473	44.10440927
0	6.449225473	44.10440927
0	6.449225473	44.10440927
0	6.449225473	44.10440927
0	6.449225473	44.10440927
0	5.269413183	35.99567054
0	2.856190872	19.508472
0	2.856190872	19.508472
0	3.176075783	21.68007686

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	2.97252411	20.07231686
0	8.355626895	56.32885616
0	8.355626895	56.32885616
0	8.355626895	56.32885616
0	8.355626895	56.32885616
0	8.355626895	56.32885616
0	8.355626895	56.32885616
0	8.355626895	56.32885616
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0	8.355626895	56.32885616
0	8.355626895	56.32885616
0	8.355626895	56.32885616
0	8.355626895	56.32885616
0	4.462799082	30.08370592
0	3.121148869	20.89770772
0	3.589079467	23.9770497
0	3.589079467	23.9770497
0	3.589079467	23.9770497
0	3.317564516	22.11856001
0	2.92800135	19.4216726
0	2.78073012	18.36992877
0	2.664762993	17.6008465
0	2.664762993	17.6008465
0	5.018220793	33.11147439
0	5.018220793	33.11147439
0	5.018220793	33.11147439
0	3.874534161	25.51782825
0	3.874534161	25.51782825
0	3.874534161	25.51782825
0	6.018955823	39.46106759
0	6.018955823	39.46106759
0	6.018955823	39.46106759
0	6.018955823	39.46106759
0	6.018955823	39.46106759
0	6.018955823	39.46106759
0	6.018955823	39.46106759
0	4.303183542	28.16559728
0	4.303183542	28.16559728
0	4.303183542	28.16559728
0	4.303183542	28.16559728
0	3.252340291	21.23426428

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	12.02502005	78.28461648
0	12.02502005	78.28461648
0	12.02502005	78.28461648
0	12.02502005	78.28461648
0	12.02502005	78.28461648
0	12.02502005	78.28461648
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0	12.02502005	78.28461648
0	12.02502005	78.28461648
0	12.02502005	78.28461648
0	2.446152659	15.83215897
0	2.517273954	16.18706537
0	3.766706924	24.1787755
0	3.766706924	24.1787755
0	3.766706924	24.1787755
0	2.842827375	18.19704936
0	3.18962469	20.39481489
0	2.70913915	17.31153824
0	2.70913915	17.31153824
0	7.519662921	48.0393836
0	7.519662921	48.0393836
0	7.519662921	48.0393836
0	7.519662921	48.0393836
0	7.519662921	48.0393836
0	7.519662921	48.0393836
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0	7.519662921	48.0393836
0	7.519662921	48.0393836
0	7.519662921	48.0393836
0	7.519662921	48.0393836
0	7.519662921	48.0393836

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	7.519662921	48.0393836
0	7.519662921	48.0393836
0	2.422945781	15.46359889
0	3.425573218	21.8553007
0	4.789864075	30.5440443
0	4.789864075	30.5440443
0	4.789864075	30.5440443
0	4.789864075	30.5440443
0	4.789864075	30.5440443
0	4.15457597	26.41159911
0	2.967173421	18.75495232
0	5.64246988	35.49956547
0	5.64246988	35.49956547
0	5.64246988	35.49956547
0	5.64246988	35.49956547
0	5.64246988	35.49956547
0	3.129275715	19.59730168
0	3.129275715	19.59730168
0	3.664708186	22.9318643
0	4.01587557	24.80344985
0	4.581364462	28.24802699
0	4.581364462	28.24802699
0	22.53245192	137.6905759
0	22.53245192	137.6905759
0	22.53245192	137.6905759
0	22.53245192	137.6905759
0	22.53245192	137.6905759
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0	22.53245192	137.6905759
0	22.53245192	137.6905759
0	22.53245192	137.6905759

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	22.53245192	137.6905759
0	22.53245192	137.6905759
0	22.53245192	137.6905759
0	22.53245192	137.6905759
0	22.53245192	137.6905759
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0	22.53245192	137.6905759
0	22.53245192	137.6905759
0	22.53245192	137.6905759
0	22.53245192	137.6905759
0	22.53245192	137.6905759
0	3.568077803	21.768895
0	6.835692397	41.46706321
0	6.835692397	41.46706321

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

	0	6.835692397	41.46706321
	0	6.835692397	41.46706321
	0	6.835692397	41.46706321
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	0	6.835692397	41.46706321
	0	6.835692397	41.46706321
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	0	6.835692397	41.46706321
	0	6.835692397	41.46706321
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	0	6.835692397	41.46706321
	0	6.835692397	41.46706321
	0	10.02031542	60.62207809
	0	10.02031542	60.62207809
	0	10.02031542	60.62207809
	0	10.02031542	60.62207809
	0	10.02031542	60.62207809
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	0	10.02031542	60.62207809
	0	10.02031542	60.62207809
	0	10.02031542	60.62207809
	0	10.02031542	60.62207809
	0	10.02031542	60.62207809
	0	10.02031542	60.62207809

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	10.02031542	60.62207809
0	10.02031542	60.62207809
0	10.02031542	60.62207809
0	10.02031542	60.62207809
0	10.02031542	60.62207809
0	10.02031542	60.62207809
0	10.02031542	60.62207809
0	10.02031542	60.62207809
0	10.02031542	60.62207809
0	10.02031542	60.62207809
0	2.11695935	12.80425979
0	5.3102764	32.0897578
0	5.3102764	32.0897578
0	5.3102764	32.0897578
0	5.3102764	32.0897578
0	5.3102764	32.0897578
0	3.01516129	18.1175912
0	3.886123582	23.32540037
0	2.827633172	16.88021898
0	4.390239818	26.1860594
0	3.206405267	19.10860404
0	3.476402824	20.68257189
0	3.476402824	20.68257189
0	2.292407097	13.4503798
0	2.78398212	16.30745785
0	3.764481094	21.96380424
0	3.764481094	21.96380424
0	3.764481094	21.96380424
0	5.014993307	29.13178459
0	5.014993307	29.13178459
0	5.014993307	29.13178459
0	4.214405145	24.32711093
0	4.214405145	24.32711093
0	4.214405145	24.32711093
0	4.214405145	24.32711093
0	4.214405145	24.32711093
0	4.214405145	24.32711093
0	6.265716961	36.15509499
0	6.265716961	36.15509499
0	6.265716961	36.15509499
0	6.265716961	36.15509499
0	6.265716961	36.15509499

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	6.265716961	36.15509499
0	6.265716961	36.15509499
0	6.265716961	36.15509499
0	6.265716961	36.15509499
0	1.642360278	9.440597349
0	3.650210878	20.70678476
0	3.650210878	20.70678476
0	3.306468717	18.7145075
0	8.588383549	48.5107264
0	8.588383549	48.5107264
0	8.588383549	48.5107264
0	8.588383549	48.5107264
0	8.588383549	48.5107264
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0	8.588383549	48.5107264
0	8.588383549	48.5107264
0	8.588383549	48.5107264
0	8.588383549	48.5107264
0	2.700589064	15.23202894
0	2.175065693	12.24988899
0	4.052096216	22.64521827
0	4.052096216	22.64521827
0	4.052096216	22.64521827
0	4.750792644	26.54785806
0	4.750792644	26.54785806
0	4.750792644	26.54785806
0	4.750792644	26.54785806
0	4.750792644	26.54785806
0	4.750792644	26.54785806

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	4.750792644	26.54785806
0	4.750792644	26.54785806
0	2.021811403	11.25518019
0	2.546377693	14.1526246
0	2.810142154	15.55677543
0	3.227570738	17.82171388
0	3.227570738	17.82171388
0	3.542662439	19.54396269
0	3.542662439	19.54396269
0	5.783430053	31.79234174
0	5.783430053	31.79234174
0	5.783430053	31.79234174
0	5.783430053	31.79234174
0	5.783430053	31.79234174
0	5.783430053	31.79234174
0	5.783430053	31.79234174
0	5.783430053	31.79234174
0	5.783430053	31.79234174
0	5.783430053	31.79234174
0	5.783430053	31.79234174
0	2.33360024	12.78493239
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
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0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	15.02083333	82.09239322
0	2.954290499	16.09773381
0	2.622030389	14.24216835
0	2.763158602	14.9884519
0	3.90181017	21.11850911
0	3.90181017	21.11850911
0	3.90181017	21.11850911
0	2.028143213	10.94750812
0	3.152342433	16.98330267
0	3.152342433	16.98330267
0	3.152342433	16.98330267
0	3.152342433	16.98330267
0	4.513012048	24.27656581
0	4.513012048	24.27656581
0	4.513012048	24.27656581
0	4.513012048	24.27656581
0	4.513012048	24.27656581
0	4.513012048	24.27656581
0	3.441259625	18.46623214
0	3.441259625	18.46623214
0	1.910732183	10.20977117
0	2.897322259	15.44091568
0	2.717715494	14.44560068
0	7.514434643	39.77620347
0	7.514434643	39.77620347

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	7.514434643	39.77620347
0	7.514434643	39.77620347
0	7.514434643	39.77620347
0	7.514434643	39.77620347
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0	3.080533597	16.19503549
0	5.370041275	28.16010506
0	5.370041275	28.16010506
0	5.370041275	28.16010506
0	5.370041275	28.16010506
0	5.370041275	28.16010506
0	5.370041275	28.16010506
0	5.370041275	28.16010506
0	5.370041275	28.16010506
0	3.762258842	19.72844098
0	3.762258842	19.72844098
0	3.762258842	19.72844098
0	3.762258842	19.72844098
0	2.547897555	13.32943171
0	3.345490301	17.4655751

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	2.673738293	13.92678438
0	1.804178993	9.351561141
0	4.297877223	22.26883835
0	4.297877223	22.26883835
0	4.297877223	22.26883835
0	4.297877223	22.26883835
0	3.011916264	15.45308237
0	3.011916264	15.45308237
0	2.631157194	13.43066573
0	3.632331744	18.45920222
0	3.632331744	18.45920222
0	3.632331744	18.45920222
0	2.295156585	11.64133711
0	5.011771001	25.10052692
0	5.011771001	25.10052692
0	5.011771001	25.10052692
0	5.011771001	25.10052692
0	5.011771001	25.10052692
0	2.946282294	14.7539749
0	2.946282294	14.7539749
0	4.10230011	20.48504273
0	4.10230011	20.48504273
0	4.10230011	20.48504273
0	4.10230011	20.48504273
0	2.738846971	13.66221653
0	6.67914105	33.23419995
0	6.67914105	33.23419995
0	6.67914105	33.23419995
0	6.67914105	33.23419995
0	6.67914105	33.23419995
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0	6.67914105	33.23419995
0	6.67914105	33.23419995
0	6.67914105	33.23419995
0	6.67914105	33.23419995

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

	0	6.67914105	33.23419995
	0	6.67914105	33.23419995
	0	6.67914105	33.23419995
	0	6.67914105	33.23419995
	0	11.26502404	55.79649531
	0	11.26502404	55.79649531
	0	11.26502404	55.79649531
	0	11.26502404	55.79649531
	0	11.26502404	55.79649531
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	0	11.26502404	55.79649531
	0	11.26502404	55.79649531
	0	11.26502404	55.79649531
	0	11.26502404	55.79649531
	0	11.26502404	55.79649531

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	11.26502404	55.79649531
0	11.26502404	55.79649531
0	11.26502404	55.79649531
0	11.26502404	55.79649531
0	11.26502404	55.79649531
0	11.26502404	55.79649531
0	11.26502404	55.79649531
0	3.169073125	15.667948
0	3.169073125	15.667948
0	1.839270634	9.087848565
0	3.511066452	17.29723652
0	1.624432008	7.919318913
0	3.923729701	18.89285351
0	3.923729701	18.89285351
0	3.923729701	18.89285351
0	3.087649813	14.85911364
0	4.69828451	22.49704824
0	4.69828451	22.49704824
0	4.69828451	22.49704824
0	4.69828451	22.49704824
0	2.64246434	12.61678699
0	2.823218599	13.47199234
0	1.968792976	9.310113872
0	6.010906175	28.187918
0	6.010906175	28.187918
0	6.010906175	28.187918
0	6.010906175	28.187918
0	6.010906175	28.187918
0	6.010906175	28.187918
0	6.010906175	28.187918
0	6.010906175	28.187918
0	6.010906175	28.187918
0	6.010906175	28.187918
0	6.010906175	28.187918
0	6.010906175	28.187918
0	6.010906175	28.187918
0	6.010906175	28.187918
0	6.010906175	28.187918
0	6.010906175	28.187918
0	6.010906175	28.187918
0	6.010906175	28.187918
0	6.010906175	28.187918
0	3.010297667	14.10342404

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

0	2.176266158	10.16802951
0	2.596765678	12.13112332
0	2.596765678	12.13112332
0	2.596765678	12.13112332
0	2.765454008	12.88364792
0	2.765454008	12.88364792
0	3.760040161	17.46567016
0	3.760040161	17.46567016
0	3.760040161	17.46567016
0	3.760040161	17.46567016
0	2.437037476	11.24975616
0	2.437037476	11.24975616

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

Genes
IL1RN;TNFRSF6B;IL23R;ICAM1;SOX2;MT2A;PSMD7;PSMD4;MYC;AKT1;TNF
CD86;CSF3;IL1RN;CSF2;IL23R;CD80;IL5RA;RORA;AQP4;TNF;ICAM1;SOX2;
CD86;APP;CSF2;IL23R;CD80;SERPINE1;RORA;PARK7;TNF;CYP1B1;IL12B;I
CD86;APP;CSF3;NCF1;EPO;IRS1;CD80;PARK7;FGF1;TNF;IGF1R;NR3C2;SO
APP;SERPINE1;RORA;PARK7;TNF;ETS1;IL12B;CCN3;GHSR;ADIPOQ;FOXP
IL1RN;HP;CXCL13;TNF;C3AR1;LGALS9;TNFRSF4;CMKLR1;SLC11A1;F2R;C
TNFRSF6B;PARK7;CLU;TNF;IKZF3;MPO;IGF1R;LGALS1;MYC;CFL1;KDR;TN
CD86;APP;CSF3;CSF2;EPO;IRS1;REG1A;SIRPG;FGF1;CLU;ETS1;IGF1R;ST
SERPINE1;ENO1;TNF;IGF1R;GJA1;CFL1;LEPR;IL12B;CMKLR1;GHSR;IL4R;
TNFRSF6B;PARK7;TNF;MPO;IGF1R;MYC;CFL1;KDR;AKT1;HGF;F2R;LIG4;P
APP;TNFAIP3;HSPB1;PTPN22;HMGB1;CLU;CX3CL1;VSIR;IFIH1;IL12B;LGAL
APP;CSF2;FMR1;HFE;PARK7;RBPJ;FGF1;CLU;TNF;ETS1;ACTB;ACTG2;AC
CD86;CSF3;CSF2;EPO;IRS1;FMR1;REG1A;SIRPG;HP;FGF1;TNF;ETS1;CXC
APP;SERPINE1;RBPJ;SOX2;KAT5;ZMIZ1;MYC;AKT1;TNFSF11;KAT8;TP63;S
APP;CSF2;HFE;FMR1;PARK7;RBPJ;FGF1;CLU;TNF;ETS1;ACTG2;ACTG1;G
APP;CSF3;HFE;CD80;FMR1;PARK7;FGF1;TNF;CCND1;KDR;ENPP2;LEPR;A
APP;TNFAIP3;PTPN22;HMGB1;TNF;CX3CL1;IFIH1;C1QTNF3;LGALS9;LBP;I
APP;CD40;LRRK2;PTPN22;HMGB1;FGF1;TNF;ADRA1A;CX3CL1;PIK3CG;IC
APP;CRTC2;CSF3;SERPINE1;RORA;PARK7;AHR;RBPJ;NR3C1;FGF1;ETS1;
TNFRSF6B;PARK7;MPO;IGF1R;MYC;CFL1;KDR;AKT1;HGF;MIF;PRLR;YME1
CD86;CSF3;CSF2;EPO;IRS1;REG1A;SIRPG;IL5RA;RBPJ;FGF1;TNF;IGF1R;G
CD86;CXCL9;CXCL8;CD80;IL23R;GFI1;SERPINE1;TNFAIP3;PTPN22;CXCL1
APP;LPL;HMGB1;NOD2;BCL10;TNF;AGER;AIF1;HSPD1;IFIH1;MBP;LBP;LGA
CD86;APP;HSPB1;HMGB1;CLU;IFIH1;IL12B;LBP;LGALS9;EPHB2;JAK2;CCR
APP;CSF2;HFE;RORA;PARK7;AHR;RBPJ;NR3C1;FGF1;ETS1;CLU;TNF;ACT
CIITA;AQP4;CX3CL1;ICAM1;MT2A;CASP1;LGALS9;JAK2;B2M;HLA-DPA1;JA
APP;CD40;CSF3;CRTC2;PARK7;CLU;TNF;CX3CL1;SHH;FLOT1;AKT1;TNFSF
APP;HSPB1;LPL;HMGB1;NOD2;PSEN1;CLU;THBS1;AGER;RASGRP1;IFIH1;
IL21;APP;SERPINE1;TNF;ETS1;CX3CL1;MDK;IL12B;LBP;CCR2;IL15;IL18;IL1
CD40;TNFRSF6B;CXCL8;BRCA1;TNFRSF13C;TNF;CX3CL1;TNFSF13B;PSM
CD86;IL21;CD274;CD40;CD80;IL23R;TNFRSF13C;CD1D;AIF1;TNFSF13B;HL
CD86;IL21;CD274;CD80;IL23R;SIRPG;TNFRSF13C;NOD2;GATA3;CD1D;AIF1
IL21;APP;SERPINE1;TNF;ETS1;CX3CL1;MDK;IL12B;CCR2;IL15;IL18;PRKCA
IL23R;IFNA2;TNFAIP3;PTPN22;HMGB1;TNF;CX3CL1;VSIR;IFIH1;C1QTNF3;K
IL21;CSF3;CD40;CSF2;EPO;CD80;IL23R;IFNA2;TNF;ENPP2;IL12B;IL12A;JAK
CD86;CXCL9;CXCL8;CD80;GFI1;SERPINE1;TNFAIP3;PTPN22;CXCL1;HMGB
CD86;CXCL9;CXCL8;NCF1;IRS1;GFI1;CD80;SERPINE1;TNFAIP3;RORA;CXC
CRP;PLA2G1B;SERPINE1;PTPN22;PARK7;HMGB1;NOD2;BCL10;TNF;RELA
IL21;APP;SERPINE1;TNF;ETS1;CX3CL1;MDK;IL12B;CCR2;IL15;IL18;IL16;IL1
APP;CSF1R;AIRE;LPL;HMGB1;TNF;HIF1A;AGER;AIF1;HMOX1;MBP;LGALS9
CD86;IL21;CD274;CD80;IL23R;EBI3;HMGB1;TNFRSF13C;CD1D;AGER;AIF1;

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

ITGB1;BMPR2;FAM107A;PIK3CD;LAMC2;FGF1;VSIR;CXCL16;ACTG1;IGF1R
APP;PTPN22;HMGB1;TNF;ADRA1A;CX3CL1;ICAM1;SPRED2;KDR;TIMP3;CC
APP;CSF3;CD40;CIITA;IL23R;CXCL16;IL18BP;CASP8;CASP3;SMPD1;TIMP2
CD86;ITGB1;CSF3;IRS1;CD80;PIK3CD;PARK7;PIK3CB;FGF1;TNF;CX3CL1;P
ITGB1;CD40;BTG1;CXCL8;SERPINE1;TNFAIP3;HSPB1;PIK3CD;FASLG;PRL;
CD86;IL21;CD274;CD80;IL23R;IL27;TNFRSF13C;CD1D;AIF1;LGALS3;HLA-D
CD86;ITGB1;CSF3;IRS1;CD80;PIK3CD;PARK7;PIK3CB;FGF1;TNF;CX3CL1;P
ITGB1;FAM107A;PIK3CD;LAMC2;FGF1;VSIR;CXCL16;ACTG1;IGF1R;MDK;K
CD86;NCF1;EPO;CD80;RORA;AHR;TNF;ETS1;SOX2;SALL1;KAT5;ZMIZ1;CD
APP;CD40;CLU;TNF;CX3CL1;FLOT1;TNFSF11;LGALS9;MAP3K7;PRKCB;SP
PLA2G1B;SERPINE1;PARK7;HMGB1;NOD2;BCL10;TNF;RELA;RIPK1;LBP;L
ITGB1;SERPINE1;FAM107A;PIK3CD;LAMC2;FGF1;VSIR;CX3CL1;CXCL16;A
IL21;CD274;IL23R;EBI3;PTPN22;IL27;HMGB1;RASGRP1;VSIR;HSPD1;IL12B
CD86;CXCL9;CXCL8;CD80;GFI1;SERPINE1;TNFAIP3;CXCL1;HMGB1;CXCL1
DDR1;APP;CD40;FMR1;LRRK2;IFNA2;FGF1;TNF;IGF1R;MYDGF;CCND1;KD
APP;PTPN22;HMGB1;TNF;ADRA1A;CX3CL1;ICAM1;KDR;TNFSF11;CCR7;LG
IRS1;CD80;LRRK2;TNFAIP3;SLC2A4;RBPJ;GLI1;FGF1;SHH;CDH3;SALL1;ZM
CD40;IL23R;HMGB1;MEFV;THBS1;AGER;HSPD1;MDK;IL12B;CCR7;LGALS9
CX3CR1;APP;GSTP1;TNFAIP3;HSPB1;LPL;NOD2;NLRC4;MEFV;TNF;AGER;
CD274;IL23R;HMGB1;NOD2;AGER;VSIR;HSPD1;IL12B;LGALS9;TIGIT;JAK3;
ITGB1;CD40;ITGB2;PTPN22;AHR;ICAM5;CXCL13;ITGAL;PVR;ICAM1;FCGR3
IL21;PIK3CD;TNF;PIK3CG;IFIH1;C1QTNF3;CASP8;FLOT1;IL12B;CCR7;LGAL
CD86;CXCL9;CXCL8;IRS1;GFI1;CD80;SERPINE1;TNFAIP3;RORA;CXCL1;AH
HMGB1;CXCL13;ADRA1A;GRM1;EDNRA;C3AR1;CCR9;BDKRB1;CCR8;CCR
CCL13;CXCL9;CXCL8;CCL11;PLA2G1B;ITGB2;PIK3CD;CXCL1;CXCL13;CXC
PSMD10;PSMD12;CD40;TNFRSF6B;TNFRSF11B;TNFRSF11A;TNFRSF13C;
CCL13;CXCL9;CXCL8;CCL11;PLA2G1B;ITGB2;PIK3CD;CXCL1;CXCL13;CXC
CX3CR1;CXCL8;LRRK2;CXCR5;CXCR4;CXCR6;EGFR;TRPM2;EDNRB;CXC
CCL13;CXCL9;CXCL8;CCL11;PLA2G1B;ITGB2;PIK3CD;CXCL1;CXCL13;CXC
CDKN1C;APP;BTG1;CXCL8;BMPR2;SIRPG;TNFAIP3;CXCL1;ETS1;ADRA1A;
HP;MPO;LGALS3;PSMD7;ANPEP;C3AR1;PRSS3;B2M;CD177;SLC11A1;HLA
APP;EPO;SIRPG;ENO1;PARK7;CLU;ETS1;GJA1;STK11;MYC;CYP1B1;CCN3
APP;CSF3;CD80;IL23R;ITGB2;EGFR;IL22RA2;NTF3;ENPP2;ABL1;IL12B;TNF
CSF1R;APP;AIRE;LPL;TNF;HIF1A;AGER;AIF1;HMOX1;LGALS9;IL6R;EGR1;I
CX3CR1;CXCL8;LRRK2;CXCR5;CXCR4;CXCR6;HRH1;EDNRB;CXCR1;CXC
APP;IFNA2;ITGB2;PRF1;ATN1;FASLG;AHR;ADRA1A;CASP9;STK11;CASP8;
CIITA;PTAFR;ICAM1;MT2A;NCAM1;JAK2;FCGR1A;B2M;HLA-DQA2;HLA-DQ
IL21;CSF1R;CD40;CSF2;EPO;IL23R;IFNA2;TNF;IL22RA2;SOCS3;SOCS1;CC
GPI;SERPINA3;SNAP25;SERPINA1;ITGAM;ITGB2;CTSZ;HP;HBB;CXCL1;HM
CXCL8;IL23R;TNFAIP3;PTPN22;TNFRSF11A;CXCL2;PRDX3;CYP27B1;IRAK
GPI;SERPINA3;SNAP25;SERPINA1;ITGAM;ITGB2;CTSZ;HP;HBB;CXCL1;HM
GRN;ITGAM;PLA2G1B;IL23R;ITGB2;NOD2;CD1D;GPR151;HLA-DMB;CCL5;I

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

ITGB1;FOXC2;CD40;GRN;CXCL8;BTG1;SERPINE1;HSPB1;PIK3CD;BRCA1;F
CCL13;CD40;CIITA;CCL11;IL23R;AQP4;MEFV;AIF1;CX3CL1;CXCL16;CYP27
APP;HSPB1;LPL;HMGB1;NOD2;NLRC4;TNF;AGER;MALT1;PANX1;CASP8;IF
IL21;CSF1R;CD40;CSF2;EPO;IL23R;IFNA2;TNF;SOCS3;CCL5;IL12B;IL12A;J
APP;CD40;FMR1;LRRK2;FGF1;TNF;MYDGF;KAT5;CCND1;SMPD1;KDR;LEP
APP;CD40;FMR1;LRRK2;ITGB2;HSPB1;PARK7;FGF1;TNF;MYDGF;CCND1;K
CCL13;CXCL9;FOXC1;CXCL8;CCL11;CXCL1;CXCL13;CXCL2;CX3CL1;CXCL
APP;HSPB1;LPL;NOD2;NLRC4;TNF;AGER;MALT1;PANX1;CASP8;IFI16;CAS
CSF2;GSTP1;SERPINE1;TNFAIP3;FASLG;PARK7;BRCA1;TNF;THBS1;RELA
CSF3;NCF1;EPO;MAZ;PIK3CD;PIK3CB;TNF;PIK3CG;IGF1R;INS;MYDGF;ER
ITGB1;BTG1;FASLG;HMGB1;CLU;TNF;CASP9;CASP8;SMPD1;CASP3;TNFS
CCL13;CXCL9;FOXC1;CXCL8;CCL11;CXCL1;CXCL13;CXCL2;CX3CL1;CXCL
RNASEL;TNFAIP3;SPATA2;TNF;USP18;SOCS3;CASP8;SOCS1;IRAK1;RIPK
CX3CR1;PTGER4;CXCR5;LPAR2;CXCR4;LPAR3;ITPR3;HMGB1;CXCR6;CXC
CD86;APP;PTPN22;NOD2;PHB;TNF;AGER;RELA;EGFR;NR3C2;C1QTNF3;IR
IL21;IL23R;EBI3;PTPN22;IL27;RASGRP1;HSPD1;IL12B;IL12A;LGALS9;CD14
ITGB1;CD40;GRN;CXCL8;BTG1;SERPINE1;HSPB1;PIK3CD;BRCA1;FGF1;ET
TNFAIP3;PHB;TNF;THBS1;AIF1;CX3CL1;CCL5;AKT1;IL12B;MFN2;HMOX1;IL
GPI;FOXC2;CD40;GRN;BMPR2;HSPB1;PIK3CD;PIK3CB;HMGB1;GATA3;FGF
IL23R;PTPN22;TNFRSF11A;FOXO3;PRDX3;CYP27B1;IRAK1;BGLAP;SPP1;C
IFNA1;IFNA2;PIK3CD;PTPN22;GATA3;RASGRP1;PIK3CG;HSPD1;INS;DPP4;
VIPR2;TNFAIP3;ADM;RORA;C1QTNF3;FCGR3A;MDK;CCN3;IL10;GHSR;IL13
CCR1;CCL21;CXCR4;HMGB1;PIK3CG;TRPM2;CXCR1;GPR183;CCL5;CXCR
FASLG;TNF;CASP9;CASP8;ERBB3;BAG3;CASP3;IL12A;RIPK1;JAK2;BID;IL6
CCR1;CCL21;CXCR4;HMGB1;PIK3CG;TRPM2;CXCR1;GPR183;ALOX5;CCL5
APP;CXCL8;IFNA2;PTPN22;PARK7;TNF;MECP2;YY1;KDR;LGALS9;CD34;HA
SEMA7A;GRN;ALOX15;SPATA2;XIAP;CXCR4;PTPN22;PARK7;NOD2;PTGS2
APP;CD40;CIITA;NCF1;IL23R;PIK3CD;HMGB1;PIK3CG;CXCL16;IFIH1;SMPD
IL21;PRNP;TGFB1;IL15;IL23R;SPHK1;OSM;IL18;PHB;NOD2;FOXP3;VSIR;IL2
APP;CCL13;CD40;CXCL8;CCL11;TNFRSF11A;HIF1A;CX3CL1;RELA;IRAK1;C
CD86;APP;NOD2;PHB;TNF;AGER;RELA;EGFR;NR3C2;IRAK1;IL12B;LGALS9
PSMD10;GSTP1;IQGAP1;ADRB2;HMGB1;RASGRP1;ADRA1A;CX3CL1;EGFR
CD40;IL23R;IL16;HMGB1;MAPK14;AGER;HLA-G;HSPD1;CD40LG;IFNG;MDK
ITGB1;LRRK2;PRF1;FASLG;HMGB1;CLU;TNF;CASP9;CASP8;SMPD1;CASP
CSF1R;SERPINE1;HMGB1;PTN;THBS1;AIF1;PLA2G7;MDK;CCL5;MAPK1;CC
CX3CR1;APP;C1QA;GRN;ITGAM;IFNGR1;ITGB2;CLU;TNF;AGER;AIF1;CX3C
BLK;IL21;CD40;TNFRSF13C;AHR;IKZF3;TNFSF13B;CTLA4;CD38;EPHB2;TN
PSMD10;CSF1R;CEMIP;CD40;LRRK2;MST1R;ADRB2;NOD2;FGF1;TNF;RAS
CSF3;NCF1;EPO;MAZ;PIK3CD;PIK3CB;TNF;PIK3CG;EGFR;IGF1R;INS;MYD
CSF2;EPO;EHMT2;GFI1;ATN1;IKZF1;ENO1;AHR;RBPJ;NR3C1;TNF;YY1;SO
GSTP1;FASLG;PARK7;BCL10;TNF;THBS1;RELA;LGALS3;CASP8;TNFSF10;
CD40;HSPB1;PRCP;HMGB1;TNF;ETS1;THBS1;HIF1A;MECP2;KDR;AKT1;AP

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

NCF1;LRRK2;GSTP1;PARK7;FOXO3;HIF1A;AIF1;EGFR;ARNTL;PRDX3;PRD
PIK3CD;PTPN22;PIK3CB;PSMD7;PSMD4;GRAP2;CTLA4;CD38;MAP3K7;ICO
BMPR2;ADM;RBPJ;BRCA2;TNF;SLC6A4;SPRED2;GJA1;SHH;STK11;MDK;TI
C1QA;GRN;ITGAM;ITGB2;FOXO3;CLU;TNF;CCL3;FYN;MAP3K5;SNCA;EGR1
CXCL8;IRS1;PTH;FMR1;HBB;PARK7;PLD1;GLI1;PTGS2;CLU;TNF;HIF1A;TH
CD40;TNFAIP3;HSPB1;RORA;FASLG;TNF;CX3CL1;GJA1;LGALS1;CASP8;T
CCL13;CCL11;CCL22;CCL21;CCL20;PIK3CD;CXCL13;CYP7B1;CX3CL1;PIK3
CIITA;IRS1;PTH;FMR1;NOD2;PLD1;GLI1;THBS1;EGFR;INS;MYC;KDR;AKT1;
CXCL8;UHRF1;FMR1;GATA3;THBS1;INS;CCL5;NTF3;AKT1;RIPK1;APOE;SN
LRRK2;SLC1A1;RORA;AHR;BRCA1;NR3C1;TFPI;TNF;ACTB;EGFR;ZFP36L1
LRRK2;IKZF3;CLU;TNF;LGALS1;CASP1;AKT1;JAK2;JAK3;TP63;HTATIP2;TG
APP;EHMT2;GFI1;SERPINE1;IKZF1;ENO1;RBPJ;IKZF3;BACH2;SOX2;EDNR
IL21;CD40;RNASEL;IFNA2;PRF1;PHB;RELA;IFIH1;IFI16;FLNA;NLRP1;IFNL3;
CSF1R;IL23R;AGAP2;IQGAP1;ADRB2;CLU;TNF;STK11;RAP1A;ERBB3;CCL5
C1QA;ITGAM;LRRK2;CTSZ;ITGB2;PARK7;CLU;GRM4;CCL5;AKT1;FYN;CD3
CCL13;CD40;CXCL8;CCL11;GATA3;TNFRSF11A;BRCA1;CX3CL1;RELA;CXC
CSF1R;CSF3;CSF2;GLO1;PIK3CD;TNFRSF11A;CASP8;IFI16;TNFSF11;CCR
IL21;CD40;RNASEL;IFNA2;PRF1;RELA;IFIH1;IFI16;FLNA;NLRP1;IFNL3;MICA
PTPN22;RELA;HSPD1;IFIH1;IFI16;IRAK1;FLOT1;STAT6;CD14;HSP90AA1;DD
IL10;CD274;GHSR;ARG2;IL37;GSTP1;ADIPOQ;TNFAIP3;PTPN22;LILRB1;IG
STAT5A;FOXC2;CD40;TGFB1;ANXA1;NOS3;HSPB1;PRKCA;HMGB1;PTGS2;
CD274;TSLP;STAT3;IL13;HMGB1;NOD2;HSPD1;IL4;IL6;CD40LG;IL23A;TLR9
GRN;SEMA7A;ALOX15;SPATA2;XIAP;PTPN22;PARK7;NOD2;PTGS2;USP18
APP;C1QA;ITGAM;IFNGR1;SLC11A1;ITGB2;IL13;CLU;TNF;AGER;AIF1;CX3C
CD86;PARK7;PHB;TXN;ADRB2;FGF1;MALT1;INS;STK11;IRAK1;NTF3;ABL1;
CD86;APP;UHRF1;CD80;IL23R;TNFAIP3;BCL10;PSEN1;CLU;TNF;RASGRP1
CD40;RGS14;LRRK2;GSTP1;MST1R;PIK3CB;NOD2;FGF1;TNF;RASGRP1;PI
CSF2;IRS1;LRRK2;IL5RA;PIK3CB;FGF1;TNF;PSMD7;PSMD4;MYC;KDR;CTS
NOTCH2;GRN;BMPR2;CCL11;TGFA;PIK3CD;NOD2;PTN;FGF1;HIF1A;RTN4;
RNASEL;IFNA1;IFNA2;IRAK1;JAK1;IFNAR2;EGR1;STAT1;IFNB1;IFNA17;MX
RNASEL;IFNA1;IFNA2;IRAK1;JAK1;IFNAR2;EGR1;STAT1;IFNB1;IFNA17;MX
IL10;GHSR;ARG2;IL37;GSTP1;ADIPOQ;TNFAIP3;PTPN22;LILRB1;IGF1;CX3
IL10;EDN1;STAT1;MMP2;IL18;PHB;IGF1;THBS1;TNF;AIF1;MMP9;CX3CL1;F
LRRK2;SLC1A1;TNF;TRPM2;CYP27B1;BGLAP;CCL5;SPP1;CCL3;CYP1B1;C
APP;CXCL8;FMR1;IFNA2;PTPN22;PARK7;TNF;MECP2;YY1;KDR;LGALS9;C
CCL13;CCL11;ANXA1;CCL22;CCL21;CCL20;TNFRSF11A;CX3CL1;LGALS3;I
FOXC1;NOTCH1;CXCL8;BMPR2;HSPB1;IQGAP1;LRP2;NR3C1;RELA;EGFR;
PSMD10;PSMD12;WAS;PIK3CD;PTPN22;BCL10;GATA3;PIK3CB;RELA;MALT
DDR1;NCF1;IRS1;PLAT;PIK3CB;FGF1;ACTB;ACTG1;IGF1R;SPRED2;CASP3
CSF3;BTG1;CSF2;BMPR2;GJA1;MDK;KDR;AKT1;CD34;IL6R;TP63;CMKLR1;
GPI;FOXC2;GRN;BMPR2;PIK3CD;PIK3CB;GATA3;FGF1;ETS1;THBS1;HIF1A
BMPR2;CCL11;PIK3CD;HMGB1;HIF1A;MYDGF;MDK;KDR;AKT1;HMOX1;STA

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

FASLG;BCL10;HMGB1;NLRC4;TNF;MALT1;HSPD1;CASP9;CASP8;MYC;TNF
ACHE;FH;HDAC3;EPAS1;CXCR4;ADRB2;TNF;IGF1R;INS;GJA1;UCP2;LEPR;
CCR1;SERPINE1;HMGB1;TNF;AGER;AIF1;PLA2G7;IL4;LGALS3;CXCL10;CX
ITGAM;ITGB2;HMGB1;BCL10;HSPD1;CASP8;IRAK1;UBC;RIPK1;LBP;LGALS
ACHE;FH;HDAC3;EPAS1;CXCR4;ADRB2;IGF1R;GJA1;UCP2;LEPR;MFN2;ST
CX3CR1;CXCR5;CXCR4;CXCR6;CX3CL1;CXCR1;CXCR3;CXCR2;CCR9;CCR
CD40;LRRK2;TNFRSF11A;NOD2;MST1R;FGF1;TNF;RASGRP1;PIK3CG;EGF
GRN;LRRK2;AGAP2;PARK7;ERBB3;MDK;NTF3;AKT1;CCL2;APOE;PPARGC
IL33;SPHK1;MMP3;IL18;IGF1;MMP8;TNFRSF1B;PTGS2;TNF;MMP9;IL4;CD2
IL10;EGR1;TGFB2;TGFB1;STAT3;PRL;GATA3;FOS;NR3C1;FOXO3;KLF4;TN
EPO;EHMT2;GFI1;ATN1;ENO1;RBPJ;NR3C1;TNF;YY1;SOX2;SALL1;EDNRB;
APP;CSF3;IFNA1;IFNA2;PARK7;TXN;TNF;EGFR;NTF3;AKT1;NOS1;SNCA;IL
C1QA;ITGAM;LRP1;LRRK2;ITGB2;HP;HBB;PHB;CLU;TNF;RIPK1;FYN;HTATI
NCF1;LRRK2;GSTP1;PARK7;FOXO3;AIF1;PRDX3;PRDX2;PRDX5;ABL1;PPA
IL10;EGR1;TGFB2;TGFB1;STAT3;PRL;GATA3;FOS;NR3C1;FOXO3;KLF4;TN
CD40;FASLG;BCL10;NOD2;TNF;CX3CL1;RELA;MALT1;GJA1;LGALS1;CASP
CD86;ITGB1;CD40;IFNA1;IFNA2;PIK3CD;PHB;RASGRP1;MALT1;HSPD1;CA
CSF1R;CSF3;BMPR2;LRRK2;SLC1A1;CXCR4;PARK7;LRP2;TNF;IL18BP;MA
CD86;PRNP;ANXA1;CD80;TNFAIP3;TRAF2;FOXP3;MALT1;IL1A;PTPRC;KAT
IL21;CD74;CD40;XBP1;FCRL3;TNFRSF13C;MIF;NOD2;IL2;TNFSF13B;IL4;IL6
GRN;AGAP2;PARK7;FOXO3;TNF;GRM4;ERBB3;MDK;NTF3;CCL3;CCL2;APO
IL21;HSP90AA1;DDX58;IFNB1;FMR1;MAPK14;HIF1A;IRGM;IFIH1;CXCL10;IL
IL10;IL11;CD40;ITGA4;SERPINE1;IL13;TNFAIP3;FASLG;GATA3;THBS1;TNF;
BLK;APP;SERPINA3;SERPINA1;SERPINE1;PLG;CLU;THBS1;KNG1;TIMP3;F
NCF1;TXNRD2;GSTP1;HP;HBB;FOS;SOD2;MMP9;SIRT1;HIF1A;EGFR;SOD1
CCL13;CCL11;CCL22;CCL21;CCL20;MSN;GATA3;CX3CL1;CCL7;CCL5;TBX2
CX3CR1;EDN1;HSP90AA1;CAV1;HBB;PTGS2;MMP8;KLF4;CLU;TNF;P2RX4;
PSMD10;CCL13;IL1RN;PSMD12;CD40;CXCL8;CCL11;NOD2;HIF1A;CX3CL1;
IL10;XBP1;IL23R;LILRB1;PHB;IL2;HLA-DMB;PTPRC;IFNG;IL23A;IL1B;IL12B;
IL10;NOTCH1;EGF;IL10RB;CAV1;IL10RA;F2R;PRL;TNF;SOCS3;GH1;IL6;SO
CXCL8;IRS1;LRRK2;TNFAIP3;PIK3CB;TNF;CX3CL1;SMPD1;AKT1;IL12B;IL12
ITGB1;CCL13;CD40;CCL11;RASGRP1;CX3CL1;DOCK11;MAPK8;RAP1A;CC
GPI;FOXC2;GRN;BMPR2;PIK3CD;PRCP;PIK3CB;PTN;GATA3;FGF1;ETS1;TH
LRP1;KMT2A;FMR1;SIRPG;PON1;TNF;ACTB;CDH3;SMPD1;FLOT1;APOE;C
APP;EPHA4;PRNP;XBP1;VCAM1;ITGA4;LRP1;CAV1;PTPN22;NOD2;ADRB2;
CRP;PLA2G1B;IL23R;SERPINE1;NOD2;NLRC4;CXCL13;PLA2G6;CFP;MPO;I
BMPR2;CCL11;PIK3CD;PRL;THBS1;HIF1A;MYDGF;ALOX5;KDR;KRIT1;AKT1
ANXA1;NCF1;TNFAIP3;PARK7;FOS;MMP9;SIRT1;RELA;EGFR;PRDX3;TRPM
NOS3;SERPINE1;TNFAIP3;TNFRSF10B;FASLG;TNFRSF10A;TRAF2;PARK7;
CD274;PRNP;IL23R;IL18;HMGB1;IGF1;PDCD1LG2;AGER;FOXP3;IL2;IL23A;P
BMPR2;FMR1;PSEN1;PRL;PTN;TNF;RTN4;INS;GJA1;SHH;MDK;CFL1;NLRP
IL21;CD74;CD40;FCRL3;TNFRSF13C;MIF;IL2;TNFSF13B;IL4;PTPRC;IL7;GP

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

IL21;ITGAM;NOS2;IL23R;HLA-B;CD1D;HLA-A;HLA-F;PVR;RASGRP1;HLA-G;
FASLG;NLRC4;TNF;HSPD1;CASP9;CASP8;CASP1;TNFSF10;RIPK1;NLRP1;
STAT5A;STAT5B;PRNP;ANXA1;IRS1;STAT1;MMP2;REG1A;STAT3;MMP3;NO
IL21;TGFB1;IL15;IL23R;SPHK1;OSM;IL18;PHB;NOD2;IL2;IL6;IL23A;IL12B;CC
WWOX;TNFRSF12A;IFNB1;CAV1;TNFSF12;TRAF2;BCL10;TNF;TGFBR1;AG
BLK;APP;SNAP25;SERPINA3;SERPINA1;SERPINE1;PLG;CLU;THBS1;KNG1
TGFB1;EIF2AK3;RORA;BRCA1;PTGS2;HIF1A;C3;IL1A;SARS1;IL6;IL1B;CYP1
ITGB2;SIRPG;TNF;ETS1;RELA;HSPD1;IL6;IRAK1;MDK;TRAF6;HLA-DPB1;TN
IL21;IFNAR2;STAT5A;STAT5B;STAT1;IL15;CTR9;STAT3;IFNG;LEP;STAT4;C
TGFB1;PRKCE;IL18;PTPN22;BCL10;TNF;IRAK1;IL1B;CCL5;CCL3;CCL2;LBP;
CD274;IL23R;LILRB1;PDCD1LG2;MMP8;AGER;FOXP3;VSIR;TYROBP;IL23A;
PSMD10;CX3CR1;GSTP1;MAZ;PARK7;CLU;TNF;THBS1;CX3CL1;RELA;LGA
IL23R;HLA-B;TRAF2;CD1D;HLA-A;HLA-F;HLA-G;MALT1;HSPD1;IL23A;IL1B;T
CDKN1C;CIITA;CSF2;GFI1;IFNA2;ENO1;AHR;IKZF1;BRCA1;RBPJ;NR3C1;TN
ITGB1;VCAM1;ITGA4;ITGB2;MSN;ITGAL;SELE;ICAM1;SELP;NT5E;CD40LG;
PSMD10;SLC44A4;BTG1;BMPR2;FAM107A;ENO1;PHB;EGFR;RTN4;CXCL16
IL10;IL1RN;NOTCH1;TGFB1;JAG1;NOTCH4;ADIPOQ;APOA1;PLG;KLF4;VEG
PTGER4;MACIR;SERPINE1;TNFAIP3;RORA;GATA3;MEFV;C1QTNF3;IFI16;A
SNAP25;ACHE;PLA2G1B;ITPR3;HMGCR;TNF;ARNTL;INS;DPP4;RAP1A;ALO
APP;CSF3;PARK7;TXN;TNF;EGFR;NTF3;AKT1;NOS1;SNCA;IL11;HSP90AA1
DDR1;APP;BMPR2;LRRK2;PIK3CD;STK19;IGF1R;STK11;KDR;AKT1;JAK2;E
TRAF2;BCL10;TNF;RELA;TNFRSF1A;RELB;NFKBIA;TRAF6;UBC;BCL3;TLR9
APP;ENTPD1;IL18;TXN;MEFV;C3;P2RX7;NT5E;P2RX4;IL1B;C3AR1;CASP1;T
ITGB1;IL10;EDN1;NCF1;HDAC1;EGF;HFE;TGFA;PARK7;ADRB2;HIF1A;ADR
FOXC2;SIRPG;ALOX15;TNF;ADGRG1;MDK;CCL5;IL12B;CCR7;IL12A;JAK2;T
NOS3;SERPINE1;TNFAIP3;TNFRSF10B;FASLG;TNFRSF10A;TRAF2;BRCA1;
CD86;IL21;IL10;GPI;XBP1;SPHK2;PTPN22;PHB;NOD2;IL2;IL6;PTPRC;TLR9;
CDKN1C;CIITA;CSF2;BMPR2;FMR1;GFI1;IFNA2;ENO1;AHR;IKZF1;BRCA1;R
BLK;CSF1R;CSF2;LILRB1;IKZF1;RELB;VEGFA;IL4;BMP4;TRPM2;IFI16;AXL;I
CHGA;IL11;NOTCH1;ANXA1;LIF;OSM;LILRB1;HMGCR;TNFRSF1B;INS;TNFR
APP;CEMIP;TGFB1;DMTN;EGF;SPHK1;IRGM;BMP7;SIRT2;SMAD7;SPRED2
HSP90AA1;DDX58;LILRB1;PTPN11;RELB;YY1;IFIH1;MAVS;OAS1;STING1;T
ANXA1;HP;HBB;TNFAIP3;PARK7;SIRT1;RELA;SOD1;PRDX3;TRPM2;IL6;CA
APP;CSF3;FOXC1;LRP1;HFE;LRRK2;PON1;HMGB1;TXN;PSEN1;STMN1;FL
APP;PRNP;EPHA4;VCAM1;LRP1;ITGA4;MMP2;MMP3;PSEN1;ADRB2;IGF1;A
HFE;TRAF2;HLA-A;TNFRSF1B;HLA-F;FOXP3;MALT1;SMAD7;TRAF6;B2M;M
PTGER4;VIPR2;PTH;ALOX15;TNFAIP3;ADM;ADRB2;CRHR1;PTHLH;LGALS3
DDX58;IL23A;IL23R;CD80;IL1B;IL18;TLR9;IL12B;PAEP;IL17F;IL17D;RASGRP
PTGER4;MACIR;TNFAIP3;RORA;GATA3;MEFV;C1QTNF3;IFI16;ALOX5;NLR
S100A1;HMGB1;NOD2;BCL10;TLR1;IRAK1;TRAF3;TRAF6;UBC;TLR9;TLR8;T
CD86;IL10;CD274;ARG1;IFNB1;CD80;IFNA2;PTPN22;LILRB1;PDCD1LG2;HL
DDR1;CSF1R;AGAP2;MST1R;IQGAP1;TNF;EGFR;IGF1R;RAP1A;ERBB3;KD

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

FOXC1;SERPINE1;FASLG;PIK3CB;PRL;TNF;THBS1;MECP2;ADAMTS1;ALO
APP;CCL21;AIRE;CCL20;AIF1;CXCL10;CD200R1;CXCL12;CCL5;TNFRSF14;
SMAD4;SELPLG;STAT1;CTR9;STAT3;PTPN11;PHB;RELA;NFKB1;SOCS3;IL
CD86;IL21;IL10;GPI;XBP1;FCRL3;PHB;IL2;IL4;IL6;PTPRC;TLR9;MZB1;EPHB
TGFB1;PIK3R3;IGF1;TNF;SIRT2;ZFP36L1;IL1B;CCL5;KDR;TYRO3;CCL3;AKT
IL10;TGFB2;TGFB1;TGFB3;HFE;APOA1;LILRB1;HLA-F;TNF;FOXP3;JAK3;S M
DDX58;IL23A;IL23R;CD80;IL1B;IL18;TLR9;IL12B;PAEP;IL17D;RASGRP1
IL33;EDN1;IFNG;GSTP1;KDR;TLR9;CCL2;NOD2;JAK2;TLR4;TLR2
IL10;TGFB3;IGFBP3;ADIPOQ;TNFAIP3;SOD2;AIF1;APLN;IFNG;MFN2;HMOX
IL10;SERPINB2;ANXA2;GSTO1;MSN;TALDO1;MIF;SOD2;LMNB1;SOD1;IFNG
CX3CR1;GRN;TGFB3;BDNF;F2R;AGAP2;LIG4;PARK7;NGF;SOD2;HIF1A;CX
MACIR;NOS2;STAT3;NOD2;MEFV;MAPK14;TNF;HIF1A;IL17RA;IL6;ALOX5;L
CD274;PRNP;LILRB1;HMGB1;PDCD1LG2;FOXP3;VSIR;AXL;DDIT3;RARA;LG
IL23R;HLA-B;LILRB1;CD1D;HLA-A;HLA-F;AGER;HLA-G;CEACAM1;PTPRC;IL
ITGB1;IFNA1;IFNA2;PIK3CD;PTPN22;IKZF1;GATA3;RELB;DLL4;LEPR;JAK3;
TGFB1;EIF2AK3;RORA;BRCA1;PTGS2;HIF1A;C3;IL1A;IL6;IL1B;CYP1B1;HPS
PTGER4;CD40;TNFSF14;TNFRSF10B;TNFRSF10A;BCL10;NFKB1;TNFRSF1
CRP;ITGAM;TGFB1;GSTP1;ITGB2;MMP8;MAPK14;THBS1;AGT;SOD1;ACE2;
HSP90AA1;NOS3;S100A1;CAV1;PIK3CB;TNF;HIF1A;EGFR;INS;IL1A;DDAH1;
XBP1;IFNB1;IFNA2;GATA3;FOXP3;IL2;SOD1;IL4;IFNG;MDK;ZMIZ1;IL7;TBX2
APP;NCF1;SEMA3A;HMGB1;NOD2;AGER;RASGRP1;RIPK1;CCR7;CCL19;M
FTO;XBP1;TGFB1;ADIPOQ;LPL;RORA;GATA3;TNF;SIRT1;SIRT2;ZFP36L1;A
BMP4;CSF1R;CSF2;CASP8;PARP1;IFNG;IL15;MMP9;SIRT1;HLA-DRB1;VEG
DDR1;ITGB1;APP;ITGAM;NCAN;SERPINE1;ITGB2;LAMC2;ICAM5;ITGAL;ICA
CD86;ANXA1;CD80;TRAF2;MALT1;IL1A;PTPRC;IL1B;TRAF6;CD28;PRKD2;M
PSMD10;PSMD12;TNFSF15;TNFRSF10B;TRAF2;TNFRSF10A;RELA;MALT1;
P2RY12;TGFB1;CCL21;HSPB1;PTN;THBS1;AIF1;VEGFA;IL6;ADAM17;P2RX
ITGB1;FOXC2;XBP1;ANXA1;DMTN;PRKCE;SERPINE1;F2R;THBS1;MTOR;A
IL10;SERPINB2;ANXA2;GSTO1;MSN;TALDO1;MIF;SOD2;LMNB1;SOD1;IFNG
XIAP;HMGB1;BCL10;TNF;THBS1;MALT1;SOX2;MYC;CASP1;TNFSF10;AKT1
CD74;EDN1;TSLP;GFI1;CXCR4;HIF1A;IRGM;MAVS;ADAM17;IL7;AXL;CASP1
HSP90AA1;DDX58;PTPN11;IFIH1;MAVS;OAS1;STING1;IRF1;FLOT1;TLR9;TL
CCR1;CD74;IL23R;LIF;PRKCA;TNF;ZFP36L1;CASP8;IFNG;IL23A;TRAF6;TNF
ITGB1;CCL13;CD40;CCL11;LRRK2;RASGRP1;CX3CL1;DOCK11;KLRK1;RAP
EDN1;HSP90AA1;HBB;PTGS2;MMP8;KLF4;CLU;TNF;P2RX4;DDAH1;IFNG;IL
SPHK1;GSTP1;ADIPOQ;TNFAIP3;APOA1;SPATA2;TRAF2;TRAF1;TNF;TNFR
SIRPG;IL27;PTPN22;TNFRSF1B;HSPD1;LGALS3;CCL5;TBX21;ABL1;HLA-DP
ITGB1;ANXA1;DMTN;TNFRSF12A;CAV1;PRKCE;SERPINE1;F2R;TNFAIP3;A
CRP;NOTCH1;NOTCH4;CTR9;RORA;GATA3;TNF;EGFR;PTHLH;ARNTL;SOX
IL10;NOTCH1;TSLP;IL10RB;IL10RA;F2R;PRL;TNF;GH1;IL6;CCL5;MGAT5;LE
CCL13;LGALS3;CCL11;CCL21;CCL7;CCL5;CCL4;CCL3;CCL2;CCL1;CX3CL1
CCL13;LGALS3;CCL11;CCL21;CCL7;CCL5;CCL4;CCL3;CCL2;CCL1;CX3CL1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

SELP;IL6;IRAK1;MDK;TRAF6;ALOX5;ITGB2;TNF;SELE;ETS1;RELA
CCR1;PLA2G1B;SPHK2;CAV1;F2R;P2RX7;LGALS3;P2RX5;CXCL12;P2RX4;
FOXC1;TGFB2;STAT1;FASLG;PRL;KLF4;HLA-G;THBS1;DCN;PML;MECP2;C
CD74;OAS1;LPL;F2RL1;MBP;HMGB1;KLF4;TNF;TLR4;FOXP1
VDR;S100A1;PIK3CB;PARK7;TNF;HIF1A;INS;CYP27B1;CDH3;IFNG;IL1B;AK
EDN1;HSP90AA1;HBB;PTGS2;MMP8;KLF4;CLU;TNF;P2RX4;DDAH1;IFNG;IL
APP;EPHA4;TYROBP;FAM107A;ABL1;PTN;APOE;AGER
JAG1;CD8A;STAT3;EBI3;IL18;IL12B;PHB;CD46;TLR4;BACH2;HLA-DRB1;IL1 B
IL21;CST3;CEACAM1;TGFB1;IL15;MDK;IL23A;LEP;IL18;LEPR;IL12B;IL2
XBP1;IL23R;GATA3;HLA-G;VSIR;IL4;SHH;SOCS1;MDK;ZMIZ1;IL7;IL23A;IL1 2
IL10;NOTCH1;IL10RB;IL10RA;F2R;PRL;TNF;PRLR;IL4;GH1;IL6;CCL5;LEP;C
IL10;CD40;IFNA1;TNFSF14;IFNB1;IFNA17;IFNA2;MSN;RASGRP1;PIK3CG;H
CXCL8;TGFB1;TGFB3;F2R;APOA1;HSD17B13;MMP8;MTOR;INS;BMP4;CRE
FOXC1;NOTCH1;ANXA1;SPHK1;VEGFB;HSPB1;MAPK14;RELA;VEGFA;DLL
CEMIP;CXCL9;PLA2G1B;CAV1;F2R;CX3CL1;P2RX7;CXCL10;CXCL11;P2RX
APP;CEMIP;TGFB1;EGF;SPHK1;IRGM;BMP7;MAPK1;CHI3L1;CALM3;S1PR2
APP;CCL21;CCL20;CXCL13;AIF1;CXCL10;ADAM17;CXCL12;WNK1;CCL5;TN
IFNAR2;STAT5A;STAT5B;STAT1;CTR9;STAT3;IFNG;STAT4;CCL2;STAT6;JA
IL10;IL1RN;ADIPOQ;APOA1;KLF4;TNF;AGER;BMP7;WNK1;IL1B;FLOT1;MBP
IL10;STAT1;DDX58;HSPD1;IFIH1;MAVS;TLR9;TLR8;IRF5;TLR7;TLR4;TLR3; H
IL4;IL6;IL1B;TRAF6;IL18;NLRP3;TRAF2;HLA-A;B2M;MAP3K7;MALT1;IL18R1
STAT1;STAT3;EBI3;CANX;STAT4;IL12A;IL6ST;JAK2;JAK1
IL33;IFNG;KDR;TLR9;CCL2;NOD2;JAK2;TLR4;TLR2
BLK;CXCL12;CCL21;AXL;LILRB1;CCR7;CCL19;LGALS9;GAS6
CRP;TGFB1;ITGAM;TYROBP;GSTP1;ITGB2;F2RL1;MAPT;SOD1;CD177
DAXX;SORT1;TNFRSF10C;TNFRSF10B;FASLG;TNFRSF10A;NGF;TNF;TNF R
IL21;LILRB1;HLA-F;PVR;RASGRP1;HLA-G;NCR1;KLRK1;LEP;IL12A;CD226;L
APP;PRNP;EPHA4;VCAM1;LRP1;ITGA4;PSEN1;ADRB2;IGF1;AGER;IGF1R;I
CD86;IL10;CD274;PRNP;ARG1;CD80;LILRB1;PDCD1LG2;HLA-G;FOXP3;PR
SIRPG;NOD2;HSPD1;IL6;TYROBP;IL23A;TLR9;HLA-DPB1;TNFSF11;IL12B;C
ITGB1;CXCL8;ITGAM;LRP1;ITGB2;HP;HBB;ADM;ADRB2;LRP2;RABEPK;CXC
TGFB2;ARG2;PLA2G1B;DDX58;CDKN2A;IL15;FMR1;CD80;ADIPOQ;GATA3;
XBP1;EPO;LRRK2;SYVN1;HSPB1;PARK7;ENO1;SOD2;CLU;MMP9;SIRT1;IN
IL23R;HLA-B;CD1D;HLA-A;HLA-F;PVR;HLA-G;IL23A;IL12B;HLA-DRA;IL12A;H
NOTCH2;NOTCH1;CXCL8;PRCC;XIAP;GATA3;IQGAP1;BRCA1;THBS1;ARNT
SOCS3;SMAD4;IL6;STAT1;STAT3;CTR9;PTPN11;IL6ST;JAK2;IL6R;JAK1
CXCL10;CXCL11;CCL20;GPR183;S1PR1;CCL3;MSN;PIK3CD;CCR6;PIK3CG;
IL10;GHSR;IL37;TNFAIP3;PTPN22;TNF;CX3CL1;C1QTNF3;CD200R1;TLR9;P
CRP;ABCA1;CSF2;ADIPOQ;PLA2G2A;IL18;LPL;NR1H3;NFKB1;AGT;NFKBIA;
CCR1;IL23R;TNF;MTOR;IL4;IFNG;BGLAP;IL23A;TRAF6;CCL3;TNFSF11;IL12
FOXC1;TGFB1;EGF;GZMA;TXN;HMGB1;IGF1;MMP8;NGF;MMP9;SIRT2;NFK
FOXC1;TGFB2;SMAD4;NOTCH1;TGFB1;JAG1;TGFB3;MTOR;TGFBR1;BMP2

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

APP;BMPR2;LRRK2;PIK3CD;STK19;PIK3CB;PIK3CG;STK11;AKT1;JAK2;EPH
CAV1;NR1H3;PTPN22;HMGB1;RTN4;TLR1;NINJ1;FLOT1;TLR9;F2RL1;LBP;T
EDN1;DMTN;CAV1;SERPINE1;F2R;TFPI;THBS1;KNG1;F2RL1;APOE;HPSE;E
OAS1;STAT1;MX1;STAT3;EBI3;CANX;IL27;IL6ST;JAK2;JAK1
CCR1;TYROBP;IFNG;IL23A;IL23R;TRAF6;TNFSF11;IL12B;TNF;IL17A
CRP;TGFB1;ITGAM;TYROBP;GSTP1;ITGB2;F2RL1;MAPT;SOD1;CD177
PARK7;CLU;TNF;LGALS3;APOE;BID;ABCA1;ATF7IP;HSP90AA1;TGFB1;GSN
CAST;IL10;IL11;SERPINE1;IL13;TNFAIP3;GATA3;ICAM1;IL4;MDK;KDR;KRIT
APP;NCF1;CCL21;SEMA3A;TRAF2;HMGB1;TRAF1;NOD2;MMP8;AGER;RAS
CEMIP;ITGAM;HDAC3;ITGB2;PSEN1;NPEPPS;MAPK8;CASP8;CDH1;BAG3;
PSMD10;SMAD4;RGS14;GSTP1;CAV1;ADIPOQ;PIK3CB;PHB;BMP7;SORL1;
SOCS3;SOCS1;IFNG;STAT1;ARG1;IFNGR1;CDC37;NR1H3;PPARG;JAK2;IR
IL4;CSF1R;LGALS3;MDK;CCL5;MSN;MAPK1;THBS1;TNF;AIF1;BMP5;CMKLR
STAT5A;STAT5B;SOCS1;CISH;TSLP;IRS1;IL7;STAT3;IL7R;JAK3;JAK1
DLL4;TGFB2;NOTCH1;NOG;ADGRG6;S1PR1;NRG1;RBPJ;BMP7;TGFBR1;B
STAT5A;STAT5B;SOCS1;CISH;TSLP;IRS1;IL7;STAT3;IL7R;JAK3;JAK1
LGALS3;LEP;MZB1;TNFSF9;IL12B;IL27;PTPN22;IL12A;AHR;TNFRSF1B;IKZF
CSF1R;WAS;GATA3;FGF1;NTN1;EGFR;DUOX1;ERBB3;LMNA;ENPP2;PLXN
CXCL12;CCL21;AXL;LILRB1;CCR7;NOD2;CCL19;MERTK;GAS6
HSP90AA1;DAXX;HSPA5;HSPA1L;HSPA4;HSPB8;HSPB1;HSPB3;HSPA2;H
PTGER4;CXCL9;PTH;LPAR2;LPAR3;ADM;ADRB2;ADRA1A;CRHR1;PTHLH;A
CSF2;PARK7;CXCL13;CLU;TNF;LGALS3;BID;SNCA;ABCA1;HSP90AA1;TGF
CXCL12;CCL21;AXL;LILRB1;CCR7;CCL19;GAS6
GH1;IL23A;IL23R;CCL5;IL12B;IL6R;AGT
CYP27B1;IFNG;VDR;IL1B;GFI1;TNF;NFKB1
ANXA2;CCL21;EGF;FMR1;HFE;SERPINE1;CLU;SELE;VEGFA;C3;IL4;GH1;A
DDR1;IL21;BLK;EPHA4;CSF1R;IL15;PRLR;EGFR;IGF1R;IL4;LEP;KDR;BTK;A
BLK;IL4;TRPM2;CSF2;AXL;IRF8;F2RL1;LILRB1;CCR7;CCL19;LGALS9;GAS6
PRNP;TGFB2;GRN;ITGAM;TYROBP;DDIT3;CCL3;CTNNB1;BAX;FOXO3;TNF
IL10;SPHK2;BTK;APOA1;F2RL1;LILRB1;TNFRSF14;NOD2;TNFRSF1B;TNF;C
IL1A;HSP90AA1;DDAH1;VDR;NOS3;CAV1;IL1B;LEP;AKT1;CALM1;EGFR;SN
APP;HDAC3;NCF1;SEMA3A;HMGB1;NOD2;AGER;RASGRP1;EGFR;IGF1R;R
BLK;CD86;IL10;CD274;ARG1;CD80;LILRB1;PDCD1LG2;HLA-G;FOXP3;TYRO
IRAK1;TNFSF15;TRAF6;TNFRSF10B;CHI3L1;TNFRSF10A;TRAF2;MAP3K7;
IL10;CEACAM1;ANXA1;F2R;CCR7;HMGB1;MEFV;GAS6;TLR4;FOXP1
IL23A;IL23R;IL18;TNFSF9;IL12B;HMGB1;IGF1;CD24;AGER;IL2;ICOSLG
IFIH1;MAVS;STAT1;DDX58;TLR9;TLR8;IRF5;TLR7;TLR4;TLR3;HSPD1
EDN1;IRS1;PIK3CD;PIK3CB;GATA3;IGF1;PIK3CG;SIRT2;ZFP36L1;IGF1R;E
FOXC1;TGFB1;EGF;TXN;PARK7;HMGB1;GATA3;IGF1;MMP8;NGF;MMP9;SI
PRNP;EPHA4;IFNGR1;IGF1;CLU;TNF;SORL1;RTN4;RELA;IFNG;SP1;CASP3
WWOX;TNFRSF12A;CAV1;TNFSF12;TRAF2;BCL10;THBS1;TNF;AGT;PML;T
CCR1;KL;BMPR2;TGFB1;AHSG;PTH;TGFB3;PTN;BMP7;BMP4;P2RX7;CYP2

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

LRP1;DCTN1;PARK7;CLU;TNF;IGF1R;LGALS3;SMPD1;FLOT1;APOE;CCL19
IFNAR2;RNASEL;IFNB1;TNFAIP3;XIAP;PTPN22;PTPN11;CD1D;USP18;CAS
EHMT2;LRRK2;HSPB1;PTPN22;BRCA1;FGF1;TNF;STK11;KAT5;RAC2;AKT1
CSF2;NOTCH4;GATA3;TNF;PTHLH;ZFP36L1;KLK6;INS;LGALS3;SHH;MDK;A
STAT5A;STAT5B;XBP1;ANXA1;IRS1;STAT1;SORT1;CAV1;REG1A;STAT3;SI
CD86;IL21;IL10;GPI;XBP1;PHB;IL2;IL6;PTPRC;TLR9;MZB1;TP53BP1;EPHB2
BLK;DDR1;CSF1R;BMPR2;MST1R;PIK3CB;PTN;EGFR;IGF1R;ERBB3;NTF3;
APP;PTH;EGF;IFNA2;BCL10;PSEN1;MIF;THBS1;EGFR;AR;IFNG;CCL5;SNCA
IL33;CD74;SPHK1;NR1H3;MIF;MMP8;THBS1;HSPD1;IL4;IL6;LBP;TLR4;CD20
IL10;PSMD10;CDKN2A;GFI1;TNFAIP3;KLF4;SIRT1;FOXP3;BMP7;NFKBIA;IT
ITGB1;PRNP;CEMIP;ITGAM;LRP1;PRKCE;ITGB2;GZMB;TNF;YWHAZ;EGFR;
PCSK1;CPB1;TMPRSS6;CTSZ;PLAT;PRCP;PLG;PSEN1;PHEX;MALT1;DPP4
ANXA1;PIK3CD;LIG4;PTPN22;GATA3;IL2;ZFP36L1;DLL4;SHH;ADAM17;PTP
CXCL8;CXCR4;TNF;KNG1;PIK3CG;ADGRG1;ERBB3;MDK;CXCR3;CCL5;PLX
IL10;NOTCH2;CSF1R;TGFB2;CSF2;SELPLG;TGFB1;JAG1;KMT2A;FST;NOT
IL10;C1QTNF3;IL6;OAS1;GSTP1;F2RL1;APOD;LGALS9;MEFV;KLF4
IL6;STAT3;NOD2;IL17D;TNF;HIF1A;TLR4;MYD88;IL17RA;IL17A
IL15;AHSG;SLC11A1;SIRPG;APOA1;MERTK;TNF;C2;C3;PTPRC;IFNG;IL1B;I
IL10;SIRPG;CXCL13;TNF;AGER;BMP7;CX3CL1;SMAD7;MDK;CCL5;IL1B;FLO
LAG3;SOCS1;IFNG;MDK;IRF1;IL2RA;CTLA4;CD46;HLA-G;FOXP3;VSIR;IL2
PSMD10;GFI1;TNFAIP3;IRAK1;CYP1B1;NLRP3;FLNA;TNFRSF4;CMKLR1;HA
RNASEL;CXCL8;IFNB1;MX1;EIF2AK2;TNF;IFIH1;BST2;ISG20;MAVS;OAS1;IF
CSF1R;PRNP;EPHA4;ACE;NCF1;EGF;BDNF;TGFA;AGT;ADAM17;ERBB3;NO
SNAP25;NOS2;ABCC8;HFE;PRKCA;ITPR3;GCG;TNF;ARNTL;INS;DPP4;IL6;R
TOR1A;LRP1;CCL21;HFE;SERPINE1;CLU;C3;IL4;AXL;SMPD1;FLOT1;F2RL1
DHRS11;VDR;NR1I2;DHCR24;LRP2;CYP2C19;CYP7B1;HSD17B7;CYP3A4;P
DDX58;XRCC5;TNFAIP3;PTPN22;RELA;NFKB1;NFKB2;IFIH1;ITCH;MAVS;IFI
STAT5A;STAT5B;GH1;STAT3;STAT6;PRL;JAK2;PRLR;JAK3
IL10;TLR8;LILRB1;CCR7;MEFV;TIGIT;THBS1;JAK3;CMKLR1
IL4;GRN;CD200R1;PTPRC;IGF1;TNFRSF1B;LDLR;CX3CL1;CD200
CEACAM1;PTPRC;HFE;LILRB1;AHR;HLA-F;HLA-G;FOXP3;SMAD7
OPN1SW;CCND1;MMP1;MMP2;MMP3;AKT1;TIMP1;MMP9;EGFR
ITGB1;CX3CR1;CXCL9;NCF1;TRAT1;PRF1;HLA-G;RELA;NCR1;TYROBP;CX
APP;EDN1;TGFB1;UHRF1;NR1H3;FOXO3;KLF4;AGT;NFKB1;INS;NFKBIA;AT
IL10;CD40;IFNA1;IFNB1;IFNA17;IFNA2;RASGRP1;HSPD1;PTPRC;CD40LG;C
ADAM17;CCL21;CCL7;WNK1;CCL5;CCL4;CCL3;CXCL13;CCL27;CCR2
TGFB2;SMAD4;FN1;LILRB1;LGALS9;PTGS2;CD46;HIF1A;CD34;CD200
ERN1;DAXX;HSPA5;HSPA1L;BAG3;HSPB8;BAX;HSPA2;HSPA14;HSPA1B;H
IL10;IL4;IL11;SERPINE1;IL13;KDR;KRIT1;TNFAIP3;GATA3;GAS6;ICAM1;NFE
CSF1R;DUOX1;STK11;ADAM17;CCL21;CCR7;CCL19;ETS1;NTN1;DUOX2;TG
IL10;HGF;IL10RA;STAT3;HP;PTPN22;SORL1;SIRT2;MTOR;INS;CST3;LEP;A
IL21;STAT1;STAT3;IL21R;STAT4;JAK3;JAK1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

IL21;STAT1;STAT3;IL21R;STAT4;JAK3;JAK1
GH1;IL23A;IL23R;CCL5;IL12B;IL6R;AGT
CD40;SERPINA1;KMT2A;HDAC1;HFE;LRRK2;CTSZ;USO1;WAS;TGFA;MEFV
PRNP;IFNG;DDIT3;IL12B;IL12A;TLR4;FOXP3;VSIR
IGFBP1;CXCL8;HSPA5;DDIT3;EIF2AK3;CCL2;NFE2L2;ATF4
CXCL10;CXCL11;GPR183;CCL3;PIK3CD;PIK3CG;CCR2;CXCL16
DDR1;CSF1R;MST1R;EGFR;IGF1R;ERBB3;MYC;KDR;MAPK1;EPHB2;ROS1;
CD40;IL6;GSN;RGCC;CD40LG;ITGA4;PLA2G1B;CCL2;FASLG;THBS1;HLA-G
CD86;CD40LG;DDIT3;CD28;RARA;NLRP3;GATA3;LGALS9;FOXP3;HLA-DRB
SPHK2;TRAF2;NOD2;HLA-A;HLA-F;HLA-G;MALT1;TRAF6;F2RL1;TNFRSF14
IL4;HSP90AA1;MAVS;AIM2;STING1;STAT1;DDX58;IL23A;IL23R;IL12B;PTPN
ITGB1;DUOX1;GRN;OCLN;ANXA1;DMTN;CLDN3;MDK;PRKCE;PTN;DUOX2;
IL10;IL4;IL6;CD19;FCRL3;TLR9;MZB1;TNFAIP3;NOD2;AHR;IKZF3;ZFP36L1
APP;IRS1;LRRK2;PSEN1;PIK3CB;HMGB1;FOXO3;MEFV;TNF;HIF1A;INS;ST
CSF1R;EDN1;IRS1;PTAFR;PIK3CD;PIK3CB;GATA3;IGF1;NGF;PIK3CG;SIRT
SERPINA3;SERPINA1;SERPINB2;AHSG;HDAC1;SERPINE1;VSIR;KNG1;AG
P2RY12;CSF1R;P2RX4;MDK;CCL5;CCL3;MAPK1;THBS1;CX3CL1;CMKLR1
CCR1;CXCL10;CXCL12;CCL5;SERPINE1;CCL1;HMGB1;AIF1;PLA2G7;CCR2
TYROBP;AXL;IL23A;IL23R;IL18;IL12B;IL12A;HLA-F;GAS6
ITGB1;CCL13;CD40;CCL11;CXCL13;RASGRP1;CX3CL1;DOCK11;RAP1A;C
APP;CSF3;LRP1;BDNF;HFE;LRRK2;CAV1;PSEN1;MMP9;BMP4;CLDN5;BMP
IL15;AHSG;SPHK1;SLC11A1;SIRPG;ADIPOQ;APOA1;MERTK;TNF;PTPRC;IF
CHGA;LRRK2;TRAF2;PARK7;TNFRSF1B;HLA-F;CLU;BMP7;SORL1;BMP4;C
CEMIP;CXCL9;GSTO1;F2R;CX3CL1;CXCL10;CXCL11;CD19;CALM3;HAP1;C
PSMD10;SEMA7A;TGFB2;EDN1;SLC44A4;SYT1;BDNF;SPHK1;IGF1;NGF;NT
PRNP;EDN1;AGAP2;PHB;HMGCR;CLU;SIRT2;EGFR;NFKB1;INS;EDNRB;FL
PSMD10;PSMD12;EPO;EPAS1;HIF1A;PSMB8;PSMB9;VEGFA;PSMB6;MUC1
MUC1;NOTCH1;HSPA5;DDIT3;RBPJ;HIF1A;TP53;ATF3;VEGFA;NFE2L2;ATF
TLR1;IRAK1;TNIP1;TRAF6;UBC;BTK;CD14;MAP3K7;TLR4;MYD88;HSPD1;TL
IL4;LGALS3;IL6;ADAM17;MDK;F2RL1;PTN;TNF;AIF1;IL6R;ICAM1;VEGFA
DDR1;ITGB1;APP;ITGAM;NCAN;SERPINE1;COL11A2;ITGB2;LAMC2;ICAM5;
MACIR;LRP1;SERPINE1;FOXO3;CX3CL1;GJA1;ADGRG1;SHH;CDH1;CYP1B
PSMD10;GSTP1;TNFAIP3;RORA;PIK3CB;THBS1;RELA;ARNTL;C1QTNF3;CA
MMP7;GSN;MMP1;TMPRSS6;MMP2;MMP3;PLG;MMP8;MMP9;MMP12;BMP1
MMP7;GSN;MMP1;TMPRSS6;MMP2;MMP3;PLG;MMP8;MMP9;MMP12;BMP1
CAST;HGF;XIAP;DHCR24;NGF;KLF4;TNF;THBS1;VEGFA;IFI16;AKT1;GAS6;
ANXA1;TNFAIP3;PARK7;SIRT1;RELA;TRPM2;IL6;ABL1;CYP1B1;RIPK1;FXN;
EPHA4;SPHK2;IFNGR1;FMR1;PLD1;PLA2G6;CLU;TNF;THBS1;RELA;MTOR;
PSMD10;PSMD12;SPATA2;TNFAIP3;GATA3;BRCA1;ADRB2;HIF1A;USP18;A
IL23A;IL1B;SLC11A1;IL23R;IL18;IL12B;IL18R1;CCR2
LGALS3;LGALS1;HLA-B;LILRB1;HMGB1;LGALS9;AGER;HLA-G
EOMES;TGFB2;NOTCH1;TGFB1;NOTCH4;HGF;NOG;RBPJ;HIF1A;BMP7;TG

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

SHH;IL23A;IL23R;EBI3;HLA-DRA;IL12B;IL12A;HLA-A;HLA-DRB1;CCR2
IL4;XBP1;MDK;IL7;AXL;ZMIZ1;BTK;CD27;GATA3;GAS6
EGR1;HSP90AA1;DAXX;ITCH;EPAS1;ZMIZ1;HIF1A;TGFBR1;HSPA1B;HSPA
ITGB1;CLDN5;GJA1;OCLN;IL6;CLDN3;SLC1A1;PECAM1;MBP;ACTB;VCL;AC
CX3CR1;IL10;GHSR;CEACAM1;GSTP1;TNFAIP3;NLRP3;APOA1;IGF1;MEFV
CREB1;IL1B;ADIPOQ;AKT1;APOA1;HSD17B13;PPARG;APOE;PPARA;MTO R
IL4;LRP1;IFNG;HDAC1;IFNGR1;HMGCR;APOE;CLU;TNF
PTGER4;CXCL9;VIPR2;PTH;LPAR2;LPAR3;ADM;ADRB2;CRHR1;PTHLH;AD
STAT5A;STAT5B;STAT1;IL9;STAT3;JAK3;JAK1
IL23A;IL23R;STAT3;STAT4;IL12B;P4HB;JAK2
STAT5A;STAT5B;STAT1;IL9;STAT3;JAK3;JAK1
IFNB1;TBX21;HFE;IFNA2;HLA-F;FOXP3;SMAD7
IFNG;CDKN2A;MFN2;IL12B;PPARG;IL12A;SOD2
CXCL8;NOTCH1;IL1B;NOTCH4;CAV1;FLOT1;APOA1
CCL21;SLC11A1;CCR7;NOD2;CCL19;CD68;THBS1
EBI3;IL18;IL12B;HMGB1;TLR4;HLA-DRB1;IL18BP
P2RY12;FN1;HBB;HSPB1;PIK3CB;PIK3CG;ACTB;ACTG1;TYRO3;FLNA;TLN1
HSP90AA1;STAT1;DDX58;IL23R;TNFAIP3;PTPN22;LILRB1;IL4;MAVS;AIM2;S
PSMD10;PSMD12;EPO;EPAS1;RORA;PTGS2;HIF1A;ZFP36L1;PSMB6;NPEP
NOTCH3;TGFB2;NOTCH1;JAG1;EGF;NOS3;NOTCH4;STAT3;NOD2;RBPJ;EG
HGF;XIAP;DHCR24;PARK7;NGF;KLF4;TNF;MMP9;THBS1;VEGFA;AKT1;GAS
PTGER4;SPEF2;PTH;NCAN;COL11A2;TNFRSF11B;PHEX;PTHLH;GJA1;BGL
F2R;HMGB1;NLRC4;BCL10;MEFV;TNF;SIRT1;MALT1;CASP8;AIM2;IFI16;MY
CX3CR1;NOTCH1;CCL11;RGS14;LIG4;LRP2;TNF;SORL1;CX3CL1;ARNTL;IL
NTF3;IL18;AKT1;NRG1;TXN;PARK7;IGF1;FGF1;GAS6;ADRA2B;MTOR;INS
P2RY12;CSF1R;DUOX1;TGFB1;CCL21;F2RL1;CCR7;CCL19;THBS1;NTN1;AI
PTPRC;PRKCB;TRAT1;PRKD2;CD226;BCL10;RELA;CARD11;NECTIN2;FOX
GPR151;TGFB2;ANXA1;PLA2G1B;IL15;PIK3CD;PIK3CB;LGALS9;HLA-G;VE G
XBP1;SMAD4;BMP2;NOTCH1;RBPJ;HIF1A;RELA;VEGFA;NFE2L2;ATF4
CCR1;CXCL10;CXCL12;CCL5;SERPINE1;CCL1;CCN3;HMGB1;AIF1;PLA2G7
STAT1;CAV1;PRL;THBS1;DLL4;RGCC;ALOX5;KRIT1;IL12B;CCL2;IL12A;PPA
IL10;TGFB3;MMP2;ADIPOQ;IGF1;SOD2;MMP9;APLN;ERN1;GJA1;ADAMTS1
IFNA1;IFNB1;IFNA17;IFNA2;PIK3CD;RASGRP1;IL2;NCR1;CASP8;KLRK1;PT
APP;STK19;PLAT;PARK7;STK11;PSMD7;LGALS1;PSMD4;AKT1;ROS1;MAP3
FOXC2;NOTCH1;IL15;GSTP1;ADIPOQ;NR1H3;RBPJ;ARNTL;STK11;ADAM17
RNASEL;STAT1;IFNB1;MX1;EIF2AK2;TNF;PML;IFIH1;BST2;ISG20;MAVS;OA
NOTCH2;DLL4;BMP4;BMP2;TGFB1;NOTCH1;JAG1;NOG;RBPJ
PSMD10;PSMD12;TNFAIP3;GATA3;BRCA1;ADRB2;HIF1A;USP18;ACTB;IFIH
IL6;IRAK1;MDK;TRAF6;ITGB2;TNF;ETS1;RELA
IL6;PTPRC;TSLP;EGF;MGAT5;IL7R;JAK2;JAK3
LRRK2;GSTP1;HSPB1;PARK7;C9ORF72;SPRED2;NTF3;AKT1;EPHB2;SNCA
DDR1;ITGB1;APP;ITGAM;NCAN;SERPINE1;COL11A2;ITGB2;LAMC2;ICAM5;

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

NOTCH2;NOTCH1;BMPR2;BTG1;ENO1;PHB;RTN4;CYP27B1;STK11;MT2A;G
CDKN1C;RGS14;CDKN2A;GSTP1;ADIPOQ;PIK3CB;SIRT1;BMP7;SORL1;AG
DUOX1;PRDX2;NCF1;NOS2;NOS3;NOX3;CYBB;NOX4;NOX5;SOD2;DUOX2;
CRTC2;IRS1;RPS6;ADIPOQ;STAT3;GCG;PARK7;SLC2A4;SIRT1;HIF1A;IGF1
P2RY12;FN1;HBB;HSPB1;PIK3CB;PIK3CG;ACTB;ACTG1;CEACAM5;TYRO3;
DDR1;CDKN1C;EPHA4;CSF1R;CD74;INSRR;MST1R;MERTK;EGFR;IGF1R;S
NOTCH1;TGFB1;ANGPT2;HMGB1;THBS1;TNF;DCN;DLL4;MECP2;RGCC;KR
PTGER4;VIPR2;PTH;ADM;ADRB2;CRHR1;PTHLH;FCGR3A;GNG2;FYN;FCG
BRCA1;TNFRSF1B;SIRT1;PML;CASP9;IFI16;DDIT4;BCL3;ABL1;BCL2;BAX;A
FOXC1;TGFB2;NOTCH1;TGFB1;HGF;NOTCH4;NOG;RBPJ;HIF1A;BMP7;TGF
CDKN1C;TGFB2;TGFB1;VDR;STAT1;CAV1;PRL;GATA3;BRCA2;MCC;THBS1
ACHE;EDN1;TGFB2;TGFB1;PLA2G1B;TGFB3;IGF1;UNC13D;CD2AP;IL1A;BM
P2RY12;EGR1;XBP1;DMTN;AHR;TRPV1;BRCA1;ACTB;RELA;MTOR;ZFP36L
PTGER4;VIPR2;PTH;ADM;ADRB2;CRHR1;PTHLH;FCGR3A;GNG2;FYN;FCG
TGFB2;NOTCH1;JAG1;NOS3;NOTCH4;STAT3;NOD2;RBPJ;DLL4;ZMIZ1;CCN
ANXA1;TYROBP;LRP1;ALOX15;RAC2;TYRO3;RARA;NR1H3;HMGB1;GAS6;T
STAT1;NOS3;TNFSF12;VEGFA;DPP4;NR4A1;PIK3CA;ADGRA2;ABL1;CYP1B
CHGA;IRS1;F2R;NR1H3;HMGCR;INS;IL1B;IL12B;IL12A;CCN3;APOE;DRD2;
IL10;IL1RN;WNK1;ADIPOQ;APOA1;MBP;KLF4
IL10;IL1RN;WNK1;ADIPOQ;APOA1;MBP;KLF4
BLK;CHGA;SNAP25;NOS2;IRS1;ABCC8;PRKCA;ITPR3;GCG;TNF;ARNTL;DP
NOTCH1;TGFB1;JAG1;DMTN;FZD4;SERPINE1;PLG;CX3CL1;KNG1;MUC1;P
ARG2;DDAH1;NOS2;NOS3;ARG1;NOS1
CD74;LPL;MBP;HMGB1;TNF;TLR4
KLRK1;CCL7;CCL5;CCL4;CCL3;CCL2
CEACAM1;IL12B;IL12A;CD226;PVR;NECTIN2
IL23A;IL23R;LEP;IL18;IL12B;PTPN22
NOTCH2;BMP4;TGFB2;BMPR2;NOTCH1;JAG1;NOS3;TNFRSF1B;TNFRSF1
STAT5A;STAT5B;APP;GHSR;GH1;GDF15;PRL;IGF1;SOD1
BMP4;IL6;TGFB1;MYCN;RIPK1;TNF;ESR1;TP53;EGFR
ADAM17;ITGA4;MDK;SP1;CCL2;PPARG;HMGB1;APLN;FGFR1
CX3CR1;P2RY12;GPR17;F2R;ADRA1A;ESR1;GRM1;AGT;HRH1;GNA11;P2R
LRRK2;HSPB1;AKT1;FYN;TXN;PARK7;SOD2;SIRT1;INS;NFE2L2;ATF4
CD74;PLA2G1B;MYC;SPHK1;FN1;LIG4;MIF;IGF1;WNT1;GAS6;AGT
CD74;IFNA1;MDK;IFNB1;SLC11A1;IFNA17;IFNA2;F2RL1;LILRB1;ITGAL;ICAM
PSMD10;PSMD12;HDAC1;LRRK2;XIAP;PSEN1;GLI1;EGFR;ARNTL;SOX2;PS
CD74;PLA2G1B;GSTP1;SPHK1;FN1;LIG4;MIF;IGF1;AGT;MYC;CTNNB1;WNT
PTGER4;EGF;MYC;KDR;APOA1;CTSH;MAPK1;IGF1;LGALS9;ZFP36L1
NFKBIA;LRP1;CAV1;ADIPOQ;PON1;NR1H3;APOA1;PPARG;APOE;SIRT1
BMP4;GJA1;EGF;MDK;NOG;LIF;ITGAX;PIK3CD;AGT;VEGFA
HSP90AA1;CASP8;CDC37;FLOT1;SPATA2;RIPK1;ARHGEF2;SLC25A4;BIRC
BLK;HSP90AA1;PRKCE;WAS;PIK3CB;PLA2G6;ACTB;ACTG1;FCGR3A;FCGR

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

APP;CXCL10;CXCL12;CCL21;CCL20;CCL5;TNFRSF14;AIF1
CD86;ANXA1;CD80;IL18;RARA;NLRP3;CCL19;MALT1
CD86;IL4;CD74;IL6;IL18;RARA;NLRP3;NOD2
CD74;TGFB2;SEMA7A;TGFB1;TGFB3;LILRB1;SIRT1;HLA-G
SOCS3;SOCS1;IFNG;STAT1;IFNGR1;CDC37;JAK2;JAK1
IL21;PTGER4;IL4;IL6;GPR183;IL12B;HMGB1;FOXP1
NOS3;KCNMA1;F2RL1;ADRB2;NOS1;SOD2;INS;SOD1
DLL4;MECP2;NOTCH1;TGFB1;ANGPT2;RGCC;PPARG;HMGB1;APOE;KLF4;
DPP4;P2RY12;FOXC2;MUC1;TGFB2;CCL21;SERPINE1;LIF;CYP1B1;PTPN11
EDN1;SERPINB2;F10;NOS3;SERPINE1;PLAT;PLG;TFPI;KNG1;SERPING1;A
KL;TGFB2;BMPR2;TGFB1;PTH;TGFB3;PTPN11;PTN;BMP7;P2RX7;BMP4;BM
GFI1;IKZF1;ENO1;RBPJ;IKZF3;BACH2;SOX2;KAT5;ZMIZ1;MYC;AKT1;KAT8;
RNASEL;IFNB1;MX1;EIF2AK2;TNF;AICDA;IFIH1;BST2;ISG20;MAVS;OAS1;IF
ITGB1;IL10;IL11;VCAM1;IFNA1;ITGA4;IFNB1;IFNA17;IFNA2;SYVN1;AICDA;IL
APP;RGS14;CD80;LRRK2;ALOX15;RORA;GATA3;GLI1;CLU;CX3CL1;GRK2;I
PSMD10;HGF;IGF1;CLU;MMP9;TNFSF10;AKT1;BAX;BID;DNM1L;FXN;TP53;
CRP;ACE2;EDNRA;EDN1;EDNRB;ACE;NOS3;AGTR1;F2RL1;NOS1;AGT;INS
FOXC1;TGFB2;SMAD4;TGFB1;TGFB3;GATA3;TGFBR1;MTOR;BMP5;SMAD
IL33;TSLP;CD226;LBP;HAVCR1;THBS1;TLR4;NECTIN2;HSPD1
EDN1;AGTR1;ABL1;PARK7;NOD2;TNF;FXN;AGT;SIRT3
TGFB3;NOTCH4;CAV1;NRG1;PRL;JAK2;PRLR;WNT3;APLN;VEGFA
CHGA;TGFB1;MMP1;MMP3;NRG1;PRKCA;PARK7;CLU;TNF;BMP7;CX3CL1;
EPAS1;RORA;PTGS2;SIRT1;HIF1A;BMP7;SIRT2;MTOR;ZFP36L1;VEGFA;NP
TGFB2;SMAD4;TGFB1;BMPR2;BTG1;SPHK2;CDKN2A;RNF6;ENO1;PHB;SIR
ITGB1;CX3CR1;APP;PXK;SYT1;BDNF;FMR1;LRRK2;ADIPOQ;SYN3;NGF;TN
PSMD10;DAXX;HSP90AA1;HDAC3;CAV1;LRRK2;SPHK1;FAM107A;TNFAIP3
IL1RN;ARG1;GSTP1;ADIPOQ;APOA1;NR1H3;USP18;IL6;PTPRC;OAS1;PADI
NOS2;NOS1;S100A9;GAPDH;S100A8
IFNG;HLA-DRA;LGALS9;FOXP3;HLA-DRB1
LGALS3;LGALS1;HMGB1;LGALS9;AGER
NOTCH1;RBPJ;HIF1A;NFE2L2;VEGFA
CDKN1C;GRN;TGFB2;TGFB1;UHRF1;TGFA;NOD2;IGF1;FGF1;MCC;EGFR;Z
STAT5A;STAT5B;IL2RA;IL2RB;JAK3;IL2;JAK1
STAT5A;STAT5B;IL2RA;IL2RB;JAK3;IL2;JAK1
IL4;TSLP;SPHK2;RARA;IL18;GATA3;LGALS9
BLK;ANXA1;CDKN2A;PIK3CD;PIK3CB;LGALS9;SIRT1
BMP4;IL6;TGFB1;MYCN;RIPK1;TP53;EGFR
ATP6AP2;LGALS9;CD46;PTGS2;THBS1;CD34;CD200
C1QTNF3;OAS1;IL1B;GSTP1;ADIPOQ;APOD;LGALS9
IL1B;WAS;HMGB1;TNFRSF1B;AGER;CCR2;TRPM4
IL10;AGAP2;PHB;HMGCR;EGFR;SIRT2;INS;CST3;TIMP2;FLNA;TIMP3;TIMP
BMP4;TGFB2;BMPR2;NOTCH1;JAG1;LRP1;NOG;LRP2;TGFBR1;SMAD7;VE

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

ITGB1;CD200R1;VCAM1;ITGA4;ITGB2;NINJ1;ITGAX;CTNNA3;DSG2;CD1D;C
CRP;IL22;IL6;AHSG;LBP;IL6R;INS;MBL2
IGFBP1;CXCL8;HSPA5;DDIT3;EIF2AK3;CCL2;NFE2L2;ATF4
P2RY12;LGALS3;EDNRB;P2RX4;CCL5;CCL3;CCL2;CCR2
BMPR2;NOS2;NOS3;ADIPOQ;PRCP;NOS1;DRD2;APLN
CX3CR1;CEACAM1;PTPRC;LILRB1;LGALS9;HLA-F;HLA-G;MICA
IFIH1;CD74;MAVS;TSLP;DDX58;IL7;AXL;GAS6
GRN;IL6;PTPRC;SPHK1;CCL3;MMP8;LDLR;CX3CL1
CXCL10;ADAM17;CCL21;WNK1;CCL5;CXCL13;CCL27;CCR2
CYP27B1;CYP24A1;VDR;CYP2R1;LRP2;CYP3A4;GC;FGF23
CRTC2;IRS1;RPS6;ADIPOQ;STAT3;GCG;PARK7;SLC2A4;IGF1R;INS;STK11;
TGFB2;DST;SLC11A1;NOG;ALOX15;NRG1;PRCP;IGF1;FGF1;TGFBR1;INS;M
LRRK2;HSPB1;PTPN22;PIK3CB;HMGB1;MEFV;FOXO3;C9ORF72;STK11;MA
BMP4;CYP27B1;TGFB2;BMP2;BMPR2;NOTCH1;MDK;AHSG;S1PR1;PTPN11
TNFRSF10B;TRAF2;BRCA1;TNFRSF1B;PML;ERN1;CASP9;STK11;IFI16;DDI
ITGB1;CXCL8;LRP1;CAV1;ITGB2;MX1;ADM;LILRB1;CEACAM1;GRK2;CXCR
SERPINA3;SERPINA1;SERPINB2;LRP1;AHSG;SERPINE1;PARK7;KNG1;AGT
PSMD10;EGR1;IL1RN;PSMD12;NOD2;RELA;NFKB1;PSMB8;PSMB9;PSMB6;
ACHE;NCAN;ATN1;CXCL1;MTR;SHH;EDNRB;CDH1;MDK;ADGRA2;SMPD1;M
PSMD10;PSMD12;BCL10;PIK3CB;FOS;NFKB1;RELA;MALT1;PSMB8;PSMB9
LGALS3;PRNP;CXCL12;EGF;SPHK2;FCRL3;CCL3;CCL2;CTNNB1;FYN
HSP90AA1;PRKCE;WAS;PIK3CB;PLA2G6;ACTB;ACTG1;FCGR3A;FCGR2A;
STAT5A;STAT5B;GH1;STAT3;STAT6;PRL;JAK2;PRLR;JAK3
IL21;KLRK1;IL12B;IL12A;CD226;HLA-F;PVR;RASGRP1;NECTIN2
IL4;IL6;GSTP1;OSM;NLRP3;DNASE1;IL6ST;INS;PTGES
ITGAM;OAS1;IRAK1;PRKCE;ITGB2;LBP;CD14;LGALS9;TLR4
CD86;P2RY12;PTH;BDNF;LPAR2;PHB;ADRA1A;SELE;ESR1;EGFR;EDNRA;N
PSMD10;PSMD12;BCL10;PIK3CB;FOS;NFKB1;RELA;MALT1;PSMB8;PSMB9
HLA-B;HLA-C;HLA-A;HLA-F;B2M;HLA-G
IL1B;RAC2;BMP7;S100A9;CD44;S100A8
MYO1C;KDR;PIK3CD;HSPB1;PRKD2;VEGFA
CCL21;IL12A;CCR7;LGALS9;CCR6;GAS6
IL4;XBP1;CIITA;IFNG;JAK2;SIRT1
ANXA1;CDKN2A;ADIPOQ;PIK3CD;PIK3CB;SIRT1
FOXC2;XBP1;ALOX5;SERPINE1;TNFAIP3;TNF
DLL4;TGFB2;NOTCH1;NRG1;RBPJ;TGFBR1
HSP90AA1;PRKCE;WAS;PIK3CB;PLA2G6;ACTB;ACTG1;FCGR3A;FCGR2A;
TGFB2;SMAD4;BMPR2;TGFB1;TGFB3;GDF15;HFE;NOG;RGMB;BMP7;RGM
NOTCH2;NOTCH3;NOTCH1;HDAC3;HDAC1;NOTCH4;MAZ;NR1I2;RORA;RB
IL6;NOTCH1;CCL11;IL1B;LILRB1;IGF1;TNF;B2M;SORL1;PTHLH
CD74;MUC1;CXCL12;BCL2;ACKR3;MIF;CLU;SIRT1;CD44;BCL2L1
CEACAM1;HLA-B;LILRB1;HLA-A;LGALS9;HLA-F;HLA-G;MICA

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

IL23A;EBI3;IL18;IL12B;PTPN22;HLA-A;LGALS9;CCR2
CD40;RGCC;CD40LG;ITGA4;CCL2;FASLG;THBS1;HLA-G
CD74;SEMA7A;MAVS;DDX58;LILRB1;BCL10;SIRT1;HLA-G
IL4;TSLP;SPHK2;IFNA2;IL18;RARA;GATA3;LGALS9
ACE;EPO;STAT1;NOS3;SOD1;DLL4;ACE2;CXCL10;CXCL12;C3AR1;AGTR1;
PXK;EGF;TRAT1;ADIPOQ;NR1H3;NRG1;LILRB1;BST2;LGALS3;ERBB3;CRY
PSMD10;PSMD12;NCF1;HLA-B;TAP1;HLA-C;CYBB;HLA-A;HLA-F;HLA-G;PS
EPHA4;CD74;JAG1;SERPINE1;ADIPOQ;NOG;WAS;MIF;GATA3;FOXO3;CX3
ERN1;DAXX;HSPA5;HSPA1L;BAG3;HSPB8;BAX;HSPA2;HSPA14;HSPA1B;H
P2RY12;TGFB1;P2RX4;CCL21;ADGRA2;GPR183;CXCR4;F2RL1;CCL19;THB
APP;ERBB3;ATN1;BCL2;LIG4;FAS;NLRP1;BID;GAPDH
MAVS;TYROBP;ITGAM;DDX58;ITGB2;F2RL1;CD177
IL33;IL6;IL1B;CCL3;IL18;MMP8;TNF
IL4;IL10;XBP1;CIITA;IFNG;JAK2;SIRT1
TYROBP;IL23A;LEP;IL12B;PTPN22;IL12A;MICA
ITGB1;TGFB2;SMAD4;TGFB1;BMPR2;TGFB3;GDF15;HFE;APOA1;FOS;RGM
GFI1;CAV1;MST1;ADIPOQ;DKKL1;BRCA1;NFKB1;INS;C1QTNF3;CEACAM1;
PARP1;FMR1;RELA;EGFR;YY1;CASP9;MAPK8;MC1R;CCND1;MYC;SMPD1;
CDKN1C;APP;EGF;CDKN2A;IFNA2;FN1;HSPB1;MIF;BCL10;PSEN1;HIF1A;B
CSF1R;APP;PRNP;EPHA4;ACE;PTPRC;ERBB3;CAV1;NOX4;FCGR1A;GAS6;
IFIH1;ITCH;CASP8;IRAK1;DDX58;TRAF6;UBC;TNFAIP3;NOD2;MAP3K7
EPO;GSTO1;FMR1;CALM3;DRD2;EPHB2;CALM1;MMP9;CALM2;CRHR1
BMP4;IL6;TGFB1;MYCN;FMR1;STAT3;AGO2;RIPK1;TP53;EGFR
IL1A;EDN1;RGCC;EGF;IL1B;CD28;TGFA;IGF1;SIRT2;INS
GFI1;FCRL3;IRF1;FLOT1;TLR9;TYRO3;BIRC2;TLR3;TLR2;BIRC3
SMAD4;NOTCH1;TGFB1;BMPR2;FST;CAV1;NOG;LRP2;SIRT1;SORL1;TGFB
PSMD10;PSMD12;LRRK2;TNFAIP3;XIAP;EGFR;ARNTL;PSMB6;PSMD7;CDH
P2RX7;IL4;APP;IFNG;ENO1;PSEN1;IGF1;PPARA;HIF1A;PPARGC1A;INS
NFKBIA;SHH;LRP1;CAV1;PON1;ADIPOQ;NR1H3;APOA1;PPARG;APOE;SIRT
SPRED2;DMTN;DDIT4;CALM3;CALM1;CALM2;SIRT2;SMAD7
BMP4;TGFB2;BMPR2;NOG;GATA3;BMP7;TGFBR1;BMP5
CXCL8;CXCL12;NTF3;VEGFB;KDR;F2RL1;IL16;VEGFA
CLDN5;IL1B;S1PR3;S1PR2;TNF;VCL;TNFRSF1A;VEGFA
CCR1;TGFB1;NOTCH1;NOS3;AHSG;CCL3;GAS6;FGF23;TRPM4
CSF1R;TYROBP;ANXA2;GLO1;GPR183;TNFSF11;TNFRSF11A;MAPK14;FOX
EPHA4;IFNG;IFNGR1;SP1;CASP3;CLU;TNF;AGER;RELA
IL4;CD74;CXCL8;CCL21;MDK;RAC2;CCR7;CCL19;DNM1L
CRP;FTO;C3;NFKBIA;IL6;LPL;TNF;SIRT1;NFKB1
CSF1R;DDT;MDK;CCL5;MST1;MAPK1;MIF;THBS1;CMKLR1
IL10;IFNG;IL1B;TIMP2;TIMP3;APOE;TIMP1;TNFRSF1B;TNF
IFIH1;IL3;MAVS;IRAK1;DDX58;APOA1;KLF4;CD24;SH2B3
CDKN1C;TGFB2;SMAD4;BMPR2;NOTCH1;TGFB1;TGFB3;GDF15;HFE;RBPJ

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

PSMD10;TGFB2;SLC44A4;SPHK1;TGFBR1;EGFR;IL2;CXCL16;INS;GH1;ADA
APP;CSF3;LRP1;HFE;CAV1;LRRK2;CTSZ;PARK7;PSEN1;SORL1;ACTB;BMP
DAXX;CCL21;XRCC5;GSTP1;AGAP2;HSPB1;PARK7;IQGAP1;TNF;SIRT1;SO
FOXC2;NOTCH1;IL15;ADIPOQ;NR1H3;RBPJ;ARNTL;STK11;ADAM17;DDIT3;
ITCH;CASP8;IRAK1;TRAF6;UBC;TNFAIP3;NOD2;MAP3K7;IRGM;RELA
P2RY12;TGFB1;CCL21;IRS1;CD19;AGAP2;CCR7;NOD2;AMBRA1;CCL19
P2RX5;P2RX4;P2RX3;TRAT1;P2RX2;LRRK2;CCL4;CCL3;MAPT;CMKLR1
IL1A;CSF2;IL1B;BCL2;AKT1;TNF;HSPA1B;BCL2L1;FGFR1;HSPA1A
IFNAR2;BST2;AIM2;IFI16;OAS1;STAT1;IFNB1;IRF1;XAF1;IRGM
BLK;PTPRC;PRKCB;CD19;BCL2;BTK;PIK3CD;CTLA4;CD38;BAX;MS4A1
DLL4;TGFB2;SMAD4;NOTCH1;TGFB1;NOG;NRG1;LRP2;RBPJ;TGFBR1;SMA
PARP1;MMP1;FMR1;MMP2;MMP3;MMP9;SIRT1;YY1;CASP9;STK11;OPN1S
IL25;IL17F;IL17C;IL17RC;IL17A;IL17RA
IL25;IL17F;IL17C;IL17RC;IL17A;IL17RA
BLK;CRP;IL33;GSTP1;TNFAIP3;LILRB1
CASP8;RIPK1;ARHGEF2;SLC25A4;BIRC2;BIRC3
PRDX3;NOS2;PARK7;NOS1;S100A9;S100A8
IL23A;IL23R;HLA-DRA;IL12B;CD46;HLA-DRB1
IL4;IL10;IL11;TGFB2;CFH;IL13
CSF2;IFNG;TLR4;MYD88;IL17A;IL17RA
NCR1;NOS2;LEP;DNASE1;AGER;ICAM1
IFNG;CDKN2A;IL12B;IL12A;IGF1;SIRT1
IL23A;SLC11A1;IL23R;IL12B;IL27;CCR2
CCND1;LEP;STAT3;LEPR;LRP2;SIRT1
HSP90AA1;TGFB1;UHRF1;FMR1;MSN;NR1H3;PLD1;KLF4;THBS1;AGT;MTO
LRP1;LRRK2;CTSZ;HP;HBB;DHCR24;PARK7;PHB;TNFRSF1B;CLU;BMP7;B M
STAT5A;STAT5B;IL15;STAT3;IL2RB;JAK3;JAK1
STAT5A;STAT5B;IL15;STAT3;IL2RB;JAK3;JAK1
CYP27B1;BMP2;GFI1;APOE;NFKB1;SOD1;BMP5
CRP;ABCA1;NFKBIA;ADIPOQ;NR1H3;PPARG;PPARA
XBP1;NOTCH1;HDAC3;HDAC1;BDNF;CEACAM5;CCN3
P2RX5;P2RX4;P2RX3;TRAT1;P2RX2;CCL4;CCL3
IL4;NOS2;NOS3;ENO1;NOS1;PPARA;PPARGC1A
ADAM17;ITGA4;MDK;SP1;HMGB1;APLN;FGFR1
HFE;BCL2;HIF1A;HAMP;FXN;B2M;SNCA
NOTCH2;CX3CR1;GRN;ADGRA2;IL1B;AKT1;CTNNB1;CLOCK;CX3CL1;WNT
SOX2;STAT5B;BMPR2;RPS6KB1;MYC;SPHK1;AKT1;CTNNB1;LRP2;NOS1;K
PSMD10;PSMD12;NCF1;HLA-B;TAP1;HLA-C;CYBB;HLA-A;HLA-F;HLA-G;PS
CD74;LAG3;HLA-DRB5;DCTN1;HLA-A;HLA-F;HLA-DMA;HLA-DMB;KIF5A;CA
RGS14;GSTP1;ADIPOQ;PTPN22;PIK3CB;SORL1;BMP7;AGT;BMP4;SMPD1;I
IL1A;CSF2;IL1B;BCL2;AKT1;TNF;HSPA1B;BCL2L1;HSPA1A
IL1A;CSF2;IL1B;BCL2;AKT1;TNF;HSPA1B;BCL2L1;HSPA1A

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

SMAD4;MUC1;SPHK2;IL1B;LIF;BRCA1;NOS1;FOXP3;PPARGC1A
EDN1;TRAF6;TLR9;TRAF2;TNFRSF11A;TNF;MAP3K7;ARHGEF5;MAP3K5
IL21;KLRK1;IL12A;CD226;HLA-F;PVR;HLA-G;RASGRP1;NECTIN2
SOX2;AIM2;IFI16;FYN;MEFV;NGF;BIRC2;PSMB9;BIRC3
LBP;CD14;MAPK14;RELA;TLR2
CD274;SOCS1;HFE;LILRB1;VSIR
CCL21;SLC11A1;CCR7;NOD2;CCL19
CCL21;SLC11A1;CCR7;NOD2;CCL19
IL1B;TNFSF11;TNFRSF11A;PTGS2;TNF
IL12B;IL12A;CD226;PVR;NECTIN2
IL12B;IL12A;CD226;PVR;NECTIN2
ANXA2;BDNF;HFE;B2M;MMP9
LGALS3;HLA-DMB;LILRB1;LGALS9;HAVCR2
LBP;CD14;MAPK14;RELA;TLR2
IL6;MAG;NOTCH1;CCL11;IL1B;GORASP1;PTN;TNF;B2M;SORL1;RTN4
EDN1;GSTP1;TRAF6;TLR9;PTPN22;TRAF2;TNFRSF11A;TNF;MAP3K7;ARH G
C3;CEACAM1;CREB1;ADIPOQ;AKT1;APOA1;HSD17B13;APOE;PPARA;MTO
LGALS3;PRNP;CEACAM1;TRAT1;PTPN22;PRKD2;CD226;BCL10;RELA;CAR
IFIH1;MAVS;IFNA1;STING1;DDX58;IFNB1;IFNA17;CAV1;IFNA2;FLOT1;TLR3
ITGB1;CX3CR1;SELP;SELPLG;VCAM1;ITGA4;TNF;SELE
EPHA4;IFNG;IFNGR1;SP1;CASP3;CLU;TNF;RELA
CD86;CD40LG;CD28;RARA;NLRP3;GATA3;LGALS9;HAVCR2
HSPB1;AKT1;P4HB;SOD2;SIRT1;INS;SOD1;NFE2L2
GGCT;BCL2;BAX;SOD2;BID;DNM1L;CLU;BCL2L1
IFNAR2;BST2;RO60;AXL;EIF2AK2;GATA3;GAS6;IFNAR1
SERPINA3;SERPINA1;SERPINB2;AHSG;SERPINE1;SORL1;KNG1;AGT;IFI16
NOTCH2;GPR17;NOTCH1;EPO;F2R;APOA1;STK19;PIK3CB;IGF1;NGF;RASG
PRDX3;DUOX1;PRDX2;PRDX5;CAT;HBB;PARK7;MPO;DUOX2;SOD1
EDN1;CLDN3;ALOX5;SERPINE1;APOE;TFPI;TNF;CD34;CRK;KNG1
HFE;CAV1;ITPR3;THBS1;HIF1A;IL1A;MT2A;KCNMA1;BCL2;CALM3;MAPT;C A
TGFB2;GSTP1;EIF2AK2;NOD2;AGER;RASGRP1;EGFR;IGF1R;MYC;MAPK1;
HSPA5;XRCC5;PON1;APOA1;LILRB1;HSPA2;CLU;TNF;SORL1;VEGFA;LGAL
H2AX;ANXA1;LIG4;BRCA1;MAPK14;SIRT1;STK11;COP1;KAT5;IFI16;FANCD
APP;PTH;AHR;PSEN1;MEFV;HIF1A;AIF1;PTHLH;ZFP36L1;SOX2;RO60;SHH;
DLL4;BMP4;BMP2;BMPR2;NOTCH1;TGFB1;JAG1;NOS3;GATA3;TNFRSF1B;
IL1A;HSP90AA1;DAXX;BAG3;HMOX1;TRPV1;MAPT;FGF1;THBS1;HSPA1B; H
IL6;TGFB1;ADIPOQ;RORA;GATA3;WNT1;TNF;SIRT1;TRIB2;SIRT2;ARNTL
P2RX7;BMP4;KL;BMP2;BMPR2;TGFB1;PTH;TGFB3;ALOX5;PTN;BMP7
GNG2;LRRK2;ABL1;MAPK1;SIRT2;GABPA;TGM2;SNCA;ATF4
P2RX7;APP;IFNG;EGF;IGF1;PSEN1;HIF1A;NFKB1;INS
EDN1;SMAD4;NOTCH1;P2RX4;PARP1;PRKCA;IGF1;IL6ST;AGT
SPHK2;BRCA1;MAPK14;THBS1;SIRT2;AGT;ACE2;ALOX5;RAC2;AGTR1;CY P

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

H2AX;BLK;OGG1;FMR1;XIAP;BRCA1;PARK7;PSEN1;YY1;CASP9;STK11;CC
XBP1;PARP1;IRS1;PLA2G1B;CAV1;ADIPOQ;GCG;SLC2A4;CRHR1;NFKB1;R
CYP2C9;GSTM1;ACOT7;GPX4;CYP2D6;GSTP1;ALOX5;ALOX15;CYP3A4;PT
APP;EPHA4;TYROBP;FAM107A;ABL1;PTN;APOE;EPHB2;AGER;INS
ACE2;BMPR2;ACE;CAV1;F2R;AGTR1;ADM;ADRA1A;AGT;TRPM4
TGFB1;CCL21;TH;CCL3;SDF4;CCR7;CCL19;CCR5;TGFBR1;SOD1
CD40;CASP8;TRAF3;UBC;RIPK1;CD14;TLR4;BIRC2;TLR3;BIRC3
C1QA;CFH;PHB;CFP;CLU;C2;C3;IL1B;CD19;C3AR1;SERPING1;CD46;CFB
CST3;IL10;PRNP;EPHA4;LRRK2;TIMP2;AKT1;TIMP3;PLAT;TIMP1;KNG1;INS
TAP1;HLA-DRA;HLA-A;HLA-F;HLA-G;B2M;HLA-DRB1
HLA-B;NOD2;NLRC4;HLA-A;CD1D;NAIP;HLA-DRB1
BMP4;LAG3;IFNB1;MDK;IRF1;IFNA2;CTLA4
IL4;ITGAM;SPHK2;ITGB2;F2RL1;HLA-F;CD177
SOCS1;HLA-DRA;CD46;HLA-G;FOXP3;VSIR;HLA-DRB1
ADAM17;CCL21;WNK1;CCL5;CXCL13;CCL27;CCR2
TRAT1;PRKD2;CD226;BCL10;RELA;CARD11;NECTIN2
FOXC1;MYO1C;PIK3CA;VEGFB;KDR;PIK3CD;VEGFA
ITGB1;CX3CR1;SELP;SELPLG;VCAM1;ITGA4;TNF;SELE
IL6;NOTCH1;CCL11;IL1B;TNF;SORL1;B2M;TLR2
HSPB1;AKT1;PARK7;SOD2;SIRT1;HIF1A;INS;NFE2L2
XBP1;BMP2;NOTCH1;HDAC3;HDAC1;BDNF;CEACAM5;CCN3
CD74;CXCL8;CCL21;MDK;RAC2;CCR7;CCL19;DNM1L
AIM2;CASP8;GZMA;CASP1;GZMB;NLRC4;NLRP1;NAIP
IGFBP1;GH1;BMP2;CDH3;IGFBP3;IGF1;WNT1;BMP5
ITGB1;CXCL8;TGFB1;LRP1;CAV1;ITGB2;MX1;ADM;LILRB1;GRK2;CXCR1;C
TGFB2;SMAD4;BMPR2;TGFB1;TGFB3;GDF15;HFE;NOG;BMP7;TGFBR1;BM
LRRK2;ABL1;MAPK1;GABPA;TGM2;ATF4
TLR9;TLR7;MAP3K7;TLR4;TLR3;TLR2
CST3;DPP4;TGFB1;NOTCH1;TNFRSF1B;TNFRSF1A
IL11;GJA1;IL1B;LIF;OSM;FGF23
CD274;CCL5;PDCD1;LGALS9;TP53;IDO1
IL21;IL15;IL23A;IL18;IL12B;IL2
IL23A;IL23R;HLA-DRA;IL12B;CD46;HLA-DRB1
LRRK2;ABL1;MAPK1;GABPA;TGM2;ATF4
HSP90AA1;TGFB1;EGF;TGFA;NRG1;PRKCA;PTPN11;IQGAP1;EGFR;ADAM
XBP1;LPL;PTGS2;BMP7;ZFP36L1;INS;BMP2;CREB1;AKT1;PPARG;RREB1;C
TGFB2;BMPR2;PRKCE;PTN;MCC;HIF1A;RTN4;IL4;CEACAM1;IFNG;ENPP2;
XBP1;LRRK2;ALOX5;SYVN1;NR1H3;PARK7;CLU;BCL2L1;HSPA1A
IL11;ERBB3;TRAT1;IGFBP3;IL1B;ADIPOQ;LIF;OSM;FGF23
DPP4;CD74;CXCL8;CCL21;MDK;RAC2;CCR7;CCL19;DNM1L
CD40;CASP8;TRAF3;UBC;RIPK1;CD14;TLR4;BIRC2;TLR3;BIRC3
PSMD10;CD74;CXCL12;DDX39B;ACKR3;MIF;CLU;SIRT1;CD44;BCL2L1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

C1QTNF3;XBP1;IL18;LPL;NR1H3;APOA1;RORA;APOE;ANGPTL4;SIRT1
CD74;LAG3;HLA-DRB5;MARCHF1;DCTN1;HLA-DMA;HLA-DMB;KIF5A;CANX;
IL10;LRRK2;HGF;IL10RA;STAT3;PTPN22;SIRT2;MTOR;PIK3CA;LEP;LEPR;B
PSMD10;PSMD12;NOTCH1;EPO;EPAS1;RBPJ;HIF1A;SIRT2;PSMB8;PSMB9;
HSP90AA1;NCF1;VEGFB;HSPB1;CYBB;PIK3CB;MAPK14;VEGFA;PIK3CA;AX
CAV1;EIF2AK3;MMP9;DDIT3;BCL2;BAX;P4HB;DNM1L;BID;S100A9;TP53;S10
CXCL9;CEMIP;GSTO1;F2R;CX3CL1;CXCL10;CXCL11;CD19;CALM3;NOS1;C
CX3CR1;NR4A2;BDNF;IFNB1;MAZ;BCL2;FAS;TRAF1;TNF;CX3CL1;TGFBR1
ERN1;BMP4;IL6;TGFB1;MYCN;IL1B;RIPK1;TP53;RELA;EGFR;NFKB1;HSPA1
MBTPS1;CXCL8;HSPA5;ALOX15;EIF2AK3;SYVN1;TNFRSF10B;TRAF2;RNF
CRP;ABCA1;NFKBIA;IL6;NR1H3;PPARG;PPARA;TNF
APP;MAPK8;IFNG;EGF;GATA3;KLF4;TNF;NFKB1
HSP90AA1;CASP8;CDC37;FLOT1;SPATA2;RIPK1;BIRC2;BIRC3
NOTCH2;NOTCH3;NOTCH1;JAG1;STAT1;NOTCH4;PSEN1;RBPJ;DLL4;ADA
P2RY12;P2RX7;P2RX4;P2RX3;P2RY2;P2RY1;TRPV1
IFIH1;MAVS;STING1;DDX58;IFNB1;CAV1;FLOT1
NQO1;ARG2;NOS2;NOS3;AKT1;CYP1B1;NOS1
IL6;IL1B;OSM;PARK7;PTGS2;IL6ST;TNF
IL10;IL1B;FLOT1;TNF;AGER;BMP7;CD44
DDR1;DPP4;CST3;IL6;TGFB1;LRP1;FSCN1
BMP4;AR;NR3C1;ESR1;BMP7;ESR2;NR3C2
DUOX1;NCF1;NOX3;CYBB;NOX4;NOX5;DUOX2
TNFSF14;SLC11A1;MSN;LILRB1;RASGRP1;TNFRSF4;PIK3CG
CD86;P2RY12;EDNRA;PTH;BDNF;LPAR2;PHB;ADRA1A;SELE;EGFR
C3;GH1;OCLN;PTH;IRS1;ADIPOQ;AKT1;PTPN11;IGF1;INS
DLL4;FOXC2;NOTCH1;ANXA1;KDR;HMOX1;PTGS2;KLF4;THBS1;VEGFA
CD40;KMT2A;HFE;WAS;FAM107A;AIF1;ACTB;RTN4;ACTG1;CHAF1A;RAC2;
CX3CR1;GHSR;GSTP1;TNFAIP3;NLRP3;APOA1;IGF1;MEFV;CX3CL1
MAPK8;CASP8;BCL2;GZMB;BID;YWHAZ;TP53;TP63;TP73
MAPK8;CASP8;BCL2;GZMB;BID;YWHAZ;TP53;TP63;TP73
HSP90AA1;CISH;SPHK1;FAM107A;TRAF2;PTPN11;PARK7;SSRP1;TNF;IRG
HSPB8;ADRB2;SIRT1;C9ORF72;IRGM;DCN;IL4;STING1;BAG3;KDR;MAP3K7
C1QA;CFH;CFP;CLU;C2;C3;CD19;C3AR1;SERPING1;HLA-DRA;CD46;CFB;H
PSMD10;PSMD12;TGFB1;EGF;CAV1;LRRK2;ATP6AP2;XIAP;NFKB1;EGFR;
HLA-B;HLA-C;HLA-A;HLA-F;HLA-G
HLA-B;HLA-C;HLA-A;HLA-F;HLA-G
ALOX5;IL18;AKT1;IL18R1;IL18BP
CASP8;TRAF2;RIPK1;TNF;TNFRSF1A
P2RY12;TGFB2;P2RX4;CCL3;CCL2
ALOX5;IL18;AKT1;IL18R1;IL18BP
ANXA1;IFNB1;TBX21;IFNA2;CCR2
CSF2;IFNG;MYD88;IL17A;IL17RA

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

TSLP;SPHK2;CD226;HAVCR1;NECTIN2
IL23A;IL23R;IL18;IL12B;IL12A
P2RY12;CX3CR1;P2RX4;CCL3;CX3CL1
CD74;ANXA1;IL1B;PTGS2;SIRT1
ANXA1;CD80;IL27;CCL19;JAK3
S1PR1;AKT1;PIK3CB;S1PR2;PIK3CG
HSP90AA1;NOTCH1;RAP1A;MSN;PTPN11;TRAF2;APOE;CCL19;IRGM;AGT;
C3;IL4;CCL21;HFE;SERPINE1;APOC1;FLOT1;PIK3CB;CCL19;CLU;B2M
CD74;CIITA;LGALS1;GSN;IFNA2;PTX3;LGALS9;P4HB;HLA-DRB1;NECTIN2;L
MAVS;HDAC3;TGFB1;IFNG;BAG3;CDH1;IL1B;FLNA;PSEN1;ANP32B;GAS6;T
PSMD10;PIAS3;HDAC3;LRRK2;SPHK1;CAV1;FAM107A;XIAP;BRCA1;BCL10;
IGFBP3;APOA1;NR1H3;KLF4;CLU;SIRT1;FOXP3;HLA-G;DDAH1;ERBB3;ALO
SHMT1;PRF1;AQP4;MIF;BCL10;TRPV1;NLRC4;SOD2;HLA-G;CRYZ;TRPM2;
CD74;CD40;DMTN;KMT2A;HFE;WAS;FANCC;TRAF2;TRAF1;PML;CD2AP;OC
PRNP;DAXX;DMTN;NCF1;SYT1;HFE;LRRK2;ALOX15;IQGAP1;FOS;MMP9;E
MCAM;KDR;PRCP;HPSE;CD34;VEGFA
SPAST;NEFL;MAPT;HAP1;HIF1A;SYBU
OPN1SW;MMP1;MMP2;MMP3;TIMP1;MMP9
CXCL8;CXCL12;NTF3;VEGFB;IL16;VEGFA
CD274;PRNP;PRKAR1A;PDCD1LG2;LGALS9;FOXP3
CASP8;RIPK1;ARHGEF2;SLC25A4;BIRC2;BIRC3
IL4;ANXA1;TBX21;JAK3;FOXP3;SMAD7
LGALS3;CD274;CCL5;PDCD1;JAK3;IDO1
IL4;IL6;IFNB1;TBX21;IFNA2;NLRP3
C1QA;CFH;CXCL13;CFP;CLU;C2;C3;CD19;C3AR1;SERPING1;CCR7;CD46;C
ACE;HFE;CANX;HLA-B;HLA-C;TAP1;HLA-A;HLA-F;B2M;HLA-G
NFKBIA;LRP1;CAV1;PON1;ADIPOQ;NR1H3;APOA1;PPARG;APOE;SIRT1
FOXC1;TGFB2;ACE;GATA3;BMP7;TGFBR1;AGT;VEGFA;BMP4;SHH;SALL1;
SELP;PRNP;TRPM2;DMTN;VCAM1;PTPRC;CCL20;KDR
IL4;CASP9;ERBB3;CASP3;BCL2;FAS;BAX;BCL2L1
IL11;ERBB3;IGFBP3;IL1B;ADIPOQ;LIF;OSM;FGF23
RAP1A;SORT1;BDNF;CASP3;NTF3;DDIT4;HAP1;NGF
IL10;ERN1;GJA1;ADAMTS1;MMP2;MFN2;IGF1;MMP9
BMP4;TGFB2;SMAD4;BMP2;BMPR2;TGFB1;TGFB3;GDF15;HFE;BMP7;TGF 3
CAV1;DDIT3;BCL2;BAX;BID;DNM1L;S100A9;TP53;S100A8;SOD1;BCL2L1
CRP;IL22;IL6;AHSG;HP;LBP;IL6R;INS;MBL2
MT2A;MAPK8;DAXX;NCF1;AKT1;MAPK1;FOS;MMP9;EGFR
STAT5B;STAT1;STAT3;FOXO3;MAPK14;ETS1;HIF1A;HSPA1B;HSPA1A
TRPM2;PTPRC;CCL21;F2R;ITPR3;FASLG;CCR7;CCL19;DRD2
IL10;IL1RN;IL6;ANXA1;FAM107A;NR3C1;TNF;SSTR4;ZFP36L1
FASLG;RIPK1;TRPM7;CD14;DNM1L;TLR4;TLR3
SPRED2;ZEB1;IFNG;NOTCH4;CAV1;IL13;MMP9

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

IL4;GRN;PTPRC;NR1H3;LDLR;CX3CL1;CD200
PSMD10;HGF;AKT1;IGF1;CLU;FXN;BCL2L1
CXCL8;TYROBP;IL15;CCL5;CXCR2;F2RL1;DNASE1
NQO1;ARG2;NOS2;NOS3;AKT1;CYP1B1;NOS1
IRS1;PRKCE;ADIPOQ;AKT1;ADM;PPARG;PPARA
DLL4;AGTR1;HMOX1;IL12B;IL12A;THBS1;VEGFA
IL11;EDN1;ANXA1;LIF;OSM;FGF23;VAMP2
JAG1;AIRE;CD8A;CTSH;HLA-A;CD46;MICA
NOTCH2;NOTCH3;SEMA7A;NOTCH1;SEMA3A;CXCR4;PIK3CD;LAMC2;PIK3
TGFB2;SMAD4;BMPR2;TGFB1;TGFB3;GDF15;HFE;RGMB;BMP7;RGMA;BMP
ABCA1;XBP1;CAV1;IL18;APOA1;LPL;NR1H3;RORA;CYP7B1;SIRT1;SOAT1;A
XBP1;ANXA1;TGFB3;NOTCH4;CAV1;MSN;NRG1;PRL;TGFBR1;SOD1;SOX2;
ANXA1;CDKN2A;FAM107A;KLF4;AIF1;EGFR;ADAM17;RGCC;CCND1;APC;A
PSMD10;PSMD12;FOXC1;KMT2A;OSM;EIF2AK2;GATA3;PSMB8;PSMB9;PS
PSMD10;PSMD12;BCL10;NFKB1;RELA;MALT1;PSMB8;RELB;PSMB9;PSMB
PSMD10;PSMD12;BCL10;NFKB1;RELA;MALT1;PSMB8;RELB;PSMB9;PSMB
CDKN1C;IL10;BMP4;FOXC1;BTG1;TGFB1;RGCC;PRCC;BUB1B;CTNNB1;BM
MAPK8;CASP8;BCL2;GZMB;BAX;BID;YWHAZ;TP53;TP63;TP73
P2RX7;BMP4;KL;BMP2;BMPR2;TGFB1;PTH;TGFB3;ALOX5;PTN;BMP7
BLK;EPHA4;CSF1R;EGFR;KDR;BTK;ABL1;FYN;PTPN6;EPHB2;JAK2;JAK3;F
ABCA1;XBP1;CAV1;IL18;APOA1;LPL;NR1H3;RORA;CYP7B1;SIRT1;SOAT1;A
CCL13;CXCL9;CXCL8;PLA2G1B;REG1A;CXCL1;CXCL13;CXCL2;CXCL5;CX
CD74;LAG3;HLA-DRB5;DCTN1;HLA-DMA;HLA-DMB;KIF5A;CANX;HLA-DPB1
TGFB2;TGFB1;CCL21;TGFB3;CAV1;NR1H3;CCR7;CCL19;THBS1
CYP2C9;CYP2B6;CYP2D6;NR1I2;CYP2R1;NOS1;CYP3A4;CYP2C19
MBTPS1;ADAM17;TGFB1;MMP7;TRAF6;PSEN1;RELA;NFKB1
PRNP;PTPRC;KAT5;TBX21;TNFAIP3;FOXP3;CD34;HAVCR2
CX3CR1;DLL4;MDK;CTNNB1;LRP2;DRD2;CX3CL1;VEGFA
CD74;CXCL8;CCL21;MDK;RAC2;CCR7;CCL19;DNM1L
XBP1;LRRK2;DDIT3;EIF2AK3;SYVN1;PARK7;BCL2L1;HSPA1A
FOXC2;TGFB2;FOXC1;NOTCH1;TGFB1;NOTCH4;FN1;PTPN11;TGFBR1;WD
CST3;IL1B;APOC1;AGAP2;FLNA;PHB;HMGCR;PPARA;TNF;SIRT2;EGFR;INS
LRRK2;PIK3CB;PARK7;HMGB1;MEFV;FOXO3;SIRT1;C9ORF72;IRGM;DCN;I
CHGA;NOS2;IL23R;SLC11A1;SERPINE1;IRGM;SELP;IL6;IL23A;TLR9;IL12B;
ADAM17;ANXA1;RGCC;CCND1;ADAMTS1;AKT1;GLI1;AIF1;EGFR;EZH2
CREB1;AKT1;NR1H3;APOA1;HSD17B13;APOE;PPARA;LDLR;MTOR;INS
P2RY12;TGFB1;CCL21;IRS1;CD19;PIK3R3;CCR7;NOD2;AMBRA1;CCL19
FOXC1;TGFB2;ACE;STAT1;GATA3;TGFBR1;AGT;VEGFA;BMP4;SALL1;WT1
EDN1;SERPINE1;APOE;TFPI;CD34;KNG1
BST2;CSF1R;IL5RA;IL12B;MAPK1;IL12A
PRNP;IGF1;HAP1;APOE;CLU;SORL1;RTN4
IL33;CCL3;LBP;MMP8;THBS1;TLR4;HSPD1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

CX3CR1;LRRK2;CTNNB1;PTN;DRD2;CX3CL1;VEGFA
P2RX7;DUOX1;TRPM2;P2RX4;STAT1;P2RY1;DUOX2
CSF1R;TGFB2;TGFB1;TGFB3;F2R;PVR;CLDN5;OCLN;CDH3;CDH1;FSCN1;F
NOTCH2;CSF1R;DMTN;LRP1;FAM107A;IQGAP1;C9ORF72;MTOR;BST2;TRP
PSMD10;PSMD12;NOTCH1;JAG1;KMT2A;OSM;EIF2AK2;PTN;GATA3;PSMB8
RO60;AXL;GATA3;GAS6;IFNAR1
CCL21;PRF1;MSN;CCR7;CCL19
CYP27B1;GFI1;GLA;NFKB1;SNCA
GSN;CASP8;FAS;LGALS9;JAK2
ITGB1;TGFB1;DMTN;PRKCE;THBS1
P2RY12;P2RX4;CCL3;CX3CL1;CCR2
LGALS3;LGALS1;HMGB1;LGALS9;AGER
C3;CCL2;HMGB1;TGM2;C2
ABCA1;RALBP1;ABL1;APOA1;APOE
IL12A;CCR7;LGALS9;CCR6;GAS6
TGFB2;TGFB1;TGFB3;NOG;TGFBR1
BMP2;NOTCH1;RGCC;TNFRSF1B;TNFRSF1A
BLK;LGALS3;CD274;BTK;JAK3
CD86;ANXA1;RARA;IL18;NLRP3
CAV1;FLOT1;TNFAIP3;F2RL1;PTPN22
IL21;IL15;LEP;JAK2;JAK3
CASP8;TRAF3;IRF1;XIAP;PTPN22;CX3CL1;BIRC2;FOXP1;BIRC3
MT2A;MAPK8;DAXX;NCF1;AKT1;MAPK1;FOS;MMP9;EGFR
PSMD10;PSMD12;BCL10;NFKB1;RELA;MALT1;PSMB8;RELB;PSMB9;PSMB
NOTCH2;NOTCH3;NOTCH1;HDAC3;HDAC1;NOTCH4;MAZ;NR1I2;RORA;RB
ARNT2;TGFB1;TGFB3;NOG;LIG4;BRCA1;GATA3;BMP7;TGFBR1;VEGFA;BM
CCR1;EGF;FCRL3;F2R;IL16;LILRB1;P2RX4;CCL5;CCL4;CCL3;BCL2;CTNNB
BMPR2;NOTCH1;HGF;NOG;IGF1;BMP7;BMP4;BMP2;IL6;PPARG;IL6ST;IL6R
CYP2C9;CYP2B6;CYP2D6;NR1I2;CYP2R1;NOS1;CYP3A4;CYP2C19
GH1;AHI1;EGF;FMR1;NTF3;SELE;APLN;VEGFA
HSPA5;S100A1;PLP1;PADI2;MBP;CALM3;NDRG2;CALM1;CALM2;ACTB;SIR
SPAST;DST;DCTN1;NEFL;KIF1B;MAPT;HAP1;HIF1A;SYBU;SOD1
CHGA;SCN10A;P2RX4;CALM3;NOS1;CALM1;ADRA1A;CALM2;PIK3CG;SMA
BMP4;MAVS;HDAC3;TGFB1;IFNG;BAG3;CDH1;FLNA;APOD;PSEN1
GRN;PARK7;PHB;CLU;RTN4;HSPD1;BAG3;FLOT1;FLNA;PPARGC1A;ATF7IP
PSMD10;PSMD12;FOXC1;KMT2A;OSM;EIF2AK2;GATA3;PSMB8;PSMB9;PS
CSF1R;PIK3CA;RPS6KB1;IRS1;PTAFR;PIK3CD;PIK3CB;IGF1;NGF;PIK3CG;I
P2RY12;TGFB1;CCL21;IRS1;CD19;CCR7;NOD2;AMBRA1;CCL19
MAVS;HDAC3;TGFB1;IFNG;BAG3;CDH1;FLNA;PSEN1;ARHGEF5
NOTCH2;NOTCH1;EPO;STK19;IGF1;JAK2;NGF;RASGRP1;TGM2
DLL4;BMP4;SHH;BMP2;SALL1;WT1;NOTCH4;MYC;KDR;CTNNB1;VEGFA
IFIH1;MAVS;STING1;DDX58;IFNB1;CAV1;FLOT1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

CIITA;IL6;CEACAM1;GSTP1;PARK7;PPARA;INS
NOS2;DDAH1;NOS3;NOS1;APOE;AGT;INS
P2RY12;FOXC2;TGFB2;CCL21;CCL5;LIF;CXCL13
BMP2;TGFB1;NOTCH1;MDK;CXCR4;PTN;TNFRSF1B
CSF2;PLA2G2A;IL18;AGTR1;LPL;NFKB1;AGT
S100A1;AKT1;PIK3CB;APOE;TNF;HIF1A;INS
PTPA;PTPRC;FCRL3;CALM3;CALM1;CALM2;MTOR
FASLG;RIPK1;TRPM7;CD14;DNM1L;TLR4;TLR3
XBP1;FCRL3;TLR9;BTK;CD27;IKZF3;ZFP36L1
FTO;LEP;PTGS2;SIRT1;BMP7;RREB1;INS
STAT5B;CSF3;STAT1;STAT3;FOXO3;MAPK14;ETS1;HIF1A;HSPA1B;HSPA1
STAT5B;STAT1;STAT3;FOXO3;MAPK14;ETS1;HIF1A;HSPA1B;ZFP36L1;HS
OCLN;PTH;IRS1;PLA2G1B;LEP;ADIPOQ;AKT1;PTPN11;IGF1;INS
BMP2;NCF1;SPHK1;IL1B;LEP;PTPN22;LGALS9;AGER;RASGRP1;VEGFA
MBTPS1;CLDN3;TRAT1;LRRK2;ICA1;LEPR;ACTB;VAMP2;ACTG1;SNCA
GSTK1;CPT1A;TGFB1;STAT1;SOX10;CNN3;VEGFA;LGALS3;AHI1;BMP2;SH
APP;SERPINA1;PLG;PLAT;AFP;PSEN1;RNF5;PHEX;KNG1;C3;CST3;LGALS
CD74;IFNA1;IFNB1;MDK;IFNA17;GPR183;IFNA2;F2RL1
CCR1;NOTCH1;AHSG;MDK;CCL3;RBPJ;FGF23;TRPM4
ITCH;CASP8;IRAK1;TRAF6;UBC;TNFAIP3;NOD2;MAP3K7
CD74;LGALS1;AXL;FMR1;TYRO3;P4HB;LGALS9;HLA-DRB1
DDR1;MMP12;CEACAM1;ADAM17;TOR1A;FLNA;ARHGAP24;CD44
CX3CR1;NOTCH1;NOS3;F2R;PLA2G2A;CCN3
ACE;ANXA1;NOS2;PLA2G1B;LEP;DRD2
NOTCH2;IL21;DOCK11;IL6;POU2AF1;GPR183
SPAST;NEFL;MAPT;HIF1A;LRPPRC;SYBU
IL10;HGF;LRRK2;TXN;PARK7;NFE2L2
CD74;MUC1;BCL2;MIF;SIRT1;CD44
IL23A;SLC11A1;IL23R;IL1B;IL12B;CCR2
ARG2;CDKN2A;LMNA;SIRT1;HLA-G;B2M
TSLP;IFNA2;IL9;RARA;GATA3;LGALS9
CD86;LEP;ABL1;PHB
TNF;B2M;RELA;NFKB1
CXCL13;THBS1;TNF;S100A9
NOTCH1;LRP2;TGFBR1;VEGFA
F2RL1;CCR7;CCL19;LGALS9
LRP1;TIMP2;TIMP3;TIMP1
LAG3;MDK;IRF1;CTLA4
KDR;HSPB1;PRKD2;VEGFA
CCL7;CCL5;CCL4;CCL3
IL23A;IL23R;IL18;IL12B
CD74;ANXA1;IL1B;PTGS2

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

P2RX4;IL1B;TNFSF11;TNFRSF11A
CXCL10;ITGAX;FGF1;FOXP1
IL1B;PTGS2;TNF;PTGES
CX3CR1;TYROBP;ITGAM;CX3CL1
CRP;IL12B;LILRB1;IL12A
FOXC1;NOTCH1;TGFB1;NOS3;NOTCH4;MIF;CST3;BMP4;SHH;BMP2;MAPT;
CDKN1C;PRNP;TGFB1;CDKN2A;LRRK2;IGFBP3;PARK7;SIRT1;C9ORF72;B
NOTCH2;TGFB2;NOTCH1;EPO;STK19;MYO9B;IGF1;NGF;RASGRP1;BCR;S
SOCS1;RPS6KB1;IRS1;AHSG;PRKCB;IL1B;MZB1;PTPN11;SORL1;SIRT1;IN
NQO1;ARG2;NOS2;NOS3;SPHK2;SPHK1;AKT1;CYP1B1;NOS1
CD74;HPGDS;EDN1;GSTM1;GSTP1;PLA2G4A;MIF;PTGS2;PTGES
STAT5A;APP;STAT5B;LEP;ABL1;PRL;APOE;IGF1;SOD1
SMAD4;TMPRSS6;HFE;SLC11A1;SLC40A1;CP;SOD1;MYC;LCN2;HMOX1;B2
FOXC2;TGFB2;FOXC1;NOTCH1;TGFB1;BMPR2;FN1;PTPN11;BMP7;TGFBR
CCR1;CAV1;ATP2B2;PSEN1;TRPV1;PANX1;P2RX7;TRPM2;CYP27B1;P2RX
DMTN;CCL21;ALOX15;FN1;APOA1;CX3CL1;MDK;ABL1;FLNA;CCR7;P4HB;J
ACE;DMTN;IL1B;FAM107A;APOD;THBS1;TNF;TLR2
TRPM2;PTPRC;CCL21;F2R;ITPR3;CCR7;CCL19;DRD2
XBP1;NOTCH1;HDAC3;HDAC1;BDNF;CEACAM5;CCN3;MAPK14
BMP4;BMP2;SHH;SALL1;WT1;MYC;FGF1
NOTCH2;DLL4;TGFB2;BMP2;BMPR2;NOTCH1;NOG
PRNP;IGF1;HAP1;APOE;CLU;SORL1;RTN4
CD74;EDN1;HPGDS;PLA2G4A;MIF;PTGS2;PTGES
BMP4;CIITA;IL6;TGFB1;RGCC;TGFB3;F2R
IL6;ADAM17;MDK;MST1;F2RL1;PTN;IL6R
P2RY12;P2RX7;P2RX4;P2RX3;P2RY2;P2RY1;TRPV1
BMP4;BMP2;SHH;SALL1;WT1;MYC;GATA3
STK11;PIK3CA;AKT1;MAP3K7;MTOR
ITGB1;CD86;CD40;CD40LG;PHB
LEP;STAT3;EBI3;LEPR;SIRT1
CRP;NFKBIA;IL6;NR1H3;TNF
IL10;FCRL3;APOA1;LILRB1;TNF
DLL4;BMP2;NOTCH1;BMP7;BMP5
IL10;XBP1;BTK;CD27;IL2
APOC1;AGTR1;APOA1;APOE;AGT
CD74;SEMA7A;LILRB1;SIRT1;HLA-G
CD40;MC1R;SPHK2;ADRA1A;VEGFA
CD274;IRF1;HFE;LILRB1;HLA-A
ACE2;ACE;IL1B;CAV1;AGT
MST1;GATA3;BRCA2;RREB1;RTN4
ACE2;BCL2;ACTB;INS;SNCA
CX3CR1;CD274;PARK7;CD47;FOXP1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

CX3CR1;C3;C1QA;ITGAM;CX3CL1
PTGER4;NOD2;MAPK14;NFKB1;ZFP36L1;MAPK8;IRAK1;TRAF6;UBC;MAPK
CCR1;CCL13;CD40;EDN1;CCL11;CAV1;RMDN3;ATP2B2;CYP27B1;CXCL12;
NOTCH2;APP;NOTCH3;SEMA7A;NOTCH1;SEMA3A;CXCR4;PIK3CD;PIK3CB
MBTPS1;ADAM17;TGFB1;MMP7;TMPRSS6;TRAF6;CTSH;PSEN1;RELA;NFK
ATXN2;EDN1;EDNRB;TRAT1;PTX3;BRCA1;APOE;NFKB1;SIRT2;INS
BMP4;CSF1R;SHH;TGFB1;ACE;PTPRC;FST;KDR;TP53
CX3CR1;C3;CXCL8;CCL5;ADIPOQ;CD47;JAK2;TNFRSF1B;SIRT1
NOTCH2;NOTCH3;NOTCH1;HDAC3;HDAC1;NOTCH4;CTR9;CSTF2;NR1I2;M
CXCL10;OAS1;DDX58;MX1;PHB;NLRP1
DLL4;SHH;NOTCH4;KDR;CTNNB1;VEGFA
CSF1R;CLDN3;DCTN1;F2R;F2RL1;CD177
ITGB1;ABCA1;ITGB2;LPL;PPARG;LDLR
PLA2G2A;AGTR1;LPA;MPO;PLA2G7;AGT
EDN1;SERPINE1;APOE;TFPI;CD34;KNG1
IL33;CCL21;SOAT1;CCR7;IGF1;CCL19
CSF1R;MDK;CCL5;MAPK1;THBS1;CMKLR1
BMP4;SMAD4;TGFB1;TGFB3;JAK2;TGFBR1
CD74;MUC1;BCL2;MIF;SIRT1;CD44
CYP27B1;CYP24A1;SPP1;HSD17B6;CYP3A4;FGF23
SHH;ADAM17;PTPRC;LIG4;CCR6;ZFP36L1
PSMD10;APP;PSMD12;SERPINA1;EPAS1;AFP;HIF1A;KNG1;C3;CST3;PSMB
APP;C1QA;TGFB2;TGFB1;TGFB3;PSEN1;ACTB;ACTG1;VMP1;OCLN;CLDN3
BLK;ACHE;TGFB2;TGFB1;PLA2G1B;TGFB3;IGF1;CD2AP;C1QTNF3;IL1A;F2
ADAM17;ANXA1;RGCC;CCND1;ADAMTS1;AKT1;AIF1;EGFR
OCLN;PTH;IRS1;ADIPOQ;AKT1;PTPN11;IGF1;INS
CASP8;TNIP1;STAT1;GSTP1;ADIPOQ;TNFAIP3;RORA;RIPK1;ESR1;SIRT1
MAPK8;XRCC5;CAV1;ABL1;APOA1;NOD2;PSEN1;MAPK14;FXN;SOD1
IFNG;GSTO1;CCL2;CALM3;ADRB2;HAP1;EPHB2;CALM1;CALM2;CCR2
GPRC6A;TRPM2;IL6;MRGPRX1;SYVN1;IRF5;TRPV1;DRD2;RNF5;MTOR
AIM2;OAS1;IFI16;STAT1;IFNB1;IRF1;IRGM
CHGA;EDN1;TGFB2;ADM;ADRA1A;APLN;TRPM4
FCRL3;TBX21;TLR9;ABL1;IKZF3;ZFP36L1;CCR2
ACE;LRP1;IGFBP3;CCL5;SERPINE1;IGF1;SORL1
GGCT;BCL2;BAX;BID;DNM1L;SOD2;CLU;HSPD1;BCL2L1
CEACAM1;S100A1;ALOX5;PIK3CB;FGF1;KLF4;THBS1;JAK1;VEGFA
FOXC1;BTG1;NOTCH1;AIRE;OGG1;NR1I2;CTR9;RORA;RNF6;AHR;PHB;BR
DDR1;EPHA4;CSF1R;LRRK2;INSRR;EIF2AK3;EIF2AK2;EGFR;MTOR;IGF1R;
SHH;TGFB1;WT1;CAV1;SLC1A1;KDR;CYP1B1;ADM;RBPJ;TGFBR1;VEGFA;
NPEPPS;MAPK8;CASP8;HSPA1L;RAC2;BCL2;GZMB;BID;YWHAZ;TP53;TP6
APP;RGS14;SYT1;FMR1;TNF;ADRA1A;AGER;INS;FLOT1;CCL2;HAP1;EPHB
ABCA1;GPR17;RALBP1;F2R;APOA1;MYO9B;BCR;ADGRG1;STMN1;ABL1;F2

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

APP;CSF3;EDN1;CCL11;CCL21;DCTN1;PRKCE;ALOX15;PSEN1;CLU;CX3CL
APP;BTG1;EHMT2;OGG1;RORA;AHR;BRCA2;NR3C1;ELAVL2;SOX2;NCOA2
ITGB1;TGFB2;VCAM1;ITGAM;ITGB2;ITGAL;PVR;SELE;ICAM1;SELP;CLDN11
PSMD10;SERPINA3;NCOA2;NQO1;PSMD12;HDAC3;HMGCR;PSMB8;INS;PS
GSTK1;CPT1A;JAG1;ANXA1;HDAC1;GATA3;GLI1;CNN3;VEGFA;BMP4;LGAL
DPP4;PIK3CA;ADGRA2;STAT1;NOS3;TNFSF12;ABL1;CYP1B1;PKN2;PRSS3
PRDX3;LRRK2;ABL1;BCL2;AKT1;BAX;PARK7;MAPT;SOD1;BCL2L1
ITGA4;HFE;LRRK2;CAV1;CTSZ;ADIPOQ;PARK7;ADRB2;SORL1;ACTB;MAP K
CYP2C9;HPGDS;CYP2B6;GPX4;CYP2D6;ALOX5;ALOX15;CYP1B1;PLA2G4A
ACE2;CLDN5;CLDN3;BDNF;CAV1;DLG5;KDR;FLOT1;ABL1;EPHB2;AGT;VE G
GHSR;ADCYAP1;EDN1;IL6;ANXA1;PARK7;VIP;CRHR1
CXCL10;CEMIP;CXCL9;CXCL11;CD19;F2R;CX3CL1;SNCA
IL6;ADGRA2;LEP;HMOX1;CTNNB1;CXCL13;ETS1;HTATIP2
P2RY12;CCL21;TGFB3;FMR1;P2RX7;DOCK11;OCLN;PIK3CA;APC;RAC2;FS
PSMD10;HGF;AKT1;IGF1;MAPT;CLU;FXN;BCL2L1;HSPA1A
AR;TGFB2;TGFB1;TGFB3;CAV1;NR1H3;NR3C1;TFPI;THBS1
GPX4;PON2;ALOX5;PON1;ALOX15;PTGS2
XBP1;LRRK2;SYVN1;PARK7;BCL2L1;HSPA1A
SORT1;BDNF;CASP3;DDIT4;HAP1;NGF
P2RX4;KDR;HSPB1;PRKD2;VEGFA;FGFR1
CD74;EDN1;PLA2G4A;MIF;PTGS2;PTGES
APP;PSEN1;APOE;CLU;CRYAB;LDLR
NOTCH1;P2RX4;HSPB1;PRKD2;FGF1;THBS1
DDAH1;NOS2;NOS3;ARG1;NOS1
CXCL8;IL15;CCL5;CXCR2;F2RL1
LEP;STAT3;EBI3;LEPR;SIRT1
NOTCH1;RGCC;NOTCH4;PLG;VEGFA
SACS;HSPA2;SORL1;HSPA1B;HSPA1A
IL10;HFE;ADIPOQ;NOG;B2M
CDH3;TYROBP;FN1;LILRB1;CD24
FMR1;CALM3;DRD2;CALM1;CRHR1
APP;PRNP;DCTN1;PSEN1;INS
CD74;LGALS1;P4HB;LGALS9;HLA-DRB1
DMTN;F2R;SERPINE1;HPSE;THBS1
DMTN;F2R;SERPINE1;HPSE;THBS1
NINJ1;NR1H3;F2RL1;PTPN22;LBP
CD74;LGALS1;P4HB;LGALS9;HLA-DRB1
DPP4;WNK1;CCL5;CXCL13;ADA
LRRK2;RIPK1;TXN;PARK7;NFE2L2
P2RY12;CX3CR1;CD200R1;MST1;CD200
GSN;IL5;CSF2;FSCN1;TNF
BDNF;HFE;ADIPOQ;B2M;MMP9

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

IL4;TBX21;FOXP3;MALT1;SMAD7
EGR1;HSP90AA1;IFNG;CLU;SORL1
PRKCA;ACTB;ACTG1;SMAD7;CLDN11;CLDN5;GJA1;GJB1;FSCN1;CTNNB1;
PSMD10;APP;TGFB2;SPHK1;PRKCA;EGFR;ADAM17;RGCC;CCND1;RPS6K
BMP4;TGFB2;BMP2;BMPR2;NOTCH1;NOS3;NOG
IFI16;DDIT4;BCL3;SIRT1;TP53;PML;TP73
EPHA4;CLDN3;MDK;ALOX5;SERPINE1;CRK;CERS2
P2RX7;APP;IFNG;IGF1;PSEN1;HIF1A;INS
PTPA;BMP2;IFNG;CALM3;CALM1;CALM2;MTOR
P2RX7;APP;IFNG;IGF1;PSEN1;HIF1A;INS
FOXC1;TGFB1;IFNG;TRAF6;PARK7;IGF1;GATA3
GRIA2;SNAP25;SLC1A1;LPAR3;SLC1A4;GRM1;HRH1;GRM4;GRM7;NPY;MP
XBP1;PARP1;IRS1;PLA2G1B;SORT1;ADIPOQ;SLC2A4;SIRT1;ZFP36L1;CEA
HACE1;CDKN2A;WAS;MYO9B;PARK7;IGF1;PLD1;MAPK14;RASGRP1;NTN1
APP;DCTN1;MAPT;SPG11
PIK3CD;CXCL13;CYP7B1;GAS6
TGFB1;SOAT1;STAT1;PPARG
MDK;ALOX5;NINJ1;PTN
TGFB1;SOAT1;STAT1;PPARG
CYP2C9;CYP2D6;CYP3A4;CYP2C19
DLL4;IL12B;IL12A;THBS1
PECAM1;PIK3CD;PIK3CG;CD177
HLA-DMA;HLA-DMB;HLA-DRA;HLA-DRB1
CX3CR1;AKT1;TNF;CX3CL1
P2RY12;P2RX4;CCL3;CX3CL1
CD86;RARA;IL18;NLRP3
CAV1;FLOT1;F2RL1;PTPN22
CEACAM1;XBP1;MDK;PTN
BMP4;IL1A;SHH;IL1B
IL4;IL10;CD226;NECTIN2
THBS1;EGFR;INS;VEGFA
IL23A;IL23R;IL12B;IL12A
IL23A;IL23R;TBX21;IL12B
CD74;NLRP3;NOD2;CCR2
IFNG;GFI1;TNF;NFKB1
SMAD4;TMPRSS6;HFE;MYC;SLC11A1;SLC40A1;LCN2;HMOX1;FXN;CP;HA M
SPRED2;SMAD4;PTPRC;RGS14;TNIP1;GSTP1;ADIPOQ;TIMP3;PHB;EPHB2;
ADAM17;ERBB3;EGF;ABL1;NRG1;PKN2;RAF1;ETS1;TGFBR1;EGFR;VEGFA
GSTO1;FMR1;TLR9;CALM3;DRD2;CALM1;CALM2;CRHR1
MAVS;HDAC3;TGFB1;IFNG;BAG3;CDH1;FLNA;PSEN1
SPHK2;ALOX5;PARK7;MMP8;PPARA;TLR4;INS;SNCA
BMP4;TGFB2;SMAD4;BMPR2;NOTCH1;NOG;TGFBR1;SMAD7

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

SMAD4;BMPR2;NOTCH1;FST;NOG;XIAP;LRP2;RBPJ;SORL1;SMAD7;BMP4;
ITGB1;WWOX;TGFB2;SMAD4;TGFB1;TGFB3;GDF15;APOA1;FOS;NR3C1;SI
IFIH1;YY1;IL10;ITCH;MAVS;DDX58;TNFAIP3;LILRB1;RELB;HAVCR2
DPP4;CEACAM1;TGFB1;JAG1;CDH1;SIRPG;CD47;WNT1;ADA;SMAD7
NOTCH1;DMTN;FZD4;ALOX15;RAC2;PLG;PIK3CB;WNT1;JAK2;CX3CL1
SNAP25;GRM4;SYT1;SNPH;GAD1;GAD2;SYN3;VAMP2;STX1A;SNCA
HDAC3;TGFB1;EIF2AK3;LIF;PARK7;PSEN1;INS;MAVS;IFNG;CDH1;BAG3;AK
BLK;SELP;NOS3;PLA2G4A;PRKCA;APOE;TLR4
NOS2;DDAH1;NOS3;ARG1;GAD1;NOS1
ITGB1;NOTCH1;PIK3CA;CAV1;CEACAM5;BCL2
LGALS3;GRN;LILRB1;CD47;INS;HAVCR2
IL4;PARP1;SPHK2;ENO1;PPARA;PPARGC1A
SPHK2;SPHK1;PLA2G6;TNF;TNFRSF1A;SIRT3
BMPR2;ACE;DDAH1;ADM;PRCP;DRD2
IL1A;EDN1;RGCC;EGF;IL1B;CD28;TGFA;IGF1;INS
GH1;AHI1;ATXN2;EGF;FMR1;NTF3;FLOT1;SELE;VEGFA
PCSK1;MYRF;HP;PSEN1;MMEL1;VSIR;PHEX;KLK6;ADAM17;ADAMTS13;F9;
ERN1;DDIT3;BCL2;TNFRSF10B;BAX;TRAF2;MAP3K5;ATF4
IL4;CEACAM1;MYC;ADIPOQ;CCL3;RARA;TLR4;TLR3
TMPRSS6;HFE;SLC11A1;SLC40A1;XIAP;HMOX1;B2M;CP
PRDX3;IL11;CSF2;IFI16;EPO;CASP3;TET2;KAT8;IKZF1;JAK2;JAK3
H2AX;CASP9;BCL3;ABL1;ATM;TP53BP1;WNT1;BID;MAPK14;TP53;CLOCK
SNAP25;GRM4;SYT1;SNPH;GAD1;GAD2;SYN3;VAMP2;STX1A;SNCA
BMP4;BMP2;IL6;BMPR2;HGF;IGF1;IL6ST;IL6R;BMP7;TP63
CD74;CD19;CD27;TLR8;HLA-G
HGF;STMN1;MST1;MST1R;SIRT2
IRS1;EIF2AK3;AKT1;IGF1;IGF1R
BMP4;CSF1R;IFI16;PPARG;VEGFA
CD200R1;AKT1;PADI2;APOD;CD200
LILRB1;LGALS9;HLA-F;HLA-G;MICA
SOCS3;SOCS1;CAV1;BCL3;SH2B3
BMP2;GFI1;DKKL1;NFKB1;BMP5
NOTCH2;DLL4;NOTCH1;JAG1;RBPJ
IL4;IFNG;IL10RB;PARK7;IFNAR1
SPHK2;PLA2G6;TNF;TNFRSF1A;SIRT3
TGFB1;CASP8;LIF;PRKCA;RIPK1
CX3CR1;CTNNB1;DRD2;CX3CL1;VEGFA
SPHK2;PLA2G6;TNF;TNFRSF1A;SIRT3
HSPA5;DDIT3;TP53;ATF3;ATF4
GSN;FAS;PARK7;LGALS9;MMP9
FCRL3;TLR9;PTPN22;HMGB1;RTN4
PTGER4;GNG2;CCL21;CCR7;CCL19

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

TGFB1;CCL3;RORA;CCR5;TGFBR1
TNFSF14;FAS;AKT1;JAK3;FOXP3
CX3CR1;C1QA;ITGAM;MYRF;NCAN;GSTP1;ATN1;CXCR4;KLK6;C3;SHH;AD
HSP90AA1;RGCC;POLG2;XRCC5;MYC;HGF;MAPK1;CTNNB1;PRKD2;ATM;H
PXK;TOR1A;SYT1;HFE;P2RX7;SCN10A;P2RX4;CA2;WNK1;NOS1;DRD2;B2M
CRP;CHGA;PLA2G1B;PLA2G2A;HLA-A;ADAM17;IL6;IL12A;TNFRSF14;LBP;M
ABCA1;APOA1;HMGCR;CYP7B1;NR0B2;CYP27A1;IL4;SOAT1;CYP21A2;CYP
ITGAM;GSN;ITGB2;RAC2;ELMO1;FCGR1A;HAVCR1;THBS1;AIF1
NOTCH2;BMP4;GJA1;SMAD4;BMP2;BMPR2;NOTCH1;NRG1;MSC;BMP7;BM
CXCL8;GRK2;RGS14;CCL5;STMN1;ADA;SNCA
BMP4;SMAD4;TGFB1;TGFB3;CCN3;JAK2;TGFBR1
NINJ1;FLOT1;NR1H3;TNFAIP3;F2RL1;PTPN22;LBP
GH1;RPS6KB1;FAM107A;PRL;CD68;MTOR;ATF4
HSP90AA1;HSPA1L;HSPB8;SIRT1;MTOR;ARNTL;CASP9;BAG3;ALOX5;ABL 1
ITGB1;TGFB2;SMAD4;TGFB1;TGFB3;GDF15;APOA1;FOS;SIRT1;TGFBR1;S
EPHA4;AIM2;STAT3;MBP;FYN;MEFV;AGER;VSIR
SCN10A;GRK2;P2RX4;CALM3;NOS1;CALM1;CALM2;SMAD7
IFNAR2;RNASEL;MAVS;OAS1;CDC37;PTPN11;PTPN6;USP18
CD74;MUC1;BCL2;MIF;SIRT1;CD44
IL10;TGFB3;ADIPOQ;PPARG;SOD2;APLN
DMTN;F2R;SERPINE1;PLG;HPSE;THBS1
BMP4;TGFB1;RGCC;TGFB3;F2R;VSIR
PSMD10;ADAM17;RGCC;CCND1;AKT1;EGFR
EDN1;PARP1;PRKCA;IGF1;IL6ST;AGT
NOTCH2;BMP4;TGFB2;NOTCH1;JAG1;NOS3
IL10;IL11;TGFB2;MAPK8;CFH;ICAM1
SMAD4;BMPR2;NOTCH1;NOG;LRP2;THBS1;SORL1;AGT;APLN;SMAD7;IL4;
ITGB1;TGFB1;LRP1;PRKCE;TNF;ACTB;EGFR;INS;LGALS3;AR;IFNG;AKT1;E
TGFB1;EIF2AK3;LIF;PARK7;TNF;RTN4;INS;TYROBP;APC;AKT1;FYN;MAPT;
SHMT1;AQP4;TRPV1;SOD2;CRYZ;TRPM2;MIP;HPRT1;B2M;MS4A1;HLA-DR
GRN;IFI16;OAS1;TYRO3;TNFAIP3;SERPING1;A2M;USP18;INS
CX3CR1;BMP4;TYROBP;RGS14;IFNG;ADIPOQ;LIG4;LRP2;TGM2
EDN1;ANXA2;SYT1;CD80;ADIPOQ;GATA3;HCRT;TNF;SNCA
SEMA7A;MAG;SEMA3A;ABL1;RNF6;APOE;MAPT;NTN1;RTN4
STAT5B;GH1;TGFB1;ANXA1;KAT5;STAT3;CTNNB1;ESR1;EGFR
TGFB2;SMAD4;BMPR2;NOTCH1;SALL1;NOG;GATA3;TGFBR1;SMAD7
SHH;HSP90AA1;TOR1A;PARP1;EGF;BDNF;HFE;CTNNB1;GPC5;MAPT
TGFB2;TGFB1;TGFB3;MSN
EPO;ARHGEF2;TLR3;ICOSLG
IL4;GSTP1;NLRP3;INS
IL10;TIMP2;TIMP3;TIMP1
IL4;TBX21;FOXP3;SMAD7

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

DLL4;NOTCH1;BMP7;BMP5
BMP4;TGFB2;BMPR2;NOG
TGFB2;NOTCH1;JAG1;TGFBR1
IL6;IL1B;LRP2;TNF
TSLP;IL9;RARA;GATA3
IL10;CCL5;PDCD1;IDO1
MECP2;DCTN1;HSPA1B;HSPA1A
MMP3;RIPK1;TLR4;SOD1
IL5;CSF2;FSCN1;TNF
IL23A;IL23R;IL12B;MALT1
CD74;ANXA1;IL1B;PTGS2
TGFB1;NOTCH1;RGCC;AGT
CX3CR1;AKT1;TNF;CX3CL1
CLDN3;LRP1;TIMP2;TIMP1
CXCL10;GJA1;FGF1;FOXP1
AGTR1;PARK7;AGT;INS
ACE2;ACE;AGTR1;AGT
HMGB1;AHR;HLA-DRB1;HSPD1
IL2RA;HLA-B;HLA-G;FOXP3
TGFB2;SMAD4;CDH3;HIF1A
MFN2;PPARG;IGF1;SOD2
FAS;AKT1;RIPK1;FASLG
CYP2C9;CYP2D6;CYP3A4;CYP2C19
CASP8;TNFRSF10C;TNFRSF10B;TNFRSF10A
MCAM;KDR;CD34;VEGFA
CST3;APP;GSN;UBC;APOA1;RIPK1;PRL;MAPT;B2M;SORL1;INS;SNCA
H2AX;MECP2;RGCC;WT1;MYC;HGF;PRKD2;HMGB1;BRCA1;SIRT1;EGFR;P
CX3CR1;RGS14;LIG4;LRP2;NGF;CX3CL1;VEGFA;IFNG;CUX1;PLXNA2;CTN
SOCS3;SOCS1;DMTN;PTPRC;CAV1;NTF3;PTPN6;SH2B3
CX3CR1;S100A12;BCL10;CLEC4E;S100A9;GAPDH;S100A8
BMP2;NCF1;SPHK1;IL1B;LEP;AGER;VEGFA
XRCC5;FANCD2;MYC;LIG4;ATM;CRYAB;TP53
EDN1;EGF;PRKCE;CXCR5;TGFA;IGF1;SIRT2;INS;IL1A;SPAST;RGCC;OPN1
ACE2;ACE;ATP6AP2;CTSZ;REN
JAG1;NPHS1;WT1;IQGAP1;CD24
LGALS3;EDNRB;CCL5;CCL3;CCL2
BLK;IL10;TYROBP;CTLA4;ATM
TGFB1;PPARG;TNF;ESR1;POU5F1
IL6;TGFB1;STAT3;TNF;ESR1
CYP27B1;CYP24A1;HSD17B6;CYP3A4;FGF23
ARG2;CDKN2A;B2M;SIRT1;HLA-G
ACE2;ACE;ATP6AP2;CTSZ;REN

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

EPHA4;BMP2;IL6;NOTCH1;NOG
BLK;IL10;BTK;IL2;FOXP1
APOC1;AGTR1;APOA1;APOE;AGT
LGALS3;CSF2;PRKCB;PTN;IL17D
LANCL1;MMP3;FYN;P4HB;PARK7
PSMD10;HDAC3;LRRK2;SPHK1;CAV1;FAM107A;XIAP;BRCA1;BCL10;MALT L
CCR1;CCL13;CD40;EDN1;CCL11;SLC11A1;CAV1;RMDN3;ATP2B2;MT2A;CX
CSF1R;MST1;ADRB2;SIRT1;IRGM;ACTB;CCND1;IFNG;CDC37;ABL1;AKT1;C
PSMD10;PSMB6;NQO1;PSMD12;PSMD7;PSMD4;CAV1;PPARA;SIRT1;PSMB
KL;CXCL8;PTPN11;FGF1;ZFP36L1;DLL4;SPRED2;NR4A1;CCL5;CCL2;MAPK
PSMD10;PSMD12;CDKN2A;FAM107A;KLF4;PSMB8;ZFP36L1;PSMB9;PSMB6
ERN1;BMP4;BMPR2;HMOX1;NOX5;CD34
IL10;ANXA1;BCL3;TLR9;PTPN22;KLF4
WNK1;AKT1;PTPN22;PPARA;TIGIT;JAK3
IL1B;APOC1;AKT1;TNF;SORL1;INS
EDN1;PARP1;PRKCA;IGF1;IL6ST;AGT
FOXC2;ANXA1;KDR;HMOX1;PTGS2;VEGFA
ADIPOQ;NR1H3;APOA1;PPARG;PPARA;PPARGC1A
IFNA1;IFNG;IFNB1;IFNA17;IFNA2;LIF
BMP4;BMP2;BMPR2;BMP1;MDK;PTHLH
P2RY12;TYROBP;P2RX4;MTR;APOD;SOD1
HACE1;TNFSF12;AGAP2;TNFAIP3;PHB;HMGCR;TNF;SORL1;SIRT2;EGFR; G
PARP1;NOS3;LRRK2;TWNK;MX1;PARK7;PHB;FANCG;SIRT3;HSPD1;PRDX3
HSP90AA1;ERBB3;PIK3CA;EGF;CDC37;NRG1;PRKCA;EGFR
MMP12;JAG1;DMTN;CDKN2A;SERPINE1;FAM107A;APOD;THBS1
CCR1;HRH1;ANXA1;MC1R;CNR2;MTNR1B;CNR1;NPY;CCL2;LPAR3;SSTR4;
TGFB2;S100A1;ITPR3;ATP2B2;AGT;APLN;SMAD7;ACE2;SCN10A;P2RX4;TH
IGFBP1;PSMD10;PSMD12;FZD4;HDAC1;CAV1;NOG;DKKL1;MCC;GLI1;PSM
MYRF;MPZ;ADGRG6;PLP1;PMP22;CXCR4;MBP;SOX10;SIRT2;KLK6
IL18;LPL;NR1H3;APOA1;RORA;APOE;ANGPTL4
CYP27B1;CYP24A1;VDR;CYP2R1;LRP2;CYP3A4;GC
ERBB3;BDNF;NTF3;ADGRG6;PMP22;NGF;SOX10
NOTCH1;JAG1;DMTN;FZD4;CDKN2A;PLG;WNT1;THBS1;CX3CL1
EDN1;FMR1;SHMT1;EIF2AK3;EIF2AK2;GZMB;PLAT;KNG1;NFKB1;INS;CST3
BMP4;IL1A;EDN1;RGCC;EGF;IL1B;CD28;TGFA;IGF1;BMP7;INS
ITGB1;SEMA7A;DST;ITGB2;FN1;APOA1;PTN;CEACAM1;ADAMTS13;CD40L
CCR1;CCL13;CD40;EDN1;CCL11;CAV1;RMDN3;ATP2B2;CXCL12;CCL7;CCL
IL3;TGFB2;CXCL8;SALL1;TGFB1;KMT2A;KDR;GATA3;RBPJ;TNF;SH2B3;ATF
PRKCB;PRKCE;LRRK2;EIF2AK3;PRKCA;MAPK14;TGFBR1;MTOR;ERN1;MA
HSP90AA1;HACE1;TNFSF12;TNFAIP3;MSN;TNFRSF1B;TNF;SORL1;ITCH;IF
FTO;PSMD10;PSMD12;FMR1;SLC11A1;TNFSF13;HSPB1;PRKCA;YWHAZ;P
P2RX7;ANXA1;ANXA2;LIG4;ADRB2;PPARGC1A;IRGM;RAB3GAP1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

KMT2A;IL1B;PARK7;BRCA1;NOS1;PPARGC1A;FOXP3;SNCA
SHH;NOTCH1;TGFB1;WT1;CAV1;KDR;ADM;VEGFA
HSP90AA1;NOS3;SPHK2;SPHK1;AKT1;CALM1
BMP4;TGFB2;BMP2;NOTCH1;NOS3;NOG
PRNP;RGS14;SLC2A4;APOE;SGK1;LDLR
HMOX1;PDCD1;IL17D;HLA-G;FOXP3;CD200
NOTCH1;RGCC;NOTCH4;FLOT1;PLG;VEGFA
CEACAM1;IFNG;CAV1;GATA3;CD24;DSPP
C3;GH1;OCLN;PLA2G1B;PRKCB;IL1B
IFNA1;IFNG;IFNB1;IFNA17;IFNA2;LIF
BMP4;FOXC1;BMP2;SALL1;WT1;BMP7
IL3;KMT2A;KDR;SH2B3;ATF4
ALOX5;ADIPOQ;ALOX15;PLA2G7;PPARGC1A
CX3CR1;GRN;TYROBP;IFNG;LBP
IL10;AR;EDN1;TGFB1;GSTP1
TGFB2;BMP2;TGFB1;TGFBR1;SMAD7
LGALS3;CXCL12;SPHK2;CCL3;CCL2
PTH;IRS1;PRKCE;AKT1;SNCA
IRS1;PTPN11;SORL1;SIRT1;INS
APOC1;AGTR1;APOA1;APOE;AGT
KMT2A;ADIPOQ;PON1;NR1H3;SGK1
BLK;CCL5;TNFSF11;PRKCA;JAK1
SELPLG;CHI3L1;PHB;RELA;NFKB1
PTPN22;IRF5;NOD2;ARHGEF2;NLRP1
MMP3;MTR;CCR7;TXN;CCL19
IRAK1;TRAF6;TLR9;TLR7;MYD88
NCOA2;STAT5B;XBP1;CAV1;STAT3;NR3C1;TFPI;ZFP36L1;AR;WT1;LEP;RA
CCR1;CCL13;CD40;EDN1;CCL11;CAV1;RMDN3;ATP2B2;PSEN1;PML;CXCL1
NR4A2;C1QTNF3;IL11;NR4A1;ADIPOQ;SDF4;PPARG;KLF4;SIRT1;PPARGC
RALBP1;KDR;TNFSF10;BAX;PARK7;DNM1L;BID;MMP9;TP53;PPARGC1A;D
ADIPOQ;IL12B;IL12A;HMGCR;APOE;DRD2;INS
ACE2;ZGPAT;HFE;PPARG;EPHB2;PPARA;TNF
CYP27B1;NOTCH1;TGFB1;NOS3;AHSG;S1PR1;GAS6
RPS6KB1;RPS6;AKT1;EIF4EBP2;GATA3;MTOR;CARD11
PRNP;FMR1;SPHK1;SHMT1;EIF2AK3;EIF2AK2;GZMB;IGF1;CLU;SORL1;RTN
XBP1;BMPR2;HSPA5;EHMT2;LRRK2;EIF2AK3;EIF2AK2;FOXO3;SIRT1;MTO
CA2;AGTR1;RELA;NFKB1
NOTCH1;LRP2;TGFBR1;VEGFA
CXCR4;GAS6;CCR5;NECTIN2
CXCL12;FN1;MZB1;CX3CL1
CXCR4;GAS6;CCR5;NECTIN2
IL6;ADAM17;ACE;PLA2G1B

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

IFNG;IFNGR1;HMGCR;TNF
CD200R1;DDT;MIF;CD200
GRN;PTPRC;LDLR;CX3CL1
LRRK2;TXN;PARK7;NFE2L2
CEACAM1;PTPRC;LILRB1;HLA-G
IL4;TBX21;FOXP3;SMAD7
PIK3CA;PIK3CD;PIK3CB;PIK3CG
SOCS1;HLA-DRA;FOXP3;HLA-DRB1
DMTN;CCL5;TNFSF11;JAK1
GH1;CDH3;IGF1;WNT1
ITGAM;UHRF1;ITGB2;NOD2
OAS1;IL1B;ADIPOQ;LGALS9
MDK;CXCR4;PTN;TNFRSF1B
GSTO1;CALM3;CALM1;CALM2
IRF1;EBI3;TNFRSF14;CCR2
IRF1;PTPN22;HLA-A;VSIR
EDN1;PADI2;HIF1A;SH2B3
PRNP;FYN;APOE;INS
GZMA;AKT1;HMGB1;SIRT1
IFNG;APOE;TNF;LDLR
GFI1;XIAP;BIRC2;BIRC3
ANGPT2;KDR;F2RL1;VEGFA
MAPK14;SIRT1;TP53;ARNTL
MTRR;CBS;MTHFR;MTR
IGFBP1;PSMD10;WWOX;PSMD12;LRP1;FZD4;HDAC1;CAV1;NOG;DKKL1;M
APP;PRNP;SMAD4;TMPRSS6;HFE;SLC11A1;SLC40A1;CP;SOD1;MT2A;MYC
ACHE;SLC44A4;PLA2G1B;PON1;PLA2G2A;APOA1;PLA2G4A;NR1H3;PLA2G
ADAM17;NCF1;EGF;TGFA;AKT1;HAP1;MMP9;AGT
ACE2;OCLN;SCN10A;PRKCB;BCL2;ACTB;INS;SNCA
TRPM2;PTPRC;CCL21;F2R;ITPR3;CCR7;CCL19;TRPV1;DRD2
CX3CR1;IL1B;CTNNB1;PTN;TNFRSF1B;CX3CL1;WNT3;SIRT2;ARNTL
BMP4;TGFB2;BMP2;NOTCH1;RBPJ;TGFBR1
FOXC2;BTK;IKZF1;JAK2;IKZF3;VEGFA
APP;DMTN;ANXA2;SH2B3;FOXP1;TLR2
BST2;CIITA;GSN;IFNA2;PTX3;LY6E
PSMD10;ADAM17;RGCC;CCND1;AKT1;EGFR
CSF1R;MDK;CCL5;MAPK1;THBS1;CMKLR1
MC1R;PRKAR1A;LRRK2;ADIPOQ;MIF;ADRB2
NOTCH1;GZMA;HP;NOS1;TIMP1;SIRT1;TP53
CCR1;SLC11A1;CAV1;ATP2B2;LRP2;PSEN1;PANX1;TRPM2;CYP27B1;CCL 5
LRRK2;CAV1;GZMA;CTSZ;PARK7;SORL1;ACTB;NFKBIA;MAPK8;IFI16;CYP2
ACHE;IL1A;TGFB2;TGFB1;PLA2G1B;TGFB3;IGF1;DNM1L;TNF;ARHGEF5;VA

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

HSP90AA1;HSPA1L;HSPB8;SIRT1;MTOR;BAG3;MAPK1;ATM;MAPT;CD34;C
CD40;BTLA;LILRB1;CD24;HLA-G
CCR1;AHSG;CCL3;FGF23;TRPM4
PSMD10;CD74;MIF;SIRT1;CD44
BMP4;PPARG;PPARA;RELA;POU5F1
CD74;ERBB3;EGF;NR1H3;NRG1
LRP1;IGFBP3;ADIPOQ;SERPINE1;AIF1
ACHE;SLC44A4;NOS1;SLC6A3;SLC6A4
IRS1;PTPN11;SORL1;SIRT1;INS
MAPK8;NOS2;NOS3;NOS1;MAPK14
PTH;IRS1;AKT1;IGF1;INS
PRKAR1A;ADIPOQ;MST1;ADRB2;SIRT1
CD40;MC1R;SPHK2;ADRA1A;VEGFA
FOXC1;CXCL12;CCL21;WNK1;SH2B3
CYP27B1;AR;CAV1;RARA;BRCA1;GATA3;CD24;ESR1
TRPM2;TBC1D2;DMTN;P2RX4;FMR1;CAV1;SGSM3;FSCN1;WAS;CCR7;PLD
SMAD4;BMP2;BMPR2;NOTCH1;NOG;PPARG;LRP2;WNT1;SORL1;SMAD7
PTGER4;PRRT2;HSPA5;PARK7;HMGB1;RAF1;MEFV;CLU;CRYAB;SORL1
TRPM2;MIP;SHMT1;AQP4;HPRT1;TRPV1;SOD2;B2M;CRYZ;TRPM4
LGALS3;LRP1;SMPD1;SPHK1;FLOT1;ABL1;LILRB1;APOE;CCL19;CD177;SN
CDKN1C;IL10;FOXC1;BTG1;TGFB1;CDKN2A;LILRB1;GATA3;BMP7;BMP4;N
TWNK;PRF1;NLRC4;BCL10;SPAST;STING1;NINJ1;YME1L1;TP53BP1;DNM1
DDR1;ITGB1;VCAM1;ITGA4;CCL21;ITGB2;FN1;ITGAL;BCR;ADAMTS13;HPS
CDKN1C;SMAD4;TGFB1;CAV1;SIRT1;THBS1;TGFBR1;SMAD7;SPRED2;ST
EDN1;SYT1;CD80;ADIPOQ;GATA3;HCRT;TNF
GPR17;F2R;C3AR1;AGTR1;F2RL1;DRD2;GRM1
PSMD10;SPRED2;CD74;ATM;MIF;SIRT1;CD44
DLL4;BMP4;TGFB2;NOTCH1;TGFB1;JAG1;GATA3;RBPJ;SMAD7
AR;DAXX;ZMIZ1;PADI2;PHB;NR3C1;ESR1;ESR2;NR3C2
SHH;SPAST;OPN1MW;PRKCE;CXCR5;PKN2;FGF1;DRD2;SIRT2
SHH;SPP1;HSD17B6;HSD17B7;CYP3A4;CYP17A1
PRDX3;PRDX2;PRDX5;CAT;HBB;MPO
ITGB1;NOTCH1;PIK3CA;CAV1;CEACAM5;BCL2
NOTCH1;NOG;GLI1;RBPJ;TGFBR1;TP73
ITGB1;TGFB1;DMTN;MACIR;PRKCE;THBS1
SORT1;APOC1;NR1H3;LPL;APOA1;ANGPTL4
TGFB2;TGFB1;TGFB3;CAV1;NR1H3;THBS1
STK11;IFI16;DDIT4;BCL3;SIRT1;TP53;PML;TP73
DMTN;MDK;ABL1;FLNA;APOA1;P4HB;RREB1;CRK
NCOA2;AR;HDAC1;RNF6;PHB;PARK7;SIRT1;FOXP1
CDH3;ALB;HSPB1;LCN1;B2M;ACTB;ACTG1;SOD1
CDKN1C;PRDX3;CEACAM1;PTPRC;GSTP1;HSPB1;AKT1;PARK7;MAPT;TRI

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

MBTPS1;XBP1;HSPA5;DDIT3
NR4A1;CCN3;CXCL13;VEGFA
GSTM1;ALOX5;GSTP1;ALOX15
GSTM1;ALOX5;GSTP1;ALOX15
CD274;HFE;LILRB1;TNFRSF14
TGFB1;NOTCH1;NOS3;GAS6
CEACAM1;LGALS9;HLA-F;CCR2
F10;SERPING1;A2M;TFPI
BMPR2;PRCP;ADRB2;SOD2
IL4;ENO1;PPARA;PPARGC1A
MC1R;ADIPOQ;MIF;ADRB2
XIAP;PTPN22;NOD2;BIRC2
ADAM17;CASP1;HSPA1B;HSPA1A
CXCL12;PIK3CA;WAS;C9ORF72
MUC1;RGS14;DDIT3;RELA
IL1B;TNF;VCL;TNFRSF1A
CEACAM1;ZEB1;BTG1;NOTCH4
IL6;NOTCH1;IL1B;TNF
LIF;CTNNB1;GATA3;CD24
CYP27B1;CYP24A1;BGLAP;SPP1
CYP27B1;CYP24A1;BGLAP;SPP1
PSMD10;PSMD12;FMR1;TNFSF13;HSPB1;PRKCA;YWHAZ;PSMB8;ZFP36L1
DMTN;LRP1;FAM107A;IQGAP1;MTOR;BST2;P2RX7;FSCN1;ABL1;RAC2;MA
OPN1SW;IFI16;OPN1MW;OPN1MW2;LIG4;MAPK14;SIRT1;CLOCK;TP53
CX3CR1;RGS14;IFNG;BDNF;DLG5;LIG4;LRP2;EPHB2;TGM2
CASP8;F9;IFI16;HP;CTSH;PLAT;NLRC4;PRSS3;VSIR
CSF3;EDN1;CCL11;CCL21;PRKCE;ALOX15;CX3CL1;P2RX7;NTF3;ABL1;F2R
NPEPPS;ADAMTS13;ACE;CYP2D6;ANPEP;ENPP2;PLA2G4A;CYP3A4;PLA2
SERPINA3;NCOA2;HDAC3;CAV1;RORA;HMGCR;SP1;IL1B;APOC1;GNB3;PP
LRP1;AKR1B1;APOA1;LPL;LRP2;CYP3A4;PLB1;OPN1SW;OPN1MW;CYP2D
CSF1R;AKT1;IRF6;JAK2;WNT3
JAG1;EPAS1;SDC1;NRG1;IGF1
IL4;GRN;NR1H3;CD200;HAVCR2
PRNP;LRRK2;SERPINE1;CTSZ;THBS1
DDR1;KDR;ABL1;EGFR;IGF1R
PTH;IRS1;AKT1;IGF1;INS
SMAD4;KMT2A;CTR9;CTNNB1;BRCA1
NOS2;NOS3;PARK7;NOS1;FXN
IFNG;IL1B;APOE;TNFRSF1B;TNF
BAG3;IL1B;ANP32B;GAS6;TP53
S100A1;FGF1;KLF4;VEGFA;JAK1
FCRL3;LEP;CD19;CCL5;IKZF3

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

CASP8;ADIPOQ;LIF;PRKCA;RIPK1
NTF3;ABL1;ESR1;RASGRP1;FGFR1
EPHA4;TGFB1;CDX2;LRRK2;TNFAIP3;CXCL13;ETS1;IL6;CEACAM1;CLDN3;
CST3;SHH;ITCH;CASP8;TRAF3;CAV1;AKT1;PLAT;KNG1;INS
SOX2;SHH;MYRF;ERBB3;ADGRG6;STAT3;SOX10
CDKN1C;PRDX3;ABL1;PARK7;MAPT;TP53;SMAD7
PTPA;BMP2;TGFB1;SMPD1;CALM3;CALM1;CALM2
BMPR2;RGCC;MYC;HGF;ADIPOQ;ATM;PRKD2
PRNP;CEMIP;ITGAM;DMTN;MYO1C;ITGB2;FYN
NOTCH2;CSF1R;TRPM2;CSF3;MDK;NTF3;ABL1;CCL27
SNAP25;GRM4;SYT1;SNPH;GAD1;SLC1A1;GAD2;SYN3;SLC6A3;STX1A;VA
RAP1A;BDNF;NTF3;AKT1;MAPT;NGF
BLK;IL10;TYROBP;TNFAIP3;CTLA4;ATM
LGALS3;TNFAIP3;PTPN22;TIGIT;JAK3;MICA
CDKN1C;BMP4;CDKN2A;SIRT1;BMP7;TP53
VMP1;GSTO1;CALM3;HAP1;CALM1;CALM2
OPN1SW;OPN1MW;LRP1;AKR1B1;APOA1;LPL;SDC1;GPC5;LRP2;APOE;PL
MECP2;ATF7IP;CSF1R;IL6;CCND1;CDKN2A;BAX;CTNNB1;TP53;RELA;NFK 3
GRM4;GRM7;SYT1;LRRK2;CCL2;DRD2;TNF;GRM1;CCR2
DUOX1;RAP1A;DMTN;STAT1;WT1;AHR;DUOX2;ZFP36L1
AHI1;AIRE;TIMELESS;SOX10;ACTB;VCL;ACTG1
ITGAM;GSN;ITGB2;ELMO1;FCGR1A;HAVCR1;AIF1
BMP4;BMP2;NOG
IRGM;ATG12;ATG5
SMAD4;NOTCH1;NRG1
NOTCH1;NRG1;RBPJ
CDH1;CTNNB1;BRCA1
AR;SPP1;MSN
TGFB2;TH;SNCA
SMAD4;NOTCH1;NRG1
EOMES;SOX2;POU5F1
CCL21;CCR7;CCL19
LRRK2;MAPT;DNM1L
PECAM1;CD47;CCR2
TGFB1;PPARG;POU5F1
MMP3;HP;FYN
CXCL12;CCL21;KLF4
TGFB2;TGFB1;TGFB3
SERPINE1;CTSZ;THBS1
TGFB1;PPARG;POU5F1
KCNMA1;ADRB2;SOD1
CD200R1;APOD;CD200

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

CYP27B1;GFI1;NFKB1
ITGB1;IL4;IFNG
LGALS9;MAPK14;ZFP36L1
ACE2;GRK2;STX1A
ADIPOQ;ADRB2;SIRT1
IL23A;IL23R;IL12B
BMP4;SMAD4;RBPJ
IL6;IL1B;TNF
CCL21;IGF1;CCL19
IL1B;PTGS2;TNF
SMAD4;SPHK2;BRCA1
CLDN3;STAT3;MBP
LRP1;LRP2;LDLR
IL1B;IL18;IL18R1
PTPN22;HMGB1;RTN4
MFN2;PPARG;SOD2
BMP4;JAG1;LRP2
ACE2;GAS6;ICAM1
FOXC1;IFNG;PSEN1
P2RY12;CX3CR1;GPR183
BMP4;IL6R;BMP7
TSLP;CD34;HAVCR2
NOS2;NOS3;NOS1
GRN;MDK;ALOX5
AR;TGFB2;S100A9
CX3CR1;TYROBP;ITGAM
ITGAM;ITGB2;CD177
IL23A;IL18;IL12B
XIAP;BIRC2;BIRC3
BMP4;TGFB1;ARHGEF5
GRN;LBP;INS
LRP1;APOC1;TSPO
IL1B;IL18;IL18R1
CDH1;CTNNB1;BRCA1
CCL21;CCR7;CCL19
TGFB2;TGFB1;TGFB3
TGFB2;TGFB1;TGFB3
CLDN11;CLDN5;ACTG1
CYP27A1;CYP27B1;CYP2R1
ADAM17;TGFB1;PIK3CA;EGF;TGFA;AKT1;PTPN11;IQGAP1;EGFR
CD40LG;IFNB1;GPR183;CD19;LIG4
ANXA1;FAM107A;NR3C1;SSTR4;ZFP36L1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

DDR1;CEACAM1;TOR1A;FLNA;CD44
BMP4;BMP2;BMPR2;BMP7;TGFBR1
EPHA4;SEMA3A;RAC2;LAMC2;NTN1
SOCS3;SOCS1;CAV1;BCL3;SH2B3
APP;PRNP;DCTN1;PSEN1;INS
BMP4;TGFB1;RGCC;TGFB3;F2R
IL4;CD40;TGFB1;TNFSF13;TP53BP1
ABCA1;NR1H3;LPL;PPARG;PPARA
BLK;IL4;SPHK2;LGALS9;UNC13D
CD74;MYC;HLA-DRB1;ZFP36L1;FOXP1
IL4;GNB3;PSEN1;CD24;SIRT2
ACE2;EDN1;ACE;NOS3;AGTR1
P2RX7;DUOX1;P2RX4;STAT1;DUOX2
DST;KIF5A;NEFL;HAP1;SOD1
CTNNB1;ACTB;VCL;SMAD7
ACE;ANXA1;PLA2G1B;DRD2
ACE;ANXA1;PLA2G1B;DRD2
XBP1;STAT6;GATA3;JAK3
AKT1;CD68;TLR4;MYD88
EOMES;SOX2;CTR9;POU5F1
BMP4;CTNNB1;PRKD2;RBPJ
JAG1;KDR;PECAM1;CD34
ANXA1;ITGB2;CCL3;CD177
CD74;CD19;CD27;TLR8
VMP1;LRP1;PRKCB;PPARG
BMP4;SALL1;WT1;GATA3
UBC;ENO1;B2M;TLR2
DLL4;NOTCH1;BMP7;BMP5
MYRF;CXCR4;CLU;SOD1
CD274;TNFRSF14;LGALS9;VSIR
MUC1;WNK1;SERPINE1;CYP1B1
ABCA1;NR1H3;PPARG;PPARA
CD200R1;HMOX1;CD200;BMP5
MUC1;CREB1;PHB;SMAD7
PRKCB;IL1B;AKT1;THBS1
IL12B;IL12A;PIK3CB;DCN
RAP1A;BDNF;NTF3;NGF
C3;APP;C1QA;CX3CL1
ENPP2;PLA2G4A;PLA2G6;PLA2G7
PRKCB;IL1B;PRKD2;HIF1A
CEACAM1;RAP1A;KDR;CD34
MECP2;KMT2A;WT1;MYC

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

ERN1;XBP1;HSPA5;BAX
CDH3;HPSE;CLOCK;ARNTL
SELP;CXCL12;CCL21;SELE
TSLP;CD226;HAVCR1;NECTIN2
MECP2;DCTN1;HSPA1B;HSPA1A
ATF7IP;HMGB1;ESR1;TP53
IL23A;IL23R;IL12B;SMAD7
PRDX2;NOS3;SOD2;SOD1
ABCA1;KLF4;SMAD7;NFE2L2
MC1R;CAT;SDF4;ERCC5
BLK;APP;EPHA4;TOR1A;BDNF;LRRK2;HMGB1;NGF;AGER;BMP7;ADCYAP1
MMP3;PARK7;BRCA1;PPARA;SIRT2;INS
ACE;CALM3;CALM1;CALM2;INS;VEGFA
BLK;PRKCB;FCRL3;CD19;PTPN22;FOXP1
BAG3;IL1B;PARK7;ANP32B;GAS6;TP53
PIK3CA;ABL1;PARK7;MAPT;APOE;C9ORF72
XBP1;BMPR2;LRRK2;EHMT2;ALB;FAM107A;LPL;PPARA;CD68;SIRT1;MTOR
PTGER4;AR;GNG2;SPHK2;SPP1;MSN;AHR;NR3C1
SHH;MYC;NLRP5;TXNIP;CALM3;FGF1;CALM1;CALM2;TP63;SIRT2;POU5F1;
CYP21A2;AKR1B1;TSPO;HSD17B6;DHCR7;HSD17B7;CYP17A1
CYP2C9;GPX4;CYP2D6;PON2;ALOX5;PON1;ALOX15;CYP1B1;PLA2G4A;PT
IFI16;XRCC5;LIG4;ATM;MAPK14;SIRT1;CRYAB;CLOCK;TP53
APP;SHH;MAPK8;ACE;TRAF3;IL17F;APOE;KLF4;LDLR
FOXC2;XBP1;PARP1;IRS1;PLA2G1B;ADIPOQ;PIK3R3;SLC2A4;IGF1R;ZFP3 6
CYP27A1;ABCA1;IL4;SOAT1;APOA1;DHCR24;HMGCR;APOE;DHCR7;HSD17
PTGER4;GH1;GJA1;PTPRC;BGLAP;WNT1;TP53;TGM2
TGFB2;CXCL8;SALL1;EDNRB;CDX2;NPY;GLI1;TNF
DDIT3;AKT1;PIK3CB;DRD2;PPARA;SH2B3;SIRT1;HLA-G
ABCA1;SOAT1;APOC1;APOA1;APOE;ABCG4
CEACAM1;IL1B;APOC1;APOD;TNF;INS
PRNP;CEMIP;ITGAM;MYO1C;ITGB2;FYN
DLL4;BMP4;NOTCH1;TGFB1;JAG1;NOS3;GATA3
ITGA4;MMP2;ITGB2;CTR9;FN1;MMP8;MMP9
CPT1A;FABP4;RPS6KB1;LCN1;PPARG;SLC25A20;APOE
HDAC1;PHB;BRCA1;SIRT1;CLOCK;ARNTL;FOXP1
OCLN;PIK3CA;ENPP2;RAC2;FSCN1;WNT1;RREB1
GRIA2;APP;IFNG;NEFL;CCL2;EPHB2;CCR2
TGFB2;BMP2;NOTCH1;NOS3;NOG
BMP4;FOXC1;SALL1;WT1;BMP7
CIITA;GSN;IFNA2;PTX3;LY6E
EDN1;NOTCH1;IGF1;GLI1;RBPJ
MDK;ADAMTS1;CCL5;IGF1;AIF1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

NOTCH3;NOTCH1;STAT1;NOTCH4;RBPJ
IL4;NOS2;IFNG;IL10RB;IFNAR1
SEC14L2;MBTPS1;APOE;FGF1;SOD1
GJA1;ACE;PTPRC;EIF2AK2;ZFP36L1
CCL13;CCL11;LRRK2;TNFAIP3;HSD17B13;PARK7;PHB;SYNE1;PRDX3;VPS
PTGER4;MAPK8;IRAK1;TRAF6;UBC;NOD2;MAP3K7;MAP3K5
DOCK11;TRPM2;DMTN;CCL21;TGFB3;FMR1;FSCN1;CCR7
DMTN;CUX1;MDK;ABL1;APOA1;FLNA;P4HB;CRK;RREB1
CSF1R;F2R;F2RL1;CD177
PRDX2;NOS3;SOD2;SOD1
MYRF;PLP1;CLU;SOX10
XBP1;APOE;SIRT1;INS
CD40LG;LIG4;CCR6;HSPD1
VMP1;LRP1;PRKCB;PPARG
BMP4;GATA3;FGF1;BMP7
IL10;PARK7;HIF1A;ATF4
LRP1;ADIPOQ;APOD;SNCA
PTPRC;APOA1;KLF4;SH2B3
SPP1;TNFSF11;PRKCA;TNFRSF11A
MDK;AGER;CCR2;ICAM1
ADAM17;NCF1;EGF;TGFA
C3;LRP1;LPL;NFKB1
SPHK2;ALOX5;GSTP1;SNCA
CAV1;F2R;F2RL1;EPHB2
SMAD4;KMT2A;SPHK2;BRCA1
SACS;HSPA2;HSPA1B;HSPA1A
LRRK2;KDR;BCL2;DCN
LRP1;RASGRP1;FGFR1;SNCA
IL10;IL1RN;IL6;TNF
HSP90AA1;NOS3;AKT1;CALM1
CRP;EDNRA;EDN1;EDNRB
PSMD10;COP1;LRRK2;RNF19A;CAV1;CLU;TRIB2;SIRT2;HSPA1B;SMAD7;H
PSMD10;H2AX;BRD2;DAXX;PSMD12;PARP1;GTF2H4;PSMB8;PSMB9;PSMB
HSP90AA1;ALCAM;SEMA3A;CTNNB1;IQGAP1;C9ORF72;SPG11
SART3;FMR1;IL1B;BRCA1;NOS1;PPARGC1A;FOXP3
TOR1A;TYROBP;EGF;BDNF;HFE;CTNNB1;TNF
ARNT2;BMP2;TGFB3;LIG4;TGFBR1;VEGFA
PXK;WNK1;LILRB1;NOS1;VIP;SNCA
AKT1;HAP1;RBPJ;MMP9;RTN4;AGT
TNFSF10;BAX;BID;DNM1L;MMP9;TP53
CAV1;CTNNA3;DSG2;CALM3;CALM1;TRPM4
LRP1;APOC1;TSPO;NR1H3;APOA1;NFKB1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

RALBP1;LRRK2;KDR;MAPT;DNM1L;DCN
IFNA1;DDX58;IFNB1;IFNA17;IFNA2;TLR3
PSMD10;CDKN1C;IL10;APP;PSMD12;FOXC1;TGFB1;BTG1;SPHK1;BUB1B;P
CDKN1C;GSTP1;CAV1;HSPB1;PARK7;SORL1;CEACAM1;PTPRC;IFNG;ABL1
YY1;CASP9;OPN1SW;PARP1;OPN1MW;FMR1;MYC;SMPD1;OPN1MW2;TP5
ABCA1;SOAT1;CAV1;APOC1;APOA1;APOE;CLU;ABCG4;LDLR
PSMD10;PSMB6;NQO1;PSMD12;PSMD7;PSMD4;PSMB8;INS;PSMB9
SELP;ALCAM;VCAM1;CEACAM5;ITGAL;PVR;SELE;ICAM1
SOCS3;SOCS1;CISH;PIK3CA;PIK3CD;PIK3R3;PIK3CB;PIK3CG
ACHE;ADAM17;PSEN1;APOE;KLK6
NR4A1;KDR;PIK3R3;AKT1;VEGFA
ANXA1;FAM107A;NR3C1;SSTR4;ZFP36L1
PSMD10;CD74;MIF;SIRT1;CD44
GSTP1;ADIPOQ;APOA1;F2RL1;GAS6
BMP4;BMP2;BMPR2;BMP1;MDK
BMP2;IL6;TGFB1;RGCC;FSCN1
IRF1;ALOX15;AHR;IL6ST;SIRT1
CAV1;ADIPOQ;PPARG;PPARA;INS
BLK;CEACAM1;DMTN;PRKCA;SH2B3
EGR1;PIAS3;ZMIZ1;CTNNB1;PARK7
LRRK2;C9ORF72;SIRT1;DCN;MTOR;ERN1;IL4;MAPK8;PIK3CA;STING1;CAS
IL4;JAK2;PRLR
NRG1;ADRB2;PRLR
CX3CR1;C1QA;CX3CL1
EPO;AKR1B1;ARHGEF2
TLR1;CD14;TLR2
C1QTNF3;XBP1;SIRT1
IFIH1;DDX58;TLR3
CCL21;CCR7;CCL19
ANGPT2;PECAM1;CD34
DUOX1;DUOX2;SOD1
BAX;RIPK1;FASLG
PTGER4;CXCL12;CCL21
DDAH1;ENO1;CD34
PHB;CLOCK;ARNTL
SORT1;APOC1;ANGPTL4
CX3CR1;LGALS9;CCR2
BMP2;GATA3;CD34
MAPK8;PRKD2;VEGFA
TIMP3;THBS1;ATF3
ACE2;CAV1;AGT
CD274;HLA-DRB1;HSPD1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

BMP4;MYC;NOG
IFNG;NOS2;PRF1
EGR1;HSP90AA1;CLU
HLA-B;HLA-A;HLA-G
SORL1;SIRT1;TRPM4
CST3;CEACAM1;TGFB1
F2R;F2RL1;GAS6
PRNP;FYN;CX3CL1
TGFB1;EGF;NFKB1
IFNB1;TNFRSF1B;S100A9
CDKN2A;NOD2;SIRT1
CSF1R;IL33;MAPK1
PTPN22;HSPA1B;HSPA1A
HLA-DRA;IL27;HLA-DRB1
BMP4;JAK3;TP53
IL6;IRF5;RELA
AR;SPP1;MSN
NOG;LRP2;TGFBR1
MECP2;CSF1R;IL6;CCND1;CDKN2A;BAX;CTNNB1;TP53;RELA;NFKB1
PTPA;PRNP;OCLN;TGFB1;LRRK2;IGFBP3;XRCC1;PARK7;MAPT;EPHB2;SI R
CYP2C9;XBP1;ACOT7;GPX4;CYP2D6;PLA2G1B;ALOX5;ALOX15;LPL;CYP3A
PTPA;TGFB1;SMPD1;CALM3;CALM1;CALM2;MTOR
OCLN;DMTN;PIK3CA;WAS;RAC2;FSCN1;WNT1
BMP4;NOTCH1;BTG1;TGFB1;IGFBP3;MAPK14;ZFP36L1
PARP1;PRKCB;PRKCE;LRRK2;EIF2AK3;PRKCA;MAPK14;TGFBR1;MTOR;M
GHSR;GH1;SEMA7A;SYT1;BDNF;LEP;MAPT;NGF;NTN1
ITGB1;LGALS3;IFNG;LRP1;PRKCE;AKT1;EPHB2;TNF;EGFR
ITGB1;LGALS3;IFNG;LRP1;PRKCE;AKT1;EPHB2;TNF;EGFR
BMP4;NR4A1;ADGRA2;KDR;VEGFB;AKT1;PIK3R3;THBS1;VEGFA
AIM2;MYC;IL1B;ADIPOQ;GAS6;TP53
HSPA5;HSPA1L;HSPA2;HSPA14;HSPA1B;HSPA1A
APP;MYRF;MDK;SOX10;S100A9;TLR2
DOCK11;CCL21;TGFB3;FMR1;FSCN1;CCR7
SMAD4;KMT2A;CTR9;CTNNB1;BRCA1;SIRT1
MYRF;ITGAX;EIF2AK3;PTN;TNFRSF1B;SIRT2
XBP1;IFI16;HSPA5;EIF2AK3;FOXO3;HNRNPA1;TP53;ATF4
GGCT;GSTK1;HPGDS;GSTM1;GSTP1;GSR;PARK7;SOD1
PSMD10;PSMD12;HACE1;SYVN1;SIRT1;RNF5;SIRT2;PSMB8;PML;ARNTL;P
GPI;CRTC2;OAS1;ADIPOQ;APOD;ENO1;GAPDH;PPARGC1A;BRS3;ATF4
TPX2;SMAD4;PIK3CA;APC;STMN1;ARHGEF2;APOE;CLU;CRYAB;LDLR;SN C
TGFB2;TH;GATA3;SNCA
CYP27B1;CYP24A1;CYP3A4;FGF23

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

CA2;MB;MYC;HBB
MTRR;CBS;MTHFR;NOX4
LRRK2;MAPT;HAP1;DNM1L
CRP;CFL1;PTX3;APOE
APOE;CLU;CRYAB;LDLR
SMAD4;NOTCH1;P2RX4;LMNA
IL12B;IL12A;PIK3CB;DCN
CEACAM1;APOC1;BRCA1;SIRT1
DDT;PADI2;CCN3;MIF
GZMA;HP;INS;SNCA
GSTO1;CALM3;CALM1;CALM2
GSTO1;CALM3;CALM1;CALM2
CLDN5;CEACAM1;DDAH1;VEGFA
ABCA1;APOC1;APOA1;APOE
APC;CCL21;F2RL1;CCR7
IL23A;IL23R;IL12B;MALT1
EPHA4;GRN;PTN;CERS2
SOCS1;HLA-DRA;HMGB1;HLA-DRB1
CAV1;CALM3;CALM1;CALM2
STAT3;LEPR;GNB3;INS
MDK;WNK1;AKT1;PPARA
SERPINE1;CTSZ;ENO1;THBS1
APC;CCL21;F2RL1;CCR7
CAV1;DSG2;CTNNA3;TRPM4
CDKN2A;SERPINE1;ATM;TP53
CASP8;OAS1;RIPK1;TLR3
SHH;ANXA1;AMH;EPHB2
BCR;ANXA1;CDSN;JAG1;HDAC1;CASP3;TXNIP;CTNNB1;GLI1
TGFB2;SMAD4;BMP2;BMPR2;NOTCH1
TGFB2;TH;COMT;DRD2;SNCA
LRRK2;ALB;MFN2;HAP1;NECTIN2
CHGA;C3;PRKCA;PHB;KLK6
CLDN5;OCLN;CLDN3;MYO1C;TNF
SMAD4;KMT2A;CTR9;CTNNB1;BRCA1
NOTCH1;MDK;CXCR4;PTN;TNFRSF1B
MYO1C;IL12B;IL12A;PIK3CB;DCN
DLL4;IL4;KRIT1;APOE;MCC;THBS1;DCN
ACE2;ACE;TH;S100A1;AGTR1;AGER;AGT
CX3CR1;BCR;PXK;BDNF;NTF3;EIF4EBP2;NGF
BMP4;SHH;SPEF2;WT1;CHI3L1;FGF1;VEGFA
PCSK1;NPEPPS;GSTK1;HPGDS;ADAMTS13;ACE;GSTM1;ANPEP;GSTP1;G
TRPM2;SLC44A4;P2RX3;ABCC8;TRPM7;SLC25A20;TRPM8;TRPM4

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

BST2;DMTN;LRP1;FAM107A;RAC2;FSCN1;ABL1;IQGAP1;CRK;ARHGEF5;M
GRIA2;SNAP25;SLC1A1;LPAR3;GRM1;HRH1;GRM4;GRM7;NPY;MPZ;KIF5A;
SOCS1;RPS6KB1;IRS1;AHSG;PRKCB;IL1B
CLDN5;OCLN;RAP1A;MYO1C;CLDN3;FLOT1
APP;ADAM17;ZGPAT;NCF1;EGF;TGFA
MAPK8;UBC;MAPK1;MAP3K7;NFKB1;MAP3K5
PSMD10;PSMB6;NQO1;PSMD12;PSMD7;PSMD4;PSMB8;INS;PSMB9
DMTN;FAM107A;KDR;ABL1;APOD;THBS1;VCL;ACTG1;VEGFA
PTGER4;RGCC;TGFB3;STMN1;WAS;ABL1;APOA1;CD47;TGFBR1;ARHGEF5
FBXW4;SHH;TGFB2;SALL1;HDAC1;NOG;CTNNB1
EOMES;ITGA4;MMP2;ITGB2;FN1;MMP8;MMP9
TLR9;TYRO3;TNFAIP3;F2RL1;CD14;TLR4;TLR3
HDAC3;PARP1;HDAC1;LIG4;MTHFR;SIRT1;GEM;SOX2;MYC;UBC;ABL1;PAD
BCL2;BAX;PSEN1;PML;TGM2
IL4;CCL3;LILRB1;TLR4;TLR3
BMP4;CYP27B1;FOXC1;VDR;PLAAT4
C1QTNF3;EDN1;HFE;SPP1;INS
IL1B;BRCA1;NOS1;FOXP3;PPARGC1A
PIAS3;CAV1;TNFAIP3;AKT1;CTNNB1;PARK7;HSPA1B;SMAD7;HSPA1A
GPI;LDHA;SLC16A1;GLO1;BSG;ENO1;SLC16A3;DLD;GAPDH
STAT5B;FOXC1;PTPN11;IQGAP1;EGFR;ZFP36L1
SOCS1;RPS6KB1;IRS1;AHSG;PRKCB;IL1B
MECP2;OCLN;DCTN1;MAPT;HSPA1B;HSPA1A
ADIPOQ;GNB3;RORA;APOE;PPARA;SIRT1
CYP27A1;DHRS11;AMACR;CYP21A2;HMGCR;DHCR7;CYP7B1;LBR;PRLR;C
BMP4;TGFB2;JAG1;GATA3
PRNP;CLDN3;FYN;IGF1R
SYT1;CALM3;CALM1;CALM2
CDH1;CXCR4;CTNNB1;CCR5
ABCA1;BMP1;APOA1;APOE
HDAC1;CCL5;CCL4;CCL3
CD274;HMGB1;LGALS9;VSIR
C1QTNF3;ADIPOQ;MST1;INS
FYN;PARK7;PPARA;INS
SOCS1;HLA-DRA;LGALS9;HLA-DRB1
LRP1;ADIPOQ;SPP1;APOE
HSP90AA1;NOS3;AKT1;CALM1
BLK;PTPRC;CD19;PTPN22
LMNA;MIF;WNT1;ARNTL
CAV1;CALM3;CALM1;CALM2
GZMA;HP;ABL1;NOD2
KAT5;PARK7;SIRT1;ARNTL

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

ACE2;ACE;NOS3;AGTR1
CHGA;GSN;P2RX4;PIK3CA
STK11;IL12B;IL12A;RELA
ACE2;ACE;NOS3;AGTR1
CA2;CAV1;AGTR1
MYRF;PLP1;SOX10
OAS1;CTSH;VEGFA
APOC1;APOE;LDLR
C3;CFP;CFB
CAV1;SOD2;HIF1A
JAG1;NPHS1;IQGAP1
JAG1;NPHS1;IQGAP1
BMP4;SHH;LIG4
UBC;B2M;TLR2
ARG1;NR1H3;PPARG
APP;ADIPOQ;PSEN1
CD14;TLR4;TLR3
PIAS3;CTNNB1;PARK7
ARG1;NR1H3;PPARG
BMP4;TGFB1;SIRT2
BMP4;CCL5;JAK3
NOD2;IRGM;RELA
MB;MYC;HBB
IL4;LRP1;APOE
GRK2;VIP;STX1A
EGF;PIK3CD;GATA3
EGR1;GATA3;HIF1A
IL1B;CCR7;PHB
KDR;DCN;TRPM4
CD226;HLA-F;HLA-G
CHGA;GSTO1;ADRA1A
ANXA1;ANXA2;SNCA
MDK;LEP;LEPR
BMP2;H6PD;BMP5
GRN;SIRT2;FOXP1
ITGAM;ITGB2;HPRT1
CXCL13;FGF1;FGFR1
PHB;CLOCK;ARNTL
SPHK2;PRKD2;VEGFA
LRP1;LRP2;LDLR
CD226;HLA-F;HLA-G
TYROBP;ATP6AP2;THBS1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

CCL3;FASLG;CCR5
UBC;B2M;TLR2
DDR1;PLAT;CCN3
P2RY12;NTN1;CD2AP
OAS1;CTSH;VEGFA
TH;SLC6A3;SNCA
GSTM1;GSTO1;CRYZ
DMTN;EPO;CASP3;IKZF1;JAK2;JAK3;SH2B3;VEGFA
HSP90AA1;XRCC5;MYC;MAPK1;CTNNB1;ATM;KLF4;TP53
GPI;ISYNA1;TGFB1;GPX4;SPHK2;SPHK1;LRRK2;STAT3;PLA2G2A;LPL;PIK3
SPAST;KIF5A;HSPB1;NEFL;KIF1B;HAP1;SOD1
APP;TNXB;PLA2G1B;DCTN1;COL11A2;LAMC2;PRL;KRT20;INS;CST3;SPAS
RAP1A;CLDN3;PECAM1;MSN;F2RL1;ICAM1
CEACAM1;ADIPOQ;APOC1;NR1H3;APOA1;BRCA1
C1QTNF3;ADIPOQ;MST1;PPARGC1A;SIRT1;INS
BMP4;SHH;TGFB1;EIF2AK3;LIF;AKT1;PARK7;INS
EDNRB;SEMA3A;FN1;GATA3;SOX10
BMP4;AR;NR3C1;TFPI;BMP7
IFNA1;IFNB1;IFNA17;IFNA2;VAMP2
P2RX7;P2RX4;CCL2;CCR2;PTGES
ITCH;HACE1;APC;IL1B;TNFSF12;TNFAIP3;VIP;TNF;SORL1;VSIR
CASP8;IFNG;TNIP1;IL1B;CTSH;NLRC4;APOE;TNFRSF1B;TNF
DAXX;HDAC1;EHMT2;TOP3A;BRCA1;SSRP1;MAPK14;PML;MTOR;TPX2;ST
TGFB2;BMP2;BMPR2;NOTCH1
HDAC1;MBD2;PARK7;SIRT1
ACE;NOX4;FYN;SOD1
NOS3;APOE;LDLR;CD200
DLL4;NOTCH1;KLF4;THBS1
PTGS2;BMP7;RREB1;INS
IRS1;AKT1;SIRT1;PPARGC1A
GCG;PLA2G6;HLA-DRB1;TRPM4
ADRB2;TNF;IRGM;IGF1R
C3;P2RX7;GH1;CA2
DMTN;FLNA;TIMP1;CD177
ALOX5;EIF2AK3;NR1H3;CLU
F2R;CCL3;CCN3;VIP
GJA1;AGO2;TIMP1;VEGFA
CEACAM1;RAP1A;KDR;CD34
ANXA1;XRCC5;LIG4;ATM
P2RY12;PTPRC;NTN1;CD2AP
SHH;AIRE;TGFBR1;SOD1
H2AX;PARP1;TIMELESS;XRCC1;HMGB1;BRCA1;SIRT1;EGFR

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

APP;WWOX;LRP1;LRRK2;ATP6AP2;TNFAIP3;PSEN1;FOXP3;ESR1;BMP2;S
NR4A2;CDH3;APC;FZD4;LRRK2;CAV1;CTNNB1;GATA3;WNT1;WNT3
SPRED2;ADAM17;TGFB1;CAV1;UBC;PPARA;SIRT1;TGFBR1;SMAD7;HSPA1
RPS6KB1;FMR1;ALKBH1;CCL5;AGO2;EIF2AK3;HSPB1;EIF4EBP2;ATF3;ATF
VMP1;ATG16L2;STING1;ATG16L1;MFN2;AMBRA1;IRGM;ATG12;ATG5
MECP2;ADAM17;ANXA1;RGCC;CCND1;ADAMTS1;AKT1;AIF1;EGFR
DLL4;NOTCH3;EGF;AKT1;EGFR;DLK1
PLA2G1B;PLA2G2A;NR1H3;PLA2G4A;PLA2G6;PLB1
CHGA;GRK2;SYT1;DRD2;STX1A;SNCA
AR;GSN;FYN;GPC5;ACTB;INS
APP;GRM7;ACTBL2;PLP1;MTR;MAPT;EPHB2;DRD2;S100B;ACTB;RTN4
SOX2;BMP2;ZEB1;BDNF;LRRK2;NTF3;ARHGEF2;NGF;ADRA2B;BMP7;FGF R

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

SF11;IL12B;IL12A;B2M;HLA-B;TALDO1;HLA-C;MIF;HLA-A;HLA-F;HLA-G;I
MT2A;CCND1;MYC;GRAP2;LEPR;AKT1;TNFSF11;IL12B;IL12A;LGALS9;IL
L12A;LGALS9;MAP3K7;IL6R;SLC11A1;ADIPOQ;F2R;MIF;HLA-A;HLA-G;FO
X2;GJA1;LGALS1;KDR;TNFSF10;TNFSF11;IL12B;LGALS9;MAP3K7;TGM2
1;ACE2;IL23A;NINJ1;AGTR1;TYRO3;S100A9;S100A8;PTGES;SEMA7A;AL
YBB;AGTR1;S100A9;NAIP;S100A8;CSF1R;PXK;ALOX15;MEFV;PRDX5;HR
FSF10;AKT1;CYP1B1;TP63;MAP3K5;TGM2;DAXX;IGFBP3;HGF;RPS6;MIF
K11;MYC;KDR;AKT1;CYP1B1;IL6R;IGFBP3;RPS6;F2R;FOXP3;PRLR;AR;A
SLC11A1;FST;ADIPOQ;F2R;MIF;HLA-G;PRLR;ADCYAP1;IL23A;EPAS1;AD
RKCA;MIF;PRLR;MAG;TYRO3;YME1L1;IL6ST;RAF1;TP53;NAIP;NOTCH2;P
S9;LBP;EPHB2;JAK2;CD34;CCR2;HAVCR2;IL10;GHSR;ARG2;DDX58;SPH
TG1;GJA1;CDH3;MYC;AKT1;LGALS9;EPHB2;SLC11A1;MIF;ERN1;AR;CLD
L16;IGF1R;CDH3;CCND1;MYC;KDR;AKT1;IL12B;IL12A;IL6R;TGM2;EPHA4
LC11A1;SOX10;AR;DDX39B;DDIT3;PADI2;PRKD2;CLOCK;TP53;ATF3;AT
JA1;CDH3;MYC;AKT1;LGALS9;EPHB2;SLC11A1;AR;CLDN5;CLDN3;TYRO
KT1;IL6R;DAXX;RALBP1;HGF;ADIPOQ;MIF;ADCYAP1;ADAM17;CLDN3;PR
L6R;IL10;GHSR;DDX58;SPHK2;F2R;HLA-B;IL16;MMP8;IL17RA;TLR1;IL1A;
AM1;IGF1R;SOX2;MYDGF;GRM4;KDR;TNFSF11;CCR7;LGALS9;IL11;EDN1
TNF;YY1;SOX2;SALL1;KAT5;ZMIZ1;MYC;TNFSF11;KAT8;TP63;EOMES;ZB
L1;IL6ST;RAF1;TP53;NAIP;NOTCH2;PSMD10;GLO1;PSEN1;PRDX3;PRDX
JA1;MYC;KDR;AKT1;IL6R;RPS6;F2R;LIG4;MIF;PRLR;FOXP1;AR;CLDN5;A
;HMGB1;CXCL13;CXCL2;CXCL5;CASP1;IL12A;LGALS9;LBP;NOS1;CCR5;
LS9;IL6R;CD74;IL33;XBP1;TSLP;NOS2;SPHK2;DDX58;F2R;STAT3;IL16;P
2;HAVCR2;SPHK2;DDX58;IFNGR1;MIF;MMP8;TLR1;IL1A;TYROBP;OAS1;I
G2;ACTG1;YY1;SOX2;GJA1;CDH3;CDH1;MYC;KDR;AKT1;IL12B;LGALS9;E
K1;IFNGR1;HLA-B;HLA-C;HLA-A;HLA-F;HLA-G;OAS1;IFNG;IRF1;IRF8;IRF
F11;LGALS9;MAP3K7;IL10;EDN1;PRKCB;DDX58;SPHK1;IL18;TRAF2;TRAF
DDT;CCL3;IL12B;RIPK1;LBP;LGALS9;CD14;CCL19;EPHB2;JAK2;CCR2;HA
6;MMP8;TNFRSF1A;IL17RA;IFNG;IL23A;IL1B;NINJ1;TLR9;AGTR1;TLR7;C
D7;PSMD4;AKT1;TNFSF11;JAK2;TNFRSF4;TNFRSF12A;TRAF2;TRAF1;TN
A-DMB;CCL5;CD38;IL12B;IL12A;CCL19;EPHB2;TNFRSF4;JAK3;HLA-DPA1
;HSPD1;HLA-DMB;MDK;ZMIZ1;CCL5;TNFSF11;IL12B;CCL2;CCR7;LGALS
;IL16;IL17RA;TNFRSF1A;IFNG;IL23A;IL1B;NINJ1;AGTR1;TLR9;TLR8;TLR7
AT5;IL12B;IL12A;CCR7;LGALS9;CD34;JAK3;CMKLR1;HAVCR2;IL10;GHS
2;IL6R;EPHA4;IL11;IL15;HGF;IL18;MIF;TNFRSF1A;IFNG;IL23A;PECAM1;A
1;CXCL13;TNF;CXCL2;CXCL5;CASP1;LBP;CCR5;IL10;PRKCE;IL18;PDCD
L1;MTR;AHR;HMGB1;CXCL13;CXCL2;ACTB;CXCL5;KAT5;CASP1;AKT1;L
;RIPK1;LBP;LGALS9;CD14;IL10;CD74;ANXA1;NOS2;DDX58;ADIPOQ;F2R;
7RA;TNFRSF1A;IFNG;IL23A;IL1B;NINJ1;AGTR1;TLR9;TLR8;TLR7;CD47;S
;IL6R;CD74;EGR1;IL33;TSLP;ADIPOQ;IL18;EIF2AK2;IL17RA;ADCYAP1;AD
HLA-DMB;CCL5;IL12B;CCL19;JAK3;ICOSLG;CCR2;HLA-DPA1;CD276;ANX

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

;MDK;KDR;ENPP2;ITGAX;CTSH;EPHB2;CCR2;EDN1;MMP7;PRKCE;SPHK
R7;LGALS9;EPHB2;ROS1;ADIPOQ;F2R;PRKCA;MIF;YWHAZ;ADCYAP1;C
;CASP1;TIMP3;CCR7;LGALS9;TIMP1;JAK2;IL6R;JAK3;IFNAR2;ANXA1;SL
IK3CG;IGF1R;MYDGF;RAC2;CCR7;HSP90AA1;HGF;IL18;NRG1;TGFBR1;
BRCA1;CXCL13;FGF1;ETS1;MECP2;MYDGF;ADGRA2;ADAMTS1;KDR;IT
MB;CCL5;IL12B;CCL19;JAK3;HLA-DPA1;CD276;IL10;ANXA1;VCAM1;IL15;
IK3CG;IGF1R;MYDGF;RAC2;AKT1;CCR7;HSP90AA1;HGF;IL18;NRG1;HLA
DR;ITGAX;CTSH;CCR7;EPHB2;EDN1;MMP7;SPHK1;HGF;F2R;PRKCA;MM
H1;MYC;AKT1;KAT8;TP63;MAP3K5;EOMES;F2R;SOX10;FOXP3;AR;MYCN
HK1;IL18;TRAF2;TRAF1;AR;AIM2;TRAF6;IL1B;BTK;TLR9;PRKD2;ARHGEF
GALS9;CD14;CD74;NOS2;DDX58;ADIPOQ;F2R;STAT3;TLR1;IL6;MAVS;IL1
CTG1;IGF1R;SHH;CDH1;MDK;ITGAX;KDR;ENPP2;AKT1;CYP1B1;CTSH;EP
;CCR7;IL12A;LGALS9;CD14;CCR2;HAVCR2;HLA-DPA1;CD276;PRNP;SLC
3;CXCL2;CXCL5;CASP1;LBP;CCR5;IL10;PDCD1LG2;TNFRSF1B;SIRT2;IL
R;LEPR;FLOT1;AKT1;EPHB2;ROS1;EPHA4;DAXX;RALBP1;HSP90AA1;HG
ALS9;F2R;PRKCA;MIF;ADCYAP1;CHI3L1;PRKD2;GAS6;CD44;NOTCH2;C
IZ1;TNFSF11;CCN3;JAK2;TP63;PRKCB;ADIPOQ;ATP6AP2;PRKCA;SIRT1
;CCL19;TIGIT;JAK3;CMKLR1;IL10;HLA-B;IL16;LILRB1;MAPK14;HLA-G;FO
CX3CL1;MALT1;PANX1;CASP8;IFI16;CASP1;CCL3;NLRP3;CCR7;LGALS9
CD34;TSLP;STAT3;IL13;LILRB1;PDCD1LG2;MMP8;FOXP3;IL4;IL6;TYROB
A;CASP8;FCGR3B;B2M;CD34;LAG3;ITGA4;IL15;HLA-B;HLA-C;HLA-A;HLA
S9;ICOSLG;CCR2;IL10;ANXA1;DDX58;IL15;SLC11A1;HLA-B;MIF;TNFRSF
R;HMGB1;CXCL13;NR3C1;CXCL2;CXCL5;KAT5;CASP1;LBP;CCR5;IL10;S
7;CCR6;CCR5;CCR4;CCR3;CMKLR1;CCR2;EDN1;F2R;ADCYAP1;AGTR1;
L2;CX3CL1;CXCL5;PIK3CG;LGALS3;CXCR1;CCL7;CCL5;BSG;CXCR2;CC
FOXO3;TNF;RELA;TNFSF13B;PSMB6;PSMD7;PSMD4;TNFSF11;TNFRSF1
L2;CX3CL1;CXCL5;PIK3CG;LGALS3;CXCR1;CCL7;CCL5;BSG;CXCR2;CC
R1;CXCR3;CXCR2;KDR;CCR9;CCL3;TNFSF11;CCR8;CCR7;CCR6;CCR5;C
L2;CX3CL1;CXCL5;PIK3CG;LGALS3;CXCR1;CCL7;CCL5;BSG;CXCR2;CC
SOX2;STK11;ADAMTS1;MYC;CYP1B1;IL12B;CCN3;IL12A;JAK2;B2M;IL10;
-B;HLA-C;CYBB;MIF;UNC13D;ADAM17;TYROBP;PADI2;S100A9;S100A8;V
;EPHB2;IGFBP3;F2R;ADIPOQ;MIF;FOXP3;AR;CLDN3;TXNIP;RAF1;TP53;N
RSF14;FYN;JAK2;IL6R;IL11;CD74;PRNP;TGFB1;DMTN;IL15;HGF;LIF;OSM
L33;CD74;TSLP;IL18;EIF2AK2;FOXP1;IL6;ADAM17;IFNG;IL7;TLR9;F2RL1;
R3;CXCR2;CCR9;CCL3;CCR8;TNFSF11;CCR7;CCR6;NOS1;APOE;CCR5;C
MYC;CASP3;CASP1;AKT1;JAK2;MAP3K7;TP63;PARP1;PRKCE;LIG4;IL1A;
A1;HLA-DPA1;JAK1;HLA-DRB5;VCAM1;IFNGR1;STAT1;HLA-B;HLA-C;HLA-
L5;IL12B;IL12A;JAK2;IL6R;SH2B3;TSLP;IL15;STAT3;IL18;LIF;OSM;IGF1;IL
GB1;ITGAL;MPO;LGALS3;PSMD7;FCGR3B;ANPEP;C3AR1;TIMP2;ITGAX;
1;IL12A;LBP;NOS1;LGALS9;CD14;JAK2;SNCA;IL10;NOS2;NOS3;SLC11A1
GB1;ITGAL;MPO;LGALS3;PSMD7;FCGR3B;ANPEP;C3AR1;TIMP2;ITGAX;
L12B;NLRP3;CCR7;LGALS9;CD177;IL10;CD74;TGFB2;XBP1;IL15;SPHK2;I

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

GF1;ETS1;HIF1A;THBS1;MYDGF;MDK;KDR;ITGAX;CYP1B1;HMOX1;CTS
B1;CCL7;CCL5;CCL4;CASP1;CCL3;CCL2;CCL1;LGALS9;CCL19;CCL18;CC
I16;CASP1;CCL3;NLRP3;LGALS9;NLRP1;CCL19;JAK2;EGR1;STAT3;IL16;
AK2;IL6R;TSLP;IL15;STAT3;IL18;LIF;OSM;IGF1;IL2;TNFRSF1A;VEGFA;IL4
R;FLOT1;AKT1;DAXX;RALBP1;HSP90AA1;HGF;ADIPOQ;SIRT1;MMP9;AD
DR;LEPR;FLOT1;AKT1;EPHB2;DAXX;RALBP1;HSP90AA1;HGF;IGFBP3;A
5;CCL7;CCL5;CCL4;CCL3;CCL2;CCL1;CCL19;CCL18;SH2B3;CCL17;CCR2
P1;CCL3;NLRP3;LGALS9;NLRP1;CCL19;JAK2;EGR1;STAT3;P2RX7;IL6;TY
;ICAM1;LGALS3;CASP8;TNFSF10;AKT1;HMOX1;RIPK1;NOS3;TNFRSF10B
BB3;CCL5;NTF3;KDR;JAK2;TGFB2;EGF;HGF;F2R;IL18;FN1;OSM;IGF1;SIR
F10;CYP1B1;CTLA4;DNM1L;TP63;MAP3K5;TGM2;TNFRSF12A;SPHK2;IGF
5;CCL7;CCL5;CCL4;CCL3;CCL2;CCL1;CCL19;CCL18;SH2B3;CCL17;CCR2
1;JAK2;JAK1;IFNAR2;CD74;TSLP;IFNGR1;STAT1;SPHK1;TRAF2;PTPN11;
L13;ADRA1A;KNG1;EDNRA;CXCR1;CXCR3;P2RY1;CXCR2;C3AR1;ABL1;
AK1;IL12B;NLRP3;CCN3;LGALS9;CD14;CCL19;TNFSF14;SPHK1;EIF2AK2
;CCR2;HLA-DPA1;CD276;SLC11A1;IL18;LILRB1;HLA-A;IL23A;IL1B;TLR9;H
S1;HIF1A;THBS1;MYDGF;KDR;ITGAX;CYP1B1;HMOX1;CTSH;CD34;CCR
12A;APOD;IL6R;EDN1;STAT1;XRCC5;IGFBP3;IL18;IGF1;FOXP1;BMP4;IL6
1;ETS1;THBS1;HIF1A;PIK3CG;KDR;ABL1;AKT1;STAT5A;EDN1;TGFB1;EG
TSH;IL12A;LGALS9;LBP;NOS1;JAK2;SNCA;STAT5B;TGFB1;ANXA1;NOS2
DLL4;CASP8;MDK;LEPR;CCR7;CCL19;TNFRSF4;ICOSLG;MICA;CD276;C
;ADIPOQ;GPBAR1;APOA1;TNFRSF1B;TNFRSF1A;ADCYAP1;CD200R1;A
2;CCR7;CCL19;CCR6;CCR5;CCR2;TRPM4
R;DAXX;TGFB2;TGFB1;SORT1;TNFSF12;TNFRSF10B;TRAF2;TNFRSF10
;CXCR2;CCR7;CCL19;CCR6;CCR5;CCR2;TRPM4
VCR2;MIF;MMP8;SIRT1;FOXP1;CLDN5;CLDN3;MYCN;IFNG;MAPT;CD46;
;USP18;CX3CL1;RELA;CASP8;ADGRA2;ALOX5;CASP1;NLRP1;EPHB2;JA
1;LBP;B2M;MBL2;DDX58;SLC11A1;CYBB;TYROBP;OAS1;BTK;TLR9;TLR8
;IL6;IFNG;IL23A;DDIT3;IL12B;CCL1;IL12A;TLR4;MYD88
CL7;SMPD1;CCL5;CCL4;CCL3;CCL2;CCL1;LGALS9;CCL19;CCL18;CCL17
;CD14;CCL19;TNFSF14;SPHK1;EIF2AK2;MMP8;IL23A;IL1B;TRAF6;TLR9;C
;IGF1R;INS;SOX2;MYDGF;GRM4;KDR;MAPK1;ROS1;IL11;CD74;EGF;GD
;IL23A;TLR9;IL12B;CCR7;IRF5;CCL19;LGALS9;TLR4;TLR3;IL17A;TLR2
3;TNFSF10;CYP1B1;CTLA4;DNM1L;HTATIP2;MAP3K5;TGM2;TNFRSF12A;
R7;IL12A;CCL1;CCR6;LGALS9;IL6R;CCR2;CMKLR1;CCR1;VEGFB;VEGFA
L1;IL4;TYROBP;IFNG;MAPT;JAK2;SNCA
FRSF4;IL10;CD74;FCRL3;MIF;IL2;IL4;TYROBP;PTPRC;IL7;GPR183;TLR9;
GRP1;PIK3CG;EGFR;CCND1;IRAK1;AKT1;TNFSF11;S100A12;SNCA;EDN
GF;ERBB3;CCL5;NTF3;KDR;MAPK1;JAK2;TGFB2;EGF;HGF;F2R;FN1;IL18;
X2;SALL1;EDNRB;CCND1;KAT5;MYC;KAT8;TNFRSF4;TP63;EOMES;DAXX
RIPK1;BID;WWOX;TNFRSF12A;CAV1;TNFSF12;TNFRSF10B;TRAF2;TNFR
OE;STAT5A;TGFB1;ANGPT2;NOS3;PRKCA;MAPK14;SIRT1;VEGFA;ADAM

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

X2;PRDX5;MAPK8;ABL1;AKT1;HMOX1;MAPK1;PPARGC1A;SNCA;PARP1;
SLG;HLA-DPA1;PRKCB;HLA-A;PIK3CA;TRAF6;BTK;PRKD2;MS4A1;CARD
MP1;IL10;IL15;IFNGR1;SLC11A1;IL13;ADIPOQ;F2R;APOA1;FOXP3;ADAM
;PRNP;TGFB2;DAXX;FOS;TYROBP;IFNG;DDIT3;DDIT4;BAX;CTNNB1;MA
BS1;EGFR;INS;CDH3;MYC;CCL5;AKT1;CCL19;PPARGC1A;LDLR;SNCA;E
NFSF10;CASP1;CCR7;LGALS9;MAP3K7;PRKCB;SPHK2;ADIPOQ;F2R;TRA
CG;CXCL16;CXCL10;CXCL11;CCL7;CCL5;GPR183;CCL4;CCL3;CCL2;CC
CCL2;CCL19;JAK2;IL33;TGFB2;XBP1;CCL21;EGF;HGF;IGF1;KLF4;SIRT1;
CA;TGFB1;ANXA2;EGF;IL10RB;ADIPOQ;APOA1;NR1H3;MAPK14;KLF4;SE
;TRPM2;HRH1;RAP1A;GNG2;KAT5;CDH1;CASP3;P2RY2;CCL5;P2RY1;SP
M2;DAXX;HSP90AA1;IGFBP3;TRAF2;SIRT1;TNFRSF25;SGK1;RAF1;TP53
B;KAT5;ZMIZ1;MYC;TNFSF11;KAT8;TP63;PRKCB;SLC11A1;SOX10;AR;PR
MICA;IFNAR2;DDX58;STAT1;IFNB1;MX1;EIF2AK2;LILRB1;AICDA;ISG20;B
;IL12B;CCR7;CCL19;FCGR1A;IL6R;SNCA;EPHA4;EGR1;PRNP;DAXX;TGF
4;PPARGC1A;MAP3K5;SNCA;CHGA;EGR1;PRNP;DAXX;LANCL1;TRAF2;D
L16;ZFP36L1;CASP8;CCL7;CASP3;SMPD1;CCL5;CCL4;CCL3;AKT1;CCL2
7;LGALS9;CCL19;PARP1;IL15;MAPK14;MMP9;SIRT1;PML;FOXP1;VEGFA;
;IFNAR2;DDX58;STAT1;IFNB1;MX1;EIF2AK2;LILRB1;AICDA;ISG20;BST2;
X58;STAT1;XRCC5;PTPN11;NFKB1;NFKB2;MAVS;OAS1;STING1;IRF1;TL
F1;CX3CL1;VSIR;IL4;POMC;MC1R;RARA;PTPN6;LBP;LGALS9;GAS6;CD34
MAPK14;THBS1;ETS1;HIF1A;SIRT1;VEGFA;ADAM17;P2RX4;SP1;KDR;AK
;CD28;IL12B;F2RL1;LGALS9;TIGIT;CD46;CD34;TLR4
;RELA;CASP8;ALOX5;CASP1;NLRP1;APOE;JAK2;CCR2;ANXA1;AHSG;IL3
L1;FOXP1;TLR1;IL4;IFNG;LBP;MAPT;JAK2;TLR4;SNCA
AKT1;JAK2;MAP3K7;TGFB2;TNFSF15;SLC11A1;IL18;TNFRSF10B;TNFRS
;INS;MAPK8;AKT1;IL12B;APOE;TGFB1;HACE1;DDX58;TNFSF12;IL18;NR1
K3CG;EGFR;IRAK1;SMPD1;TNFSF11;S100A12;APOE;SH2B3;EDN1;TGFB
H;NEFL;LGALS9;CCR5;JAK2;JAK3;MAP3K7;JAK1;MAP3K5;HGF;IL18;APO
EGFR;MYDGF;CDH3;MDK;MYC;KDR;AKT1;RREB1;STAT5A;XBP1;EGF;TN
1;HLA-B;HLA-C;HLA-A;HLA-F;HLA-G;PSMB8;BST2;ISG20;OAS1;IRF1;IRF8
1;HLA-B;HLA-C;HLA-A;HLA-F;HLA-G;PSMB8;BST2;ISG20;OAS1;IRF1;IRF8
CL1;VSIR;IL4;POMC;MC1R;RARA;PTPN6;LBP;LGALS9;GAS6;CD34;TLR4;
OXP1;ERN1;BMP4;GJA1;IL6;ADAMTS1;CCL5;MFN2;AKT1;HMOX1;IL6R
CL2;DRD2;STAT5B;ANXA1;TGFB1;MRGPRX1;STAT3;IL18;TRPV1;ESR1;G
D34;HAVCR2;IL10;SLC11A1;MIF;MMP8;SIRT1;FOXP3;FOXP1;ERN1;CLDN
L6;CCL7;CCL5;CCL4;CCL3;TNFSF11;CCL2;S100A12;CCL1;CCL19;CCL18;
ZFP36L1;DLL4;RAP1A;CCL5;KDR;AKT1;CCL2;NOS1;STAT5B;WWOX;SMA
1;PSMB6;PSMD7;PSMD4;GRAP2;CTLA4;FYN;MAP3K7;HLA-DQA2;ICOSL
;STMN1;KDR;AKT1;JAK2;EPHB2;ROS1;EPHA4;HSP90AA1;HGF;MMP2;IN
HGF;IGFBP3;IL18;NGF;ADRA2B;TGFBR1;AR;CEACAM1;ZEB1;CREB1;IL1
;PIK3CG;RTN4;KDR;ENPP2;ABL1;AKT1;CTSH;RREB1;EDN1;TGFB2;EGF;
T5A;ITGA4;EGF;TNFSF12;VEGFB;PRKCA;SIRT1;TGFBR1;APLN;VEGFA;

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

SF10;CASP1;NLRP3;RIPK1;LGALS9;NLRP1;JAK2;BID;MAP3K5;SNCA;GS
MFN2;STAT6;TRPM8;HCRT;JAK2;PPARGC1A;CMKLR1;DECR1;CCR2;IL4
CL12;CCL5;CCL1;IL12A;CCR7;LGALS9;CCR6;GAS6;CCR2
9;CD14;MAP3K7;S100A1;TLR1;OAS1;TNIP1;TRAF3;TRAF6;TLR9;BTK;TLR
AT6;TRPM8;HCRT;JAK2;PPARGC1A;CMKLR1;DECR1;CCR2;IL4R;CAV1;A
8;CCR7;CCN3;CCR6;CCR5;CCR4;CCR3;CCR2;CCR1;CCL21;CCL20;HGF
R;IRAK1;TNFSF11;S100A12;MAP3K7;MAP3K5;EDN1;TGFB1;EGF;TRAF2;
1A;CD34;SNCA;CHGA;TGFB3;BDNF;F2R;LIG4;TRAF2;HLA-F;TNFRSF1B;N
00R1;IL6;IL1B;CD200
F;ETS1;HIF1A;RELA;POU5F1;APLN;BMP4;WT1;PPARG;PPARA;TP53
KAT5;CCND1;MYC;EOMES;ZGPAT;FST;SOX10;FOXP3;FOXP1;AR;DDIT3
11;HSP90AA1;TGFB1;BDNF;IFNB1;IFNA17;CAV1;LIF;OSM;MIF;NGF;IRGM
P2;MAP3K5;SNCA;EGR1;PRNP;DAXX;MMP3;FOS;BMP4;TYROBP;IFNG;A
RGC1A;SNCA;PARP1;TXNRD2;CAV1;TXNRD1;GSR;CYBB;FANCC;SOD2;
F;ETS1;HIF1A;RELA;APLN;WT1;PPARG;TP53
8;IRAK1;TNFSF10;CASP1;S100A12;HMOX1;FLNA;RIPK1;CCR7;LGALS9;C
SP8;EPHB2;JAK3;IL10;IL11;VCAM1;ITGA4;PRKCB;IFNB1;IFNA17;AICDA;IL
PK8;CCL5;CASP1;CCL3;CYP1B1;CCL2;CCR7;NOS1;STAT5B;NCOA2;TGF
5;TBX21;IL1B;TRAF6;CD28;IL17F;PRKD2;MAP3K7;CD34;CARD11;CCR2;H
;PTPRC;IL7;GPR183;TLR9;BTK;BCL2;CD38;CD27;TP53BP1;EPHB2;TNFR
E;PPARGC1A;PRNP;TGFB2;TGFB3;BDNF;F2R;LANCL1;LIG4;NGF;SOD2;
6;OAS1;CCL5;POU2AF1;BAX;IL12A;CCL19;LGALS9;LGALS8
HLA-G;ICAM1;IL4;RGCC;CD40LG;KDR;KRIT1;CCL2;GAS6;NFE2L2
LNA;TIMP1;A2M;TGFB2;TGFB1;TGFB3;AHSG;EGF;HGF;ANXA5;FN1;VEG
;PRDX3;CRYGD;MAPK8;PRDX5;CAT;AKT1;HMOX1;MAPK1;FYN;APOD;M
1;CCL4;S1PR1;CCL3;CCL2;CCL1;CCL19;CCR6;CCL18;CCL17
DDAH1;IFNG;IL1B;AKT1;CD47;JAK2;CD34;GLA;TLR4
RELA;PSMB6;PSMD7;PSMD4;IRAK1;CCL7;CCL5;UBC;CCL4;CCL3;CCL2;
HLA-DRA;LBP;LGALS9;CD46;HLA-DRB1;CCR2
CS1;PTPRC;CCL5;LEP;BCL3;CYP1B1;JAK2;JAK3;SH2B3
A;IL10;PRKCB;AHSG;IGFBP3;NOG;ADIPOQ;DCN;IL1B;DDIT4;TYRO3;TLR
L7;RGS1;CCL5;CCL4;CCL3;CTSH;CCL2;CCL1;CCL19;CCL18;CCL17;TGM2
BS1;PIK3CG;DLL4;KDR;KRIT1;ABL1;AKT1;APOE;EDN1;EGF;PRKCA;DCN
CL19;BID;SNCA;ANXA1;ANXA2;IL15;AHSG;SLC11A1;APOA1;NR1H3;MER
PSEN1;IGF1;AGER;IGF1R;ICAM1;ZFP36L1;GJA1;TIMELESS;FYN;ARHGE
L12B;S100A12;IL12A;TNFRSF14;NLRP1;LBP;IL6R;MICA;MBL2;CHGA;NO
;APOE;STAT5A;EGF;STAT1;CAV1;TNFSF12;VEGFB;PRKCA;SIRT1;TGFB
2;CRYGD;MAPK8;PRDX5;IL6;ABL1;AKT1;CYP1B1;MAPK1;RIPK1;MAPT;F
BRCA1;ICAM1;BMP5;CASP8;TNFSF10;HMOX1;FAS;RIPK1;ARHGEF2;BC
RKAR1A;IL12B;TNFSF9;LGALS9;CD24;ICOSLG;IDO1
5;LMNA;KDR;ENPP2;APOE;TP53BP1;DNM1L;RREB1;TRPM4;RALBP1;XBP
R183;TLR9;BCL2;CD38;EPHB2;TNFRSF4

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

KLRK1;TYROBP;IL23A;IL12B;HLA-DRA;IL12A;CD226;HLA-DRB1;NECTIN2
JAK2;BID;SNCA;TNFSF15;F2R;EIF2AK3;TNFRSF10B;TRAF2;TNFRSF10A;
D2;AGER;MMP9;MMP12;STAT4;STAT6;FYN;IRF5;NLRP1
L1;MYD88
T;PML;DDIT3;TNFSF10;BCL2;FAS;BAX;RIPK1;DNM1L;BID;S100A9;TP53;S
;TIMP3;SDF4;FLNA;TIMP1;A2M;SNCA;TGFB2;TGFB1;SYT1;TGFB3;AHSG;
B1;HPSE;IL6ST;CCR2;ATF4
FSF11;CCL2;CD47;CD44;CCR2;HLA-DPA1
CL2;STAT6;JAK2;JAK3;CCR2;IFNAR1
CD14;TLR4
IL12B;JAK3;TRIB2
LS3;AKT1;RIPK1;BDNF;HGF;IGF1;MMP9;TGFBR1;IL4;BMP4;NR4A2;AR;B
RAF6;IL12B;HLA-DRA;IL12A;B2M;MAP3K7;HLA-DRB1
F;MECP2;SALL1;KAT5;KAT8;CD38;CIC;TNFRSF4;TP63;DAXX;ZGPAT;ZB
TNIP1;CCL5;PECAM1;OLR1;CD177
;INS;CYP27B1;GJA1;STK11;AKT1;CCN3;ROS1;TGFB2;SMAD4;TGFB1;CIS
FA;BMP2;RGCC;CDH1;WNK1;AKT1;MBP;WNT1;PPARA
LOX5;NLRP3;CCN3;APOE;DRD2;IL10;EPHA4;GHSR;ADIPOQ;IL13;APOA1
X5;CCL5;IL12B;IL12A;APOE;DRD2;DNM1L;TGFB2;TGFB1;NOS2;TGFB3;A
;TGFB1;DMTN;BDNF;CAV1;LIF;OSM;MIF;NGF;IRGM;SMAD7;VEGFA;IL6;D
PHB2;JAK3;MAP3K7;ROS1;JAK1;MAP3K5;HTATIP2;BRD2;EPHA4;PRKCB;
;AKT1;TLR8;TLR7;RIPK1;CD14;MAP3K7;TLR4;TLR3;CARD11;BIRC2;TLR2
XNIP;NLRP3
A2B;ADAM17;IFNG;CCL2;EPHB2;JAK2;CCR2
GM2;P2RY12;EPHA4;TGFB2;CCL21;LIF;PRKCA;VEGFA;SMAD7;CXCL12;
THBS1;ICAM1;BMP5;LGALS3;CASP8;TNFSF10;HMOX1;FAS;RIPK1;ARHG
MZB1;F2RL1;TNFRSF14;EPHB2;TNFRSF4
BPJ;NR3C1;TNF;MECP2;SALL1;KAT5;KAT8;CD38;CIC;TNFRSF4;TP63;DA
RF8;PPARG;GAS6
SF1A;GRM7;IL12B;IL12A;APOE;DRD2;FGF23;SNCA
;DDIT4;MAPK1;CHI3L1;CALM3;S1PR2;CALM1;CALM2
RAF3;IRF1;FLOT1;TLR9;TLR8;IRF5;TLR7;TLR4;TLR3;TLR2
T;ABL1;CYP1B1;HMOX1;RIPK1;FYN;FXN;MAP3K5;NFE2L2
OT1;APOE;B2M;EGF;CAV1;IGF1;MMP8;NGF;MMP9;SIRT2;BMP4;CLDN5;B
GER;MMP9;IGF1R;ICAM1;MMP12;GJA1;FYN;TLR4
AP3K7;CCR2;TRPM4
;FCGR3A;GNG2;IFI16;FYN;FCGR1A;CCR2;HAVCR2;IL10;CD163;GPBAR1
1
P3;CCN3;APOE;IL10;GHSR;IL13;ADIPOQ;APOA1;NR1H3;KLF4;SIRT2;TNF
LR7;LBP;CD14;CLEC4E;MAP3K7;S100A9;TLR4;S100A8;TLR3;MYD88;TLR
A-G;FOXP3;LGALS3;CEACAM1;DLG5;TIGIT;JAK3;HLA-DRB1;HAVCR2
R;CCR7;CCL19;EPHB2;ROS1;EPHA4;CD74;DAXX;CCL21;XRCC5;INSRR;M

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

X5;KRIT1;CCR2;GTF2I;TGFB2;STAT1;KLF4;HLA-G;DCN;PML;CLDN5;CXC
APOD;CCR6;CD200
6;JAK2;IL6ST;IL6R;JAK1
2;TNFRSF4
1;CCL2;GAS6
AD7

1;IL12B;IL12A;APOD;PPARG;VIP
;CFL1;STAT4;IL12B;IL12A;P4HB;CD47;JAK2;JAK1
3CL1;SOD1;MAG;ERBB3;MDK;NTF3;TYRO3;BCL2;CCL2;APOE;PPARGC1
EP;APOD;PPARA;IL17D;TLR4;MYD88;IL17A
ALS9;GAS6;TLR4;HLA-DRB1;HAVCR2
23A;IL12B;HLA-DRA;IL12A;HLA-DRB1
IL10;IL11;VCAM1;ITGA4;IFNB1;IFNA17;IL2;AICDA;IL4;ADAM17;PTPRC;AX
E;IL6ST;ATF4
A;MAPK8;CASP8;IL1B;IRF1;CASP1;TLR8;FAS;TLR7;TLR4;TLR3;MYD88
TYROBP;AGTR1;F2RL1;RIPK1;MAPT;TLR4;TP53;CD177
IL1B;LEP;AKT1;APOE;CALM1;GLA
1;IL2RA;ABL1;CTLA4;CCR2
AP3K5;TGFB2;CCL21;SPHK1;EIF2AK2;TRAF2;TRAF1;MMP8;VEGFA;BMP
RNTL;BMP2;IL6;CREB1;ALOX5;LEP;AKT1;GNB3;PPARG;WNT1;TRIB2;CM
FA
M1;CDH1;ADAMTS1;BSG;KDR;TIMP2;FLOT1;ITGAX;CYP1B1;TIMP1;TPS
AP3K7;CARD11;CCR2
PSMB8;RELB;PSMB9;NFKB2;PSMB6;PSMD7;PSMD4;IRAK1;TRAF6;AKT1;
4;MDK;KDR;F2RL1;PRKD2;CCL19;IL6R;CCR2
CTG1;DUOX1;OCLN;CLDN3;HPSE;RREB1;DUOX2
;CFL1;STAT4;IL12B;IL12A;P4HB;JAK2;JAK1
;NLRP3;MAP3K5;SNCA;HGF;F2R;DHCR24;NGF;KLF4;SIRT1;VEGFA;GAS
;RIPK1;GAS6;HSPA1B;HSPA1A
R8;IRF5;TLR7;TLR4;TLR3;TLR2
SF11;IL12B;RIPK1;HLA-DRB1;IL17A
1A;CCL7;RGS1;CCL5;CCL4;PLXNA2;CCL3;CCL2;CCL1;CCL19;CCL18;CC
1B;AKT1;TLR4
SF1A;ADAM17;CASP8;CASP1;F2RL1;RIPK1;GAS6;BIRC2;HSPA1B;BIRC3
B1;TNFSF11;CCL2;TNFSF9;CD47;TIGIT;JAK3;CCR2;HLA-DPA1
CTG1;DUOX1;OCLN;CLDN3;ALOX5;F2RL1;EPHB2;CRK;DUOX2
2;SPRED2;SHH;WNT1;FGF23;TRPM4;ABCA1;TGFB1;JAG1;CAV1;ADIPO
P;CYP1B1;IL7R

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

P2RX3;P2RX2;CCL5;CCL4;CCL3;CCL2
LDN5;CXCL10;SARS1;RGCC;ADAMTS1;ALOX5;KRIT1;CTNNB1;PPARG;IL

T1;APOE;FGF23
1B;AKT1;TLR4

BP

B;HLA-DRA;TNFSF9;CD46;HLA-DRB1
YP1B1;JAK2
SPD1;PTPRC;CD40LG;BCL2;TNFRSF4;MS4A1
B1;RGCC;CCL5;AKT1;APOE;PPARA;TLR4
4;ERN1;NR4A1;PIK3CA;KDR;PRKD2
5;P2RX4;P2RX3;P2RX2;CD19;SNCA
;CALM1;CALM2
FRSF14;CCL27;CCR2
K2;CCR2;IFNAR1
;CD44
AVCR2

SF1A;CASP8;BAG3;BCL2;BAX;BID
GALS9;MICA;NECTIN2
CAM1;GJA1;FYN;TLR4
KAR1A;DLG5;TNFRSF14;LGALS9;HLA-DRB1
CL2;IL12A;CD47;CCR2;HLA-DPA1
L16;GRK2;CXCR1;CXCR2;APOE;FCGR1A;LDLR;PDLIM7;SNCA;CD163;H
SIRT1;HLA-G;IFIH1;GPR151;MAVS;MYC;B2M
S;CXCL12;BCL2;AKT1;ACKR3;ARHGEF2;HSPA1A;NFE2L2;BCL2L1
LA-DRB1;NECTIN2
L;SOX2;STK11;CCND1;MYC;ABL1;IL12B;MFN2;IL12A;TGFB2;TGFB1;CDK

CXCL16
TPN6;GAS6;TLR4;CD200
AGTR1;PPARG;PPARA
B;TLR4;TLR3;IL17A
BIA;MAPK8;IFI16;BCL3;PPARG;JAK2
;IL6;RGCC;MDK;IL1B;CTNNB1;EZH2

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

B2;JAK3;ROS1;JAK1;MAP3K5;BRD2;PRKCB;SPHK2;PRKCE;SPHK1;IGFB
LR3;TLR2
PHB2;CD34

;HSPA5;MMP1;MMP3;EIF2AK2;TRAF2;NRG1;PTPN11;SORL1;IRGM;GFA
1;PPARA;GAS6;NFE2L2
GRP1;TRAF3;IL1B;TRAF6;TLR9;CD27;F2RL1;CCR7;RIPK1;CCL19;MAP3K
RAC2;FLNA;FYN;BID;TP63;PRNP;TGFB1;HSPA1L;GZMB;YWHAZ;SORL1;
AGT;BMP4;P2RX7;SPRED2;PTPRC;TNIP1;MYC;SMPD1;IL1B;TIMP3;APOE
GM;JAK1
1

MP5

3
A2;ABL1;AKT1;FLNA;CCR7;CCL19;FGF23;DUOX2;TGFB1;HACE1;CCL21;

PA14;HSPD1;ERN1;BAG3;DDIT3;BAX;HSPA1B;HSPA1A
DGRG1;GNG2;CNR2;CNR1;ADGRG6;S1PR1;S1PR3;S1PR2;DRD2;S1PR5
B1;PARP1;MMP1;MMP3;NRG1;ESR1;GTF2H4;VEGFA;IL5;IFNG;FSCN1;BA

HI1;NTF3;CCL19;B2M
BL1;FYN;PTPN6;EPHB2;JAK2;JAK3;FGFR1

;ATF4
CR2;TRPM4
CA
IPK1;CCR7;CCL19;MAP3K5;CCL21;TRAF2;TRAF1;MMP8;ITCH;TRAF3;TR
BP;DLG5;CTLA4;ATM;HLA-DRB1
ALT1;TLR3

BB3;PIK3CA;TYRO3;AKT1
RT2;TRAF6;PPARG
;APOE;HAP1
NFSF10;RIPK1;BID
7B1;BMP2;ALOX5;S1PR1;CCL3;FGF23;TRPM4

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

;BID;SNCA;TGFB2;TGFB1;TGFB3;MMP1;MMP3;NRG1;BMP7;TGFBR1;VE
P8;IFI16;IRF1;CDC37;CCL5;TYRO3;TLR8;PTPN6;BIRC2;BIRC3
;TNFSF11;ROS1;TP63;CMKLR1;DAXX;RALBP1;SPHK2;TOP3A;ATP6AP2;
LOX5;NTF3;TGFB1;PRKCB;BDNF;LIF;EIF2AK2;NGF;KLF4;TGFBR1;SMAD
RT1;ZFP36L1;CREB1;LEP;STAT4;AKT1;STAT6
;TNFRSF4
KDR;FYN;EPHB2;JAK2;ROS1;JAK3;EPHA4;BDNF;INSRR;LIF;NGF;MERTK;

0
CH;AIM2;IRAK1;TRAF3;DDIT3;TLR9;CYP1B1;NLRP3;CD200;HAVCR2;CMK
LGALS3;MAPK8;CASP8;MYO1C;IFNG;BCL2;AKT1;FYN;EPHB2;BID;TP53;
;NPEPPS;ADAMTS13;CASP8;ANPEP;CASP3;CASP1;CTSH;OLR1;NLRP1;
RC;CD8A;LEP;LEPR;CD28
NA2;ABL1;RAC2;IL12B;IL12A;CCR7;EPHB2;TGM2;EPHA4;IL18;PRKCA;PT
CH4;TET2;PRDX3;BMP4;IL3;PTPRC;IFI16;KDR;KAT8;CD34;TP53;SH2B3;A

L2RB;CCL2;F2RL1;CD47;GAS6
T1;TNFSF11;CD47;CD44;JAK1

VCR2;EOMES;PRNP;CDKN2A;KLF4;FOXP3;NR0B2;ESR1;BMP7;SIRT1;S
I16;TNIP1;CCL5;CD28;PKN2;PPARA;IFNL3;FKBP6
X4;FYN;FCGR1A;GAS6
AP1A;IFNG;MTNR1B;IL1B;ALOX5;CCL5;CLOCK;STX1A
;APOE;CCL19;B2M;SNCA
RLR;CYP17A1;CYP27A1;CYP27B1;CYP2C9;SHH;CYP2B6;AMACR;CYP24
16;IRAK1;STING1;TRAF3;IRF1;IRF8;CTNNB1;IRF5;STAT6;CD14;GAPDH;

CR2;CCR9;LBP;CCR6;CCR5;CCR3
XN2;EDNRB;AGTR1;AKT1;APOE
D19;BCL2;MS4A1

SPD1;HSPA1A
2L2
FBR1;VEGFA
POC1;TIMP2;LEPR;BCL2;AKT1;TIMP3;TIMP1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

;TNF;CX3CL1;CASP8;KAT5;MYC;RIPK1;DNM1L;PPARGC1A;CD74;DMTN;

EPHA4;CD74;HSP90AA1;TGFB1;XRCC5;ADIPOQ;INSRR;MERTK;KLF4;PL

1;HAVCR2
;CD226;B2M;MAP3K7
22;LILRB1
ACTG1

K11;KAT5;APOE;SNCA;HSP90AA1;MSN;APOA1;IGF1;TNFRSF1B;IRGM;D
2;IGF1R;ZFP36L1;PIK3CA;ERBB3;RPS6KB1;TYRO3;AKT1;FGFR1
;PSMB8;PSMB9;TIMP2;AKT1;TIMP3;SERPING1;TIMP1;GAPDH;BIRC2;BI

L7;RGS1;CCL5;NTF3;CCL4;CCL3;CCL2;CCR7;CCL1;CCL19;CCL18;CCL1
2;STING1;FLOT1;ABL1;APOE;B2M
NG;IL1B;IL2RB;CD47;GAS6;TGM2;TLR2
D200R1;ALB;AKT1;CCN3;FYN;CD34;PPARGC1A;CD200;HSPA1B;SNCA;A
ALM1;CALM2;SNCA
N1;IL2;TGFBR1;EGFR;CXCL16;INS;ADAM17;BCL2;AKT1;MAPT;S100A9;F
NA;PTX3;APOE;CRYAB;LDLR
;PSMD7;PSMD4;BAG3;DDIT3;UBC;HMOX1;TP53;ATF3;ATF4;HSPA1A;NF
4
R2

ITGAL;THBS1;ICAM1;ADAMTS13;CDH1;ADAMTS1;BSG;KDR;SPP1;ITGAX
1;HMOX1;TIMP1;DRD2;EPHA4;CD74;JAG1;IGFBP3;ADIPOQ;NOG;MIF;MC
SP8;AKT1;NLRP3;CCN3;RIPK1;DRD2;SH2B3;STAT1;CAV1;ADIPOQ;MAP
;BSG;TIMP2;FLOT1;TIMP1;TPSAB1;A2M;CD44
;BSG;TIMP2;FLOT1;TIMP1;TPSAB1;A2M;CD44
RAF1;NAIP;CD44;SNCA
MAP3K5;NFE2L2
TNFRSF1A;SIRT3;IL6;IFNG;RPS6KB1;SP1;CASP3;BCL3;CD28
CTB;IFIH1;PSMB6;YY1;PSMD7;PSMD4;MYC;UBC;NLRP3;RIPK1;MAP3K7;

FBR1;BMP2;DLG5;CTNNB1;FGFR1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

1A
TG1
;GAS6;CX3CL1
;INS

GRG1;CNR2;RGS1;CNR1;GNA11;ADGRG6;S1PR1;OXER1;S1PR3;S1PR2;

;CLIC1;VCL
TING1;IL23A;IL12B
PS;PSMD7;PSMD4;MYC;UBC;LMNA;HMOX1;BMP7;SIRT1;SIRT2;MTOR;P
FR;DLK1;DLL4;ZMIZ1;AKT1;CCN3;IL6ST;CD46;WNT1;TP63
6;RAF1;NAIP;CD44;SNCA
AP;WNT1;TGM2;CMKLR1;WWOX;TGFB2;AHSG;NOG;EIF2AK3;IGF1;BMP
C;CASP1;TNFSF10;NLRP3;FYN;MAP3K5
6;IFNG;IL1B;CTNNB1;B2M;WNT3;TGM2

F1;DUOX2
P1
FA

;CCR2
RG;APOE
;MFN2;PPARG
PRC;AXL;IL21R;IL12B
K5;TGM2;CHGB;FBXW4;IGFBP1;CISH;PRKCB;PRKCE;IGFBP3;PRKCA;B
;IL1B;DDIT3;APOC1;TLR4;IL18R1;ATF4
S1;IFI16;TNIP1;CCL5;PTX3;IFNL3;MBL2

1;PSMB6;YY1;PSMD7;PSMD4;MYC;UBC;NLRP3;RIPK1;MAP3K7;IL33;SMA

;PRNP;TGFB1;DMTN;IGFBP3;CAV1;ADIPOQ;NOG;SIRT2;SMAD7;OCLN;C
ITGAL;THBS1;ICAM1;ADAMTS13;CDH1;ADAMTS1;BSG;KDR;SPP1;ITGAX

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

JA1;CCN3;TGFB2;SMAD4;TGFB1;SPHK2;CDKN2A;SIRT1;ESR2;PML;BST
T;BMP4;APC;PRKAR1A;SMPD1;IL1B;ABL1;AKT1;APOE;SH2B3
SOD1
R;INS;STK11;IL6;OAS1;MTNR1B;ALOX5;LEPR;PPARG;PPARGC1A
FLNA;TLN1;CLIC1;VCL
OD1;PRDX3;ERBB3;AXL;KDR;TYRO3;MAPT;EPHB2;ROS1;HLA-DRB1;FG
IT1;PPARG;APOE
R1A;IL10;CD163;GPBAR1;GCG;MAPK14;POMC;ADCYAP1;ADAM17;IL6;M
TM;TP53;TP73;BCL2L1
BR1;BMP2;DLG5;CTNNB1;FGFR1
;SOX2;CEACAM1;RGCC;ALOX5;KRIT1;APOE;B2M
P2;GRK2;RGCC;P2RX4;IL1B;DNM1L;STX1A;SNCA
1;P2RX7;TRPM2;HRH1;RAP1A;P2RX4;P2RX3;CDH1;WT1;P2RY2;P2RY1;
R1A;IL10;CD163;GPBAR1;GCG;MAPK14;POMC;ADCYAP1;ADAM17;IL6;M
3;WNT1;IL6ST;TP63
HBS1;TGM2
1;CCN3;PRSS3;LGALS8
D200

P4;IL6;RAP1A;IFNG;MTNR1B;IL1B;ALOX5;CCL5;CCN3;CLOCK;STX1A
TPRC;ERBB3;MDK;CDH1;PLXNA2;CYP1B1;EPHB2;WNT1

Y1;CXCR2;C3AR1;AGTR1;F2RL1;DRD2;VIP;TGM2;CMKLR1

1
MB6;STK11;PSMD7;CDH3;PSMD4;ADGRA2;MDK;GPC5;APOE;TRPM4;IG
1;GAS6;TP53

2;BIRC3
2A;MYO1C;PIK3CA;ELMO1;ABL1;MAPK1;FYN;FCGR1A;CRK

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

THBS1;TNF
;PIK3CG;ADA
POE;A2M;CD34
P2;ALOX5
TP63;DAXX;PRKCB;SOX10;AR;PRKAR1A;DDIT3;CLOCK;TP53;ATF3;ATF4
I16;TNIP1;CCL5;IFNL3
4;ADAM17;PTPRC;JAK3;MS4A1
RAK1;ERBB3;NCAM1;FYN;TIMP1;CD177;IGFBP1;PRNP;TGFB1;IGFBP3;A
BCL2L1

;SPRED2;BMP2;IL6;RGCC;MDK;IL1B;CTNNB1;EZH2

VEGFA;LGALS3;CLDN3;RGCC;IFNG;FLOT1;BAX;SDC1;BID
EPPS;RGCC;MYC;LMNA;HMOX1;P4HB;TP53
T1;RTN4;ESR2;PML;BST2;CYP27B1;STK11;GJA1;MAG;WT1;CCN3;TP53;
F;AGER;GRM1;BCR;GRM4;GRM7;IL1B;NTF3;EIF4EBP2;DRD2;HCRT
;XIAP;PARK7;BCL10;BRCA1;TGFBR1;MALT1;SMAD7;TRAF6;AKT1;BIRC2
2;F2RL1;PPARG;GAS6;SH2B3

FP36L1;VEGFA;BMP5;SOX2;BMP4;NR4A1;MYC;LEP;B2M

1;SNCA
GFA

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

D200

IL6;OAS1;MTNR1B;ALOX5;LEPR;PPARG

MP12;ERBB3;SMPD1;HMOX1;HPSE;RAF1

PK8;KAT5;IFI16;CASP3;LEPR;ABL1;AKT1;KAT8;DNM1L;IL10;IL10RA;HGF

;PTN;RBPJ

T3;ABL1;BCL2;CYP1B1;BAX;ATM;CD24;TP53;MAP3K5;ATF4;TP73;BCL2L

1;CXCR2;ACKR3;SNCA

;CST3;TIMP2;AKT1;TIMP3;SERPING1;TIMP1;GAPDH

NFKBIA;IL1A;PSMD7;PSMD4;IRAK1;IL1B;TRAF6;UBC;MAP3K7;MYD88

PZ;EPHB2;NOG;LIG4;NRG1;NGF;SOX10;TGFBR1;NINJ1;TYRO3;HAP1;N

;PSMB6;MAPK8;PSMD7;PSMD4;PIK3CA;GRAP2;TRAF6;BTK;MAPK1;CAL

MYO1C;PIK3CA;ELMO1;ABL1;MAPK1;FYN;FCGR1A;CRK

TF3;FGFR1

;PSMB6;MAPK8;PSMD7;PSMD4;PIK3CA;GRAP2;TRAF6;BTK;MAPK1;CAL

MYO1C;PIK3CA;ELMO1;ABL1;MAPK1;FYN;FCGR1A;CRK

A;BMP5;SMAD7;BMP4;BMP2;AMH

PJ;NR3C1;NR3C2;PPARGC1A;VDR;NR1H3;NR0B2;ESR1;GTF2H4;ESR2;N

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

OLR1;SERPING1;LPA
AB;HAMP;TLR2;SNCA
MB8;PSMB9;PSMB6;PSMD7;PSMD4;FCGR1A;B2M
CL1;SMAD7;BST2;CLDN5;SHH;CLDN3;CDH1;DLG5;CYP1B1;DRD2;CRK;V
SPA1A
S1;AIF1

B;BMP7;SIRT1;TGFBR1;SMAD7;BMP5;RGMA;BMP4;CLDN5;BMP2;ZMIZ1;
APOC1;FYN;CD34;GLA
BCL3;CAT;AKT1;IL12B;SDF4;IL12A;ERCC5;TP53;ATF4
MP7;SIRT1;THBS1;SIRT2;EGFR;PML;IL4;BMP4;AR;SOCS1;CCL5;CD24
AGT

R1;SMAD7;SPRED2;ADAM17;BMP2;UBC;CCN3;PPARG;WNT1;PPARA;HS
3;SALL1;PSMD4;ADGRA2;GPC5;TRPM4;TGFB1;EGF;CAV1;ATP6AP2;NF

1

P1

;THBS1;BMP7;TGFBR1;BMP5;BMP4;STK11;ADAM17;BMP2;JAK2

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

M17;LEP;BCL2;AKT1;S100A9;FXN;S100A8
4;CLDN5;BMP2;MAPK8;STING1;FLOT1;AKT1;BAX;B2M;CRK;GAS8
D1;ADCYAP1;CEACAM1;RAP1A;PTPRC;AKT1;CCR7;CCL19;GAS6;TRIB2;
TLR4;IL18R1;ATF4

D7
W;MC1R;MYC;SMPD1;TIMP1;TP53;ATF4

R;INS;NFKBIA;IL6;CASP8;RPS6KB1;BCL3;AGTR1;CD28;AKT1
MP4;APC;CCL5;CCN3;CRYAB;HSPA1B;ATG5;SNCA;HSPA1A

3;INS;ARNTL
LF4;TGFBR1
MB8;PSMB9;PSMB6;PSMD7;PSMD4;FCGR1A;B2M
NX;HLA-DPB1;HLA-DRA;HLA-DOA;CTSE;HLA-DQA2;HLA-DQA1;HLA-DRB
L1B;APOE;SH2B3

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

EF5;MAP3K5
R;INS
D11;NECTIN2

;TIMP2;AKT1;TIMP3;SERPING1;TIMP1;GAPDH
RP1;PIK3CG;ADGRG1;F2RL1;JAK2

LM1;FXN;CALM2;HAMP;SNCA
FAS;F2RL1;LGALS9
S3;AR;SACS;RAF1;CRYAB;HSPA1B;HSPA1A
2;MYC;SMPD1;ATM;TP53;CLOCK
SART3;CDH1;MYC;PCBP1;FLOT1;APOE;LDLR;KDM6A;TCF19;IL10;SORT
TNFRSF1A
SPA1A

1B1;RIPK1;TP53;SNCA

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

ND1;MYC;ALKBH1;ABL1;CTLA4;TP53BP1;BID;WNT1;MICA;PARP1;XRCC
ELA;ZFP36L1;NR4A2;NR4A1;CEACAM1;RPS6KB1;PRKAR1A;AKT1;PPAR
GS2

XCR2;ACKR3;SNCA
P5;SMAD7;BMP4;BMP2

17;PIK3CA;ERBB3;CDC37;AKT1;MAPK1
MKLR1;TRPM4
CTSH;RREB1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

;HLA-DPB1;HLA-DRA;HLA-DOA;CTSE;HLA-DQA2;HLA-DQA1;HLA-DRB1;H
CL2;AKT1;SNCA
VEGFA;PSMB6;PSMD7;PSMD4;UBC;NFE2L2
L;KDR;ELMO1;PRKD2;FYN;CRK
0A8;BCL2L1
ALM1;CALM2;SNCA

A
;THBS1;ERN1;DDIT3;BCL2;FLOT1;BAX;P4HB;TP53;ATF3;MAP3K5;ATF4

M17;BMP2;ITCH;MDK;MYC

FLNA;DNM1L;PPARGC1A;CD74;DMTN;GSN;TGFB1;FANCC;TRAF2;TRAF

M;AGT;MTOR;GFAP;STK11;CEACAM1;ITCH;RAP1A;AGTR1;ABL1;APOE;S
;SLC25A4;RAB3GAP1
LA-DRB1
SMB8;ARNTL;PSMB9;PSMB6;PSMD7;CDH3;PSMD4;ADGRA2;WNK1;GPC

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

GFAP

Y6E
P53
MALT1;SMAD7;TNIP1;TRAF6;BIRC2;BIRC3
X5;PDCD1;CD34;SH2B3
SPAST;P2RX3;MIP;NINJ1;HPRT1;TP53BP1;B2M;CARD11;TRPM4;ASIC1
LN;APC;IL2RB;FAS;DNM1L;TP53;PPARGC1A;VAMP2;SKAP2
GFR;TRPM2;MT2A;MAPK8;P2RX4;CDH1;SMPD1;AKT1;MAPK1;B2M;SNCA

FB

WT1;AGTR1;CTSH;REN

R1;BMP5

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

CB;NTN1;SHH;ALCAM;BSG;KIF5A;RAC2;PLXNA2;MAPK1;NCAM1;FYN;EP
5;SMAD7;BMP4;BMP2;AMH
POE;CD24;ABCG4;LDLR
SHH;SALL1;MDK;WT1
DAMTS1;TFDP3;AKT1;CCL2;PTPN6
MB6;ITCH;PSMD7;PSMD4;ABL1;TP73
6;MUC1;PSMD7;TYROBP;PSMD4;TRAF6;FYN;CLEC4E;RAF1;MAP3K7;CA
6;MUC1;PSMD7;TYROBP;PSMD4;TRAF6;FYN;CLEC4E;RAF1;MAP3K7;CA
P7;ZFP36L1

GFR1
POE;CD24;ABCG4;LDLR
CL10;CXCL11;S100A12;S100A9;GAPDH
;HLA-DRA;HLA-DOA;CTSE;HLA-DQA2;HLA-DQA1;HLA-DRB1;HLA-DQB2;H

R11;STK11;BMP2;SHH;SALL1;CASP8;TH;PIK3CA;ERBB3;WT1;PDLIM7;K

L4;STK11;KAT5;IFNG;STING1;KDR;MAP3K7
TNFRSF14;LBP;IL6R;TLR4

;AGTR1;REN

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

2RL1;DSG2;TLN1;NECTIN2;CD177
M2;PIK3CA;MDK;RAC2;FSCN1;ABL1;CRK;ARHGEF5
;PSMB9;PSMB6;ITCH;PSMD7;PSMD4;ABL1;TP73

6;MUC1;PSMD7;TYROBP;PSMD4;TRAF6;FYN;CLEC4E;RAF1;MAP3K7;CA
PJ;NR3C1;NR3C2;PPARGC1A;VDR;NR1H3;NR0B2;ESR1;GTF2H4;ESR2;N
P5;BMP2;FGFR1
1;NOS1
;FGF23;TP63;ATF4;TRPM4

T2

D7

;EPHA4;HSP90AA1;SYVN1;APOA1;IGF1;IRGM;SMAD7;TYROBP;CREB1;
MB6;ITCH;PSMD7;PSMD4;ABL1;TP73
GF1R;FGFR1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

A

A1A

H;SALL1;WT1;KDR;TIMELESS;PPARG;JAK2;CD34;VCL;WNT3
1;SPP1;ABL1;EIF4EBP2;CTSH;RIPK1;TIMP1;APOE;FGF23;CHGB;IGFBP1;

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

ANP32B;GAS6;WNT1;IL17D
MP7;PRDX3;BMP4;OCLN;MAPT;EPHB2;PPARA
GSM3;MFN2;ARHGEF2;EPHB2;JAK2;RAF1
S

M;FXN;HAMP
1;BMP5;APLN;VEGFA;WDR11;BMP4;BMP2;SHH;SALL1;CASP8;TH;ERBB3
4;CCL5;CCL3;TRPM7;FYN;TRPM8;CCR5;GAS6;MS4A1;TRPM4
AK2;CRK;RREB1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

1;LGALS9;MAP3K7;MAP3K5
CCL7;CCL5;CCL3;CCL1;CCL19;CCR2;SNCA
;C9ORF72;ACTB;SHH;BSG;KIF5A;MAPK1;NCAM1;FYN;EPHB2;DRD2;SPG
B1

AZ;GLIS3;RORA;RBPJ;NR3C1;NR3C2;PPARGC1A;RREB1;GTF2I;XBP1;P

6;SOCS3;COP1;PSMD7;LGALS1;PSMD4;SPP1;APOE;TIMP1;FGF23;CHG
;FLNA;MAPT;SNCA
RL1;DNM1L;TLR4;TLR2

CA2;NR3C1;HIF1A;RELA;ELAVL2;ARNTL;INS;SOX2;ZMIZ1;TBX21;ABL1;M
ERN1;STK11;IRAK1;KDR;TYRO3;ABL1;AKT1;PRKD2;RIPK1;ATM;JAK2;FG
SMAD7
3;TP73
2;VAMP2;CCR2
RL1;ARHGEF2;APOE;RAF1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

1;OCLN;F2RL1;CCR7;MAPT;APOE
;DAXX;ZBTB38;FOXP3;POU5F1;TGFBR1;DDIT3;CLOCK;TP53;ATF4;FOXC
;CLDN5;MAG;CEACAM1;CDH3;ALCAM;CDH1;MPZ;CEACAM5;BSG;PECA
MB9;PSMB6;PSMD7;PSMD4;SP1;PPARG;APOE;DHCR7;PPARA;LDLR;CE
S3;CRYGD;WT1;KDR;AKT1;PPARG;IRF6

8;AKT1;BAX;B2M
;CYP2C19;PTGS2;PTGES
FA

CN1;F2RL1;CCR7;CCL19;WNT1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

PKN2;TLN1;VCL
B1;RARA;AKT1;PKN2

Z;KIF5A;MAPK1;KIF1B;MBP;APOE;HCRT;DRD2;SPG11;SNCA;NQO1;SYT
CAM1;RPS6KB1;LEP;AKT1;PPARG;VAMP2
;AIF1;ADGRG1;RAP1A;GRAP2;SGSM3;CFL1;ELMO1;AGTR1;RAC2;TP53;

P;SOD1
TLR4

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

BMP2;PPARG;WNT1
RT1;TGFBR1;ZFP36L1;SMAD7;CLDN5;ZMIZ1;UBC;MAP3K7

T1;FLNA

CASP1;YME1L1;CTSH;PRSS3;FXN;METAP2

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

GRG1;ADGRA2;APOD;PHGDH;MBP;CIC;EOMES;ARNT2;GSN;MOG;STAT
NRNPA1;KLF4
;VAMP2;SNCA
YD88;MBL2;TLR2
1B1;APOE;DHCR7;LBR

P5

;MAPK1;ATM;MAPT;CRYAB;ATF3;HSPA1B;ATF4;HSPA1A
MAD7;CLDN5;ZMIZ1;UBC;MAP3K7

BMP2;PPARG;WNT1
PHB2;BCL2L1
GAS8
B1;SNCA;TRPM4

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

ML
NB1;DRD2;TGM2

MW;IL1B;CD28;PKN2;DRD2

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

;SMAD7;TRAF6;BIRC2;BIRC3
CL12;CCL7;CCL5;CCL3;CCL1;CCL19;CCR2
ALM3;CALM1;TRIB2;CALM2;EZH2;SNCA
8;INS;PSMB9
1;HNRNPA1;FGF23;CD44;FGFR1
;PSMD7;RGCC;PSMD4;APC;TFDP3;CCL2

FAP;INS;ITCH;APC;FLNA;VIP
;POLG2;YME1L1;TSPO;MFN2;BAX;HAP1;DNM1L;BID;PPARGC1A;SLC25

AGT
;CALM3;NOS1;CALM1;CALM2
B8;PSMB9;SOX2;PSMB6;STK11;BMP2;PSMD7;PSMD4;APC;MDK;DDIT3;A

;EDNRB;AKT1;APOE;GAPDH

G;ADAMTS1;ABL1;CD47
5;KCNMA1;CCL3;CCL1;CCL19;CCR2
4
PK8;GRK2;RPS6KB1;WNK1;AKT1;MAPK1;PRKD2;RIPK1;ATM;PKN2;GAS
NG;APC;IL1B;APOE;VIP
SMB8;ZFP36L1;PSMB9;PSMB6;PSMD7;PSMD4;APEX1;UBC;AKT1;VIP;HS

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

RA;CTSH
2;CCL7;CCL5;BCL2;CCL3;BAX;CCL1;CCL19;CCR2
1A;PSMB8
CN

4;HAP1;APOE;GAPDH
R;MAPK8;IFI16;ALB;MAPK1;FAS;PPARA;HNRNPA1;TP53;MAP3K5;ATF4;A

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

CC;GLI1;PSMB8;PSMB9;SOX2;PSMB6;STK11;BMP2;PSMD7;PSMD4;APC
;LCN2;HMOX1;FXN;HAMP
6;PLAAT4;PLA2G7;PLB1;ENPP2

;CCL3;FYN;TRPM7;CCR5
D6;AKT1;BAX;JAK2
MP2;CD2AP

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

RYAB;HSPA1B;HSPA1A

1;ATG5

CA
R4A1;BMP2;APC
L;MS4A1;CARD11;HLA-DRB1;SNCA
E;SIGLEC1;CD34;VCL;CD44
11;ADAM17;UBC;IL17F;PPARA;HSPA1A

B2;SNCA

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

;PSMB9;PSMB6;PSMD7;PSMD4;APEX1;UBC;AKT1;HSPA1A
PK1;MAPT;S100A9;CRK;S100A8;ARHGEF5

L1;CCR7;CCL27
G6;PLA2G7;MTOR
ARG;DHCR7;PPARA;CERS2
6;CYP1B1;SDC1;GPC5;APOE

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

ADGRA2;LEP;CFL1;HMOX1;CTNNB1;MAPT;HTATIP2

MP2;SLC6A4

B1
1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

;IL6;GRM7;NPY;STMN1;NTF3;PLP1;APOE;MAPT;EPHB2;SGK1

BCL2L1

GS2

L1;INS;CEACAM1;APC;RPS6KB1;AKT1;PPARG;VAMP2
B7;LBR;NR0B2

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

51;CCL7;MDK;MYC;CFL1;CCL3;CCL2;APOE;DNM1L;PPARGC1A;GABPA;

SPA1A;NFE2L2
6;PSMD7;CHAF1A;SART3;PSMD4;UBC;ERCC5;PADI4;ANP32B

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

RKCA;IQGAP1;SIRT1;PSMB8;PSMB9;PSMB6;PSMD7;PSMD4;RPS6KB1;P
;AKT1;TRIB2;SNCA
3;ATF4

P3;KDR;AKT1;MAP3K7;GAPDH

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

T1;C9ORF72
4;PTGS2

APK8;GRK2;RPS6KB1;WNK1;AKT1;MAPK1;PRKD2;ATM;PKN2;GAS6;SGK

SMB9;PSMB6;ITCH;COP1;PSMD7;PSMD4;KAT5;DDIT3;TBX21;CTNNB1;C

A

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

SR;PSEN1;SOD1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

TOR

MAPK1;MBP;HCRT;SPG11;SNCA;SYT1;GAD1;GAD2;PRKAR1A;MTNR1B;

;ACTG1

I2;PADI4;EZH2

YP17A1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

CD;PLA2G4A;PIK3CB;PLAAT4;PLB1;PIK3CG;MTOR;INPP4B;PTPRC;PIK3

T;STMN1;NLRP5;UBC;RAC2;CYP1B1;NEFL;RIPK1;B2M;SNCA;TGFB2;GS

K11;KAT5;AKT1;ATM;SGK1;TP53;TP63;TP73

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

ALL1;CTNNB1;LGR6;TLR2

A

4

1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

L23A;TP53;STX1A;CTR9;EBI3;GATA3;HIF1A;IL22RA2;HMOX1;HLA-DQA2;
6R;IFNAR2;IL4R;IFNA17;HGF;PRLR;IL23A;FSCN1;IL6ST;TP53;STX1A;IFN
XP1;ADAM17;TYROBP;IL23A;DDIT3;PRKD2;CD226;IL6ST;CARD11;ATF4;
;PRKCB;HGF;F2R;ADIPOQ;MIF;IL23A;DDIT3;PRKD2;S100A9;TP53;S100A
OX15;LPL;SPATA2;GATA3;MEFV;PLA2G7;S100A12;NLRP3;RIPK1;APOE;
H1;NLRP3;CD14;TAC1;CCR1;TGFB1;SELE;NFKB1;IL4;CXCL10;CXCL11;B
;PRLR;YME1L1;IL6ST;RAF1;TP53;NAIP;ATF4;NOTCH2;PXT1;PSMD10;GL
CE2;CLDN5;ADAM17;CLDN3;AGTR1;TIMELESS;IL6ST;RAF1;TP53;CSF1R
RB2;RTN4;CYP27B1;NLRP5;TRPM8;APOE;TP53BP1;HCRT;PPARGC1A;R
SMD10;NOTCH1;GLO1;MAZ;AGAP2;PSEN1;PRDX3;PRDX2;PRDX5;IRAK
K2;IFNGR1;ADIPOQ;MIF;MMP8;FOXP1;TLR1;IL1A;TYROBP;OAS1;IFNG;I
N5;CLDN3;TYROBP;MYCN;TP53;ATF4;NOTCH1;MAZ;PIK3R3;PHB;PSEN1
;SLC11A1;RPS6;F2R;PRKCA;PRLR;AR;CLDN5;ADAM17;MIP;PRKD2;IL6S
F4;AIRE;EPAS1;GATA3;BCL10;HIF1A;SEC14L2;PCBP1;APOE;TP53BP1;P
BP;MYCN;TP53;ATF4;NOTCH1;MAZ;PIK3R3;PHB;PSEN1;HIF1A;PPARGC
KD2;RAF1;TP53;CSF1R;CEMIP;AGAP2;PIK3R3;TXN;IQGAP1;AGER;RAS
CD200R1;TYROBP;IFNG;IL1B;TLR9;TLR8;TLR7;ARHGEF2;CD47;GAS6;TL
;FCRL3;F2R;PRKCA;MIF;MMP8;ADRA2B;ADCYAP1;TLR9;CHI3L1;PRKD2
TB38;SLC11A1;HGF;FOXP3;AR;ADCYAP1;MYCN;DDIT3;PRKD2;ERG;CL
2;PRDX5;IRAK1;BAG3;UBC;RIPK1;WNT1;XBP1;CDSN;TSLP;HSPA5;DHC
DAM17;IL6ST;CSF1R;NOTCH1;MAZ;TGFA;PHB;TNFRSF11A;MST1R;PRD
JAK2;IL10;SLC11A1;F2R;PDCD1LG2;TNFRSF1B;FOXP1;IL1A;ADAM17;TR
TPN11;MMP8;IL17RA;TLR1;IL1A;IL6;MAVS;TYROBP;IFNG;IL1B;POU2AF1;
FNG;IL23A;TLR9;ARHGEF2;TLR4;TLR3;TLR2;LPL;NOD2;BCL10;PSEN1;T
PHB2;ICOSLG;DAXX;ZBTB38;SLC11A1;MIF;FOXP3;FOXP1;AR;ACE2;CL
5;IRF6;CD47;TLR4;GAPDH;HLA-DQB2;CD44;TLR2;HLA-DQB1;CCL13;CCL
1;AR;AIM2;DDIT3;IL1B;TRAF6;BTK;TLR9;PRKD2;PPARG;ARHGEF2;CLO
VCR2;IL33;SPHK2;DDX58;IFNGR1;STAT3;PTPN11;MIF;MMP8;TLR1;IL1A;
D47;IL6ST;S100A9;TLR4;S100A8;TLR3;TLR2;PTGER4;GRN;LPL;PLA2G7;
FRSF1B;SIRT1;TNFRSF1A;ADAM17;AIM2;TRAF3;TRAF6;LTA;CHI3L1;TN
;CD276;CD74;ANXA1;VCAM1;IL15;FCRL3;IL18;PDCD1LG2;MIF;IL2;IL4;IL6
9;CCL19;JAK3;CCR2;HLA-DPA1;CD276;XBP1;ANXA1;VCAM1;IL15;PDCD1
;CD47;S100A9;TLR4;S100A8;TLR3;TLR2;PTGER4;GRN;LPL;PLG;CD1D;P
R;ANXA1;DDX58;SLC11A1;APOA1;PDCD1LG2;MMP8;FOXP3;CD200R1;S
RHGEF2;IL6ST;GAS6;TP53;CD44;CSF1R;SOCS3;ERBB3;CCL5;NTF3;AB
1LG2;TNFRSF1B;IL1A;TRAF6;IL1B;TLR4;CX3CR1;CD274;GSTP1;CTR9;B
BP;CCR5;TGM2;IL10;MMP3;GPBAR1;PDCD1LG2;FOS;TNFRSF1B;MMP9;
STAT3;KLF4;TLR1;IL6;MAVS;PTPRC;IL1B;DDIT3;LEP;BCL3;TLR9;TLR8;C
100A9;TLR4;S100A8;TLR3;TLR2;PTGER4;GRN;LPL;CD1D;PLA2G7;DDT;C
AM17;IL6;MAVS;OAS1;IFNG;IL7;IL1B;TLR9;F2RL1;TLR7;IL17F;TLR4;TLR
A1;VCAM1;IL15;IL18;PDCD1LG2;IGF1;IL2;IL4;IL6;PTPRC;CD40LG;IL23A;I

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

1;HGF;F2R;PRKCA;MMP9;TGFBR1;ADAM17;CLDN3;IFNG;IL1B;PECAM1;
EACAM1;IL1B;CHI3L1;PRKD2;GAS6;TLR4;ARHGEF5;CD44;NOTCH2;CCL
C11A1;SPHK1;ADIPOQ;PRKCA;TRAF6;IL1B;CHI3L1;IL6ST;CSF1R;CD274;
PIK3CA;CHI3L1;GAS6;CX3CR1;MAZ;TGFA;MST1R;PHB;TXN;GATA3;LRP2
GAX;CYP1B1;CTSH;CD34;CCR3;CCR2;HTATIP2;GTF2I;PRKCB;SPHK1;PR
ARG1;LILRB1;PDCD1LG2;TNFRSF1B;FOXP3;HLA-G;IL4;IL6;PTPRC;CD40
-G;SIRT1;TGFBR1;PIK3CA;DDIT3;CHI3L1;GAS6;PPARA;CX3CR1;MAZ;TG
P9;TGFBR1;ADAM17;CLDN3;IL1B;PECAM1;CSF1R;GRN;CEMIP;SEMA7A;
;DDIT3;CLOCK;TP53;ATF4;NOTCH1;KMT2A;AIRE;NOTCH4;MAZ;BCL10;G
2;S100A9;CLOCK;TLR4;S100A8;CARD11;TLR2;CX3CR1;PLA2G1B;BCL10
B;DDIT3;LEP;TLR9;TLR8;CHI3L1;F2RL1;TLR7;PRKD2;IL17D;TLR4;TLR3;H
HB2;EPHA4;EDN1;ANXA1;MMP7;DDX58;SPHK1;HGF;F2R;ADIPOQ;NOG;
11A1;IL18;LILRB1;PDCD1LG2;HLA-A;FOXP3;IL23A;AXL;IL1B;DDIT3;TLR9;
1A;TRAF6;IL1B;TLR4;TLR2;CX3CR1;CD274;GSTP1;CTR9;BCL10;NOD2;R
F;INSRR;ADIPOQ;MIF;SIRT1;MMP9;AR;ADAM17;CLDN3;IFNG;IL1B;TYRO
SF1R;CCL13;SEMA7A;NOTCH1;CCL11;ALOX15;PHB;TNFRSF11A;NOD2;
;TGFBR1;ERN1;IL1B;PRKD2;CD226;HAP1;GAS6;IL6ST;GAS8;TLR2;NOTC
XP1;CD40LG;IFNG;IL23A;TLR9;TLR8;IRF5;CD47;TLR4;TLR3;TLR2;IL17A
;NLRP1;CCL19;JAK2;GHSR;EGR1;F2R;STAT3;APOA1;IGF1;FOXP1;P2RX
P;CD40LG;IL23A;TLR9;CD28;F2RL1;CD47;CD46;TRIB2;TLR4;HLA-DRB1
-F;FOXP3;HLA-G;FOXP1;NCR1;CD200R1;TYROBP;CD8A;TRAF3;IRF1;CD
1B;FOXP3;FOXP1;ACE2;IL1A;IFNG;TRAF3;IRF8;CD47;GAPDH;CRP;PTGE
PHK2;GPBAR1;PDCD1LG2;TNFRSF1B;AR;IL1A;CREB1;IL1B;TRAF6;TLR4
CX3CR1;PTGER4;PLA2G1B;CXCR5;LPAR2;CXCR4;LPAR3;ITPR3;CXCR6;
L4;CCL3;S100A12;CCL2;CCL1;CCL19;CCL18;CCL17;CD177;EDN1;TGFB2
7;RIPK1;TNFRSF14;JAK2;TNFRSF4;TNFSF14;TNFRSF12A;TNFSF15;STA
L4;CCL3;S100A12;CCL2;CCL1;CCL19;CCL18;CCL17;EDN1;TGFB2;ANXA1
CR4;CCR3;TRPM4;CCR2;CCR1;P2RY12;PRNP;EDN1;VCAM1;DMTN;CCL
L4;CCL3;S100A12;CCL2;CCL1;CCL19;CCL18;CCL17;EDN1;TGFB2;CCL22
IGFBP3;NOG;F2R;NGF;FOXP3;SIRT2;SSTR4;AR;IL1A;CLDN3;DDAH1;IFN
CL;PSMD12;IQGAP1;PSEN1;CFP;PLD1;C3;TRPM2;RAP1A;S100A12;CD14
OTCH1;NOTCH4;GATA3;PHB;KNG1;RTN4;CYP27B1;ADGRG1;PLXNA2;D
;PTPN11;MIF;IGF1;AGT;VEGFA;IL3;GH1;IL6;IL5;PTPRC;IL23A;PECAM1;P
TLR7;TLR4;TLR3;TLR2
CR4;CCR3;CCR2;TRPM4;CCR1;P2RY12;EDN1;NOS2;NOS3;SPHK1;EIF2
PIK3CA;IFNG;IL1B;IRF1;DDIT4;ELMO1;LTA;TNFRSF25;RAF1;GAPDH;TLR
A;HLA-F;HLA-G;PML;OAS1;IFNG;IRF1;HLA-DPB1;IRF8;HLA-DRA;IRF5;IR
2;TNFRSF1A;VEGFA;IL4;IL3;GH1;IL6;IFNG;IL23A;IL6ST
OLR1;CTSH;PRSS3;B2M;CD177;HSP90AA1;ANXA2;ARG1;AHSG;SLC11A
;F2R;SELE;SIRT2;FOXP1;SELP;ADAM17;IL6;IL1B;TLR9;IRF5;CD24;S100A
OLR1;CTSH;PRSS3;B2M;CD177;HSP90AA1;ANXA2;ARG1;AHSG;SLC11A
FNB1;LILRB1;SIRT1;IL2;PTPRC;IFNG;IL23A;TLR8;HLA-DRA;F2RL1;CD226

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

H;CD34;CCR3;JAK1;XBP1;S100A1;PRKCB;NOS3;TNFSF12;SPHK1;VEGF
L17;HLA-DPA1;SNCA;CD74;CCL22;CCL21;CCL20;STAT1;SLC11A1;BST2
P2RX7;IL6;TYROBP;AIM2;IFNG;TLR8;F2RL1;TLR4;MYD88;IL17A
;IL3;GH1;IL6;IFNG;IL23A;IL6ST
AM17;CLDN3;IFNG;IL1B;PECAM1;GAS6;CSF1R;HDAC3;PIK3R3;TXN;AGE
DIPOQ;SIRT1;MMP9;ADAM17;CLDN3;IFNG;IL1B;PECAM1;GAS6;ATF3;AT
;CCR1;CCL22;CCL21;CCL20;CXCL10;CXCL11;CXCL12;WNK1;ACKR3
ROBP;AIM2;IFNG;TLR8;F2RL1;TLR4;MYD88;IL17A
;TRAF2;TNFRSF10A;IGF1;TGFBR1;BMP5;IL4;BMP4;IL1A;AR;IL1B;BCL2;F
T1;DCN;AGT;SELP;GH1;PIK3CA;LEP;F2RL1;PTPN6;FGFR1
BP3;ADIPOQ;RPS6;NGF;SIRT1;SIRT2;TGFBR1;DDIT3;TRAF6;KCNMA1;IR
;CCR1;CCL22;CCL21;CCL20;CXCL10;CXCL11;CXCL12;WNK1;ACKR3
TRAF1;TNFRSF1A;IL3;PTPRC;IFNG;IL7;AXL;CDC37;PTPN6;GAS6;CD24;B
CCR9;BDKRB1;CCR8;CCR7;S1PR3;CCL1;CCR6;DRD2;TAC1;CCR5;CCR4
;MMP8;BMP7;NFKBIA;IL23A;IL1B;TRAF6;BCL3;TLR9;CD27;TLR7;TLR4;TL
LA-DPB1;TLR8;F2RL1;TLR7;CD226;TLR4;TLR3;IL18R1
3;XBP1;PRKCB;NOS3;TNFSF12;SPHK1;VEGFB;PRKCA;SIRT1;VEGFA;IL1
;IFNG;CTNNB1;PPARG;VIP
F;NOS3;PRKCA;MAPK14;SIRT1;AGT;FOXP1;VEGFA;BMP4;ADAM17;P2R
;NOS3;SLC11A1;F2R;STAT3;SELE;ESR1;FOXP1;SELP;GH1;ADAM17;CY
D74;CCL21;TNFSF14;IFNB1;IFNA17;MSN;FOXP3;IL2;IL4;PTPRC;CD8A;LE
DAM17;CREB1;PRKAR1A;TYRO3;PPARG;PPARA;PTGER4;GRN;MACIR;P

A;TNFRSF1B;NGF;TNFRSF1A;IL4;P2RX7;IFNG;BCL2;FAS;BAX;CD27;TLR3

NOTCH2;NOTCH1;PTH;HDAC1;PSEN1;HIF1A;DLL4;ATXN2;CCL3;APOE;L
K2;CCR2;P2RY12;ANXA1;AHSG;IL37;CAV1;F2R;SELE;FOXP1;CAMKMT;A
;PPARG;IRF5;MASP1;CLEC4E;TLR4;CFB;TLR3;TLR2;BLK;CRP;CX3CR1;P

;SNCA;ANXA1;CCL22;CCL21;CCL20;PRKCA;SELE;NFKB1;IL1B;TRAF6;C
D27;TLR7;TLR4;TLR3;TLR2
F15;CAV1;FCRL3;F2R;ATP6AP2;FN1;LIF;OSM;IGF1;MMP8;ADRA2B;YWH

SPHK2;IGFBP3;RPS6;NGF;SIRT1;IFNG;TRAF6;KCNMA1;IRF5;ARHGEF2;
;CXCL10;ADAM17;IL6;CXCL12;F2RL1;GAS6

BCL2;MZB1;ATM
1;TGFB1;EGF;ADIPOQ;SIRT1;IRGM;VEGFA;GH1;ADAM17;RGCC;IFNG;IL1
OSM;IGF1;SIRT1;DCN;AGT;SELP;GH1;CEACAM1;PIK3CA;LEP;F2RL1;PT
;ZGPAT;FST;ZBTB38;ADIPOQ;FOXP3;SOX10;FOXP1;AR;DDIT3;TIMELES
SF10A;TRAF1;IGF1;TGFBR1;AGT;PML;IL4;BMP4;AR;FAS;FGFR1
17;RGCC;P2RX4;SP1;PPARG;PRKD2;FGFR1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

TXNRD2;TXNRD1;GSR;CYBB;FANCC;FOS;SOD2;MMP9;SIRT2;SOD1;CR
11;HLA-DQB2;HLA-DQB1;BLK;PSMD10;PSMD12;WAS;BCL10;GATA3;REL
17;IFNG;DDIT3;IL1B;GAS6;TLR4;ATF4;PTGER4;FOXC2;GRN;NOTCH1;PO
PT;TLR4;ATF4
GR1;EDN1;HSP90AA1;CCL21;EGF;HGF;APOA1;NR1H3;IGF1;MMP8;KLF4;
F2;TRAF1;SIRT1;TNFRSF1A;TRAF3;IL1B;TRAF6;TLR9;GAPDH;CARD11;B
L1;CCL19;CCL18;GAS6;CCL17
NFKB1;MTOR;IL4;AR;IL6;RGCC;IFNG;RPS6KB1;IL1B;BCL3;CD28;TLR9;PR
LE;AGT;VEGFA;IL4;NFKBIA;ACE2;GH1;AHI1;IFNG;APOC1;AGTR1;PPAR
P1;CCL3;CYP1B1;CCL2;TGM2;P2RY12;EGR1;TGFB1;DMTN;IL18;MSN;GP
;BIRC2;BIRC3;PHB;NLRC4;RTN4;MALT1;PRDX2;NTF3;ABL1;RIPK1;BID;S
KAR1A;DDIT3;PRKD2;CLOCK;TP53;ATF3;ATF4;AIRE;EPAS1;SP140;CTR
ST2;CXCL10;MAVS;IL6;PTPRC;OAS1;STING1;IRF1;DDIT4;BCL2;TLR9;TL
B2;HSP90AA1;ACE;CCL21;XRCC5;SLC11A1;IRGM;AGT;VEGFA;ADCYAP
HCR24;FOS;TNFRSF1B;HLA-F;SORL1;CD200R1;TYROBP;IFNG;DDIT4;M
;RIPK1;CCL1;CCL19;JAK2;CCL18;CCL17;CCL22;CCL21;CCL20;SPHK1;AD
IL4;BMP4;TYROBP;IFNG;GPR183;RARA;F2RL1;PPARG;HLA-DRB1
MAVS;IL6;PTPRC;OAS1;STING1;IRF1;DDIT4;BCL2;TLR9;TLR8;F2RL1;TLR
R9;TLR8;CTNNB1;IRF5;TLR7;TLR4;GAPDH;TLR3;MYD88;TLR2
;TLR4;HAVCR2
T1;HMOX1;PRKD2;FGFR1

7;SELE;FOXP1;ACE2;TRAF3;IRF1;AGTR1;BIRC2;MYD88;PTGES;BIRC3

F10A;TRAF2;NRG1;IGF1;PRLR;ADRA2B;MTOR;VEGFA;IL4;TPX2;PRKAR1
H3;KLF4;SORL1;AGT;NFKBIA;ITCH;APC;IL23A;IL1B;AGTR1;TLR9;PAEP;I
1;EGF;ADIPOQ;BMP7;SORL1;AGT;VEGFA;BMP4;GH1;IL1B;CD24;TRIB2;F
A1;NRG1;PIK3CA;IL1B;RAF1;PTGER4;PSMD10;PSMD12;TGFA;RASGRP1
FSF12;MST1;VEGFB;PRKCA;IGF1;SIRT1;TGFBR1;BMP5;VEGFA;BMP4;M
;IRF5;IRF6;XAF1;MYD88;IFNAR1
;IRF5;IRF6;XAF1;MYD88;IFNAR1
HAVCR2

H1;CYP24A1;STING1;IL1B;CTNNB1;TLR3
5;CLDN3;MYCN;IFNG;MAPT;CD46;GAPDH;PTGER4;NOTCH2;NOTCH1;P
IL6R;CCL17
D4;TGFB1;ANXA1;HGF;SPHK1;PTPN11;MAPK14;KLF4;BMP7;TGFBR1;SI
G;HLA-DQA1;CD276;HLA-DPA1;HLA-DRB5;MOG;TRAT1;HLA-A;BTNL2;NF
SRR;MST1;CYBB;NRG1;NGF;PRLR;MMP9;SIRT2;PIK3CA;CD8A;DDIT4;TY
B;AGTR1;PPARG;ARHGEF2;IL6ST;FOXC1;LPL;PTN;ARNTL;ZFP36L1;INS;
PRKCE;PRKCA;MMP9;AGT;MTOR;FOXP1;VEGFA;BMP4;IFNG;PRKD2
BMP4;NR4A1;ADAM17;BMP2;SP1;AGTR1;PRKD2;VIP;FGFR1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

N;TNFSF15;F2R;EIF2AK3;TNFRSF10B;TNFRSF10A;TRAF2;NGF;SIRT1;FA
R;CAV1;ADIPOQ;IL13;IL18;PRLR;VEGFA;IL4;ADCYAP1;FABP4;IFNG;APC;

8;TLR7;S100A9;TLR4;S100A8;TLR3;BIRC2;MYD88;TLR2;BIRC3
DIPOQ;IL13;IL18;PRLR;VEGFA;IL4;ADCYAP1;FABP4;APC;LEP;LCN2
;VEGFA;NR4A1;CXCL12;AGTR1;ACKR3;ACKR2
VEGFA;GH1;TRAF6;TLR9;CD24;ARHGEF5;FGFR1;EZH2
GF;SOD2;SORL1;SOD1;MAG;CD200R1;TYRO3;BCL2;NAIP;CD200;ATF4

;TP53;ATF3;ATF4;PSMD10;NOTCH1;NOTCH4;MAZ;CTR9;GLIS3;GATA3;P
;VEGFA;IL6;IFNG;PRKD2;GAS6;RAF1;CD44
PC;DDIT4;MAPT
SIRT2;SOD1;PIK3CA;CAT;NOX4;FAS;NOX5;ATM;HSPA1B;ATF4;NFE2L2;

CL19;MAP3K7;CD74;CCL21;PRKCB;F2R;ADIPOQ;TNFRSF10B;TRAF2;S1
4;ADAM17;PTPRC;CD40LG;GPR183;BTK;BCL2;MS4A1
B1;IL37;SPHK1;STAT3;IL18;PTPN11;KLF4;TGFBR1;STING1;RPS6KB1;TR
AVCR2
SF4
SOD1;MAG;DDIT3;TYRO3;BCL2;BAX;CTNNB1;NAIP;ATF4

FB;APOA1;IGF1;VEGFA;SOD1;SELP;MMRN1;ALB;PECAM1;SERPING1;TL
APT;APOE

CCL1;CCL19;CCL18;MAP3K7;CCL17;EGR1;CCL22;CCL21;CCL20;NFKB1;P

9;CD47;CX3CR1;NOTCH3;LRP1;RGS14;MAZ;GATA3;NTN1;THBS1;EGFR
;RALBP1;CCL22;CCL21;CCL20;F2R;APOA1;ADCYAP1;BMP2;TBC1D2;SG
;AGT;FOXP1;VEGFA;BMP4;CEACAM1;PRKD2
TK;IFNG;IL1B;IL2RB;BAX;CD47;GAS6;SGK1
F2;TLR4;TP53
S2;SLC11A1;PLA2G2A;HLA-A;IRGM;SELP;ADAM17;MAVS;IL6;OAS1;IL23A
R1;VEGFA;BMP4;NR4A1;BMP2;RGCC;LEP;PRKD2;VIP
XN;MAP3K5;NFE2L2
L2L1

1;FZD4;FST;MST1;BMP7;SIRT1;SORL1;DCN;BMP5;VEGFA;BMP4;AR;BM

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

NGF;FAS;BAX;PPARG;MAPT;ANP32B;S100A9;S100A8

100A8;BCL2L1
EGF;HGF;ANXA5;FN1;VEGFB;APOA1;IGF1;VEGFA;SOD1;SELP;MMRN1;

CL2;FXN;HSPA1A;BCL2L1

TB38;ADIPOQ;NRG1;SIRT1;FOXP3;SIRT2;FOXP1;ZEB1;IFNG;DDIT3;TRA

H;SPHK2;CDKN2A;SPHK1;SIRT1;AGT;ESR2;IL2;TGFBR1;PML;MTOR;BS

;NR1H3;KLF4;SIRT2;TNFRSF1A;IL4;ITCH;CLDN3;TYRO3;PPARG;PPARA
BCC8;PRKCA;GCG;IGF1;CD2AP;IL1A;IL6;IFNG;MTNR1B;IL1B;CLOCK;ST
DIT4;PRKD2;RAF1;GAS6;CD44
PRKCE;IGFBP3;INSRR;PRKCA;YWHAZ;TGFBR1;BCR;ERN1;CREB1;TYR
;BIRC3

MIP;PRKD2;ATM;CD47;P4HB
EF2;BCL2L1

XX;ZGPAT;ZBTB38;ADIPOQ;NRG1;SIRT1;FOXP3;SIRT2;FOXP1;ZEB1;IFN

MP2;STING1;RARA;PPARG

;GCG;LILRB1;MAPK14;FOXP3;HLA-G;SIRT2;POMC;ADCYAP1;ADAM17;IL

RSF1A;IL4;ITCH;TYRO3;PPARG;PPARA
2

ERTK;ADCYAP1;PTPRC;AXL;TYRO3;MAPT;GAS6;HLA-DRB1;FGFR1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

L10;SARS1;RGCC;CTNNB1;PPARG;IL17F

A;NAIP

L;LEP;MS4A1

2;TRAF3;TRAF6;IL1B;LEP;TLR9;CD27;F2RL1
KLR1;TRPM4

AB1;MMP7;ITGA4;DST;MMP1;MMP2;MMP3;MMP8;MMP9;TGFBR1;DCN;M

CHI3L1;MAP3K7;TLR3;BIRC2;BIRC3

6;RAF1;NAIP;CD44

L17;TGM2;EPHA4;RALBP1;CCL22;CCL21;CCL20;F2R;SOD1;ADCYAP1;TB

;HSPA1A

Q;NOG;NR1H3;PTPN11;BMP7;SIRT1;TGFBR1;SIRT2;SMAD7;BMP5;NFKBI

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

17F;CCR2;GTF2I

SP90AA1;CAV1;MX1;APOA1;LILRB1;SORL1;ALB;CANX;ACKR3;MASP1

N2A;STAT3;LILRB1;DHCR24;MIF;SIRT1;BMP7;SND1;SIRT2;TGFBR1;PML

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

P3;PRKCA;YWHAZ;TGFBR1;BCR;ERN1;CREB1;PIK3CA;RARA;BTK;FAM

P;VEGFA;SELP;IFNG;BAX;RAF1;CRYAB

5
MAVS;MYO1C;IFNG;IL1B;BCL2;ANP32B;GAS6;TP53;VAMP2;TP73
;EPHB2;TLR4;SH2B3

DDX58;EGF;NRG1;CEACAM1;PKN2;RAF1;SGK1;CRK

;ABCA1;ADRA2B;ADCYAP1;CXCL10;CXCL11;MC1R;VIP
X;ATM;ERCC5;TP53;TLR4;MYD88

AF6;IL1B;TLR9;CD27;F2RL1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

GFA;AR;CLDN3;IFNG;BAX

TRAF2;TRAF1;BCR;CEACAM1;PRKAR1A;TRAF3;TRAF6;IL1B;DDIT4;PRKD
7;AR;APC;GNB3;ANP32B;RAF1;CD24;BIRC2;ATF4;FGFR1

AHI1;CD8A;AXL;TYRO3;IL6ST;FGFR1

LR1
TP63;TP73
PRSS3;TPSAB1;CTSE;PGPEP1;MBTPS1;ACE;MMP7;DESI2;MMP1;HGF;M

PN11;VEGFA;CXCL12;MIP;PRKD2;ATM;P4HB
TF4

MAD7;NFKBIA;ITCH;AIM2;TRAF3;TFDP3;DDIT3;TLR9;GAS6;CD200

A1;CYP2D6;CYP21A2;CYP2R1;CYP1B1;TSPO;GC
MYD88

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

FN1;FANCC;TRAF2;TRAF1;PML;CD2AP;TNFRSF1A;P2RX7;OCLN;CXCL1

AAT4;SORL1;POLG2;AXL;TYRO3;CTNNB1;CD200;HLA-DRB1;FGFR1

CN;P2RX7;ITCH;IFNG;AADAC;IL1B;PPARA

RC3

7;TGM2;RALBP1;CCL22;CCL21;CCL20;F2R;ARHGAP24;BCR;ADCYAP1;T

TG5;HSPA1A

XN;S100A8

E2L2

;VCAM1;MMP7;ITGA4;MMP1;MMP2;MMP3;FN1;MMP8;MMP9;TGFBR1;DC
C;SMAD7;BST2;IL4;CLDN5;CLDN3;DLG5;VCL
K14;HLA-G;SIRT1;ESR1;BMP7;MMP9;CD2AP;P2RX7;TNIP1;DDIT3;DLG5;

IL33;SMAD4;DDX58;DESI2;ADRM1;TRAF2;ESR1;PSMB8;TGFBR1;PSMB9

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

S1PR5;CCR3;ABCA1;P2RY12;GCG;ADCYAP1;CXCL10;CXCL11;MC1R;VI

SMB8;PSMB9;VEGFA;RGCC;P4HB;TP53

7;TGFBR1;BMP5;DSPP;BMP2;BMP1;CHI3L1;IL17F;CD44;FGFR1

CR;ERN1;BTK;SPARCL1;PRKD2;PADI4;ERG;TRIB2;PSMD10;PSMD12;PX

D4;TOR1A;DDX58;DESI2;ADRM1;TRAF2;ESR1;PSMB8;TGFBR1;PSMB9;

EACAM1;PTPRC;DDIT4;CALM3;PTPN6;CALM1;TRIB2;CALM2
;VCAM1;MMP7;ITGA4;MMP1;MMP2;MMP3;FN1;MMP8;MMP9;DCN;DSPP;

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

2;WT1;TP53;HSPA1B;HSPA1A

FR1

C1R;CREB1;FCGR2A;PRKAR1A;VIP;HLA-DRB1

CTNNB1

C1R;CREB1;FCGR2A;PRKAR1A;VIP;HLA-DRB1

FBP1;TGFB1;FZD4;EGF;CAV1;NOG;ATP6AP2;DKKL1;MCC;PSMB8;NFKB

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

;L3MBTL3;AIRE;EPAS1;SP140;CTR9;MYNN;TGFA;GATA3;BCL10;HIF1A;S

DIPOQ;SIRT1;FOXP3;ESR1;WDR11;ADCYAP1;IL3;MZB1;CD24;CD46;CRK

HSPA1B;HSPA1A

;HSPA1B;BIRC3;HSPA1A

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

;STAT3;IRGM;SIRT2;DCN;MTOR;GFAP;ERN1;IFNG;DDIT3;LEP;BCL2;ATM

1

AIP;NOTCH2;DCTN1;GSTP1;CXCR4;MST1R;PTN;HMGCR;KLK6;ERBB3;N
M1;MAP3K7;CARD11

M1;MAP3K7;CARD11

R4A2;AR;NR4A1;RARA;PPARG;PPARA

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

CL

UBC;AMH;MAP3K7

PA1A
KB1;PSMB8;PSMB9;BMP2;WNK1;LGR6;TLR2

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

SNCA

1;HLA-DQB2;HLA-DPA1;HLA-DQB1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

1;IGF1;POU5F1;FOXP1;PTPRC;GNB3;ADNP;TP73

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

5;ZBTB38;FANCC;TNFRSF1B;MAPK14;SIRT1;GTF2H4;FANCG;PML;FOXP
G;VAMP2

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

LA-DQB2;HLA-DPA1;HLA-DQB1

1;YWHAZ;PML;CD2AP;VMP1;OCLN;APC;IL2RB;FSCN1;FAS;GAS6;TP53;V

GK1;ROS1;CD177

5;LGR6;TRPM4

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

HB2;PDLIM7;EPHA4;BDNF;PRKCA;PTPN11;VEGFA;CXCL12;PIK3CA;LG

RD11
RD11

LA-DPA1;HLA-DQB1

DM6A

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

RD11

R4A2;AR;NR4A1;RARA;PPARG;PPARA

PER3;CDC37;CRYAB;GAPDH;HSPA1B;HSPA1A

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

MBTPS1;AHSG;MMP1;IGFBP3;MMP2;RPS6;FN1;APOA1;RPSA;IGF1;CP;B

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

;WT1;PDLIM7;KDM6A

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

11;PDLIM7;EPHA4;HSP90AA1;BDNF;PRKCA;PTPN11;S100B;CXCL12;AC

ARP1;VDR;ADRM1;NR1H3;SSRP1;NR0B2;GTF2H4;ESR1;NFKB1;ESR2;NR

B;ATG5;FBXW4;IGFBP1;MBTPS1;CISH;AHSG;IGFBP3;FN1;APOA1;CP;PS

SC;PPARGC1A;RREB1;NCOA2;ARNT2;DAXX;ZBTB38;STAT3;FOXP3;ESR
FR1;HTATIP2

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

1;NOTCH1;AIRE;NR1I2;CTR9;RNF6;PHB;FOXO3;HIF1A;RELA;ARNTL;INS
M1;DSG2;NECTIN2;CD177
RS2

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

1;GAD1;GAD2;SYN3;TH;PRKAR1A;MTNR1B;SNPH;PLP1;PMP22;HAP1;CA

RREB1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

3;ATP6AP2;LIG4;PTPN11;S100B;SOX10;NR4A2;AHI1;DDIT4;HAP1;RAB3G

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

A4;GABPA;BCL2L1

POE

6;SGK1

PA1A

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

TG5

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

;MDK;DDIT3;APOE

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

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CHGA;HACE1;DMTN;TOR1A;DST;PARP1;SORT1;NOS3;CAV1;TWNK;EIF2

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

KN2;TP73

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

1

LOCK;BIRC2;NFE2L2

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

PLP1;PMP22;HAP1;CALM1;KCNK3

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

CA;AKT1;EPHB2;CALM1

N;DST;APOA1;SORL1;TGFBR1;CD2AP;GFAP;BMP1;MYO1C;ELMO1;MAPT

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

HLA-DQA1;STAT5A;CCR1;STAT5B;EGR1;HLA-DRB5;TSLP;TNFSF14;TNF
AR1;CSF1R;SHMT1;EBI3;ALOX15;GATA3;PHB;FOXO3;HIF1A;IL22RA2;ZF
CSF1R;CD274;AIRE;EBI3;LPL;BCL10;GATA3;PHB;HIF1A;AGER;RASGRP
8;CARD11;MAZ;TGFA;BCL10;GATA3;IQGAP1;PHB;MST1R;TXN;ADRB2;A
NLRP1;TSLP;SELE;IL2;IL4;NFKBIA;IL6;CD200;MYD88;IL21;TNFAIP3;CX3C
MP2;IL6;IL9;NOX4;SERPINA3;IL22;CD40;CXCL9;CIITA;CXCL8;IFNA2;ITG
O1;BCL10;PHB;PSEN1;FOXO3;KNG1;RTN4;PRDX3;PRDX2;PRDX5;IRAK1
;NOTCH1;MAZ;TGFA;GATA3;PHB;TNFRSF11A;MST1R;ZFP36L1;PRDX3;
REB1;DECR1;TRPM4;ABCA1;XBP1;TGFB2;SMAD4;TGFB1;TGFB3;VDR;C
1;BAG3;UBC;RIPK1;APOE;WNT1;PPARGC1A;XBP1;TSLP;HSPA5;BDNF;T
L23A;TLR9;RARA;ARHGEF2;CD47;GAS6;TLR4;TLR3;TLR2;CX3CR1;GSTP
;PLD1;HIF1A;RIPK1;PPARGC1A;FGF23;WNT3;EGR1;TGFB1;VDR;FN1;EIF
T;S100A9;S100A8;PSMD10;CSF1R;NOTCH1;MAZ;TGFA;PHB;TNFRSF11A
PARGC1A;RREB1;STAT5B;EGR1;XBP1;JAG1;FZD4;EIF2AK3;LIF;IGF1;NR
1A;FGF23;WNT3;EGR1;TGFB1;VDR;FN1;EIF2AK3;MSN;IGF1;NR0B2;SELE
GRP1;C3;RAP1A;ABL1;RIPK1;TNFRSF14;FGF23;PRNP;TGFB2;SMAD4;TG
R4;TLR3;TLR2;LPL;BCL10;NOD2;AGER;AIF1;HSPD1;MBP;CD74;IL33;XBP
;GAS6;CD44;NOTCH2;CCL13;CSF1R;SEMA7A;CCL11;NOTCH1;ALOX15;
OCK;TP53;ATF3;ATF4;NOTCH3;NOTCH1;KMT2A;AIRE;EPAS1;NOTCH4;G
R24;IGF1;NFKB1;IL2;TNFRSF10D;IL4;NFKBIA;BMP4;AHI1;IL6;IL7;ALB;BC
X3;DPP4;HMOX1;WNT1;FGF23;TRPM4;XBP1;TGFB2;TGFB1;TSLP;TGFB
AF6;IL1B;S100A9;TLR4;S100A8;IFNAR1;CX3CR1;CD274;GSTP1;CTR9;BC
LEP;TLR9;TLR8;F2RL1;TLR7;IL17F;ARHGEF2;IL17D;TLR4;TLR3;MYD88;T
HBS1;AGER;RASGRP1;DDT;CCL3;RIPK1;CD14;CCL19;IL33;STAT3;PTPN1
DN5;CLDN3;TYROBP;MYCN;DDIT3;ADNP;CLOCK;TP53;ATF4;NOTCH2;N
11;PTAFR;AIF1;CCL7;CCL5;CCL4;CCL3;CCL2;NCAM1;CCL1;CCL19;FCGR
CK;TLR4;S100A9;ARHGEF5;S100A8;CARD11;TLR2;CX3CR1;PLA2G1B;BC
IL6;MAVS;TYROBP;PTPRC;OAS1;IFNG;IL23A;TLR9;ARHGEF2;TLR4;TLR
DDT;CCL3;S100A12;RIPK1;CCL1;SNCA;IL33;TSLP;PLA2G2A;OSM;AGT;IL
FRSF25;ARHGEF2;TP53;BIRC2;BIRC3;PSMD10;CCL13;PSMD12;CCL11;T
;PTPRC;CD40LG;IL23A;IL7;IL1B;LEP;GPR183;TLR9;CD28;BCL2;HLA-DPB
LG2;HLA-A;IL4;IL6;PTPRC;CD40LG;IL23A;IL7;IL1B;LEP;CD28;HLA-DPB1;
TN;PLA2G7;THBS1;AIF1;DDT;CCL5;CCL3;S100A12;RIPK1;CCL1;CCL19;S
ARS1;CEACAM1;TYROBP;IFNG;IL23A;DDIT3;TLR9;RARA;TLR8;GAS6;PP
L1;TNFRSF14;FCGR1A;PRNP;CD74;TGFB1;ACE;TSLP;STAT3;LIF;OSM;PT
CL10;NOD2;RELA;MAPK8;IRAK1;CCL5;CCL3;NLRP3;CCL2;CD14;XBP1;T
IL1A;CREB1;IL1B;TRAF6;MAPT;TLR4;TLR2;CX3CR1;CD274;SHMT1;GSTP
HI3L1;F2RL1;TLR7;PRKD2;IL17F;IL17D;TLR4;TLR3;HSPA1B;MYD88;TLR2
CL5;CCL3;S100A12;RIPK1;CCL1;SNCA;IL33;TSLP;IFNB1;PLA2G2A;OSM;
3;TLR2;IL17A
L1B;LEP;CD28;HLA-DPB1;TNFSF9;IL6ST;CD46;CD24

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

ARHGEF2;CSF1R;GRN;CEMIP;SEMA7A;CCL11;NOTCH1;SEMA3A;MAZ;P
13;CSF1R;SEMA7A;CCL11;NOTCH1;RGS14;GSTP1;ALOX15;PHB;NOD2;
CXCR4;TNFRSF11A;MEFV;RELA;RELB;CYP27B1;MAPK8;IRAK1;RIPK1;S
;THBS1;RTN4;EGFR;INS;ERBB3;CD19;CCL3;FYN;CCL19;FGF23;P2RY12;
KCA;HLA-G;SIRT1;DCN;CLDN5;IL1A;CEACAM1;SARS1;IL1B;NINJ1;CHI3
LG;IL23A;IL1B;LEP;DLG5;CD28;HLA-DPB1;TNFSF9;IL6ST;CD46;HLA-DRB
FA;MST1R;TXN;GATA3;PHB;LRP2;THBS1;EGFR;RTN4;INS;ERBB3;CD19
CCL11;NOTCH1;SEMA3A;MAZ;PIK3R3;AIF1;NTN1;THBS1;EGFR;INS;DUO
ATA3;PHB;PSEN1;FOXO3;HIF1A;SEC14L2;APOE;TP53BP1;WNT1;PPAR
;TNFRSF11A;NOD2;NLRC4;AGER;RELA;MALT1;INS;PRDX3;IRAK1;UBC;N
SPA1B;MYD88;TLR2;HSPA1A
PRKCA;MIF;MMP9;TGFBR1;CLDN5;CEACAM1;ADAM17;CLDN3;IL1B;PEC
RARA;HLA-DPB1;TLR8;F2RL1;TLR7;CD226;CD47;GAS6;TLR4;TLR3;IL18R
ELA;MAPK8;IRAK1;NLRP3;CCL2;CD14;XBP1;IL37;NR1H3;LILRB1;MAPK1
3;PECAM1;GAS6;CSF1R;HDAC3;PIK3R3;MST1R;BCL10;PSEN1;HIF1A;AG
AGER;RASGRP1;EGFR;RAP1A;CCL7;DDT;CCL5;P2RY1;CCL4;CCL3;CCL2
H1;NOTCH4;GATA3;PHB;NOD2;HIF1A;KLK6;INS;C3;DLL4;CYP27B1;MGA

7;IL6;TYROBP;AIM2;IFNG;TLR8;F2RL1;TLR4;MYD88;IL17A

226;BIRC2;BIRC3;KLRB1;PLA2G1B;XIAP;CD1D;KIR2DL3;C3;GPR151;KLR
R4;GATA3;INS;IFI16;ALOX5;CD276;IL33;MOG;NOS2;EIF2AK2;BTNL2;MA
;CX3CR1;CD274;GSTP1;CTR9;LPL;BCL10;NOD2;TFPI;RELA;EGFR;MAPK
KNG1;CXCR1;CXCR3;P2RY1;CXCR2;ABL1;S1PR3;CCL1;DRD2;TAC1;TRP
;CCL22;CCL21;CCL20;CXCL10;CXCL11;PECAM1;S100A9;S100A8
T1;TNFRSF9;TNFSF12;TNFSF13;TRAF2;TRAF1;TNFRSF1B;PSMB8;TNFR
;CCL22;CCL21;CCL20;CXCL10;CXCL11;S100A9;S100A8
20;SPHK1;EIF2AK3;SELE;IRGM;SELP;P2RX7;PTPRC;P2RX4;AGTR1;BTK
;CCL21;CCL20;CXCL10;CXCL11;S100A9;S100A8
G;IL1B;IRF1;PPARG;IRF6;RAF1;TP53;GAS8;NOTCH1;GSTP1;PLG;GATA3
;ACE;XRCC5;NFKB1;BST2;IL6;PTPRC;LCN2;HPSE;GPI;SERPINA3;SNAP
RD2;WNT1;ATG5;TGFB2;SMAD4;TGFB1;TGFB3;VDR;EIF2AK3;EIF2AK2;B
TPN6;ARHGEF2;TP53;CD44

AK3;SELE;AGT;P2RX4;DDAH1;AGTR1;BTK;ACKR3;ACKR2
2;NOTCH2;CXCR4;RTN4;HSPD1;ERBB3;NLRP3;RIPK1;CD14;NLRP1;BID;
F6;HLA-DQB2;CD44;HLA-DRB1;HLA-DQB1

1;ATP6AP2;HLA-B;HLA-C;CYBB;MIF;TNFRSF1B;MMP8;MMP9;UNC13D;AP
9;TLR4;S100A8;IFNAR1
1;ATP6AP2;HLA-B;HLA-C;CYBB;MIF;TNFRSF1B;MMP8;MMP9;UNC13D;AP
;IL6ST;CD46;HLA-DRB1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

B;PRKCA;KLF4;SIRT1;VEGFA;IL1A;SP1;IL1B;NINJ1;AGO2;CHI3L1;PRKD2
;IRF8;CD47;TLR4;GAPDH;TLR2

R;RASGRP1;EGFR;ARNTL;C3;PTPA;P2RY1;ABL1;RIPK1;FGF23;CD74;AC
F4;CSF1R;HDAC3;PIK3R3;C9ORF72;AGER;RASGRP1;EGFR;C3;SOCS1;P

AS;ARHGEF2;HSPA1B;HSPA1A;BCL2L1

F5;ARHGEF2;TP53;ARHGEF5;ATF4;PXT1;GRN;BCL10;PSEN1;NLRC4;FO

IRC2;BIRC3
;CCR3;CMKLR1;TRPM4;CCR2;CCR1;EDN1;CAV1;F2R;ATP2B2;ESR1;AD
R3;TLR2

A;SP1;IL1B;NINJ1;AGO2;CHI3L1;PRKD2;ANGPTL4

X4;SP1;PRKD2;FGFR1
P24A1;IL1B;RARA;CTNNB1;PPARG;PPARA;S100A9;TLR4;S100A8;IFNAR1
P;CD28;F2RL1;CD44;ADA
TH;GSTP1;GATA3;ADRB2;MEFV;CRHR1;PTHLH;INS;GNG2;ALOX5;NLRP

;BCL2L1

DLR;CCR1;TGFB2;TGFB1;NOS2;VDR;TRAT1;IGF1;KLF4;NR0B2;ESR1;AIC
CE2;P2RX4;TRAF3;IRF1;AGTR1;F2RL1;CALM1;MYD88;BIRC2;PTGES;BI
LA2G1B;BCL10;PHB;NOD2;CFP;MEFV;AGER;RELA;MALT1;RELB;C3;CY

HI3L1;CD47;MYD88

AZ;P2RX7;BMP2;IL6;CEACAM1;PTPRC;IL1B;LEP;TLR9;FAS;REN;PTPN6;C

TP53;ARHGEF5;ATF4;PXT1;BCL10;PSEN1;NLRC4;FOXO3;KNG1;HSPD1;

B;CALM3;CALM1;CD24;CALM2;FGFR1;EZH2
PN6;FGFR1
S;CLOCK;TP53;ATF3;ATF4;PSMD10;L3MBTL3;NOTCH1;NOTCH4;MAZ;CT

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

YGD;CAT;NOX4;NOX5;MAPT;TP53;HSPA1B;ATF4;NFE2L2;HSPA1A
A;MALT1;PSMB6;CD19;FYN;HLA-DQA2;HLA-DQA1;CD276;HLA-DRB5;MO
N1;GATA3;HMGCR;AGER;EGFR;ARNTL;INS;TGFB1;GDF15;NOS3;NR1H3

SIRT1;MTOR;IL6;RGCC;P2RX4;DDAH1;IFNG;RPS6KB1;SP1;IL1B;BCL3;C
IRC2;BIRC3;GSTP1;BCL10;NOD2;RELA;MALT1;IRAK1;S100A12;HMOX1;

KD2;TLR4;TLR2
G;PPARA;TP53;IFNAR1
BAR1;TRPV1;ESR1;P2RX7;AR;P2RX4;STING1;P2RX3;WT1;IL1B;CTNNB1
TAT1;TNFRSF10C;TNFRSF10B;TNFRSF10A;AGT;TNFRSF10D;CXCL10;A
9;MYNN;TGFA;GATA3;HIF1A;PCBP1;APOE;TP53BP1;PPARGC1A;RREB1;
R8;F2RL1;TLR7;MYD88;TLR3;BCL2L1;TLR2
1;TPX2;GH1;PTPRC;IFNG;IL23A;TRAF6;NOX4;CALM3;CALM1;GAS6;CAL
APT;CD200
DIPOQ;SELE;SIRT1;CHI3L1;ARHGEF2;NFE2L2

7;MYD88;TLR3;BCL2L1;TLR2

A;TRAF6;LEP;CHI3L1;GAS6;TLR3
L17F;VIP;IL17D
GFR1;EZH2
;EGFR;ZFP36L1;PSMB6;MAPK8;ERBB3;CCL5;UBC;CCL3;CCL2;MAPK1;M
MP12;NR4A1;BMP2;PRKD2;VIP

TH;HDAC1;SHMT1;PSEN1;HIF1A;DLL4;CCL3;APOE;CCR1;TGFB2;TGFB1;

RT2;SMAD7;VEGFA;ERN1;BMP4;NR4A1;BMP2;RPS6KB1;CTNNB1;PRKD
KB1;PSMB8;PSMB9;PTPRC;PIK3CA;WNK1;TRAF6;CD28;HLA-DPB1;HLA
RO3;ELMO1;PRKD2;HAP1;CRK;BLK;CSF1R;FOXC2;FOXC1;RGS14;PIK3
RAP1A;ABL1;TRPM4;XBP1;TGFB2;SMAD4;TGFB1;TGFB3;PLA2G2A;IGF1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

S;BAX;PPARG;ANP32B;MAPT;S100A9;S100A8
LEP;LCN2

HB;PSEN1;FOXO3;BAG3;UBC;RREB1;SMAD4;VDR;CAV1;NR0B2;ESR1;N

HSPA1A

00B;TNFRSF1A;BST2;MAVS;TRAF6;TLR9;F2RL1;GAPDH;CARD11;MYD88

AF6;IL1B;CTNNB1;PTPN6;IL18R1

N1;CALM1;GAS6;VCL

SMB8;PSMB9;NFKBIA;IL1A;TRAF6;IL1B;CD47;MYD88

;DLL4;SOCS1;ERBB3;CCL5;APOD;DRD2;SNCA;WWOX;GDF15;BDNF;EG
SM3;F2RL1;CALM3;CALM1;CALM2;CD200;RAB3GAP1;EZH2

;LCN2;TLR9;S100A9;HAMP;TLR4;NAIP;S100A8;MYD88;TLR3;TLR2

P2;BMP1;WT1;DLG5;LEP;AGO2;FGFR1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

ALB;PECAM1;SERPING1;TLN1;CALM1;GAS6;STX1A;VCL;VAMP2

F6;IRF1;RARA;TIMELESS;PPARG;GAS6;CLOCK;CRYAB;TP53;L3MBTL3;N

T2;CEACAM1;ITCH;ADAM17;WT1;AGTR1;BCL2;SGK1;TP53;S100A9;FXN;

;CRK;CERS2
X1A

O3;RARA;BTK;TLR9;FAM20C;PRKD2;TLR7;ERG;GAS6;SGK1;TRIB2;TLR4

G;DDIT3;TRAF6;IRF1;RARA;TIMELESS;PPARG;GAS6;CLOCK;CRYAB;G

6;ITCH;MC1R;CREB1;FCGR2A;PRKAR1A;TYRO3;PDCD1;VIP;HLA-DRB1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

MP12;PECAM1;CD47;GAS6;CD44;TMPRSS6;COL11A2;PLG;THBS1;ADAM

C1D2;WNK1;SGSM3;F2RL1;CRK;ARHGEF5;RAB3GAP1;EZH2

A;BMP4;IL6;IFNG;PPARG;ANP32B;PPARA;TRIB2

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

;ERN1;BMP4;NR4A1;BMP2;PTPRC;RGCC;IFNG;APC;IRF1;LEP;RARA;AT

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

20C;PRKD2;ERG;GAS6;SGK1;TRIB2;RNASEL;PXK;CCL11;MAPK8;GRK2;I

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

2;MAPT;ARHGEF2;SGK1;CRK;TP53;BIRC2;ARHGEF5;BIRC3;HDAC1;XIA

MP2;GZMA;MMP3;GZMB;MMEL1;MMP8;MMP9;MMP12;ADAM17;F9;BMP

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

2;AIM2;STING1;APC;GORASP1;IL2RB;MZB1;CTNNB1;FAS;TP53;VAMP2;

BC1D2;SGSM3;F2RL1;ARHGEF5;RAB3GAP1;EZH2

N;DSPP;MMP12;PECAM1;CD47;CD44

DDIT4;BCL2;PPARA;BCL2L1

;SMAD7;NFKBIA;AR;APC;TNIP1;TRAF3;TRAF6;TP53;BIRC2;BIRC3;OTUB

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

P

K;EPAS1;HIF1A;KNG1;C3;SOCS3;COP1;GRK2;IRAK1;ABL1;APOE;FGF23;

SMAD7;NFKBIA;AR;APC;TNIP1;TRAF3;TRAF6;TP53;BIRC2;BIRC3;OTUB1

MMP12;PECAM1;CD47;CD44

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

1;PSMB9;BMP2;APC;WNK1;DDIT3;CTNNB1;LGR6

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

EC14L2;APOE;TP53BP1;PPARGC1A;RREB1;STAT5A;STAT5B;EGR1;XRC

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

;MAPT;GAPDH

TF3;ADGRG6;MBP;DRD2;ARNT2;JAG1;GSN;TGFB1;MOG;BDNF;STAT3;F

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

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Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

1;APC;TFDP3;DDIT3;APEX1;BCL3;TIMELESS;BCL2;BAX;ATM;TP53;TP73;

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

AMP2;GAS8;SKAP2

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

R6

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

MP4;SARS1;ADAM17;IL6;TNIP1;AGO2;ALB;YME1L1;SPARCL1;FAM20C;P

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

TBL2;PIK3CA;LGR6

4A2;AR;NR4A1;SP1;RARA;INTS4;PPARG;PPARA;ATF4

MB8;PSMB9;BMP4;IL6;ALB;SPARCL1;FAM20C;P4HB;GAS6

1;POU5F1;PML;ESR2;TGFBR1;NFKB2;BMP2;WT1;SP1;DDIT3;SP3;CLOC

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

;ATXN2;TBX21;ABL1;MSC;PPARGC1A;RREB1;ARNT2;STAT3;ESR1;PML;

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

LM1;STX1A;VAMP2;KCNK3

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

AP1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

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AK3;LIG4;FANCG;GEM;SIRT3;VMP1;POLG2;GORASP1;YME1L1;NECTIN2

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

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Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

;ARHGEF2;P4HB

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

SF15;TNFSF12;TNFSF13;FN1;LIF;BST2;TNFSF9;SDC1;CD27;HLA-DRB1;IL
P36L1;SOCS3;SOCS1;IRAK1;UBC;HMOX1;RIPK1;STAT5A;CCR1;STAT5B;
1;C3;IRAK1;HMOX1;NLRP3;RIPK1;MBP;TNFRSF14;CD14;DRD2;CD276;EG
GER;RTN4;IRAK1;CD19;S100A12;HMOX1;RIPK1;CD14;FGF23;KL;TGFB2;
L1;C1QTNF3;MDK;CASP1;JAK2;CCR2;IL10;ANXA1;IL15;AHSG;SPHK1;IL1
B2;PIK3CD;ADM;CXCL1;HMGB1;ITGAL;CXCL2;CX3CL1;CXCL5;PIK3CG;O
;BAG3;UBC;ABL1;RIPK1;WNT1;XBP1;TSLP;HSPA5;TGFB3;TNFRSF10C;T
DPP4;CYP27B1;ADGRG1;DRD2;WNT1;FGF23;TRPM4;STAT5A;STAT5B;X
AV1;EIF2AK2;IL2;IL4;BMP4;GH1;BMP2;IL6;RGCC;BMP1;AGO2;CD28;LCN
GFB3;CAV1;DHCR24;IGF1;NFKB1;IL2;TNFRSF10D;NR4A2;IL4;NFKBIA;B
1;LPL;PSEN1;NOD2;AGER;RASGRP1;THBS1;DDT;CCL3;RIPK1;CD14;CC
2AK3;EIF2AK2;MSN;IGF1;NR0B2;BMP7;IL4;BMP4;OCLN;BMP2;IL6;RGCC
;MST1R;ZFP36L1;PRDX3;DPP4;ADGRG1;WNT1;FGF23;TRPM4;XBP1;TG
0B2;MC1R;AGO2;ATM;HLA-DRB1;TP73;CDKN1C;CD40;IFNA2;BRCA1;BR
;BMP7;IL4;BMP4;GH1;AHI1;OCLN;BMP2;IL6;RGCC;SP1;AGO2;CD28;ATM
FB1;XRCC5;TGFB3;BDNF;CAV1;LIF;IGF1;BMP7;BMP5;BMP4;IL3;GH1;MA
1;TSLP;NOS2;IL37;STAT3;PTPN11;MAVS;IL6;POU2AF1;LEP;F2RL1;PTPN
MST1R;IQGAP1;ADRB2;PHB;NOD2;AGER;RASGRP1;EGFR;INS;RAP1A;IR
LIS3;GATA3;FOXO3;HIF1A;PCBP1;UBC;ABL1;NLRP3;RIPK1;TP53BP1;PP
L3;CD28;BCL2;CD27;MYD88;BCL2L1;HSPB1;CX3CL1;MYDGF;SHH;CASP3
3;TNFSF13;FN1;LIF;IGF1;IL2;BMP5;BST2;IL4;BMP4;IL3;BMP2;IL6;PTPRC;
L10;TNFRSF11A;NOD2;RELA;PRDX3;CYP27B1;MAPK8;IRAK1;NLRP3;CC
LR2;IL17A
1;IL6;MAVS;PTPRC;IL17F;IL17A
OTCH1;AIRE;MAZ;CTR9;PIK3R3;GATA3;PSEN1;PHB;MEFV;HIF1A;ZFP36L
1A;CCL18;HLA-DQA2;CCL17;HLA-DQA1;HLA-DRB5;VCAM1;CCL22;CCL2
L10;TNFRSF11A;NOD2;NLRC4;AGER;RELA;MALT1;INS;PRDX3;IRAK1;U
3;TLR2;IL17A
2;NFKBIA;IL6;TNIP1
NFRSF11B;GATA3;TNFRSF11A;FOXO3;RELA;ZFP36L1;PSMB6;CCL7;CC
1;IL6ST;CD46
CD47;IL6ST;CD46
NCA;P2RY12;IL33;TGFB1;TSLP;CCL21;IFNB1;PLA2G2A;OSM;IL2;AGT;NF
ARA;TRIB2;TLR4;PTGER4;CD274;MACIR;MEFV;AGER;THBS1;TBX21;APO
PN11;IGF1;IL2;AGT;VEGFA;IL4;IL3;GH1;IL6;IL5;PTPRC;NOX4
GFB1;IL37;NR1H3;LILRB1;MAPK14;IRGM;NFKB1;CXCL10;CXCL11;IL6;AX
1;CTR9;LPL;BCL10;NOD2;RELA;EGFR;ZFP36L1;PRDX3;PRDX5;MAPK8;
;HSPA1A
IL2;AGT;NFKBIA;TNIP1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

IK3R3;HIF1A;AIF1;THBS1;EGFR;RTN4;INS;CCL7;MGAT5;CCL5;NTF3;CCL
AGER;RASGRP1;EGFR;RAP1A;CCL7;DDT;CCL5;P2RY1;CCL4;CCL3;CCL2
NCA;CD74;STAT1;IL37;MX1;STAT3;EIF2AK2;PTPN11;SELE;PML;SELP;BS
KL;TGFB1;F10;CCL21;EGF;GDF15;TRAT1;OSM;PTPN11;ESR1;MC1R;P2R
L1;PRKD2;PPARG;ANGPTL4;FOXC1;GRN;HIF1A;THBS1;ALOX5;KRIT1;HM
1;IDO1
;CCL3;FYN;CCL19;DRD2;FGF23;SH2B3;P2RY12;KL;TGFB1;CCL21;F10;G
X1;CCL7;MGAT5;CCL5;NTF3;CCL3;CCL19;DUOX2;CCR1;XBP1;TGFB1;C
GC1A;RREB1;EGR1;SMAD4;TGFB1;FZD4;TGFB3;IGF1;NR0B2;ESR1;BMP
LRP3;S100A12;RIPK1;CAV1;STAT3;EIF2AK2;NFKB1;AGT;NFKB2;NFKBIA

AM1;SGK1;VCL;CSF1R;GRN;CEMIP;SEMA7A;CCL11;NOTCH1;SEMA3A;
1;HLA-DRB1
4;IRGM;NFKB1;CXCL10;CXCL11;IL6;AXL;CD68;MYD88
ER;RASGRP1;THBS1;EGFR;INS;C3;ERBB3;CCL5;P2RY1;ABL1;RIPK1;FG
;CCL1;APOE;CCL19;CCL18;CCL17;CCR1;CD74;TGFB1;CCL22;CCL21;CC
T5;NTF3;FLNA;WNT1;CD74;XBP1;TGFB2;JAG1;DMTN;TSLP;IFNB1;BDNF

K1;CD19;FCGR1A;MICA;LAIR1;CD276;TGFB2;VCAM1;LILRB1;KIR3DL1;IL
PK14;AGT;SOD1;IL6;RGCC;PTPRC;STING1;LEP;CD28;NOX5;IL17F;HLA-D
8;IRAK1;SPP1;NLRP3;CCL2;CD14;WNT3;XBP1;FZD4;IL37;NR1H3;MSN;L
M4;CCR1;GPR17;CAV1;ESR1;P2RX7;P2RX5;P2RX4;P2RX3;P2RX2;F2RL

SF1A;PSMB9;NFKBIA;ADAM17;AIM2;CD40LG;TRAF3;TRAF6;LTA;TNFSF9

;ACKR3;ACKR2

;PHB;AIF1;PTHLH;DLL4;CYP27B1;ADGRG1;LMNA;HMOX1;MFN2;APOD;D
25;SERPINA1;ITGAM;ITGB2;CTSZ;HBB;CXCL1;HMGB1;ITGAL;FCGR3B;TI
MP7;AICDA;ESR2;BMP5;BST2;BMP4;NR4A1;BMP2;IL6;RGCC;DLG5;BCL

TNFSF14;TNFSF12;GZMA;MX1;TNFRSF10B;GZMB;TNFRSF10A;DHCR24;

RT;CEACAM3;CEACAM1;TYROBP;CAT;PECAM1;PADI2;CHI3L1;CD47;DN

RT;CEACAM3;CEACAM1;TYROBP;CAT;PECAM1;PADI2;CHI3L1;CD47;S1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

;ANGPTL4

E;TGFB1;VEGFB;IRGM;VEGFA;BMP4;MAVS;BMP2;LEP;FAS;CDK2AP1;C
2RY1;ABL1;RIPK1;FYN;FGF23;CD74;PRNP;TGFB1;FN1;EIF2AK3;VEGFB;

XO3;KNG1;HSPD1;PTPA;MAPK8;UBC;ABL1;CCL3;RIPK1;BID;SNCA;PRN

CYAP1;AGTR1;F2RL1;ACKR3;ACKR2;CD24

3;FYN;APOE;FCGR1A;CD163;NR1H3;GCG;IGF1;MAPK14;KLF4;IL4;POMC

DA;NFKB1;VEGFA;APLN;BMP4;OCLN;BMP2;AGO2;CD28
RC3;METAP2
P27B1;IRAK1;S100A12;FYN;NLRP1;IFNL3;SNCA;CHGA;CD74;NOS2;MX1;

D24;HLA-DRB1;ARHGEF5;FGFR1

PTPA;MAPK8;UBC;ABL1;RIPK1;BID;SNCA;NOS2;TGFB3;GZMA;DKKL1;TN

R9;GLIS3;GATA3;PSEN1;PHB;FOXO3;PRDX5;UBC;RREB1;SMAD4;TGFB

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

G;TRAT1;BTNL2;NFKB1;PSMB8;PSMB9;PTPRC;WNK1;CD28;BCL2;HLA-D
;MCC;SMAD7;BMP5;IL4;BMP4;BMP2;RGCC;PAEP;IL17D;IL18R1

D28;PRKD2;TLR4
FLNA;RIPK1;CCL19;CD74;CCL21;STAT1;TNFRSF10B;S100B;ESR1;BST2;

PEX1;ALB;BCL3;TNFSF9;FAS;BAX;ATM;PTPN6;ANP32B;TP73
STAT5A;STAT5B;EGR1;XBP1;JAG1;LIF;IGF1;NR0B2;MC1R;AGO2;ATM;H

M2;EZH2

BP;NCAM1;FYN;FGF23;KL;TGFB1;EGF;IGF1;PSMB8;NFKB1;IL2;PSMB9;I

NOS2;VDR;EIF2AK3;EIF2AK2;GZMB;IGF1;KLF4;NR0B2;ESR1;NFKB1;VEG

2;MAPT;CD44
-DRA;PRKD2;CARD11;HLA-DRB1;HLA-DQB2;HLA-DQB1
R3;MST1R;ADRB2;PSEN1;EGFR;INS;ERBB3;NTF3;MAPK1;FYN;HNRNPA1
;MAPK14;BMP7;AGT;NFKB1;MTOR;BMP4;BMP2;IL6;RGCC;CTNNB1;EZH2

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

FKB1;ESR2;SMAD7;NR4A2;IL4;BMP4;BMP2;HAMP;EZH2;CIITA;FASLG;H

;HLA-DRB1;BIRC2;BIRC3

F;AGT;DLK1;BMP5;APLN;NR4A2;BMP2;PTPRC;RPS6KB1;BCL2;EZH2

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

OTCH1;HDAC3;HDAC1;TMPRSS6;NR1I2;GATA3;PHB;RELA;ARNTL;IFI16

HSPA1B;S100A8;HSPA1A

;TLR3;TLR2;BLK;CSF1R;RNASEL;PXK;CCL11;EGFR;MAPK8;GRK2;IRAK1

APDH;TP53;L3MBTL3;NOTCH1;HDAC3;HDAC1;TMPRSS6;SHMT1;NR1I2;G

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

TS13;SPP1;A2M;TGFB2;GSN;TGFB1;VCAM1;FN1;DSPP;BMP1;P4HB

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

M;IRF6;TP53;BIRC2;TP73;BIRC3

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

RAK1;ABL1;CCL2;MAPK1;FYN;TGFB2;TGFB1;STAT3;EIF2AK3;EIF2AK2;M

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

P;AGER;EGFR;RELA;MAPK1;A2M;MYO9B;SSRP1;MAPK14;MTOR;PML;A

1;YME1L1;LCN1;REN;METAP2

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

SKAP2

1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

ATG5;TGFB2;TGFB1;FN1;EIF2AK3;EIF2AK2;CP;BMP4;BMP2;IL6;PTPRC;

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

C5;FZD4;IGF1;NR0B2;HLA-DRB1;SLC2A4RG;EZH2;TP73;CDKN1C;BTG1;

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

N1;MERTK;S100B;VEGFA;IL3;AHI1;P2RX5;GJB1;APC;AXL;PMP22;RBM45

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

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BCL2L1;OTUB1

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ADI4;IGFALS;P4HB;GAS6

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

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K;TP53;SLC2A4RG;ATF4;EZH2

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

ESR2;NFKB2;BMP2;WT1;SP1;SP3;SLC2A4RG;EZH2

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;RAB3GAP1

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21;IL22;CD40;IFNA1;IL25;IFNA2;IL27;TNFRSF13C;CX3CL1;IL18BP;TIMP1
EGR1;XBP1;TGFB1;VCAM1;FN1;LIF;NFKB1;IL2;IL4;CXCL10;IL3;IL6;CXCL
R1;XBP1;TGFB1;TSLP;XRCC5;EIF2AK3;EIF2AK2;NFKB1;IL2;NFKB2;IL4;
TGFB1;TNFSF14;CAV1;FN1;LIF;EIF2AK2;TNFRSF10B;IGF1;ESR1;BST2;S
3;MMP3;IL18;APOA1;IL16;MMP8;TNFRSF1B;MMP9;IL17RA;TNFRSF1A;C
LR1;CCR7;CCR5;CCR3;CCR2;ANXA1;IL18;FOS;TNFRSF1A;TLR1;IL1A;IF
NFRSF10B;TNFRSF10A;DHCR24;IGF1;NFKB1;IL2;TNFRSF10D;IL4;NFKB
BP1;TGFB2;JAG1;TGFB1;TSLP;XRCC5;TGFB3;VDR;TNFRSF9;TNFSF13;F
2;NOX5;EZH2;IL21;ACHE;BMPR2;PIK3CD;PRL;ADRA1A;PIK3CG;C1QTNF
MP4;AHI1;IL6;IL7;ALB;BCL3;BCL2;CD28;CD27;MYD88;BCL2L1;ITGB1;HSP
L19;IL33;IL37;STAT3;LILRB1;PTPN11;IGF1;IL4;POMC;MAVS;IL6;MC1R;PT
;SP1;AGO2;BCL3;CD28;NOX5;ATM;MYD88;NFE2L2;IL21;CXCL8;PIK3CD;
FB2;TGFB1;TSLP;TGFB3;CAV1;TNFSF13;FN1;LIF;IGF1;IL2;BMP5;IL4;BMP
CA2;GLI1;CX3CL1;MYDGF;SHH;CD38;GABPA;HTATIP2;IL10;NCOA2;IL11;
;MYD88;NFE2L2;CXCL8;PIK3CD;PTPN22;BRCA1;PIK3CB;VSIR;ITGAX;CT
VS;BMP2;IL6;PTPRC;IL5;CALM3;CALM1;CALM2;HLA-DRB1;CD40;BMPR2
6;IL17F;IL17D;CD200;MYD88;IL17A
AK1;CCL7;DDT;CCL5;P2RY1;CCL4;CCL3;S100A12;CCL2;CCL1;APOE;CC
ARGC1A;RREB1;STAT5B;EGR1;XBP1;TGFB2;SMAD4;JAG1;TGFB1;VDR;
;CD38;CTSH;HTATIP2;IL10;ANXA1;GPX4;SPHK1;ANXA5;NGF;SIRT1;MM
IL7;IL9;BCL2;HPSE;IL7R;EZH2;FGFR1;IL21;LAMC2;PRL;GLI1;CX3CL1;CX
L2;CD14;SNCA;XBP1;NOS2;NOS3;IL37;NR1H3;LILRB1;MAPK14;SELE;IR

1;PCBP1;ABL1;APOE;MSC;PPARGC1A;FGF23;RREB1;WNT3;CD276;CCR
1;CCL20;STAT1;PML;HLA-DPB1;HLA-DRA;HLA-DRB1
BC;S100A12;NLRP3;RIPK1;TP53BP1;WNT1;PPARGC1A;FZD4;CAV1;STAT

L5;CCL4;CCL3;TNFRSF17;CCL2;RIPK1;TNFRSF14;CCL1;CCL19;CCL18;C

KBIA;TNIP1;F2RL1
D;TIGIT;PRNP;IL37;FN1;LILRB1;KLF4;MAVS;IL6;ITCH;RGCC;PTPRC;AXL

L;CD68;MYD88
RAP1A;GNG2;IRAK1;P2RY2;P2RY1;NLRP3;CCL2;MAPK1;CD14;WNT3;P2

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

3;RREB1;CCR1;XBP1;TGFB2;DMTN;TGFB1;F10;HSPA5;EGF;CAV1;STAT
;CCL1;APOE;CCL19;CCL18;CCL17;CCR1;CD74;SMAD4;CCL22;TGFB1;C
T2;BCL2;PTPN6;XAF1;MYD88;IL18R1;BCL2L1
X4;AXL;LEP;CD28;HPSE;FGFR1
OX1;XBP1;TGFB2;STAT1;NOS3;TNFSF12;VEGFB;KLF4;PML;VEGFA;CX

DF15;EGF;TRAT1;OSM;PTPN11;ESR1;MC1R;P2RX4;AXL;LEP;CD28;HPSE
CL21;F10;HSPA5;EGF;CAV1;STAT3;IGF1;SOD2;VEGFA;IL4;BMP2;CXCL1
7;NFKB1;ESR2;IL4;BMP4;BMP2;IL6;SP1;SP3;BCL3;HLA-DRB1;TP73;CDK
;IL6;CD40LG;MYD88;HSPA1B;IL18R1;HSPA1A

MAZ;PIK3R3;FOXO3;AIF1;THBS1;EGFR;INS;CCL7;CCL5;MGAT5;NTF3;LM

F23;CD74;TGFB1;EGF;VEGFB;IGF1;MERTK;IRGM;VEGFA;BMP4;P2RX7;
L20;PLA2G2A;PTPN11;BMP2;PTPRC;GPR183;F2RL1;ACKR3;HLA-DRB1
;NOS3;STAT3;PTPN11;IGF1;SORL1;GH1;BMP2;IL6;PTPRC;MYO1C;AXL;I

4;FCGR2A;CD40LG;HLA-DRA;PDCD1;CD200;HLA-DRB1;NECTIN2
RB1
ILRB1;MAPK14;ESR1;IRGM;NFKB1;CXCL10;CXCL11;IL6;AXL;ATM;CD68;
1;ACKR3;ACKR2;CD24

;CD27;TNFRSF25;TP53;BIRC2;BIRC3

RD2;SH2B3;TGFB2;TGFB1;CDKN2A;TGFB3;VDR;NOS3;OSM;EIF2AK2;M
MP2;ITGAX;OLR1;CTSH;HSP90AA1;ANXA2;ARG1;AHSG;ATP6AP2;TNFR
2;NOX4;ANP32B;CD200;BTG1;BMPR2;CXCL8;CXCL1;ADRA1A;SHH;MDK;

MTOR;NFKBIA;IL2RA;BCL2;PAEP;FAS;BAX;NOX5;MYD88;IL17A;BCL2L1

ASE1;S100A9;VAMP2;S100A8;CD44;VCL;TLR2;GRN;PSMD12;GSTP1;PT

00A9;VAMP2;S100A8;CD44;VCL;TLR2;GRN;PSMD12;GSTP1;PTAFR;PRC

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

ALM3;CALM1;CALM2;HLA-DRB1;RAB3GAP1
BMP7;IRGM;PML;VEGFA;SOD1;BMP4;OCLN;MAVS;BMP2;LEP;FAS;CDK2

P;TGFB2;IFNB1;TGFB3;GZMA;DKKL1;TNFRSF10C;TNFRSF10B;LILRB1;T

;IL6;MC1R;FCGR2A;VIP;CD200;HLA-DRB1

S100B;IRGM;PML;BST2;IL4;CXCL10;MAVS;STING1;LCN2;PTX3;MYD88

FRSF10C;TNFRSF10B;LILRB1;TNFRSF10A;SOD1;BMP4;BMP2;IL6;APC;C

1;XRCC5;VDR;CAV1;NR0B2;BMP7;ESR1;NFKB1;ESR2;SMAD7;IL4;BMP4;

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

PB1;HLA-DRA;HLA-DRB1

MAVS;TNIP1;F2RL1;HLA-DRB1;MYD88

AMP;SLC2A4RG;EZH2;TP73;CD40;BRCA1;GLI1;CX3CL1;MECP2;MYDGF;

L3;IL5;IL2RA;IL2RB;CALM1;BCL2L1;FGFR1

FA;APLN;BMP4;OCLN;BMP2;RGCC;AGO2;CD28;HSPA1B;EZH2;HSPA1A

;FGF23;KL;ANGPT2;BDNF;SORT1;GDF15;STAT3;EIF2AK3;VEGFB;PTPN
;FGFR1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

MGB1;MECP2;SHH;EDN1;NCOA5;PARP1;NOG;SIRT1;SIRT2;POU5F1;SAR

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

;TBX21;ATF7IP;SMAD4;TGFB1;CDKN2A;XRCC5;VDR;MBD2;KLF4;NR0B2;

;ABL1;CCL2;MAPK1;FYN;RIPK1;TGFB2;TGFB1;EIF2AK3;EIF2AK2;MERTK

ATA3;PHB;RELA;ARNTL;IFI16;TBX21;ATF7IP;SMAD4;TGFB1;CDKN2A;X

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

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ERTK;MTOR;BMP2;WNK1;PKN2;ATM;FGFR1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

RHGAP24;VEGFA;NFKBIA;TPX2;BCL3;F2RL1;REN;ATM;CD24;TP73

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

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WNK1;ALB;ATM;FGFR1;SERPINA1;BMPR2;LRRK2;PIK3CD;PTPN22;PHEX

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

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OGG1;IFNA2;BRCA1;BRCA2;GLI1;MECP2;SHH;CD38;CIC;GABPA;HTATIP

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;JAK2;CCR5;JAK3;HLA-DPA1;JAK1;CCR2;IL10;IL11;ANXA1;SERPINB2;AN
12;IL5;WNK1;IL7;LCN2;BCL2;SDC1;BCL2L1;NFE2L2;ITGB1;IL22;CD40;ITG
MAVS;IL6;PTPRC;RGCC;IL7;IL9;CD28;PAEP;NOX5;HPSE;CD200;MYD88;I
ELP;GH1;MAVS;BMP2;IL6;PTPRC;MC1R;DLG5;BCL2;CD28;CD27;HPSE;H
D200R1;IFNG;IL1B;TLR9;TLR7;PPARG;CD47;DNASE1;PPARA;TLR4;VAM
NG;IL1B;CHI3L1;TLR4;CD44;TLR2;PTGER4;CRP;CCL13;CCL11;CXCR4;N
IA;BMP4;CXCL10;AHI1;BMP2;IL6;IL7;ALB;BCL3;BCL2;CD28;TNFSF9;CD2
N1;LIF;EIF2AK2;IGF1;IL2;BMP5;IL4;BMP4;CXCL10;IL3;CXCL11;BMP2;IL6;
3;SHH;MDK;FLOT1;ITGAX;LBP;JAK2;CCR2;IL10;IL15;MST1;IL13;NOG;IL1
B1;CX3CL1;MYDGF;SHH;MDK;CASP3;CD38;CTSH;HTATIP2;IL10;ANXA1;
PRC;PTPN6;IL17A
PTPN22;PIK3CB;BRCA1;VSIR;PIK3CG;C1QTNF3;ITGAX;FLOT1;CTSH;AM
4;IL3;IL6;CXCL12;IL7;IL9;BCL2;ATM;IL7R;EZH2;FGFR1;IL21;SLC44A4;HB
EDN1;PARP1;IL18;TET2;FOS;RGMB;SIRT1;SIRT2;POU5F1;RGMA;MMP12
SH;AMH;CD34;GABPA;ANXA2;IFNGR1;DDX58;IL13;NOG;MMP8;NGF;TGF
;LRRK2;CX3CL1;MYDGF;FLOT1;CCR7;NOS1;JAK2;IL11;HSP90AA1;IL15;

L19;CCL18;CCL17;CCR1;CD74;TGFB2;CCL22;TGFB1;CCL21;CCL20;GDF
TGFB3;LIF;IGF1;ESR1;NFKB1;NFKB2;BMP5;SMAD7;IL4;BMP4;NR4A2;NF
P9;YWHAZ;CEACAM5;TRAF6;CAT;ANGPTL4;GAS6;CRYAB;FXN;CD44;BIR
CL5;MECP2;SHH;MDK;ITGAX;CTSH;TIMP1;IL11;EDN1;IL15;SPHK1;IL18;N
GM;NFKB1;SELP;CXCL10;CXCL11;IL6;AXL;CD68;MYD88

1;EGR1;TGFB2;TGFB1;VDR;FN1;EIF2AK3;MSN;IGF1;BTNL2;NR0B2;BMP

3;EIF2AK2;ESR1;AGT;NFKB1;ESR2;VEGFA;NFKB2;NFKBIA;MAVS;IL6;CD

CL17;CCL22;TNFSF14;CCL21;TNFSF15;CCL20;STAT1;TNFSF12;TNFRSF

;BCL3;F2RL1;PTPN6;CD200;HLA-DRB1

RY12;EGR1;XBP1;DMTN;FZD4;IL37;NR1H3;LILRB1;TRPV1;MAPK14;ESR1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

3;FN1;IGF1;SOD2;MTOR;VEGFA;IL4;BMP2;PTPRC;CXCL12;MYO1C;APC;
CL21;CCL20;PLA2G2A;FN1;PTPN11;BMP2;PTPRC;TNIP1;GPR183;F2RL1;

CL10;IL6;RGCC;SP1;LEP;AGO2;CTNNB1;IL17F

;FGFR1
2;MYO1C;APC;F2RL1;ATM;LGR6
N1C;CIITA;IFNA2;BRCA1;GLI1;BRCA2;SHH;CD38;NOS1;IL10;FOS;RGMB;

NA;PLXNA2;CCL3;FLNA;DRD2;FGF23;CCR1;CD74;XBP1;JAG1;HACE1;AC

MAVS;BMP2;AXL;LEP;FAS;CDK2AP1;HLA-DRB1;FGFR1

L7;DLG5;FAS;BAX;LGR6;IL7R

MYD88

CC;KLF4;SOD2;PML;BMP5;BMP4;BMP2;IL6;RGCC;APC;WT1;DLG5;NOX4;
SF1B;MMP8;MMP9;APRT;CEACAM3;CEACAM1;CAT;PECAM1;CHI3L1;CD
ADAMTS1;NOS1;JAK2;CD34;IL10;SPHK2;APOA1;TNFRSF1B;NGF;SIRT1;

AFR;PRCP;IQGAP1;PSEN1;RETN;CFP;PLD1;C3;CST3;TRPM2;RAP1A;CX

P;IQGAP1;PSEN1;RETN;CFP;PLD1;C3;CST3;TRPM2;RAP1A;CXCR1;ALO

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

AP1;HLA-DRB1

NFRSF10A;SOD1;BMP4;BMP2;IL6;APC;CTNNB1;FAS;BAX;ATM

TNNB1;FAS;BAX;ATM

NR4A2;BMP2;SP3;BCL3;HAMP;EZH2;CDKN1C;CIITA;IFNA2;FASLG;BRCA

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

SHH;CIC;GABPA;HTATIP2;IL11;NCOA2;BRD2;EDN1;NCOA5;PARP1;NOG;

11;IGF1;MERTK;MAPK14;VEGFA;GH1;AHI1;APC;AXL;FGFR1

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

S1;ZEB1;IFNG;TRAF6;RARA;IRF8;PPARG;PPARA;FOXC2;FOXC1;HDAC3

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

BMP7;PML;IL4;BMP4;BMP2;WT1;SP3;BCL3;CTNNB1;EZH2

;MAPK14;GTF2H4;MTOR;SMAD7;BMP4;BMP2;RPS6KB1;WNK1;PKN2;PT

RCC5;VDR;MBD2;EIF2AK3;EIF2AK2;GZMB;KLF4;NR0B2;BMP7;PML;IL4;B

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

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;FCGR3A;TIMP1;JAK2;JAK3;JAK1;BRD2;ANXA1;PARP1;AHSG;APOA1;SI

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

2;IL10;NCOA2;BRD2;FOS;RGMB;SIRT1;SIRT2;POU5F1;ZEB1;IL1B;RARA

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XA2;TNFRSF12A;IFNGR1;GSTO1;IL15;IL13;IL18;IL16;FOS;SIRT1;IL17RC;
AM;CXCL8;IFNA1;ITGB2;IFNA2;PIK3CD;FASLG;CXCL1;PIK3CB;BRCA1;C
L21;CD40;PIK3CD;IL27;PTPN22;BRCA1;HMGB1;PIK3CG;IFIH1;C1QTNF3;
LA-DRB1;MYD88;BCL2L1;FGFR1;ITGB1;CD40;PIK3CD;FASLG;PIK3CB;H
P2;TLR3;BIRC2;TLR2;BIRC3;PTGER4;GRN;MACIR;XIAP;NOD2;PTGS2;US
LRC4;AIF1;THBS1;RELA;RELB;CCL7;CCL5;CXCR2;CCL4;CCL3;CCL2;CCL
7;ATM;ANP32B;MYD88;BCL2L1;TP73;ITGB1;HSPB1;FASLG;HMGB1;CX3C
RGCC;IL7;DLG5;IL9;BCL2;NOX4;IL7R;CD200;EZH2;FGFR1;IL21;CXCL9;B
8;PLAAT4;SIRT1;TGFBR1;IL1A;IFNG;IL1B;HAP1;GAS6;GAPDH;PTGER4;F
SPHK1;ANXA5;NGF;SIRT1;MMP9;YWHAZ;PIK3CA;TRAF6;CEACAM5;CAT

H;CD34;GABPA;IL10;SPHK2;IFNGR1;IL15;DDX58;IL13;NOG;NGF;MMP8;T
B;LAMC2;PRL;GLI1;CX3CL1;CXCL5;MECP2;SHH;MDK;ITGAX;FLOT1;CTS
;IL1B;RARA;TLR9;PPARG;NCOA7;ARHGEF2;PPARA;TLR4;TLR3;TLR2;FO
BR1;IL1A;IFNG;IL1B;TLR9;GAS6;CD46;TLR4;TLR3;TLR2;CRP;INS;DLL4;M
SPHK1;NGF;SIRT1;MMP9;TGFBR1;IFNG;IL1B;PECAM1;CHI3L1;ARHGEF2

15;EGF;PLA2G2A;LIF;OSM;EIF2AK2;PTPN11;IGF1;VEGFA;GH1;BMP2;IL6;
KBIA;CXCL10;AHI1;NR4A1;BMP2;IL6;MAVS;RGCC;MC1R;SP1;AGO2;SP3;
C2;BIRC3;HDAC3;HDAC1;GSTP1;XIAP;LRP2;THBS1;RELA;EGFR;MALT1
RG1;SIRT1;TGFBR1;IFNG;IL1B;RARA;CD47;GAS6;FXN;GRN;HDAC1;PLA

7;ESR1;NFKB1;ESR2;NFKB2;IL4;BMP4;BMP2;IL6;OCLN;RGCC;PTPRC;SP

40LG;RGCC;STING1;CTNNB1;CD200;HSPA1B;IL18R1;MYD88;HSPA1A

9;TNFSF13;PSMB8;PSMB9;NFKBIA;CD40LG;TNFSF9;CD27;NFE2L2

;IRGM;NFKB1;MTOR;P2RX7;CXCL10;CRYGD;CXCL11;IL6;P2RX4;P2RX3;

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

AGO2;F2RL1;ATM;LGR6

ACKR3;PTPN6;HLA-DRB1

TGFBR1;CREB1;IL1B;IRF1;RARA;PPARG;IRF6;PPARA;FOXC2;FOXC1;MY

E;TGFB1;F10;HSPA5;EGF;CAV1;STAT3;IGF1;SOD2;SORL1;VEGFA;SMA

CTNNB1;PTPN6;VIP;CD200;HSPA1B;TP73;HSPA1A

47;VAMP2;CD44;TLR2;GRN;PLA2G1B;GSTP1;PTAFR;PRCP;RETN;CST3;

SIRT2;SSTR4;IL1A;DDAH1;IL1B;IRF1;IRF6;CRYAB;GAS8;TLR2;PLG;PTHL

CR1;ALOX5;CXCR2;S100A12;MAPK1;AGA;CD14;LAIR1;GSN;XRCC5;MAP

X5;CXCR2;S100A12;MAPK1;AGA;CD14;LAIR1;GSN;XRCC5;MAPK14;NFK

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

1;HMGB1;MECP2;SHH;CD38;CIC;EDN1;NCOA5;PARP1;NOG;NRG1;SIRT

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

IL18;TET2;FOS;SIRT1;SIRT2;POU5F1;RGMA;MMP12;ZEB1;RARA;TLR9;A

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

;HDAC1;UHRF1;TMPRSS6;NR1I2;RELA;DLL4;IFI16;CUX1;TBX21;JAZF1;S

Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

PN6;ATM;FGFR1

MP4;BMP2;WT1;SP3;BCL3;CTNNB1;EZH2

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RT1;YWHAZ;SIRT2;TGFBR1;SIRT3;CREB1;RARA;FAM20C;GAS6;SGK1;R

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Supplementary 7. GO enrichment analysis of overlapped genes between MS and urologic diseases

;AHRR;PPARG;NCOA7;PPARA;GAS6;CRYAB;FOXC2;FOXC1;MYRF;TMP

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