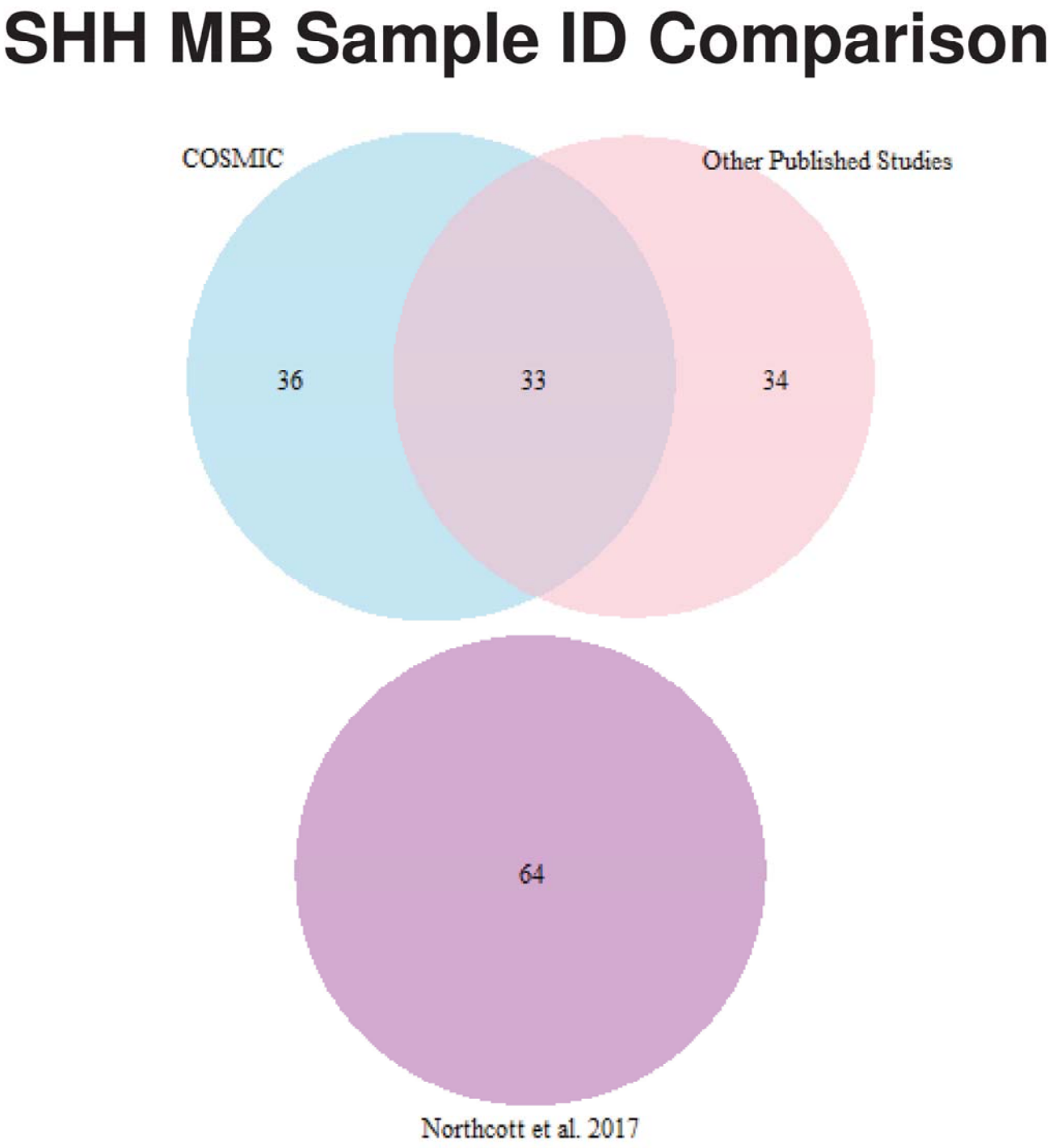
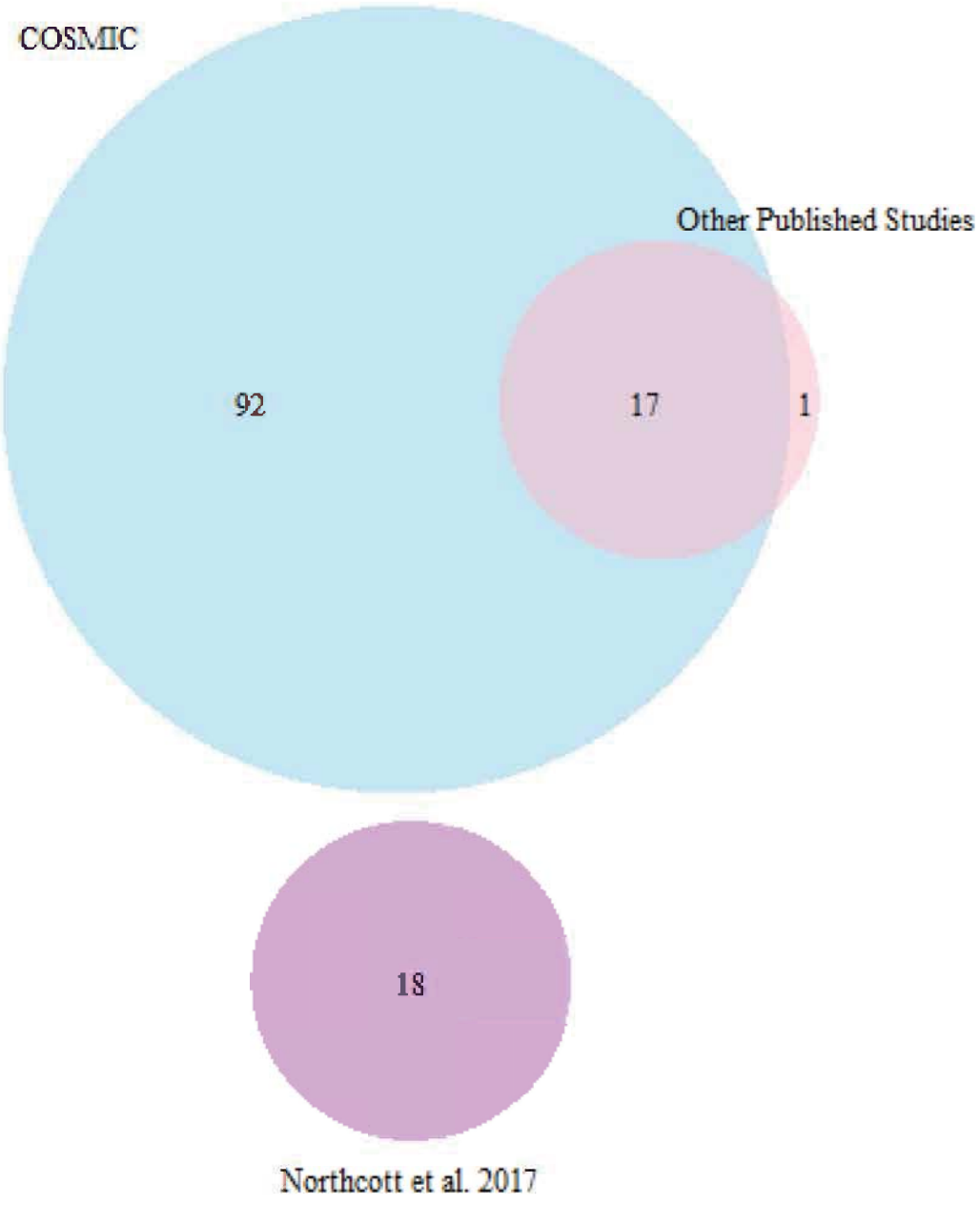
S1 File - SHH


SHH MB Sample ID Comparison
COSMIC
Other Published Studies
36
33
34
64
Northcott et al. 2017

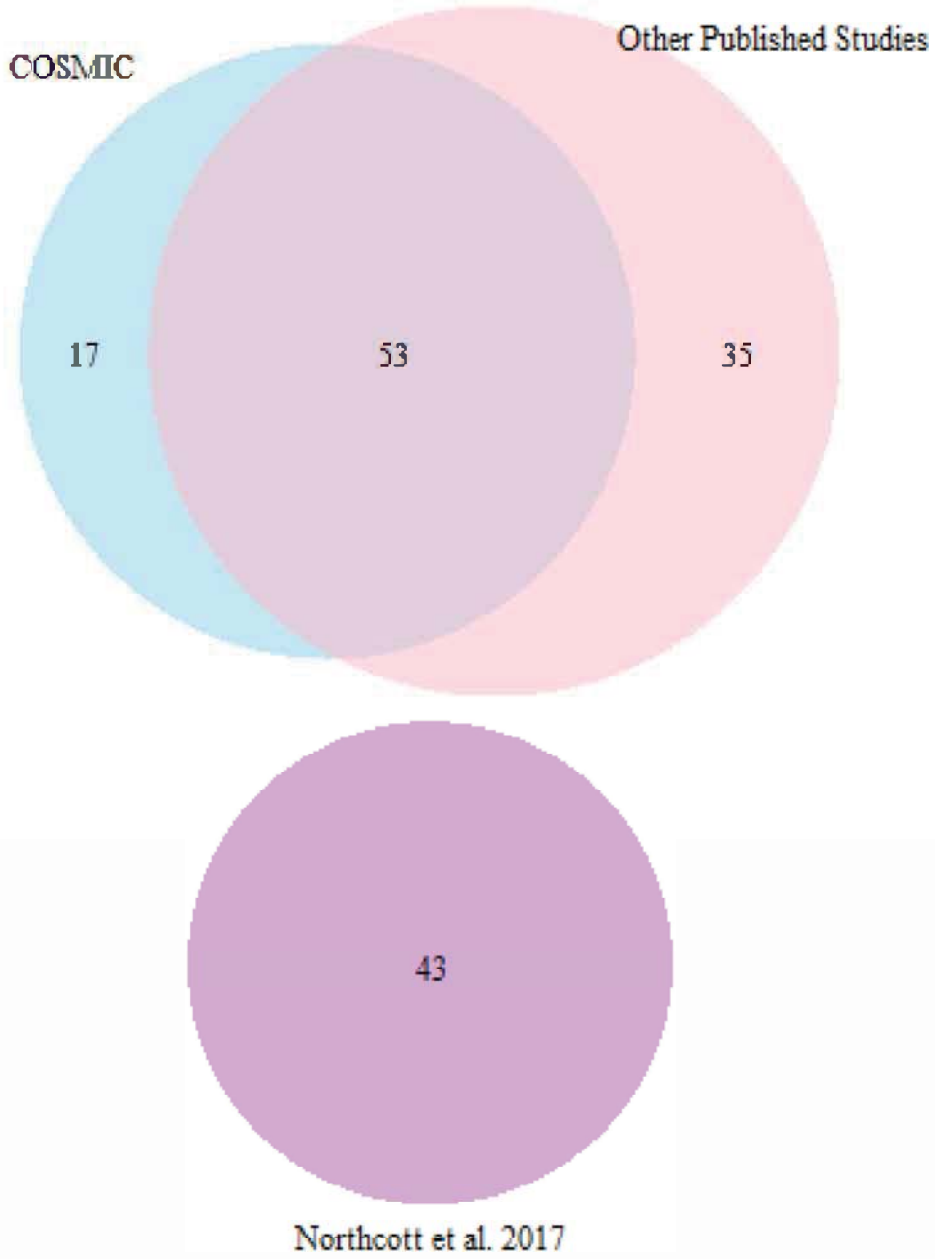
S1 File - Wnt

WNT MB Sample ID Comparison



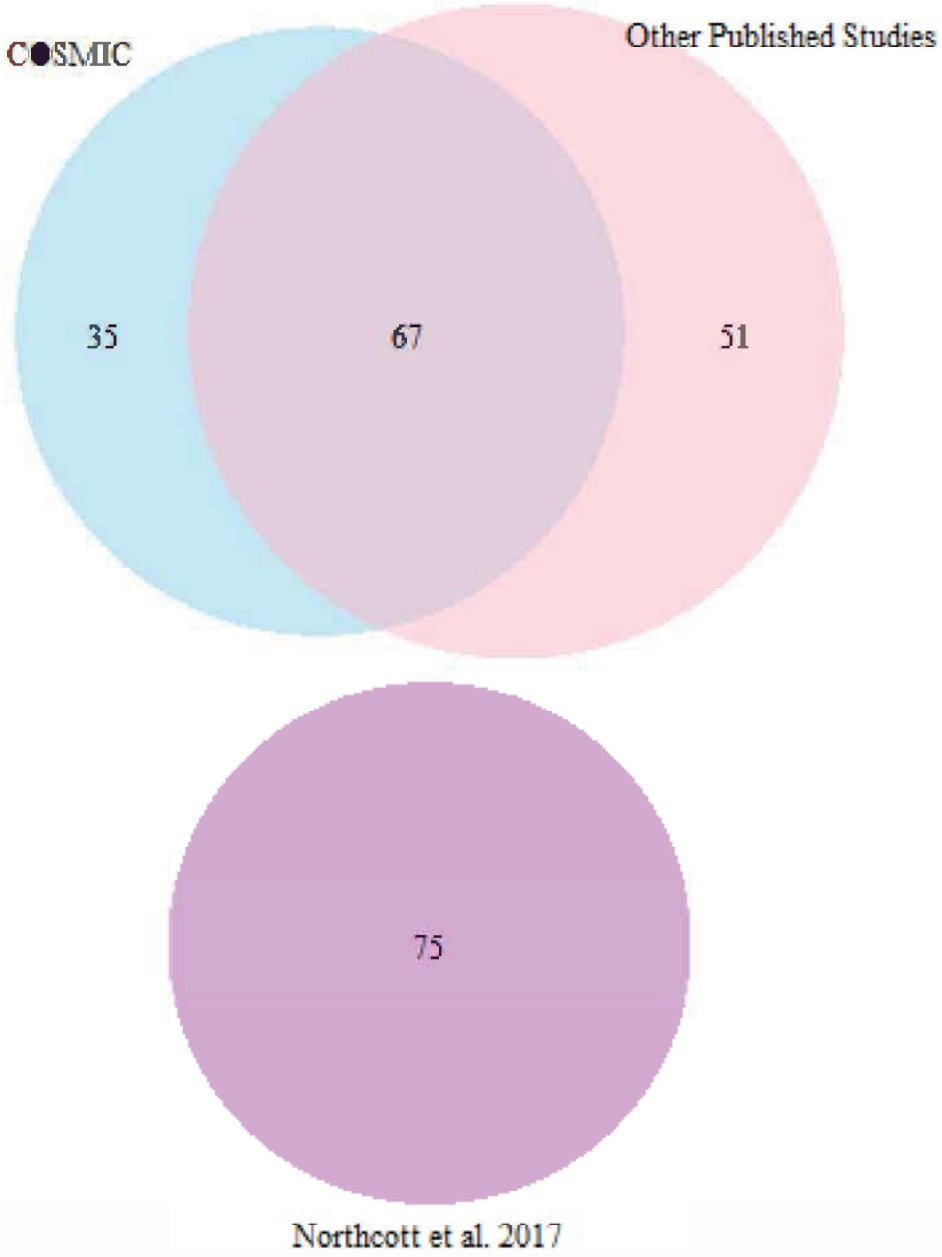
S1 File - Group 3

Group 3 MB Sample ID Comparison



S1 File - Group 4

Group 4 MB Sample ID Comparison



S1 Table

Gene	Gene Description	ATRT (182)				SHH Wildtype (65)				SHH TP53 (8)				WNT (114)				Group 3 (76)				Group 4 (121)			
		Act†	Inact	Total Mut	Total PT	Act†	Inact	Total Mut	Total PT	Act†	Inact	Total Mut	Total PT	Act†	Inact	Total Mut	Total PT	Act†	Inact	Total Mut	Total PT	Act†	Inact	Total Mut	Total PT
ACAN	Aggrecan core protein	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (22.2)	0 (0)	9	3 (3.95)	-	-	-	-
AKAP9	A-kinase anchor protein 9	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (33.3)	0 (0)	6	3 (3.95)	-	-	-	-
ALPK2	Alpha-protein kinase 2	-	-	-	-	2 (66.7)	0 (0)	3	3 (4.62)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
ARID2	AT-rich interactive domain-containing protein 2	-	-	-	-	-	-	-	-	-	-	-	-	0 (0)	3 (100)	3	1 (0.877)	-	-	-	-	-	-	-	-
ATP12A	Potassium-transporting ATPase alpha chain 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (50)	0 (0)	4	3 (3.95)	-	-	-	-
BCOR	BCL-6 corepressor	-	-	-	-	0 (0)	8 (100)	8	4 (6.15)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BRAF	Serine/threonine-protein kinase B-raf	12 (100)	0 (0)	12	5 (2.75)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
CACNA1D	Voltage-dependent L-type calcium channel subunit alpha-1D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (40)	0 (0)	5	3 (2.48)
CAST	Calpastatin	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (40)	0 (0)	5	3 (2.48)
CDH1	Cadherin-1	-	-	-	-	-	-	-	-	-	-	-	-	2 (66.7)	0 (0)	3	3 (2.63)	-	-	-	-	-	-	-	-
CDKN2A	Cyclin-dependent kinase inhibitor 2A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (25)	0 (0)	8	1 (0.826)
CHD7	Chromodomain-helicase-DNA-binding protein 7	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0 (0)	5 (100)	5	5 (4.13)
CR1	Complement receptor type 1	-	-	-	-	0 (0)	4 (100)	4	1 (1.54)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
CREBBP	CREB-binding protein	-	-	-	-	-	-	-	-	-	-	-	-	2 (40)	3 (60)	5	4 (3.51)	-	-	-	-	-	-	-	-
CSNK2B	Casein kinase II subunit beta	-	-	-	-	-	-	-	-	-	-	-	-	2 (50)	0 (0)	4	4 (3.51)	-	-	-	-	-	-	-	-
CTDNEP1	CTD nuclear envelope phosphatase 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0 (0)	3 (100)	3	3 (3.95)	-	-	-	-
CTNNB1	Catenin beta-1	-	-	-	-	-	-	-	-	-	-	-	-	73 (33.8)	0 (0)	216	110 (96.5	-	-	-	-	-	-	-	-
CUL1	Cullin-1	-	-	-	-	2 (100)	0 (0)	2	1 (1.54)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DDX3X	ATP-dependent RNA helicase DDX3X	-	-	-	-	4 (33.3)	0 (0)	12	8 (12.3)	-	-	-	-	8 (22.9)	0 (0)	35	19 (16.7)	-	-	-	-	-	-	-	-
DDX60	Probable ATP-dependent RNA helicase DDX60	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0 (0)	4 (100)	4	2 (2.63)	-	-	-	-
DHX9	ATP-dependent RNA helicase A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (100)	0 (0)	2	1 (0.826)
DNAH1	Dynein heavy chain 1, axonemal	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (50)	0 (0)	4	3 (2.48)
DNAH14	Dynein heavy chain 14, axonemal	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (25)	0 (0)	8	4 (5.26)	-	-	-	-
DNAJB9	DnaJ homolog subfamily B member 9	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3 (100)	0 (0)	3	3 (2.48)
DOCK8	Dedicator of cytokinesis protein 8	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (33.3)	0 (0)	6	3 (3.95)	-	-	-	-
DYNC1H1	Cytoplasmic dynein 1 heavy chain 1	-	-	-	-	-	-	-	-	2 (100)	0 (0)	2	2 (25)	-	-	-	-	1 (0)	2 (66.7)	3	3 (3.95)	-	-	-	-
EML4	Echinoderm microtubule-associated protein-like 4	-	-	-	-	1 (0)	2 (66.7)	3	3 (4.62)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
EPHA7	Ephrin type-A receptor 7	-	-	-	-	-	-	-	-	-	-	-	-	2 (33.3)	3 (50)	6	3 (2.63)	-	-	-	-	-	-	-	-
EPHB3	Ephrin type-B receptor 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (66.7)	0 (0)	3	3 (3.95)	-	-	-	-
FAT1	Protocadherin Fat 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3 (60)	0 (0)	5	3 (2.48)
FBXW7	F-box/WD repeat-containing protein 7	-	-	-	-	4 (50)	0 (0)	8	1 (1.54)	-	-	-	-	0 (0)	4 (100)	4	1 (0.877)	-	-	-	-	-	-	-	-
FCRL2	Fc receptor-like protein 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (33.3)	2 (33.3)	6	4 (5.26)	-	-	-	-
FGFR2	Fibroblast growth factor receptor 2	-	-	-	-	1 (0)	0 (0)	5	1 (1.54)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
GABRG1	Gamma-aminobutyric acid receptor subunit gamma-1	-	-	-	-	4 (100)	0 (0)	4	4 (6.15)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
GPAM	Glycerol-3-phosphate acyltransferase 1, mitochondrial	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0 (0)	4 (100)	4	4 (3.31)
HIVEP3	Transcription factor HIVEP3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (66.7)	0 (0)	3	3 (3.95)	-	-	-	-
IDH1	Isocitrate dehydrogenase [NADP] cytoplasmic	-	-	-	-	4 (100)	0 (0)	4	1 (1.54)	-	-	-	-	2 (100)	0 (0)	2	1 (0.877)	-	-	-	-	-	-	-	-
IFIT3	Interferon-induced protein with tetratricopeptide repeats 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (50)	0 (0)	4	4 (3.31)
KDM1A	Lysine-specific histone demethylase 1A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3 (60)	0 (0)	5	3 (2.48)
KDM4C	Lysine-specific demethylase 4C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (28.6)	3 (42.9)	7	3 (2.48)
KDM6A	Lysine-specific demethylase 6A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0 (0)	7 (100)	7	3 (3.95)	2 (8.33)	18 (75)	24	14 (11.6)
KIAA1107	Uncharacterized protein KIAA1107	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0 (0)	3 (100)	3	2 (1.65)
KMT2C	Histone-lysine N-methyltransferase 2C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (0)	8 (57.1)	14	5 (4.13)
KMT2D	Histone-lysine N-methyltransferase 2D	-	-	-	-	1 (0)	31 (93.9)	33	8 (12.3)	-	-	-	-	1 (0)	6 (60)	10	4 (3.51)	0 (0)	10 (83.3)	12	5 (6.58)	2 (22.2)	5 (55.6)	9	3 (2.48)

Gene	Gene Description	ATRT (182)				SHH Wildtype (65)				SHH TP53 (8)				WNT (114)				Group 3 (76)				Group 4 (121)			
		Act†	Inact	Total Mut	Total PT	Act†	Inact	Total Mut	Total PT	Act†	Inact	Total Mut	Total PT	Act†	Inact	Total Mut	Total PT	Act†	Inact	Total Mut	Total PT	Act†	Inact	Total Mut	Total PT
LDB1	LIM domain-binding protein 1	-	-	-	-	1 (0)	2 (40)	5	4 (6.15)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LRP1B	Low-density lipoprotein receptor-related protein 1B	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (50)	0 (0)	4	3 (3.95)	-	-	-	-
LRRK2	Leucine-rich repeat serine/threonine-protein kinase 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (33.3)	0 (0)	6	3 (2.48)
MUC16	Mucin-16	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4 (33.3)	0 (0)	12	3 (2.48)
MUC4	Mucin-4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4 (100)	0 (0)	4	2 (1.65)
NRAS	GTPase NRas	3 (100)	0 (0)	3	1 (0.549)	2 (100)	0 (0)	2	1 (1.54)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
OR51L1	Olfactory receptor 51L1	-	-	-	-	2 (100)	0 (0)	2	2 (3.08)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
OTOF	Otoferlin	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (25)	0 (0)	8	3 (3.95)	-	-	-	-
OTOGL	Otogelin-like protein	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0 (0)	3 (100)	3	3 (2.48)
PBRM1	Protein polybromo-1	-	-	-	-	0 (0)	5 (100)	5	2 (3.08)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PCBP2	Poly(rC)-binding protein 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0 (0)	3 (100)	3	1 (1.32)	-	-	-	-
PCDH11X	Protocadherin-11 X-linked	-	-	-	-	4 (28.6)	0 (0)	14	2 (3.08)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PCDH9	Protocadherin-9	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (66.7)	0 (0)	3	3 (2.48)
PFKP	ATP-dependent 6-phosphofructokinase, platelet type	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (25)	0 (0)	8	4 (5.26)	-	-	-	-
PIK3CA	Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit alpha isoform	-	-	-	-	4 (50)	0 (0)	8	2 (3.08)	-	-	-	-	4 (40)	0 (0)	10	3 (2.63)	-	-	-	-	2 (50)	0 (0)	4	1 (0.826)
POLR2B	DNA-directed RNA polymerase II subunit RPB2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (66.7)	0 (0)	3	3 (3.95)	-	-	-	-
PRKAG2	5'-AMP-activated protein kinase subunit gamma-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0 (0)	4 (100)	4	2 (2.63)	-	-	-	-
PRLR	Prolactin receptor	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (66.7)	0 (0)	3	3 (2.48)
PTCH1	Protein patched homolog 1	-	-	-	-	4 (3.28)	95 (77.9)	122	21 (32.3)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PTCHD4	Patched domain-containing protein 4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (33.3)	0 (0)	6	3 (2.48)
RAB11FIP1	Rab11 family-interacting protein 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (50)	2 (50)	4	3 (3.95)	-	-	-	-
SERPINB2	Plasminogen activator inhibitor 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (0)	2 (66.7)	3	3 (3.95)	-	-	-	-
SETD2	Histone-lysine N-methyltransferase SETD2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0 (0)	6 (100)	6	1 (1.32)	-	-	-	-
SF3B1	Splicing factor 3B subunit 1	-	-	-	-	-	-	-	-	-	-	-	-	2 (100)	0 (0)	2	1 (0.877)	-	-	-	-	-	-	-	-
SGCA	Alpha-sarcoglycan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4 (100)	0 (0)	4	2 (1.65)
SMARCA4	Transcription activator BRG1	-	-	-	-	-	-	-	-	-	-	-	-	4 (30.8)	2 (15.4)	13	9 (7.89)	4 (36.4)	0 (0)	11	8 (10.5)	-	-	-	-
SMARCB1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1	7 (3.55)	188 (95.4	197	164 (90.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SPHKAP	A-kinase anchor protein SPHKAP	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (33.3)	0 (0)	6	3 (3.95)	-	-	-	-
SPTB	Spectrin beta chain, erythrocytic	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (50)	1 (0)	4	3 (3.95)	-	-	-	-
SUFU	Suppressor of fused homolog	-	-	-	-	0 (0)	5 (100)	5	3 (4.62)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SYNCRIP	Heterogeneous nuclear ribonucleoprotein Q	-	-	-	-	-	-	-	-	-	-	-	-	0 (0)	6 (100)	6	3 (2.63)	-	-	-	-	-	-	-	-
TCF4	Transcription factor 4	-	-	-	-	0 (0)	6 (100)	6	4 (6.15)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
TNXB	Tenascin-X	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (33.3)	0 (0)	6	4 (5.26)	-	-	-	-
TOP2B	DNA topoisomerase 2-beta	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (100)	0 (0)	2	1 (0.826)
TP53	Cellular tumor antigen p53	-	-	-	-	-	-	-	-	8 (7.92)	25 (24.8)	101	8 (100)	4 (15.4)	0 (0)	26	4 (3.51)	-	-	-	-	-	-	-	-
TRIML1	Probable E3 ubiquitin-protein ligase TRIML1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (0)	2 (66.7)	3	3 (3.95)	-	-	-	-
TTN	Titin	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (11.1)	0 (0)	18	4 (3.31)
ZMYM3	Zinc finger MYM-type protein 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (22.2)	6 (66.7)	9	6 (4.96)
ZNF462	Zinc finger protein 462	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0 (0)	4 (100)	4	3 (3.95)	-	-	-	-
ZRANB2	Zinc finger Ran-binding domain-containing protein 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0 (0)	4 (100)	4	2 (2.63)	-	-	-	-

Total PT: total number of patients

† : *Number of activating mutations at identical positions in the protein*

S2 Table

DG.name	GRP3_20-20Rule	GRP4_20-20Rule	SHH_20-20Rule	SHHTP53Mutant_20-20Rule	SHHWildtype_20-20Rule	WNT_20-20Rule
SMARCB1	NA	NA	NA	NA	NA	NA
NRAS	NA	NA	Oncogene	NA	Oncogene	NA
BRAF	NA	NA	NA	NA	NA	NA
TP53	NA	NA	Tumor Suppressor	Tumor Suppressor	NA	**Oncogene**
KMT2D	Tumor Suppressor	Tumor Suppressor	Tumor Suppressor	NA	Tumor Suppressor	Tumor Suppressor
PTCH1	NA	NA	Tumor Suppressor	NA	Tumor Suppressor	NA
KDM6A	Tumor Suppressor	Tumor Suppressor	NA	NA	NA	NA
CTDNEP1	Tumor Suppressor	NA	NA	NA	NA	NA
KMT2C	NA	Tumor Suppressor	NA	NA	NA	NA
ARID1A	NA	NA	NA	NA	NA	NA
PTEN	NA	NA	NA	NA	NA	NA
CTNNB1	NA	NA	NA	NA	NA	Oncogene
SUFU	NA	NA	Tumor Suppressor	NA	Tumor Suppressor	NA
DYNC1H1	Tumor Suppressor	NA	Oncogene	Oncogene	NA	NA
FCRL2	Tumor Suppressor	NA	NA	NA	NA	NA
SERPINB2	Tumor Suppressor	NA	NA	NA	NA	NA
RAB11FIP1	Tumor Suppressor	NA	NA	NA	NA	NA
TRIML1	Tumor Suppressor	NA	NA	NA	NA	NA
SETD2	Tumor Suppressor	NA	NA	NA	NA	NA
DDX60	Tumor Suppressor	NA	NA	NA	NA	NA
PCBP2	Tumor Suppressor	NA	NA	NA	NA	NA
PRKAG2	Tumor Suppressor	NA	NA	NA	NA	NA
ZRANB2	Tumor Suppressor	NA	NA	NA	NA	NA
ZNF462	Tumor Suppressor	NA	NA	NA	NA	NA
SMARCA4	Oncogene	NA	NA	NA	NA	Tumor Suppressor?
DNAH14	Oncogene	NA	NA	NA	NA	NA
PFKP	Oncogene	NA	NA	NA	NA	NA
ACAN	Oncogene	NA	NA	NA	NA	NA
AKAP9	Oncogene	NA	NA	NA	NA	NA
ATP12A	Oncogene	NA	NA	NA	NA	NA
DOCK8	Oncogene	NA	NA	NA	NA	NA
EPHB3	Oncogene	NA	NA	NA	NA	NA
HIVEP3	Oncogene	NA	NA	NA	NA	NA
OTOF	Oncogene	NA	NA	NA	NA	NA
POLR2B	Oncogene	NA	NA	NA	NA	NA
SPHKAP	Oncogene	NA	NA	NA	NA	NA
TNXB	Oncogene	NA	NA	NA	NA	NA
LRP1B	Oncogene	NA	NA	NA	NA	NA
SPTB	Oncogene	NA	NA	NA	NA	NA
GPAM	NA	Tumor Suppressor	NA	NA	NA	NA
CHD7	NA	Tumor Suppressor	NA	NA	NA	NA
KDM4C	NA	Tumor Suppressor	NA	NA	NA	NA
OTOGL	NA	Tumor Suppressor	NA	NA	NA	NA
ZMYM3	NA	Tumor Suppressor	NA	NA	NA	NA
KIAA1107	NA	Tumor Suppressor	NA	NA	NA	NA
PIK3CA	NA	Oncogene	Oncogene	NA	Oncogene	Oncogene
DNAJB9	NA	Oncogene	NA	NA	NA	NA
IFIT3	NA	Oncogene	NA	NA	NA	NA
CAST	NA	Oncogene	NA	NA	NA	NA
DNAH1	NA	Oncogene	NA	NA	NA	NA
FAT1	NA	Oncogene	NA	NA	NA	NA
KDM1A	NA	Oncogene	NA	NA	NA	NA
LRRK2	NA	Oncogene	NA	NA	NA	NA
MUC16	NA	Oncogene	NA	NA	NA	NA
PCDH9	NA	Oncogene	NA	NA	NA	NA
PRLR	NA	Oncogene	NA	NA	NA	NA
PTCHD4	NA	Oncogene	NA	NA	NA	NA
CDKN2A	NA	Oncogene	NA	NA	NA	NA
SGCA	NA	Oncogene	NA	NA	NA	NA
MUC4	NA	Oncogene	NA	NA	NA	NA
TOP2B	NA	Oncogene	NA	NA	NA	NA
DHX9	NA	Oncogene	NA	NA	NA	NA
CACNA1D	NA	Oncogene	NA	NA	NA	NA
TTN	NA	Not Classified	NA	NA	NA	NA
SF3B1	NA	NA	NA	NA	NA	Oncogene
EML4	NA	NA	Tumor Suppressor	NA	Tumor Suppressor	NA
BCOR	NA	NA	Tumor Suppressor	NA	Tumor Suppressor	NA
TCF4	NA	NA	Tumor Suppressor	NA	Tumor Suppressor	NA
LDB1	NA	NA	Tumor Suppressor	NA	Tumor Suppressor	NA
PBRM1	NA	NA	Tumor Suppressor	NA	Tumor Suppressor	NA
CR1	NA	NA	Tumor Suppressor	NA	Tumor Suppressor	NA
FBXW7	NA	NA	Oncogene	NA	Oncogene	Tumor Suppressor
IDH1	NA	NA	Oncogene	NA	Oncogene	Oncogene
DDX3X	NA	NA	Oncogene	NA	Oncogene	Oncogene
CUL1	NA	NA	Oncogene	NA	Oncogene	NA
GABRG1	NA	NA	Oncogene	NA	Oncogene	NA
PCDH11X	NA	NA	Oncogene	NA	Oncogene	NA
ALPK2	NA	NA	Oncogene	NA	Oncogene	NA
OR51L1	NA	NA	Oncogene	NA	Oncogene	NA
FGFR2	NA	NA	**Oncogene**	NA	**Oncogene**	NA
SYNCRIP	NA	NA	NA	NA	NA	Tumor Suppressor
CREBBP	NA	NA	NA	NA	NA	Tumor Suppressor
EPHA7	NA	NA	NA	NA	NA	Tumor Suppressor
ARID2	NA	NA	NA	NA	NA	Tumor Suppressor
CDH1	NA	NA	NA	NA	NA	Oncogene
CSNK2B	NA	NA	NA	NA	NA	Oncogene

Bold *classifications are classifications from SomInAClust that differed from the "20/20" Rule*

DG.name	GRP3_DG.Percent	GRP4_DG.Percent	SHH_DG.Percent	SHHTP53Mutant_DG.Percent	SHHWildtype_DG.Percent	WNT_DG.Percent
SMARCB1	NA	NA	NA	NA	NA	NA
NRAS	NA	NA	1.370	NA	1.538	NA
BRAF	NA	NA	NA	NA	NA	NA
TP53	NA	NA	10.959	100.000	NA	3.509
KMT2D	6.579	2.479	10.959	NA	12.308	3.509
PTCH1	NA	NA	28.767	NA	32.308	NA
KDM6A	3.947	11.570	NA	NA	NA	NA
CTDNEP1	3.947	NA	NA	NA	NA	NA
KMT2C	NA	4.132	NA	NA	NA	NA
ARID1A	NA	NA	NA	NA	NA	NA
PTEN	NA	NA	NA	NA	NA	NA
CTNNB1	NA	NA	NA	NA	NA	96.491
SUFU	NA	NA	4.110	NA	4.615	NA
DYNC1H1	3.947	NA	2.740	25.000	NA	NA
FCRL2	5.263	NA	NA	NA	NA	NA
SERPINB2	3.947	NA	NA	NA	NA	NA
RAB11FIP1	3.947	NA	NA	NA	NA	NA
TRIML1	3.947	NA	NA	NA	NA	NA
SETD2	1.316	NA	NA	NA	NA	NA
DDX60	2.632	NA	NA	NA	NA	NA
PCBP2	1.316	NA	NA	NA	NA	NA
PRKAG2	2.632	NA	NA	NA	NA	NA
ZRANB2	2.632	NA	NA	NA	NA	NA
ZNF462	3.947368421	NA	NA	NA	NA	NA
SMARCA4	10.526	NA	NA	NA	NA	7.895
DNAH14	5.263	NA	NA	NA	NA	NA
PFKP	5.263	NA	NA	NA	NA	NA
ACAN	3.947	NA	NA	NA	NA	NA
AKAP9	3.947	NA	NA	NA	NA	NA
ATP12A	3.947	NA	NA	NA	NA	NA
DOCK8	3.947	NA	NA	NA	NA	NA
EPHB3	3.947	NA	NA	NA	NA	NA
HIVEP3	3.947	NA	NA	NA	NA	NA
OTOF	3.947	NA	NA	NA	NA	NA
POLR2B	3.947	NA	NA	NA	NA	NA
SPHKAP	3.947	NA	NA	NA	NA	NA
TNXB	5.263157895	NA	NA	NA	NA	NA
LRP1B	3.947368421	NA	NA	NA	NA	NA
SPTB	3.947368421	NA	NA	NA	NA	NA
GPAM	NA	3.306	NA	NA	NA	NA
CHD7	NA	4.132	NA	NA	NA	NA
KDM4C	NA	2.479	NA	NA	NA	NA
OTOGL	NA	2.479	NA	NA	NA	NA
ZMYM3	NA	4.959	NA	NA	NA	NA
KIAA1107	NA	1.653	NA	NA	NA	NA
PIK3CA	NA	0.826	2.740	NA	3.077	2.632
DNAJB9	NA	2.479	NA	NA	NA	NA
IFIT3	NA	3.306	NA	NA	NA	NA
CAST	NA	2.479	NA	NA	NA	NA
DNAH1	NA	2.479	NA	NA	NA	NA
FAT1	NA	2.479	NA	NA	NA	NA
KDM1A	NA	2.479	NA	NA	NA	NA
LRRK2	NA	2.479	NA	NA	NA	NA
MUC16	NA	2.479	NA	NA	NA	NA
PCDH9	NA	2.479	NA	NA	NA	NA
PRLR	NA	2.479	NA	NA	NA	NA
PTCHD4	NA	2.479	NA	NA	NA	NA
CDKN2A	NA	0.826	NA	NA	NA	NA
SGCA	NA	1.653	NA	NA	NA	NA
MUC4	NA	1.653	NA	NA	NA	NA
TOP2B	NA	0.826	NA	NA	NA	NA
DHX9	NA	0.826	NA	NA	NA	NA
CACNA1D	NA	2.479338843	NA	NA	NA	NA
TTN	NA	3.306	NA	NA	NA	NA
SF3B1	NA	NA	NA	NA	NA	0.877
EML4	NA	NA	4.110	NA	4.615	NA
BCOR	NA	NA	5.479452055	NA	6.153846154	NA
TCF4	NA	NA	5.479452055	NA	6.153846154	NA
LDB1	NA	NA	5.479452055	NA	6.153846154	NA
PBRM1	NA	NA	2.739726027	NA	3.076923077	NA
CR1	NA	NA	1.369863014	NA	1.538461538	NA
FBXW7	NA	NA	1.369863014	NA	1.538461538	0.877192982
IDH1	NA	NA	1.370	NA	1.538	0.877
DDX3X	NA	NA	10.959	NA	12.308	16.667
CUL1	NA	NA	1.370	NA	1.538	NA
GABRG1	NA	NA	5.479	NA	6.154	NA
PCDH11X	NA	NA	2.739726027	NA	3.076923077	NA
ALPK2	NA	NA	4.109589041	NA	4.615384615	NA
OR51L1	NA	NA	2.739726027	NA	3.076923077	NA
FGFR2	NA	NA	1.369863014	NA	1.538461538	NA
SYNCRIP	NA	NA	NA	NA	NA	2.632
CREBBP	NA	NA	NA	NA	NA	3.509
EPHA7	NA	NA	NA	NA	NA	2.631578947
ARID2	NA	NA	NA	NA	NA	0.877192982
CDH1	NA	NA	NA	NA	NA	2.632
CSNK2B	NA	NA	NA	NA	NA	3.509

DG.name	GRP3_OG.Ratio	GRP3_TSG.Ratio	GRP4_OG.Ratio	GRP4_TSG.Ratio	SHH_OG.Ratio	SHH_TSG.Ratio	SHHTP53Mutant_OG.Ratio	SHHTP53Mutant_TSG.Ratio	SHHWildtype_OG.Ratio	SHHWildtype_TSG.Ratio	WNT_OG.Ratio	WNT_TSG.Ratio
SMARCB1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NRAS	NA	NA	NA	NA	1	0	NA	NA	1	0	NA	NA
BRAF	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TP53	NA	NA	NA	NA	0.079207921	0.247524752	0.079207921	0.247524752	NA	NA	0.153846154	0
KMT2D	0	0.833333333	0.222222222	0.555555556	0	0.939393939	NA	NA	0	0.939393939	0	0.6
PTCH1	NA	NA	NA	NA	0.032786885	0.778688525	NA	NA	0.032786885	0.778688525	NA	NA
KDM6A	0	1	0.083333333	0.75	NA	NA	NA	NA	NA	NA	NA	NA
CTDNEP1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
KMT2C	NA	NA	0	0.571428571	NA	NA	NA	NA	NA	NA	NA	NA
ARID1A	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PTEN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CTNNB1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.337962963	0
SUFU	NA	NA	NA	NA	0	1	NA	NA	0	1	NA	NA
DYNC1H1	0	0.666666667	NA	NA	1	0	1	0	NA	NA	NA	NA
FCRL2	0.333333333	0.333333333	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SERPINB2	0	0.666666667	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
RAB11FIP1	0.5	0.5	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TRIML1	0	0.666666667	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SETD2	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DDX60	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PCBP2	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRKAG2	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZRANB2	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF462	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SMARCA4	0.363636364	0	NA	NA	NA	NA	NA	NA	NA	NA	0.30769230B	0.153846154
DNAH14	0.25	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PFKP	0.25	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ACAN	0.222222222	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AKAP9	0.333333333	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ATP12A	0.5	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DOCK8	0.333333333	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EPHB3	0.666666667	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
HIVEP3	0.666666667	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
OTOF	0.25	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
POLR2B	0.666666667	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SPHKAP	0.333333333	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TNXB	0.333333333	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LRP1B	0.5	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SPTB	0.5	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GPAM	NA	NA	0	1	NA	NA	NA	NA	NA	NA	NA	NA
CHD7	NA	NA	0	1	NA	NA	NA	NA	NA	NA	NA	NA
KDM4C	NA	NA	0.285714286	0.428571429	NA	NA	NA	NA	NA	NA	NA	NA
OTOGL	NA	NA	0	1	NA	NA	NA	NA	NA	NA	NA	NA
ZMYM3	NA	NA	0.222222222	0.666666667	NA	NA	NA	NA	NA	NA	NA	NA
KIAA1107	NA	NA	0	1	NA	NA	NA	NA	NA	NA	NA	NA
PIK3CA	NA	NA	0.5	0	0.5	0	NA	NA	0.5	0	0.4	0
DNAJB9	NA	NA	1	0	NA	NA	NA	NA	NA	NA	NA	NA
IFIT3	NA	NA	0.5	0	NA	NA	NA	NA	NA	NA	NA	NA
CAST	NA	NA	0.4	0	NA	NA	NA	NA	NA	NA	NA	NA
DNAH1	NA	NA	0.5	0	NA	NA	NA	NA	NA	NA	NA	NA
FAT1	NA	NA	0.6	0	NA	NA	NA	NA	NA	NA	NA	NA
KDM1A	NA	NA	0.6	0	NA	NA	NA	NA	NA	NA	NA	NA
LRRK2	NA	NA	0.333333333	0	NA	NA	NA	NA	NA	NA	NA	NA
MUC16	NA	NA	0.333333333	0	NA	NA	NA	NA	NA	NA	NA	NA
PCDH9	NA	NA	0.666666667	0	NA	NA	NA	NA	NA	NA	NA	NA
PRLR	NA	NA	0.666666667	0	NA	NA	NA	NA	NA	NA	NA	NA
PTCHD4	NA	NA	0.333333333	0	NA	NA	NA	NA	NA	NA	NA	NA
CDKN2A	NA	NA	0.25	0	NA	NA	NA	NA	NA	NA	NA	NA
SGCA	NA	NA	1	0	NA	NA	NA	NA	NA	NA	NA	NA
MUC4	NA	NA	1	0	NA	NA	NA	NA	NA	NA	NA	NA
TOP2B	NA	NA	1	0	NA	NA	NA	NA	NA	NA	NA	NA
DHX9	NA	NA	1	0	NA	NA	NA	NA	NA	NA	NA	NA
CACNA1D	NA	NA	0.4	0	NA	NA	NA	NA	NA	NA	NA	NA
TTN	NA	NA	0.111111111	0	NA	NA	NA	NA	NA	NA	NA	NA
SF3B1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1	0
EML4	NA	NA	NA	NA	0	0.666666667	NA	NA	0	0.666666667	NA	NA
BCOR	NA	NA	NA	NA	0	1	NA	NA	0	1	NA	NA
TCF4	NA	NA	NA	NA	0	1	NA	NA	0	1	NA	NA
LDB1	NA	NA	NA	NA	0	0.4	NA	NA	0	0.4	NA	NA
PBRM1	NA	NA	NA	NA	0	1	NA	NA	0	1	NA	NA
CR1	NA	NA	NA	NA	0	1	NA	NA	0	1	NA	NA
FBXW7	NA	NA	NA	NA	0.5	0	NA	NA	0.5	0	0	1
IDH1	NA	NA	NA	NA	1	0	NA	NA	1	0	1	0
DDX3X	NA	NA	NA	NA	0.333333333	0	NA	NA	0.333333333	0	0.228571429	0
CUL1	NA	NA	NA	NA	1	0	NA	NA	1	0	NA	NA
GABRG1	NA	NA	NA	NA	1	0	NA	NA	1	0	NA	NA
PCDH11X	NA	NA	NA	NA	0.285714286	0	NA	NA	0.285714286	0	NA	NA
ALPK2	NA	NA	NA	NA	0.666666667	0	NA	NA	0.666666667	0	NA	NA
OR51L1	NA	NA	NA	NA	1	0	NA	NA	1	0	NA	NA
FGFR2	NA	NA	NA	NA	0	0	NA	NA	0	0	NA	NA
SYNCRIP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	1
CREBBP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.4	0.6
EPHA7	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.333333333	0.5
ARID2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	1
CDH1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.666666667	0
CSNK2B	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.5	0

S3 File

		% Patients Affected	OncodriveCLUST	OncodriveFM	SomInAClust
AT/RT	SMARCB1	90.1			
	BRAF	2.75			
	NRAS	0.549			
Group 3	SMARCA4	10.5			
	KMT2D	6.58			
	DNAH14	5.26			
	FCRL2	5.26			
	PFKP	5.26			
	TNXB	5.26			
	SERPINB2	3.95			
	KDM6A	3.95			
	ACAN	3.95			
	AKAP9	3.95			
	ATP12A	3.95			
	DOCK8	3.95			
	EPHB3	3.95			
	HIVEP3	3.95			
	OTOF	3.95			
	POLR2B	3.95			
	RAB11FIP1	3.95			
	SPHKAP	3.95			
	TRIML1	3.95			
	CTDNEP1	3.95			
	DYNC1H1	3.95			
	LRP1B	3.95			
	SPTB	3.95			
	ZNF462	3.95			
	DDX60	2.63			
	PRKAG2	2.63			
	ZRANB2	2.63			
	SETD2	1.32			
	PCBP2	1.32			
Group 4	KDM6A	11.6			
	ZMYM3	4.96			
	CHD7	4.13			
	KMT2C	4.13			
	GPAM	3.31			
	IFIT3	3.31			
	TTN	3.31			
	DNAJB9	2.48			
	KDM4C	2.48			
	CAST	2.48			
	DNAH1	2.48			
	FAT1	2.48			
	KDM1A	2.48			
	LRRK2	2.48			
	MUC16	2.48			
	OTOGL	2.48			
	PCDH9	2.48			
	PRLR	2.48			
	PTCHD4	2.48			
	KMT2D	2.48			
	CACNA1D	2.48			
	SGCA	1.65			
	MUC4	1.65			
	KIAA1107	1.65			
	PIK3CA	0.826			
	CDKN2A	0.826			
	TOP2B	0.826			
	DHX9	0.826			

		% Patients Affected	OncodriveCLUST	OncodriveFM	SomInAClust
SHH TP53 Mutant	TP53	100			
	DYNC1H1	25			
SHH Wildtype	PTCH1	32.3			
	DDX3X	12.3			
	KMT2D	12.3			
	GABRG1	6.15			
	BCOR	6.15			
	TCF4	6.15			
	LDB1	6.15			
	SUFU	4.62			
	ALPK2	4.62			
	EML4	4.62			
	OR51L1	3.08			
	PIK3CA	3.08			
	PBRM1	3.08			
	PCDH11X	3.08			
	FBXW7	1.54			
	IDH1	1.54			
	CR1	1.54			
	FGFR2	1.54			
	NRAS	1.54			
	CUL1	1.54			
WNT	CTNNB1	96.5			
	DDX3X	16.7			
	SMARCA4	7.89			
	CREBBP	3.51			
	CSNK2B	3.51			
	TP53	3.51			
	KMT2D	3.51			
	PIK3CA	2.63			
	SYNCRIP	2.63			
	CDH1	2.63			
	EPHA7	2.63			
	IDH1	0.877			
	FBXW7	0.877			
	SF3B1	0.877			
	ARID2	0.877			

Legend

- *1.00E-05*
- *q ≤ 0.05*
- *NA*
- *"20/20" only*

S3 Table: Tabulated functions of identified putative driver genes

SHH Subtype (Green = novel; highlighted = unique to a subtype)

Driver Gene Name	Reference(s)	Additional Comments	Function
PTCH1	[1,2]	-	SHH receptor that associates with the smoothened protein (SMO) to transduce the hedgehog's proteins signal. Seems to have a tumor suppressor function. PTCH1 and SMO are both augmented in astrocytes. Involved in the development of the brain and face, which depends on X-linked inhibitory apoptosis mediation of PTCH1-regulated cell survival and apoptosis during embryogenesis.
DDX3X	[1,2]	-	ATP-dependent RNA helicase involved in several steps of gene expression, including transcription, mRNA maturation, mRNA export and translation.
KMT2D	[2]	-	Histone methyltransferase that methylates 'Lys-4' of histone H3 (H3K4me). H3K4me represents a tag for epigenetic transcriptional activation. Decreased levels of of KMT2D result in inhibited cancer cell proliferation and defective cell migration.
TP53	[1,2]	-	Tumor-suppressor gene involved in many cellular processes like cell cycle regulation, apoptosis, and Notch signaling. Potently limits the growth of immature and mature neurons when under cellular stress. Excessive p53 function has been implicated in neural tube defects, embryonic lethality, and neuronal degradation.
BCOR	[2]	-	Transcriptional corepressor that specifically inhibits gene expression when recruited to promoter regions by sequence-specific DNA-binding proteins. This repression may be mediated in part by histone deacetylase activities. BCOR plays a role in the gene expression regulation early in the differentiation of the embryonic stem cells.
GABRG1	[1]	Mutation mentioned, but not classified as a driver gene [2]	GABA, the major inhibitory neurotransmitter in the vertebrate brain, mediates neuronal inhibition by opening an integral chloride channel.
LDB1	[2]	-	Binds to the LIM domain of many LIM domain-containing transcription factors. It regulates the transcriptional activity of these associated proteins by determining specific partner interactions. It has been shown to play a role in the development of interneurons and motor neurons.
TCF4	[2]	-	Transcription factor that binds to the immunoglobulin enchancer Mu-E5/KE5-motif. It helps initiate neuronal differentiation and can activate transcription.

S3 Table: Tabulated functions of identified putative driver genes

ALPK2	[1]	-	Kinase that recognizes phosphorylation sites where surrounding peptides have an alpha-helical conformation.
EML4	-	-	May make microtubules slightly longer, but more dynamic. It is a highly developmentally regulated gene with high expression in the developing nervous system.
SUFU	-	Mutation mentioned, but not classified as a driver gene [2]	Negative regulator of the hedgehog signaling pathway. Decreases activity of GLI1-mediated transactivation of target genes and GLI2-mediated transactivation of target genes.
DYNC1H1	[1]	-	Cytoplasmic dynein 1, acts as a motor for the retrograde motility of vesicles and organelles along microtubules.
OR51L1	-	-	Odorant receptor initiates a neuronal response that triggers the perception of smell.
PBRM1	-	-	Involved in transcriptional activation and repression of some genes through chromatin remodeling.
PCDH11X	-	-	A calcium-dependent cell-adhesion protein that is responsible for cell-cell interactions during development of the CNS.
PIK3CA	[1]	-	Recruits PH domain-containing proteins to the membrane and activates signaling cascades involved in cell growth. Mutations of PIK3CA in an embryo can result in developmental birth defects.
CR1	-	-	The gene encodes a monomeric type I membrane glycoprotein that mediates cellular binding to particles and immune complexes. It acts as a negative regulator of the complement cascade, mediate immune adherence and phagocytosis.
CUL1	-	-	This protein plays an important role in protein degradation and protein ubiquitination. This is an essential component of the SCF (SKP1-CUL1-F-box protein) E3 ubiquitin ligase complex that regulates the ubiquitination of proteins involved in cell cycle progression and transcription.
FBXW7	-	-	Substrate recognition component of the SCF (SKP1-CUL1-F-box protein) E3 ubiquitin-protein ligase complex. This complex regulates the ubiquitination and subsequent proteasomal degradation of target proteins. It recognizes and binds phosphorylated sites within target proteins and then brings them to the SCF complex for ubiquitination.

S3 Table: Tabulated functions of identified putative driver genes

FGFR2	-	-	Upon ligand binding, FGFRs induce intracellular signaling networks which regulate processes like cell proliferation, survival, migration, and differentiation. Aberrant FGFR signaling can alter tissue.
IDH1	-	-	Isocitrate dehydrogenase facilitates the oxidation of isocitrate to oxalosuccinate. IDH is the rate-limiting enzyme of the citric acid cycle.
NRAS	-	-	The encoded proteins are involved in Golgi-to-endoplasmic reticulum (ER) retrograde transport.

WNT Subtype

Driver Gene Name	Reference(s)	Additional Comments	Function
CTNNB1	[1,2]	-	An important constituent of the canonical Wnt signaling pathway. In the absence of Wnt, it forms a complex with AXIN1, AXIN2, APC, CSNK1A1 and GSK3B that promotes phosphorylation and ubiquitination of CTNNB1. In the presence of Wnt, CTNNB1 is not ubiquitinated and accumulates in the nucleus, where it acts as a coactivator for transcription factors of the TCF/LEF family, leading to the activation of Wnt responsive genes. It is involved in the regulation of cellular adhesion.
DDX3X	[1,2]	-	ATP-dependent RNA helicase involved in several steps of gene expression, including transcription, mRNA maturation, mRNA export and translation.
SMARCA4	[1,2]	-	Chromatin remodeling enzyme that is involved oligodendrocytes differentiation. Fucntions as a transcriptional coactivator by cooperating with nuclear hormone receptors to potentiate transcriptional activation. It is part of the CREST-BRG1 complex that regulates promoter activation. Regulates E-cadherin transcription and helps induce epithelial-mesenchymal transitioning (EMT) by ZEB1.AKAP
CREBBP	[1]	Mutation mentioned, but not classified as driver gene [2]	The encoded protein acetylates histones, tagging for transcriptional activation. It also acetylates non-histone proteins and binds specifically to phosphorylated CREB. It enhances the transcriptional activity of cAMP-responsive genes.
CSNK2B	[1]	Mutation mentioned, but not classified as driver gene [2]	Regulates the basal catalytic activity of the alpha subunit in the Wnt pathway.
KMT2D	[2]	-	Histone methyltransferase that methylates 'Lys-4' of histone H3 (H3K4me). H3K4me represents a tag for epigenetic transcriptional activation. Decreased

S3 Table: Tabulated functions of identified putative driver genes

			levels of of KMT2D result in inhibited cancer cell proliferation and defective cell migration.
TP53	[2]	-	Tumor-suppressor gene involved in many cellular processes like cell cycle regulation, apoptosis, and Notch signaling. Potently limits the growth of immature and mature neurons when under cellular stress. Excessive p53 function has been implicated in neural tube defects, embryonic lethality, and neuronal degradation.
CDH1	[1]	-	Calcium-dependent cell adhesion protein that regulates cell-cell adhesions, mobility and proliferation of epithelial cells.
EPHA7	-	-	This receptor tyrosine kinase binds to GPI-anchored ephrin-A family ligands residing on adjacent cells. It regulates brain development through a caspase-dependent proapoptotic activity.
PIK3CA	[1]	-	Recruits PH domain-containing proteins to the membrane and activates signaling cascades involved in cell growth. Mutations of PIK3CA in an embryo can result in developmental birth defects.
SYNCRIP	-	-	The encoded protein is a heterogenous nuclear ribonucleoprotein (hnRNP) that is implicated in mRNA processing mechanisms.
ARID2	-	-	Participates in the transcriptional activation and repression of particular genes through chromatin remodeling. It is essential for the stability of the SWI/SNF chromatin remodeling complex and is potentially involved in targeting the complex to different genes.
FBXW7	-	-	Substrate recognition component of the SCF (SKP1-CUL1-F-box protein) E3 ubiquitin-protein ligase complex. This complex regulates the ubiquitination and subsequent proteasomal degradation of target proteins. It recognizes and binds phosphorylated sites within target proteins and then brings them to the SCF complex for ubiquitination.
IDH1	-	-	Isocitrate dehydrogenase facilitates the oxidation of isocitrate to oxalosuccinate. IDH is the rate-limiting enzyme of the citric acid cycle.
SF3B1	[1]	-	The splicing factor 3b protein complex can interact with splicing factor 3a and a 12S RNA unit to form a small nuclear ribonucleoproteins complex that binds to pre-mRNA upstream of the intron in a sequence-independent way and may anchor the snRNP to the pre-mRNA.

S3 Table: Tabulated functions of identified putative driver genes

Group 3 Medulloblastoma

Driver Gene Name	Reference(s)	Additional Comments	Function
SMARCA4	[3]	SMARCA4 is also a DG in WNT in Robinson *et al.* paper	Chromatin remodeling enzyme that is involved oligodendrocytes differentiation. Fucntions as a transcriptional coactivator by cooperating with nuclear hormone receptors to potentiate transcriptional activation. It is part of the CREST-BRG1 complex that regulates promoter activation. Regulates E-cadherin transcription and helps induce epithelial-mesenchymal transitioning (EMT) by ZEB1.
KMT2D (MLL2)	[4,5]	KMT2D was reported as a DG in Gijjar *et al.*, but as only mutated in Kijima *et al.*	Histone methyltransferase that methylates 'Lys-4' of histone H3 (H3K4me). H3K4me represents a tag for epigenetic transcriptional activation.
DNAH14	[6]	-	Dynein heavy chain of a motor protein for motile cilia. No mention of brain function.
FCRL2	[7]	-	Potential regulatory role in normal and neoplastic B cell development. SH3/SH2 adaptor activity.
PFKP	[8]	PFKP in Robinson *et al.* paper was identified in group 4 and WNT	Catalyzes the phosphorylation of D-fructose 6-phosphate to fructose 1,6-bisphosphate by ATP, the first step of glycolysis.
TNXB	[9]	Mentioned in Northcott *et al*. as mutated, but not as driver gene.	Mediate interactions between cells and their surrounding extracellular matrix. A substrate-adhesion molecule that inhibits cell migration and a potential role in supporting epithelial tumor growth.

S3 Table: Tabulated functions of identified putative driver genes

ACAN	[10]	-	A major component of extracellular matrix that binds to hyaluronic acid via an N-terminal globular region, to metal ions, and carbohydrates.
AKAP9	[11]	-	Scaffolding protein that assembles protein kinases and phosphatases on the centrosome and Golgi apparatus. Help maintain the Golgi apparatus integrity. Required for microtubule nucleation.
ATP12A	[12]	-	Catalyzes the hydrolysis of ATP coupled with the exchange of H^+ and K^+ ions across the plasma membrane. Aids in potassium absorption in different tissue types.
CTDNEP1	[13]	CTDNEP1 listed as novel driver gene in Gijjar *et al.* and Vriend *et al.*	Serine/threonine protein phosphatase that forms an active phosphatase complex with CNEP1R1.
DYNC1H1	[14]	DYNC1H1 is a novel driver gene for SHH subtype	Cytoplasmic dynein 1, acts as a motor for the retrograde motility of vesicles and organelles along microtubules.
DOCK8	[15]	-	Potential guanine nucleotide exchange factor (GEF). Involved in NK-mediated cytotoxicity by regulating the polarization of microtubule-organizing center (MTOC), and possibly controlling CCDC88B-mediated lytic granule transport to MTOC during cell killing.
EPHB3	[16]	-	Receptor tyrosine kinase that binds to transmembrane ephrin-B family ligands on adjacent cells, causing contact-dependent bidirectional signaling in neighboring cells. Functions in axon guidance during development, development and maturation of dendritic spine, and the formation of excitatory synapses. Controls

S3 Table: Tabulated functions of identified putative driver genes

			other aspects of development by regulating cell migration, angiogenesis, palate development and thymic epithelium development.
HIVEP3	[17–19]	-	Plays a role of transcription factor. Involved in cell growth. Strongly inhibits TNF-alpha-induced NF-kappa-B activation by interacting with TRAF. Homologue of the mouse Krc, whose overexpression inhibited, while antisense or dominant-negative Krc enhanced, NF-kappa-B-dependent transactivation and JNK phosphorylation and consequently inhibited apoptosis and cytokine gene expression. In T cells, Krc was induced by T cell signaling and enhanced IL2 production. CD4 T cells from $Krc^{-/-}$mice produced significantly less IL2 after TCR stimulation but were able to respond to exogenous IL2.
KDM6A	[20,21]	-	Histone demethylase that demethylates 'Lys-27' of histone H3. It mediates the removal of repressive trimethyls to mediate chromatin accessibility for transcription. Plays a central role in regulating posterior development.
LRP1B	[22]	LRP1B as a novel driver gene in Gijjar *et al.*	Cell surface proteins involved in receptor-mediated endocytosis.
OTOF	[23]	-	Important calcium ion sensor involved in the fusion of synaptic vesicle-plasma membrane and controls neurotransmitter release at these synapses.
POLR2B	[24]	-	A large component of RNA polymerase II that catalyzes DNA transcription into RNA. Believed to contribute to the polymerase catalytic activity.
RAB11FIP1	[25]	RAB11FIP1 is also present in group 4 in Robinson *et al.*paper	A Rab11 effector protein involved in the recycling process of endosomes and membrane trafficking along the phagocytic pathway and in phagocytosis.
SERPINB2	[26,27]	-	Inhibitor of the urokinase-type plasminogen activator. Functions as a serine protease inhibitor.

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SPHKAP	[28,29]	-	Anchoring protein that binds preferentially to the type I regulatory subunit of c-AMP-dependent protein kinase (PKA type I) to target it to distinct subcellular compartments.
SPTB	[30,31]	Listed in Northcott et al., but not as driver gene.	Spectrin beta, which along with ankyrin plays a role in cell membrane organization and stability. Involved in axon guidance.
TRIML1	[32]	-	Potential E3 ubiquitin-protein ligase, which plays an important role in the development of the blastocyst.
ZNF462	[33]	-	Involved in DNA and metal ion binding; a potential role in transcriptional regulation.
DDX60	[34]	DDX60 also found in group 4 in Robinson *et al.*paper	Positively regulates type I interferon and interferon inducible gene expression in response to viral infection.
PRKAG2	[35,36]	PRKAG2 is a was a novel driver gene for SHH subtype but found in Robinson *et al.*paper	AMP/ATP-binding subunit of AMP-activated protein kinase (AMPK). Functions as an energy sensor protein kinase, which has a key role in regulating cellular energy metabolism.
ZRANB2	[37]	-	Important splice factor for alternative splicing of TRA2B/SFRS10 transcripts.
PCBP2	[38,39]	-	Single-stranded nucleic acid binding protein, which binds preferentially to oligo dC. Negatively regulates antiviral responses mediated by mitochondrial antiviral-signaling protein (MAVS) and acts as an adapter between MAVS and the E3 ubiquitin ligase ITCH, thereby inducing MAVS ubiquitination and degradation.
SETD2	[40,41]	-	Histone methyltransferase that tri-methylates 'Lys-36' of histone H3 (H3K36me3) using di-methylated 'Lys-36' (H3K36me2) as substrate. H3K36me3 is a specific tag for epigenetic transcriptional activation and plays an essential role in the

S3 Table: Tabulated functions of identified putative driver genes

			maintenance of a heterochromatic state via the recruitment of DNA methyltransferase DNMT3A.

Group 4 Medulloblastoma

Driver Gene Name	Reference(s)	Additional Comments	Function
KDM6A	[20]	-	Histone demethylase that demethylates 'Lys-27' of histone H3. Plays a central role in regulating posterior development.
ZMYM3	[42,43]	Only mentioned as mutated in 3% of cases in Chiang et al.	Plays a role in the regulation of cellular morphology and organization of the cytoskeleton. Found to play a supportive role in the cell's ability to repair damaged DNA.
CHD7	[44]	Only mentioned as mutated in Massimoso et al. and Chiang et al.	Probable transcription regulator.
KMT2C (previously MLL3)	[45]	-	Histone methyltransferase of 'Lys-4' of histone H3. This methylation represents a specific tag for epigenetic transcriptional activation. KMT2C is a central component of the MLL2/3 complex, which is involved in transcriptional coactivation. KMT2C/MLL3 is a potential catalytic subunit of this complex.
GPAM	[46,47]	-	Esterifies acyl-group from acyl-ACP to the sn-1 position of glycerol-3-phosphate, which is an essential step in glycerolipid biosynthesis.

S3 Table: Tabulated functions of identified putative driver genes

IFIT3	[48,49]	-	IFN-induced antiviral protein. It acts as an inhibitor of cellular and viral processes such as cell migration, proliferation, signaling, and viral replication. Exhibits an antiproliferative activity through the up-regulated expression of the cell cycle negative regulators CDKN1A/p21 and CDKN1B/p27.
TTN	[50]	-	In non-muscle cells it seems to play a role in the condensation and segregation of chromosomes during mitosis.
CACNA1D	[51,52]	-	Voltage-sensitive calcium channels (VSCC) that are involved in a variety of calcium-dependent processes, including muscle contraction, hormone or neurotransmitter release, gene expression, cell division, cell motility, and cell death.
CAST	[53]	-	The protein encoded by this gene is an endogenous calpain (calcium-dependent cysteine protease) inhibitor. It is involved in the proteolysis of amyloid precursor protein. The calpain/calpastatin system is involved in numerous membrane fusion events, such as neural vesicle exocytosis and platelet and red-cell aggregation. The encoded protein is also thought to affect the expression levels of genes encoding structural or regulatory proteins.
DNAH1	[54,55]	-	Force generating protein of respiratory cilia. Produces force towards the minus ends of microtubules. Dynein has ATPase activity; the force-producing power stroke is thought to occur on release of ADP. Involved in sperm motility; implicated in sperm flagellar assembly.
DNAJB9	[56]	-	Involved in endoplasmic reticulum-associated degradation (ERAD) of misfolded proteins. Acts as a co-chaperone with an Hsp70 protein.
FAT1	[57]	-	Low expression of FAT1 has been correlated with negative outcomes in medulloblastoma patients. Plays an essential role for cellular polarization, directed cell migration and modulating cell-cell contact.

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KDM1A	[58,59]	-	Histone demethylase that demethylates both 'Lys-4' (H3K4me) and 'Lys-9' (H3K9me) of histone H3. Thus, acts as a coactivator or a corepressor, depending on the context. Required for gastrulation during embryogenesis and a potential role in the repression of neuronal genes.
KDM4C	[60,61]	Listed as recurrently mutated in Northcott *et al.*	Histone demethylase that specifically demethylates 'Lys-9' and 'Lys-36' residues of histone.
KMT2D (MLL2)	[4,5]	KMT2D was reported as a driver gene in Gijjar *et al.*, but as only mutated in Kijima *et al.*	Histone methyltransferase that methylates 'Lys-4' of histone H3 (H3K4me). H3K4me represents a tag for epigenetic transcriptional activation. Decreased levels of of KMT2D result in inhibited cancer cell proliferation and defective cell migration.
LRRK2	[62,63]	-	Positive regulator of autophagy through a calcium-dependent activation of the CaMKK/AMPK signaling pathway. In intact central nervous system, LRRK2 is involved in the regulation neuronal morphologic processes. Plays a role in synaptic vesicle trafficking and a potential role in the phosphorylation of proteins central to Parkinson disease.
MUC16	[64,65]	-	Interact with beta-catenin through c-terminal region resulting in the subsequent activation of WNT pathway.
OTOGL	[66,67]	-	Expressed in the inner ear with highest reported expression being during embryonic development and lowest in adults.
PCDH9	[68,69]	-	Downregulated expression was noticed in metastatic gastric and hepatocellular carcinoma. It was shown to regulate epithelial to mesenchymal transitioning by increasing the activity of GSK-3β and inhibiting Snail1.
PRLR	[70,71]	-	A receptor for the anterior pituitary hormone prolactin (PRL).

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PTCHD4	[72]	-	Previously known as *PTCH53, a*cts as a potential repressor of the canonical hedgehog signaling by antagonizing the effects of SMO.
KIAA1107	[73]	-	AP2-interacting clathrin-endocytosis protein (APache)
MUC4	[74,75]	-	A suggested role in tumor progression and an ability to promote tumor growth by repressing of apoptosis. Involved in cell proliferation and differentiation of epithelial cells via the induction of specific phosphorylation of ERBB2. The MUC4-ERBB2 complex results in site-specific phosphorylation of the ERBB2 'Tyr-1248'. MUC4-ERBB2-ERBB3-NRG1 complex formation leads down-regulated CDKN1B and results in the repression of apoptosis and stimulation of proliferation.
SGCA	[76,77]	-	A component of the sarcoglycan complex, which is a subcomplex of the dystrophin-glycoprotein complex that links the F-actin cytoskeleton to the extracellular matrix.
TOPB2	[78,79]	-	Releases DNA supercoiling and torsional tension introduced during the DNA replication and transcription, by transiently cleaving and rejoining one strand of the DNA duplex. Introduces a single-strand break via transesterification at a target site in duplex DNA.
PIK3CA	[1,80,81]	-	Recruits PH domain-containing proteins to the membrane and activates signaling cascades involved in cell growth. Mutations of PIK3CA in an embryo can result in developmental birth defects.
DHX9	[82]	-	Unwinds double-stranded DNA and RNA in a 3' to 5' direction. Functions as a transcriptional activator. Component of the CRD-mediated complex that promotes MYC mRNA stability. Positively regulates HIV-1 LTR-directed gene expression.
CDKN2A	[83]	-	Acts as a negative regulator of normal cell proliferation by interacting strongly with CDK4 and CDK6, which inhibits their ability to interact with cyclins D and phosphorylate the retinoblastoma protein.

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Functions were mostly obtained from UniprotKB: https://www.uniprot.org/, NCBI: https://www.ncbi.nlm.nih.gov/gene/, and reactome: https://reactome.org/. Further information on function can be found in the cited papers.

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		SHH Wildtype (65)	SHH TP53 (8)	WNT (114)	Group 3 (76)	Group 4 (121)
Age						
	0-5yrs	19 (29)	-	1 (0.88)	18 (24)	10 (8.3)
	6-15yrs	16 (25)	6 (75)	30 (26)	17 (22)	56 (46)
	16+ years	3 (4.6)	-	4 (3.5)	1 (1.3)	2 (1.7)
	Not Available	27 (42)	2 (25)	79 (69)	40 (53)	53 (44)
Gender						
	Male	34 (39.1)	3 (37.5)	44 (38.6)	54 (71.1)	84 (69.4)
	Female	29 (33.3)	5 (62.5)	63 (55.3)	21 (27.6)	36 (29.8)
	Not Available	24 (27.6)	-	7 (6.1)	1 (1.3)	1 (0.8)
Histology						
	Classic	17 (26)	2 (25)	37 (32)	46 (61)	86 (71)
	Desmoplastic	28 (43)	-	-	5 (6.6)	2 (1.7)
	Large Cell	11 (17)	5 (62)	2 (1.8)	16 (21)	12 (9.9)
	Medullomyoblastoma	4 (6.2)	1 (12)	5 (4.4)	6 (7.9)	19 (16)
	Melatonic	1 (1.5)	-	-	-	-
	Not Available	4 (6.2)	-	70 (61)	3 (3.9)	2 (1.7)
Sample Somatic Mutations						
	Synonymous Mutations	330	44	123	424	365
	Non-Synonymous Mutations	1081	207	726	1403	1169
	Tumors with NS DGs	43 (66)	8 (100)	114 (100)	27 (36)	58 (48)
	NS DG Mutations	224	107	345	123	162
	Average DG Mutations	3.72	12.88	3.03	1.62	1.34
	STDEV DG Mutations	4.35	4.91	2.45	3.30	1.99

S4 Table. Patient demographics, histology, and somatic mutations of medulloblastoma subgroups. Numbers in parenthesis under each subgroup indicate sample size. Numbers in parenthesis for other cells indicate percentages. NS = Non-synonymous, DG = putative driver gene.