

Table S1. Clinical characteristics of human neuroblastoma tumor samples

Characteristics	Number of Patients
Age (months)	
Median age at diagnosis	17
Age range	2 to 180
Gender	
Female	10
Male	7
INRGSS*	
L1	5
L2	3
M	9
COG Risk Stratification	
High Risk	11
Intermediate Risk	6
Low Risk	4
MYCN Status	
Amplified	5
Non-Amplified	16

Table S2: Top 20 genes with a statistically significant expression changes (p value <0.05) in MYCN non-amplified human neuroblastoma tumor compared with MYCN amplified tumor.

Gene ID	Linear fold change (MYCN non-amp /MYCN amp)	p-value	Probe ID
S100A12	14.50	0.001	NM_005621.1:260
CCL19	9.83	0.003	NM_006274.2:401
ITK	9.75	0.001	NM_005546.3:3430
POU2AF1	9.44	0.003	NM_006235.2:1675
PAX5	8.94	0.001	NM_016734.1:2288
CD7	8.64	0.001	NM_006137.6:440
CD2	8.48	0.002	NM_001767.3:687
TNFRSF9	7.72	0.003	NM_001561.4:255
CD5	7.70	0.003	NM_014207.2:1295
CD8B	7.23	0.002	NM_004931.3:440
LTF	7.17	0.003	NM_002343.2:590
CD27	7.04	0.003	NM_001242.4:330
SLAMF1	6.89	0.005	NM_003037.2:580
LCK	5.77	0.005	NM_005356.2:1260
CD96	5.73	0.004	NM_005816.4:1355
TIGIT	5.12	0.004	NM_173799.2:1968
CTSW	4.64	0.004	NM_001335.3:1075
KLRB1	4.41	0.001	NM_002258.2:85
FOXP3	2.83	0.005	NM_014009.3:1230
CXCL3	-14.56	0.003	NM_002090.2:540

Table S3. Top 20 T cell function genes differentially expressed in MYCN non-amplified human neuroblastoma tumor compared with MYCN amplified tumor (p value<0.05).

Gene ID	Linear fold change (MYCN non-amp /MYCN amp)	p-value
CD7	8.64	0.001
CD2	8.48	0.002
CD5	7.7	0.003
CD3E	7.33	0.005
CD8B	7.23	0.002
CD27	7.04	0.003
IRF4	6.14	0.006
LCK	5.77	0.005
TIGIT	5.12	0.004
CD1C	5.05	0.007
CTLA4	4.41	0.017
CXCR3	4.12	0.028
IL18RAP	3.98	0.031
CXCL9	3.19	0.118
TBX21	3.14	0.060
CD38	3.07	0.037
MS4A1	3.06	0.159
FOXP3	2.83	0.005
CD8A	2.23	0.049
TP53	-1.89036	0.0379

Table S4: Top 50 statistically significantly upregulated genes in MYCN non-amplified human neuroblastoma cells compared with MYCN amplified cells.

	Linear fold change (MYCN non amp /MYCN amp)	P-value	probe.ID
ANXA1	5540	2.12E-08	NM_000700.1:515
COL3A1	5460	7.26E-08	NM_000090.3:180
CCL2	1040	9.43E-08	NM_002982.3:123
MAGEA3	696	2.63E-08	NM_005362.3:849
PLAU	568	6.03E-08	NM_002658.2:793
ITGA2	530	3.13E-06	NM_002203.2:475
AXL	505	3.68E-07	NM_021913.2:2190
IFITM2	356	2.84E-05	NM_006435.2:390
THBS1	246	3.01E-07	NM_003246.2:3465
IL8	199	0.000241	NM_000584.2:25
MAGEA12	195	1.64E-05	NM_001166386.1:567
TNFSF12	187	9.99E-08	NM_003809.2:339
PSMB8	183	1.79E-09	NM_004159.4:1215
VCAM1	175	2.68E-07	NM_001078.3:2535
ITGA6	161	2.31E-11	NM_000210.1:3065
MICB	159	7.92E-11	NM_005931.3:1387
F2RL1	145	0.000129	NM_005242.3:940
TAP1	118	7.06E-07	NM_000593.5:2075
ITGB3	89.9	6.21E-15	NM_000212.2:4485
MME	84.3	0.000107	NM_000902.2:5059
IL32	82.3	9.69E-07	NM_004221.4:358
IL13RA1	78.8	7.49E-07	NM_001560.2:1230
IKBKE	77.8	1.57E-05	NM_014002.2:2470
CXCL2	75.8	1.93E-05	NM_002089.3:854
TNFRSF9	74.4	1.5E-15	NM_001561.4:255
ICAM1	74.1	5.21E-06	NM_000201.2:2253
CD274	69.8	5.43E-06	NM_014143.3:1245
APOE	61.5	0.000014	NM_000041.2:96
TGFB2	60.9	1.46E-06	NM_003238.2:1125
MICA	59.5	2.66E-15	NM_000247.1:550
PDGFC	57.3	0.000571	NM_016205.2:1632
MAGEC1	53.6	0.00011	NM_005462.4:2920
CTSS	50.8	1.98E-07	NM_004079.3:685
TPTE	47.6	0.000267	NM_199259.2:142
HLA-C	47	0.00261	NM_002117.4:895
IFI35	44.8	3.2E-06	NM_005533.3:415
SSX1	43.4	0.0392	NM_005635.2:174
SERPINB2	41.1	0.000334	NM_002575.1:305
MAGEB2	39.8	0.000262	NM_002364.4:1026
IRAK2	38.8	3.8E-07	NM_001570.3:1285
VEGFC	38.7	0.0247	NM_005429.2:565
IFIT1	34.8	1.44E-05	NM_001548.3:1440
LIF	32.7	9.73E-06	NM_002309.3:1240
PSMB9	31.2	3.41E-08	NM_002800.4:455

C1S	31	4.29E-06	NM_001734.2:775
KLRC1	31	0.0113	NM_002259.3:335
PIK3CD	30.8	7.67E-06	NM_005026.3:2978
IFITM1	30.3	0.000339	NM_003641.3:482
DUSP6	29.7	1.54E-08	NM_001946.2:1535
PDCD1LG2	29	0.00718	NM_025239.3:235

Table S5. Clinical characteristics of human melanoma tumor samples

Characteristic	Patients with MYCN amplification (n = 30)	Patients without MYCN amplification (n = 324)
Age at diagnosis—years		
Mean ± S.E.M	59.4 ± 3.2	56.1 ± 0.9
Sex—no. (%)		
Male	25 (83%)	199 (61.4)
Female	5 (17%)	125 (38.6)
Overall Survival Months		
Mean ± S.E.M	73.8 ± 3.8	66.9 ± 10.8

Table S6: Top 20 genes differentially expressed in Myc inhibitor treated B16 cells compared with untreated B16 cells

Gene ID	Linear fold change (Myc inhibitor treated /untreated)	P-value	Probe ID
Tnfrsf12a	18.6	5.42E-14	NM_001161746.1:517
Mcam	10.6	6.64E-15	NM_023061.2:630
Il17ra	2.7	5.07E-10	NM_008359.1:312
Cd63	2.3	4.68E-14	NM_001042580.1:220
Cd164	2.3	6.22E-13	NM_016898.2:688
Il6st	2.1	1.14E-10	NM_010560.2:2325
Psen1	2.1	9.85E-12	NM_008943.2:2770
Jam3	2.0	3.45E-10	NM_023277.4:145
Casp3	2.0	4.27E-11	NM_009810.2:630
Hspb2	1.6	1.54E-10	NM_024441.3:667
Map2k2	1.6	8.03E-13	NM_023138.4:1440
Ifitm2	-1.7	4.89E-10	NM_030694.1:87
Gpi1	-2.4	9.33E-11	NM_008155.4:1540
Stat6	-2.9	6.14E-13	NM_009284.2:3465
Ifi27	-3.3	1.23E-10	NM_026790.2:166
Vegfa	-5.1	5.33E-11	NM_001025250.3:3015
Cd9	-5.4	6.28E-13	NM_007657.3:620
Bst2	-5.8	1.9E-12	NM_198095.2:468
Ddx58	-7.7	1.52E-11	NM_172689.3:1751
Icam2	-19.8	1.4E-10	NM_010494.1:375