

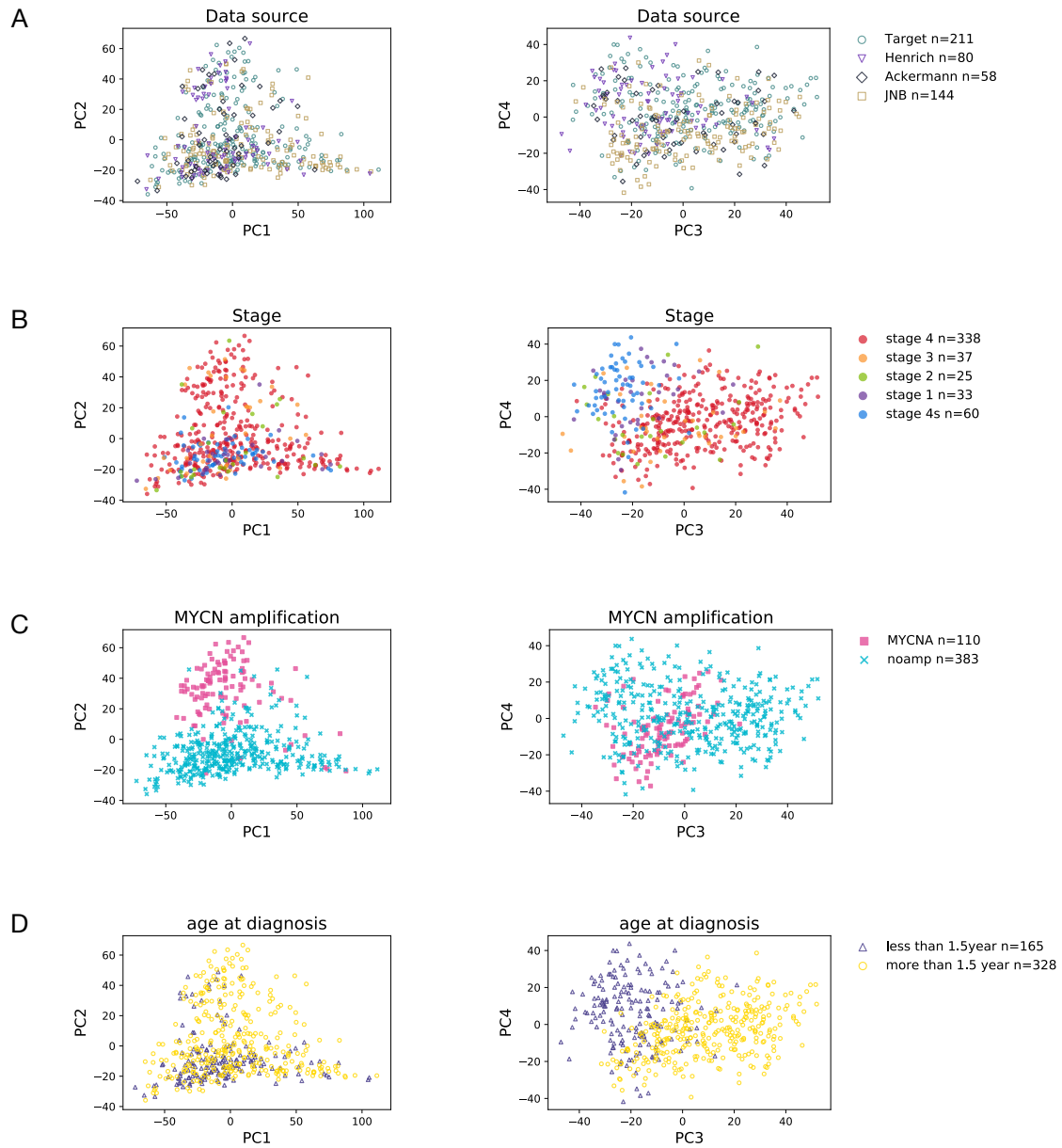


Fig. S1 PCA result for sample categories. PC1-4 were colored by each classification scheme. Marker information were listed in each figure. A) Data source. B) INSS stage. C) *MYCN* amplification status. D) Age at diagnosis.

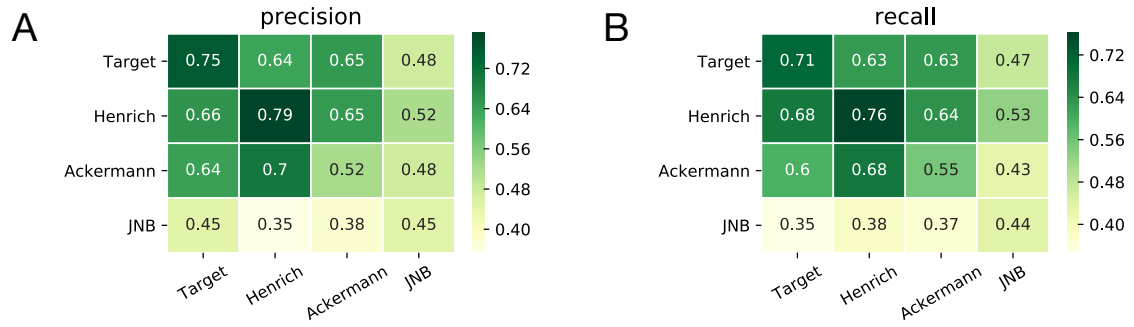


Fig. S2 Intra-dataset prediction ability. Training dataset were listed on y-axis and test data was listed on x-axis. (A) Precision. (B) recall.

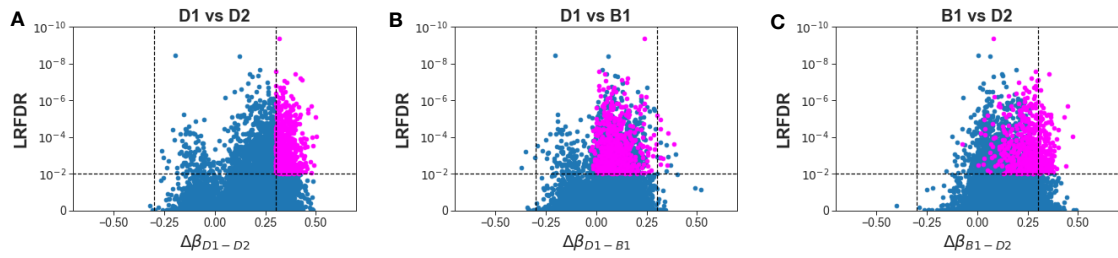


Fig. S3 Relationship between $\Delta\beta_{|D1-D2|}$ and log rank test's FDR (LRFDR). (A) $\Delta\beta_{|D1-D2|}$ was calculated between D1 and D2. (B) $\Delta\beta_{|D1-D2|}$ was calculated between B1 and D2. (C) $\Delta\beta_{|D1-D2|}$ was calculated between B1 and D2. Purple marker indicated $\Delta\beta_{|D1-D2|} > 0.3$ and LRFDR < 0.01.

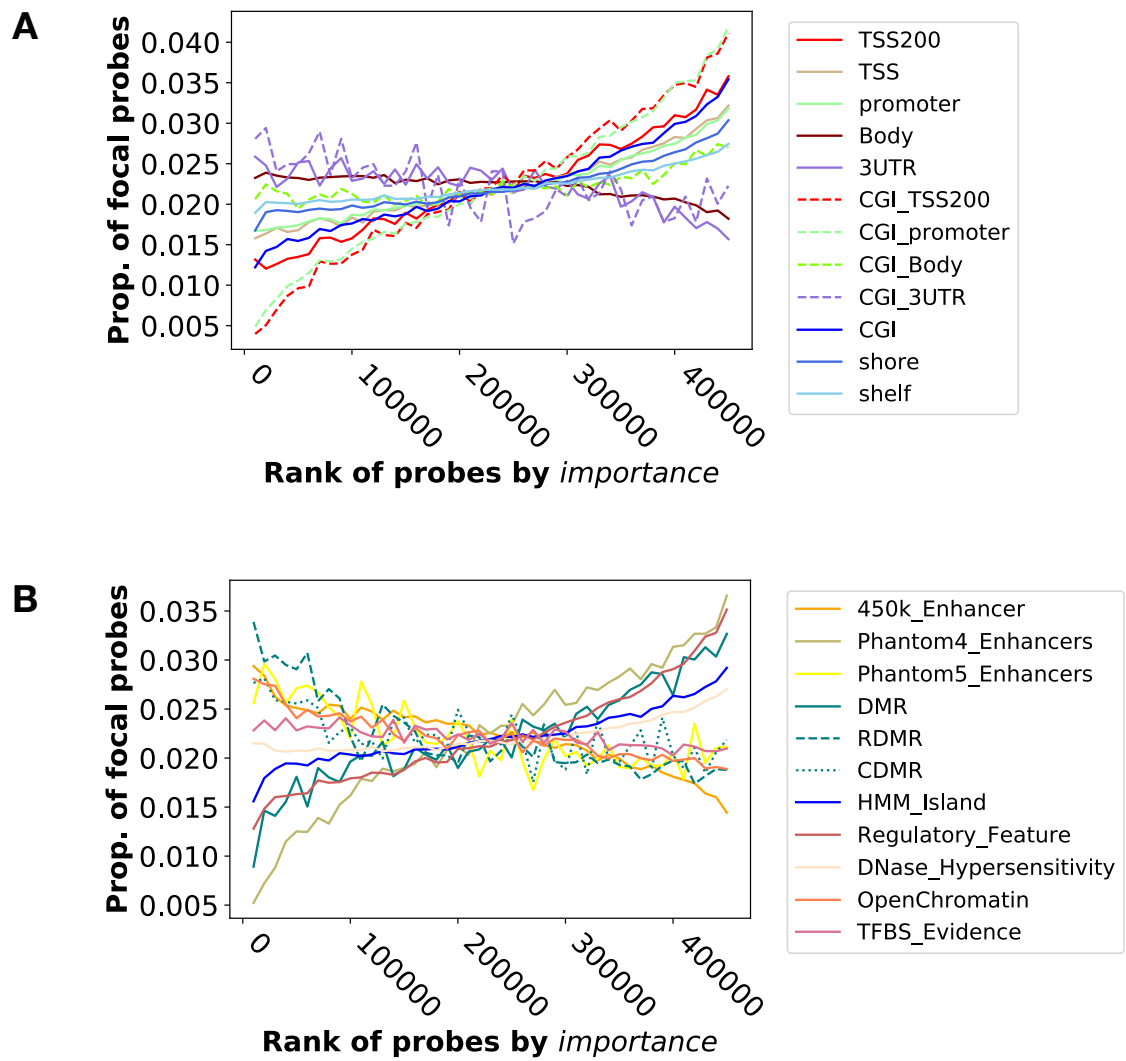


Fig. S4 Distribution of probe annotation groups in binned *importance*. x-axis is the ranked probes by *importance*. y-axis is the proportion of probes in the focal bin. Probe annotation group was colored.

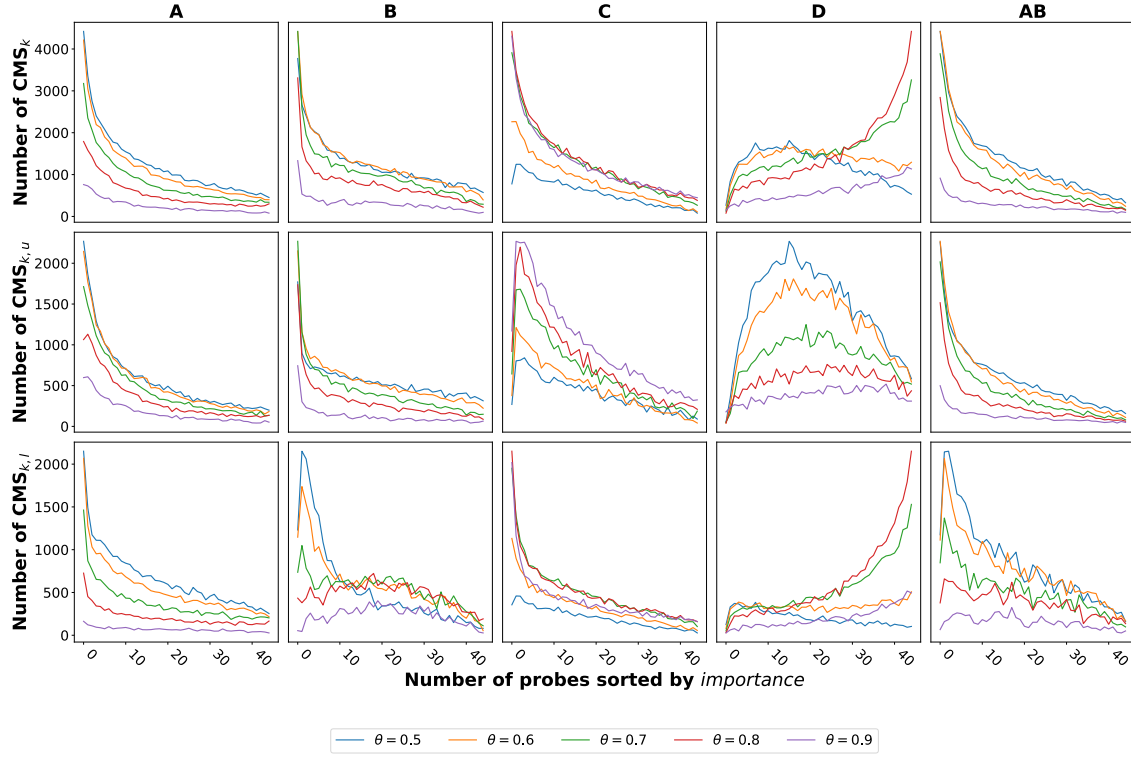


Fig. S5 Relationship between rank by *importance* and number of classifying probes.

A) x-axis is the ranked probes by *importance*. y-axis is the number of classifying probes.

Line color illustrated each θ . Top row showed the number of CMS_k. In the middle and bottom rows, it was shown the number of CMS_k with upper and lower than r_0 , respectively. Column label indicated focal class.

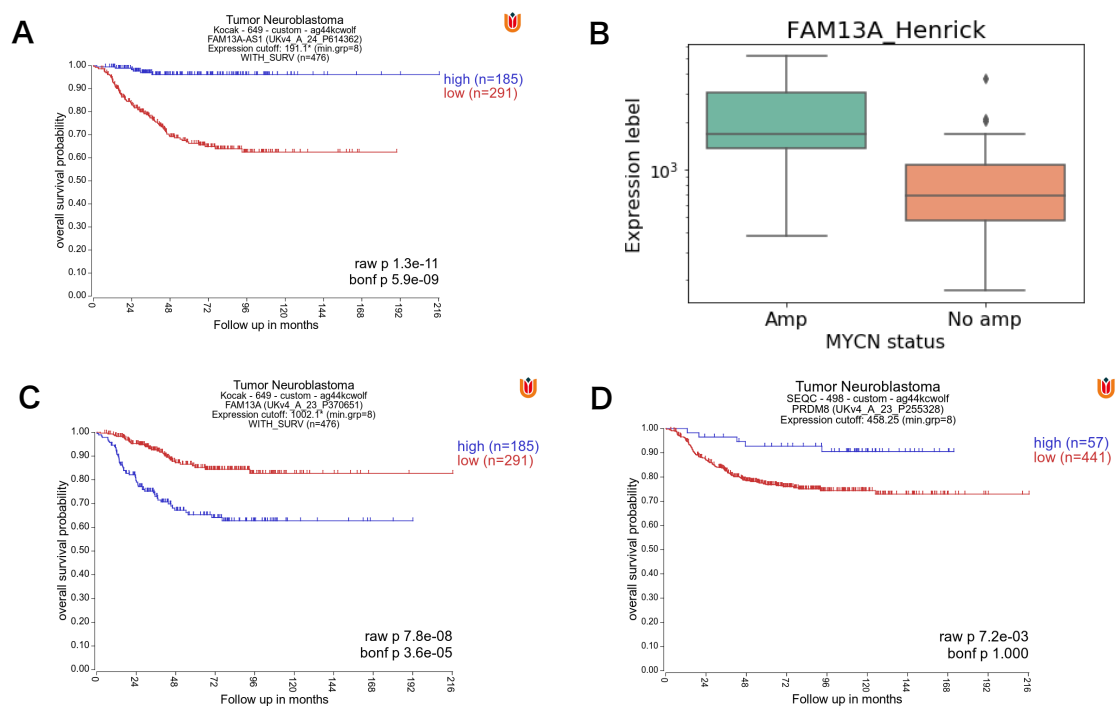


Fig. S6 A) Survival time analysis of 476 NB patients divided by gene expression

level of *FAM13A-AS*. Gene expression data and survival time data were obtained from the R2 database (<https://hgserver1.amc.nl/>). Kocak data were selected. “Scan” option was selected for sample grouping. B) Gene expression level of *FAM13A* for the data of Henrich *et al.* [22]. Box plot of *FAM13A* gene expression in MYCN-amplified (n = 33) and non-amplified (n = 72) tumors. C) Kaplan–Meier survival curves of 476 patients with NB divided by *FAM13A* expression, with same setting of Fig. S6A. D) Kaplan–Meier survival curves of 498 patients with NB divided by *PRDM8* expression with same setting of Fig. S6A. Gene expression data were obtained from the SEQC data.

Dataset	Target	Henrich	Ackerman	JNB	total
INSS stage					
4	165	41	29	103	338
3	6	8	5	18	37
2	1	8	9	7	25
1	15	8	7	3	33
4s	24	15	8	13	60
Total	211	80	58	144	493
MYCN amplification					
Y	50	25	15	20	110
N	161	55	43	124	383
Total	211	80	58	144	493

Table S1. Number of samples used in this study.

Probe annotation	probe_num	A_fl	B_fl	var
promoter	78798	0.8955	0.8650	0.0096
TSS200	58151	0.8724	0.8597	0.0068
TSS	78798	0.8917	0.8682	0.0092
Body	163726	0.8912	0.8670	0.0136
3UTR	18534	0.8692	0.8576	0.0142
CGI	138386	0.8867	0.8528	0.0073
shore	58921	0.9021	0.8660	0.0098
shelf	23349	0.8839	0.8666	0.0107
CGI_promoter	26416	0.8337	0.8018	0.0038
CGI_TSS200	36313	0.8545	0.8065	0.0031
CGI_Body	39719	0.8688	0.8574	0.0104
CGI_3UTR	2259	0.8724	0.8409	0.0136
pha5enha	7269	0.8887	0.8584	0.0163
450Kenha	95986	0.8983	0.8698	0.0172
pha5enha_CGI	2070	0.8862	0.8219	0.0104
450Kenha_CGI	14017	0.8978	0.8489	0.0119
DMR	34643	0.8992	0.8551	0.0132
DNase	275166	0.8928	0.8664	0.0115
TFBS	54338	0.8837	0.8653	0.0132
OpenChr	58724	0.8778	0.8661	0.0134
SNP	369310	0.8985	0.8749	0.0133

Table S2. Prediction ability of each probe annotation for group A and B

	2yrs	5yrs	8yrs
selP5>RF	0.609±0.044	0.657±0.037	0.678±0.037
selP5>PCA>RF	0.591±0.041	0.643±0.041	0.653±0.035
selP5>LDA>RF	0.613±0.045	0.655±0.037	0.677±0.036
selP5>CNN	0.61±0.046	0.644±0.051	0.665±0.049
selP5>PCA>CNN	0.602±0.04	0.638±0.041	0.664±0.037
selP5>LDA>CNN	0.607±0.039	0.637±0.036	0.666±0.04
selP5>SVM_rbf	0.6±0.036	0.55±0.053	0.575±0.048
selP5>PCA>SVM_rbf	0.585±0.042	0.576±0.049	0.599±0.05
selP5>LDA>SVM_rbf	0.61±0.037	0.629±0.038	0.659±0.041
selP5>SVM_linear	0.618±0.042	0.628±0.04	0.654±0.039
selP5>PCA>SVM_linear	0.607±0.038	0.661±0.038	0.678±0.032
selP5>LDA>SVM_linear	0.612±0.036	0.636±0.035	0.668±0.038
selP5>logistic	0.621±0.038	0.637±0.039	0.664±0.035
selP5>PCA>logistic	0.604±0.038	0.652±0.04	0.673±0.036
selP5>LDA>logistic	0.611±0.036	0.636±0.034	0.669±0.038

Table S5. Mean accuracy and its standard deviation