Table SI. SNPs in the patient cohort (n=79).

Genes	SNPs
ABCB1	rs3213619
ABCC1	rs212090
ABCC1	rs2301666
ABCC1	rs4148356
ABCC1	rs4148380
ABCC2	rs12826
ABCC4	rs1059751
ABCC4	rs11568658
ABCC4	rs1189466
ABCC4	rs4148553
ABCC4	rs6650282
ABCC5	rs1132776
ABCC5	rs3749440
ABCC5	rs7624838
ABCG2	rs1448784
AKT3	rs1058304
BDNF	rs6265
BDNF	rs7124442
CDKN1B	rs7330
CYP2C8	rs11188150
CYP2E1	rs2515641
EGFR	rs10228436
EGFR	rs1140475
EGFR	rs2293347
ERCC1	rs3212933
FOXO1	rs17592236
GRIN3A	rs10512285
GRIN3A	rs10989591
GRIN3A	rs3824473
GRIN3A	rs942142
GRIN3A	rs3739724
GSK3B	rs2037547
GSK3B	rs3732361
HMMR	rs2303078
HMMR	rs299290
HMMR	rs299295
INSR	rs1864193
INSR	rs2229431
INSR	rs3745551
MAP3K1	rs832575
MAP3K1	rs832582
MAPK1	rs13515

MTOR	rs1057079
MTOR	rs12124598
MTOR	rs17036508
MTOR	rs2076658
NOS3	rs3918227
NR1I2	rs1523130
NR1I2	rs3814057
NR1I2	rs6438550
NTRK2	rs1047896
NTRK2	rs10780691
NTRK2	rs1624327
NTRK2	rs2013566
NTRK2	rs3654
PDK1	rs11904158
PDK1	rs1530864
PERP	rs514552
PHOX2B	rs6826373
PIK3CA	rs9838117
PIK3CG	rs12667819
PIK3R1	rs3756668
PIK3R1	rs706713
PRRC2A	rs11538264
PTEN	rs11202607
RB1CC1	rs2305427
SERPINA5	rs2067060
SERPINA5	rs2070005
SERPINA5	rs7069
SERPINA5	rs7070
SERPINA5	rs938
SLC31A1	rs10759637
STAT5B	rs2230097
TPMT	rs2842934
TSC1	rs10491534
TSC1	rs2809244
TSC1	rs4962081
TSC1	rs739441
VEGFA	rs3025039

SNP, single nucleotide polymorphism.

Table SII. Significant differences in the frequencies of copy number aberrations between NB and GNB.

A, Gain			
Chromosomal regions[a]	NB (n=25), n (%)	GNB (n=20), n (%)	P-value
1p	5 (20.0)	1 (5.0)	0.303
1q	6 (24.0)	0 (0.0)	0.056
1	4 (16.0)	0 (0.0)	0.178
2p	6 (24.0)	1 (5.0)	0.182
2q	2 (8.0)	0 (0.0)	0.571
2	7 (28.0)	0 (0.0)	0.031
3q	1 (4.0)	0 (0.0)	>0.999
4q	2 (8.0)	1 (5.0)	>0.999
4	3 (12.0)	0 (0.0)	0.316
5q	3 (12.0)	1 (5.0)	0.770
5	4 (16.0)	1 (5.0)	0.491
6p	1 (4.0)	1 (5.0)	>0.999
6q	1 (4.0)	0 (0.0)	>0.999
6	6 (24.0)	0 (0.0)	0.056
7p	2 (8.0)	0 (0.0)	0.571
7q	5 (20.0)	1 (5.0)	0.303
7	11 (44.0)	1 (5.0)	0.003
8p	1 (4.0)	0 (0.0)	>0.999
8q	1 (4.0)	0 (0.0)	>0.999
8	4 (16.0)	0 (0.0)	0.178
9p	1 (4.0)	0 (0.0)	>0.999
9q	1 (4.0)	0 (0.0)	>0.999
9	4 (16.0)	0 (0.0)	0.178
10	3 (12.0)	0 (0.0)	0.316
11p	2 (8.0)	2 (10.0)	>0.999
11	2 (8.0)	0 (0.0)	0.571
12q	5 (20.0)	0 (0.0)	0.100
12	9 (36.0)	0 (0.0)	0.009
13q	2 (08.0)	0 (0.0)	0.571
13	9 (36.0)	2 (10.0)	0.095
14q	1 (4.0)	0 (0.0)	>0.999
15q	1 (4.0)	0 (0.0)	>0.999
15	3 (12.0)	0 (0.0)	0.316
16p	1 (4.0)	0 (0.0)	>0.999
16q	2 (8.0)	0 (0.0)	0.571
16	2 (8.0)	0 (0.0)	0.571
17p	1 (4.0)	0 (0.0)	>0.999
17q	14 (56.0)	1 (5.0)	<0.001
17	9 (36.0)	0 (0.0)	0.009
18q	3 (12.0)	1 (5.0)	0.770

18	8 (32.0)	2 (10.0)	0.161
19q	1 (4.0)	0 (0.0)	>0.999
20q	1 (4.0)	1 (5.0)	>0.999
20	5 (20.0)	0 (0.0)	0.100
21q	1 (4.0)	0 (0.0)	>0.999
21	4 (16.0)	0 (0.0)	0.178
22q	2 (8.0)	0 (0.0)	0.571
22	5 (20.0)	0 (0.0)	0.100

B, LOH

Chromosomal regions[a]	NB (n=25), n (%)	GNB (n=20), n (%)	P-value
1p	9 (36.0)	0 (0.0)	0.009
1q	0 (0.0)	1 (5.0)	0.910
2p	1 (4.0)	1 (5.0)	>0.999
2q	1 (4.0)	1 (5.0)	>0.999
2	1 (4.0)	0 (0.0)	>0.999
3p	5 (20.0)	1 (5.0)	0.303
3q	1 (4.0)	0 (0.0)	>0.999
3	2 (8.0)	0 (0.0)	0.571
4p	4 (16.0)	1 (5.0)	0.491
4q	2 (8.0)	0 (0.0)	0.571
4	2 (8.0)	0 (0.0)	0.571
5p	2 (8.0)	0 (0.0)	0.571
5	2 (8.0)	0 (0.0)	0.571
6q	1 (4.0)	1 (5.0)	>0.999
7p	1 (4.0)	1 (5.0)	>0.999
7q	2 (8.0)	0 (0.0)	0.571
8p	1 (4.0)	0 (0.0)	>0.999
8q	2 (8.0)	0 (0.0)	0.571
8	4 (16.0)	0 (0.0)	0.178
9p	3 (12.0)	0 (0.0)	0.316
9	1 (4.0)	1 (5.0)	>0.999
10p	0 (0.0)	1 (5.0)	0.910
10	3 (12.0)	0 (0.0)	0.316
11p	1 (4.0)	0 (0.0)	>0.999
11q	9 (36.0)	2 (10.0)	0.095
11	3 (12.0)	0 (0.0)	0.316
12	2 (8.0)	0 (0.0)	0.571
13	1 (4.0)	0 (0.0)	>0.999
14q	3 (12.0)	0 (0.0)	0.316
14	5 (2.0)	0 (0.0)	0.100
15q	2 (8.0)	2 (10.0)	>0.999
15	4 (16.0)	0 (0.0)	0.178
16q	2 (8.0)	0 (0.0)	0.571

16	2 (8.0)	0 (0.0)	0.571
17p	2 (8.0)	0 (0.0)	0.571
17q	0 (0.0)	1 (5.0)	0.910
18p	2 (8.0)	0 (0.0)	0.571
18	1 (4.0)	0 (0.0)	>0.999
19p	3 (12.0)	0 (0.0)	0.316
19q	7 (28.0)	1 (5.0)	0.107
19	2 (8.0)	0 (0.0)	0.571
20p	0 (0.0)	1 (5.0)	0.910
20	1 (4.0)	0 (0.0)	>0.999
21	6 (24.0)	0 (0.0)	0.056
22q	3 (12.0)	0 (0.0)	0.316
X	3 (12.0)	0 (0.0)	0.316

C, Amplification

Chromosomal regions[a]	NB (n=25), n (%)	GNB (n=20), n (%)	P-value
MYCN	6 (24.0)	0 (0.0)	0.056
ALK	2 (8.0)	0 (0.0)	0.571

D, Y LOH in male patients

Chromosomal regions[a]	NB (n=16) n (%)	GNB (n=11) n (%)	P-value
Y LOH	7 (44.0)	0 (0.0)	0.022

[a]Relatively large change (typically >5 Mb) in chromosomal regions. LOH, loss of heterozygosity (including copy-neutral loss of heterozygosity); NB, neuroblastoma; GNB, ganglioneuroblastoma.

Table SIII. Clinicopathological characteristics of patients with NB and GNB.

Clinicopathological characteristic	Total, n (%)	NB, n (%)	GNB, n (%)	P-value
All	45	25 (55.6)	20 (44.4)	
Sex				0.540
Male	27 (60.0)	16 (64.0)	11 (55.0)	
Female	18 (40.0)	9 (36.0)	9 (45.0)	
Age, months				0.047
<18	8 (17.8)	7 (28.0)	1 (0.050)	
18-60	24 (53.3)	14 (56.0)	10 (50.0)	
≥60	13 (28.9)	4 (16.0)	9 (45.0)	
INSS stage				<0.001
Stages 1, 2, 4s	22 (48.9)	6 (24.0)	16 (80.0)	
Stage 3	11 (24.4)	9 (36.0)	2 (10.0)	
Stage 4	12 (26.7)	10 (40.0)	2 (10.0)	
Risk stratification				<0.001
Low	16 (35.6)	3 (12.0)	13 (65.0)	
Intermediate	11 (24.4)	6 (24.0)	5 (25.0)	
High	18 (40.0)	16 (64.0)	2 (10.0)	
Size, cm				<0.001
<5	19 (42.2)	4 (16.0)	15 (75.0)	
5-10	13 (28.9)	8 (32.0)	5 (25.0)	
>10	13 (28.9)	13 (52.0)	0 (0.0)	
Copy number aberrations (>5 Mb)				<0.001
Yes	26 (57.8)	23 (92.3)	3 (15.0)	
No	19 (42.2)	2 (8.0)	17 (85.0)	

NB, neuroblastoma; GNB, ganglioneuroblastoma; INSS, International Neuroblastoma Staging System.