

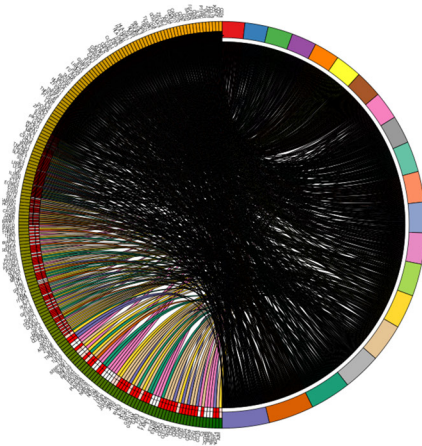
Table S1 Kaplan-Meier survival analyses of *ADRB2* in different subtypes of BRCA patients

<i>ADRB2</i> original order	Nodal status	Estrogen receptor status	Progesterone receptor status	Event status	P value	Hazard ratio	95% confidence interval	Good prognosis' RNA level	No. patients	No. events
1	N-	ER all	PR all	OS	<0.0001	0.47	0.35–0.62	High	2415	196
2	N-	ER+	PR all	OS	<0.0001	0.49	0.35–0.67	High	2018	154
3	N all	ER+	PR+	OS	<0.0001	0.56	0.44–0.72	High	3160	262
4	N all	ER all	PR all	OS	<0.0001	0.57	0.46–0.69	High	4307	435
5	N all	ER all	PR+	OS	<0.0001	0.57	0.44–0.72	High	3210	270
6	N all	ER+	PR all	OS	<0.0001	0.59	0.47–0.73	High	3588	315
7	N-	ER-	PR+	OS	–	–	–	–	23	1
8	N-	ER+	PR+	OS	0.0001	0.5	0.35–0.71	High	1784	132
9	N-	ER all	PR+	OS	0.0001	0.5	0.35–0.71	High	1810	134
10	N-	ER all	PR-	OS	0.0027	0.36	0.19–0.70	High	372	36
11	N+	ER all	PR all	OS	0.0049	0.64	0.47–0.87	High	1646	203
12	N all	ER-	PR-	OS	0.0064	0.49	0.30–0.82	High	422	61
13	N+	ER all	PR+	OS	0.0082	0.59	0.40–0.87	High	1232	116
14	N all	ER-	PR all	OS	0.0116	0.53	0.33–0.87	High	469	66
15	N-	ER-	PR-	OS	0.0129	0.33	0.14–0.79	High	229	21
16	N+	ER+	PR+	OS	0.0131	0.6	0.40–0.90	High	1213	111
17	N all	ER all	PR-	OS	0.0254	0.63	0.43–0.95	High	711	98
18	N-	ER-	PR all	OS	0.0269	0.38	0.16–0.90	High	254	22
19	N-	ER+	PR-	OS	0.0297	0.28	0.09–0.88	High	143	15
20	N+	ER+	PR all	OS	0.0357	0.66	0.45–0.97	High	1377	133
21	N all	ER+	PR-	OS	0.0715	0.42	0.16–1.08	High	288	36
22	N+	ER-	PR all	OS	0.0975	0.59	0.31–1.10	High	179	40
23	N+	ER-	PR-	OS	0.1254	0.59	0.30–1.16	–	161	36
24	N+	ER all	PR-	OS	0.1307	0.54	0.24–1.20	–	285	53
25	N all	ER-	PR+	OS	0.2049	4.75	0.43–52.69	–	44	4
26	N+	ER+	PR-	OS	0.2531	2.39	0.54–10.61	–	123	16
27	N+	ER-	PR+	OS	0.2947	0.22	0.01–3.68	–	17	3

Table S2 Co-expression genes of ADRB2 in BRCA

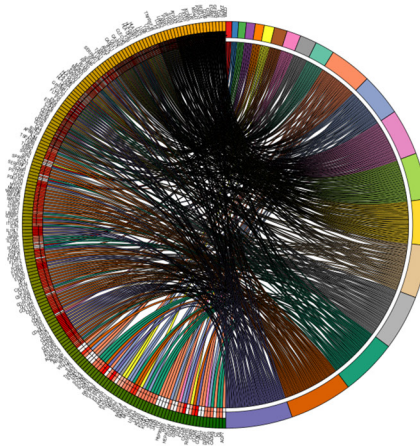
Correlated with ADRB2	Cytoband	Spearman's correlation	P value	q value
ITM2A	Xq21.1	0.621457723	1.62E-118	3.28E-114
FLU1	11q24.3	0.605435057	5.47E-111	5.52E-107
TGFB2	3q24.1	0.603290809	5.17E-110	3.48E-106
GIMAP8	7q36.1	0.599110672	5.92E-108	1.98E-104
MFNG	22q13.1	0.596562487	3.31E-107	2.15E-103
RIMP	12q12.1	0.595015896	2.56E-106	8.60E-103
PTGER4	5p13.1	0.593837389	8.42E-106	4.52E-102
SELP	10q24.2	0.589531355	6.02E-104	1.25E-100
GIMAP6	7q36.1	0.588291565	2.17E-103	4.81E-100
CCDC69	5q23.1	0.588188493	2.38E-103	4.41E-100
GAB3	Xq28	0.587003455	3.66E-103	1.40E-99
GGTA1P	9q32.3	0.585960996	2.13E-102	3.59E-99
ACKR1	10q23.2	0.585595077	3.04E-102	4.72E-99
IGF1	12q23.2	0.584846172	6.36E-102	9.17E-99
SIPR1	1p21.2	0.584231823	1.16E-101	1.56E-98
ABC11	7q21.12	0.581307375	1.98E-100	2.50E-97
IL16	15q25.3	0.577783506	5.83E-99	6.93E-96
KCTD12	15q23.1	0.577509225	7.58E-99	8.50E-96
ACTA6	17q24.2-q24.3	0.577206914	1.01E-98	1.07E-95
GIMAP7	7q36.1	0.576384154	2.21E-98	2.23E-95
ABIBP	3q12.2	0.574383971	1.47E-97	1.41E-94
MFAP4	17p11.2	0.573309334	4.03E-97	3.70E-94
PRDM8	4q21.21	0.572943064	5.57E-97	4.98E-94
CAVIN2	2q32.3	0.5693823	1.67E-95	1.32E-92
CLIC2	Xq28	0.567354883	1.02E-94	8.26E-92
GIMAP5	7q36.1	0.565643866	4.92E-94	3.82E-91
DNASE1L3	3p14.3	0.565518078	5.52E-94	4.13E-91
LRRN4CL	11q12.3	0.565281329	6.86E-94	4.94E-91
VSR	10q22.1	0.564492641	1.41E-93	9.48E-91
ALDH1A1	9q21.13	0.564112867	1.98E-93	1.33E-90
SLC9A9	3q24	0.563925913	2.36E-93	1.58E-90
LRN3	1q44	0.562889931	6.04E-93	3.81E-90
ABC9A	6p21.32	0.562815264	6.47E-93	3.96E-90
TXN3	16p21.33-q21.32	0.562715559	6.73E-93	3.99E-90
TMEM273	10q11.23	0.56198426	1.37E-92	7.75E-90
HSD17B11	4q22.1	0.561963211	1.38E-92	7.75E-90
ABC8	17q24.2	0.560884128	3.70E-92	2.02E-89
LRR2	3p21.31	0.560569087	4.91E-92	2.61E-89
INMT	7p14.3	0.56028076	6.37E-92	3.03E-89
IL33	9p24.1	0.557924262	5.24E-91	2.65E-88
INPP5D	2q37.1	0.557339377	8.83E-91	4.35E-88
STARSD8	Xq13.1	0.556480255	1.89E-90	9.10E-88
TMEM119	12q23.3	0.55626709	2.29E-90	1.07E-87
CD1C	1q23.1	0.556166385	2.50E-90	1.15E-87
ALDH1A2	15q21.3	0.555867925	3.26E-90	1.44E-87
JAM2	21q12.3	0.555855775	3.29E-90	1.44E-87
FREM1	9p22.3	0.553890491	1.86E-89	8.00E-87
PAPLN	14q24.2	0.553865381	1.91E-89	8.01E-87
INPP2	8q24.12	0.553266838	3.22E-89	1.63E-86
CLEC10A	17p13.1	0.551437832	1.60E-88	6.34E-86
CLEC1A	12p13.2	0.548979446	1.47E-87	5.82E-85
LPAR6	13p14.2	0.548785484	1.59E-87	6.19E-85
C7	5p13.1	0.547058026	7.06E-87	2.68E-84
SEV1P	9q31.3	0.54630718	1.35E-86	5.03E-84
FECAM1	17q23.3	0.545617044	2.43E-86	8.91E-84
FCE1A	1q23.2	0.54468865	5.36E-86	1.93E-83
FLG2	7q11.23	0.542557875	3.28E-85	1.16E-82
CD69	12p13.31	0.542408921	3.72E-85	1.29E-82
ANGPT1	1q25.2	0.542153735	4.61E-85	1.58E-82
JAML	11q23.3	0.541982282	5.33E-85	1.79E-82
P2RY13	3q25.1	0.54189751	5.72E-85	1.89E-82
RASGRP4	19q13.2	0.541687159	6.84E-85	2.23E-82
SH2	1q21.3	0.541221719	1.01E-84	3.24E-82
CCL14	17q12	0.539214305	4.68E-84	1.72E-81
COL14A1	8q24.12	0.538695163	7.30E-84	2.25E-81
GPR34	Xp11.4	0.538859163	7.34E-84	2.25E-81
GIMAP1	7q36.1	0.538664305	8.64E-84	2.60E-81
CNRP1	2p14	0.538006358	1.50E-83	4.44E-81
LHFPL6	13q13.3-q14.11	0.537753318	1.85E-83	5.40E-81
FXR1	19q13.12	0.537047773	3.32E-83	9.58E-81
ITIH5	10p14	0.536774943	4.17E-83	1.18E-80
LINC00341	14q32.13	0.536682222	4.70E-83	1.32E-80
TESP1	12q13.2	0.536489048	5.28E-83	1.46E-80
MEOX1	17q21.31	0.535452044	1.25E-82	3.40E-80
SCARAS5	8p21.1	0.534924701	1.92E-82	5.18E-80
ZCCCH24	10q22.3	0.534715459	2.29E-82	6.07E-80
RC3TB2	13q14.2	0.534274934	3.29E-82	8.62E-80
CLIC5	6p21.1	0.534036038	5.06E-82	1.04E-79
DPYD	1p21.3	0.533608992	6.68E-82	1.45E-79
MAP1LC3C	1q43	0.53326411	6.08E-82	1.56E-79
ATOH8	2p11.2	0.533399167	6.75E-82	1.63E-79
PEAR1	1q23.1	0.533327005	7.16E-82	1.76E-79
CD1D	1q23.1	0.533046381	9.01E-82	2.18E-79
BHLHE22	8q12.3	0.5313838	3.51E-81	9.34E-79
PGM5	9q21.11	0.531221289	4.00E-81	9.51E-79
ADAM33	2p21.3	0.531029758	4.68E-81	1.10E-78
AKNA	9q32	0.530901065	5.20E-81	1.21E-78
RGS18	1q31.2	0.530252789	9.00E-81	2.06E-78
CD300LG	17q21.31	0.530052642	1.04E-80	2.35E-78
SPARCL1	4q22.1	0.529386508	1.78E-80	3.98E-78
RHHBP	5q13.3	0.528716155	3.05E-80	6.77E-78
GIPC2	1p31.1	0.527897892	5.91E-80	1.30E-77
AHMGAP25	2p13.3	0.527628294	7.34E-80	1.59E-77
DPT	10q24.2	0.527385229	8.83E-80	1.92E-77
CCDC80	3q13.2	0.526495781	1.82E-79	3.87E-77
KLRI1	12p13.31	0.526461288	1.87E-79	3.94E-77
GN2	14q22.1	0.525978094	2.76E-79	5.74E-77
TSPAN7	Xp11.4	0.525801124	3.18E-79	6.55E-77
TAL1	1p33	0.525499848	4.05E-79	8.52E-77
CLEC9A	12p13.2	0.525025831	5.91E-79	1.19E-76
GAS7	17p13.1	0.524913347	9.27E-79	1.19E-76
P2RY12	3q25.1	0.524467703	5.99E-79	1.82E-76
MEOX2	7p21.2	0.52438096	9.44E-79	1.85E-76
ADH1C	4q23	0.523861482	1.49E-78	2.90E-76
NLRP1	17p13.2	0.522476242	4.48E-78	8.61E-76
RASGRP2	11q13.1	0.51911015	6.32E-77	1.20E-74
CADM3	1q23.2	0.518593045	9.47E-77	1.78E-74
PDE2A	11q13.4	0.518582793	9.54E-77	1.78E-74
GIMAP4	7q36.1	0.518398894	1.10E-76	2.04E-74
FOXO1	13q14.11	0.518083666	1.41E-76	2.59E-74
C3	19p13.3	0.517384559	2.43E-76	4.42E-74
LRRRC70	1q22.1	0.516764491	3.92E-76	7.08E-74
PPP1R16B	2q22.2-q22.3	0.516161306	6.27E-76	1.12E-73
CSF2RB	22q12.3	0.516073497	6.72E-76	1.19E-73
MCTP1	5q15	0.515719682	8.83E-76	1.55E-73
CCDC178	18q12.1	0.515341356	1.18E-75	2.00E-73
ARHGAP15	17p13.1	0.5151089624	1.44E-75	2.48E-73
CAV1	10q11.21	0.514964786	1.58E-75	2.71E-73
CAV1	7q31.2	0.514938061	1.62E-75	2.74E-73
RASAL3	19p13.12	0.514621812	2.06E-75	3.47E-73
CEL2F	10p14	0.514522453	2.22E-75	3.71E-73
DIPK2B	Xp11.3	0.514386041	2.47E-75	4.09E-73
SIGLEC17P	19q13.41	0.512717857	8.90E-75	1.46E-72
XPNPEP2	Xq26.1	0.512512443	1.04E-74	1.69E-72
TNS1	2q35	0.511824547	1.76E-74	2.84E-72
ADGRD1	12q24.33	0.511310021	2.61E-74	4.18E-72
CTS3	1q21.3	0.511124422	3.00E-74	4.77E-72
EBF1	5q33.3	0.510794367	3.86E-74	6.09E-72
EBF3	10q26.3	0.510716224	4.10E-74	6.41E-72
HLA-DPB1	6p21.32	0.510260317	5.79E-74	9.00E-72
KL	13p13.1	0.510049702	6.80E-74	1.05E-71
ADCY4	14q12	0.509399852	1.11E-73	1.70E-71
CHRD1	Xq23	0.509285844	1.21E-73	1.84E-71
MIRN1	4q22.1	0.509203285	1.29E-73	1.95E-71
NKML	6p22.1	0.50914224	1.35E-73	2.02E-71
MIRN2	10q23.3	0.508943575	1.57E-73	2.33E-71
HLA-DOA	6p21.32	0.508874546	1.68E-73	2.44E-71
ACSM5	16p12.3	0.507794294	3.74E-73	5.47E-71
AVP2R	Xq28	0.507694435	4.03E-73	5.86E-71
C16orf54	16p11.2	0.507476524	4.75E-73	6.85E-71
LDB2	15q15.32	0.507064974	4.68E-73	9.27E-71
GDF10	10q11.22	0.506949973	7.06E-73	1.00E-70
FLPP3	1p32.2	0.506835802	7.69E-73	1.09E-70
RGS13	1q31.2	0.506503521	9.87E-73	1.38E-70
P2RY8	Xp22.33			
TNFRSF1B	1p36.22	0.506121941	1.51E-72	1.82E-70
SPN	16p11.2	0.505907573	1.54E-72	2.12E-70
TMEM132C	12q24.32-q24.33	0.505707919	1.79E-72	2.44E-70
PTGD5	9q34.3	0.505627174	1.90E-72	2.58E-70
ELMO1	7p14.2-p14.1	0.505556251	2.00E-72	2.69E-70
PPP1R16B	20q11.23	0.505538007	2.03E-72	2.72E-70
ABC110	17q24.3	0.505065848	2.89E-72	3.84E-70
GYPE	4q31.21	0.504905517	3.26E-72	4.30E-70
TNXP	1q21.1	0.504888803	3.30E-72	4.30E-70
BMX	Xp22.2	0.504687733	3.84E-72	5.00E-70
ZFP98L2	2p21	0.504192721	5.55E-72	7.18E-70
WIF1	12p13.31	0.504120721	5.85E-72	7.53E-70
CHL1	3p26.3	0.503812874	7.36E-72	9.40E-70
SCN3A	2q24.3	0.503202694	1.16E-71	1.47E-69
ABPB1P	10p12.1	0.503060735	1.29E-71	1.62E-69
EPG	21q22.2	0.502835803	1.76E-71	2.21E-69
PRKCB	16p12.2-q12.1	0.502337178	2.20E-71	2.74E-69
TLI1	4q32.3	0.502250997	2.34E-71	2.90E-69
MAB2L1	13q13.3	0.502145913	2.52E-71	3.12E-69
CD40LG	Xq26.3	0.502036287	2.75E-71	3.36E-69
IRF8	16q24.1	0.501920798	2.99E-71	3.64E-69
PALMD	1p21.2	0.501657086	3.32E-71	4.39E-69
GLI1	12q13.3	0.501636253	3.69E-71	4.43E-69
SRH	16p13.3	0.501066237	5.62E-71	6.71E-69
CD37	19q13.33	0.500042422	1.19E-70	1.42E-68
RNAS5E	14q11.2	0.499651312	1.59E-70	1.89E-68
EMCN	4q24	0.499605846	1.64E-70	1.95E-68
ABC2D	12q12	0.499581158	1.67E-70	1.95E-68
FLRT2	14q13.3	0.49865052	3.31E-70	4.33E-68
FLOR2	11q13.4	0.498466975	3.77E-70	4.95E-68
TPO	2p25.3	0.498264817	4.38E-70	5.02E-68
T1ORF21	11p15.5	0.498116832	4.68E-70	5.57E-68
CMA1	14q12	0.497698594	6.82E-70	7.51E-68
F10	13q34	0.497236088	9.27E-70	1.05E-67
HCLS1	3q13.33	0.497043938	1.07E-69	1.20E-67
DOCK11	Xq24	0.496887005	1.19E-69	1.33E-67
ANK2	4q25-q26	0.496596286	1.48E-69	1.64E-67
EPAS1	2p21	0.496537075	1.54E-69	1.70E-67
PI16	6p21.2	0.49650115	1.58E-69	1.73E-67

GO-BP circle plot



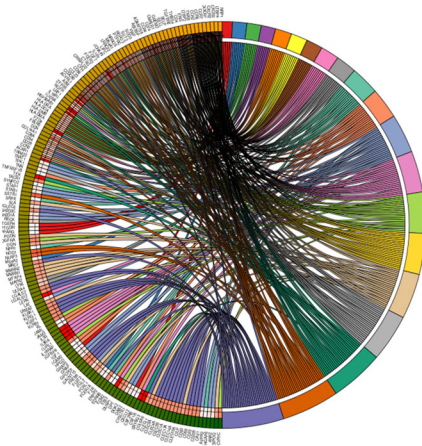
- Term**
- positive regulation of T cell activation
 - positive regulation of leukocyte cell-cell adhesion
 - lymphocyte proliferation
 - monocyte cell adhesion
 - T cell differentiation
 - leukocyte adhesion
 - positive regulation of lymphocyte activation
 - positive regulation of response to external stimulus
 - regulation of leukocyte cell-cell adhesion
 - leukocyte cell-cell adhesion
 - positive regulation of leukocyte activation
 - regulation of T cell activation
 - positive regulation of cell activation
 - lymphocyte differentiation
 - negative regulation of immune system process
 - leukocyte migration
 - regulation of lymphocyte activation
 - leukocyte differentiation
 - regulation of leukocyte activation
 - T cell activation

GO-CC circle plot



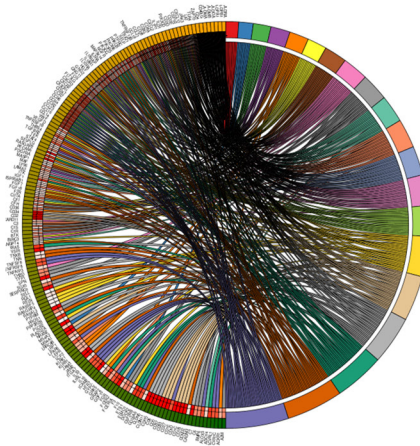
- Term**
- cell trailing edge
 - canal
 - intracellular component of external side of plasma membrane
 - MHC class II protein complex
 - MHC protein complex
 - macula cell granule
 - T cell receptor complex
 - immunological synapse
 - platelet alpha granule
 - plasma membrane cell
 - cell-cell junction
 - receptor complex
 - membrane microdomain
 - membrane cell
 - membrane region
 - external side of plasma membrane
 - collagen-containing extracellular matrix
 - plasma membrane protein complex
 - extracellular matrix
 - side of membrane

GO-MF circle plot



- Term**
- cosmid receptor activity
 - immunoglobulin binding
 - MHC class II protein complex binding
 - transmembrane growth factor factor binding
 - chemokine receptor activity
 - protein-coupled chemotactant receptor activity
 - MHC protein complex binding
 - chemokine binding
 - co-receptor activity
 - peptide receptor activity
 - integrin binding
 - protein binding, bridging
 - cytokine receptor activity
 - growth factor binding
 - positive binding
 - extracellular matrix structural constituent
 - sulfur compound binding
 - cytokine binding
 - glycosaminoglycan binding
 - carbohydrate binding

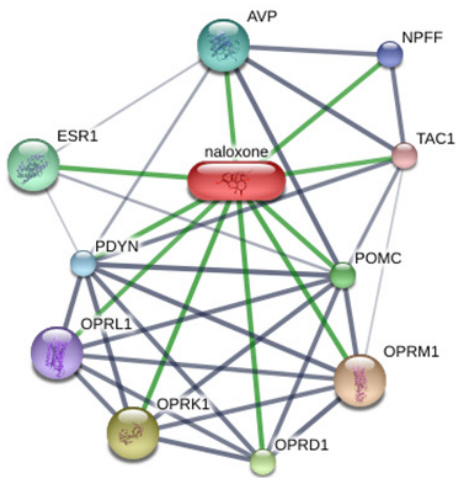
KEGG circle plot



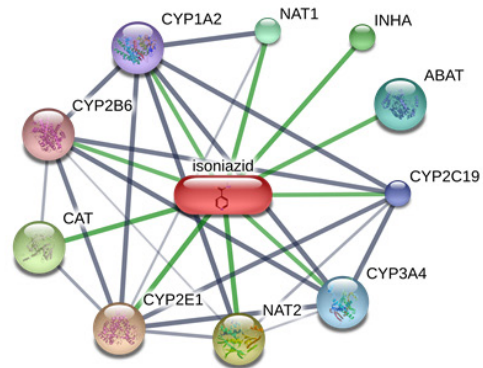
- Term**
- Allograft rejection
 - Aspirin
 - intestinal immune network for IgA production
 - Inflammasome driven disease (IDD)
 - Malaria
 - Primary immunodeficiency
 - Staphylococcus aureus infection
 - NF-kappa B signaling pathway
 - Complement and coagulation cascades
 - Transsplanosis
 - T cell receptor signaling pathway
 - IL-6 and IL-12/23 differentiation
 - Th17 cell differentiation
 - Viral protein interaction with cytokine and cytokine receptor
 - Notch signaling pathway
 - Hemostasis, cell lineage
 - Cell adhesion molecules (CAMs)
 - Chemokine signaling pathway
 - ILK-AM signaling pathway
 - Cytokine-cytokine receptor interaction

Figure S1 *ADRB2* functional enrichment circle plots of GO and KEGG pathways. GO, gene ontology.

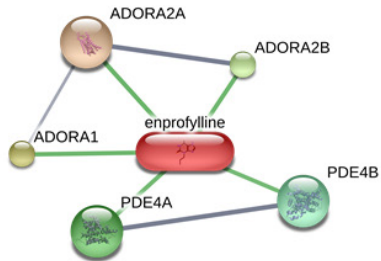
A



B



C



D

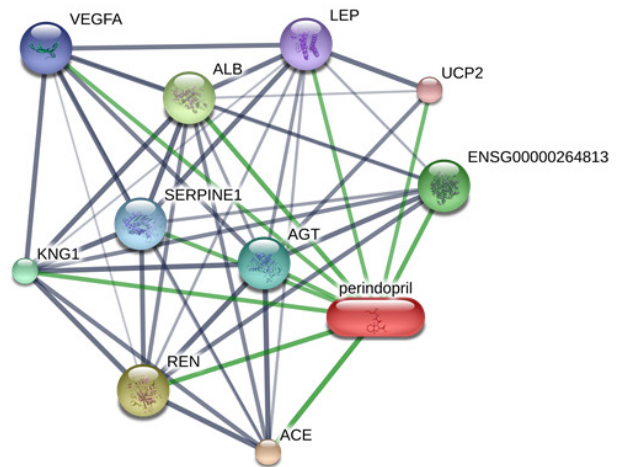


Figure S2 Correlations between candidate drugs and targeted genes. (A) The map of naloxone and targeted genes. (B) The map of isoniazid and targeted genes. (C) The map of enprofylline and targeted genes. (D) The map of perindopril and targeted genes.

Table S3 Gene markers in different kinds of major T cell subtypes

Name	Gene marker
T cell (general)	<i>CD3D, CD3E</i>
CD8 ⁺ T cell	<i>CD8A, CD8B</i>
CD4 ⁺ T cell	<i>CD4</i>
Th1	<i>CXCR3, STAT4, CD4</i>
Th2	<i>CCR4, STAT6, CD4</i>
T _{fh}	<i>IL21R, CXCR5</i>
Treg	<i>FOXP3, STAT5A, STAT5B, IL2RA, TGFB1</i>