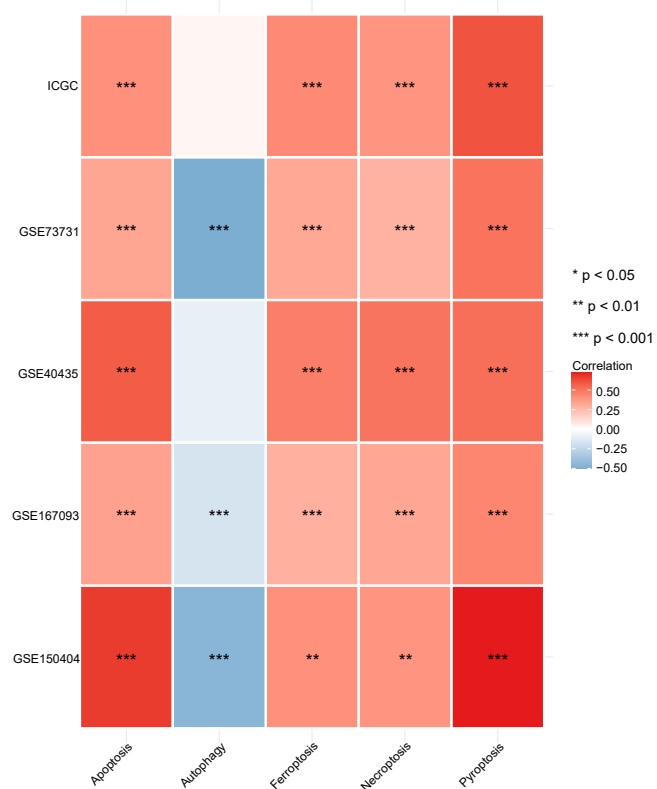
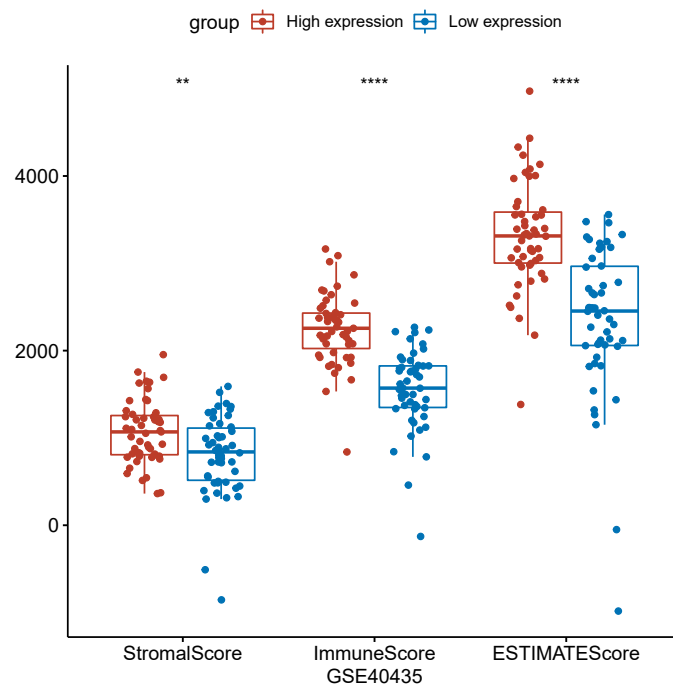
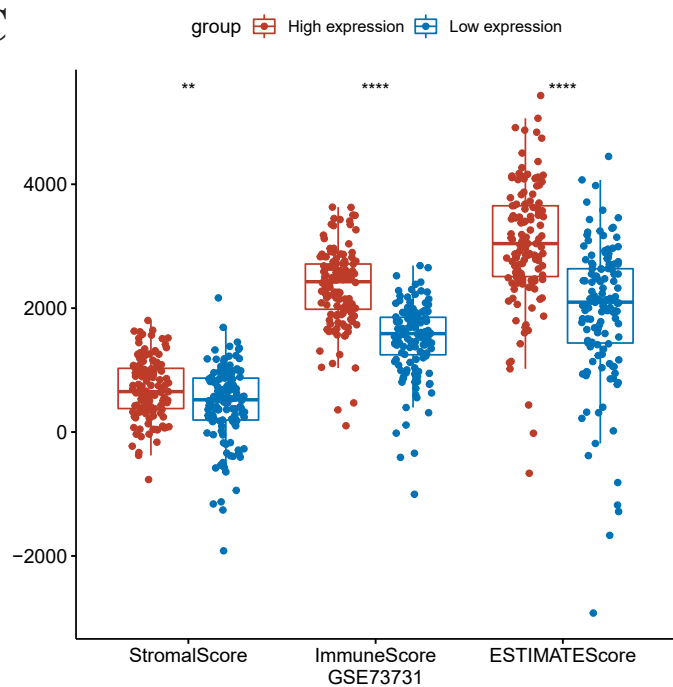
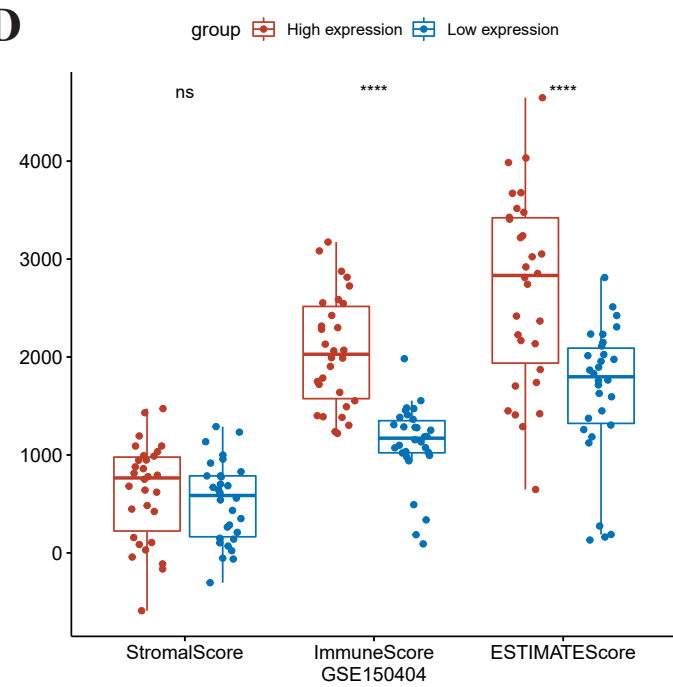
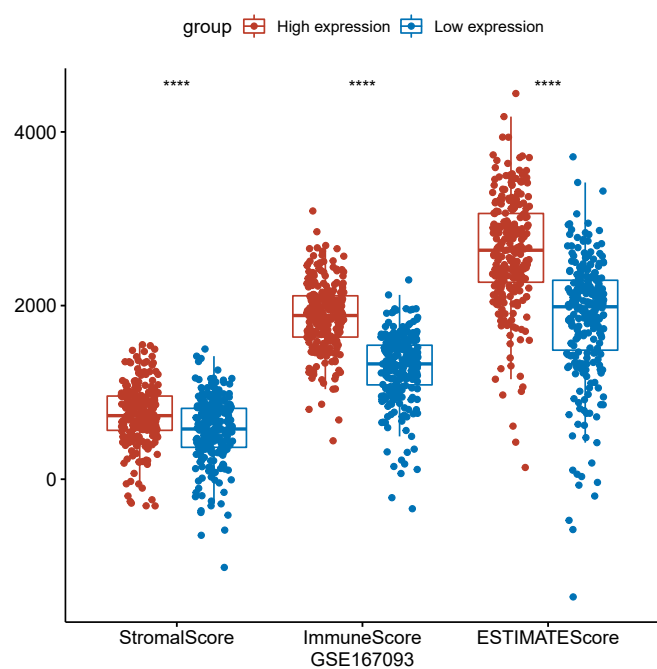
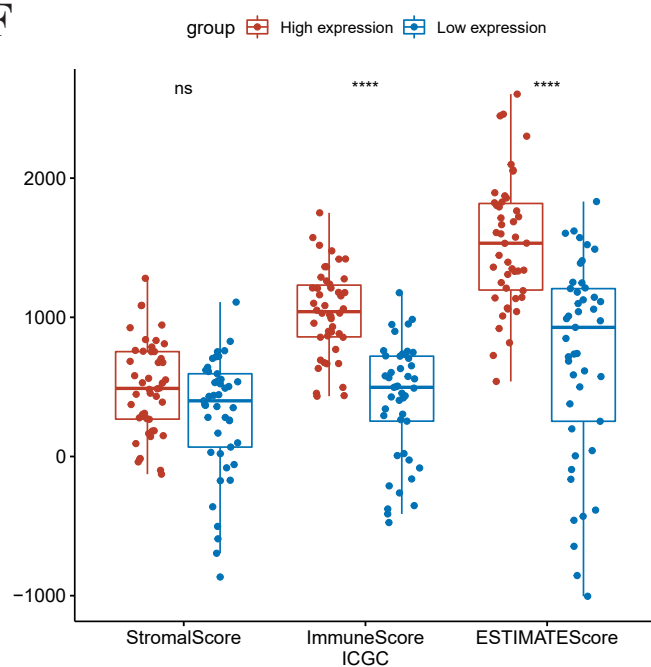
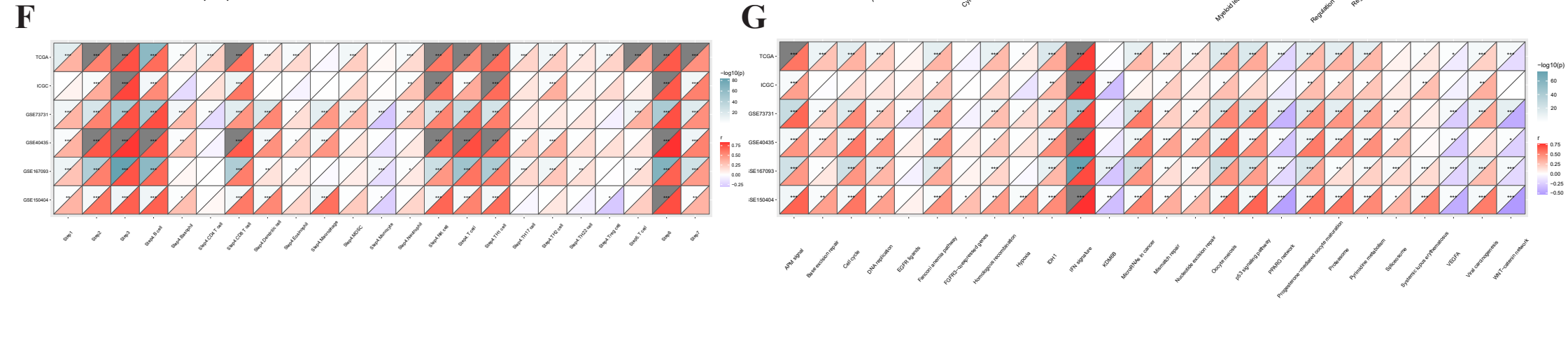
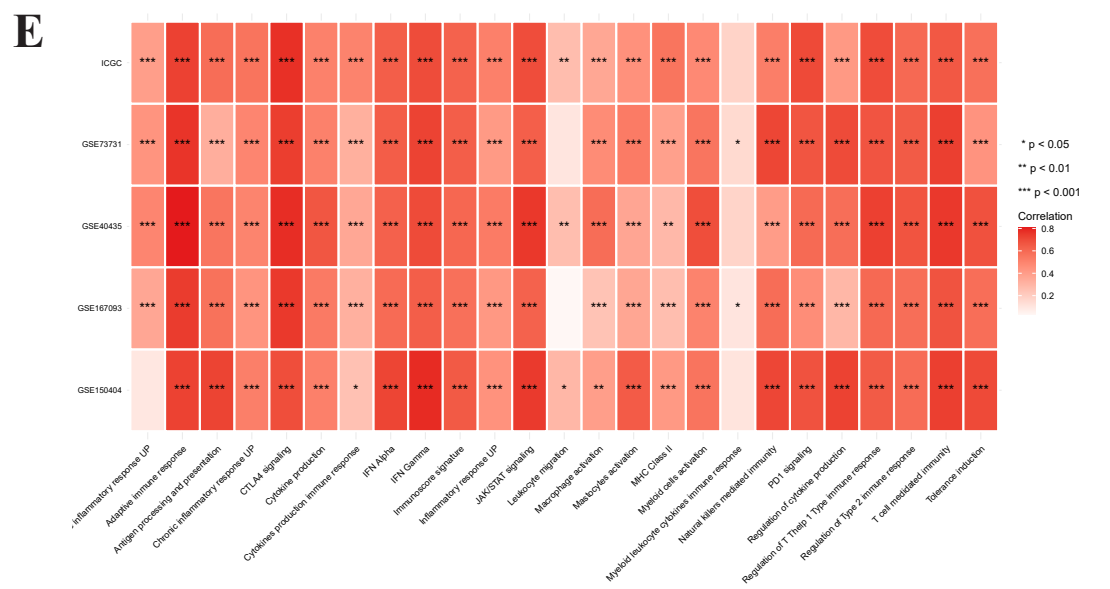
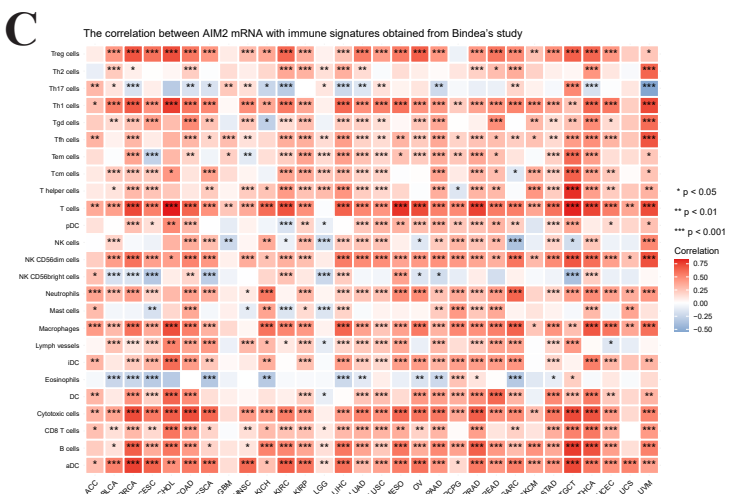
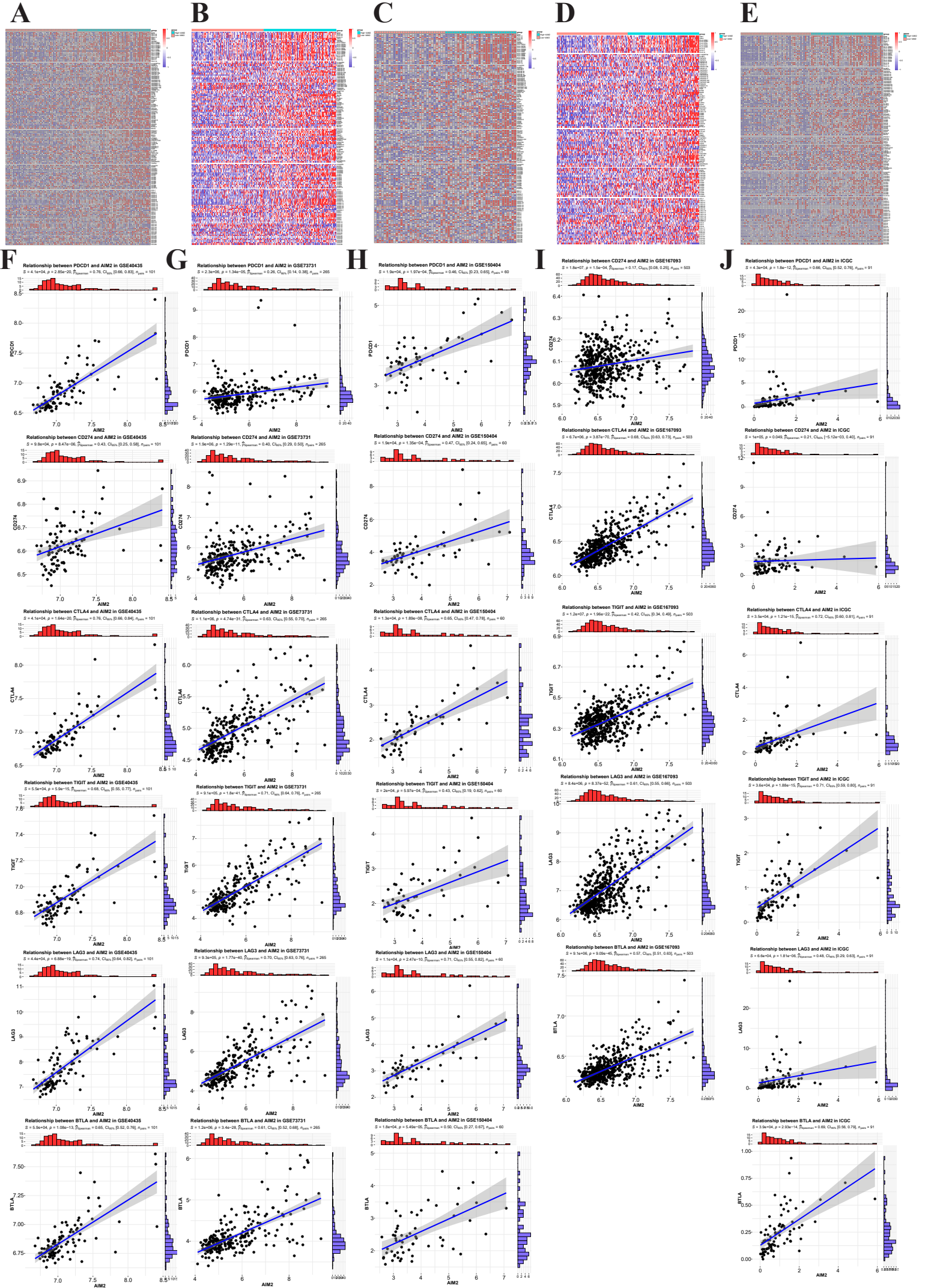


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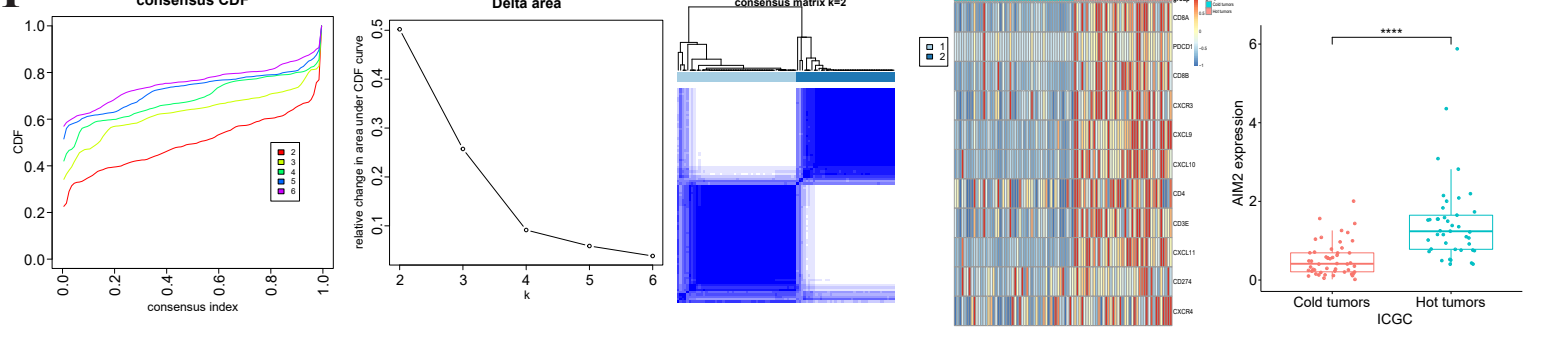
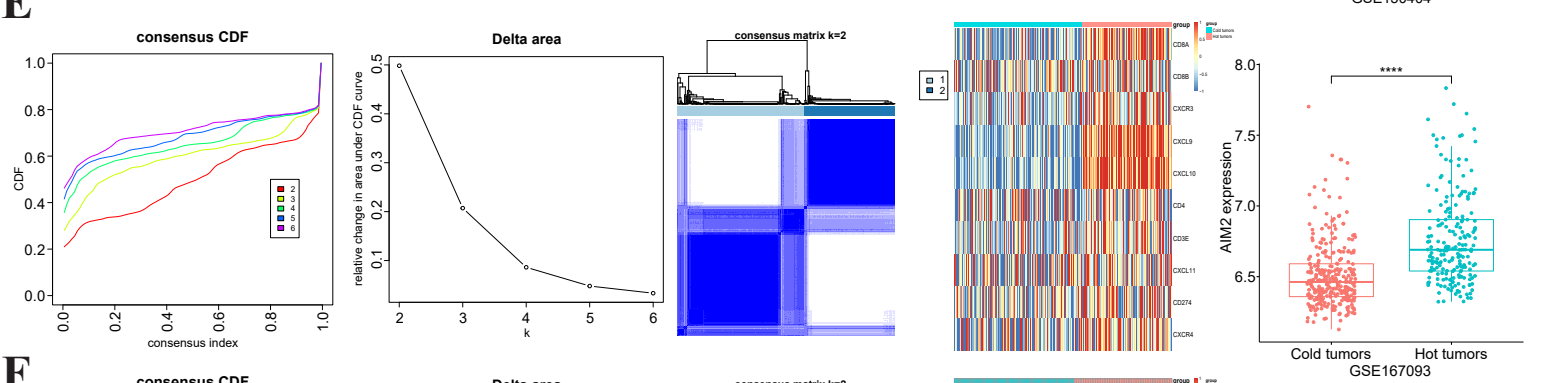
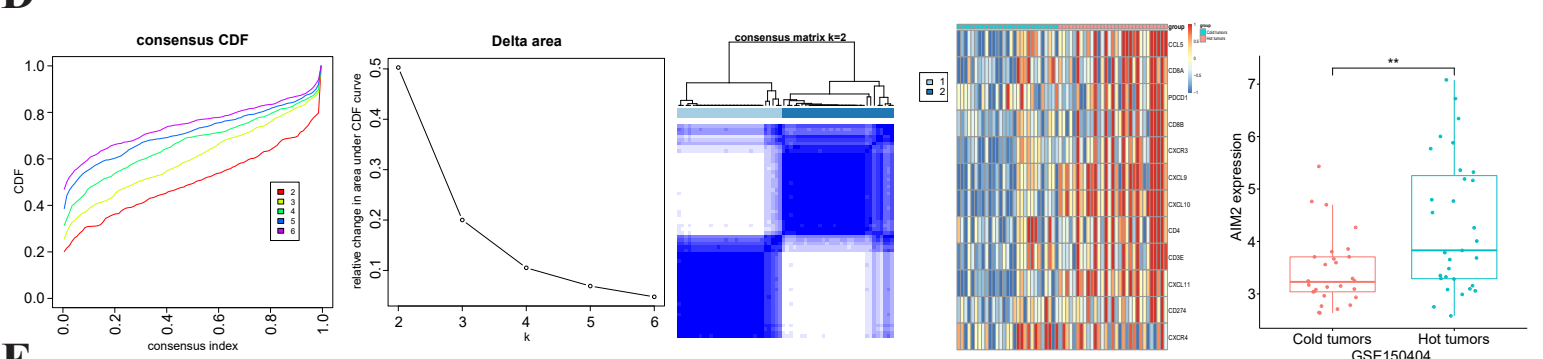
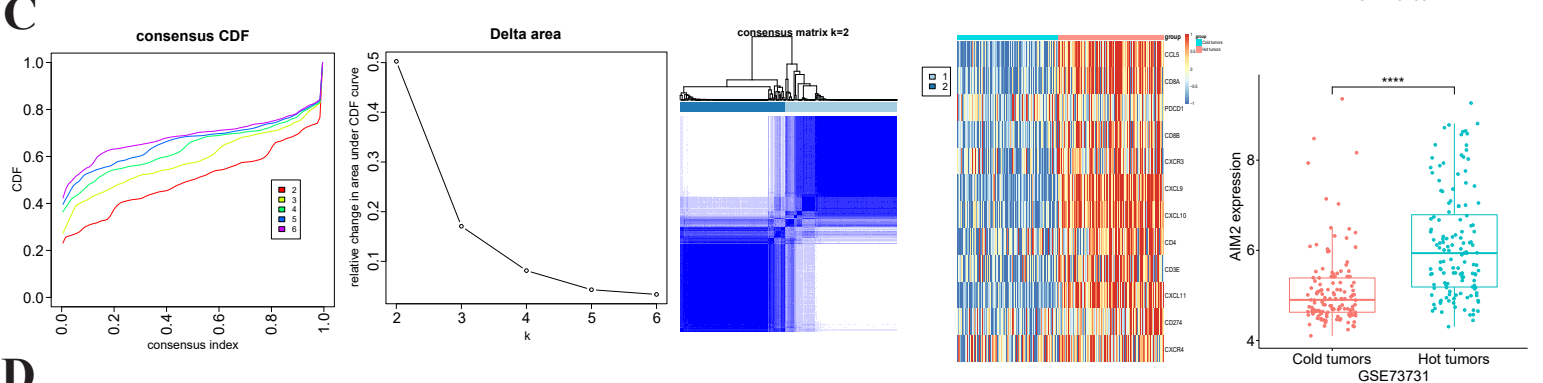
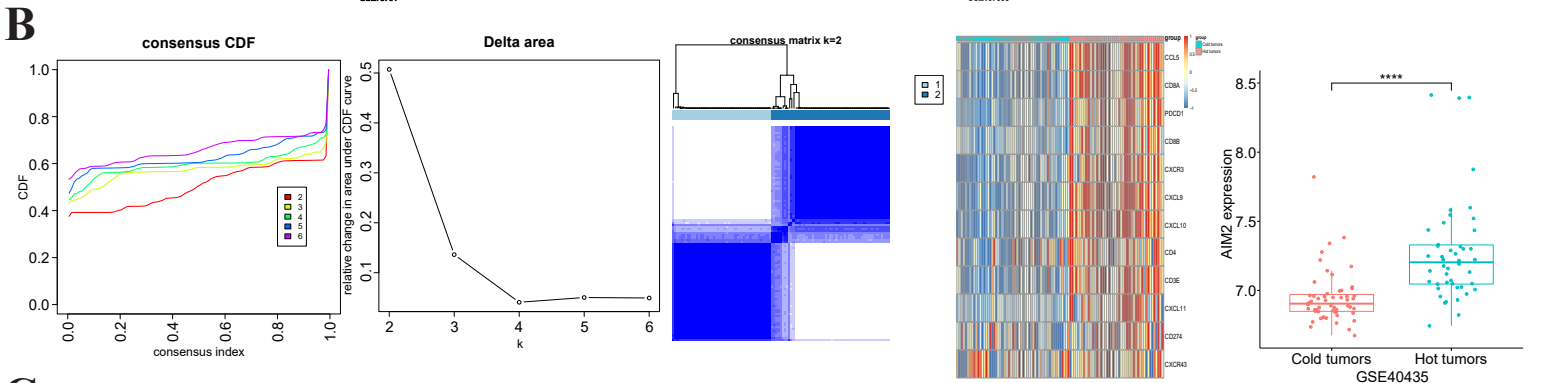
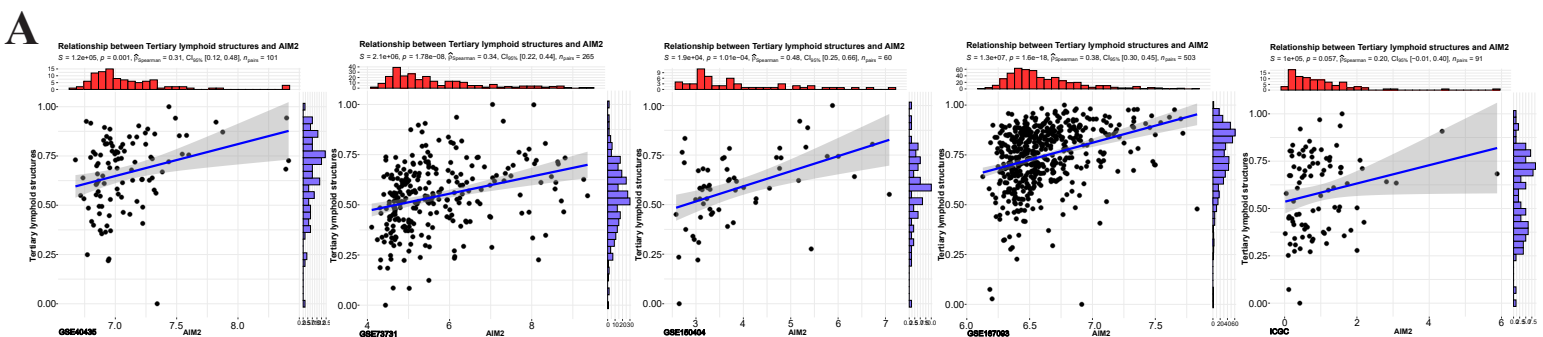
Supplementary Figure 1 | Pathway analysis and estimate score analysis suggested that AIM2 was associated with tumor immunity. (A) AIM2 mRNA expression was positively associated with apoptosis, pyroptosis, necroptosis, and ferroptosis, while showing a negative correlation with Autophagy based on ssGSEA in multiple cohorts. (B-F) AIM2 high-expression subgroup had higher immune and stromal scores in comparison with AIM2 low-expression subgroup in GSE40435, GSE73731, GSE150404, GSE167093 and ICGC cohort respectively. ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$, NS $P > 0.05$.



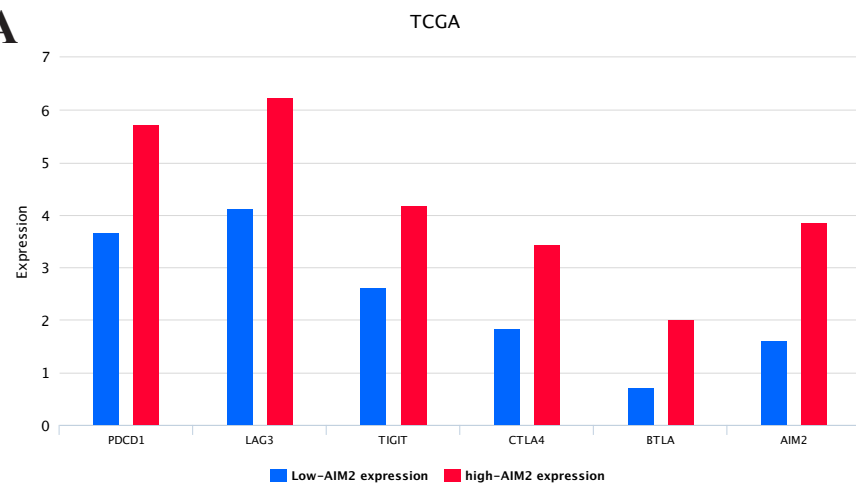
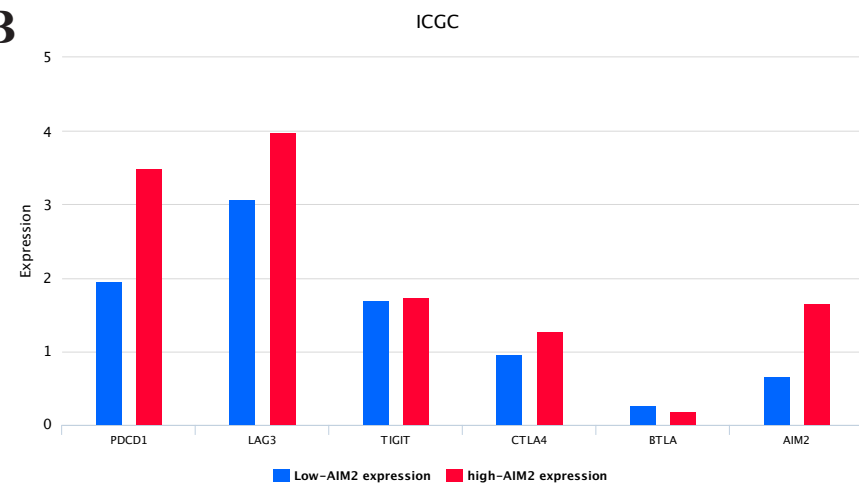
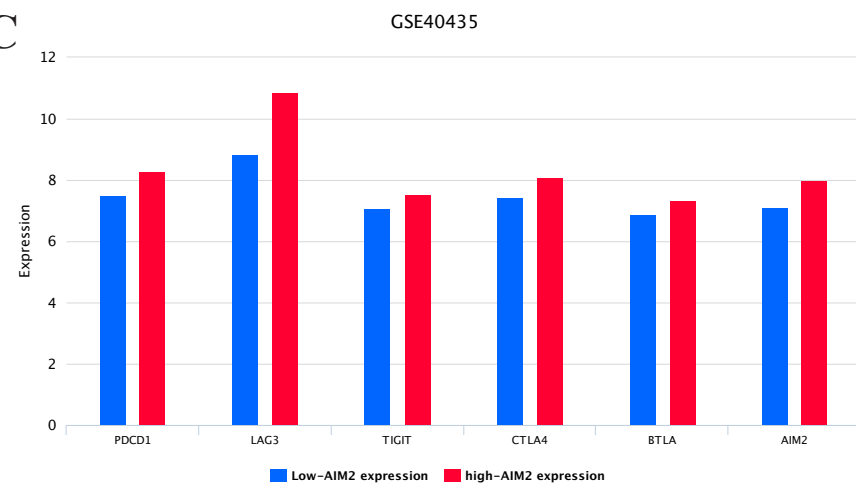
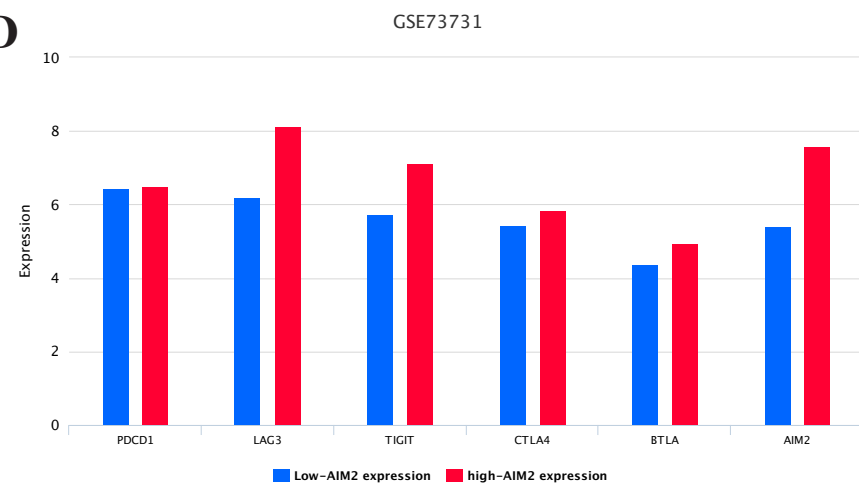
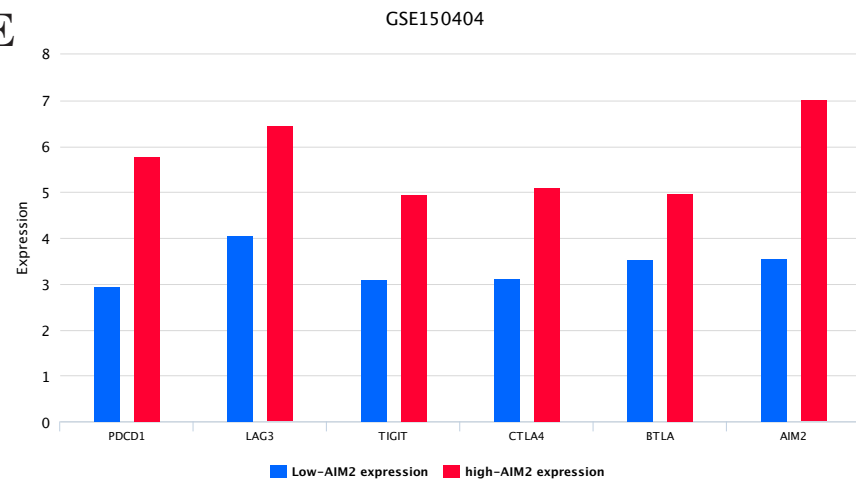
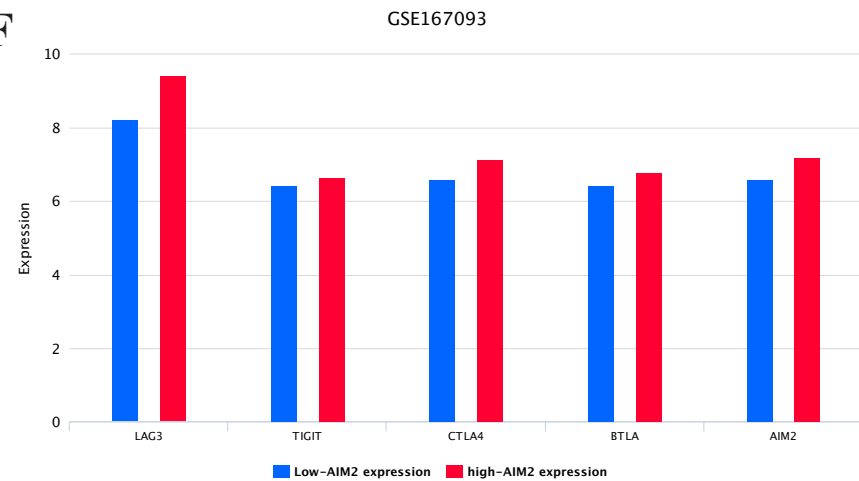
Supplementary Figure 2 | The correlation between AIM2 and immune activation as well as immune infiltration of ccRCC. (A-C) Pan-cancer analyses proved that AIM2 mRNA expression was positively correlated with a majority of TIICs in different tumors via Cibersort algorithm, TIMER algorithm and 24 types of tumor infiltrating immune cells ' gene set signatures obtained from Bindea ' s study respectively. (D) The correlation between immune cells and AIM2 mRNA expression in multiple cohorts of ccRCC. (E) The correlation between innate and adaptive immunity-related gene sets and AIM2 mRNA expression in multiple cohorts of ccRCC. (F) Correlations between AIM2 mRNA expression and the steps of the cancer immunity cycle in multiple cohorts. (G) Correlations between AIM2 mRNA expression and the enrichment scores of immunotherapy-predicted pathways in multiple cohorts. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.



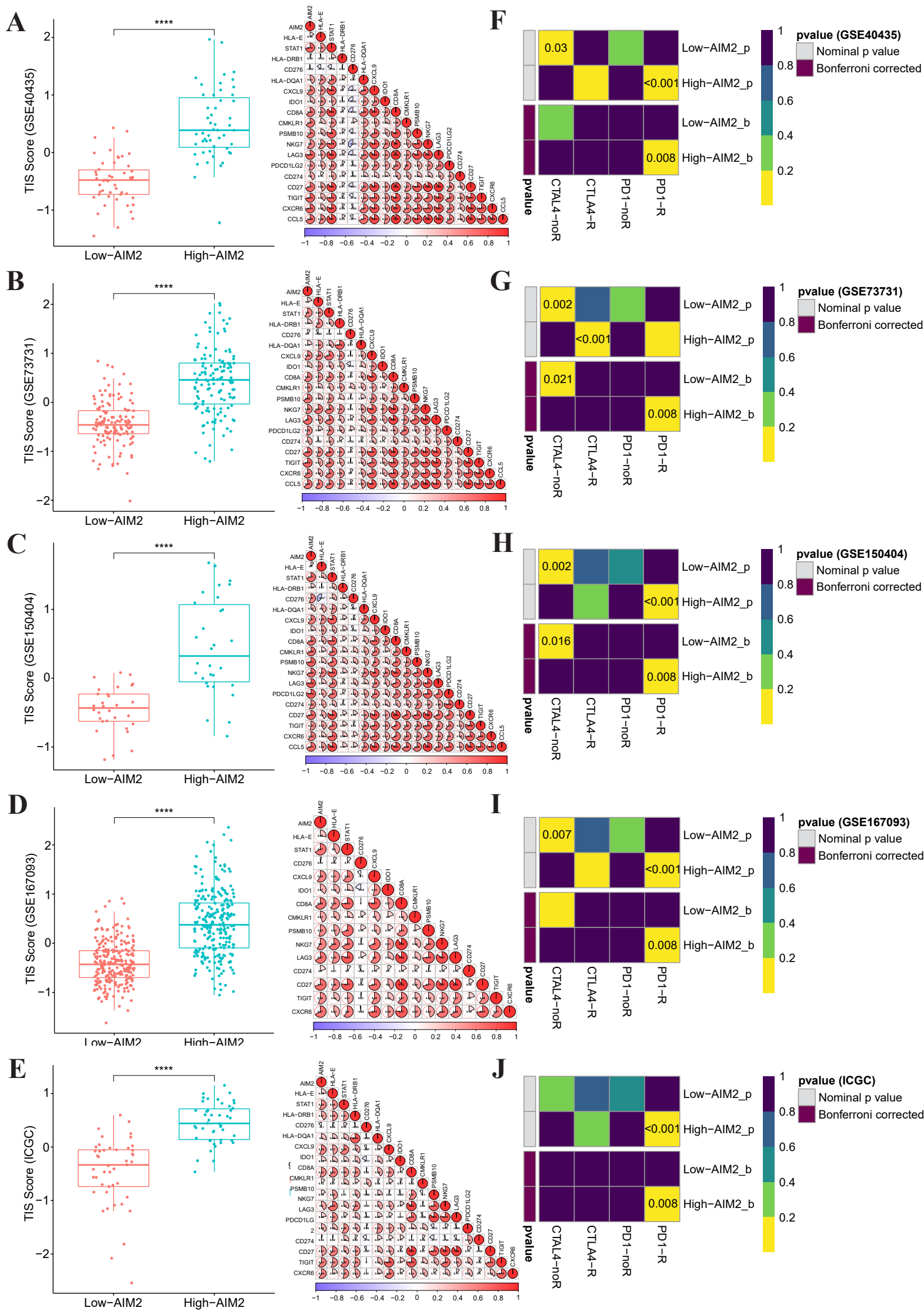
Supplementary Figure 3 | AIM2 had a remarkably positive association with most immunomodulators in multiple cohorts. (A-E) The correlation between AIM2 mRNA expression and immunomodulators in GSE40435, GSE73731, GSE150404, GSE167093 and ICGC cohort respectively. (F-J) The correlation between AIM2 mRNA expression and immune checkpoints in GSE40435, GSE73731, GSE150404, GSE167093 and ICGC cohort respectively.



Supplementary Figure 4 | The correlation between AIM2 and tertiary lymphoid structure as well as immunologically hot tumor. (A) AIM2 mRNA expression was positively correlated with the tertiary lymphoid structures in GSE40435, GSE73731, GSE150404, GSE167093 and ICGC cohort respectively. (B-F) The overexpression of AIM2 in hot tumors subgroup was also observed in GSE40435, GSE73731, GSE150404, GSE167093 and ICGC cohort respectively. ** $P < 0.01$, **** $P < 0.0001$.

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Supplementary Figure 5 | The mRNA expression of AIM2 and immune checkpoints in ccRCC tumor infiltrating CD8⁺ T lymphocytes. (A-F) The mRNA expression of AIM2, PDCD1, CTLA4, TIGIT, LAG3 and BTLA in tumor infiltrating CD8⁺ T lymphocytes of ccRCC patients were up-regulated in AIM2 high-expression subgroup of TCGA, ICGC, GSE40435, GSE73731, GSE150404 and GSE167093 cohort respectively.



Supplementary Figure 6 | Patients in AIM2 high-expression group were more likely responsive to immunotherapy. (A-E) Higher mRNA expression of AIM2 were accompanied by higher T-cell inflamed scores in GSE40435, GSE73731, GSE150404, GSE167093 and ICGC cohort respectively. (F-J) SubMap algorithm suggested that patients in AIM2 high-expression group were more responsive to anti-PD1 treatment in GSE40435, GSE73731, GSE150404, GSE167093 and ICGC cohort respectively as well. **** P < 0.0001.

Project	Histology	Stage	Tumor sample	Normal sample	Platforms
TCGA-KIRC	KIRC	I-IV	539	72	TCGA
GSE40435	KIRC	I-IV	101	101	GPL10558
GSE53000	KIRC	I-IV	56	6	GPL6244
GSE68417	KIRC	I-IV	29	14	GPL6244
GSE73731	KIRC	I-IV	265	0	GPL570
GSE150404	KIRC	I-IV	60	0	GPL17692
GSE167093	KIRC	I-IV	503	0	GPL10558
ICGC-RECA	KIRC	I-IV	91	45	ICGC

Supplementary Table 1 | The characteristics of all data sets included in this study.

Gene symbol	Primer	Sequences
AIM2	Forward primer	TGGCAAAACGTCTTCAGGAGG
AIM2	Reverse primer	AGCTTGACTTAGTGGCTTTGG
PDCD1	Forward primer	CAGTTCCAAACCCTGGTGGT
PDCD1	Reverse primer	GGCTCCTATTGTCCCTCGTG
CTLA4	Forward primer	ACGGGACTCTACATCTGCAAGG
CTLA4	Reverse primer	GGAGGAAGTCAGAATCTGGGCA
CD274	Forward primer	TGGCATTTGCTGAACGCATTT
CD274	Reverse primer	TGCAGCCAGGTCTAATTGTTTT
TIGIT	Forward primer	TGGTGGTCATCTGCACAGCAGT
TIGIT	Reverse primer	TTTCTCCTGAGGTCACCTTCCAC
LAG3	Forward primer	GCCTCCGACTGGGTCATTTT
LAG3	Reverse primer	CTTTCCGCTAAGTGGTGATGG
BTLA	Forward primer	CATCTTAGCAGGAGATCCCTTTG
BTLA	Reverse primer	GACCCATTGTCATTAGGAAGCA

Supplementary Table 2 | The sequences of primers used in this study.

T cell-inflamed score	Immunologically hot tumor signature
HLA-E	CCL5
STAT1	CD8A
HLA-DRB1	PDCD1
CD276	CD8B
HLA-DQA1	CXCR3
CXCL9	CXCL9
IDO1	CXCL10
CD8A	CD4
CMKLR1	CD3E
PSMB10	CXCL11
NKG7	CD274
LAG3	CXCR4
PDCD1LG2	
CD274	
CD27	
TIGIT	
CXCR6	
CCL5	

Supplementary Table 3 | Marker genes of T cell-inflamed score and Immunologically hot tumor.

Clinical characteristics	Total (N)	Odds ratio in AIM2 expression	P-value
Age (≤ 60 vs. > 60)	530	1.20(0.85-1.69)	0.297
Gender (male vs. female)	530	1.35(0.94-1.93)	0.102
Histological grade (G1-G2 vs. G3-G4)	522	2.02(1.42-2.86)	<0.001
Clinical stage (I-II vs. III-IV)	527	2.02(1.41-2.89)	<0.001
Tumor stage (T1-T2 vs. T3-T4)	530	1.87(1.31-2.70)	<0.001
Distant metastasis (positive vs negative)	498	2.42(1.47-4.10)	<0.001
Lymph metastasis (positive vs negative)	255	3.23(1.09-11.83)	0.047

Supplementary Table 4 | Logistic regression analysis evaluated the association between AIM2 and clinicopathological staging characteristics of ccRCC patients.

Parameter	Univariate analysis			Multivariate analysis		
	HR	95%CI	P-value	HR	95%CI	P-value
Age	1.023	1.005-1.041	0.012	1.032	1.012-1.051	0.001
Gender	1.013	0.666-1.541	0.951			
Histological grade	2.242	1.682-2.988	<0.001	1.465	1.049-2.046	0.025
Stage	1.862	1.541-2.251	<0.001	1.451	0.885-2.381	0.140
T classification	1.943	1.538-2.456	<0.001	0.954	0.596-1.527	0.846
M classification	4.073	2.634-6.300	<0.001	1.538	0.691-3.422	0.292
N classification	2.932	1.516-5.668	0.001	1.427	0.705-2.886	0.323
AIM2	1.052	1.034-1.069	<0.001	1.033	1.013-1.054	0.002

Supplementary Table 5 | Univariate and Multivariate Cox regression analysis showed AIM2 could serve as an independent predictor of favorable survival outcomes.

ONTOLOGYID	Description	GeneRatio	pvalue	p.adjust	qvalue
BP	GO:0002449 lymphocyte mediated immunity	102/517	6.97E-76	2.57E-72	2.15E-72
BP	GO:0019724 B cell mediated immunity	85/517	6.58E-75	1.21E-71	1.02E-71
BP	GO:0002460 adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	102/517	1.17E-74	1.45E-71	1.21E-71
BP	GO:0016064 immunoglobulin mediated immune response	83/517	1.11E-72	1.03E-69	8.60E-70
BP	GO:0006958 complement activation, classical pathway	69/517	7.48E-71	5.53E-68	4.62E-68
BP	GO:0002455 humoral immune response mediated by circulating immunoglobulin	71/517	2.13E-70	1.31E-67	1.10E-67
BP	GO:0002429 immune response-activating cell surface receptor signaling	109/517	1.08E-69	5.71E-67	4.77E-67
BP	GO:0006956 complement activation	71/517	1.99E-64	9.21E-62	7.70E-62
BP	GO:0006909 phagocytosis	94/517	4.42E-64	1.82E-61	1.52E-61
BP	GO:0051249 regulation of lymphocyte activation	103/517	5.83E-62	2.15E-59	1.80E-59
BP	GO:0072376 protein activation cascade	72/517	3.01E-61	1.01E-58	8.46E-59
BP	GO:0002696 positive regulation of leukocyte activation	90/517	2.71E-58	8.33E-56	6.97E-56
BP	GO:0050867 positive regulation of cell activation	91/517	6.31E-58	1.79E-55	1.50E-55
BP	GO:0051251 positive regulation of lymphocyte activation	85/517	8.97E-58	2.37E-55	1.98E-55
BP	GO:0006959 humoral immune response	87/517	1.52E-57	3.74E-55	3.13E-55
BP	GO:0050851 antigen receptor-mediated signaling pathway	79/517	5.46E-53	1.26E-50	1.05E-50
BP	GO:0050853 B cell receptor signaling pathway	55/517	2.23E-51	4.85E-49	4.06E-49
BP	GO:0038094 Fc-gamma receptor signaling pathway	56/517	5.46E-50	1.12E-47	9.37E-48
BP	GO:0002697 regulation of immune effector process	88/517	7.21E-49	1.40E-46	1.17E-46
BP	GO:0006911 phagocytosis, engulfment	51/517	4.74E-48	8.75E-46	7.32E-46
BP	GO:0002431 Fc receptor mediated stimulatory signaling pathway	55/517	5.41E-48	9.52E-46	7.96E-46

BP	GO:0002433	immune response-regulating cell surface receptor signaling pathway involved in Fc-gamma receptor	54/517	8.51E-48	1.37E-45	1.14E-45
BP	GO:0038096	signaling pathway involved in phagocytosis	54/517	8.51E-48	1.37E-45	1.14E-45
BP	GO:0099024	plasma membrane invagination	52/517	1.77E-47	2.73E-45	2.28E-45
BP	GO:0002920	regulation of humoral immune response	53/517	2.04E-47	3.02E-45	2.52E-45
BP	GO:0030449	regulation of complement activation	50/517	2.79E-47	3.96E-45	3.31E-45
BP	GO:2000257	regulation of protein activation cascade	50/517	4.78E-47	6.54E-45	5.47E-45
BP	GO:0002673	regulation of acute inflammatory response	56/517	9.59E-47	1.27E-44	1.06E-44
BP	GO:0002526	acute inflammatory	63/517	3.39E-46	4.32E-44	3.62E-44
BP	GO:0010324	membrane invagination	52/517	8.15E-46	1.00E-43	8.39E-44
BP	GO:0050864	regulation of B cell	58/517	3.21E-45	3.82E-43	3.20E-43
BP	GO:0006910	phagocytosis, recognition	43/517	1.07E-44	1.23E-42	1.03E-42
BP	GO:0050871	positive regulation of B cell activation	52/517	1.82E-44	2.04E-42	1.71E-42
BP	GO:0042113	B cell activation	70/517	1.07E-43	1.16E-41	9.70E-42
BP	GO:0050900	leukocyte migration	84/517	6.27E-42	6.61E-40	5.53E-40
BP	GO:0038093	Fc receptor signaling pathway	61/517	3.10E-41	3.18E-39	2.66E-39
BP	GO:0070613	regulation of protein processing	53/517	1.26E-39	1.26E-37	1.05E-37
BP	GO:1903317	regulation of protein maturation	53/517	2.39E-39	2.33E-37	1.95E-37
BP	GO:0050727	regulation of inflammatory response	79/517	2.48E-38	2.35E-36	1.97E-36
BP	GO:0002377	immunoglobulin production of molecular	53/517	6.96E-38	6.43E-36	5.38E-36
BP	GO:0002440	mediator of immune response	62/517	1.34E-37	1.20E-35	1.01E-35
BP	GO:0042110	T cell activation	74/517	2.98E-35	2.62E-33	2.19E-33
BP	GO:0008037	cell recognition	50/517	5.51E-32	4.73E-30	3.96E-30
BP	GO:0038095	Fc-epsilon receptor signaling pathway	45/517	1.23E-31	1.04E-29	8.67E-30
BP	GO:0016485	protein processing	58/517	3.77E-30	3.09E-28	2.59E-28
BP	GO:0006898	receptor-mediated endocytosis	54/517	2.38E-27	1.91E-25	1.60E-25
BP	GO:0050863	regulation of T cell	53/517	1.38E-26	1.08E-24	9.04E-25
BP	GO:0051604	protein maturation	59/517	1.72E-26	1.32E-24	1.11E-24

BP	GO:0030098	lymphocyte differentiation	55/517	8.91E-26	6.71E-24	5.62E-24
BP	GO:0030217	T cell differentiation	45/517	1.14E-24	8.40E-23	7.02E-23
BP	GO:0042742	defense response to bacterium	52/517	1.20E-24	8.68E-23	7.27E-23
BP	GO:0007159	leukocyte cell-cell	51/517	2.30E-23	1.64E-21	1.37E-21
BP	GO:1903037	regulation of leukocyte cell-cell adhesion	48/517	7.42E-23	5.17E-21	4.32E-21
BP	GO:0050870	positive regulation of T cell activation	39/517	5.32E-22	3.64E-20	3.04E-20
BP	GO:1903039	positive regulation of leukocyte cell-cell	40/517	1.11E-21	7.48E-20	6.26E-20
BP	GO:0046651	lymphocyte proliferation	43/517	1.34E-20	8.86E-19	7.41E-19
BP	GO:0032943	mononuclear cell proliferation	43/517	1.80E-20	1.16E-18	9.74E-19
BP	GO:0022409	positive regulation of cell-cell adhesion	41/517	5.72E-20	3.64E-18	3.05E-18
BP	GO:0070661	leukocyte proliferation	44/517	7.41E-20	4.64E-18	3.88E-18
BP	GO:0050670	regulation of lymphocyte proliferation	37/517	1.17E-19	7.18E-18	6.01E-18
BP	GO:0032944	regulation of mononuclear cell proliferation	37/517	1.38E-19	8.37E-18	7.00E-18
BP	GO:0022407	regulation of cell-cell adhesion	50/517	4.38E-19	2.61E-17	2.18E-17
BP	GO:0070663	regulation of leukocyte proliferation	37/517	1.14E-18	6.69E-17	5.60E-17
BP	GO:0042129	regulation of T cell proliferation	31/517	4.15E-18	2.39E-16	2.00E-16
BP	GO:0042102	positive regulation of T cell proliferation	25/517	5.93E-18	3.37E-16	2.82E-16
BP	GO:0042098	T cell proliferation	33/517	8.96E-18	5.01E-16	4.19E-16
BP	GO:0050671	positive regulation of lymphocyte proliferation	27/517	1.91E-16	1.05E-14	8.79E-15
BP	GO:0032946	positive regulation of mononuclear cell proliferation	27/517	2.34E-16	1.27E-14	1.06E-14
BP	GO:0070665	positive regulation of leukocyte proliferation	27/517	1.13E-15	6.04E-14	5.05E-14
BP	GO:0045785	positive regulation of cell adhesion	45/517	1.56E-15	8.25E-14	6.90E-14
BP	GO:0045619	regulation of lymphocyte differentiation	29/517	3.05E-15	1.59E-13	1.33E-13
BP	GO:0001819	positive regulation of cytokine production	47/517	1.50E-14	7.68E-13	6.43E-13
BP	GO:0032609	interferon-gamma	23/517	5.28E-14	2.67E-12	2.24E-12
BP	GO:0045058	T cell selection	16/517	6.47E-14	3.23E-12	2.70E-12

BP	GO:0045580	regulation of T cell differentiation	25/517	8.38E-14	4.13E-12	3.45E-12
BP	GO:0043368	positive T cell selection	14/517	1.10E-13	5.33E-12	4.46E-12
BP	GO:0050852	T cell receptor signaling pathway	29/517	3.57E-13	1.71E-11	1.43E-11
BP	GO:0046631	alpha-beta T cell	24/517	5.70E-13	2.70E-11	2.26E-11
BP	GO:0032623	interleukin-2 production	17/517	5.97E-13	2.79E-11	2.33E-11
BP	GO:1902105	regulation of leukocyte differentiation	33/517	1.05E-12	4.85E-11	4.06E-11
BP	GO:0030595	leukocyte chemotaxis	29/517	5.05E-12	2.30E-10	1.92E-10
BP	GO:0032663	regulation of interleukin-2 production	15/517	1.13E-11	5.09E-10	4.26E-10
BP	GO:0002695	negative regulation of leukocyte activation	25/517	1.73E-11	7.69E-10	6.43E-10
BP	GO:0032649	regulation of interferon-gamma production	19/517	3.64E-11	1.60E-09	1.34E-09
BP	GO:0002683	negative regulation of immune system process	41/517	5.70E-11	2.47E-09	2.07E-09
BP	GO:1990266	neutrophil migration	20/517	8.06E-11	3.46E-09	2.90E-09
BP	GO:0045621	positive regulation of lymphocyte differentiation	18/517	8.79E-11	3.70E-09	3.10E-09
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BP	GO:0060326	cell chemotaxis	32/517	1.02E-10	4.24E-09	3.55E-09
BP	GO:0032613	interleukin-10 production	14/517	2.01E-10	8.25E-09	6.90E-09
BP	GO:0002285	lymphocyte activation involved in immune	24/517	2.15E-10	8.72E-09	7.30E-09
BP	GO:0050866	negative regulation of cell activation	25/517	2.91E-10	1.17E-08	9.76E-09
BP	GO:0042108	positive regulation of cytokine biosynthetic	15/517	3.24E-10	1.29E-08	1.08E-08
BP	GO:0002703	regulation of leukocyte mediated immunity	25/517	3.60E-10	1.42E-08	1.18E-08
BP	GO:0030593	neutrophil chemotaxis	18/517	5.01E-10	1.95E-08	1.63E-08
BP	GO:0051250	negative regulation of lymphocyte activation	21/517	6.41E-10	2.47E-08	2.06E-08
BP	GO:0045582	positive regulation of T cell differentiation	16/517	8.88E-10	3.38E-08	2.83E-08
BP	GO:0046635	positive regulation of alpha-beta T cell	14/517	1.12E-09	4.24E-08	3.55E-08
BP	GO:0050868	negative regulation of T cell activation	18/517	1.75E-09	6.51E-08	5.45E-08
BP	GO:0045061	thymic T cell selection	9/517	1.95E-09	7.21E-08	6.03E-08
BP	GO:0097530	granulocyte migration	20/517	2.11E-09	7.71E-08	6.45E-08
BP	GO:0032729	positive regulation of interferon-gamma	14/517	2.19E-09	7.84E-08	6.56E-08

BP	GO:0072678	T cell migration	14/517	2.19E-09	7.84E-08	6.56E-08
BP	GO:0046632	alpha-beta T cell differentiation	17/517	2.38E-09	8.45E-08	7.07E-08
BP	GO:0031295	T cell costimulation	13/517	3.08E-09	1.08E-07	9.08E-08
BP	GO:0031294	lymphocyte costimulation	13/517	3.90E-09	1.36E-07	1.14E-07
BP	GO:0097529	myeloid leukocyte	24/517	4.54E-09	1.57E-07	1.31E-07
BP	GO:0046634	regulation of alpha-beta T cell activation	16/517	5.06E-09	1.73E-07	1.45E-07
BP	GO:0002706	regulation of lymphocyte mediated immunity	20/517	5.61E-09	1.90E-07	1.59E-07
BP	GO:0002699	positive regulation of immune effector process	24/517	7.96E-09	2.67E-07	2.23E-07
BP	GO:0071621	granulocyte chemotaxis	18/517	8.15E-09	2.71E-07	2.27E-07
BP	GO:0043383	negative T cell selection	7/517	8.42E-09	2.78E-07	2.32E-07
BP	GO:0032633	interleukin-4 production	10/517	1.27E-08	4.15E-07	3.47E-07
BP	GO:0042035	regulation of cytokine biosynthetic process	17/517	1.59E-08	5.14E-07	4.30E-07
BP	GO:1903706	regulation of hemopoiesis	37/517	1.65E-08	5.31E-07	4.44E-07
BP	GO:1903038	negative regulation of leukocyte cell-cell	18/517	1.76E-08	5.59E-07	4.68E-07
BP	GO:0045059	positive thymic T cell selection	7/517	1.78E-08	5.62E-07	4.70E-07
BP	GO:1902107	positive regulation of leukocyte differentiation	19/517	1.80E-08	5.63E-07	4.71E-07
BP	GO:0045076	regulation of interleukin-2 biosynthetic process	8/517	1.89E-08	5.87E-07	4.91E-07
BP	GO:0002819	regulation of adaptive immune response	20/517	1.93E-08	5.95E-07	4.98E-07
BP	GO:0032733	positive regulation of interleukin-10 production	10/517	3.23E-08	9.87E-07	8.26E-07
BP	GO:0042089	cytokine biosynthetic	17/517	5.05E-08	1.53E-06	1.28E-06
BP	GO:0042100	B cell proliferation	15/517	5.08E-08	1.53E-06	1.28E-06
BP	GO:0033077	T cell differentiation in thymus	13/517	5.44E-08	1.62E-06	1.35E-06
BP	GO:0042107	cytokine metabolic	17/517	5.71E-08	1.69E-06	1.41E-06
BP	GO:0072676	lymphocyte migration	16/517	6.86E-08	2.01E-06	1.68E-06
BP	GO:0002704	negative regulation of leukocyte mediated	11/517	7.42E-08	2.15E-06	1.80E-06
BP	GO:0042094	interleukin-2 biosynthetic process	8/517	7.44E-08	2.15E-06	1.80E-06
BP	GO:0032743	positive regulation of interleukin-2 production	9/517	7.61E-08	2.18E-06	1.82E-06
BP	GO:0032945	negative regulation of mononuclear cell proliferation	13/517	9.16E-08	2.58E-06	2.16E-06

BP	GO:0050672	negative regulation of lymphocyte proliferation	13/517	9.16E-08	2.58E-06	2.16E-06
BP	GO:0032103	positive regulation of response to external	28/517	1.07E-07	2.98E-06	2.50E-06
BP	GO:0032753	positive regulation of interleukin-4 production	8/517	1.11E-07	3.09E-06	2.59E-06
BP	GO:0070098	chemokine-mediated signaling pathway	14/517	1.29E-07	3.55E-06	2.97E-06
BP	GO:0048247	lymphocyte chemotaxis	12/517	1.59E-07	4.34E-06	3.63E-06
BP	GO:0071887	leukocyte apoptotic	15/517	1.75E-07	4.74E-06	3.96E-06
BP	GO:0006968	cellular defense response	11/517	1.76E-07	4.74E-06	3.96E-06
BP	GO:0045060	negative thymic T cell selection	6/517	1.80E-07	4.81E-06	4.03E-06
BP	GO:0070664	negative regulation of leukocyte proliferation	13/517	2.06E-07	5.48E-06	4.59E-06
BP	GO:1903708	positive regulation of hemopoiesis	20/517	2.21E-07	5.84E-06	4.88E-06
BP	GO:0001909	leukocyte mediated cytotoxicity	15/517	2.56E-07	6.70E-06	5.61E-06
BP	GO:2000404	regulation of T cell	10/517	2.59E-07	6.73E-06	5.63E-06
BP	GO:0007204	positive regulation of cytosolic calcium ion concentration	27/517	2.91E-07	7.52E-06	6.29E-06
BP	GO:0031343	positive regulation of cell killing	12/517	3.18E-07	8.16E-06	6.83E-06
BP	GO:0070227	lymphocyte apoptotic process	12/517	3.76E-07	9.57E-06	8.00E-06
BP	GO:1902622	regulation of neutrophil migration	9/517	4.32E-07	1.09E-05	9.14E-06
BP	GO:2000106	regulation of leukocyte apoptotic process	13/517	4.36E-07	1.10E-05	9.17E-06
BP	GO:0050766	positive regulation of phagocytosis	12/517	4.42E-07	1.10E-05	9.17E-06
BP	GO:1990868	response to chemokine	14/517	4.45E-07	1.10E-05	9.17E-06
BP	GO:1990869	cellular response to chemokine	14/517	4.45E-07	1.10E-05	9.17E-06
BP	GO:0002710	negative regulation of T cell mediated immunity	7/517	4.53E-07	1.10E-05	9.20E-06
BP	GO:0046641	positive regulation of alpha-beta T cell	7/517	4.53E-07	1.10E-05	9.20E-06
BP	GO:0032673	regulation of interleukin-4 production	8/517	4.57E-07	1.10E-05	9.23E-06
BP	GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II	14/517	5.07E-07	1.21E-05	1.01E-05

BP	GO:0031341	regulation of cell killing	14/517	5.07E-07	1.21E-05	1.01E-05
BP	GO:0042130	negative regulation of T cell proliferation	11/517	5.55E-07	1.31E-05	1.10E-05
BP	GO:0045730	respiratory burst	9/517	5.57E-07	1.31E-05	1.10E-05
BP	GO:0002685	regulation of leukocyte migration	20/517	5.64E-07	1.32E-05	1.10E-05
BP	GO:0002822	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	17/517	5.68E-07	1.32E-05	1.10E-05
BP	GO:0010818	T cell chemotaxis	8/517	6.25E-07	1.44E-05	1.21E-05
BP	GO:0045086	positive regulation of interleukin-2 biosynthetic process	6/517	6.37E-07	1.46E-05	1.22E-05
BP	GO:0071346	cellular response to interferon-gamma	19/517	6.42E-07	1.46E-05	1.22E-05
BP	GO:0001776	leukocyte homeostasis	13/517	6.66E-07	1.51E-05	1.26E-05
BP	GO:0022408	negative regulation of cell-cell adhesion	19/517	7.00E-07	1.58E-05	1.32E-05
BP	GO:0034341	response to interferon-gamma	20/517	7.19E-07	1.61E-05	1.35E-05
BP	GO:0002495	antigen processing and presentation of peptide antigen via MHC class II	14/517	7.38E-07	1.64E-05	1.37E-05
BP	GO:0043367	CD4-positive, alpha-beta T cell differentiation	12/517	8.25E-07	1.82E-05	1.53E-05
BP	GO:0002504	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	14/517	8.34E-07	1.83E-05	1.53E-05
BP	GO:1903557	positive regulation of tumor necrosis factor superfamily cytokine	13/517	8.73E-07	1.91E-05	1.60E-05
BP	GO:0002260	lymphocyte homeostasis	11/517	9.36E-07	2.03E-05	1.70E-05
BP	GO:0001906	cell killing	18/517	1.02E-06	2.19E-05	1.83E-05
BP	GO:0002708	positive regulation of lymphocyte mediated immunity	14/517	1.19E-06	2.56E-05	2.14E-05
BP	GO:0045088	regulation of innate immune response	32/517	1.30E-06	2.78E-05	2.32E-05
BP	GO:0002286	T cell activation involved in immune response	14/517	1.34E-06	2.84E-05	2.38E-05
BP	GO:0019882	antigen processing and presentation	21/517	1.38E-06	2.92E-05	2.44E-05

BP	GO:0035710	CD4-positive, alpha-beta T cell activation	13/517	1.47E-06	3.05E-05	2.55E-05
BP	GO:2000406	positive regulation of T cell migration	8/517	1.47E-06	3.05E-05	2.55E-05
BP	GO:0001910	regulation of leukocyte mediated cytotoxicity	12/517	1.48E-06	3.05E-05	2.55E-05
BP	GO:0048872	homeostasis of number of cells	22/517	1.48E-06	3.05E-05	2.55E-05
BP	GO:0070228	regulation of lymphocyte apoptotic process	10/517	1.63E-06	3.34E-05	2.79E-05
BP	GO:0002478	antigen processing and presentation of exogenous peptide antigen	18/517	1.84E-06	3.76E-05	3.14E-05
BP	GO:0007162	negative regulation of cell adhesion	24/517	1.86E-06	3.78E-05	3.16E-05
BP	GO:0032703	negative regulation of interleukin-2 production	7/517	2.00E-06	4.04E-05	3.38E-05
BP	GO:0002292	T cell differentiation involved in immune	11/517	2.43E-06	4.88E-05	4.08E-05
BP	GO:0046633	alpha-beta T cell proliferation	8/517	2.47E-06	4.93E-05	4.13E-05
BP	GO:0051480	regulation of cytosolic calcium ion concentration	27/517	2.59E-06	5.14E-05	4.30E-05
BP	GO:0001912	positive regulation of leukocyte mediated cytotoxicity	10/517	2.76E-06	5.44E-05	4.55E-05
BP	GO:0050764	regulation of phagocytosis	13/517	3.04E-06	5.97E-05	4.99E-05
BP	GO:0045066	regulatory T cell differentiation	8/517	3.15E-06	6.16E-05	5.15E-05
BP	GO:0019884	antigen processing and presentation of exogenous antigen	18/517	3.23E-06	6.24E-05	5.22E-05
BP	GO:0002688	regulation of leukocyte chemotaxis	14/517	3.24E-06	6.24E-05	5.22E-05
BP	GO:0002820	negative regulation of adaptive immune response	9/517	3.26E-06	6.24E-05	5.22E-05
BP	GO:0002709	regulation of T cell mediated immunity	11/517	3.26E-06	6.24E-05	5.22E-05
BP	GO:0010819	regulation of T cell chemotaxis	6/517	4.18E-06	7.92E-05	6.62E-05
BP	GO:0060263	regulation of respiratory burst	6/517	4.18E-06	7.92E-05	6.62E-05
BP	GO:0002705	positive regulation of leukocyte mediated	15/517	4.26E-06	8.01E-05	6.70E-05
BP	GO:0050777	negative regulation of immune response	16/517	4.27E-06	8.01E-05	6.70E-05

BP	GO:2000107	negative regulation of leukocyte apoptotic	9/517	4.77E-06	8.89E-05	7.44E-05
BP	GO:0048002	antigen processing and presentation of peptide antigen	18/517	5.52E-06	0.0001024	8.57E-05
BP	GO:0002698	negative regulation of immune effector process	14/517	5.96E-06	0.00011	9.21E-05
BP	GO:0030888	regulation of B cell proliferation	10/517	6.17E-06	0.0001133	9.48E-05
BP	GO:0043029	T cell homeostasis	8/517	6.23E-06	0.0001134	9.48E-05
BP	GO:2000403	positive regulation of lymphocyte migration	8/517	6.23E-06	0.0001134	9.48E-05
BP	GO:0002456	T cell mediated immunity	13/517	7.35E-06	0.0001325	0.000110886
BP	GO:0002700	regulation of production of molecular mediator of immune response	15/517	7.36E-06	0.0001325	0.000110886
BP	GO:0002707	negative regulation of lymphocyte mediated immunity	8/517	7.70E-06	0.0001381	0.000115523
BP	GO:0060333	interferon-gamma-mediated signaling	12/517	7.74E-06	0.0001381	0.000115529
BP	GO:0046637	regulation of alpha-beta T cell differentiation	10/517	8.32E-06	0.000147	0.000122956
BP	GO:2000401	regulation of lymphocyte migration	10/517	8.32E-06	0.000147	0.000122956
BP	GO:0045089	positive regulation of innate immune response	27/517	8.64E-06	0.0001519	0.000127097
BP	GO:0051209	release of sequestered calcium ion into cytosol	14/517	8.75E-06	0.0001532	0.000128164
BP	GO:0002228	natural killer cell mediated immunity	10/517	9.62E-06	0.0001675	0.00014015
BP	GO:0051283	negative regulation of sequestering of calcium	14/517	1.05E-05	0.0001828	0.000152928
BP	GO:1902624	positive regulation of neutrophil migration	7/517	1.10E-05	0.0001896	0.000158589
BP	GO:0019722	calcium-mediated	19/517	1.11E-05	0.0001896	0.000158589
BP	GO:0050854	regulation of antigen receptor-mediated signaling pathway	10/517	1.11E-05	0.0001896	0.000158589
BP	GO:0002823	negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	8/517	1.15E-05	0.0001964	0.00016427

BP	GO:0042116	macrophage activation	12/517	1.21E-05	0.0002055	0.000171932
BP	GO:0002577	regulation of antigen processing and	6/517	1.22E-05	0.0002057	0.000172051
BP	GO:0002687	positive regulation of leukocyte migration	14/517	1.27E-05	0.0002114	0.000176844
BP	GO:0051282	regulation of sequestering of calcium ion	14/517	1.27E-05	0.0002114	0.000176844
BP	GO:0046640	regulation of alpha-beta T cell proliferation	7/517	1.40E-05	0.0002324	0.000194411
BP	GO:0090022	regulation of neutrophil chemotaxis	7/517	1.40E-05	0.0002324	0.000194411
BP	GO:0032655	regulation of interleukin-12 production	9/517	1.57E-05	0.0002582	0.000216035
BP	GO:0030183	B cell differentiation	14/517	1.65E-05	0.0002698	0.000225669
BP	GO:0051208	sequestering of calcium	14/517	1.65E-05	0.0002698	0.000225669
		positive regulation of adaptive immune response based on somatic				
BP	GO:0002824	recombination of immune receptors built from immunoglobulin superfamily domains	12/517	2.06E-05	0.0003347	0.000279996
		immunoglobulin				
BP	GO:0002381	production involved in immunoglobulin mediated	9/517	2.12E-05	0.0003426	0.000286625
BP	GO:0032615	interleukin-12 production	9/517	2.12E-05	0.0003426	0.000286625
BP	GO:0045589	regulation of regulatory T cell differentiation	7/517	2.21E-05	0.0003551	0.000297042
BP	GO:0050921	positive regulation of chemotaxis	14/517	2.32E-05	0.0003716	0.000310912
BP	GO:0045807	positive regulation of endocytosis	15/517	2.35E-05	0.0003734	0.000312337
BP	GO:0030101	natural killer cell	11/517	2.48E-05	0.0003907	0.000326829
BP	GO:0032760	positive regulation of tumor necrosis factor	11/517	2.48E-05	0.0003907	0.000326829
BP	GO:0002367	cytokine production involved in immune	12/517	2.52E-05	0.0003955	0.000330884
BP	GO:0002690	positive regulation of leukocyte chemotaxis	11/517	2.76E-05	0.0004325	0.000361848
BP	GO:0002821	positive regulation of adaptive immune response	12/517	3.37E-05	0.0005256	0.000439714
BP	GO:0097553	calcium ion transmembrane import	14/517	3.50E-05	0.000543	0.00045422
BP	GO:0032677	regulation of interleukin-8 production	10/517	3.56E-05	0.0005504	0.000460413

BP	GO:0042267	natural killer cell mediated cytotoxicity	9/517	3.76E-05	0.0005783	0.000483797
BP	GO:0090023	positive regulation of neutrophil chemotaxis	6/517	3.85E-05	0.0005906	0.000494066
BP	GO:0043370	regulation of CD4-positive, alpha-beta T cell differentiation	8/517	3.98E-05	0.0006024	0.000503942
BP	GO:0046638	positive regulation of alpha-beta T cell	8/517	3.98E-05	0.0006024	0.000503942
BP	GO:0070231	T cell apoptotic process	8/517	3.98E-05	0.0006024	0.000503942
BP	GO:0019932	second-messenger-mediated signaling	28/517	4.03E-05	0.0006068	0.000507598
BP	GO:0002287	alpha-beta T cell activation involved in	9/517	4.30E-05	0.0006406	0.000535927
BP	GO:0002293	alpha-beta T cell differentiation involved in immune response	9/517	4.30E-05	0.0006406	0.000535927
BP	GO:2000514	regulation of CD4-positive, alpha-beta T cell	9/517	4.30E-05	0.0006406	0.000535927
BP	GO:0001774	microglial cell activation	8/517	4.66E-05	0.0006886	0.000576068
BP	GO:0002269	leukocyte activation involved in inflammatory	8/517	4.66E-05	0.0006886	0.000576068
BP	GO:1903555	regulation of tumor necrosis factor superfamily cytokine	15/517	4.93E-05	0.0007246	0.000606209
BP	GO:0002507	tolerance induction	6/517	4.95E-05	0.0007259	0.000607245
BP	GO:2000516	positive regulation of CD4-positive, alpha-beta T cell activation	7/517	4.98E-05	0.0007274	0.000608505
BP	GO:0002643	regulation of tolerance induction	5/517	5.42E-05	0.0007844	0.000656218
BP	GO:0010820	positive regulation of T cell chemotaxis	5/517	5.42E-05	0.0007844	0.000656218
BP	GO:0032757	positive regulation of interleukin-8 production	8/517	5.44E-05	0.0007844	0.000656224
BP	GO:0055074	calcium ion homeostasis	29/517	5.55E-05	0.0007975	0.000667128
BP	GO:0071624	positive regulation of granulocyte chemotaxis	6/517	6.29E-05	0.0009003	0.000753128
BP	GO:0071706	tumor necrosis factor superfamily cytokine production	15/517	6.97E-05	0.0009939	0.00083146
BP	GO:0043373	CD4-positive, alpha-beta T cell lineage commitment	5/517	7.50E-05	0.0010611	0.000887655
BP	GO:0045072	regulation of interferon-gamma biosynthetic	5/517	7.50E-05	0.0010611	0.000887655

BP	GO:1901623	regulation of lymphocyte chemotaxis	6/517	7.90E-05	0.0011133	0.000931361
BP	GO:0006874	cellular calcium ion homeostasis	28/517	8.40E-05	0.0011758	0.000983683
BP	GO:0001818	negative regulation of cytokine production	21/517	8.41E-05	0.0011758	0.000983683
BP	GO:0032637	interleukin-8 production	10/517	8.71E-05	0.0012132	0.001014931
BP	GO:0050729	positive regulation of inflammatory response	14/517	9.27E-05	0.0012877	0.001077238
BP	GO:0045577	regulation of B cell differentiation	6/517	9.82E-05	0.0013581	0.001136148
BP	GO:0042095	interferon-gamma biosynthetic process	5/517	0.00010148	0.0013983	0.001169807
BP	GO:0002718	regulation of cytokine production involved in immune response	10/517	0.00010695	0.0014683	0.001228337
BP	GO:0071216	cellular response to biotic stimulus	18/517	0.0001078	0.0014744	0.001233472
BP	GO:0030890	positive regulation of B cell proliferation	7/517	0.00011908	0.0016227	0.001357494
BP	GO:0050920	regulation of chemotaxis	17/517	0.00012028	0.0016331	0.001366226
BP	GO:0070229	negative regulation of lymphocyte apoptotic process	6/517	0.00012093	0.0016359	0.001368517
BP	GO:0002886	regulation of myeloid leukocyte mediated	8/517	0.00012694	0.001711	0.001431358
BP	GO:0060402	calcium ion transport into cytosol	14/517	0.00013089	0.0017578	0.001470506
BP	GO:0050663	cytokine secretion	18/517	0.00013329	0.0017835	0.00149205
BP	GO:0002363	alpha-beta T cell lineage commitment	5/517	0.0001346	0.0017945	0.001501194
BP	GO:0043372	positive regulation of CD4-positive, alpha-beta T cell differentiation	6/517	0.00014765	0.0019614	0.001640892
BP	GO:0002532	production of molecular mediator involved in inflammatory response	9/517	0.00016132	0.0021353	0.001786351
BP	GO:0042088	T-helper 1 type immune response	7/517	0.00016271	0.0021461	0.001795346
BP	GO:0002517	T cell tolerance induction	4/517	0.00016428	0.002159	0.00180619
BP	GO:0042535	positive regulation of tumor necrosis factor biosynthetic process	5/517	0.0001754	0.0022888	0.001914775
BP	GO:0043369	CD4-positive or CD8-positive, alpha-beta T cell lineage commitment	5/517	0.0001754	0.0022888	0.001914775

BP	GO:0002312	B cell activation involved in immune response	9/517	0.00017956	0.002335	0.001953381
BP	GO:0042093	T-helper cell	8/517	0.00018586	0.0023999	0.002007699
BP	GO:0061900	glial cell activation	8/517	0.00018586	0.0023999	0.002007699
BP	GO:0071622	regulation of granulocyte chemotaxis	7/517	0.00018893	0.0024311	0.002033797
BP	GO:0150076	neuroinflammatory	9/517	0.00022123	0.0028368	0.002373235
BP	GO:0002438	acute inflammatory response to antigenic	5/517	0.000225	0.0028652	0.002396961
BP	GO:0140131	positive regulation of lymphocyte chemotaxis	5/517	0.000225	0.0028652	0.002396961
BP	GO:0002294	CD4-positive, alpha-beta T cell differentiation involved in immune	8/517	0.00023638	0.0029999	0.002509618
BP	GO:0038110	interleukin-2-mediated signaling pathway	4/517	0.00024104	0.0030381	0.002541559
BP	GO:0045416	positive regulation of interleukin-8 biosynthetic process	4/517	0.00024104	0.0030381	0.002541559
BP	GO:0002437	inflammatory response to antigenic stimulus	7/517	0.0002516	0.003139	0.002626018
BP	GO:0002715	regulation of natural killer cell mediated immunity	7/517	0.0002516	0.003139	0.002626018
BP	GO:0043300	regulation of leukocyte degranulation	7/517	0.0002516	0.003139	0.002626018
BP	GO:0001914	regulation of T cell mediated cytotoxicity	6/517	0.0002567	0.0031706	0.002652407
BP	GO:0002717	positive regulation of natural killer cell	6/517	0.0002567	0.0031706	0.002652407
BP	GO:0070232	regulation of T cell apoptotic process	6/517	0.0002567	0.0031706	0.002652407
BP	GO:0050707	regulation of cytokine secretion	16/517	0.00025953	0.0031948	0.002672701
BP	GO:0072503	cellular divalent inorganic cation homeostasis	28/517	0.00028571	0.0035054	0.002932515
BP	GO:0071219	cellular response to molecule of bacterial	16/517	0.00028879	0.0035315	0.002954364
BP	GO:0060401	cytosolic calcium ion transport	14/517	0.00029924	0.0036472	0.003051147
BP	GO:0007588	excretion	8/517	0.0003328	0.0040429	0.003382154
BP	GO:0002864	regulation of acute inflammatory response to antigenic stimulus	4/517	0.00034057	0.0040968	0.003427253
BP	GO:0045078	positive regulation of interferon-gamma biosynthetic process	4/517	0.00034057	0.0040968	0.003427253

BP	GO:0071352	cellular response to interleukin-2	4/517	0.00034057	0.0040968	0.003427253
BP	GO:0032735	positive regulation of interleukin-12 production	6/517	0.00035898	0.0043043	0.00360084
BP	GO:0006885	regulation of pH	10/517	0.00038441	0.0045943	0.003843474
BP	GO:0051897	positive regulation of protein kinase B signaling	14/517	0.00040154	0.0047835	0.004001731
BP	GO:0002407	dendritic cell chemotaxis	5/517	0.0004388	0.0051773	0.004331211
BP	GO:0002861	regulation of inflammatory response to antigenic stimulus	5/517	0.0004388	0.0051773	0.004331211
BP	GO:0050857	positive regulation of antigen receptor-mediated signaling pathway	5/517	0.0004388	0.0051773	0.004331211
BP	GO:0002523	leukocyte migration involved in inflammatory	4/517	0.00046639	0.0054506	0.004559849
BP	GO:0055064	chloride ion homeostasis	4/517	0.00046639	0.0054506	0.004559849
BP	GO:0070669	response to interleukin-2	4/517	0.00046639	0.0054506	0.004559849
BP	GO:0002712	regulation of B cell mediated immunity	7/517	0.0004831	0.0055928	0.004678765
BP	GO:0002889	regulation of immunoglobulin mediated	7/517	0.0004831	0.0055928	0.004678765
BP	GO:0051452	intracellular pH reduction	7/517	0.0004831	0.0055928	0.004678765
BP	GO:0050715	positive regulation of cytokine secretion	12/517	0.00049357	0.0056961	0.004765245
BP	GO:0050714	positive regulation of protein secretion	18/517	0.00051208	0.0058913	0.004928545
BP	GO:0051453	regulation of intracellular	9/517	0.00052072	0.0059721	0.004996091
BP	GO:0032680	regulation of tumor necrosis factor production	13/517	0.0005235	0.0059854	0.005007274
BP	GO:1902106	negative regulation of leukocyte differentiation	10/517	0.00057271	0.0065279	0.005461071
BP	GO:0071222	cellular response to lipopolysaccharide	15/517	0.00061228	0.0069478	0.005812367
BP	GO:0045851	pH reduction	7/517	0.00061332	0.0069478	0.005812367
BP	GO:0002237	response to molecule of bacterial origin	21/517	0.00061995	0.0070014	0.005857208
BP	GO:0002467	germinal center formation	4/517	0.00062214	0.0070047	0.005859982
BP	GO:0032640	tumor necrosis factor production	13/517	0.00062432	0.0070079	0.005862659
BP	GO:0002360	T cell lineage commitment	5/517	0.00064879	0.0072387	0.006055681
BP	GO:0055083	monovalent inorganic anion homeostasis	5/517	0.00064879	0.0072387	0.006055681
BP	GO:0050856	regulation of T cell receptor signaling	6/517	0.00065712	0.0073095	0.006114943

BP	GO:1902476	chloride transmembrane transport	9/517	0.00073321	0.0081314	0.006802525
BP	GO:0043030	regulation of macrophage activation	7/517	0.00076995	0.0085132	0.007121961
BP	GO:0002825	regulation of T-helper 1 type immune response	5/517	0.0007783	0.0085543	0.007156322
BP	GO:0036336	dendritic cell migration	5/517	0.0007783	0.0085543	0.007156322
BP	GO:0009615	response to virus	20/517	0.00080772	0.0088399	0.007395241
BP	GO:0002295	T-helper cell lineage commitment	4/517	0.00081146	0.0088399	0.007395241
BP	GO:0043031	negative regulation of macrophage activation	4/517	0.00081146	0.0088399	0.007395241
BP	GO:0030641	regulation of cellular pH	9/517	0.00086333	0.0093772	0.007844765
BP	GO:0050728	negative regulation of inflammatory response	13/517	0.00087561	0.0094828	0.007933072
BP	GO:0050858	negative regulation of antigen receptor-mediated signaling pathway	5/517	0.00092615	0.0099716	0.008341986
BP	GO:0090383	phagosome acidification	5/517	0.00092615	0.0099716	0.008341986
BP	GO:0032496	response to lipopolysaccharide	20/517	0.00093813	0.0100713	0.008425386
BP	GO:0032958	inositol phosphate biosynthetic process	6/517	0.00098509	0.0105143	0.00879598
BP	GO:0097028	dendritic cell	6/517	0.00098509	0.0105143	0.00879598
BP	GO:0051607	defense response to virus	16/517	0.00101861	0.0108407	0.00906906
BP	GO:0031348	negative regulation of defense response	16/517	0.00106457	0.0112972	0.009451001
BP	GO:0032675	regulation of interleukin-6 production	12/517	0.00109105	0.0115422	0.009655917
BP	GO:0006929	substrate-dependent cell migration	5/517	0.0010939	0.0115422	0.009655917
BP	GO:0002793	positive regulation of peptide secretion	18/517	0.00117533	0.0123656	0.0103448
BP	GO:0034612	response to tumor necrosis factor	19/517	0.00117864	0.0123656	0.0103448
BP	GO:0055067	monovalent inorganic cation homeostasis	12/517	0.00122189	0.0127831	0.010694
BP	GO:0042269	regulation of natural killer cell mediated cytotoxicity	6/517	0.00126521	0.0131618	0.011010832
BP	GO:0090382	phagosome maturation	6/517	0.00126521	0.0131618	0.011010832
BP	GO:0001782	B cell homeostasis	5/517	0.00128315	0.0131996	0.011042484
BP	GO:0045954	positive regulation of natural killer cell mediated cytotoxicity	5/517	0.00128315	0.0131996	0.011042484
BP	GO:0050690	regulation of defense response to virus by virus	5/517	0.00128315	0.0131996	0.011042484

BP	GO:0050869	negative regulation of B cell activation	5/517	0.00128315	0.0131996	0.011042484
BP	GO:0045576	mast cell activation	7/517	0.00130142	0.0132833	0.011112444
BP	GO:0001911	negative regulation of leukocyte mediated cytotoxicity	4/517	0.00130566	0.0132833	0.011112444
BP	GO:0032693	negative regulation of interleukin-10 production	4/517	0.00130566	0.0132833	0.011112444
BP	GO:0070233	negative regulation of T cell apoptotic process	4/517	0.00130566	0.0132833	0.011112444
BP	GO:0071356	cellular response to tumor necrosis factor	18/517	0.00132043	0.0133966	0.011207277
BP	GO:0002218	activation of innate immune response	19/517	0.00152378	0.0154173	0.012897725
BP	GO:0006833	water transport	4/517	0.00161795	0.0162809	0.013620201
BP	GO:0045414	regulation of interleukin-8 biosynthetic process	4/517	0.00161795	0.0162809	0.013620201
BP	GO:0002637	regulation of immunoglobulin	7/517	0.0017365	0.0174264	0.014578474
BP	GO:0032635	interleukin-6 production	12/517	0.00178632	0.0178777	0.014956087
BP	GO:0043303	mast cell degranulation	6/517	0.00179471	0.0179132	0.014985732
BP	GO:1903532	positive regulation of secretion by cell	22/517	0.00180809	0.017998	0.015056688
BP	GO:0003014	renal system process	10/517	0.00185856	0.0184507	0.015435402
BP	GO:0002827	positive regulation of T-helper 1 type immune response	4/517	0.00197859	0.0194851	0.016300791
BP	GO:0042228	interleukin-8 biosynthetic process	4/517	0.00197859	0.0194851	0.016300791
BP	GO:0050860	negative regulation of T cell receptor signaling	4/517	0.00197859	0.0194851	0.016300791
BP	GO:0002279	mast cell activation involved in immune	6/517	0.00200396	0.0196303	0.016422237
BP	GO:0002711	positive regulation of T cell mediated immunity	6/517	0.00200396	0.0196303	0.016422237
BP	GO:0002548	monocyte chemotaxis	7/517	0.00208409	0.0203613	0.017033746
BP	GO:0019730	antimicrobial humoral response	10/517	0.00210172	0.0204793	0.017132462
BP	GO:0032621	interleukin-18 production	3/517	0.00219074	0.0212347	0.017764399
BP	GO:0071104	response to interleukin-9	3/517	0.00219074	0.0212347	0.017764399
BP	GO:0001913	T cell mediated	6/517	0.00223113	0.0215132	0.017997425
BP	GO:0002448	mast cell mediated	6/517	0.00223113	0.0215132	0.017997425
BP	GO:0030100	regulation of endocytosis	17/517	0.00224478	0.0215884	0.018060354
BP	GO:0042533	tumor necrosis factor biosynthetic process	5/517	0.00228788	0.021889	0.018311789

BP	GO:0042534	regulation of tumor necrosis factor	5/517	0.00228788	0.021889	0.018311789
BP	GO:1901739	regulation of myoblast	4/517	0.0023912	0.0228183	0.019089262
BP	GO:0002701	negative regulation of production of molecular mediator of immune response	5/517	0.00260937	0.0246455	0.020617816
BP	GO:0032689	negative regulation of interferon-gamma	5/517	0.00260937	0.0246455	0.020617816
BP	GO:0042092	type 2 immune response	5/517	0.00260937	0.0246455	0.020617816
BP	GO:0045622	regulation of T-helper cell differentiation	5/517	0.00260937	0.0246455	0.020617816
BP	GO:0015698	inorganic anion transport	12/517	0.00267719	0.0252216	0.021099754
BP	GO:0031342	negative regulation of cell killing	4/517	0.00285933	0.026733	0.022364152
BP	GO:0035584	calcium-mediated signaling using intracellular calcium	4/517	0.00285933	0.026733	0.022364152
BP	GO:0072643	interferon-gamma	4/517	0.00285933	0.026733	0.022364152
BP	GO:0018108	peptidyl-tyrosine phosphorylation	20/517	0.00288655	0.0269193	0.022520025
BP	GO:0002604	regulation of dendritic cell antigen processing and presentation	3/517	0.00295066	0.027242	0.022789993
BP	GO:0002887	negative regulation of myeloid leukocyte mediated immunity	3/517	0.00295066	0.027242	0.022789993
BP	GO:0033089	positive regulation of T cell differentiation in	3/517	0.00295066	0.027242	0.022789993
BP	GO:0098883	synapse pruning	3/517	0.00295066	0.027242	0.022789993
BP	GO:0033572	transferrin transport	5/517	0.00296236	0.0272818	0.022823262
BP	GO:0006821	chloride transport	9/517	0.00309126	0.0283276	0.023698152
BP	GO:0030004	cellular monovalent inorganic cation	9/517	0.00309126	0.0283276	0.023698152
BP	GO:0018212	peptidyl-tyrosine	20/517	0.00316829	0.0289616	0.024228592
BP	GO:0002714	positive regulation of B cell mediated immunity	5/517	0.00334856	0.0304288	0.02545603
BP	GO:0002891	positive regulation of immunoglobulin mediated immune response	5/517	0.00334856	0.0304288	0.02545603
BP	GO:0009595	detection of biotic	4/517	0.00338648	0.0304288	0.02545603
BP	GO:0010447	response to acidic pH	4/517	0.00338648	0.0304288	0.02545603
BP	GO:0010528	regulation of transposition	4/517	0.00338648	0.0304288	0.02545603
BP	GO:0010529	negative regulation of transposition	4/517	0.00338648	0.0304288	0.02545603

BP	GO:0036037	CD8-positive, alpha-beta T cell activation	4/517	0.00338648	0.0304288	0.02545603
BP	GO:0051896	regulation of protein kinase B signaling	15/517	0.00342229	0.030676	0.02566281
BP	GO:0043647	inositol phosphate metabolic process	7/517	0.00345523	0.0308962	0.025847044
BP	GO:0098661	inorganic anion transmembrane transport	9/517	0.00371447	0.0331342	0.02771924
BP	GO:0015682	ferric iron transport	5/517	0.00376968	0.0332532	0.027818778
BP	GO:0072512	trivalent inorganic cation transport	5/517	0.00376968	0.0332532	0.027818778
BP	GO:0002468	dendritic cell antigen processing and	3/517	0.00385387	0.0332532	0.027818778
BP	GO:0002863	positive regulation of inflammatory response to antigenic stimulus	3/517	0.00385387	0.0332532	0.027818778
BP	GO:0006216	cytidine catabolic process	3/517	0.00385387	0.0332532	0.027818778
BP	GO:0009972	cytidine deamination	3/517	0.00385387	0.0332532	0.027818778
BP	GO:0016554	cytidine to uridine editing	3/517	0.00385387	0.0332532	0.027818778
BP	GO:0030002	cellular anion homeostasis	3/517	0.00385387	0.0332532	0.027818778
BP	GO:0030320	cellular monovalent inorganic anion	3/517	0.00385387	0.0332532	0.027818778
BP	GO:0045579	positive regulation of B cell differentiation	3/517	0.00385387	0.0332532	0.027818778
BP	GO:0046087	cytidine metabolic process	3/517	0.00385387	0.0332532	0.027818778
BP	GO:0048302	regulation of isotype switching to IgG isotypes	3/517	0.00385387	0.0332532	0.027818778
BP	GO:0072540	T-helper 17 cell lineage commitment	3/517	0.00385387	0.0332532	0.027818778
BP	GO:1905522	negative regulation of macrophage migration	3/517	0.00385387	0.0332532	0.027818778
BP	GO:0031579	membrane raft	4/517	0.00397601	0.0341744	0.028589485
BP	GO:1903707	negative regulation of hemopoiesis	11/517	0.00397915	0.0341744	0.028589485
BP	GO:0002758	innate immune response- activating signal	17/517	0.00408975	0.0350428	0.029315928
BP	GO:0051047	positive regulation of secretion	22/517	0.00422001	0.0360551	0.030162777
BP	GO:2000816	negative regulation of mitotic sister chromatid	5/517	0.00422741	0.0360551	0.030162777
BP	GO:0001894	tissue homeostasis	14/517	0.00447506	0.0380793	0.031856172
BP	GO:0048871	multicellular organismal homeostasis	24/517	0.00462107	0.0388707	0.032518311
BP	GO:0001562	response to protozoan	4/517	0.00463123	0.0388707	0.032518311
BP	GO:0002335	mature B cell	4/517	0.00463123	0.0388707	0.032518311

BP	GO:0002719	negative regulation of cytokine production involved in immune	4/517	0.00463123	0.0388707	0.032518311
BP	GO:0090025	regulation of monocyte chemotaxis	4/517	0.00463123	0.0388707	0.032518311
BP	GO:2000482	regulation of interleukin-8 secretion	4/517	0.00463123	0.0388707	0.032518311
BP	GO:0046173	polyol biosynthetic	7/517	0.00469314	0.039301	0.032878293
BP	GO:0009268	response to pH	5/517	0.00472344	0.0393762	0.032941172
BP	GO:1905819	negative regulation of chromosome separation	5/517	0.00472344	0.0393762	0.032941172
BP	GO:0002702	positive regulation of production of molecular mediator of immune response	8/517	0.00484685	0.0401879	0.033620218
BP	GO:0035723	interleukin-15-mediated signaling pathway	3/517	0.00490786	0.0401879	0.033620218
BP	GO:0043301	negative regulation of leukocyte degranulation	3/517	0.00490786	0.0401879	0.033620218
BP	GO:0045006	DNA deamination	3/517	0.00490786	0.0401879	0.033620218
BP	GO:0048291	isotype switching to IgG isotypes	3/517	0.00490786	0.0401879	0.033620218
BP	GO:0071350	cellular response to interleukin-15	3/517	0.00490786	0.0401879	0.033620218
BP	GO:0071415	cellular response to purine-containing	3/517	0.00490786	0.0401879	0.033620218
BP	GO:1902713	regulation of interferon-gamma secretion	3/517	0.00490786	0.0401879	0.033620218
BP	GO:0032722	positive regulation of chemokine production	6/517	0.00524237	0.042832	0.035832202
BP	GO:0007520	myoblast fusion	5/517	0.00525943	0.0428766	0.035869478
BP	GO:0001916	positive regulation of T cell mediated cytotoxicity	4/517	0.00535531	0.043276	0.036203676
BP	GO:0002230	positive regulation of defense response to virus	4/517	0.00535531	0.043276	0.036203676
BP	GO:0042044	fluid transport	4/517	0.00535531	0.043276	0.036203676
BP	GO:0072539	T-helper 17 cell differentiation	4/517	0.00535531	0.043276	0.036203676
BP	GO:0032732	positive regulation of interleukin-1 production	6/517	0.00570258	0.0459817	0.038467179
BP	GO:0033048	negative regulation of mitotic sister chromatid	5/517	0.00583704	0.0469634	0.039288444
BP	GO:0001771	immunological synapse formation	3/517	0.00611917	0.0485981	0.040655976
BP	GO:0043374	CD8-positive, alpha-beta T cell differentiation	3/517	0.00611917	0.0485981	0.040655976

BP	GO:0045591	positive regulation of regulatory T cell differentiation	3/517	0.00611917	0.0485981	0.040655976
BP	GO:0045869	negative regulation of single stranded viral RNA replication via double stranded DNA	3/517	0.00611917	0.0485981	0.040655976
BP	GO:0046133	pyrimidine ribonucleoside catabolic process	3/517	0.00611917	0.0485981	0.040655976
BP	GO:0070672	response to interleukin-15	3/517	0.00611917	0.0485981	0.040655976
CC	GO:0019814	immunoglobulin complex	83/529	3.51E-88	1.24E-85	1.05E-85
CC	GO:0009897	external side of plasma membrane	94/529	1.72E-62	3.03E-60	2.57E-60
CC	GO:0042571	immunoglobulin complex, circulating	43/529	2.75E-49	3.24E-47	2.75E-47
CC	GO:0072562	blood microparticle	32/529	2.64E-20	2.33E-18	1.98E-18
CC	GO:0042101	T cell receptor complex	30/529	3.38E-20	2.39E-18	2.03E-18
CC	GO:0098802	plasma membrane receptor complex	39/529	1.72E-16	1.01E-14	8.62E-15
CC	GO:0042613	MHC class II protein complex	9/529	6.52E-11	3.29E-09	2.79E-09
CC	GO:0042611	MHC protein complex	10/529	4.04E-10	1.78E-08	1.52E-08
CC	GO:0001772	immunological synapse	11/529	1.53E-09	6.00E-08	5.10E-08
CC	GO:0030666	endocytic vesicle	19/529	1.24E-07	4.36E-06	3.71E-06
CC	GO:0030139	endocytic vesicle	26/529	2.06E-07	6.60E-06	5.61E-06
CC	GO:0071556	integral component of luminal side of endoplasmic reticulum	8/529	6.65E-07	1.81E-05	1.53E-05
CC	GO:0098553	luminal side of endoplasmic reticulum	8/529	6.65E-07	1.81E-05	1.53E-05
CC	GO:0030669	clathrin-coated endocytic vesicle membrane	9/529	2.07E-06	5.21E-05	4.43E-05
CC	GO:0030665	clathrin-coated vesicle membrane	14/529	2.51E-06	5.90E-05	5.02E-05
CC	GO:0045334	clathrin-coated endocytic vesicle	10/529	6.33E-06	0.0001396	0.000118646
CC	GO:0030136	clathrin-coated vesicle	17/529	1.33E-05	0.000276	0.000234596
CC	GO:0030662	coated vesicle membrane	15/529	0.0001219	0.0023907	0.002031735
CC	GO:0070821	tertiary granule membrane	9/529	0.00014205	0.0026392	0.002242926
CC	GO:0030667	secretory granule	20/529	0.00017188	0.0030337	0.002578256
CC	GO:0045335	phagocytic vesicle	12/529	0.00023161	0.0038669	0.003286316
CC	GO:0012507	ER to Golgi transport vesicle membrane	8/529	0.000241	0.0038669	0.003286316
CC	GO:0001931	uropod	4/529	0.00030205	0.0044427	0.003775653
CC	GO:0031254	cell trailing edge	4/529	0.00030205	0.0044427	0.003775653
CC	GO:0030135	coated vesicle	19/529	0.00032148	0.0045394	0.003857816

CC	GO:0030134	COPII-coated ER to Golgi transport vesicle	9/529	0.00087772	0.0119167	0.010127484
CC	GO:0016471	vacuolar proton-transporting V-type	4/529	0.00092319	0.0120699	0.010257714
CC	GO:0101003	ficolin-1-rich granule membrane	7/529	0.00119861	0.015111	0.01284222
CC	GO:0005765	lysosomal membrane	20/529	0.00150518	0.0183128	0.015563261
CC	GO:0098852	lytic vacuole membrane	20/529	0.00155633	0.0183128	0.015563261
CC	GO:0070820	tertiary granule	12/529	0.00160895	0.0183213	0.015570523
CC	GO:0005774	vacuolar membrane	22/529	0.00183232	0.0202128	0.017177984
CC	GO:0016323	basolateral plasma membrane	14/529	0.0022601	0.0236594	0.020107112
CC	GO:0005581	collagen trimer	8/529	0.00232602	0.0236594	0.020107112
CC	GO:0005771	multivesicular body	6/529	0.00234583	0.0236594	0.020107112
CC	GO:0031253	cell projection membrane	19/529	0.00259973	0.0254918	0.021664394
CC	GO:0035579	specific granule	8/529	0.00308346	0.0294178	0.025000993
CC	GO:0030660	Golgi-associated vesicle membrane	9/529	0.00361388	0.0335711	0.028530657
CC	GO:0030670	phagocytic vesicle membrane	7/529	0.00426085	0.0385661	0.032775754
CC	GO:0033176	proton-transporting V-type ATPase complex	4/529	0.00479164	0.0422863	0.035937336
CC	GO:0001891	phagocytic cup	4/529	0.00550753	0.0474185	0.040299034
CC	GO:0016324	apical plasma membrane	17/529	0.00571276	0.0480144	0.040805408
MF	GO:0003823	antigen binding	74/472	7.84E-74	4.26E-71	3.59E-71
MF	GO:0034987	immunoglobulin receptor binding	42/472	2.51E-46	6.82E-44	5.75E-44
MF	GO:0032395	MHC class II receptor activity	8/472	1.04E-11	1.88E-09	1.58E-09
MF	GO:0004896	cytokine receptor activity	18/472	6.80E-11	9.23E-09	7.78E-09
MF	GO:0019955	cytokine binding	17/472	5.30E-08	5.75E-06	4.85E-06
MF	GO:0042287	MHC protein binding	10/472	6.85E-08	6.20E-06	5.23E-06
MF	GO:0019864	IgG binding	6/472	1.44E-07	1.02E-05	8.60E-06
MF	GO:0042379	chemokine receptor	12/472	1.50E-07	1.02E-05	8.60E-06
MF	GO:0008009	chemokine activity	9/472	5.04E-06	0.0003039	0.000256263
MF	GO:0038187	pattern recognition receptor activity	6/472	1.35E-05	0.0006841	0.000576862
MF	GO:0042605	peptide antigen binding	7/472	1.39E-05	0.0006841	0.000576862
MF	GO:0005126	cytokine receptor binding	21/472	2.96E-05	0.0013026	0.001098448
MF	GO:0019865	immunoglobulin binding	6/472	3.12E-05	0.0013026	0.001098448
MF	GO:0005125	cytokine activity	17/472	8.99E-05	0.0034855	0.002939213
MF	GO:0048020	CCR chemokine receptor binding	7/472	0.00012882	0.0042019	0.003543317
MF	GO:0045236	CXCR chemokine receptor binding	4/472	0.00014205	0.0042019	0.003543317

MF	GO:0005164	tumor necrosis factor receptor binding	6/472	0.00014562	0.0042019	0.003543317
MF	GO:0008329	signaling pattern recognition receptor	5/472	0.00014703	0.0042019	0.003543317
MF	GO:0030506	ankyrin binding	5/472	0.00014703	0.0042019	0.003543317
MF	GO:0016493	C-C chemokine receptor activity	5/472	0.0002987	0.0081097	0.006838683
MF	GO:0019957	C-C chemokine binding	5/472	0.0003691	0.0095083	0.008018066
MF	GO:0005044	scavenger receptor	7/472	0.00038524	0.0095083	0.008018066
MF	GO:0005070	SH3/SH2 adaptor activity	7/472	0.00043508	0.0098032	0.00826676
MF	GO:0023023	MHC protein complex binding	5/472	0.00045135	0.0098032	0.00826676
MF	GO:0043027	cysteine-type endopeptidase inhibitor activity involved in	5/472	0.00045135	0.0098032	0.00826676
MF	GO:0048365	Rac GTPase binding	8/472	0.00048481	0.0101251	0.008538186
MF	GO:0001637	G protein-coupled chemoattractant receptor activity	5/472	0.00054667	0.0102965	0.008682712
MF	GO:0004950	chemokine receptor	5/472	0.00054667	0.0102965	0.008682712
MF	GO:0001664	G protein-coupled receptor binding	18/472	0.00054991	0.0102965	0.008682712
MF	GO:0001784	phosphotyrosine residue binding	6/472	0.00061983	0.0112189	0.009460526
MF	GO:0023026	MHC class II protein complex binding	4/472	0.00070458	0.0123414	0.01040714
MF	GO:0004869	cysteine-type endopeptidase inhibitor	7/472	0.00085249	0.0144657	0.01219846
MF	GO:0042277	peptide binding	18/472	0.00100563	0.0165472	0.013953737
MF	GO:0015026	coreceptor activity	6/472	0.001042	0.0166414	0.014033165
MF	GO:0043325	phosphatidylinositol-3,4- bisphosphate binding	5/472	0.00108487	0.016831	0.014193056
MF	GO:0004252	serine-type endopeptidase activity	12/472	0.00123138	0.017509	0.014764793
MF	GO:1901981	phosphatidylinositol phosphate binding	12/472	0.00129925	0.017509	0.014764793
MF	GO:0035591	signaling adaptor activity	8/472	0.00130312	0.017509	0.014764793
MF	GO:0008509	anion transmembrane transporter activity	19/472	0.00131031	0.017509	0.014764793
MF	GO:0004715	non-membrane spanning protein tyrosine kinase activity	6/472	0.00132204	0.017509	0.014764793
MF	GO:0032813	tumor necrosis factor receptor superfamily	6/472	0.00132204	0.017509	0.014764793
MF	GO:0019956	chemokine binding	5/472	0.0014674	0.0189714	0.015997972

		inorganic anion				
MF	GO:0015103	transmembrane transporter activity	11/472	0.00187211	0.0236408	0.019935568
MF	GO:0038024	cargo receptor activity	8/472	0.00192774	0.02379	0.020061388
MF	GO:0045309	protein phosphorylated amino acid binding	6/472	0.00227287	0.0274259	0.023127404
MF	GO:0015250	water channel activity	3/472	0.00265143	0.0312984	0.026392959
MF	GO:1902936	phosphatidylinositol bisphosphate binding	9/472	0.00272297	0.031459	0.026528379
MF	GO:0017048	Rho GTPase binding	12/472	0.00287874	0.0325658	0.027461697
MF	GO:0004126	cytidine deaminase	3/472	0.00346571	0.0368996	0.031116273
MF	GO:0005372	water transmembrane transporter activity	3/472	0.00346571	0.0368996	0.031116273
MF	GO:0016175	superoxide-generating NADPH oxidase activity	3/472	0.00346571	0.0368996	0.031116273
MF	GO:0008236	serine-type peptidase	12/472	0.00361027	0.0376996	0.031790881
MF	GO:0017171	serine hydrolase activity	12/472	0.00429757	0.0440298	0.037128961
MF	GO:0001540	amyloid-beta binding	7/472	0.00475389	0.047803	0.040310799
MF	GO:0043028	cysteine-type endopeptidase regulator activity involved in	5/472	0.00498519	0.0492174	0.041503471

Supplementary Table 6 | GO result of AIM2 high vs low subgroup.

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
KEGG_AUTOIMMUNE_THYRO ID_DISEASE	50	0.887389	2.71565	0	0	0
KEGG_CYTOKINE_CYTOKINE _RECEPTOR_INTERACTION	247	0.635322	2.62575	0	0	0
KEGG_INTESTINAL_IMMUNE _NETWORK_FOR_IGA_PRODU	46	0.872307	2.61134	0	0	0
KEGG_ANTIGEN_PROCESSIN G_AND_PRESENTATION	80	0.802707	2.56772	0	0	0
KEGG_VIRAL_MYOCARDITIS	67	0.80852	2.56019	0	0	0
KEGG_JAK_STAT_SIGNALING _PATHWAY	150	0.645265	2.55852	0	0	0
KEGG_NATURAL_KILLER_CE LL_MEDIATED_CYTOTOXICIT	131	0.719605	2.52375	0	1.32E-04	0.001
KEGG_PRIMARY_IMMUNODE FICIENCY	34	0.903791	2.48322	0	1.15E-04	0.001
KEGG_CELL_ADHESION_MOL ECULES_CAMS	128	0.701096	2.4782	0	1.03E-04	0.001
KEGG_LEISHMANIA_INFECTI	70	0.817561	2.44334	0	1.70E-04	0.002
KEGG_TYPE_I_DIABETES_ME	41	0.886261	2.40942	0	1.55E-04	0.002
KEGG_SYSTEMIC_LUPUS_ER YTHEMATOSUS	54	0.854075	2.40612	0	1.42E-04	0.002
KEGG_HEMATOPOIETIC_CEL L_LINEAGE	85	0.690577	2.40034	0.0020202	1.31E-04	0.002
KEGG_TOLL_LIKE_RECEPTO R_SIGNALING_PATHWAY	96	0.685132	2.36762	0	3.18E-04	0.004
KEGG_ASTHMA	28	0.865155	2.36223	0	2.97E-04	0.004
KEGG_ALLOGRAFT_REJECTI	35	0.933905	2.3362	0	2.78E-04	0.004
KEGG_T_CELL_RECEPTOR_SI GNALING_PATHWAY	105	0.717602	2.33479	0	2.62E-04	0.004
KEGG_GRAFT_VERSUS_HOST _DISEASE	37	0.898466	2.254	0	7.26E-04	0.006
KEGG_CHEMOKINE_SIGNALI NG_PATHWAY	173	0.636099	2.2255	0.00402414	0.00118537	0.013
KEGG_CYTOSOLIC_DNA_SEN SING_PATHWAY	49	0.641373	2.21335	0	0.00132036	0.013
KEGG_B_CELL_RECEPTOR_SI GNALING_PATHWAY	73	0.681006	2.18474	0.00196078	0.00166093	0.016
KEGG_NOD_LIKE_RECEPTOR _SIGNALING_PATHWAY	58	0.680493	2.16996	0	0.00177236	0.017
KEGG_FC_GAMMA_R_MEDIA TED_PHAGOCYTOSIS	91	0.638527	2.09195	0.00395257	0.00610837	0.044
KEGG_HOMOLOGOUS_RECO MBINATION	26	0.749511	1.9991	0	0.0149007	0.094
KEGG_FC_EPSILON_RI_SIGNA LING_PATHWAY	79	0.550034	1.97032	0.00796813	0.01881949	0.115

KEGG_APOPTOSIS	85	0.600014	1.92597	0.00804829	0.02687417	0.143
KEGG_DNA_REPLICATION	36	0.743794	1.90447	0.00627615	0.03101421	0.167
KEGG_CELL_CYCLE	124	0.619685	1.87863	0.01229508	0.03736225	0.188
KEGG_PROTEASOME	43	0.714574	1.8761	0.01195219	0.03678844	0.19
KEGG_BASE_EXCISION_REPA	34	0.666114	1.85233	0.01590457	0.04219111	0.214
KEGG_RIG_I_LIKE_RECEPTOR _SIGNALING_PATHWAY	66	0.544396	1.82841	0.01642711	0.04839904	0.238
KEGG_P53_SIGNALING_PATH	65	0.561669	1.81208	0.01260504	0.05378761	0.257
KEGG_LEUKOCYTE_TRANSE NDOTHELIAL_MIGRATION	114	0.502784	1.75986	0.02941177	0.07524273	0.325
KEGG_PRION_DISEASES	34	0.569906	1.70539	0.03193613	0.1001498	0.396
KEGG_SNARE_INTERACTION S_IN_VESICULAR_TRANSPOR	37	0.56994	1.6911	0.03807615	0.10534902	0.419
KEGG_PROGESTERONE_MEDI ATED_OOCYTE_MATURATIO	85	0.521911	1.68613	0.05208333	0.10559241	0.426
KEGG_REGULATION_OF_ACT IN_CYTOSKELETON	210	0.464854	1.66918	0.04848485	0.11257351	0.447
KEGG_AMINO_SUGAR_AND_ NUCLEOTIDE_SUGAR_METAB	43	0.552304	1.64735	0.06185567	0.1243782	0.477
KEGG_MISMATCH_REPAIR	23	0.659534	1.63645	0.05063291	0.12795839	0.499
KEGG_PATHOGENIC_ESCHER ICHIA_COLI_INFECTION	56	0.530407	1.61688	0.06930693	0.13922673	0.529
KEGG_AMYOTROPHIC_LATE RAL_SCLEROSIS_ALS	50	0.461969	1.61151	0.04752475	0.1396868	0.539
KEGG_O_GLYCAN_BIOSYNTH	26	0.518332	1.60394	0.04125737	0.14222346	0.55
KEGG_NUCLEOTIDE_EXCISIO N_REPAIR	43	0.573424	1.60183	0.07520326	0.14034423	0.557
KEGG_LYSOSOME	119	0.507243	1.58002	0.1053678	0.15252937	0.587
KEGG_PYRIMIDINE_METABO	96	0.476023	1.57965	0.08641975	0.1495428	0.587
KEGG_MAPK_SIGNALING_PA	262	0.408027	1.57458	0.07331976	0.14926921	0.592
KEGG_PATHWAYS_IN_CANC	318	0.421486	1.56376	0.08730159	0.15331452	0.605
KEGG_VEGF_SIGNALING_PAT	75	0.425243	1.5622	0.07056452	0.1511042	0.609
KEGG_PANCREATIC_CANCER	68	0.511805	1.55863	0.10515873	0.15107396	0.614
KEGG_COLORECTAL_CANCE	62	0.51048	1.54788	0.10040161	0.15558337	0.626
KEGG_ACUTE_MYELOID_LEU	56	0.496503	1.54582	0.1124498	0.15400834	0.628
KEGG_OTHER_GLYCAN_DEG RADATION	16	0.596059	1.53856	0.09619238	0.15551989	0.64
KEGG_OOCYTE_MEIOSIS	110	0.462354	1.52657	0.09635975	0.16206948	0.659
KEGG_COMPLEMENT_AND_C OAGULATION_CASCADES	69	0.563604	1.50482	0.07966457	0.17540964	0.695
KEGG_ABC_TRANSPORTERS	44	0.432756	1.50291	0.0546875	0.17342079	0.696
KEGG_PANTOTHENATE_AND _COA_BIOSYNTHESIS	16	0.544464	1.49195	0.07459678	0.17774561	0.711
KEGG_SMALL_CELL_LUNG_C	83	0.463957	1.48852	0.11576846	0.17689902	0.715
KEGG_NICOTINATE_AND_NIC OTINAMIDE_METABOLISM	22	0.464192	1.44252	0.10311284	0.21183257	0.764

KEGG_PURINE_METABOLISM	150	0.386333	1.43763	0.14807302	0.2124721	0.774
KEGG_GALACTOSE_METABO	26	0.466493	1.41098	0.14081633	0.23101802	0.8
KEGG_PHOSPHATIDYLINOSIT OL_SIGNALING_SYSTEM	75	0.428149	1.4075	0.1627451	0.2301695	0.805
KEGG_UBIQUITIN_MEDIATED _PROTEOLYSIS	129	0.464603	1.38833	0.20523138	0.24315488	0.817
KEGG_ENDOCYTOSIS	175	0.404805	1.37696	0.18972331	0.24907167	0.826
KEGG_ALPHA_LINOLENIC_A CID_METABOLISM	19	0.448997	1.37351	0.11111111	0.24834363	0.827
KEGG_NEUROACTIVE_LIGAN D_RECEPTOR_INTERACTION	265	0.297657	1.37049	0.07378641	0.24712673	0.829
KEGG_AXON_GUIDANCE	126	0.388715	1.36541	0.18585859	0.249159	0.839
KEGG_NEUROTROPHIN_SIGN ALING_PATHWAY	124	0.413171	1.35193	0.21062993	0.25717476	0.853
KEGG_GLYCOSPHINGOLIPID_ BIOSYNTHESIS_LACTO_AND_ NEOLACTO_SERIES	25	0.398741	1.35021	0.138	0.25459245	0.853
KEGG_TASTE_TRANSDUCTIO	51	0.416312	1.34566	0.1979798	0.25496858	0.856
KEGG_N_GLYCAN_BIOSYNTH	46	0.473433	1.34263	0.20281124	0.2541546	0.86
KEGG_ERBB_SIGNALING_PAT	86	0.400248	1.33296	0.22266401	0.25928885	0.868
KEGG_RNA_DEGRADATION	54	0.451593	1.33237	0.22088353	0.25605753	0.868
KEGG_NON_SMALL_CELL_LU NG_CANCER	53	0.43707	1.33103	0.21485944	0.25359958	0.868
KEGG_FOCAL_ADHESION	196	0.389136	1.33038	0.21242484	0.25072008	0.868
KEGG_GLYCOSPHINGOLIPID_ BIOSYNTHESIS_GANGLIO_SE	15	0.500243	1.32964	0.18871595	0.24801752	0.868
KEGG_GLYCOSAMINOGLYCA N_BIOSYNTHESIS_CHONDROI	22	0.484927	1.32362	0.20816326	0.2502448	0.872
KEGG_GLIOMA	65	0.402476	1.32185	0.22764228	0.24833678	0.873
KEGG_CHRONIC_MYELOID_L EUKEMIA	72	0.433266	1.31454	0.24404761	0.25161985	0.876
KEGG_HEDGEHOG_SIGNALIN G_PATHWAY	56	0.363209	1.29441	0.17669903	0.26590955	0.895
KEGG_SPHINGOLIPID_METAB	36	0.422344	1.29423	0.23326571	0.2627139	0.895
KEGG_GLYCEROPHOSPHOLIP ID_METABOLISM	71	0.342235	1.29162	0.17706238	0.26185507	0.895
KEGG_LONG_TERM_POTENTI	68	0.372379	1.28136	0.22983871	0.2669101	0.9
KEGG_PROTEIN_EXPORT	23	0.495994	1.27822	0.26335877	0.26633292	0.904
KEGG_DORSO_VENTRAL_AXI S_FORMATION	24	0.436499	1.2667	0.24590164	0.27303734	0.91
KEGG_ETHER_LIPID_METAB	30	0.359752	1.24799	0.20907298	0.28648326	0.919
KEGG_GLYCOSAMINOGLYCA N_DEGRADATION	21	0.420139	1.24003	0.23425196	0.29041007	0.923
KEGG_LONG_TERM_DEPRESS	68	0.334297	1.23519	0.21829522	0.29199627	0.928
KEGG_GNRH_SIGNALING_PA	101	0.32932	1.22894	0.25099602	0.29446375	0.933

KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM	33	0.400768	1.20873	0.27234927	0.30998787	0.945
KEGG_BASAL_CELL_CARCINOMA	55	0.353813	1.20208	0.264	0.3123425	0.947
KEGG_RENAL_CELL_CARCINOMA	66	0.402287	1.19829	0.31736526	0.31279054	0.948
KEGG_WNT_SIGNALING_PATHWAY	149	0.338683	1.19261	0.3111546	0.3149535	0.949
KEGG_TYPE_II_DIABETES_METABOLISM	46	0.336753	1.18108	0.25726143	0.32194835	0.952
KEGG_DILATED_CARDIOMYOPATHY	90	0.318602	1.173	0.31013918	0.32605273	0.953
KEGG_CALCIIUM_SIGNALING_PATHWAY	176	0.280601	1.17137	0.262	0.32447806	0.953
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	83	0.317446	1.16528	0.2977867	0.32665092	0.954
KEGG_GLYCEROLIPID_METABOLISM	42	0.317677	1.15425	0.27599245	0.33374628	0.958
KEGG_ONE_CARBON_POOL_BY_FOLATE	17	0.441982	1.14843	0.34210527	0.3364395	0.96
KEGG_ECM_RECEPTOR_INTERACTION	83	0.355421	1.14277	0.33958334	0.33844241	0.96
KEGG_MELANOGENESIS	101	0.311163	1.14137	0.30181086	0.3363436	0.96
KEGG_STARCH_AND_SUCROSE_METABOLISM	52	0.336618	1.1231	0.30927834	0.34989524	0.962
KEGG_MELANOMA	71	0.308801	1.11686	0.32595575	0.3527931	0.964
KEGG_INOSITOL_PHOSPHATE_METABOLISM	53	0.36289	1.10793	0.37621832	0.3577507	0.966
KEGG_REGULATION_OF_AUTOPHAGY	34	0.336796	1.10457	0.33996025	0.35785657	0.968
KEGG_PROSTATE_CANCER	87	0.339113	1.07873	0.3968254	0.38044912	0.976
KEGG_MTOR_SIGNALING_PATHWAY	51	0.350861	1.07681	0.4	0.37848112	0.976
KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	40	0.346455	1.05572	0.37037036	0.39533463	0.982
KEGG_INSULIN_SIGNALING_PATHWAY	136	0.298846	1.05028	0.39227644	0.39735445	0.984
KEGG_RNA_POLYMERASE	29	0.359769	1.04107	0.41082165	0.40298307	0.985
KEGG_BASAL_TRANSCRIPTION_FACTORS	34	0.353496	1.02439	0.4563492	0.41510186	0.986
KEGG_SPLICEOSOME	121	0.355259	1.015	0.44294003	0.42138416	0.986
KEGG_DRUG_METABOLISM_OTHER_ENZYMES	51	0.328334	1.00608	0.46680498	0.42678288	0.986
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	22	0.400949	1.00574	0.48692152	0.4233871	0.986
KEGG_ARACHIDONIC_ACID_METABOLISM	58	0.257216	1.0024	0.46625766	0.42338088	0.987
KEGG_BLADDER_CANCER	40	0.318308	0.99775	0.47011954	0.42493367	0.987
KEGG_NOTCH_SIGNALING_PATHWAY	47	0.345228	0.99708	0.48665297	0.42183363	0.987
KEGG_ADHERENS_JUNCTION	68	0.334158	0.99571	0.47211155	0.419644	0.987
KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	34	0.299251	0.95917	0.49377593	0.45508468	0.99

KEGG_ALANINE_ASPARTATE _AND_GLUTAMATE_METABO	30	0.332584	0.95561	0.5209205	0.45486835	0.99
KEGG_ADIPOCYTOKINE_SIG NALING_PATHWAY	66	0.279852	0.95018	0.5	0.45717043	0.991
KEGG_ENDOMETRIAL_CANC	52	0.319503	0.93659	0.5150301	0.46907634	0.992
KEGG_VASCULAR_SMOOTH_ MUSCLE_CONTRACTION	112	0.243466	0.90868	0.5378641	0.49562496	0.992
KEGG_GAP_JUNCTION	88	0.255503	0.89652	0.5476673	0.5047916	0.993
KEGG_PENTOSE_AND_GLUC URONATE_INTERCONVERSIO	27	0.323726	0.87402	0.59342915	0.5266095	0.998
KEGG_LINOLEIC_ACID_META BOLISM	29	0.270374	0.87384	0.64081633	0.5225554	0.998
KEGG_THYROID_CANCER	28	0.297617	0.86283	0.5836653	0.5304369	0.998
KEGG_GLYCOSAMINOGLYCA N_BIOSYNTHESIS_HEPARAN_	26	0.280664	0.85533	0.62603307	0.5347954	0.998
KEGG_TGF_BETA_SIGNALING _PATHWAY	85	0.251542	0.79908	0.66529775	0.5970172	1
KEGG_OLFACTORY_TRANSD	383	0.211167	0.74605	0.75992066	0.6573535	1
KEGG_GLYCOSYLPHOSPHATI DYLINOSITOL_GPI_ANCHOR_ BIOSYNTHESIS	24	0.251963	0.68611	0.791423	0.72659796	1
KEGG_PENTOSE_PHOSPHATE _PATHWAY	26	0.229522	0.67075	0.82815737	0.74095434	1

Supplementary Table 7 | GSEA result of AIM2 high vs low subgroup.