

Figure S1. *In vitro* assays of NRP1 functions in the HUVEC cell line with overexpression or knockdown. (A) Migration ability of HUVEC cells with NRP1 overexpression or knockdown (x200; Olympus Corporation). (B) *In vitro* tube-forming activity of HUVEC cells with NRP1 overexpression or knockdown. The number of cells or tubes were counted in five randomly selected fields under a light microscope (x40; Olympus Corporation). NC, control group; NRP1, overexpression NRP1 group; siNRP1, knockdown NRP1 group. **P<0.01 vs. NC. NRP1, neuropilin 1; HUVEC, primary human umbilical vein endothelial cells.

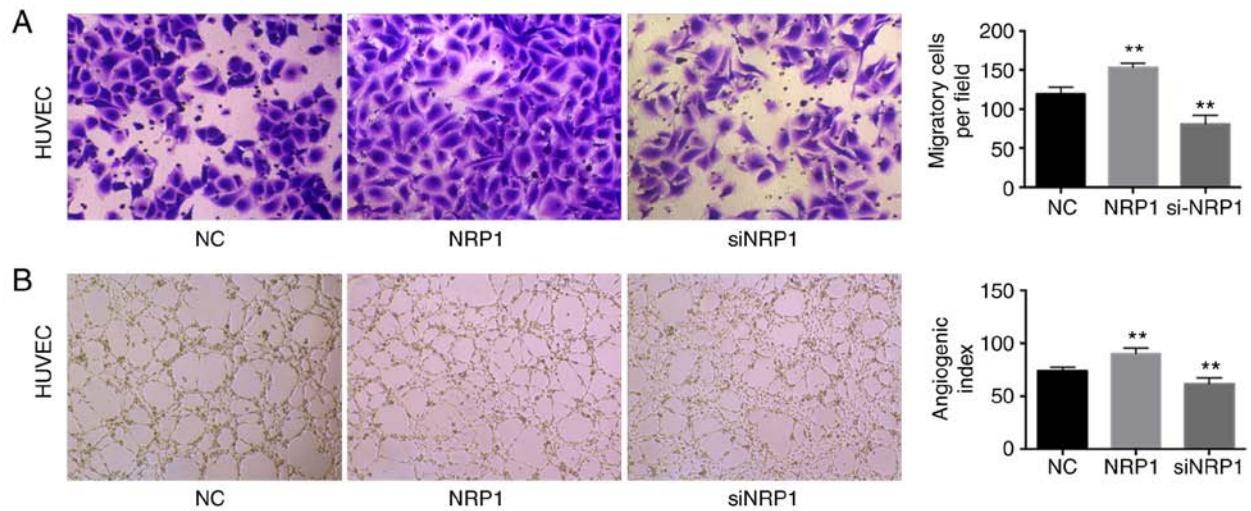


Table SI. KEGG enrichment pathway analysis.

No.	Pathway	DEGs with pathway annotation (n=33) (%)	All genes with pathway annotation (n=27474) (%)	P-value	Q-value	Pathway ID
1	Thyroid cancer	3 (9.09)	206 (0.75)	0.002	0.169	ko05216
2	Antigen processing and presentation	3 (9.09)	287 (1.04)	0.005	0.200	ko04612
3	RNA degradation	3 (9.09)	324 (1.18)	0.007	0.200	ko03018
4	IL-17 signaling pathway	2 (6.06)	346 (1.26)	0.065	0.656	ko04657
5	Bacterial invasion of epithelial cells	2 (6.06)	444 (1.62)	0.099	0.656	ko05100
6	Collecting duct acid secretion	1 (3.03)	101 (0.37)	0.115	0.656	ko04966
7	HIF-1 signaling pathway	2 (6.06)	511 (1.86)	0.125	0.656	ko04066
8	Prostate cancer	2 (6.06)	521 (1.9)	0.129	0.656	ko05215
9	AMPK signaling pathway	2 (6.06)	545 (1.98)	0.139	0.656	ko04152
10	Pathways in cancer	5 (15.15)	2385 (8.68)	0.154	0.656	ko05200
11	Insulin signaling pathway	2 (6.06)	582 (2.12)	0.154	0.656	ko04910
12	Proteasome	1 (3.03)	177 (0.64)	0.192	0.656	ko03050
13	Fructose and mannose metabolism	1 (3.03)	179 (0.65)	0.194	0.656	ko00051
14	RNA transport	2 (6.06)	681 (2.48)	0.197	0.656	ko03013
15	Fluid shear stress and atherosclerosis	2 (6.06)	683 (2.49)	0.198	0.656	ko05418
16	Protein processing in endoplasmic reticulum	2 (6.06)	690 (2.51)	0.201	0.656	ko04141
17	MicroRNAs in cancer	2 (6.06)	714 (2.6)	0.211	0.656	ko05206
18	N-Glycan biosynthesis	1 (3.03)	208 (0.76)	0.222	0.656	ko00510
19	Oxytocin signaling pathway	2 (6.06)	767 (2.79)	0.235	0.656	ko04921
20	Ferroptosis	1 (3.03)	224 (0.82)	0.237	0.656	ko04216
21	Amino sugar and nucleotide sugar metabolism	1 (3.03)	225 (0.82)	0.238	0.656	ko00520
22	Axon guidance	2 (6.06)	783 (2.85)	0.242	0.656	ko04360
23	Lysine degradation	1 (3.03)	235 (0.86)	0.247	0.656	ko00310
24	<i>Vibrio cholerae</i> infection	1 (3.03)	236 (0.86)	0.248	0.656	ko05110
25	Basal cell carcinoma	1 (3.03)	241 (0.88)	0.252	0.656	ko05217
26	Cocaine addiction	1 (3.03)	253 (0.92)	0.263	0.656	ko05030
27	VEGF signaling pathway	1 (3.03)	271 (0.99)	0.280	0.656	ko04370
28	RIG-I-like receptor signaling pathway	1 (3.03)	285 (1.04)	0.291	0.656	ko04622
29	Epithelial cell signaling in <i>Helicobacter pylori</i> infection	1 (3.03)	313 (1.14)	0.315	0.656	ko05120
30	B cell receptor signaling pathway	1 (3.03)	324 (1.18)	0.324	0.656	ko04662
31	Rheumatoid arthritis	1 (3.03)	325 (1.18)	0.325	0.656	ko05323
32	Acute myeloid leukemia	1 (3.03)	332 (1.21)	0.331	0.656	ko05221
33	Protein digestion and absorption	1 (3.03)	336 (1.22)	0.334	0.656	ko04974
34	Synaptic vesicle cycle	1 (3.03)	337 (1.23)	0.335	0.656	ko04721
35	Glycolysis/Gluconeogenesis	1 (3.03)	338 (1.23)	0.336	0.656	ko00010
36	Adipocytokine signaling pathway	1 (3.03)	339 (1.23)	0.336	0.656	ko04920
37	Inositol phosphate metabolism	1 (3.03)	342 (1.24)	0.339	0.656	ko00562
38	Cardiac muscle contraction	1 (3.03)	348 (1.27)	0.344	0.656	ko04260
39	Endometrial cancer	1 (3.03)	351 (1.28)	0.346	0.656	ko05213
40	Mitophagy-animal	1 (3.03)	367 (1.34)	0.359	0.656	ko04137
41	Fc gamma R-mediated phagocytosis	1 (3.03)	367 (1.34)	0.359	0.656	ko04666
42	Glycerophospholipid metabolism	1 (3.03)	376 (1.37)	0.366	0.656	ko00564
43	Gap junction	1 (3.03)	390 (1.42)	0.376	0.656	ko04540
44	mRNA surveillance pathway	1 (3.03)	397 (1.45)	0.382	0.656	ko03015
45	HCM	1 (3.03)	397 (1.45)	0.382	0.656	ko05410
46	Chronic myeloid leukemia	1 (3.03)	404 (1.47)	0.387	0.656	ko05220
47	ARVC	1 (3.03)	409 (1.49)	0.391	0.656	ko05412
48	Longevity regulating pathway-mammal	1 (3.03)	423 (1.54)	0.401	0.656	ko04211
49	Melanogenesis	1 (3.03)	443 (1.61)	0.415	0.656	ko04916
50	Oxidative phosphorylation	1 (3.03)	444 (1.62)	0.416	0.656	ko00190
51	ErbB signaling pathway	1 (3.03)	446 (1.62)	0.417	0.656	ko04012
52	DCM	1 (3.03)	448 (1.63%)	0.419	0.656	ko05414

Table SI. Continued.

No.	Pathway	DEGs with pathway annotation (n=33) (%)	All genes with pathway annotation (n=27474) (%)	P-value	Q-value	Pathway ID
53	GABAergic synapse	1 (3.03)	451 (1.64)	0.421	0.656	ko04727
54	GnRH signaling pathway	1 (3.03)	469 (1.71)	0.434	0.656	ko04912
55	Adherens junction	1 (3.03)	471 (1.71)	0.435	0.656	ko04520
56	Progesterone-mediated oocyte maturation	1 (3.03)	474 (1.73)	0.437	0.656	ko04914
57	Phosphatidylinositol signaling system	1 (3.03)	477 (1.74)	0.439	0.656	ko04070
58	Th17 cell differentiation	1 (3.03)	478 (1.74)	0.440	0.656	ko04659
59	Colorectal cancer	1 (3.03)	481 (1.75)	0.442	0.656	ko05210
60	TNF signaling pathway	1 (3.03)	489 (1.78)	0.447	0.656	ko04668
61	Aldosterone synthesis and secretion	1 (3.03)	525 (1.91)	0.471	0.661	ko04925
62	Glutamatergic synapse	1 (3.03)	549 (2)	0.486	0.661	ko04724
63	Ribosome	1 (3.03)	564 (2.05)	0.496	0.661	ko03010
64	Breast cancer	1 (3.03)	575 (2.09)	0.503	0.661	ko05224
65	Estrogen signaling pathway	1 (3.03)	584 (2.13)	0.508	0.661	ko04915
66	Necroptosis	1 (3.03)	585 (2.13)	0.509	0.661	ko04217
67	Alcoholism	1 (3.03)	596 (2.17)	0.515	0.661	ko05034
68	Regulation of autophagy	1 (3.03)	618 (2.25)	0.528	0.661	ko04140
69	Phagosome	1 (3.03)	629 (2.29)	0.535	0.661	ko04145
70	Neurotrophin signaling pathway	1 (3.03)	639 (2.33)	0.540	0.661	ko04722
71	MAPK signaling pathway	2 (6.06)	1499 (5.46)	0.544	0.661	ko04010
72	Ubiquitin-mediated proteolysis	1 (3.03)	650 (2.37)	0.546	0.661	ko04120
73	Hippo signaling pathway	1 (3.03)	653 (2.38)	0.548	0.661	ko04390
74	Apoptosis	1 (3.03)	687 (2.5)	0.567	0.662	ko04210
75	Wnt signaling pathway	1 (3.03)	700 (2.55)	0.574	0.662	ko04310
76	Purine metabolism	1 (3.03)	711 (2.59)	0.579	0.662	ko00230
77	NOD-like receptor signaling pathway	1 (3.03)	721 (2.62)	0.584	0.662	ko04621
78	Hepatitis B	1 (3.03)	726 (2.64)	0.587	0.662	ko05161
79	Tuberculosis	1 (3.03)	778 (2.83)	0.613	0.675	ko05152
80	Adrenergic signaling in cardiomyocytes	1 (3.03)	780 (2.84)	0.614	0.675	ko04261
81	Regulation of actin cytoskeleton	1 (3.03)	899 (3.27)	0.667	0.724	ko04810
82	Transcriptional misregulation in cancers	1 (3.03)	942 (3.43)	0.684	0.728	ko05202
83	Proteoglycans in cancer	1 (3.03)	948 (3.45)	0.686	0.728	ko05205
84	Rap1 signaling pathway	1 (3.03)	1003 (3.65)	0.707	0.741	ko04015
85	Endocytosis	1 (3.03)	1054 (3.84)	0.725	0.751	ko04144
86	HTLV-I infection	1 (3.03)	1172 (4.27)	0.763	0.781	ko05166
87	Human papillomavirus infection	1 (3.03)	1378 (5.02)	0.817	0.827	ko05165
88	PI3K-Akt signaling pathway	1 (3.03)	1444 (5.26)	0.832	0.832	ko04151

KEGG, Kyoto Encyclopedia of Genes and Genomes; DEGs, differentially expressed genes; HCM, hypertrophic cardiomyopathy; ARVC, arrhythmogenic right ventricular cardiomyopathy; DCM, dilated cardiomyopathy.