

Table S1 Efferocytosis-Related Genes from GeneCards

Gene Symbol	Description	Category	Uniprot ID	Gifts	GC Id	Relevance score	GeneCards Link
MERTK	MER Proto-Oncogene, Tyrosine Kinase	Protein Coding	Q12866	59	GC02P111898	7.120387077	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MERTK
TIMD4	T Cell Immunoglobulin And Mucin Domain Containing 4	Protein Coding	Q96H15	47	GC05M156919	5.229410648	https://www.genecards.org/cgi-bin/carddisp.pl?gene=TIMD4
CD300LF	CD300 Molecule Like Family Member F	Protein Coding	Q8TDQ1	42	GC17M074694	3.272643089	https://www.genecards.org/cgi-bin/carddisp.pl?gene=CD300LF
PLAUR	Plasminogen Activator, Urokinase Receptor	Protein Coding	Q03405	53	GC19M043646	2.550109863	https://www.genecards.org/cgi-bin/carddisp.pl?gene=PLAUR
AXL	AXL Receptor Tyrosine Kinase	Protein Coding	P30530	60	GC19P041219	2.313197136	https://www.genecards.org/cgi-bin/carddisp.pl?gene=AXL
GAS6	Growth Arrest Specific 6	Protein Coding	Q14393	52	GC13M113820	2.259215355	https://www.genecards.org/cgi-bin/carddisp.pl?gene=GAS6
MIAT	Myocardial Infarction Associated Transcript	RNA Gene		32	GC22P026646	2.102351427	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MIAT
CD47	CD47 Molecule	Protein Coding	Q08722	53	GC03M108043	2.005666494	https://www.genecards.org/cgi-bin/carddisp.pl?gene=CD47
HAVCR1	Hepatitis A Virus Cellular Receptor 1	Protein Coding	Q96D42	50	GC05M157028	1.949641228	https://www.genecards.org/cgi-bin/carddisp.pl?gene=HAVCR1
SMAD5-AS1	SMAD5 Antisense RNA 1	RNA Gene	Q9Y6J3	28	GC05M136129	1.821329117	https://www.genecards.org/cgi-bin/carddisp.pl?gene=SMAD5-AS1
HMGB1	High Mobility Group Box 1	Protein Coding	P09429	57	GC13M030456	1.744839907	https://www.genecards.org/cgi-bin/carddisp.pl?gene=HMGB1
RHOA	Ras Homolog Family Member A	Protein Coding	P61586	58	GC03M049359	1.489726067	https://www.genecards.org/cgi-bin/carddisp.pl?gene=RHOA
CD274	CD274 Molecule	Protein Coding	Q9NZQ7	54	GC09P005450	1.489726067	https://www.genecards.org/cgi-bin/carddisp.pl?gene=CD274
PLG	Plasminogen	Protein Coding	P00747	58	GC06P160702	1.455093741	https://www.genecards.org/cgi-bin/carddisp.pl?gene=PLG
TYRO3	TYRO3 Protein Tyrosine Kinase	Protein Coding	Q06418	57	GC15P041557	1.455093741	https://www.genecards.org/cgi-bin/carddisp.pl?gene=TYRO3
MIR34A	MicroRNA 34a	RNA Gene		29	GC01M013270	1.455093741	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MIR34A
FN1	Fibronectin 1	Protein Coding	P02751	59	GC02M215360	1.418220282	https://www.genecards.org/cgi-bin/carddisp.pl?gene=FN1
PROS1	Protein S	Protein Coding	P07225	57	GC03M093873	1.418220282	https://www.genecards.org/cgi-bin/carddisp.pl?gene=PROS1
SCARB1	Scavenger Receptor Class B Member 1	Protein Coding	Q8WTV0	56	GC12M124776	1.418220282	https://www.genecards.org/cgi-bin/carddisp.pl?gene=SCARB1
ITGB5	Integrin Subunit Beta 5	Protein Coding	P18084	52	GC03M124761	1.418220282	https://www.genecards.org/cgi-bin/carddisp.pl?gene=ITGB5
PHACTR1	Phosphatase And Actin Regulator 1	Protein Coding	Q9C0D0	46	GC06P012717	1.418220282	https://www.genecards.org/cgi-bin/carddisp.pl?gene=PHACTR1
KNG1	Kininogen 1	Protein Coding	P01042	57	GC03P186717	1.378604531	https://www.genecards.org/cgi-bin/carddisp.pl?gene=KNG1
SIRT1	Sirtuin 1	Protein Coding	Q96EB6	57	GC10P067884	1.378604531	https://www.genecards.org/cgi-bin/carddisp.pl?gene=SIRT1
ABCA1	ATP Binding Cassette Subfamily A Member 1	Protein Coding	O95477	56	GC09M104781	1.378604531	https://www.genecards.org/cgi-bin/carddisp.pl?gene=ABCA1
ADAM9	ADAM Metallopeptidase Domain 9	Protein Coding	Q13443	56	GC08P038996	1.378604531	https://www.genecards.org/cgi-bin/carddisp.pl?gene=ADAM9
TGM2	Transglutaminase 2	Protein Coding	P21980	56	GC20M038127	1.378604531	https://www.genecards.org/cgi-bin/carddisp.pl?gene=TGM2
CD14	CD14 Molecule	Protein Coding	P08571	55	GC05M140631	1.378604531	https://www.genecards.org/cgi-bin/carddisp.pl?gene=CD14
GABARAP	GABA Type A Receptor-Associated Protein	Protein Coding	O95166	51	GC17M007240	1.378604531	https://www.genecards.org/cgi-bin/carddisp.pl?gene=GABARAP
S1PR5	Sphingosine-1-Phosphate Receptor 5	Protein Coding	Q9H228	51	GC19M010512	1.378604531	https://www.genecards.org/cgi-bin/carddisp.pl?gene=S1PR5
IL33	Interleukin 33	Protein Coding	O95760	48	GC09P008905	1.378604531	https://www.genecards.org/cgi-bin/carddisp.pl?gene=IL33
DYNLT1	Dynein Light Chain Tctex-Type 1	Protein Coding	P63172	47	GC06M158636	1.378604531	https://www.genecards.org/cgi-bin/carddisp.pl?gene=DYNLT1
MIR126	MicroRNA 126	RNA Gene		29	GC09P136670	1.378604531	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MIR126
ST2	Suppression Of Tumorigenicity 2	Genetic Locus		10	GC11U990127	1.378604531	https://www.genecards.org/cgi-bin/carddisp.pl?gene=ST2
MPO	Myeloperoxidase	Protein Coding	P05164	61	GC17M058269	1.335524917	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MPO
NLRP3	NLR Family Pyrin Domain Containing 3	Protein Coding	Q96P20	57	GC01P247416	1.335524917	https://www.genecards.org/cgi-bin/carddisp.pl?gene=NLRP3

Table S1 (continued)

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Gene Symbol	Description	Category	Uniprot ID	Gifts	GC Id	Relevance score	GeneCards Link
<i>ANXA1</i>	Annexin A1	Protein Coding	P04083	55	GC09P073151	1.335524917	https://www.genecards.org/cgi-bin/carddisp.pl?gene=ANXA1
<i>FPR2</i>	Formyl Peptide Receptor 2	Protein Coding	P25090	54	GC19P051752	1.335524917	https://www.genecards.org/cgi-bin/carddisp.pl?gene=FPR2
<i>MSR1</i>	Macrophage Scavenger Receptor 1	Protein Coding	P21757	54	GC08M016107	1.335524917	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MSR1
<i>WDFY3</i>	WD Repeat And FYVE Domain Containing 3	Protein Coding	Q8LZQ1	49	GC04M084751	1.335524917	https://www.genecards.org/cgi-bin/carddisp.pl?gene=WDFY3
<i>LINC02605</i>	Long Intergenic Non-Protein Coding RNA 2605	RNA Gene		19	GC08P078838	1.335524917	https://www.genecards.org/cgi-bin/carddisp.pl?gene=LINC02605
<i>SIRT6</i>	Sirtuin 6	Protein Coding	Q8N6T7	52	GC19M004174	1.287874222	https://www.genecards.org/cgi-bin/carddisp.pl?gene=SIRT6
<i>RAB17</i>	RAB17, Member RAS Oncogene Family	Protein Coding	Q9H0T7	45	GC02M237574	1.287874222	https://www.genecards.org/cgi-bin/carddisp.pl?gene=RAB17
<i>SERPINA1</i>	Serpin Family A Member 1	Protein Coding	P01009	58	GC14M094376	1.233788133	https://www.genecards.org/cgi-bin/carddisp.pl?gene=SERPINA1
<i>PLCG1</i>	Phospholipase C Gamma 1	Protein Coding	P19174	57	GC20P041136	1.233788133	https://www.genecards.org/cgi-bin/carddisp.pl?gene=PLCG1
<i>VTN</i>	Vitronectin	Protein Coding	P04004	52	GC17M071093	1.233788133	https://www.genecards.org/cgi-bin/carddisp.pl?gene=VTN
<i>ABCG1</i>	ATP Binding Cassette Subfamily G Member 1	Protein Coding	P45844	51	GC21P042199	1.233788133	https://www.genecards.org/cgi-bin/carddisp.pl?gene=ABCG1
<i>ABCC11</i>	ATP Binding Cassette Subfamily C Member 11	Protein Coding	Q96J66	50	GC16M048166	1.233788133	https://www.genecards.org/cgi-bin/carddisp.pl?gene=ABCC11
<i>EDIL3</i>	EGF Like Repeats And Discoidin Domains 3	Protein Coding	O43854	45	GC05M083940	1.233788133	https://www.genecards.org/cgi-bin/carddisp.pl?gene=EDIL3
<i>SCARF1</i>	Scavenger Receptor Class F Member 1	Protein Coding	Q14162	44	GC17M016128	1.233788133	https://www.genecards.org/cgi-bin/carddisp.pl?gene=SCARF1
<i>MIR148B</i>	MicroRNA 148b	RNA Gene		28	GC12P054337	1.233788133	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MIR148B
<i>MEG8</i>	Maternally Expressed 8, Small Nucleolar RNA Host Gene	RNA Gene		27	GC14P115584	1.233788133	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MEG8
<i>CERNA3</i>	Competing Endogenous LncRNA 3 For MiR-645	RNA Gene		19	GC08P056101	1.233788133	https://www.genecards.org/cgi-bin/carddisp.pl?gene=CERNA3
<i>SMILR</i>	Smooth Muscle Induced LncRNA, Enhancer Of Proliferation	RNA Gene		15	GC08M122412	1.233788133	https://www.genecards.org/cgi-bin/carddisp.pl?gene=SMILR
<i>LINC01150</i>	Long Intergenic Non-Protein Coding RNA 1150	RNA Gene		14	GC11P007437	1.233788133	https://www.genecards.org/cgi-bin/carddisp.pl?gene=LINC01150
<i>PPARG</i>	Peroxisome Proliferator Activated Receptor Gamma	Protein Coding	P37231	61	GC03P012287	1.169632077	https://www.genecards.org/cgi-bin/carddisp.pl?gene=PPARG
<i>CALR</i>	Calreticulin	Protein Coding	P27797	60	GC19P012938	1.169632077	https://www.genecards.org/cgi-bin/carddisp.pl?gene=CALR
<i>APOE</i>	Apolipoprotein E	Protein Coding	P02649	58	GC19P103269	1.169632077	https://www.genecards.org/cgi-bin/carddisp.pl?gene=APOE
<i>IGF2R</i>	Insulin Like Growth Factor 2 Receptor	Protein Coding	P11717	55	GC06P159969	1.169632077	https://www.genecards.org/cgi-bin/carddisp.pl?gene=IGF2R
<i>NCF1</i>	Neutrophil Cytosolic Factor 1	Protein Coding	P14598	55	GC07P084363	1.169632077	https://www.genecards.org/cgi-bin/carddisp.pl?gene=NCF1
<i>RMRP</i>	RNA Component Of Mitochondrial RNA Processing Endoribonuclease	RNA Gene		30	GC09M035655	1.169632077	https://www.genecards.org/cgi-bin/carddisp.pl?gene=RMRP
<i>ITGB3</i>	Integrin Subunit Beta 3	Protein Coding	P05106	61	GC17P101809	1.086022377	https://www.genecards.org/cgi-bin/carddisp.pl?gene=ITGB3
<i>ITGAV</i>	Integrin Subunit Alpha V	Protein Coding	P06756	56	GC02P186589	1.086022377	https://www.genecards.org/cgi-bin/carddisp.pl?gene=ITGAV
<i>TREM2</i>	Triggering Receptor Expressed On Myeloid Cells 2	Protein Coding	Q9NZC2	53	GC06M090931	1.086022377	https://www.genecards.org/cgi-bin/carddisp.pl?gene=TREM2
<i>UCP2</i>	Uncoupling Protein 2	Protein Coding	P55851	55	GC11M073974	0.884170473	https://www.genecards.org/cgi-bin/carddisp.pl?gene=UCP2
<i>ACKR2</i>	Atypical Chemokine Receptor 2	Protein Coding	O00590	49	GC03P042804	0.884170473	https://www.genecards.org/cgi-bin/carddisp.pl?gene=ACKR2
<i>MBL2</i>	Mannose Binding Lectin 2	Protein Coding	P11226	55	GC10M052760	0.755260527	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MBL2
<i>MIR21</i>	MicroRNA 21	RNA Gene		31	GC17P102034	0.69923538	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MIR21
<i>NRP2</i>	Neuropilin 2	Protein Coding	O60462	52	GC02P205681	0.494434059	https://www.genecards.org/cgi-bin/carddisp.pl?gene=NRP2
<i>TGFB1</i>	Transforming Growth Factor Beta 1	Protein Coding	P01137	61	GC19M041301	0.451354474	https://www.genecards.org/cgi-bin/carddisp.pl?gene=TGFB1

Table S1 (continued)

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TGFB3	Transforming Growth Factor Beta 3	Protein Coding	P10600	56	GC14M075958	0.403703719	https://www.genecards.org/cgi-bin/carddisp.pl?gene=TGFB3
IL6	Interleukin 6	Protein Coding	P05231	60	GC07P022725	0.34961769	https://www.genecards.org/cgi-bin/carddisp.pl?gene=IL6
TLR9	Toll Like Receptor 9	Protein Coding	Q9NR96	54	GC03M053612	0.34961769	https://www.genecards.org/cgi-bin/carddisp.pl?gene=TLR9
MFGE8	Milk Fat Globule EGF And Factor V/VIII Domain Containing	Protein Coding	Q08431	51	GC15M088898	0.34961769	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MFGE8
PLGRKT	Plasminogen Receptor With A C-Terminal Lysine	Protein Coding	Q9HBL7	41	GC09M005357	0.34961769	https://www.genecards.org/cgi-bin/carddisp.pl?gene=PLGRKT
MIR7-3HG	MIR7-3 Host Gene	RNA Gene	Q8N6C7	33	GC19P102033	0.34961769	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MIR7-3HG
C3	Complement C3	Protein Coding	P01024	58	GC19M006677	0.285461634	https://www.genecards.org/cgi-bin/carddisp.pl?gene=C3
CASP3	Caspase 3	Protein Coding	P42574	58	GC04M184627	0.285461634	https://www.genecards.org/cgi-bin/carddisp.pl?gene=CASP3
CASP1	Caspase 1	Protein Coding	P29466	57	GC11M105025	0.285461634	https://www.genecards.org/cgi-bin/carddisp.pl?gene=CASP1
GATA2	GATA Binding Protein 2	Protein Coding	P23769	57	GC03M128479	0.285461634	https://www.genecards.org/cgi-bin/carddisp.pl?gene=GATA2
ANXA2	Annexin A2	Protein Coding	P07355	56	GC15M060347	0.285461634	https://www.genecards.org/cgi-bin/carddisp.pl?gene=ANXA2
ALOX12	Arachidonate 12-Lipoxygenase, 12S Type	Protein Coding	P18054	53	GC17P100409	0.285461634	https://www.genecards.org/cgi-bin/carddisp.pl?gene=ALOX12
SIRPA	Signal Regulatory Protein Alpha	Protein Coding	P78324	53	GC20P001894	0.285461634	https://www.genecards.org/cgi-bin/carddisp.pl?gene=SIRPA
IFNB1	Interferon Beta 1	Protein Coding	P01574	52	GC09M021077	0.285461634	https://www.genecards.org/cgi-bin/carddisp.pl?gene=IFNB1
XRCC4	X-Ray Repair Cross Complementing 4	Protein Coding	Q13426	52	GC05P083077	0.285461634	https://www.genecards.org/cgi-bin/carddisp.pl?gene=XRCC4
XKR4	XK Related 4	Protein Coding	Q5GH76	41	GC08P055102	0.285461634	https://www.genecards.org/cgi-bin/carddisp.pl?gene=XKR4
QPCTL	GlutaminyI-Peptide Cyclotransferase Like	Protein Coding	Q9NXS2	39	GC19P045692	0.285461634	https://www.genecards.org/cgi-bin/carddisp.pl?gene=QPCTL
ARHGEF33	Rho Guanine Nucleotide Exchange Factor 33	Protein Coding	A8MVX0	32	GC02P038958	0.285461634	https://www.genecards.org/cgi-bin/carddisp.pl?gene=ARHGEF33
MIR33A	MicroRNA 33a	RNA Gene		25	GC22P041900	0.285461634	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MIR33A
MIR33B	MicroRNA 33b	RNA Gene		25	GC17M017813	0.285461634	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MIR33B
TMEM256-PLSCR3	TMEM256-PLSCR3 Readthrough (NMD Candidate)	RNA Gene		23	GC17M016959	0.285461634	https://www.genecards.org/cgi-bin/carddisp.pl?gene=TMEM256-PLSCR3
PWAR1	Prader Willi/Angelman Region RNA 1	RNA Gene		21	GC15P025135	0.285461634	https://www.genecards.org/cgi-bin/carddisp.pl?gene=PWAR1
LINC01672	Long Intergenic Non-Protein Coding RNA 1672	RNA Gene		18	GC01P011469	0.285461634	https://www.genecards.org/cgi-bin/carddisp.pl?gene=LINC01672
PWAR6	Prader Willi/Angelman Region RNA 6	RNA Gene		18	GC15P025031	0.285461634	https://www.genecards.org/cgi-bin/carddisp.pl?gene=PWAR6
SOD2-OT1	SOD2 Overlapping Transcript 1	RNA Gene		18	GC06M159772	0.285461634	https://www.genecards.org/cgi-bin/carddisp.pl?gene=SOD2-OT1
PGR-AS1	PGR Antisense RNA 1	RNA Gene		16	GC11P101131	0.285461634	https://www.genecards.org/cgi-bin/carddisp.pl?gene=PGR-AS1
TRE-TTC3-1	TRNA-Glu (Anticodon TTC) 3-1	RNA Gene		15	GC01P019713	0.285461634	https://www.genecards.org/cgi-bin/carddisp.pl?gene=TRE-TTC3-1
LOC106694316	Enhancer Region In Introns 7-9 Of MPO	Functional Element		9	GC17P102012	0.285461634	https://www.genecards.org/cgi-bin/carddisp.pl?gene=LOC106694316
MTOR	Mechanistic Target Of Rapamycin Kinase	Protein Coding	P42345	64	GC01M011106	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MTOR
ELANE	Elastase, Neutrophil Expressed	Protein Coding	P08246	60	GC19P101835	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=ELANE
NFE2L2	NFE2 Like BZIP Transcription Factor 2	Protein Coding	Q16236	60	GC02M177227	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=NFE2L2
TLR3	Toll Like Receptor 3	Protein Coding	O15455	60	GC04P186059	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=TLR3
ALDH2	Aldehyde Dehydrogenase 2 Family Member	Protein Coding	P05091	59	GC12P111766	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=ALDH2
GAPDH	Glyceraldehyde-3-Phosphate Dehydrogenase	Protein Coding	P04406	59	GC12P035940	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=GAPDH

Table S1 (continued)

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<i>IL1RN</i>	Interleukin 1 Receptor Antagonist	Protein Coding	P18510	58	GC02P141242	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=IL1RN
<i>IL6R</i>	Interleukin 6 Receptor	Protein Coding	P08887	58	GC01P154405	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=IL6R
<i>PTPN6</i>	Protein Tyrosine Phosphatase Non-Receptor Type 6	Protein Coding	P29350	57	GC12P035963	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=PTPN6
<i>CLU</i>	Clusterin	Protein Coding	P10909	56	GC08M027596	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=CLU
<i>IL1B</i>	Interleukin 1 Beta	Protein Coding	P01584	56	GC02M112829	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=IL1B
<i>ANG</i>	Angiogenin	Protein Coding	P03950	54	GC14P043150	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=ANG
<i>IRF3</i>	Interferon Regulatory Factor 3	Protein Coding	Q14653	54	GC19M049659	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=IRF3
<i>NTN1</i>	Netrin 1	Protein Coding	O95631	54	GC17P100538	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=NTN1
<i>TNFSF13B</i>	TNF Superfamily Member 13b	Protein Coding	Q9Y275	54	GC13P108251	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=TNFSF13B
<i>EGLN3</i>	Egl-9 Family Hypoxia Inducible Factor 3	Protein Coding	Q9H6Z9	53	GC14M033924	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=EGLN3
<i>LGALS3</i>	Galectin 3	Protein Coding	P17931	53	GC14P055124	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=LGALS3
<i>CRK</i>	CRK Proto-Oncogene, Adaptor Protein	Protein Coding	P46108	52	GC17M001420	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=CRK
<i>NRF1</i>	Nuclear Respiratory Factor 1	Protein Coding	Q16656	52	GC07P129611	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=NRF1
<i>SFTPD</i>	Surfactant Protein D	Protein Coding	P35247	52	GC10M079937	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=SFTPD
<i>UBE2D3</i>	Ubiquitin Conjugating Enzyme E2 D3	Protein Coding	P61077	52	GC04M102794	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=UBE2D3
<i>ALOX15B</i>	Arachidonate 15-Lipoxygenase Type B	Protein Coding	O15296	49	GC17P008039	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=ALOX15B
<i>LGR6</i>	Leucine Rich Repeat Containing G Protein-Coupled Receptor 6	Protein Coding	Q9HBX8	49	GC01P202193	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=LGR6
<i>GPR101</i>	G Protein-Coupled Receptor 101	Protein Coding	Q96P66	48	GC0XM137030	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=GPR101
<i>FGL2</i>	Fibrinogen Like 2	Protein Coding	Q14314	47	GC07M077193	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=FGL2
<i>GPR18</i>	G Protein-Coupled Receptor 18	Protein Coding	Q14330	47	GC13M099254	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=GPR18
<i>ID3</i>	Inhibitor Of DNA Binding 3	Protein Coding	Q02535	47	GC01M023557	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=ID3
<i>CD5L</i>	CD5 Molecule Like	Protein Coding	O43866	46	GC01M160073	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=CD5L
<i>SIAH2</i>	Siah E3 Ubiquitin Protein Ligase 2	Protein Coding	O43255	46	GC03M150741	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=SIAH2
<i>FPR3</i>	Formyl Peptide Receptor 3	Protein Coding	P25089	43	GC19P051795	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=FPR3
<i>GAS5</i>	Growth Arrest Specific 5	RNA Gene		30	GC01M173947	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=GAS5
<i>MIRLET7D</i>	MicroRNA Let-7d	RNA Gene		29	GC09P094178	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MIRLET7D
<i>MIR125A</i>	MicroRNA 125a	RNA Gene		28	GC19P103569	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MIR125A
<i>MIRLET7C</i>	MicroRNA Let-7c	RNA Gene		28	GC21P017033	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MIRLET7C
<i>MIR216A</i>	MicroRNA 216a	RNA Gene		27	GC02M055988	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MIR216A
<i>LINC01587</i>	Long Intergenic Non-Protein Coding RNA 1587	RNA Gene	Q99440	26	GC04P005524	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=LINC01587
<i>MIR409</i>	MicroRNA 409	RNA Gene		25	GC14P115610	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MIR409
<i>SNHG14</i>	Small Nucleolar RNA Host Gene 14	RNA Gene		24	GC15P147532	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=SNHG14
<i>MIR379</i>	MicroRNA 379	RNA Gene		22	GC14P115605	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MIR379
<i>MIR190B</i>	MicroRNA 190b	RNA Gene		21	GC01M154193	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MIR190B

Table S1 (continued)

Table S1 (continued)

Gene Symbol	Description	Category	Uniprot ID	Gifts	GC Id	Relevance score	GeneCards Link
<i>RAB4B-EGLN2</i>	RAB4B-EGLN2 Readthrough (NMD Candidate)	RNA Gene		19	GC19P040778	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=RAB4B-EGLN2
<i>MIR1293</i>	MicroRNA 1293	RNA Gene		17	GC12M050234	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MIR1293
<i>PWAR4</i>	Prader Willi/Angelman Region RNA 4	RNA Gene		15	GC15P025211	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=PWAR4
<i>TRA-TGC7-1</i>	TRNA-Ala (Anticodon TGC) 7-1	RNA Gene		14	GC06M090560	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=TRA-TGC7-1
<i>MBL3P</i>	Mannose-Binding Lectin Family Member 3, Pseudogene	Pseudogene		9	GC10M083328	0.20185186	https://www.genecards.org/cgi-bin/carddisp.pl?gene=MBL3P

Table S2 Steiger Filtering Analysis Applied to GTEx Blood and Lung cis-eQTLs for Directional Validation with LUAD GWAS

A																					
SNP	effect_allele.exposure	other_allele.exposure	effect_allele.outcome	other_allele.outcome	beta.exposure	beta.outcome	eaf.exposure	eaf.outcome	remove	palindromic	ambiguous	id.outcome	pval.outcome	chr.outcome	pos.outcome	se.outcome	outcome	mr_keep.outcome	pval_origin.outcome	samplesize.outcome	gene.exposure
rs9749078	T	C	T	C	0.0890557	-0.067008	0.666	0.316176	FALSE	FALSE	FALSE	GCST004744	0.00017112	19	10636904	0.01783	outcome	TRUE	reported	66756	S1PR5
rs12373520	A	G	A	G	0.157826	-0.052281	0.5795	0.39824	FALSE	FALSE	FALSE	GCST004744	0.0015196	19	10641055	0.016488	outcome	TRUE	reported	66756	S1PR5
B																					
SNP	pval.exposure	se.exposure	id.exposure	exposure	mr_keep.exposure	pval_origin.exposure	data_source.exposure	F1	samplesize.exposure	action	SNP_index	mr_keep	units.outcome	units.exposure	rsq.exposure	effective_n.exposure	rsq.outcome	effective_n.outcome	steiger_dir	steiger_pval	
rs9749078	1.82E-10	0.0139683	S1PR5 cis-eQTL from GTEx Blood Tissue	S1PR5	TRUE	reported	textfile	40.6477336	670	2	1	TRUE	NA	NA	0.05735958670		0.00021153	66756	TRUE	3.57E-09	
rs12373520	2.21E-06	0.0333422	S1PR5 cis-eQTL from GTEx LungTissue	S1PR5	TRUE	reported	textfile	22.40622	515	2	1	TRUE	NA	NA	0.04184901515		0.00015059	66756	TRUE	1.08E-05	

Table S3 Summary-based Mendelian Randomization Analysis Linking GTEx Blood cis-eQTLs to LUAD GWAS Data

probeID	Probe Chr	Gene	Probe_bp	topSNP	topSNP_chr	topSNP_bp	A1	A2	Freq	b_GWAS	se_GWAS	p_GWAS	b_eQTL	se_eQTL	p_eQTL	b_SMR	se_SMR	p_SMR	p_HEIDI	nsnp_HEIDI	FDR
ENSG00000180739	19	S1PR5	10623623	rs9749078	19	10636904	T	C	0.333996	-0.067008	0.01783	0.00017112	0.0890557	0.0139683	1.82E-10	-0.752428	0.232407	0.00120563	0.5925898	5	0.02652388
ENSG00000181788	3	SIAH2	150458914	rs1991781	3	150468433	A	G	0.027833	-0.066248	0.047714	0.1650066	0.283617	0.0484465	4.79E-09	-0.233583	0.172901	0.1767069	0.3532223	5	0.6479253
ENSG00000164342	4	TLR3	186990306	rs7687961	4	187122009	A	C	0.82008	-0.029295	0.020328	0.1495562	-0.225767	0.0379508	2.70E-09	0.129758	0.092644	0.1613322	0.0865166	10	0.6479253
ENSG00000158517	7	NCF1	74188309	rs35005436	7	74134911	T	C	0.846918	-0.032003	0.022742	0.1593695	-0.121025	0.0216824	2.38E-08	0.264433	0.193791	0.1724029	0.1101009	3	0.6479253
ENSG00000073060	12	SCARB1	125261402	rs41276688	12	125399133	T	C	0.0477137	0.056631	0.0363	0.1187398	0.462405	0.0812503	1.26E-08	0.122471	0.0813987	0.1324332	0.1548123	5	0.6479253
ENSG00000167193	17	CRK	1323983	rs79151873	17	1355484	C	T	0.0914513	-0.059978	0.030751	0.051123	-0.135914	0.0240768	1.65E-08	0.441294	0.239378	0.06525561	0.9545702	3	0.6479253
ENSG00000113249	5	HAVCR1	156456424	rs7726326	5	156519685	G	A	0.822068	-0.023846	0.021265	0.2621163	0.291423	0.0383675	3.06E-14	-0.0818261	0.0737605	0.2672798	0.545358	17	0.73962362
ENSG00000127951	7	FGL2	76822688	rs66471312	7	76851105	C	T	0.166998	-0.023673	0.021919	0.2801278	-0.141848	0.0216629	5.83E-11	0.16689	0.156612	0.2865937	0.836192	12	0.73962362
ENSG00000175567	11	UCP2	73685712	rs632862	11	73693421	G	C	0.372763	-0.017316	0.016753	0.3013345	0.31768	0.0221557	1.26E-46	-0.0545077	0.0528723	0.3025733	0.2058826	20	0.73962362
ENSG00000234741	1	GAS5	173833038	rs143997356	1	173418414	A	G	0.026839	0.051698	0.061054	0.3971338	0.48145	0.0654133	1.84E-13	0.10738	0.127649	0.4002304	0.2689949	3	0.7423163
ENSG00000164305	4	CASP3	185548850	rs72689254	4	185589941	T	C	0.115308	-0.020989	0.023956	0.3809539	-0.211096	0.0249501	2.66E-17	0.0994287	0.114091	0.3834879	0.6866524	20	0.7423163
ENSG00000112137	6	PHACTR1	12717893	rs1223562	6	13194777	T	A	0.276342	0.012325	0.017715	0.4865875	-0.202751	0.024058	3.53E-17	-0.0607889	0.0876704	0.4880716	0.9468767	15	0.7423163
ENSG00000038945	8	MSR1	15965387	rs55979812	8	16405213	T	A	0.417495	-0.010133	0.016333	0.5350108	-0.429688	0.0303906	2.19E-45	0.0235822	0.0380479	0.5353868	0.5396075	20	0.7423163
ENSG00000107020	9	PLGRKT	5357973	rs2381277	9	5381870	G	A	0.646123	0.010626	0.0173	0.5390644	-0.196697	0.0200862	1.21E-22	-0.0540222	0.0881254	0.5398664	0.3435321	20	0.7423163
ENSG00000119699	14	TGFB3	76424442	rs146047341	14	76448921	A	G	0.0447316	0.02918	0.041147	0.4782158	-0.58578	0.0618709	2.86E-21	-0.0498139	0.0704399	0.4794523	0.4617974	8	0.7423163
ENSG00000225783	22	MIAT	27042392	rs6005127	22	27069557	T	C	0.26839	0.013737	0.018512	0.4580469	0.484913	0.0341089	7.23E-46	0.0283288	0.0382279	0.4586629	0.04580635	20	0.7423163
ENSG00000162711	1	NLRP3	247579458	rs56285508	1	247554488	T	G	0.0656064	-0.008829	0.034456	0.797768	0.376895	0.0511204	1.67E-13	-0.0234256	0.0914759	0.797885	0.5650376	3	0.83587952
ENSG00000120217	9	CD274	5450503	rs59906468	9	5466085	G	A	0.234592	-0.005905	0.019929	0.7670214	0.255838	0.0246864	3.63E-25	-0.023081	0.0779288	0.767092	0.6894058	11	0.83587952
ENSG00000135046	9	ANXA1	75766673	rs10081652	9	75864067	A	T	0.740557	-0.007967	0.01814	0.6605202	0.18366	0.0185912	5.14E-23	-0.0433791	0.098867	0.6608342	0.7566723	20	0.83587952
ENSG00000096717	10	SIRT1	69644427	rs10997883	10	69697965	C	T	0.666004	-0.006805	0.017484	0.6970942	-0.267655	0.0188501	9.27E-46	0.0254245	0.0653474	0.6972267	0.178144	20	0.83587952
ENSG00000140545	15	MFGE8	89441916	rs8030053	15	89480391	G	A	0.67495	-0.005719	0.017521	0.7440988	0.24976	0.0303348	1.82E-16	-0.022898	0.0702065	0.7443093	0.6247747	20	0.83587952
ENSG00000111275	12	ALDH2	112204691	rs2238151	12	112211833	C	T	0.313121	-0.001071	0.017601	0.9514902	0.172545	0.0289862	2.64E-09	-0.0062071	0.102014	0.9514821	0.846057	5	0.9514821

Table S4 Summary-based Mendelian Randomization Analysis Linking eQTLen cis-eQTLs to LUAD GWAS Data

probelD	ProbeChr	Gene	Probe_bp	topSNP	topSNP_chr	topSNP_bp	A1	A2	Freq	b_GWAS	se_GWAS	p_GWAS	b_eQTL	se_eQTL	p_eQTL	b_SMR	se_SMR	p_SMR	p_HEIDI	nsnp_HEIDI	FDR
ENSG00000180739	19	S1PR5	10626115	rs28580742	19	10635196	C	T	0.351889	-0.058607	0.017481	0.00080036	0.176582	0.00894593	1.00E-86	-0.331897	0.100414	0.00094884	0.08035937	20	0.04649294
ENSG00000126456	19	IRF3	50165979	rs7259683	19	50153332	C	T	0.256461	0.053963	0.018414	0.00338431	0.292491	0.00888771	1.60E-237	0.184495	0.0632049	0.00351166	0.2234669	20	0.0860356
ENSG00000183087	13	GAS6	114545285	rs7338868	13	114634184	G	T	0.354871	-0.04415	0.017885	0.01356773	0.171163	0.00902036	2.73E-80	-0.257941	0.105371	0.0143683	0.03229017	20	0.23468223
ENSG00000175567	11	UCP2	73690032	rs643064	11	73684715	T	C	0.133201	-0.055195	0.024195	0.02253612	0.583099	0.0107345	0	-0.0946581	0.0415304	0.02265236	0.35754	20	0.27749141
ENSG00000120885	8	CLU	27463491	rs73231005	8	27470778	G	C	0.271372	-0.041604	0.019484	0.03273277	0.0775688	0.00924121	4.71E-17	-0.536349	0.259183	0.03851032	0.1350417	20	0.31450095
ENSG00000073060	12	SCARB1	125314308	rs7954697	12	125335253	C	A	0.400596	-0.034394	0.016483	0.0369215	0.316468	0.00785742	0	-0.108681	0.0521542	0.03717472	0.5720543	20	0.31450095
ENSG00000198959	20	TGM2	36775921	rs12624511	20	36769839	A	G	0.139165	0.046116	0.023047	0.04539854	-0.128313	0.0117911	1.40E-27	-0.359403	0.182627	0.04907229	0.1445927	20	0.34350603
ENSG00000167193	17	CRK	1345219	rs76999852	17	1338258	C	G	0.0914513	-0.055754	0.030445	0.06705411	-0.224868	0.0138955	6.67E-59	0.247941	0.136254	0.06880654	0.7597706	20	0.42144006
ENSG00000136244	7	IL6	22768562	rs10265117	7	22701636	A	G	0.10338	0.045408	0.025267	0.07231358	-0.117163	0.0123228	1.95E-21	-0.387563	0.219476	0.0774195	0.8612629	20	0.42150617
ENSG00000132170	3	PPARG	12402361	rs1699346	3	12504295	C	A	0.427435	-0.027803	0.016693	0.09580385	0.252822	0.00794678	4.09E-222	-0.109971	0.0661171	0.09625826	0.7071424	20	0.47166547
ENSG00000113249	5	HAVCR1	156471277	rs1501909	5	156466179	T	G	0.357853	0.025342	0.016733	0.1299085	0.098251	0.00901336	1.14E-27	0.257931	0.171945	0.1335929	0.1376495	20	0.59509565
ENSG00000117318	1	ID3	23885347	rs2742946	1	23886073	C	T	0.480119	-0.023015	0.018332	0.2093108	0.142311	0.00870364	4.29E-60	-0.161723	0.129195	0.2106535	0.4355579	20	0.64512634
ENSG00000118257	2	NRP2	206604785	rs113185080	2	206547511	G	A	0.0626243	-0.04945	0.035676	0.1657195	0.134258	0.0182005	1.62E-13	-0.368321	0.270378	0.1731204	0.06370015	14	0.64512634
ENSG00000112137	6	PHACTR1	13003269	rs538190	6	13327777	C	T	0.217694	-0.024604	0.019247	0.2011412	0.395533	0.0135137	2.57E-188	-0.0622046	0.0487073	0.2015628	0.3102868	20	0.64512634
ENSG00000137752	11	CASP1	104934164	rs2409065	11	105063849	G	A	0.0715706	0.041182	0.031888	0.1965461	0.476604	0.0147974	1.33E-227	0.0864071	0.0669604	0.1969046	0.6106518	17	0.64512634
ENSG00000160179	21	ABCG1	43668576	rs915845	21	43635438	G	T	0.144135	-0.032269	0.023634	0.172136	0.121472	0.0113642	1.15E-26	-0.265649	0.196144	0.1756218	0.05950888	20	0.64512634
ENSG00000127951	7	FGL2	76825915	rs66471312	7	76851105	C	T	0.166998	-0.023673	0.021919	0.2801278	-0.191715	0.0112005	1.12E-65	0.12348	0.114558	0.2810881	0.4866833	20	0.81019511
ENSG00000115414	2	FN1	216263029	rs10932612	2	216215102	C	T	0.375746	-0.01229	0.016503	0.4564352	0.14333	0.00810289	5.12E-70	-0.0857459	0.115242	0.4568438	0.6839359	20	0.82546977
ENSG00000179348	3	GATA2	128205149	rs6782812	3	128317997	G	A	0.101392	0.02554	0.025209	0.3109999	-0.192735	0.0123057	2.74E-55	-0.132514	0.13107	0.3120082	0.9861424	20	0.82546977
ENSG00000164305	4	CASP3	185559756	rs72689261	4	185590897	A	C	0.115308	-0.020437	0.023949	0.3934692	-0.489507	0.0118499	0	0.0417501	0.0489351	0.3935634	0.4801363	20	0.82546977
ENSG00000164342	4	TLR3	186998280	rs7663027	4	187112629	C	G	0.370775	-0.012651	0.018006	0.4823058	-0.142497	0.00836424	4.41E-65	0.0887811	0.126468	0.4826777	0.6349484	20	0.82546977
ENSG00000158517	7	NCF1	74195984	rs810366	7	74140925	C	G	0.193837	0.016997	0.020469	0.4063303	0.429353	0.0114479	7.64E-308	0.0395875	0.0476858	0.4064403	0.06888156	20	0.82546977
ENSG00000038945	8	MSR1	16195193	rs55979812	8	16405213	T	A	0.417495	-0.010133	0.016333	0.5350108	-0.379173	0.00778131	0	0.0267239	0.0430788	0.5350273	0.4471345	20	0.82546977
ENSG00000107020	9	PLGRKT	5397925	rs2381277	9	5381870	A	G	0.353877	-0.010626	0.0173	0.5390644	0.654003	0.00823307	0	-0.0162476	0.0264533	0.5390823	0.2844861	20	0.82546977
ENSG00000129521	14	EGLN3	34662708	rs12586857	14	34500601	T	C	0.259443	0.013855	0.018888	0.4632297	-0.200203	0.00909997	2.85E-107	-0.0692048	0.0943967	0.4634809	0.5117555	20	0.82546977
ENSG00000119699	14	TGFB3	76436888	rs146047341	14	76448921	A	G	0.0447316	0.02918	0.041147	0.4782158	-0.620411	0.0207374	1.17E-196	-0.0470333	0.0663408	0.4783459	0.2971716	20	0.82546977
ENSG00000182718	15	ANXA2	60667207	rs62004990	15	60686631	T	C	0.271372	0.017672	0.018514	0.3398022	0.28109	0.00918197	8.17E-206	0.0628696	0.0658971	0.3400547	0.05688876	20	0.82546977
ENSG000000259207	17	ITGB3	45376435	rs7210182	17	45327140	A	G	0.244533	-0.013289	0.019492	0.4953693	-0.171703	0.0140751	3.15E-34	0.0773955	0.113699	0.4960584	0.5410865	20	0.82546977
ENSG00000005381	17	MPO	56352756	rs12940119	17	56373613	C	T	0.172962	0.018079	0.022113	0.4135958	0.409196	0.0111353	1.27E-295	0.0441817	0.0540535	0.4137164	0.3754051	20	0.82546977
ENSG00000197561	19	ELANE	853628	rs2007647	19	851976	A	G	0.22167	-0.016332	0.024876	0.5114721	-0.152954	0.013128	2.27E-31	0.106777	0.162895	0.5121481	0.2920602	20	0.82546977
ENSG00000124181	20	PLCG1	39795513	rs2072967	20	40003221	A	G	0.054672	-0.028907	0.038874	0.4571185	-0.135184	0.017716	2.34E-14	0.213835	0.288926	0.4592383	0.615829	20	0.82546977
ENSG000000225783	22	MIAT	27057415	rs9625066	22	27068702	A	C	0.26839	0.014311	0.018497	0.4391223	0.67544	0.00977789	0	0.0211877	0.0273868	0.439141	0.08855927	20	0.82546977
ENSG00000125730	19	C3	6704144	rs339392	19	6722022	G	T	0.183897	-0.010673	0.020189	0.5970344	-0.0919391	0.0105965	4.08E-18	0.116088	0.219998	0.5977245	0.04137854	20	0.86833289
ENSG00000187474	19	FPR3	52313929	rs7245506	19	52296292	T	C	0.374751	-0.008774	0.016844	0.6024406	0.205958	0.00823405	4.41E-138	-0.0426008	0.0818013	0.6025167	0.5017726	20	0.86833289
ENSG00000135046	9	ANXA1	75775991	rs7867580	9	75852207	A	G	0.260437	0.008602	0.018131	0.6352031	-0.410361	0.00880091	0	-0.020962	0.0441853	0.6352065	0.9627323	20	0.8892891

Table S4 (continued)

Table S4 (continued)

probelD	ProbeChr	Gene	Probe_bp	topSNP	topSNP_chr	topSNP_bp	A1	A2	Freq	b_GWAS	se_GWAS	p_GWAS	b_eQTL	se_eQTL	p_eQTL	b_SMR	se_SMR	p_SMR	p_HEIDI	nsnp_HEIDI	FDR
ENSG00000234741	1	GAS5	173835529	rs78332745	1	174453039	T	C	0.0357853	-0.014925	0.04608	0.7460261	0.175635	0.032216	4.99E-08	-0.0849774	0.262825	0.7464505	0.4870362	6	0.91701863
ENSG00000199133	9	MIRLET7D	96941159	rs10761322	9	96937478	C	T	0.384692	0.005254	0.016597	0.7515748	-0.121402	0.0107062	8.37E-30	-0.0432777	0.136764	0.7516686	0.6014805	20	0.91701863
ENSG00000111640	12	GAPDH	6645315	rs9634157	12	6648198	G	A	0.220676	-0.005987	0.020232	0.7673036	-0.395194	0.0112926	2.60E-268	0.0151495	0.0511969	0.7673013	0.4331149	20	0.91701863
ENSG00000189403	13	HMGB1	31112309	rs5026917	13	31010795	C	A	0.389662	-0.005342	0.017621	0.761753	0.0700332	0.00895542	5.27E-15	-0.0762781	0.251798	0.7619406	0.5173763	19	0.91701863
ENSG00000224078	15	SNHG14	25444656	rs7180310	15	25339337	A	C	0.0586481	-0.010412	0.034864	0.7652003	-0.232044	0.0192195	1.46E-33	0.0448708	0.150293	0.7652797	0.02860111	20	0.91701863
ENSG00000171049	19	FPR2	52264529	rs17694990	19	52267703	G	T	0.40159	0.006192	0.016506	0.7075458	-0.706067	0.00713873	0	-0.0087697	0.0233776	0.7075611	0.9116422	20	0.91701863
ENSG00000011478	19	QPCTL	46201494	rs17850756	19	46206262	A	G	0.285288	-0.004339	0.01743	0.8034223	-0.100765	0.00872002	6.92E-31	0.0430606	0.173017	0.8034529	0.8516345	20	0.93736172
ENSG00000162711	1	NLRP3	247595934	rs4925547	1	247612435	T	A	0.403579	0.002275	0.016701	0.8916501	0.270898	0.00799922	2.15E-251	0.008398	0.0616511	0.8916487	0.6886379	20	0.9554229
ENSG00000138448	2	ITGAV	187500210	rs10174098	2	187492742	G	A	0.335984	0.00126	0.017181	0.9415163	0.196577	0.00829959	5.12E-124	0.00640969	0.0874011	0.9415384	0.6039636	20	0.9554229
ENSG00000181788	3	SIAH2	150470089	rs524772	3	150447679	G	A	0.0228628	0.002871	0.051361	0.9554282	-0.460799	0.0254703	3.71E-73	-0.0062305	0.111461	0.9554229	0.2893148	12	0.9554229
ENSG00000120217	9	CD274	5460534	rs2890658	9	5465130	A	C	0.10338	-0.003336	0.028674	0.907388	0.299232	0.0141641	4.59E-99	-0.0111486	0.0958268	0.9073826	0.3963282	20	0.9554229
ENSG00000096717	10	SIRT1	69661287	rs10997832	10	69607395	C	G	0.331014	0.000982	0.017397	0.9549985	0.712669	0.0121184	0	0.00137792	0.0244111	0.9549861	0.2216805	20	0.9554229
ENSG00000111275	12	ALDH2	112226236	rs7969271	12	112156802	A	T	0.0894632	-0.002603	0.027531	0.9246679	0.450267	0.0131472	4.65E-257	-0.005781	0.061144	0.9246742	0.9995296	20	0.9554229
ENSG00000140545	15	MFGE8	89449279	rs12911703	15	89456948	A	G	0.275348	0.002859	0.018575	0.8776649	0.506632	0.00861368	0	0.00564314	0.0366638	0.8776759	0.9165302	20	0.9554229

cis-eQTL, cis-expression quantitative trait loci; LUAD, lung adenocarcinoma; GWAS, genome-wide association study; FDR, false discovery rate.

Table S5 Baseline Clinicopathological Characteristics of TCGA-LUAD Patients Stratified by *S1PR5* Expression.

Characteristics	High expression of S1PR5	Low expression of S1PR5	P
N	262	262	
Expression of S1PR5, median [IQR]	0.57 [0.45, 0.83]	0.20 [0.11, 0.27]	<0.001
Age, mean (SD)	65.66 (10.17)	64.62 (10.04)	0.25
Gender, Male, n (%)	129 (49.2)	113 (43.1)	0.19
T stage, n (%)			0.18
T1	77 (29.4)	94 (35.9)	
T2	149 (56.9)	134 (51.1)	
T3	27 (10.3)	21 (8.0)	
T4	9 (3.4)	10 (3.8)	
Unknown	0 (0.0)	3 (1.1)	
N stage, n (%)			0.03
N0	156 (59.5)	183 (69.8)	
N1	53 (20.2)	42 (16.0)	
N2	47 (17.9)	27 (10.3)	
N3	0 (0.0)	2 (0.8)	
Unknown	6 (2.3)	8 (3.1)	
M stage, n (%)			0.56
M0	173 (66.0)	180 (68.7)	
M1	15 (5.7)	10 (3.8)	
Unknown	74 (28.2)	72 (27.5)	
Stage, n (%)			0.14
Stage I	129 (49.2)	155 (59.2)	
Stage II	63 (24.0)	59 (22.5)	
Stage III	51 (19.5)	33 (12.6)	
Stage IV	15 (5.7)	11 (4.2)	
Unknown	4 (1.5)	4 (1.5)	
Race, n (%)			0.76
American Indian or Alaska native	0 (0.0)	1 (0.4)	
Asian	3 (1.1)	4 (1.5)	
Black or African American	25 (9.5)	28 (10.7)	
Unknown	36 (13.7)	30 (11.5)	
White	198 (75.6)	199 (76.0)	
Subdivision, n (%)			0.67
Acinar cell neoplasms	9 (3.4)	13 (5.0)	
Adenomas and adenocarcinomas	245 (93.5)	242 (92.4)	
Cystic, mucinous and serous neoplasms	8 (3.1)	7 (2.7)	

Table S6 Univariate and multivariate Cox regression analyses for the SENRPS model risk scores on the overall survival of TCGA-LUAD patients.

Parameters	Univariate analysis			Multivariate analysis		
	HR	95% CI	P	HR	95% CI	P
SENRPS Risk Score						
High	2.99	2.20, 4.08	<0.001	2.48	1.79, 3.43	<0.001
Low	1	1	1			
Age						
>65	1.21	0.91, 1.63	0.194			
≤65	1	1	1			
Gender						
Male	1.06	0.80, 1.42	0.684			
Famale	1	1	1			
T stage						
T1	1	1	1			
T2	1.48	1.04, 2.11	0.03	1.28	0.89, 1.85	0.18
T3	2.94	1.74, 4.94	<0.001	2.12	1.14, 3.94	0.02
T4	2.97	1.53, 5.76	0.001	1.22	0.57, 2.61	0.61
N stage						
N0	1	1	1			
N1	2.37	1.68, 3.33	<0.001	1.68	0.96, 2.94	0.07
N2	3.01	2.06, 4.40	<0.001	1.58	0.69, 3.65	0.28
N3	0	0.00, Inf	0.994	0	0, Inf	0.99
M stage						
M0	1	1	1			
M1	2.11	1.23, 3.60	0.007	0.54	0.03, 8.87	0.67
Stage						
Stage I	1	1	1			
Stage II	2.43	1.69, 3.48	<0.001	1.16	0.64, 2.13	0.63
Stage III	3.44	2.36, 5.03	<0.001	1.63	0.66, 4.05	0.29
Stage IV	3.76	2.17, 6.51	<0.001	4.45	0.25, 79.29	0.31
Race						
American Indian or Alaska native	1	1	1			
Asian	230776.97	0.00, Inf	0.994			
Black or African American	339996.49	0.00, Inf	0.994			
White	478644.3	0.00, Inf	0.994			
Subdivision						
Acinar cell neoplasms	1	1	1			
Adenomas and adenocarcinomas	2.36	0.75, 7.40	0.14			
Cystic, mucinous and serous neoplasms	1.51	0.31, 7.51	0.612			

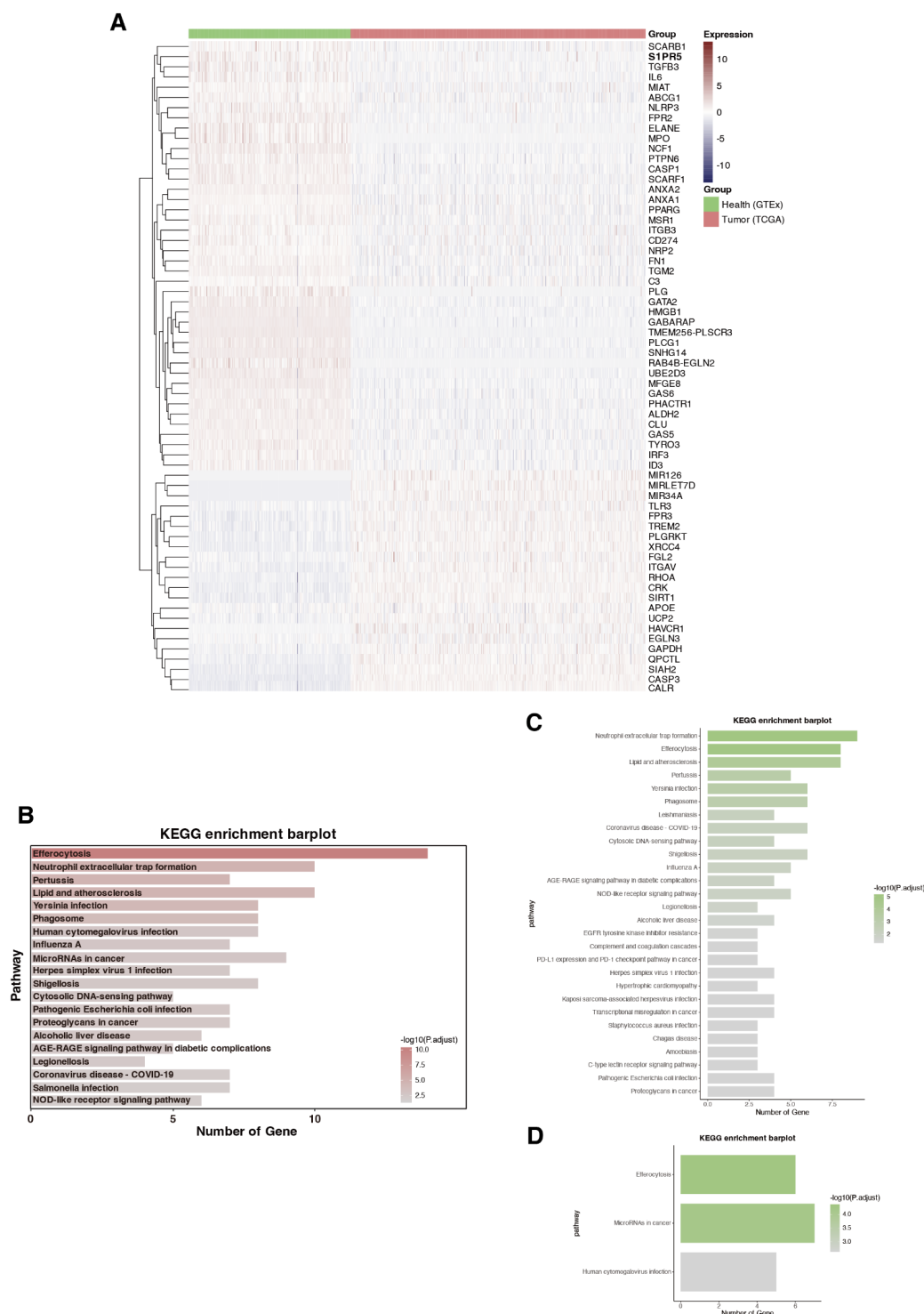
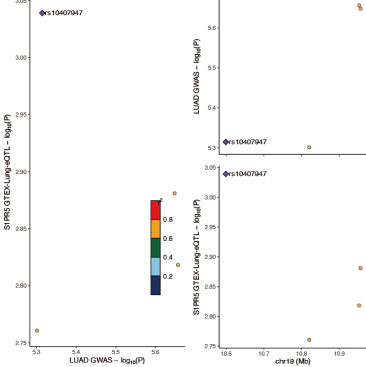


Figure S1 Expression pattern and functional analysis of differentially expressed efferocytosis-related genes (DEERGs) in TCGA-LUAD. (A) Heatmap of 64 DEERGs, with red indicating high expression and blue indicating low expression. (B) KEGG enrichment analysis of the 64 DEERGs. The x-axis represents the number of genes in each pathway, the y-axis shows the top 20 enriched pathways, and the color intensity corresponds to $-\log_{10}(P.adjust)$. (C) KEGG enrichment analysis of 42 downregulated DEERGs. (D) KEGG enrichment analysis of 22 upregulated DEERGs.

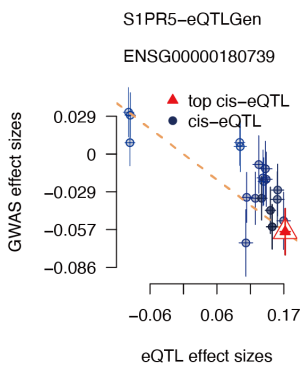
A

exposure snp	method	Pval	FDR	OR(95% CI)
ALDH2 1	Wald ratio	0.92	0.95	0.991 (0.843 to 1.166)
APOE 1	Wald ratio	0.38	0.85	0.955 (0.860 to 1.059)
CALR 1	Wald ratio	0.12	0.66	1.232 (0.946 to 1.605)
CD274 1	Wald ratio	0.60	0.89	1.035 (0.911 to 1.176)
CRK 1	Wald ratio	0.09	0.66	1.266 (0.961 to 1.668)
FPR3 1	Wald ratio	0.95	0.95	1.009 (0.765 to 1.332)
GAS5 1	Wald ratio	0.40	0.85	1.065 (0.920 to 1.233)
GATA2 1	Wald ratio	0.45	0.85	0.932 (0.778 to 1.117)
MFGE8 1	Wald ratio	0.75	0.95	1.023 (0.890 to 1.177)
MIAT 1	Wald ratio	0.44	0.85	1.040 (0.942 to 1.149)
MSR1 2	Inverse variance weighted	0.92	0.95	1.009 (0.842 to 1.209)
NLRP3 1	Wald ratio	0.46	0.85	0.924 (0.748 to 1.141)
NRP2 1	Wald ratio	0.91	0.95	1.004 (0.941 to 1.072)
PHACTR1 1	Wald ratio	0.55	0.88	0.937 (0.754 to 1.163)
PLG 1	Wald ratio	0.46	0.85	0.928 (0.760 to 1.133)
PLGRKT 1	Wald ratio	0.54	0.88	0.967 (0.870 to 1.075)
QPCTL 1	Wald ratio	0.83	0.95	1.024 (0.825 to 1.270)
S1PR5 1	Wald ratio	0.002	0.04	0.718 (0.585 to 0.881)
SIRT1 1	Wald ratio	0.27	0.85	0.857 (0.652 to 1.125)
SNHG14 1	Wald ratio	0.09	0.66	1.203 (0.970 to 1.492)
TGM2 1	Wald ratio	0.76	0.95	1.024 (0.877 to 1.196)
TREM2 1	Wald ratio	0.78	0.95	0.958 (0.710 to 1.293)
UBE2D3 1	Wald ratio	0.14	0.66	1.366 (0.905 to 2.062)
UCP2 1	Wald ratio	0.36	0.85	0.951 (0.855 to 1.058)

B



C



D

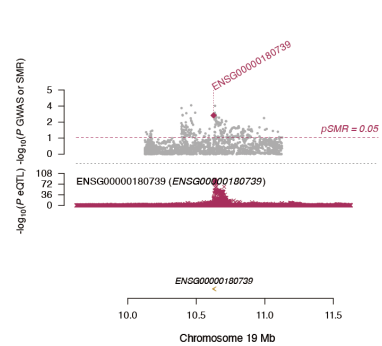


Figure S2 Mendelian Randomization and Bayesian Colocalization Analyses. (A) Mendelian randomization results using GTEx lung cis-eQTL data as the exposure and LUAD GWAS as the outcome. The odds ratios (ORs) with 95% confidence intervals are displayed for each variant. Multiple testing was adjusted using the Benjamini-Hochberg method. (B) Colocalization analysis of GTEx lung *S1PR5* cis-eQTL data and LUAD GWAS, with a posterior probability for a shared causal variant (PP.H4) of 45.6%. (C, D) Summary data-based Mendelian randomization analyses integrating eQTLGen data as the exposure and LUAD GWAS as the outcome.

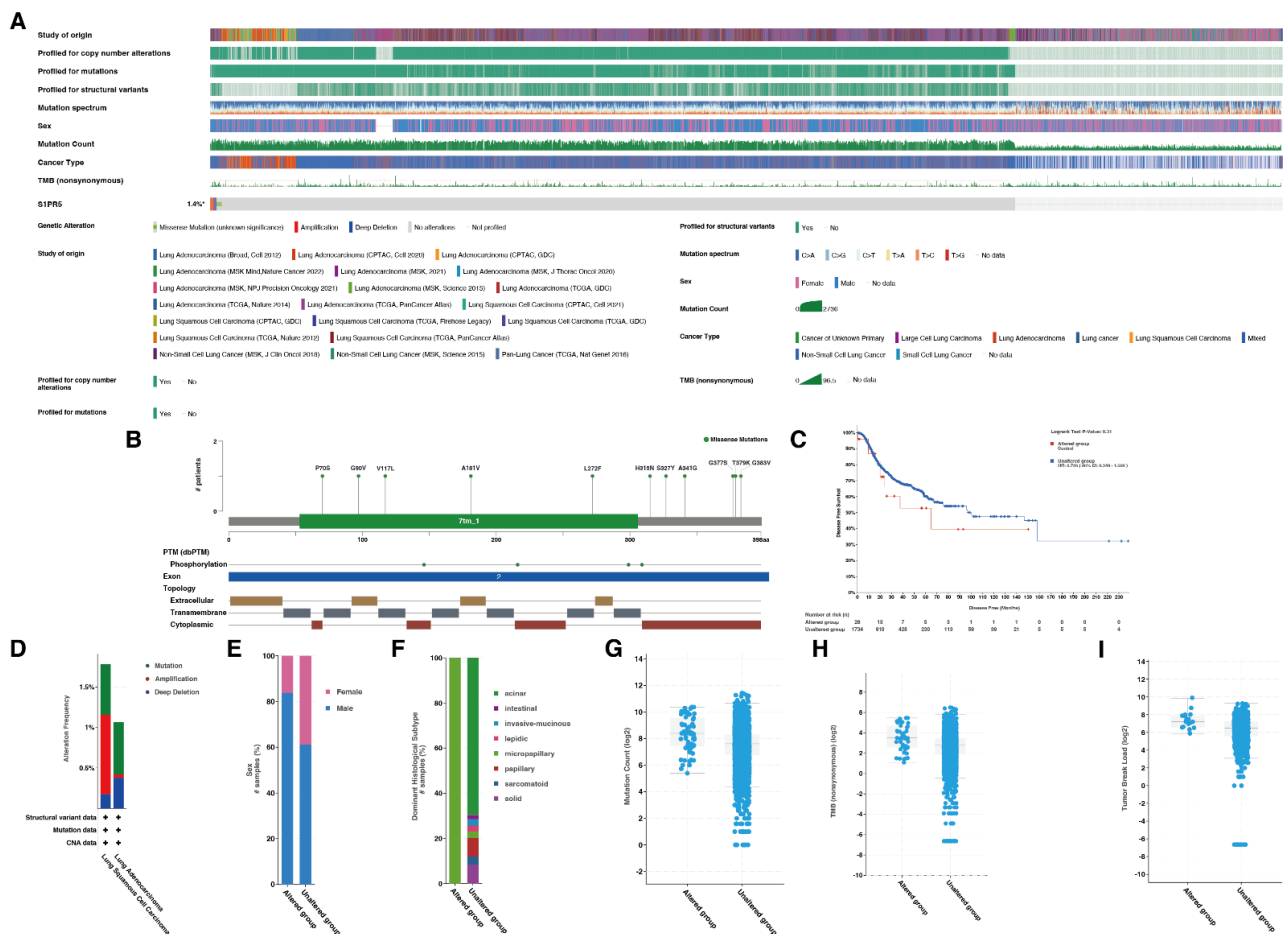


Figure S3 Comprehensive Genomic Alterations Analysis of *S1PR5* in LUAD. (A) Genetic alterations in *S1PR5* across various cancer studies. (B) *S1PR5* schematic diagram illustrating missense mutations, phosphorylation sites, exon structure, and membrane topology. (C) Kaplan-Meier survival curve comparing disease free survival between patients with *S1PR5* genetic alterations and those without. (D) Distribution of genetic alterations in *S1PR5* across different cancer types. (E) Comparison of *S1PR5* mutation rates between female and male patients. (F) Distribution of *S1PR5* genetic alterations across different histological subtypes of lung cancer. (G) Comparison of the number of mutations counts between patients with *S1PR5* genetic alterations and those without. (H) Comparison of the number of tumor mutational burden (TMB) between patients with *S1PR5* genetic alterations and those without. (I) Comparison of the number of tumor break loads between patients with and without *S1PR5* genetic alterations.

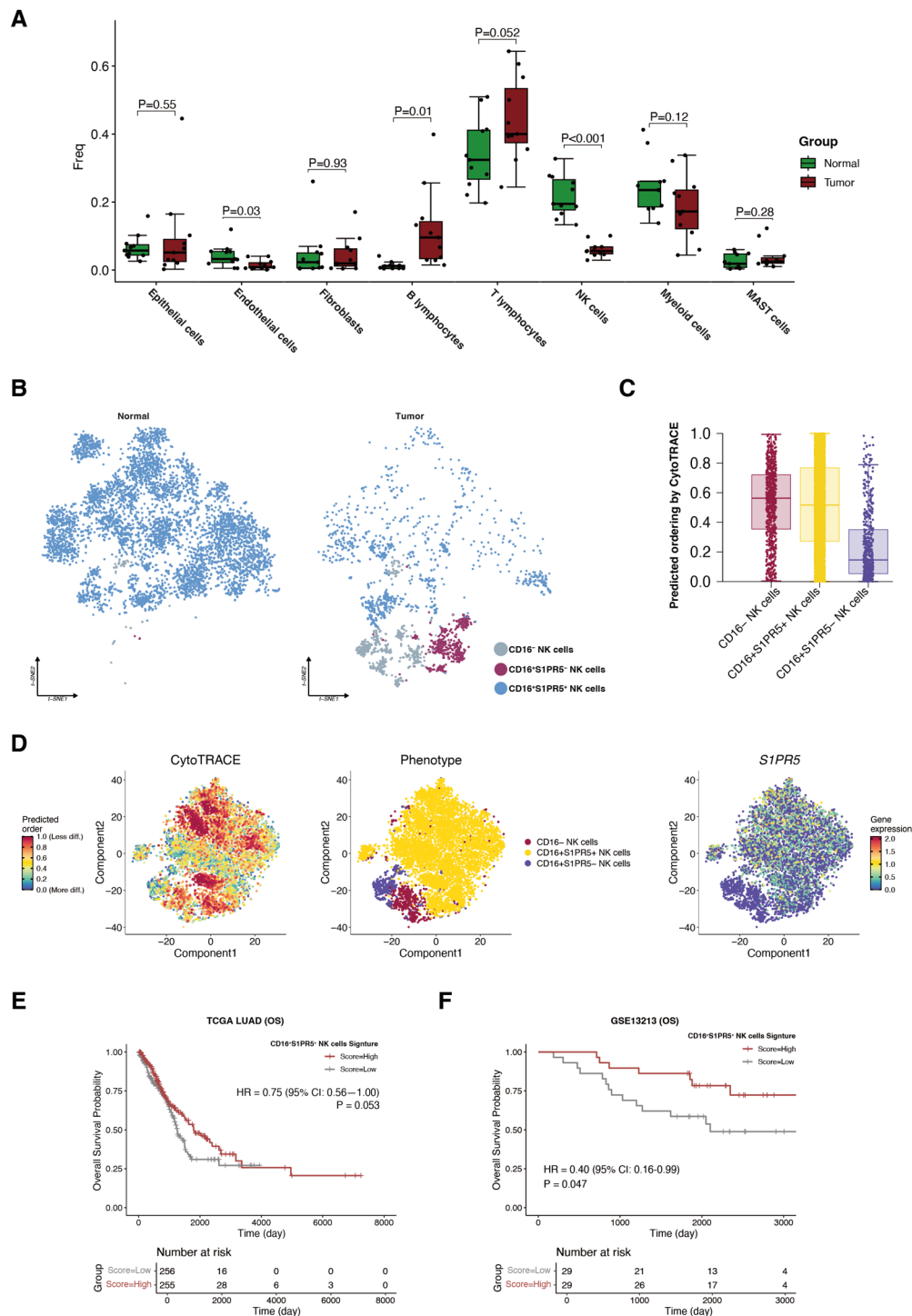


Figure S4 Single-Cell Profiling and NK Cells Subsets Analysis. (A) Boxplot showing cellular quantification in tumor and distant lung tissue. P values from t-tests are indicated for each cell type. (B) t-SNE plot illustrating the distribution of NK cell subpopulations in tumor and distant lung tissue groups. (C,D) Cytotrace analysis displaying the differentiation states and direction of the cells. (C) shows the predicted ordering by Cytotrace, and (D) visualizes the phenotype of different NK cell subpopulations. (E,F) Kaplan-Meier survival curves based on the expression of the CD16⁺S1PR5⁺ NK cell marker genes. Red lines represent high scores, and gray lines represent low scores. The hazard ratio (HR) and P values are provided for both TCGA-LUAD (E) and GSE13213 (F) datasets.

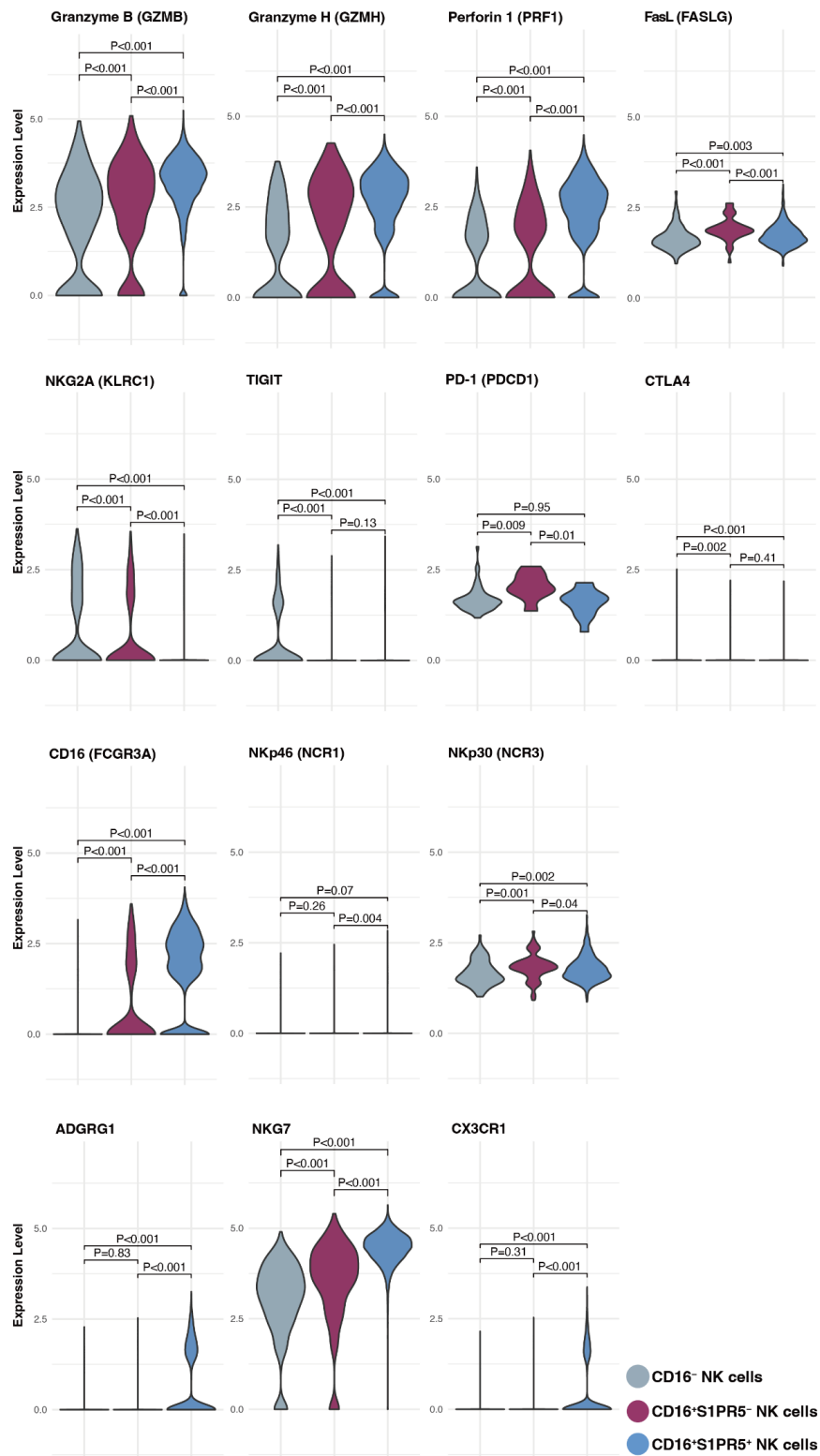


Figure S5 Violin Plots of Function-Related Gene Expression in Distinct NK Cell Subsets. The x-axis represents different NK cell subsets (CD16⁻ NK cells, CD16⁺S1PR5⁻ NK cells, and CD16⁺S1PR5⁺ NK cells), and the y-axis represents the expression levels of the genes. The P values indicate the statistical significance of the differences in expression levels between the subsets.

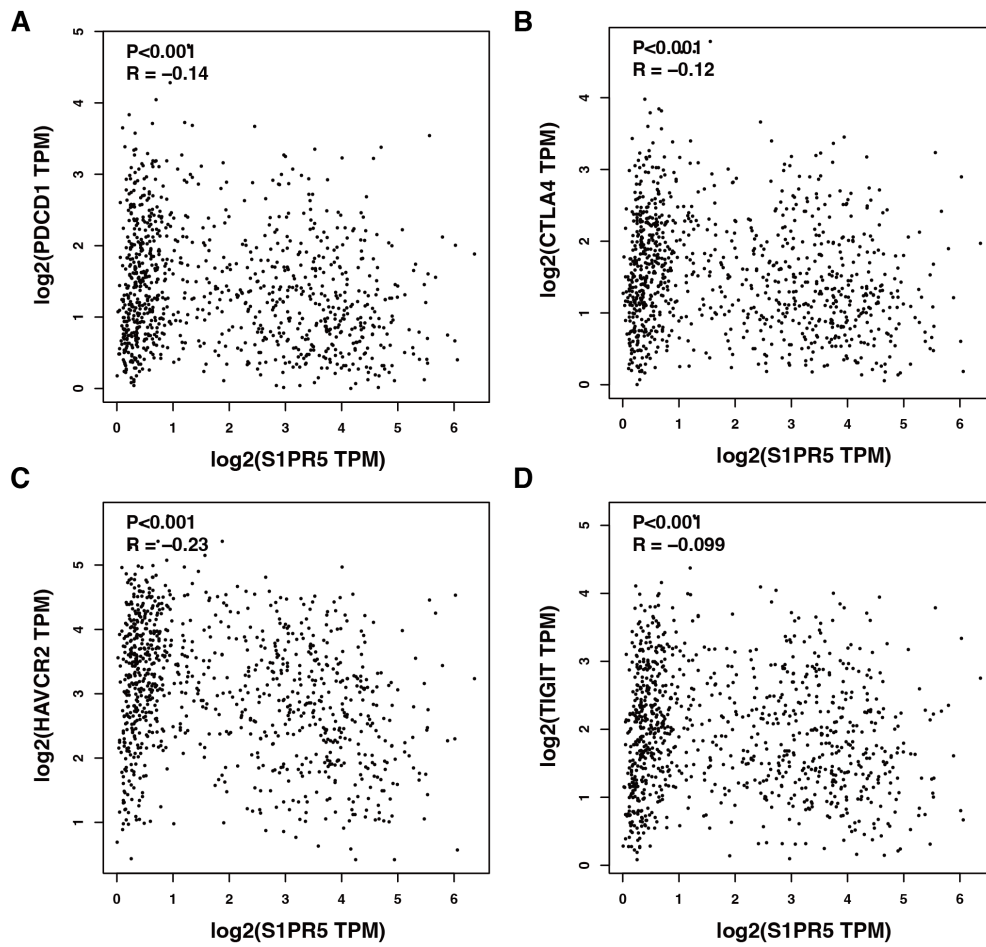


Figure S6 Correlation between *S1PR5* expression and immune checkpoint molecules. Scatter plots illustrate the correlation between $\log_2$ -transformed *S1PR5* transcripts per million (TPM) and $\log_2$ -transformed TPM values of (A) *PDCD1* (PD-1), (B) *CTLA4* (CTLA4), (C) *HAVCR2* (TIM-3), and (D) *TIGIT* (TIGIT). The Pearson correlation coefficients (R) and P values are indicated in each panel.

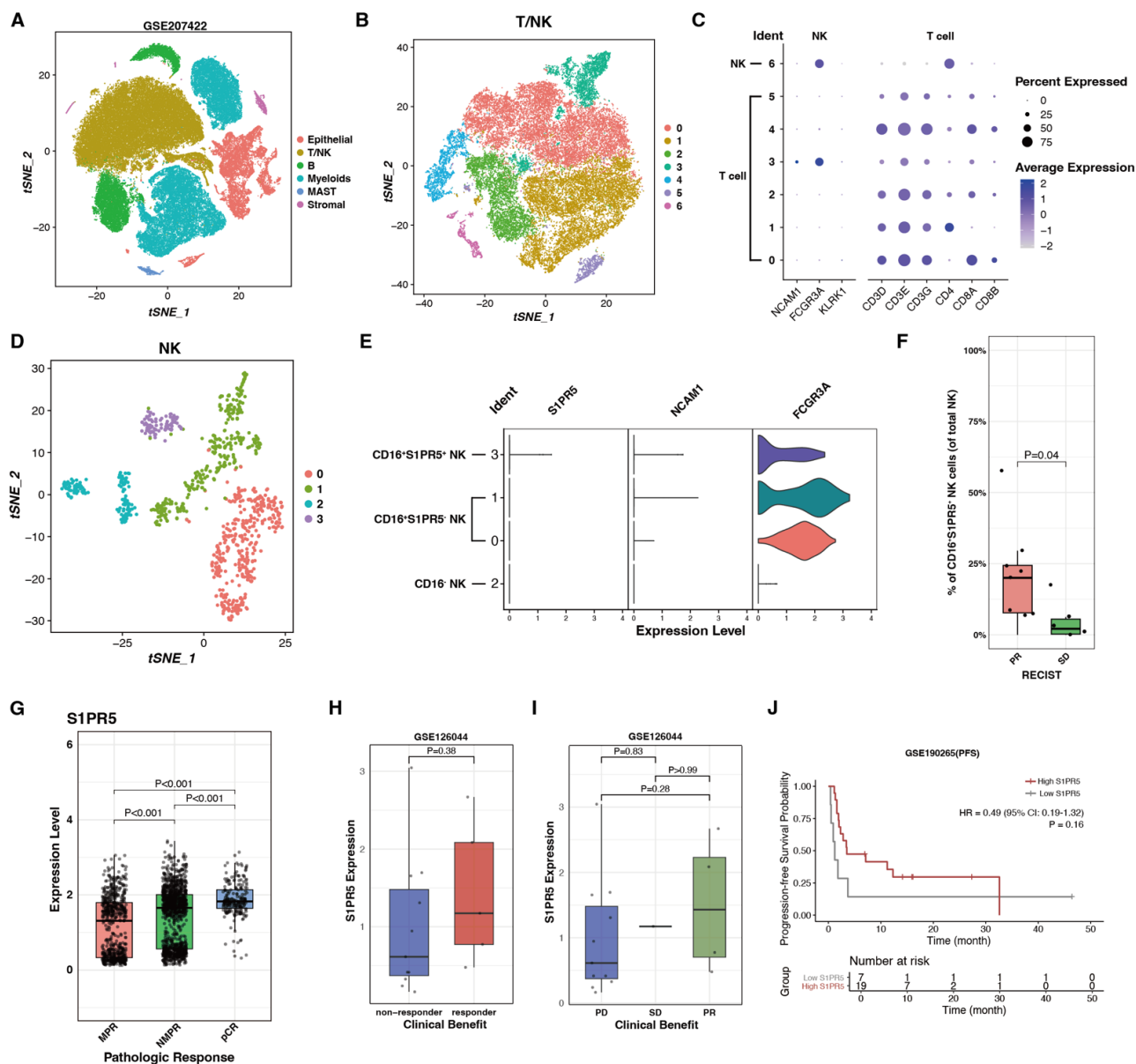


Figure S7 Association of *S1PR5* expression with treatment response and survival in NSCLC patients receiving immunotherapy. (A) t-SNE plot of scRNA-seq data from GSE207422. (B) t-SNE plot of T/NK cell subpopulations. (C) Dot plot displaying the markers of T and NK cells. Dot size indicates the percentage of cells expressing the marker, and color denotes expression level. (D) t-SNE plot highlighting NK cell subsets, with colors representing distinct subpopulations. (E) Violin plots showing the expression levels of subset-specific markers across NK cell populations. (F) Box plot comparing the proportion of CD16⁺S1PR5⁺ NK cells between responders and non-responders, and statistical significance is indicated. (G) Box plot showing *S1PR5* expression levels across different pathologic response groups, and statistical significance is indicated. (H) Box plot comparing *S1PR5* expression between responders and non-responders in the GSE126044 cohort, and statistical significance is indicated. (I) Box plot comparing *S1PR5* expression among patients with progressive disease (PD), stable disease (SD), and partial response (PR) in the GSE126044 cohort, with statistical significance indicated. (J) Kaplan-Meier curve illustrating progression-free survival stratified by *S1PR5* expression levels in the GSE190265 cohort.

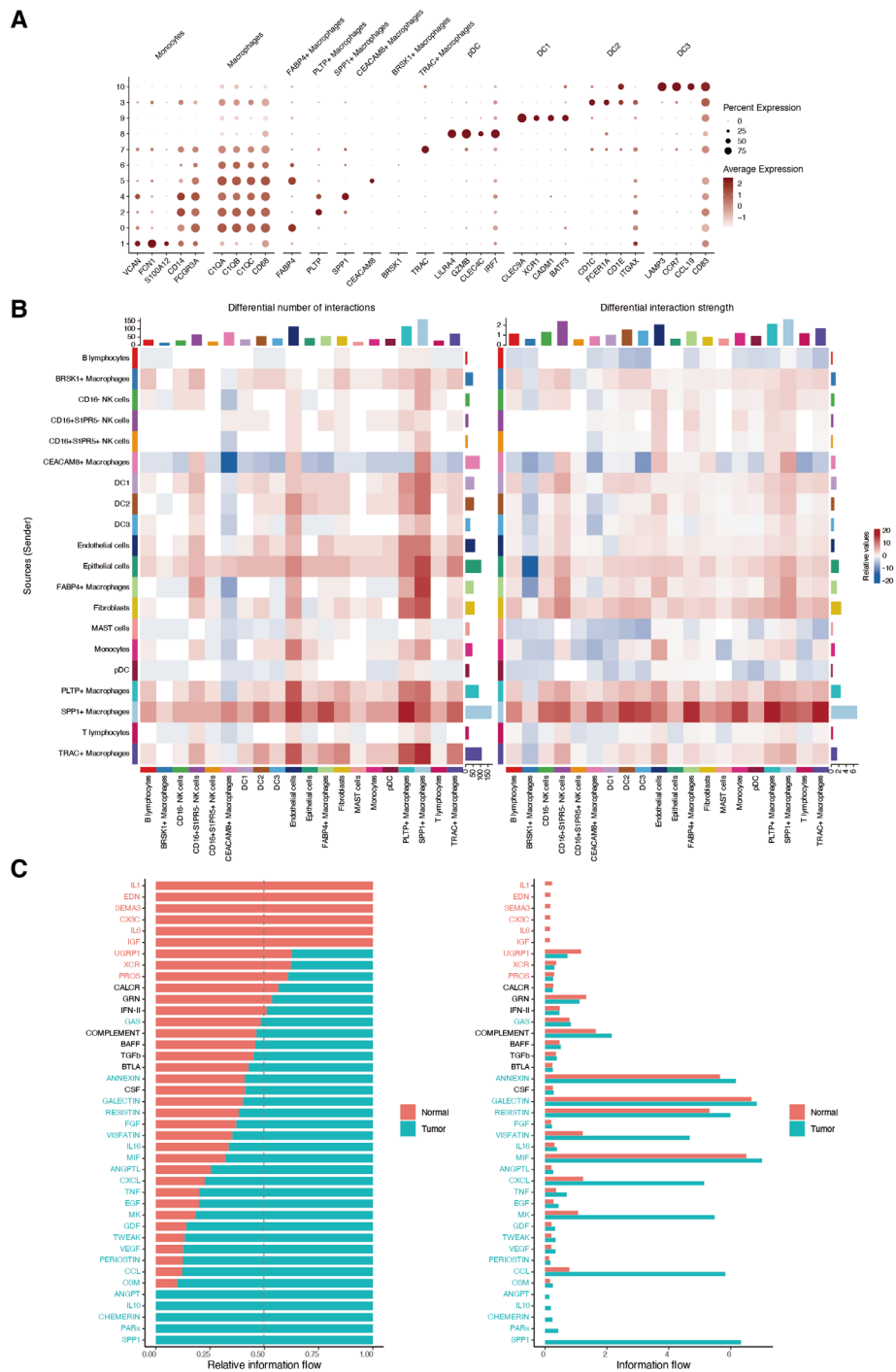


Figure S8 Annotation of myeloid cell subsets and cell communication in tumor and normal tissues. (A) Dot plot showing the expression of marker genes for myeloid cell subsets. The size of the dots represents the percentage of cells expressing the marker, and the color intensity indicates the average expression level. (B,C) Cell communication analysis comparing tumor and normal tissues. (B) Heatmap showing differential number (left) and strength (right) of interactions between cell types. Red indicates higher interactions in tumor tissue, while blue indicates higher interactions in normal tissue. (C) Bar plots showing the differential information flow in various pathways. The left panel shows the relative information flow, and the right panel shows the absolute information flow. Pink represents normal tissue, and green represents tumor tissue.

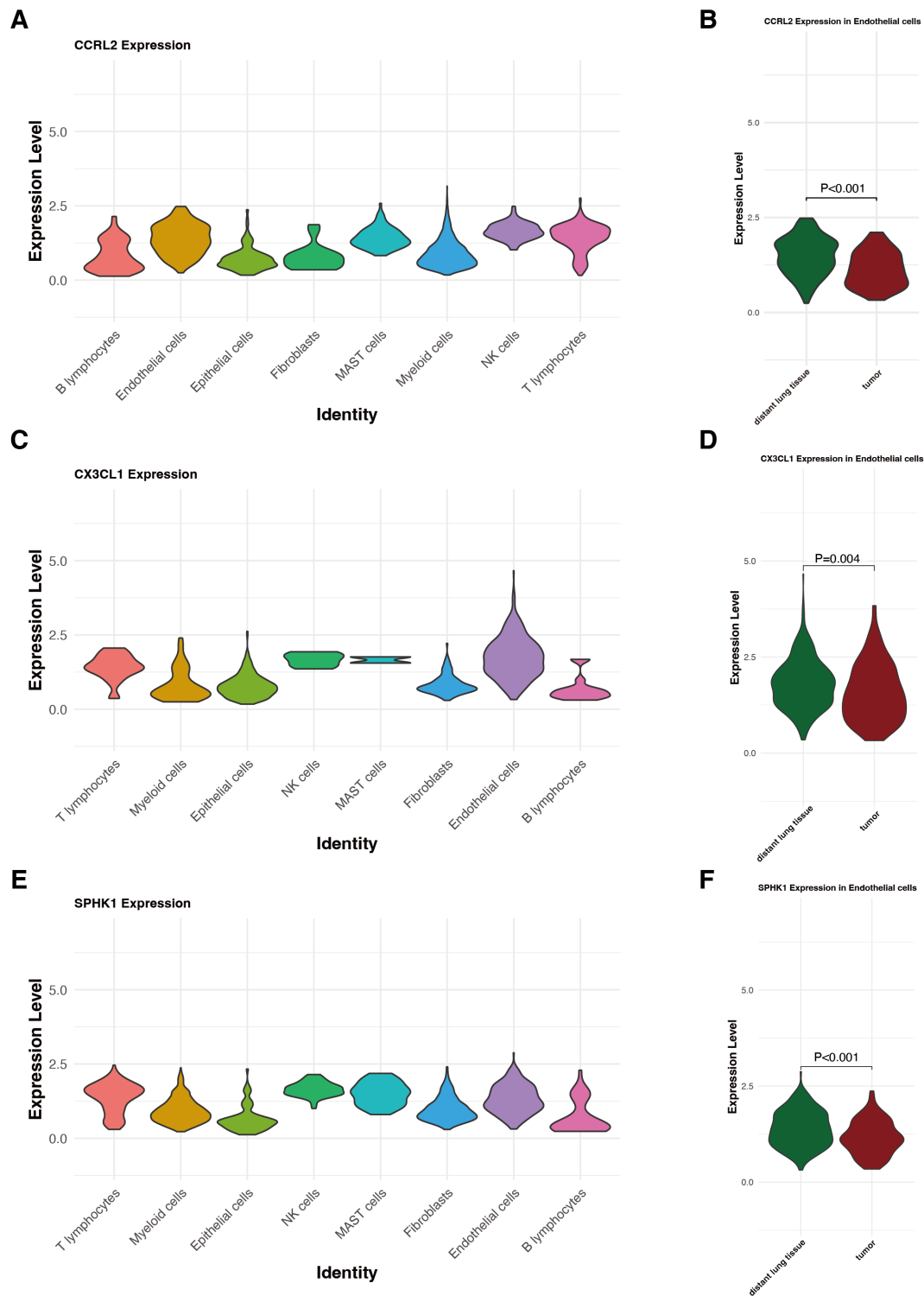


Figure S9 Expression of *CCRL2*, *CX3CL1*, and *SPHK1* in single-cell dataset. Violin plots showing the expression levels of *CCRL2*, *CX3CL1*, and *SPHK1* in various cell types, and violin plots showing the expression levels of these genes in endothelial cells from distant lung tissue and tumor. (A,B) *CCRL2* expression in different cell types (A) and in endothelial cells from distant lung tissue and tumor (B). (C,D) *CX3CL1* expression in different cell types (C) and in endothelial cells from distant lung tissue and tumor (D). (E,F) *SPHK1* expression in different cell types (E) and in endothelial cells from distant lung tissue and tumor (F).

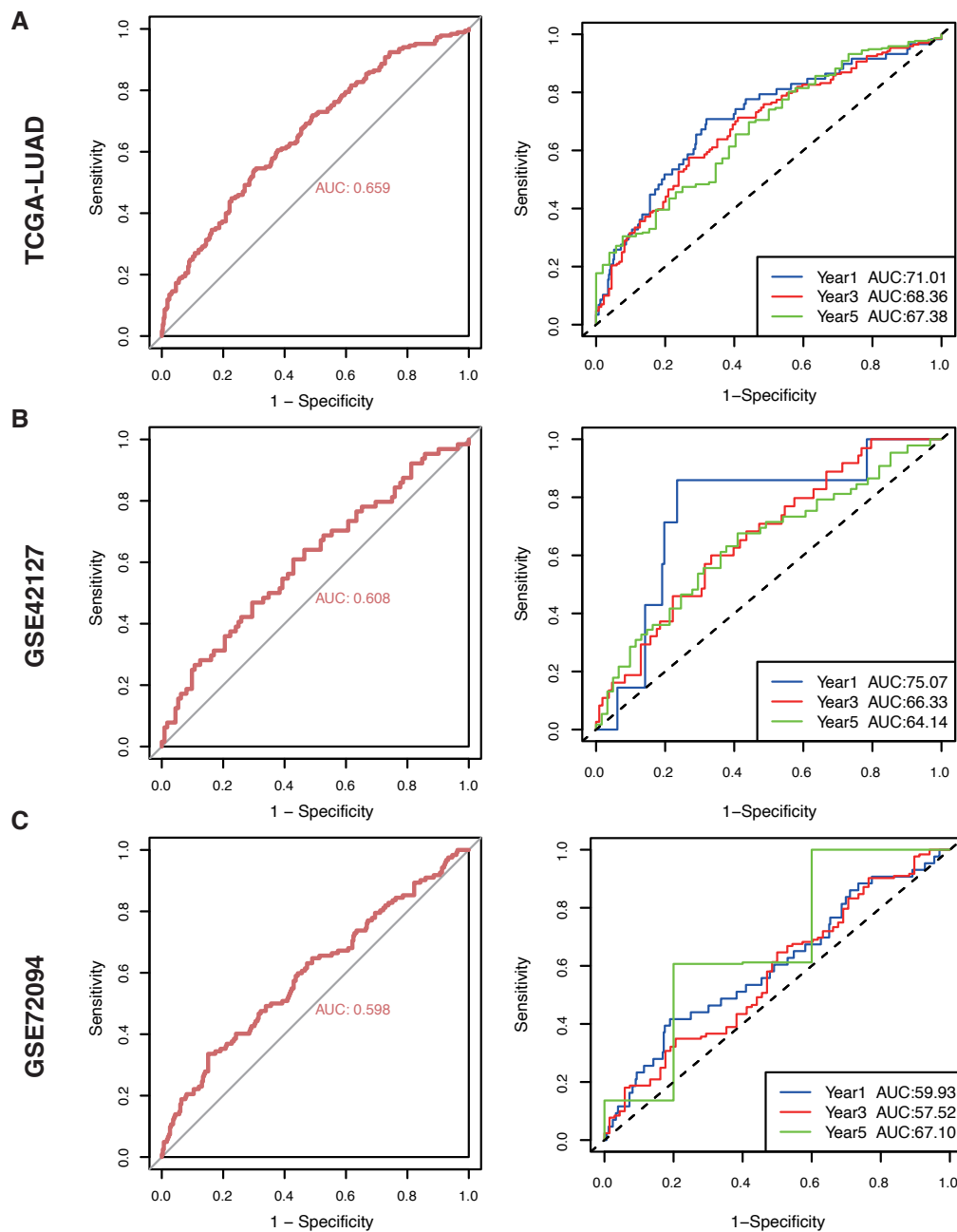


Figure S10 Evaluation of a previously published model for predicting overall and time-specific survival outcomes. The left panel presents the receiver operating characteristic (ROC) curve and corresponding AUC, reflecting the model's overall predictive accuracy. The right panel shows time-dependent ROC curves for 1-, 3-, and 5-year survival. (A) TCGA-LUAD cohort; (B) GSE42127 cohort; (C) GSE72094 cohort.

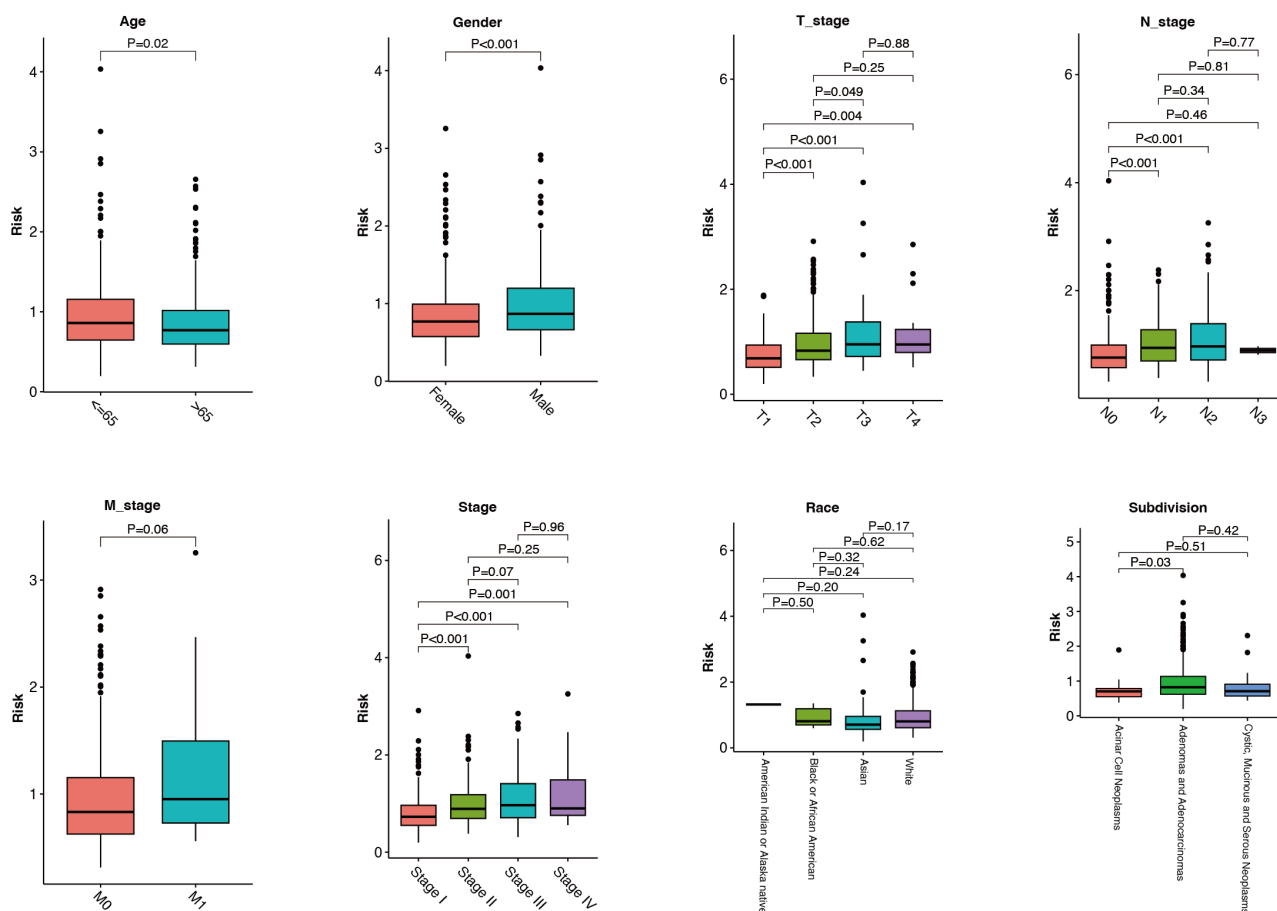


Figure S11 Clinical Relevance of the *S1PR5*-Enriched NK Cell-Related Prognostic Signature. Boxplots showing the association between the risk score of the *S1PR5*-enriched NK cell-related prognostic signature and various clinical indicators. Each panel represents a different clinical variable, including age, gender, T stage, N stage, M stage, clinical stage, race, and subdivision. The risk score is plotted on the y-axis, and the clinical variables are plotted on the x-axis. P values are indicated for each comparison.