

**S3 Table.** Results of Gene Set Enrichment Analysis with differentially expressed genes between PD-L1–high and others groups

<b>Biologic process</b>	<b>The others vs. PD-L1–high</b>
ResBP.Top.BP.n..1.of.2423	GO:0006955~immune response; FDR=1.01e-08; (ng=305); (ncommon=19)
ResBP.Top.BP.n..2.of.2423	GO:0006954~inflammatory response; FDR=6.55e-05; (ng=185); (ncommon=11)
ResBP.Top.BP.n..3.of.2423	GO:0006968~cellular defense response; FDR=1.73e-04; (ng=32); (ncommon=5)
ResBP.Top.BP.n..4.of.2423	GO:0006026~aminoglycan catabolic process; FDR=1.73e-04; (ng=7); (ncommon=3)
ResBP.Top.BP.n..5.of.2423	GO:0006030~chitin metabolic process; FDR=1.73e-04; (ng=7); (ncommon=3)
ResBP.Top.BP.n..6.of.2423	GO:0006032~chitin catabolic process; FDR=1.73e-04; (ng=7); (ncommon=3)
ResBP.Top.BP.n..7.of.2423	GO:0006959~humoral immune response; FDR=5.11e-04; (ng=44); (ncommon=5)
ResBP.Top.BP.n..8.of.2423	GO:0001817~regulation of cytokine production; FDR=5.12e-04; (ng=72); (ncommon=6)
ResBP.Top.BP.n..9.of.2423	GO:0009611~response to wounding; FDR=5.18e-04; (ng=182); (ncommon=9)
ResBP.Top.BP.n..10.of.2423	GO:0007243~protein kinase cascade; FDR=5.74e-04; (ng=187); (ncommon=9)
ResBP.Top.BP.n..11.of.2423	GO:0002455~humoral immune response mediated by circulating immunoglobulin; FDR=5.94e-04; (ng=27); (ncommon=4)
ResBP.Top.BP.n..12.of.2423	GO:0006952~defense response; FDR=8.02e-04; (ng=295); (ncommon=11)
ResBP.Top.BP.n..13.of.2423	GO:0016064~immunoglobulin mediated immune response; FDR=9.46e-04; (ng=32); (ncommon=4)
ResBP.Top.BP.n..14.of.2423	GO:0019724~B cell mediated immunity; FDR=9.46e-04; (ng=32); (ncommon=4)
ResBP.Top.BP.n..15.of.2423	GO:0002250~adaptive immune response; FDR=1.17e-03; (ng=36); (ncommon=4)
ResBP.Top.BP.n..16.of.2423	GO:0002449~lymphocyte mediated immunity; FDR=1.17e-03; (ng=36); (ncommon=4)
ResBP.Top.BP.n..17.of.2423	GO:0002460~adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains; FDR=1.17e-03; (ng=36); (ncommon= 4)
ResBP.Top.BP.n..18.of.2423	GO:0000272~polysaccharide catabolic process; FDR=1.17e-03; (ng=16); (ncommon=3)
ResBP.Top.BP.n..19.of.2423	GO:0045087~innate immune response; FDR=1.17e-03; (ng=64); (ncommon=5)
ResBP.Top.BP.n..20.of.2423	GO:0002443~leukocyte mediated immunity; FDR=1.47e-03; (ng=39); (ncommon=4)
ResBP.Top.BP.n..21.of.2423	GO:0007584~response to nutrient; FDR=2.09e-03; (ng=76); (ncommon=5)
ResBP.Top.BP.n..22.of.2423	GO:0051606~detection of stimulus; FDR=2.15e-03; (ng=44); (ncommon=4)
ResBP.Top.BP.n..23.of.2423	GO:0030198~extracellular matrix organization; FDR=2.25e-03; (ng=47); (ncommon= 4)
ResBP.Top.BP.n..24.of.2423	GO:0031328~positive regulation of cellular biosynthetic process; FDR=2.42e-03; (ng=313); (ncommon=10)

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ResBP.Top.BP.n..25.of.2423	GO:0006935~chemotaxis; FDR=2.42e-03; (ng=80); (ncommon=5)
ResBP.Top.BP.n..26.of.2423	GO:0042330~taxis; FDR=2.42e-03; (ng=80); (ncommon=5)
ResBP.Top.BP.n..27.of.2423	GO:0016485~protein processing; FDR=2.87e-03; (ng=50); (ncommon=4)
ResBP.Top.BP.n..28.of.2423	GO:0042108~positive regulation of cytokine biosynthetic process; FDR=2.90e-03; (ng=24); (ncommon=3)
ResBP.Top.BP.n..29.of.2423	GO:0002252~immune effector process; FDR=3.11e-03; (ng=52); (ncommon=4)
ResBP.Top.BP.n..30.of.2423	GO:0006958~complement activation, classical pathway; FDR=3.32e-03; (ng=26); (ncommon=3)
ResBP.Top.BP.n..31.of.2423	GO:0051604~protein maturation; FDR=3.32e-03; (ng=54); (ncommon=4)
ResBP.Top.BP.n..32.of.2423	GO:0002763~positive regulation of myeloid leukocyte differentiation; FDR=3.32e-03; (ng=8); (ncommon=2)
ResBP.Top.BP.n..33.of.2423	GO:0042116~macrophage activation; FDR=3.32e-03; (ng=8); (ncommon=2)
ResBP.Top.BP.n..34.of.2423	GO:0001816~cytokine production; FDR=3.33e-03; (ng=27); (ncommon=3)
ResBP.Top.BP.n..35.of.2423	GO:0007249~I-kappaB kinase/NF-kappaB cascade; FDR=3.33e-03; (ng=27); (ncommon=3)
ResBP.Top.BP.n..36.of.2423	GO:0009306~protein secretion; FDR=4.02e-03; (ng=9); (ncommon=2)
ResBP.Top.BP.n..37.of.2423	GO:0007626~locomotory behavior; FDR=4.02e-03; (ng=97); (ncommon=5)
ResBP.Top.BP.n..38.of.2423	GO:0009891~positive regulation of biosynthetic process; FDR=4.27e-03; (ng=416); (ncommon=11)
ResBP.Top.BP.n..39.of.2423	GO:0006684~sphingomyelin metabolic process; FDR=4.63e-03; (ng=10); (ncommon=2)
ResBP.Top.BP.n..40.of.2423	GO:0002541~activation of plasma proteins involved in acute inflammatory response; FDR=4.63e-03; (ng=32); (ncommon=3)
ResBP.Top.BP.n..41.of.2423	GO:0006022~aminoglycan metabolic process; FDR=4.63e-03; (ng=32); (ncommon=3)
ResBP.Top.BP.n..42.of.2423	GO:0006956~complement activation; FDR=4.63e-03; (ng=32); (ncommon=3)
ResBP.Top.BP.n..43.of.2423	GO:0031667~response to nutrient levels; FDR=6.22e-03; (ng=73); (ncommon=4)
ResBP.Top.BP.n..44.of.2423	GO:0042035~regulation of cytokine biosynthetic process; FDR=6.22e-03; (ng=36); (ncommon=3)
ResBP.Top.BP.n..45.of.2423	GO:0002761~regulation of myeloid leukocyte differentiation; FDR=6.22e-03; (ng=12); (ncommon=2)
ResBP.Top.BP.n..46.of.2423	GO:0007242~intracellular signaling cascade; FDR=6.56e-03; (ng=456); (ncommon=11)
ResBP.Top.BP.n..47.of.2423	GO:0006468~protein amino acid phosphorylation; FDR=6.61e-03; (ng=218); (ncommon=7)
ResBP.Top.BP.n..48.of.2423	GO:0002274~myeloid leukocyte activation; FDR=6.81e-03; (ng=13); (ncommon=2)
ResBP.Top.BP.n..49.of.2423	GO:0045639~positive regulation of myeloid cell differentiation; FDR=6.81e-03; (ng=13); (ncommon=2)
ResBP.Top.BP.n..50.of.2423	GO:0019058~viral infectious cycle; FDR=7.83e-03; (ng=14); (ncommon=2)
ResBP.Top.BP.n..51.of.2423	GO:0002526~acute inflammatory response; FDR=8.29e-03; (ng=42); (ncommon=3)

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ResBP.Top.BP.n..52.of.2423	GO:0006350~transcription; FDR=8.29e-03; (ng=766); (ncommon=1)
ResBP.Top.BP.n..53.of.2423	GO:0051240~positive regulation of multicellular organismal process; FDR=8.61e-03; (ng=82); (ncommon=4)
ResBP.Top.BP.n..54.of.2423	GO:0051605~protein maturation by peptide bond cleavage; FDR=9.06e-03; (ng=44); (ncommon=3)
<b>Pathway</b>	<b>The others vs. The high-RR</b>
ResPat.Top.Pathway.n..1.of.589	TREM1 Signaling; FDR=1.97e-06; (ng=55); (ncommon=8)
ResPat.Top.Pathway.n..2.of.589	Hepatic Fibrosis / Hepatic Stellate Cell Activation; FDR=1.97e-06; (ng=137); (ncommon=11)
ResPat.Top.Pathway.n..3.of.589	Coagulation System; FDR=1.29e-05; (ng=35); (ncommon=6)
ResPat.Top.Pathway.n..4.of.589	Atherosclerosis Signaling; FDR=1.47e-04; (ng=119); (ncommon=8)
ResPat.Top.Pathway.n..5.of.589	Granulocyte Adhesion and Diapedesis; FDR=1.81e-04; (ng=163); (ncommon=9)
ResPat.Top.Pathway.n..6.of.589	Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses; FDR=1.81e-04; (ng=91); (ncommon=7)
ResPat.Top.Pathway.n..7.of.589	Altered T Cell and B Cell Signaling in Rheumatoid Arthritis; FDR=3.24e-04; (ng=76); (ncommon=6)
ResPat.Top.Pathway.n..8.of.589	Pathogenesis of Multiple Sclerosis; FDR=3.24e-04; (ng=9); (ncommon=3)
ResPat.Top.Pathway.n..9.of.589	Tumoricidal Function of Hepatic Natural Killer Cells; FDR=3.24e-04; (ng=24); (ncommon=4)
ResPat.Top.Pathway.n..10.of.589	Intrinsic Prothrombin Activation Pathway; FDR=5.45e-04; (ng=28); (ncommon=4)
ResPat.Top.Pathway.n..11.of.589	Glioma Invasiveness Signaling; FDR=7.36e-04; (ng=57); (ncommon=5)
ResPat.Top.Pathway.n..12.of.589	Agranulocyte Adhesion and Diapedesis; FDR=7.36e-04; (ng=173); (ncommon=8)
ResPat.Top.Pathway.n..13.of.589	Oncostatin M Signaling; FDR=9.06e-04; (ng=34); (ncommon=4)
ResPat.Top.Pathway.n..14.of.589	IL-10 Signaling; FDR=9.83e-04; (ng=68); (ncommon=5)
ResPat.Top.Pathway.n..15.of.589	Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis; FDR=1.03e-03; (ng=282); (ncommon=10)
ResPat.Top.Pathway.n..16.of.589	Extrinsic Prothrombin Activation Pathway; FDR=1.04e-03; (ng=16); (ncommon=3)
ResPat.Top.Pathway.n..17.of.589	Natural Killer Cell Signaling; FDR=1.09e-03; (ng=105); (ncommon=6)
ResPat.Top.Pathway.n..18.of.589	Leukocyte Extravasation Signaling; FDR=1.21e-03; (ng=192); (ncommon=8)
ResPat.Top.Pathway.n..19.of.589	NF- $\kappa$ B Signaling; FDR=1.48e-03; (ng=157); (ncommon=7)
ResPat.Top.Pathway.n..20.of.589	VDR/RXR Activation; FDR=1.65e-03; (ng=77); (ncommon=5)
ResPat.Top.Pathway.n..21.of.589	LXR/RXR Activation; FDR=1.65e-03; (ng=121); (ncommon=6)
ResPat.Top.Pathway.n..22.of.589	Acute Phase Response Signaling; FDR=1.78e-03; (ng=167); (ncommon=7)
ResPat.Top.Pathway.n..23.of.589	Role of JAK family kinases in IL-6-type Cytokine Signaling; FDR=2.77e-03; (ng=25); (ncommon=3)

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ResPat.Top.Pathway.n..24.of.589	Sphingomyelin Metabolism; FDR=2.77e-03; (ng=7); (ncommon=2)
ResPat.Top.Pathway.n..25.of.589	HMGB1 Signaling; FDR=2.77e-03; (ng=93); (ncommon=5)
ResPat.Top.Pathway.n..26.of.589	Toll-like Receptor Signaling; FDR=2.83e-03; (ng=55); (ncommon=4)
ResPat.Top.Pathway.n..27.of.589	Fc_ Receptor-mediated Phagocytosis in Macrophages and Monocytes; FDR=2.83e-03; (ng=92); (ncommon=5)
ResPat.Top.Pathway.n..28.of.589	Complement System; FDR=4.29e-03; (ng=32); (ncommon=3)
ResPat.Top.Pathway.n..29.of.589	Tec Kinase Signaling; FDR=4.43e-03; (ng=149); (ncommon=6)
ResPat.Top.Pathway.n..30.of.589	Graft-versus-Host Disease Signaling; FDR=4.79e-03; (ng=39); (ncommon=3)
ResPat.Top.Pathway.n..31.of.589	Role of Hypercytokinemia/hyperchemokineemia in the Pathogenesis of Influenza; FDR=5.05e-03; (ng=41); (ncommon=3)
ResPat.Top.Pathway.n..32.of.589	Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis; FDR=5.15e-03; (ng=214); (ncommon=7)
ResPat.Top.Pathway.n..33.of.589	Caveolar-mediated Endocytosis Signaling; FDR=5.35e-03; (ng=71); (ncommon=4)
ResPat.Top.Pathway.n..34.of.589	Ephrin B Signaling; FDR=6.02e-03; (ng=73); (ncommon=4)

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PD-L1, programmed death-ligand 1; FDR, false discovery rate.