

Supplementary Table 1 Details of the GEO datasets included in this study.

Datasets	Reference	Platform	Sample size (tumor/control)
GSE50161	Griesinger et al. (2013)	GPL570	35 (22/13)
GSE74195	de Bont et al. (2008)	GPL570	28 (23/5)
GSE86574	Amani et al. (2017)	GPL570	26 (16/10)
GSE85217	Cavalli et al. (2017)	GPL22286	599 (599/0)
GSE37418	Giles Robinson et al. (2012)	GPL570	74 (74/0)

Supplementary Table 2 Clinicopathological characteristics of patients included in this study.

ID	Molecular Subtype	Age	Gender	OS day	OS year	Survival-status	Eisk	Coef
TG1	WNT	8	F	1341	3.673973	Y	Low	-1378.63
TG10	G4	13	M	1315	3.60274	Y	Low	-914.768
TG11	G3	5	F	896	2.454795	N	High	375.8381
TG12	G3	6	M	790	2.164384	N	High	623.496
TG13	G4	7	F	1246	3.413699	Y	High	256.2029
TG14	G4	9	M	1225	3.356164	Y	High	260.1781
TG15	SHH	2	M	1224	3.353425	Y	Low	217.285
TG18	G4	6	M	1217	3.334247	Y	High	815.8478
TG2	G3	4	F	384	1.052055	N	High	628.5418
TG20	G3	2	F	1208	3.309589	Y	High	1035.761
TG21	SHH	9	M	1207	3.306849	Y	High	962.2383
TG22	G4	13	M	1205	3.30137	Y	Low	73.70473
TG23	G4	7	M	1203	3.29589	Y	High	361.6017
TG24	G4	8	M	1217	3.334247	Y	High	758.7663
TG26	G4	3	M	1183	3.241096	Y	Low	-50.0425
TG27	WNT	6	M	1182	3.238356	Y	Low	-805.205
TG28	WNT	9	F	1179	3.230137	Y	Low	-828.031
TG29	G4	8	M	1173	3.213699	Y	Low	189.7378
TG3	G4	15	M	1334	3.654795	Y	Low	23.82234
TG30	G4	5	M	1105	3.027397	Y	Low	-399.792
TG31	G4	2	M	1105	3.027397	Y	High	1324.137
TG32	WNT	7	M	1112	3.046575	Y	Low	-1007.64
TG33	SHH	12	M	1118	3.063014	Y	High	387.1448
TG34	G4	5	M	1123	3.076712	Y	High	447.7336
TG35	SHH	2	F	1112	3.046575	Y	High	265.9618
TG36	SHH	8	F	1113	3.049315	Y	Low	253.55
TG37	G4	7	M	1049	2.873973	Y	Low	-328.347
TG38	G4	7	M	1047	2.868493	Y	High	794.7547
TG39	WNT	4	M	1134	3.106849	Y	Low	-480.459
TG4	G4	9	F	243	0.665753	N	High	1097.487
TG40	G4	15	M	1141	3.126027	Y	High	805.8612
TG41	G3	8	M	85	0.232877	N	High	295.2203
TG5	G4	6	M	1336	3.660274	Y	Low	-733.363
TG6	G4	13	M	1300	3.561644	Y	Low	-276.586
TG7	G3	7	M	1301	3.564384	Y	Low	74.29303

TG8	G3	10	M	1007	2.758904	N	High	679.8045
TG9	G3	4	F	1211	3.317808	N	Low	-56.6871

Supplementary Table 3 Univariate and multivariate Cox regression analysis of prognostic factors.

ID	Subtype	Cluster	Age	Gander	Survival Status	OS (months)
Y7	G4	C1	9	M	Decease	14
Y4	WNT	C1	14	F	Decease	41
Y6	G4	C2	5	F	Decease	20
Y1	G4	C2	7	F	Decease	15
Y5	SHH	C3	8	F	Alive	59
Y3	SHH	C3	11	M	Decease	39
Y2	SHH	C3	12	M	Decease	99
Y8	G3	C4	8	M	Alive	50

Supplementary Table 4 Metabolic genes differentially expressed among molecular subgroups.

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Supplementary Table 5 Functional enrichment analysis of metabolic subclasses.

Differentially metabolism pathways in C1			Differentially metabolism pathways in C2			Differentially m
Pathway	logFC	adj.P.Val	Pathway	logFC	adj.P.Val	Pathway
Remethylation	0,365167318	2,23E-25	Other Types of O-Glycan Biosynthesis	0,22520901	7,55E-32	Glycogen Biosynthesis
Purine Biosynthesis	0,353906708	8,65E-16	Glycolysis	-0,203709038	4,42E-55	Purine Biosynthesis
Epinephrine Biosynthesis	0,347747528	9,05E-15	Methionine Cycle	-0,205881538	1,58E-36	Selenocompound Metabolism
Neomycin, Kanamysin and Gentamicin Biosynthesis	0,340944201	2,23E-12	Cysteine and Methionine Metabolism	-0,212085953	5,87E-38	Glyoxylate and Dicarboxylate Metabolism
Sulfur Metabolism	0,336857324	2,25E-19	Prostaglandin Biosynthesis	-0,213635084	1,07E-16	Retinoic Acid Metabolism
Homocysteine Biosynthesis	0,33241013	4,03E-16	Mucin Type O-Glycan Biosynthesis	-0,218052418	1,85E-38	Pentose Phosphate
Glycogen Biosynthesis	0,325062094	6,15E-11	Retinoic Acid Metabolism	-0,221906011	5,29E-20	Steroid Biosynthesis
Norepinephrine Biosynthesis	0,303151579	3,23E-10	Pyrimidine Biosynthesis	-0,231018313	1,16E-17	Folate One Carbon Metabolism
Glycogen Degradation	0,281541338	6,79E-12	Glyoxylate and Dicarboxylate Metabolism	-0,232247417	6,27E-31	Nicotinamide Adenine Dinucleotide Biosynthesis
Prostaglandin Biosynthesis	0,276458689	8,70E-11	Remethylation	-0,247220758	1,44E-31	Ketone Biosynthesis and Metabolism
Glycosaminoglycan Biosynthesis	0,274814355	3,37E-30	Ketone Biosynthesis and Metabolism	-0,249271376	6,04E-29	Prostaglandin Biosynthesis
Cysteine and Methionine Metabolism	0,268158664	7,10E-22	Steroid Biosynthesis	-0,260835357	4,68E-31	Pyrimidine Biosynthesis
Nicotinamide Adenine Dinucleotide Biosynthesis	0,25706177	3,34E-07	Folate One Carbon Metabolism	-0,285479034	6,66E-51	Glycosphingolipid Biosynthesis
Ketone Biosynthesis and Metabolism	0,251112226	3,58E-11	Pentose Phosphate	-0,286733114	6,66E-51	Butanoate Metabolism
Folate One Carbon Metabolism	0,247985253	1,57E-13	Homocysteine Biosynthesis	-0,314699274	2,43E-40	Propanoate Metabolism

Pentose Phosphate	0,2354807	2,72E-12	Purine Biosynthesis	-0,343346834	2,59E-41	Arginine and Proline Metabolism
Methionine Cycle	0,227505453	4,03E-16	Selenocompound Metabolism	-0,359063301	2,41E-53	Fatty Acid Biosynthesis
Urea Cycle	0,222639107	1,75E-12	Glycogen Biosynthesis	-0,385869642	1,72E-41	Glycosphosphatidylinositol
Selenocompound Metabolism	0,218741786	1,96E-07				Retinoid Metabolism
Mucin Type O-Glycan Biosynthesis	0,204334872	2,07E-12				
Steroid Biosynthesis	0,203002791	1,93E-07				
Other Types of O-Glycan Biosynthesis	-0,264459123	4,03E-16				

Supplementary Table 6 Single-cell sequencing data processing and quality control.

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Supplementary Table 7 Key metabolic pathway activity scores across cell clusters.

ID	p_val	avg_log2FC	pct.1	pct.2	p_val_adj	Cluster	Gene
ATP1A2	0	2.128365	0.232	0.081	0	C1	ATP1A2
GRIK2	9.9E-35	0.800617	0.271	0.226	2.28E-31	C1	GRIK2
KCNJ6	0	2.597951	0.409	0.06	0	C3	KCNJ6
GRIA4	0	2.169276	0.303	0.039	0	C3	GRIA4
BCAT1	0	2.019461	0.394	0.092	0	C3	BCAT1
LDHB	0	2.017339	0.721	0.283	0	C3	LDHB
ADCY8	0	1.763738	0.251	0.058	0	C3	ADCY8
ABCC4	0	1.756695	0.264	0.057	0	C3	ABCC4
ATIC	0	1.577281	0.437	0.161	0	C3	ATIC
DAGLA	0	1.429621	0.255	0.07	0	C3	DAGLA
SLC6A15	0	1.340414	0.377	0.114	0	C3	SLC6A15
ST8SIA1	0	1.312467	0.234	0.095	0	C3	ST8SIA1
SLC1A5	0	0.838964	0.282	0.112	0	C3	SLC1A5
FDFT1	3.7E-252	0.671635	0.296	0.163	8.6E-249	C3	FDFT1
BDH1	2.4E-223	0.589439	0.278	0.155	5.6E-220	C3	BDH1
ATP2B4	3.3E-161	0.404279	0.385	0.259	7.5E-158	C3	ATP2B4
CA4	0	2.462984	0.338	0.055	0	C2	CA4
KCNA5	0	2.254683	0.414	0.125	0	C2	KCNA5

KCNA1	0	2.191737	0.272	0.043	0	C2	KCNA1
GLRA1	0	2.029115	0.304	0.082	0	C2	GLRA1
DGKB	0	1.783562	0.271	0.094	0	C2	DGKB
ABCC8	0	1.554835	0.287	0.111	0	C2	ABCC8
INPP5F	0	1.525382	0.407	0.196	0	C2	INPP5F
ASS1	0	1.515868	0.261	0.12	0	C2	ASS1
PDE1C	0	1.501881	0.246	0.091	0	C2	PDE1C
DPYSL4	0	1.374886	0.596	0.396	0	C2	DPYSL4
ADCY1	0	1.283728	0.545	0.33	0	C2	ADCY1
B4GALT6	1.3E-306	1.237556	0.203	0.088	3E-303	C2	B4GALT6
SLC38A1	0	1.190279	0.409	0.201	0	C2	SLC38A1
CACNA1H	3.6E-255	0.990745	0.207	0.099	8.4E-252	C2	CACNA1H
SV2B	0	0.872096	0.364	0.207	0	C2	SV2B
CLCN4	4.4E-160	0.775993	0.308	0.207	1E-156	C2	CLCN4
B3GAT1	1.47E-69	0.755937	0.258	0.201	3.38E-66	C2	B3GAT1
CACNG2	3.42E-78	0.565	0.235	0.168	7.87E-75	C2	CACNG2
CHST1	1.56E-60	0.487179	0.229	0.171	3.58E-57	C2	CHST1
NPR3	0	4.848729	0.563	0.017	0	C4	NPR3
GABRA5	0	3.891001	0.558	0.044	0	C4	GABRA5
GRIA1	0	3.415903	0.448	0.047	0	C4	GRIA1
SLC1A7	0	2.851731	0.514	0.051	0	C4	SLC1A7
SLC12A2	0	1.631638	0.363	0.12	0	C4	SLC12A2

Supplementary Table 8 Correlation analysis between 17-gene signature and immune infiltration.

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Supplementary Table 9 Prediction performance of the 17-gene signature in validation cohorts.

Gene	Beta	HR (95% CI for HR)	wald.test	p-value
DSE	-0.72	0.49 (0.36–0.65)	23	1.90E-06
ATP8A2	-0.25	0.78 (0.7–0.87)	21	4.90E-06
MTHFD2L	0.65	1.9 (1.4–2.6)	19	1.30E-05
SCN8A	-0.8	0.45 (0.31–0.65)	17	2.90E-05
CACNA1A	-0.17	0.84 (0.78–0.92)	17	4.20E-05
ODC1	0.6	1.8 (1.4–2.4)	16	5.00E-05
NALCN	-0.25	0.78 (0.68–0.89)	14	0.00022
RRM2	0.38	1.5 (1.2–1.8)	14	0.00024
SV2A	-0.26	0.77 (0.67–0.89)	13	0.00036
KCNQ2	-0.29	0.75 (0.63–0.89)	10	0.0014
QDPR	0.55	1.7 (1.2–2.4)	10	0.0016
MGAT4A	-0.29	0.75 (0.62–0.9)	9.3	0.0023
GAD1	-0.16	0.85 (0.76–0.95)	8.8	0.0031
SLC6A1	-0.24	0.79 (0.67–0.93)	8.2	0.0042
GABRD	-0.27	0.76 (0.64–0.92)	8	0.0047
LBR	0.45	1.6 (1.1–2.2)	7.5	0.0061
KCNJ6	-0.15	0.86 (0.77–0.96)	7.2	0.0072
ATP2B3	0.14	1.1 (1–1.3)	6.7	0.0095

SCN1B	-0.35	0.7 (0.54–0.92)	6.6	0.01
ANKH	-0.48	0.62 (0.43–0.9)	6.4	0.012
KCNK1	-0.16	0.85 (0.75–0.97)	6.2	0.012
CA11	-0.24	0.79 (0.65–0.95)	6.2	0.013
GRIA1	0.12	1.1 (1–1.3)	5.1	0.024
GRIA3	0.2	1.2 (1–1.5)	4.8	0.028
SLC8A2	-0.22	0.8 (0.66–0.98)	4.6	0.031
HS3ST1	0.28	1.3 (1–1.7)	4.4	0.037
KCNK12	-0.22	0.8 (0.65–0.99)	4.3	0.039
ST8SIA5	-0.16	0.85 (0.73–0.99)	4.2	0.04
TTYH1	0.17	1.2 (1–1.4)	4.2	0.041
SLC24A3	-0.15	0.86 (0.73–1)	3.9	0.049
ATP6V1G2	-0.24	0.79 (0.62–1)	3.9	0.049

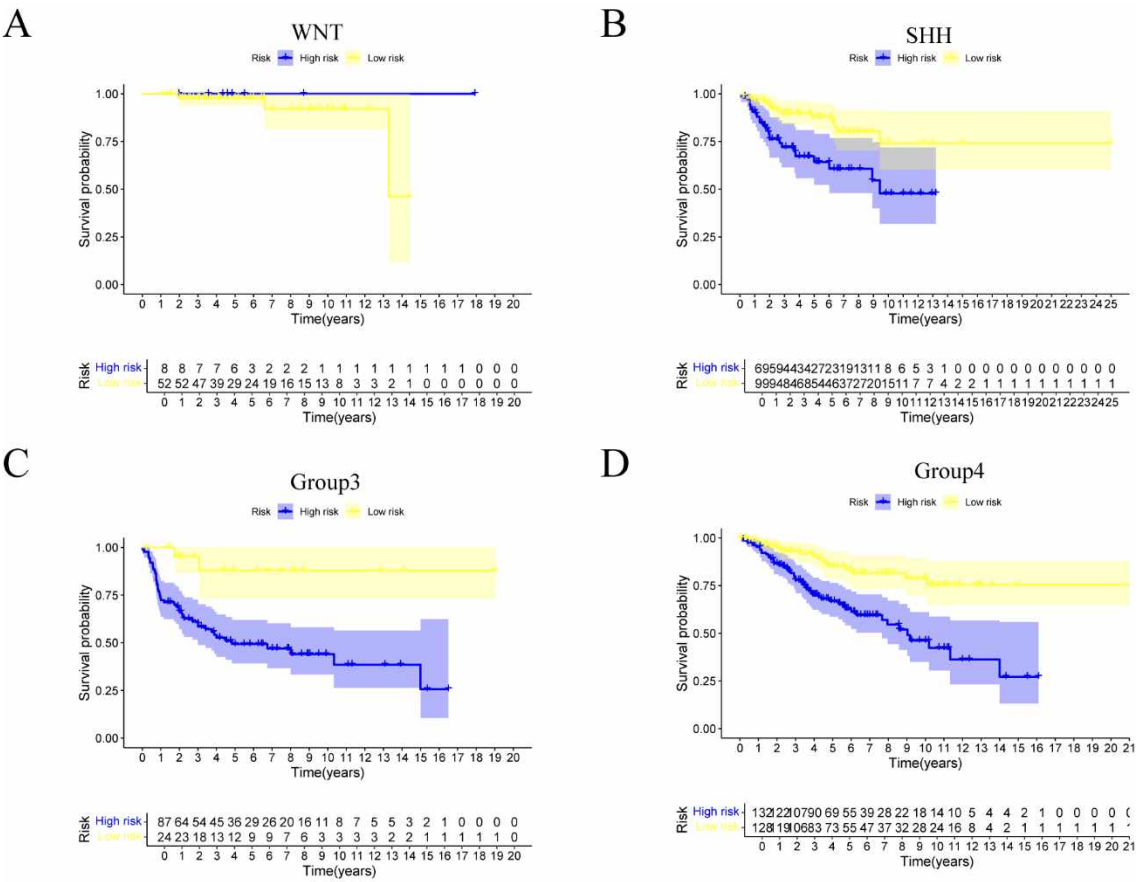
Supplementary Table 10 The clinical characteristics of the training and test sets.

Clinical characteristics	Training_set (n=400)	Testing_set (n=199)	RNAseq_set (n=37)	p-value
Gender (female)	131 (32.8%)	69 (34.7%)	10 (27.0%)	1
Age	10.28 ($\pm$ 9.35)	10.18 ($\pm$ 8.93)	7.32 ($\pm$ 3.57)	0.158
Subgroup				
WNT	41.2 (10%)	19 (9.5%)	5 (13.5%)	0.643
SHH	109 (27.3%)	59 (29.7%)	5 (13.5%)	
Group3	74 (18.5%)	37 (18.6%)	8 (21.6%)	
Group4	176 (44%)	84 (42.2%)	19 (51.4%)	

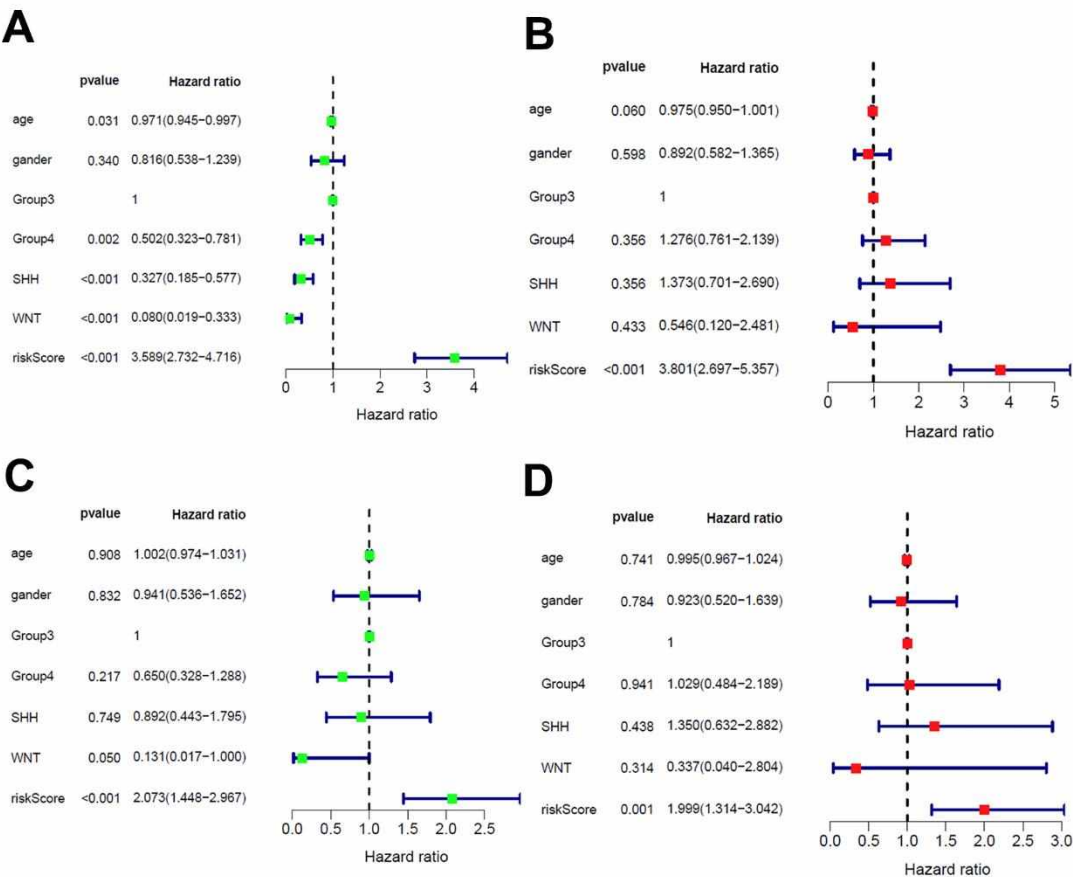
Supplementary Table 11 List of primer sequences and reagents used in this study.

Gene	Coef	Mean Expression (Training Set)	SD (Training Set)
MTHFD2L	0.66159926	5.23	0.87
QDPR	0.412769783	4.67	0.79
ODC1	0.165440545	4.89	0.72
GRIA3	0.143323094	6.11	1.03
TTYH1	0.112264197	5.76	0.91
RRM2	0.084668675	4.92	0.84
ATP2B3	0.07549509	5.38	0.89
HS3ST1	0.071117614	5.12	0.78
GRIA1	0.057104973	6.05	1.12
KCNK1	-0.009904217	5.89	0.97
NALCN	-0.055988713	5.42	0.86
GAD1	-0.07036893	5.67	0.93
ATP6V1G2	-0.122811454	6.21	1.05
ATP8A2	-0.144362938	5.98	0.99
DSE	-0.207984737	5.73	0.88
SLC24A3	-0.251598841	5.56	0.82
ANKH	-0.254280922	5.91	0.94

Supplementary Figure 1 Kaplan-Meier survival analysis of the 17-gene signature stratified by WHO molecular subgroups. The 17-gene risk score effectively stratified overall survival in SHH ($p=1.12 \times 10^{-3}$, Group 3 ($p = 1.55 \times 10^{-3}$), and Group 4 ($p = 2.75 \times 10^{-5}$) medulloblastoma subgroups, but not in the WNT subgroup ($p = 0.386$), consistent with the favorable prognosis and small sample size of WNT medulloblastoma. High-risk groups are shown in blue, and low-risk groups are shown in yellow. The number of patients at risk at each time point is listed below each survival curve.



Supplementary Figure 2 Cox regression analysis of the association between clinical factors and OS. (A–B) Univariate and multivariate Cox regression analysis in train cohort; (C–D) Univariate and multivariate Cox regression analysis in validation cohort.



Supplementary Figure 3 Nomogram combining 17-gene signature and clinical factors.

