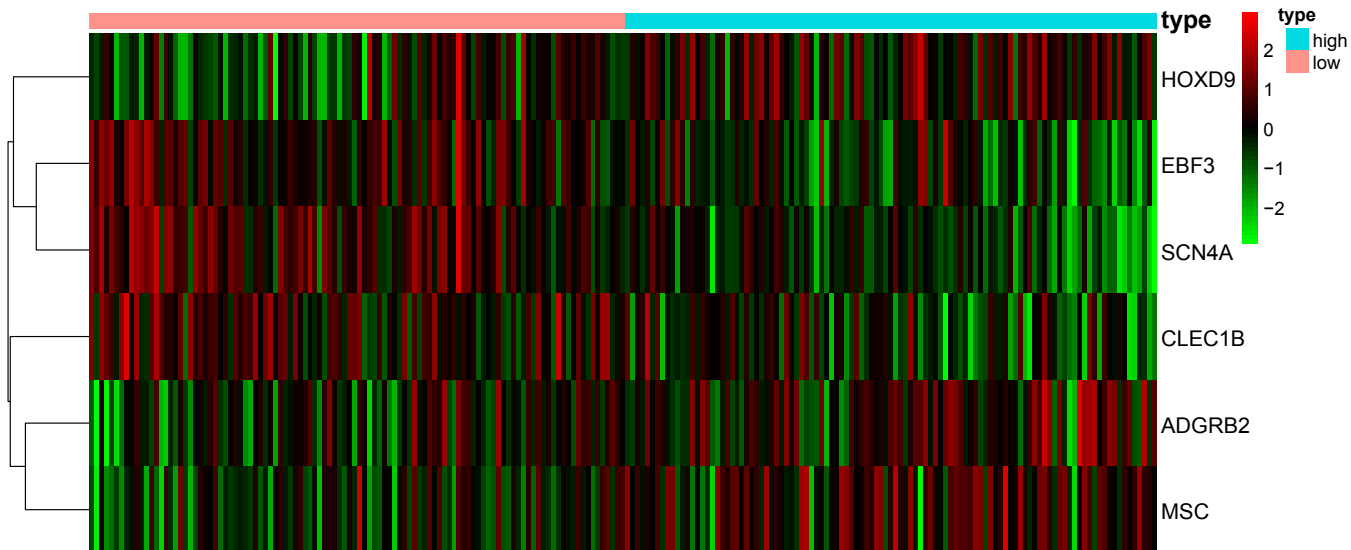
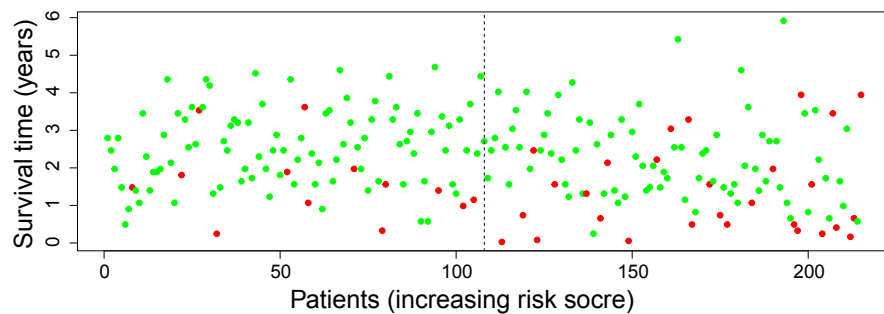
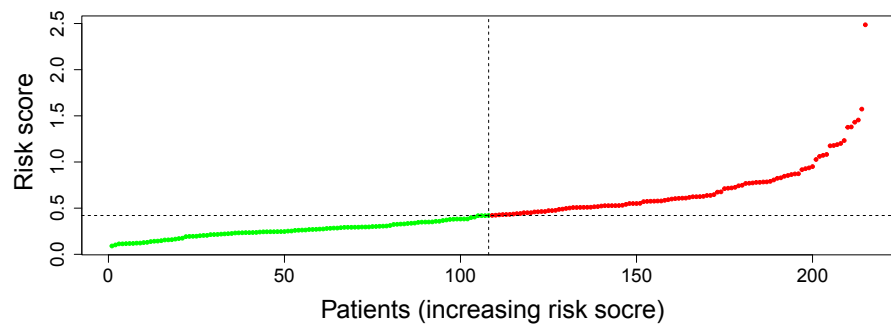
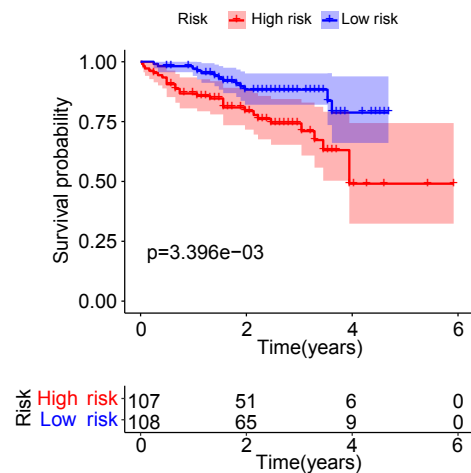
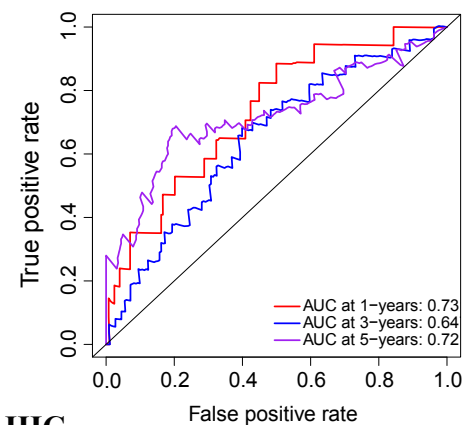


**A****B****C****D**

**Supplementary Figure.1 Validation of the MP-related risk model in ICGC-LIHC dataset.** (A, B) Expression heat map, risk score distribution and survival status. (C) Survival curve of low and high risk subgroup. (D) Time-dependent ROC curves for the efficacy evaluation of the 6-gene MP-related signature.

**Supplementary Table 1. GO and KEGG enrichment analyses of 283 differentially expressed MPRGs**

Oncology	ID	Description	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
BP	GO:0006957	complement activation alternative pathway	18/18903	8.66E-05	0.010056	0.008359	CFP/CR1/C9/C7	4
BP	GO:0001963	synaptic transmission dopaminergic	27/18903	0.000451	0.020667	0.017179	RASD2/CRHBP/PTGS2/TH	4
BP	GO:0035249	synaptic transmission glutamatergic	102/18903	0.000476	0.021512	0.017881	DGKI/UNC13A/PTGS2/GRIN2A/GRIN2B/SLC17A8/NRXN1	7
BP	GO:0051966	regulation of synaptic transmission glutamatergic	78/18903	0.000662	0.026243	0.021814	DGKI/UNC13A/PTGS2/GRIN2A/GRIN2B/NRXN1	6
BP	GO:0051968	positive regulation of synaptic transmission glutamatergic	33/18903	0.000987	0.03452	0.028694	PTGS2/GRIN2A/GRIN2B/NRXN1	4
BP	GO:0001867	complement activation lectin pathway	12/18903	0.000493	0.021682	0.018022	FCN3/FCN2/COLEC10	3
BP	GO:0050921	positive regulation of chemotaxis	144/18903	2.73E-05	0.005217	0.004336	THBS4/CDH13/NTF3/CXCL12/FPR2/P2RY12/SERPINE1/SCG2/CXCR2/DSCAM	10
BP	GO:0030509	BMP signaling pathway	167/18903	9.57E-05	0.010178	0.00846	BMPER/EGR1/CCN1/SFRP4/COMP/SFRP1/TBX20/BMP10/GDF2/BMP5	10
BP	GO:0071772	response to BMP	178/18903	0.000162	0.012841	0.010674	BMPER/EGR1/CCN1/SFRP4/COMP/SFRP1/TBX20/BMP10/GDF2/BMP5	10
BP	GO:0071773	cellular response to BMP stimulus	178/18903	0.000162	0.012841	0.010674	BMPER/EGR1/CCN1/SFRP4/COMP/SFRP1/TBX20/BMP10/GDF2/BMP5	10
BP	GO:0001936	regulation of endothelial cell proliferation	183/18903	0.000203	0.014338	0.011918	THBS4/APLN/CDH13/ECM1/CXCL12/NR4A1/EGR3/SCG2/NGFR/GDF2	10
BP	GO:0009266	response to temperature stimulus	186/18903	0.000231	0.015351	0.01276	CD34/MAPT/FOS/CXCL12/TCIM/LPL/EPHB1/PTGS2/PLAC8/NGFR	10
BP	GO:0002685	regulation of leukocyte migration	231/18903	0.00125	0.040414	0.033594	PLVAP/THBS4/ECM1/THY1/CXCL12/FPR2/P2RY12/SERPINE1/CXCR2/BMP5	10
BP	GO:0060560	developmental growth involved in morphogenesis	233/18903	0.001333	0.0413	0.03433	MAPT/SEMA5B/FSTL4/CXCL12/UNC13A/LHX2/PTK7/SFRP1/MAG/DSCAM	10
BP	GO:0097529	myeloid leukocyte migration	242/18903	0.001766	0.048268	0.040122	THBS4/CXCL12/S100A12/FPR2/P2RY12/SERPINE1/SCG2/CXCR2/CXCR1/PPBP	10

BP	GO:0050905	neuromuscular process	154/18903	8.28E-06	0.003364	0.002797	FOXS1/TCF15/SCN4A/NR4A1/UCHL1/HOXD10/STRA6/COMP/GRIN2A/SLITRK6/NRXN1	11
BP	GO:0051216	cartilage development	201/18903	9.68E-05	0.010178	0.00846	ECM1/PTH1R/CCN1/PRRX1/RFLNA/HOXD3/COMP/BMP10/GDF2/COL11A1/BMP5	11
BP	GO:0050920	regulation of chemotaxis	230/18903	0.000314	0.017582	0.014615	THBS4/CDH13/SEMA5B/NTF3/CXCL12/FPR2/P2RY12/SERPINE1/SCG2/CXCR2/DSCAM	11
BP	GO:2000116	regulation of cysteine-type endopeptidase activity	235/18903	0.000376	0.020053	0.016669	MAPT/CCN1/NR4A1/RFPL1/PTGS2/NGFR/GRIN2A/CST2/HGF/MMP9/GRIN2B	11
BP	GO:0034764	positive regulation of transmembrane transport	237/18903	0.000404	0.020549	0.017081	THY1/EHD3/TRPC6/LRRC55/F2RL3/NR4A3/CLTRN/CEMIP/ITLN1/SLC17A8/KCNH2	11
BP	GO:0045444	fat cell differentiation	244/18903	0.000516	0.02239	0.018611	EBF2/ZFP36/EGR2/LPL/NR4A1/PTGS2/NR4A3/PLAC8/FABP4/SFRP1/GDF10	11
BP	GO:0034612	response to tumor necrosis factor	254/18903	0.00072	0.027562	0.02291	PLVAP/ADAMTS13/ZFP36/TNFRSF4/CRHBP/FOS/UBD/PTGS2/HAMP/FABP4/SFRP1	11
BP	GO:0051924	regulation of calcium ion transport	268/18903	0.001115	0.037381	0.031073	THY1/EHD3/TRPC6/CXCL12/LILRA5/F2RL3/PTGS2/CEMIP/RCVRN/PLPP4/DHRS7C	11
BP	GO:0007611	learning or memory	273/18903	0.001293	0.041088	0.034153	MAPT/CRHBP/NTF3/FOS/EGR2/PTGS2/STRA6/GRIN2A/GRIN2B/NRXN1/TH	11
BP	GO:0051962	positive regulation of nervous system development	279/18903	0.001537	0.044641	0.037107	MAPT/IL1RAP/CXCL12/EGR2/LRRN3/EPHB1/MAG/DSCAM/SLITRK6/SLITRK3/NRXN1	11
BP	GO:0043542	endothelial cell migration	281/18903	0.001627	0.046407	0.038575	CDH13/BMPER/CCBE1/NR4A1/EGR3/PTGS2/SCG2/FAP/DCN/BMP10/GDF2	11
BP	GO:0007626	locomotory behavior	197/18903	1.63E-05	0.004418	0.003672	RASD2/HOXD9/EGR1/CXCL12/UCHL1/EFNB3/HOXD10/NPY1R/CEND1/DSCAM/SLITRK6/TH	12
BP	GO:0043583	ear development	221/18903	5.05E-05	0.007146	0.00594	BMPER/CTHRC1/PVALB/TCF15/PRRX1/STRA6/PTK7/COL11A1/BMP5/SLC17A8/SLITRK6/FREM2	12
BP	GO:0008037	cell recognition	230/18903	7.42E-05	0.009282	0.007715	CFP/FCN3/FCN2/COLEC10/COLEC4M/EPHB1/EFNB3/NTM/COLEC12/GAP43/DSCAM/ZBPB	12
BP	GO:0033002	muscle cell proliferation	247/18903	0.000146	0.012227	0.010163	APLN/CDH13/TRIB1/FOS/NOTCH3/EPHB1/PTGS2/NR4A3/TBX20/BMP10/HGF/MMP9	12
BP	GO:0048562	embryonic organ morphogenesis	294/18903	0.000704	0.027274	0.022671	HOXD9/CTHRC1/PRRX1/HOXD10/HOXD3/STRA6/MDFI/PTK7/TBX20/COL11A1/SLITRK6/TH	12

BP	GO:0031349	positive regulation of defense response	307/18903	0.001025	0.03509	0.029168	FCN3/FCN2/COLEC10/S100A12/LILRA5/LPL/IL1RL1/FPR2/MMP12/PTGS2/SERPINE1/FABP4	12
BP	GO:0001935	endothelial cell proliferation	199/18903	3.37E-06	0.001826	0.001518	THBS4/APLN/CD34/CDH13/ECM1/BMPER/CXCL12/NR4A1/PROK2/EGR3/SCG2/NGFR/GDF2	13
BP	GO:0050679	positive regulation of epithelial cell proliferation	224/18903	1.22E-05	0.003959	0.003291	THBS4/APLN/CDH13/ECM1/CXCL12/NR4A1/MMP12/EGR3/NR4A3/SCG2/SFRP1/GDF2/BMP5	13
BP	GO:0048705	skeletal system morphogenesis	227/18903	1.40E-05	0.004148	0.003448	HOXD9/HOXD8/TCF15/SFRP4/PRRX1/RFLNA/HOXD10/HOXD3/MDFI/COMP/HHIP/SFRP1/COL11A1	13
BP	GO:0043270	positive regulation of ion transport	289/18903	0.000167	0.012908	0.010729	THY1/EHD3/TRPC6/CXCL12/LILRA5/LRRC55/P2RY12/F2RL3/CLTRN/CEMIP/PTGES/SLC17A8/KCNH2	13
BP	GO:0001822	kidney development	309/18903	0.000319	0.0176	0.01463	CD34/BMPER/EGR1/NOTCH3/STRA6/CXCR2/PTK7/SFRP1/BMP10/MMP9/RET/FREM2/OVOL1	13
BP	GO:0072001	renal system development	318/18903	0.00042	0.020667	0.017179	CD34/BMPER/EGR1/NOTCH3/STRA6/CXCR2/PTK7/SFRP1/BMP10/MMP9/RET/FREM2/OVOL1	13
BP	GO:0006959	humoral immune response	320/18903	0.000445	0.020667	0.017179	CFP/FCN3/FCN2/COLEC10/S100A12/PGLYRP1/CXCL14/CD5L/CR1/PPBP/DEFA3/C9/C7	13
BP	GO:0048638	regulation of developmental growth	332/18903	0.000629	0.025493	0.021191	MAPT/SEMA5B/FSTL4/FOXS1/CXCL12/UNC13A/NPY1R/HAMP/PLAC8/TBX20/MAG/BMP10/DSCAM	13
BP	GO:0001655	urogenital system development	360/18903	0.001316	0.041151	0.034206	CD34/BMPER/EGR1/NOTCH3/STRA6/CXCR2/PTK7/SFRP1/BMP10/MMP9/RET/FREM2/OVOL1	13
BP	GO:0061448	connective tissue development	274/18903	2.37E-05	0.005217	0.004336	EBF2/CD34/ECM1/PTH1R/EGR1/CCN1/PRRX1/RFLNA/HOXD3/COMP/BMP10/GDF2/COL11A1/BMP5	14
BP	GO:0060326	cell chemotaxis	319/18903	0.000122	0.011322	0.009411	THBS4/CXCL12/S100A12/FPR2/NR4A1/EPHB1/EGR3/SERPINE1/SCG2/CXCL14/CXCR2/CXCR1/HGF/PPBP	14
BP	GO:0007517	muscle organ development	348/18903	0.000299	0.017032	0.014157	HOXD9/FOS/EGR1/EGR2/TCF15/NR4A1/EPHB1/EGR3/HOXD10/STRA6/TBX20/BMP10/MSC/COL11A1	14
BP	GO:0007411	axon guidance	236/18903	8.35E-07	0.000633	0.000526	SEMA5B/NOTCH3/CXCL12/EGR2/EPHB1/EFNB3/LHX2/NGFR/UNC5A/TUBB3/GAP43/DSCAM/RET/LGI1/NRXN1	15
BP	GO:0097485	neuron projection guidance	237/18903	8.81E-07	0.000633	0.000526	SEMA5B/NOTCH3/CXCL12/EGR2/EPHB1/EFNB3/LHX2/NGFR/UNC5A/TUBB3/GAP43/DSCAM/RET/LGI1/NRXN1	15

BP	GO:0030198	extracellular matrix organization	318/18903	3.08E-05	0.005277	0.004386	ADAMTS13/COL15A1/OLFML2B/OLFML2A/COL9A1/COL6A6/TCF15/EGFL6/CCN1/MMP12/FAP/COMP/MMP9/COL11A1/DPT	15
BP	GO:0043062	extracellular structure organization	319/18903	3.19E-05	0.005277	0.004386	ADAMTS13/COL15A1/OLFML2B/OLFML2A/COL9A1/COL6A6/TCF15/EGFL6/CCN1/MMP12/FAP/COMP/MMP9/COL11A1/DPT	15
BP	GO:0045229	external encapsulating structure organization	321/18903	3.43E-05	0.005313	0.004417	ADAMTS13/COL15A1/OLFML2B/OLFML2A/COL9A1/COL6A6/TCF15/EGFL6/CCN1/MMP12/FAP/COMP/MMP9/COL11A1/DPT	15
BP	GO:0050727	regulation of inflammatory response	414/18903	0.000552	0.023616	0.01963	ZFP36/S100A12/LILRA5/LPL/IL1RL1/SOCS3/FPR2/PTGS2/SERPINE1/PGLYRP1/HAMP/FABP4/PTGES/HGF/MMP9	15
BP	GO:0052547	regulation of peptidase activity	459/18903	0.001554	0.044736	0.037186	ECM1/MAPT/CCN1/NR4A1/RFPL1/PTGS2/SERPINE1/NGFR/CR1/GRIN2A/TFPI2/CST2/HGF/MMP9/GRIN2B	15
BP	GO:1904062	regulation of cation transmembrane transport	394/18903	0.0001	0.010178	0.00846	THY1/CRHBP/EHD3/KCNN2/NETO2/LRRC55/F2RL3/CLTRN/CEMIP/HAMP/GRIN2A/MMP9/GRIN2B/KCNH2/FXYD3/DHRS7C	16
BP	GO:0050678	regulation of epithelial cell proliferation	414/18903	0.000177	0.013054	0.010851	THBS4/APLN/CDH13/ECM1/ZFP36/CXCL12/NR4A1/MMP12/EGR3/NR4A3/SCG2/NGFR/SFRP1/GDF2/BMP5/OVOL1	16
BP	GO:0060537	muscle tissue development	422/18903	0.000219	0.01485	0.012343	NOX4/HOXD9/GJC1/FOS/EGR1/EGR2/NR4A1/EPHB1/HOXD10/STRA6/HAMP/TBX20/BMP10/MSC/COL11A1/BMP5	16
BP	GO:0001503	ossification	429/18903	0.000263	0.016235	0.013495	ECM1/PTH1R/CTHRC1/EGR2/CCN1/RFLNA/PTGS2/COMP/SFRP1/HGF/GDF2/MMP9/COL11A1/BMP5/GDF10/FGF23	16
BP	GO:0048568	embryonic organ development	449/18903	0.000435	0.020667	0.017179	HOXD9/CTHRC1/CCN1/SOCS3/PRRX1/HOXD10/HOXD3/STRA6/MDFI/PTK7/RSPO3/TBX20/COL11A1/BMP5/SLITRK6/TH	16
BP	GO:0050900	leukocyte migration	398/18903	3.25E-05	0.005277	0.004386	PLVAP/THBS4/CD34/ECM1/THY1/CXCL12/S100A12/FPR2/P2RY12/SERPINE1/SCG2/CXCR2/CXCR1/PPBP/MMP9/BMP5/RET	17

BP	GO:0010959	regulation of metal ion transport	423/18903	6.91E-05	0.008988	0.007471	THY1/EHD3/TRPC6/CXCL12/KCNN2/LILRA5/NETO2/LRRC55/F2RL3/PTGS2/CEMIP/HAMP/RCVRN/KCNH2/FXYD3/PLPP4/DHRS7C	17
BP	GO:0051960	regulation of nervous system development	456/18903	0.000171	0.012908	0.010729	THY1/MAPT/SEMA5B/FSTL4/IL1RAP/CXCL12/EGR2/LRRN3/EPHB1/EFNB3/LHX2/MAG/HGF/DSCAM/SLITRK6/SLITRK3/NRXN1	17
BP	GO:0032103	positive regulation of response to external stimulus	464/18903	5.67E-06	0.002634	0.002189	THBS4/CDH13/NTF3/FCN3/FCN2/COLEC10/CXCL12/S100A12/LILRA5/LPL/IL1RL1/FPR2/MMP12/P2RY12/PTGS2/SERPINE1/SCG2/CXCR2/FABP4/DSCAM	20
BP	GO:0007409	axonogenesis	438/18903	1.46E-07	0.000473	0.000393	THY1/MAPT/SEMA5B/FSTL4/NOTCH3/CXCL12/EGR2/EPHB1/UCHL1/EFNB3/LHX2/NGFR/UNC5A/TUBB3/MAG/GAP43/DSCAM/RET/SLITRK6/LGI1/SLITRK3/NRXN1	22
BP	GO:0050673	epithelial cell proliferation	481/18903	7.14E-07	0.000633	0.000526	THBS4/APLN/CD34/CDH13/ECM1/BMPER/ZFP36/DACH1/CXCL12/NR4A1/MMP12/PROK2/EGR3/NR4A3/SCG2/FAP/NGFR/SFRP1/HGF/GDF2/BMP5/OVOL1	22
BP	GO:0061564	axon development	490/18903	9.73E-07	0.000633	0.000526	THY1/MAPT/SEMA5B/FSTL4/NOTCH3/CXCL12/EGR2/EPHB1/UCHL1/EFNB3/LHX2/NGFR/UNC5A/TUBB3/MAG/GAP43/DSCAM/RET/SLITRK6/LGI1/SLITRK3/NRXN1	22
BP	GO:0038007	netrin-activated signaling pathway	10/18903	0.000275	0.016235	0.013495	UNC5A/TUBB3/DSCAM	3
BP	GO:0060245	detection of cell density	10/18903	0.000275	0.016235	0.013495	DACH1/FAP/SRPX	3
BP	GO:0098976	excitatory chemical synaptic transmission	10/18903	0.000275	0.016235	0.013495	PVALB/GRIN2A/GRIN2B	3
BP	GO:0031223	auditory behavior	12/18903	0.000493	0.021682	0.018022	STRA6/SLITRK6/NRXN1	3
BP	GO:0090177	establishment of planar polarity involved in neural tube closure	13/18903	0.000635	0.025493	0.021191	CTHRC1/PTK7/SFRP1	3
BP	GO:0007638	mechanosensory behavior	14/18903	0.0008	0.029874	0.024832	STRA6/SLITRK6/NRXN1	3
BP	GO:0050930	induction of positive chemotaxis	14/18903	0.0008	0.029874	0.024832	NTF3/CXCL12/SCG2	3

BP	GO:0042249	establishment of planar polarity of embryonic epithelium	16/18903	0.001207	0.039632	0.032943	CTHRC1/PTK7/SFRP1	3
BP	GO:0061469	regulation of type B pancreatic cell proliferation	16/18903	0.001207	0.039632	0.032943	NR4A1/NR4A3/SFRP1	3
BP	GO:0051412	response to corticosterone	17/18903	0.00145	0.043274	0.035971	FOS/FOSB/TH	3
BP	GO:0072224	metanephric glomerulus development	17/18903	0.00145	0.043274	0.035971	CD34/EGR1/RET	3
BP	GO:0097107	postsynaptic density assembly	17/18903	0.00145	0.043274	0.035971	IL1RAP/SLITRK3/NRXN1	3
BP	GO:0019896	axonal transport of mitochondrion	18/18903	0.001723	0.047897	0.039813	MAPT/UCHL1/AGBL4	3
BP	GO:0031643	positive regulation of myelination	18/18903	0.001723	0.047897	0.039813	EGR2/MAG/HGF	3
BP	GO:1903027	regulation of opsonization	11/18903	1.01E-05	0.003636	0.003022	CFP/FCN3/FCN2/COLEC10	4
BP	GO:0008228	opsonization	17/18903	6.81E-05	0.008988	0.007471	CFP/FCN3/FCN2/COLEC10	4
BP	GO:0098698	postsynaptic specialization assembly	20/18903	0.000134	0.012123	0.010077	IL1RAP/GAP43/SLITRK3/NRXN1	4
BP	GO:0060713	labyrinthine layer morphogenesis	22/18903	0.000198	0.014334	0.011915	CCN1/SOCS3/RSPO3/BMP5	4
BP	GO:0050927	positive regulation of positive chemotaxis	25/18903	0.000332	0.018007	0.014968	CDH13/NTF3/CXCL12/SCG2	4
BP	GO:0050926	regulation of positive chemotaxis	26/18903	0.000388	0.020053	0.016669	CDH13/NTF3/CXCL12/SCG2	4
BP	GO:0060669	embryonic placenta morphogenesis	26/18903	0.000388	0.020053	0.016669	CCN1/SOCS3/RSPO3/BMP5	4
BP	GO:0044342	type B pancreatic cell proliferation	27/18903	0.000451	0.020667	0.017179	DACH1/NR4A1/NR4A3/SFRP1	4
BP	GO:0099068	postsynapse assembly	29/18903	0.000598	0.024609	0.020456	IL1RAP/GAP43/SLITRK3/NRXN1	4
BP	GO:0002063	chondrocyte development	33/18903	0.000987	0.03452	0.028694	ECM1/RFLNA/COMP/COL11A1	4
BP	GO:0099084	postsynaptic specialization organization	34/18903	0.001107	0.037381	0.031073	IL1RAP/GAP43/SLITRK3/NRXN1	4

BP	GO:0040036	regulation of fibroblast growth factor receptor signaling pathway	38/18903	0.001689	0.047762	0.039701	APLN/NGFR/HHIP/SHISA2	4
BP	GO:0009595	detection of biotic stimulus	39/18903	0.001862	0.048529	0.040339	DACH1/PGLYRP1/FAP/SRPX	4
BP	GO:0030279	negative regulation of ossification	39/18903	0.001862	0.048529	0.040339	ECM1/RFLNA/SFRP1/FGF23	4
BP	GO:0090102	cochlea development	50/18903	0.000564	0.02365	0.019659	CTHRC1/PVALB/PTK7/SLC17A8/SLITRK6	5
BP	GO:0031102	neuron projection regeneration	62/18903	0.001512	0.044283	0.036809	THY1/PRRX1/MAG/HGF/GAP43	5
BP	GO:0060393	regulation of pathway-restricted SMAD protein phosphorylation	62/18903	0.001512	0.044283	0.036809	BMPER/BMP10/GDF2/BMP5/GDF10	5
BP	GO:0031100	animal organ regeneration	65/18903	0.001867	0.048529	0.040339	CXCL12/NR4A3/HAMP/HGF/NNMT	5
BP	GO:0050771	negative regulation of axonogenesis	65/18903	0.001867	0.048529	0.040339	THY1/SEMA5B/FSTL4/EFNB3/MAG	5
BP	GO:0051965	positive regulation of synapse assembly	63/18903	0.000207	0.014338	0.011918	IL1RAP/LRRN3/EPHB1/SLITRK6/SLITRK3/NRXN1	6
BP	GO:0060389	pathway-restricted SMAD protein phosphorylation	66/18903	0.000268	0.016235	0.013495	BMPER/AMHR2/BMP10/GDF2/BMP5/GDF10	6
BP	GO:0035567	non-canonical Wnt signaling pathway	72/18903	0.000431	0.020667	0.017179	CTHRC1/SFRP4/PTK7/RSPO3/SFRP1/FZD10	6
BP	GO:0007422	peripheral nervous system development	81/18903	0.000808	0.029874	0.024832	HOXD9/NTF3/EGR2/EGR3/HOXD10/ADGRB2	6
BP	GO:0048704	embryonic skeletal system morphogenesis	94/18903	0.001753	0.048268	0.040122	HOXD9/PRRX1/HOXD10/HOXD3/MDFI/COL11A1	6
BP	GO:0050918	positive chemotaxis	64/18903	2.48E-05	0.005217	0.004336	CDH13/NTF3/COLEC10/CXCL12/FPR2/SCG2/HGF	7
BP	GO:0008344	adult locomotory behavior	80/18903	0.000105	0.010386	0.008633	HOXD9/CXCL12/UCHL1/EFNB3/HOXD10/CEND1/SLITRK6	7
BP	GO:0021675	nerve development	84/18903	0.000144	0.012227	0.010163	NTF3/EGR2/EPHB1/HOXD3/NGFR/RET/SLITRK6	7
BP	GO:0007200	phospholipase C-activating G protein-coupled receptor signaling pathway	105/18903	0.000567	0.02365	0.019659	PTH1R/FPR2/P2RY12/F2RL3/CXCR2/CHRM2/LPAR4	7
BP	GO:0030282	bone mineralization	123/18903	0.001442	0.043274	0.035971	ECM1/PTH1R/CCN1/RFLNA/PTGS2/COMP/FGF23	7
BP	GO:0045471	response to ethanol	128/18903	0.001813	0.048529	0.040339	CRHBP/FOS/HAMP/GRIN2A/CSF3/GRIN2B/TH	7



BP	GO:0051928	positive regulation of calcium ion transport	129/18903	0.001895	0.048529	0.040339	THY1/EHD3/TRPC6/CXCL12/LILRA5/F2RL3/CEMIP	7
BP	GO:2000027	regulation of animal organ morphogenesis	129/18903	0.001895	0.048529	0.040339	CD34/CTHRC1/PTK7/NGFR/RSPO3/SFRP1/HGF	7
BP	GO:0019233	sensory perception of pain	103/18903	7.96E-05	0.009586	0.007968	CXCL12/PROK2/EPHB1/UCHL1/PTGS2/NPY1R/PTGES/GRIN2A	8
BP	GO:1901890	positive regulation of cell junction assembly	106/18903	9.75E-05	0.010178	0.00846	THY1/IL1RAP/LRRN3/EPHB1/SFRP1/SLITRK6/SLITRK3/NRXN1	8
BP	GO:0007631	feeding behavior	108/18903	0.000111	0.010635	0.00884	APLN/FOS/DACH1/UCHL1/STRA6/NR4A3/NPY1R/TH	8
BP	GO:0030278	regulation of ossification	122/18903	0.000259	0.016235	0.013495	ECM1/EGR2/CCN1/RFLNA/COMP/SFRP1/GDF10/FGF23	8
BP	GO:0006956	complement activation	132/18903	0.000441	0.020667	0.017179	CFP/FCN3/FCN2/COLEC10/CD5L/CR1/C9/C7	8
BP	GO:0002687	positive regulation of leukocyte migration	148/18903	0.000937	0.033843	0.028131	PLVAP/THBS4/THY1/CXCL12/FPR2/P2RY12/SERPINE1/CXCR2	8
BP	GO:0007519	skeletal muscle tissue development	164/18903	0.001805	0.048529	0.040339	HOXD9/FOS/EGR1/EGR2/NR4A1/EPHB1/HOXD10/MSC	8
BP	GO:0044344	cellular response to fibroblast growth factor stimulus	114/18903	2.50E-05	0.005217	0.004336	APLN/ZFP36/NR4A1/EGR3/NGFR/HHIP/SFRP1/SHISA2/FGF23	9
BP	GO:0001938	positive regulation of endothelial cell proliferation	115/18903	2.69E-05	0.005217	0.004336	THBS4/APLN/CDH13/ECM1/CXCL12/NR4A1/EGR3/SCG2/GDF2	9
BP	GO:0071774	response to fibroblast growth factor	120/18903	3.77E-05	0.005567	0.004627	APLN/ZFP36/NR4A1/EGR3/NGFR/HHIP/SFRP1/SHISA2/FGF23	9
BP	GO:0030534	adult behavior	143/18903	0.000147	0.012227	0.010163	HOXD9/CRHBP/CXCL12/UCHL1/EFNB3/HOXD10/CEND1/SLITRK6/NRXN1	9
BP	GO:0050770	regulation of axonogenesis	156/18903	0.000282	0.01636	0.013599	THY1/MAPT/SEMA5B/STL4/CXCL12/EFNB3/MAG/DSCAM/RET	9
BP	GO:0060538	skeletal muscle organ development	176/18903	0.000679	0.026601	0.022112	HOXD9/FOS/EGR1/EGR2/NR4A1/EPHB1/HOXD10/STRA6/MSC	9
BP	GO:0007416	synapse assembly	184/18903	0.000931	0.033843	0.028131	IL1RAP/GPM6A/LRRN3/EPHB1/GAP43/DSCAM/SLITRK6/SLITRK3/NRXN1	9
BP	GO:0002040	sprouting angiogenesis	185/18903	0.000968	0.03452	0.028694	ESM1/CDH13/BMPER/CCBE1/NR4A1/EGR3/PTGS2/NGFR/RSPO3	9

BP	GO:0034767	positive regulation of ion transmembrane transport	186/18903	0.001005	0.034772	0.028903	THY1/EHD3/TRPC6/LRRC55/F2RL3/CLTRN/CEMIP/SLC17A8/KCNH2	9
BP	GO:0031099	regeneration	192/18903	0.001255	0.040414	0.033594	THY1/CXCL12/PRRX1/NR4A3/HAMP/MAG/HGF/NNMT/GAP43	9
BP	GO:0048839	inner ear development	193/18903	0.001301	0.041088	0.034153	BMPER/CTHRC1/PVALB/PRRX1/PTK7/COL11A1/SLC17A8/SLITRK6/FREM2	9
CC	GO:0031225	anchored component of membrane	169/19869	0.000113	0.006936	0.005902	CDH13/THY1/BCAN/LY6H/PRND/CA4/NTM/LY6E/ITLN1/CEACAM7	10
CC	GO:0005581	collagen trimer	86/19869	2.46E-08	3.78E-06	3.22E-06	COL15A1/CTHRC1/FCN3/MARCO/FCN2/COL9A1/COLEC10/COL6A6/CCBE1/COLEC12/COL11A1	11
CC	GO:0150034	distal axon	278/19869	0.00046	0.017725	0.015084	THY1/MAPT/CRHBP/GPM6A/UNC13A/NGFR/CHRM2/TUBB3/GAP43/DSCAM/SLC17A8/TH	12
CC	GO:0045121	membrane raft	326/19869	0.001819	0.044203	0.037617	PLVAP/CDH13/THY1/MAPT/EPHB1/PTGS2/CR1/UNC5A/MAG/ITLN1/RET/PLPP2	12
CC	GO:0098857	membrane microdomain	327/19869	0.001866	0.044203	0.037617	PLVAP/CDH13/THY1/MAPT/EPHB1/PTGS2/CR1/UNC5A/MAG/ITLN1/RET/PLPP2	12
CC	GO:0031253	cell projection membrane	344/19869	0.000288	0.014773	0.012572	THY1/MAPT/EHD3/CSPG4/P2RY12/CLTRN/CA4/FAHP/HHIP/UNC5A/GAP43/ITLN1/SSTR3/PLA2G4F	14
CC	GO:0009897	external side of plasma membrane	462/19869	2.11E-05	0.001625	0.001383	CD34/CDH13/STAB2/THY1/TNFRSF4/CLEC4G/LIFR/FCN3/FCN2/COLEC10/CXCL12/PRND/CLEC4M/IL1RL1/CA4/CXCR2/CXCR1/ADGRE1/SLC4A3	19
CC	GO:0043025	neuronal cell body	497/19869	3.75E-07	3.85E-05	3.28E-05	GABRD/THY1/PLXDC1/MAPT/CRHBP/PVALB/KCNK2/GPM6A/UCHL1/PDE1C/NGFR/CHRM2/RCVRN/UNC5A/TUBB3/GAP43/DSCAM/SLC17A8/RET/PCSK2/CTNND2/NRXN1/TH	23
CC	GO:0062023	collagen-containing extracellular matrix	433/19869	9.98E-12	3.07E-09	2.61E-09	THBS4/COL15A1/CDH13/ECM1/CFP/BCAN/CTHRC1/FCN3/CSPG4/FCN2/COL9A1/COL6A6/CXCL12/EDIL3/ACAN/EGFL6/CCN1/SERPINE1/COMP/SFRP1/DCN/SRPX/ADAMDEC1/MMP9/COL11A1/GDF10/DPT/FREM2	28
CC	GO:1905370	serine-type endopeptidase complex	11/19869	0.000382	0.0168	0.014297	FCN3/FCN2/COLEC10	3
CC	GO:1905286	serine-type peptidase complex	13/19869	0.000649	0.022195	0.018888	FCN3/FCN2/COLEC10	3
CC	GO:0044304	main axon	63/19869	0.001678	0.044203	0.037617	THY1/MAPT/CRHBP/KCNQ3/MAG	5

CC	GO:0043204	perikaryon	154/19869	0.00127	0.039119	0.03329	CRHBP/NGFR/RCVRN/GAP43/SLC17A8/PCSK2/CTNND2/TH	8
MF	GO:0001228	DNA-binding transcription activator activityRNA polymerase II-specific	468/18432	0.001177	0.038523	0.03322	EBF2/FOS/HOXD8/EGR1/EGR2/TCF15/TLX1/FOSB/NR4A1/PRRX1/EGR3/HOXD10/HOXD3/LHX2/NR4A3/TBX20	16
MF	GO:0005178	integrin binding	156/18432	8.33E-05	0.006317	0.005447	THBS4/ADAMTS13/ESM1/THY1/CXCL12/EDIL3/EGFL6/CCN1/FAP/COMP	10
MF	GO:0008083	growth factor activity	162/18432	2.17E-05	0.003834	0.003306	THBS4/NTF3/CXCL12/BMP10/HGF/CSF3/PPBP/GDF2/BMP5/GDF10/FGF23	11
MF	GO:0005539	glycosaminoglycan binding	237/18432	3.80E-05	0.005039	0.004345	THBS4/STAB2/BCAN/ACAN/CCN1/LPL/PGLYRP1/CEMIP/COMP/RSP03/SFRP1/DCN/COL11A1	13
MF	GO:0005201	extracellular matrix structural constituent	173/18432	1.96E-07	0.000104	8.97E-05	COL15A1/ECM1/CTHRC1/COL9A1/COL6A6/EDIL3/ACAN/CCN1/COMP/DCN/TFPI2/SRPX/COL11A1/DPT	14
MF	GO:0042277	peptide binding	330/18432	0.000295	0.01472	0.012694	PTH1R/CRHBP/MARCO/CLEC4M/FPR2/NPY1R/CEMIP/NGFR/PTGES/TUBB3/GRIN2A/GRIN2B/GLP2R/SSTR3	14
MF	GO:0033218	amide binding	408/18432	0.00081	0.031444	0.027115	PTH1R/CRHBP/MARCO/CLEC4M/FPR2/NPY1R/CEMIP/NGFR/PTGES/TUBB3/GRIN2A/MAG/GRIN2B/GLP2R/SSTR3	15
MF	GO:0030246	carbohydrate binding	275/18432	2.28E-06	0.000604	0.000521	CD34/BCAN/CLEC4G/FCN3/FCN2/COL9A1/COLEC10/CRYBG2/CLEC1B/ACAN/SIGLEC7/SIGLEC11/CLEC4M/MAG/COLEC12/ITLN1	16
MF	GO:0001216	DNA-binding transcription activator activity	472/18432	0.001285	0.038523	0.03322	EBF2/FOS/HOXD8/EGR1/EGR2/TCF15/TLX1/FOSB/NR4A1/PRRX1/EGR3/HOXD10/HOXD3/LHX2/NR4A3/TBX20	16
MF	GO:0048018	receptor ligand activity	491/18432	0.000257	0.01472	0.012694	THBS4/APLN/SEMA5B/NTF3/COLEC10/CXCL12/SCG2/CXCL14/HAMP/BMP10/HGF/CSF3/PPBP/GDF2/BMP5/GDF10/GUCA2A/FGF23	18
MF	GO:0030546	signaling receptor activator activity	498/18432	0.000305	0.01472	0.012694	THBS4/APLN/SEMA5B/NTF3/COLEC10/CXCL12/SCG2/CXCL14/HAMP/BMP10/HGF/CSF3/PPBP/GDF2/BMP5/GDF10/GUCA2A/FGF23	18
MF	GO:0030169	low-density lipoprotein particle binding	17/18432	0.001684	0.042584	0.036721	CDH13/STAB2/COLEC12	3

MF	GO:0005540	hyaluronic acid binding	24/18432	0.000344	0.015212	0.013118	STAB2/BCAN/ACAN/CEMIP	4
MF	GO:0017147	Wnt-protein binding	30/18432	0.000829	0.031444	0.027115	CTHRC1/SFRP4/SFRP1/FZD10	4
MF	GO:0042056	chemoattractant activity	36/18432	0.001667	0.042584	0.036721	NTF3/COLEC10/SCG2/HGF	4
MF	GO:0071813	lipoprotein particle binding	30/18432	6.06E-05	0.005362	0.004624	CDH13/STAB2/MAPT/LPL/COLEC12	5
MF	GO:0071814	protein-lipid complex binding	30/18432	6.06E-05	0.005362	0.004624	CDH13/STAB2/MAPT/LPL/COLEC12	5
MF	GO:0050840	extracellular matrix binding	56/18432	0.000142	0.009449	0.008148	OLFML2B/ECM1/OLFML2A/CCN1/DCN/COL11A1	6
MF	GO:0008528	G protein-coupled peptide receptor activity	147/18432	0.00125	0.038523	0.03322	PTH1R/FPR2/F2RL3/NPY1R/CXCR2/CXCR1/GLP2R/SSTR3	8
MF	GO:0140375	immune receptor activity	148/18432	0.001306	0.038523	0.03322	LIFR/IL1RAP/LILRA5/IL1RL1/FPR2/CXCR2/CXCR1/CR1	8
MF	GO:0001653	peptide receptor activity	153/18432	0.001613	0.042584	0.036721	PTH1R/FPR2/F2RL3/NPY1R/CXCR2/CXCR1/GLP2R/SSTR3	8