Heatmap of selected gene markers across NMF subgroups
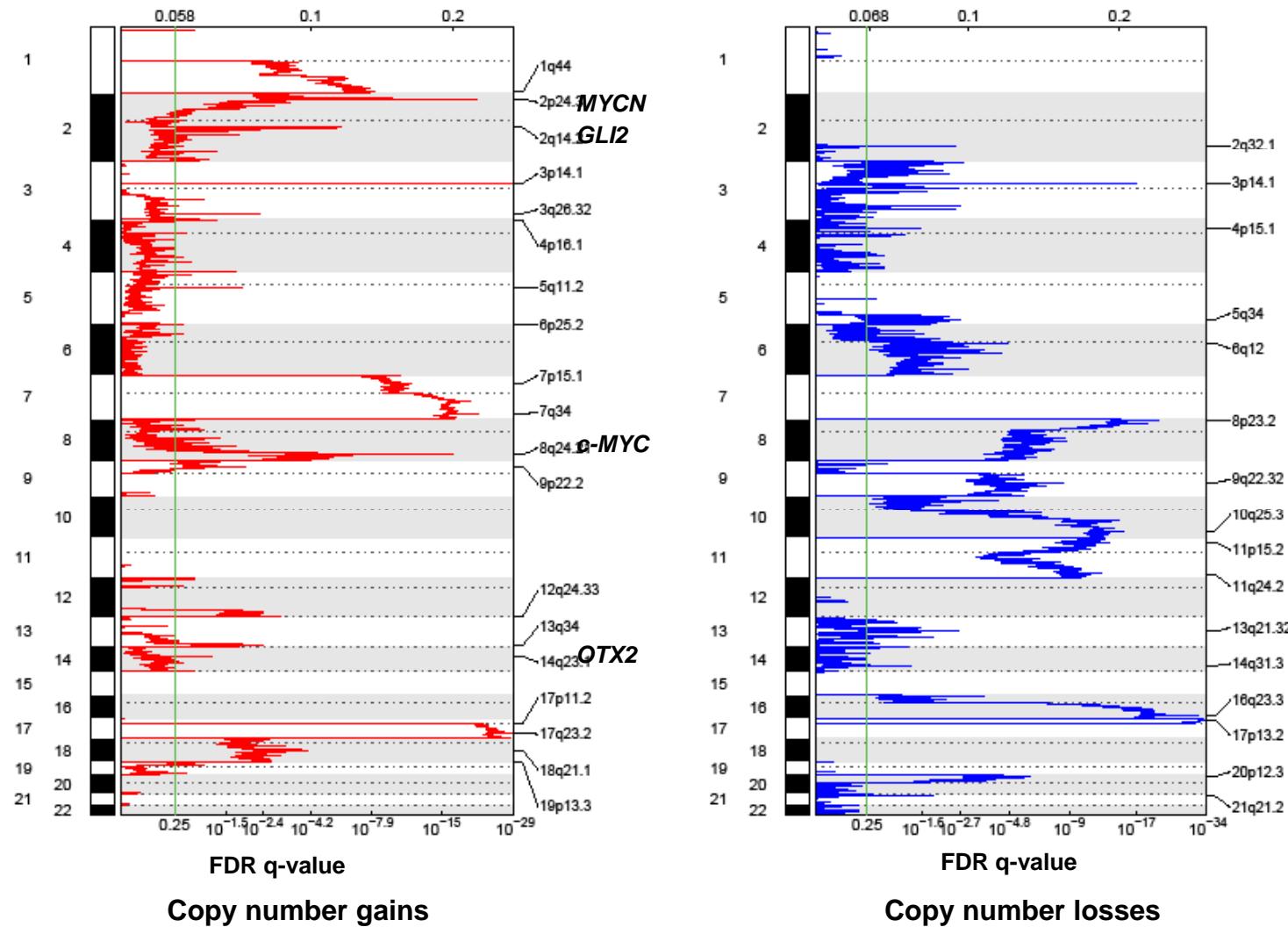
Representative 'c4' subgroup tumors immunostained with anti-CRX (red) and anti-GRM8 (brown) reveal 'mixed' subpopulations of 'photoreceptor/GABAergic' and 'neuronal/glutamatergic' cells
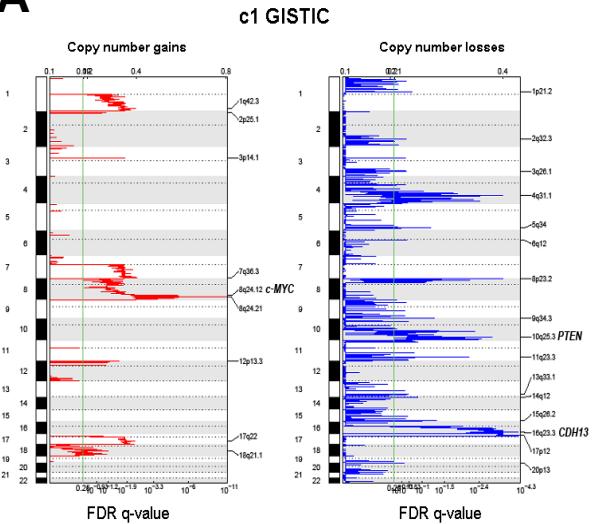
GISTIC analysis for all medulloblastoma samples
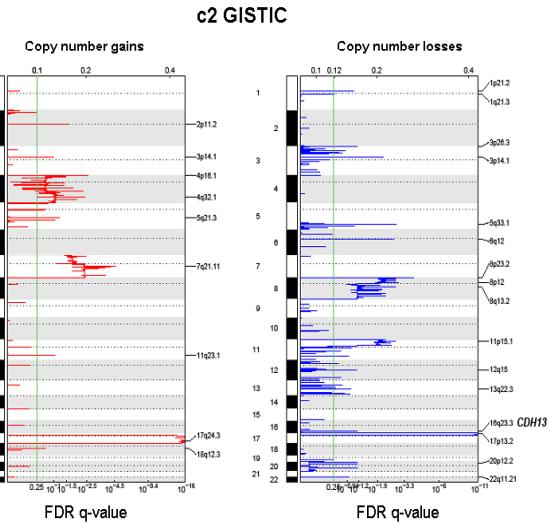
Copy number gains

Copy number losses

Supplementary Figure S4

A c1 GISTIC

B c2 GISTIC

C c3 GISTIC

D c4 GISTIC

E c5 GISTIC

F c6 GISTIC
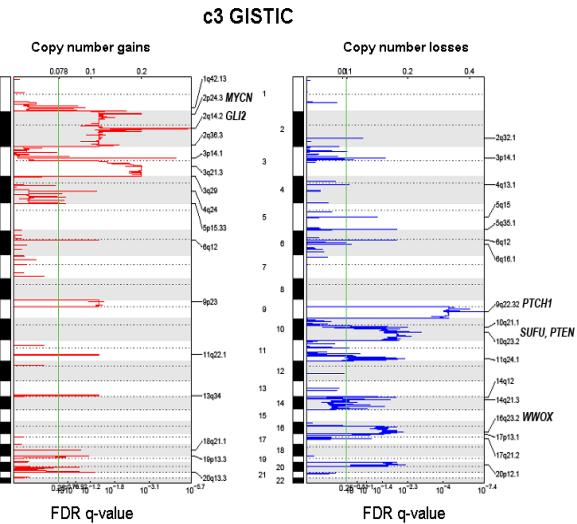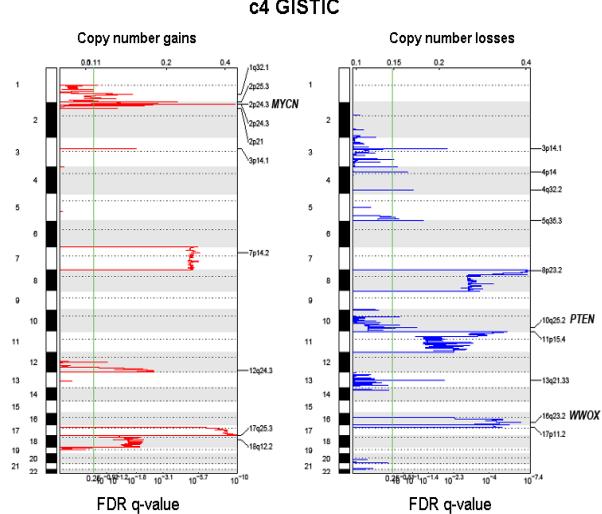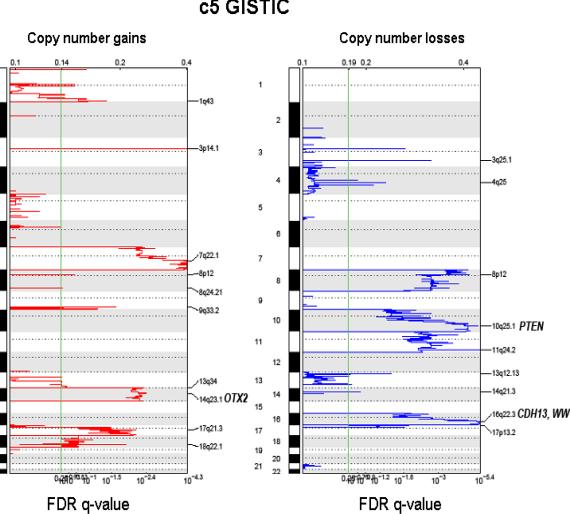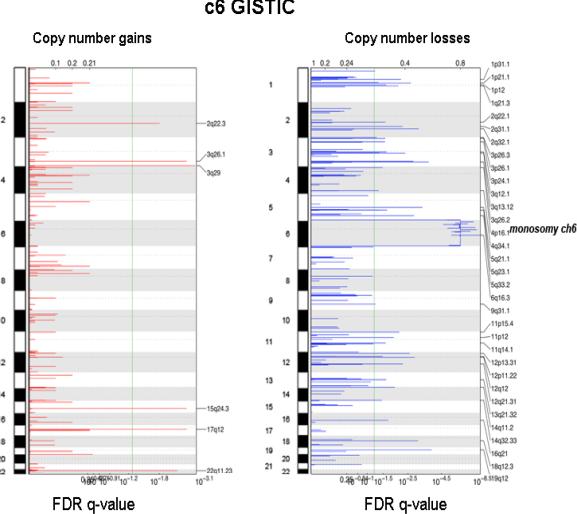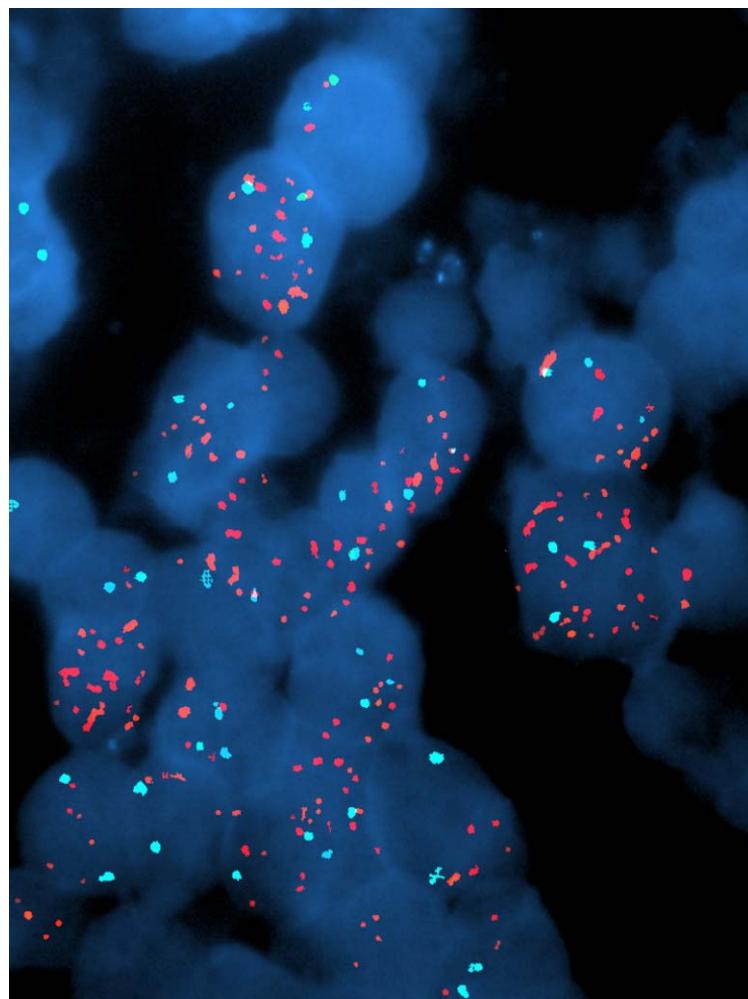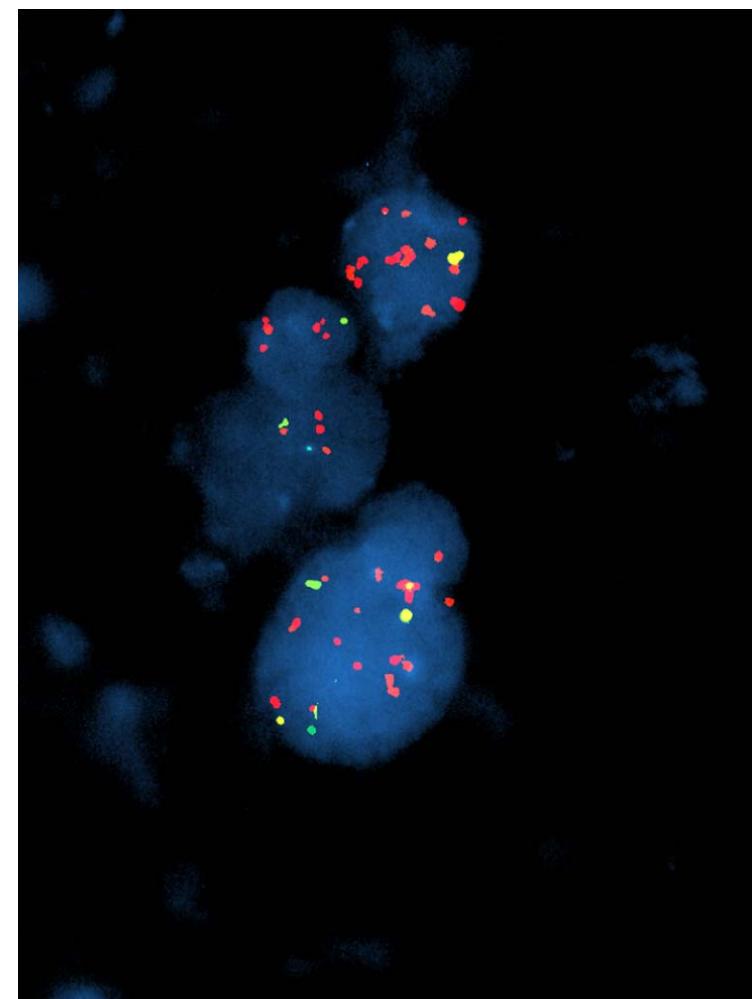
Fluorescence in situ hybridization for c-MYC (A) and MYCN (B) in representative c1 tumors confirms high-level copy number gains seen on SNP analysis

A Patient MD_29

B Patient MD_146

c-MYC amplification (orange) in c1 tumor; *CEP8* control probe (aqua)

MYCN amplification (orange) in c1 tumor; *ch2* control probe (green)

Supplementary Figure S6
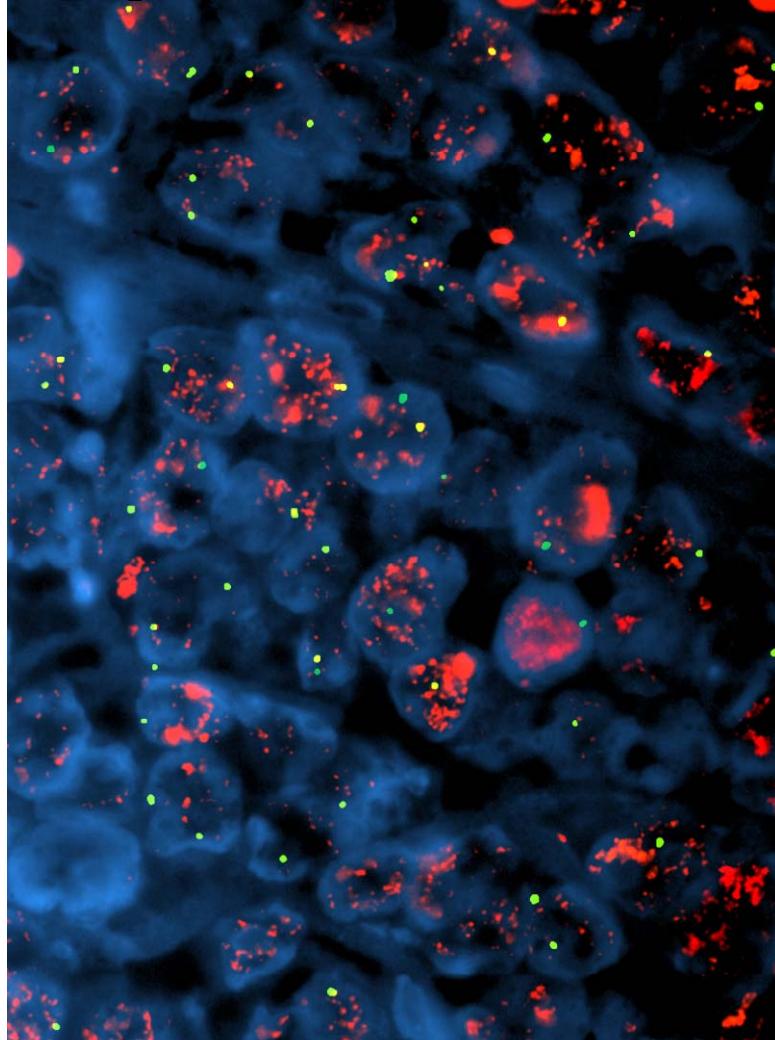
GLI2 and *MYCN* copy number gain in SHH subgroup medulloblastomas

GLI2 copy number gain

MYCN copy number gain
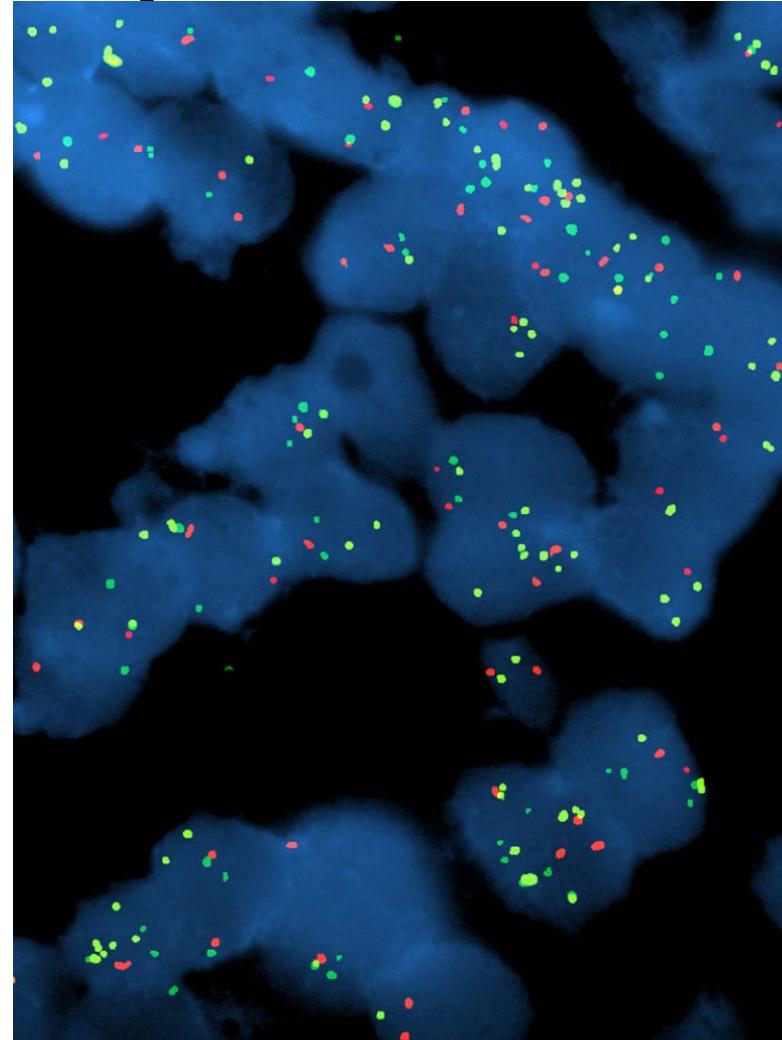
Fluorescence in situ hybridization for MYCN and GLI2 in representative c3 (SHH) subgroup tumors confirms copy number gains noted on SNP array analysis

Patient MD_7.1

Patient MD_4

MYCN amplification (orange) in c3/SHH tumor; *GLI2* control probe (green)
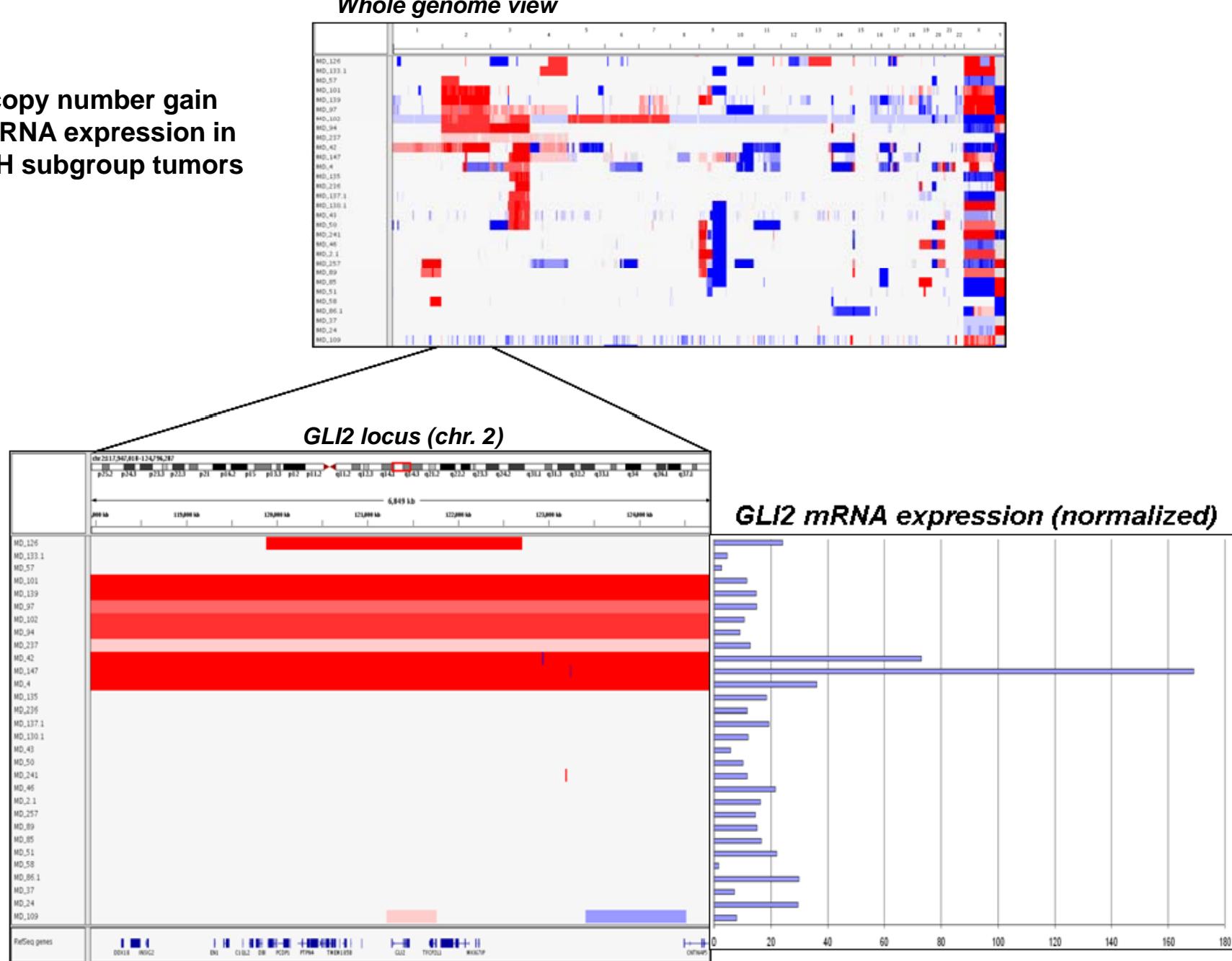
GLI2 amplification (green) in c3/SHH tumor; *MYCN* control probe (orange)
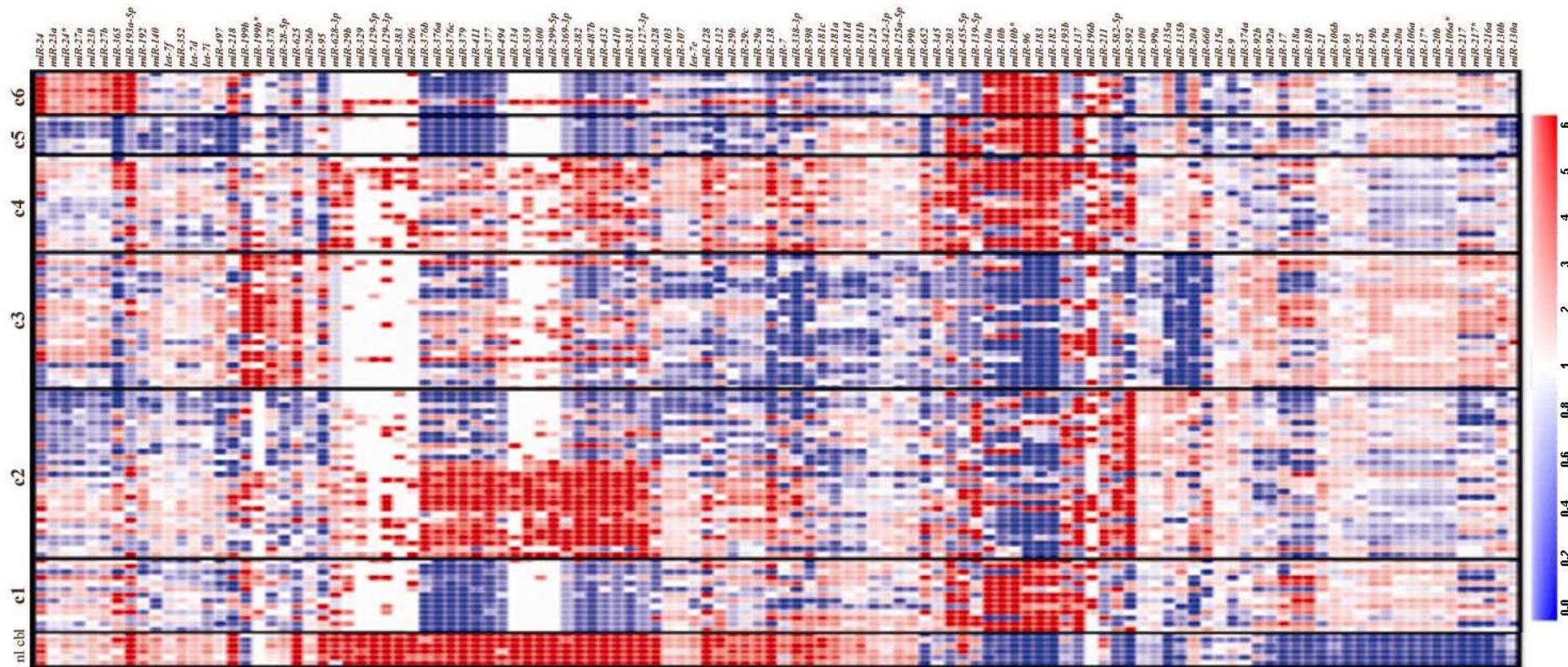
Supplementary Figure S8

GLI2 copy number gain and mRNA expression in c3/SHH subgroup tumors

Whole genome view

GLI2 locus (chr. 2)

GLI2 mRNA expression (normalized)
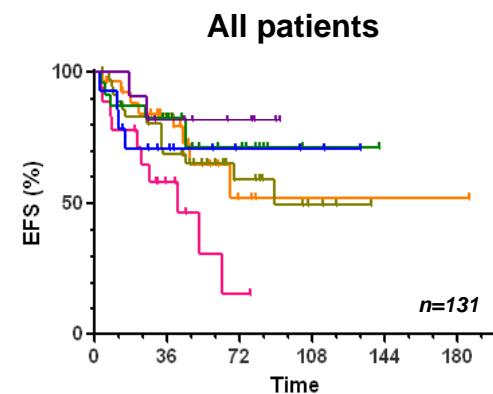
miRNA heatmap of 104 most variant miRNA probes

Supplementary Figure S10

A — All patients
D — Patients > 3y of age*
H — Patients < 3 y of age

B — Cho et al. cohort
E
I

C — Kool et al., Fattet et al., and Thompson et al. cohorts
F
J

Legend: c1, c2, c3, c4, c5, c6
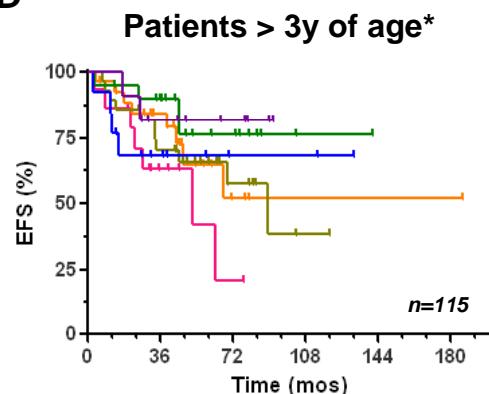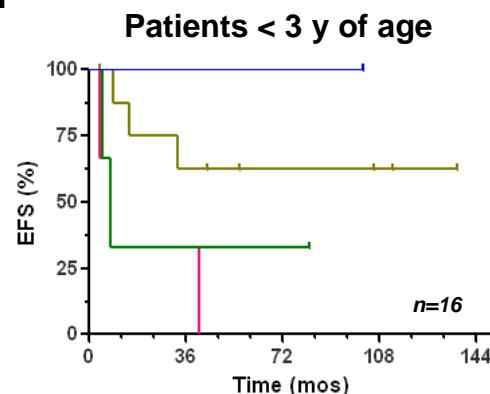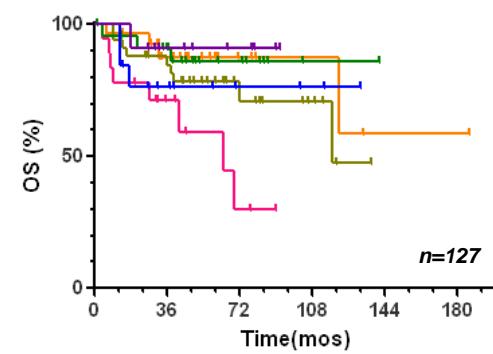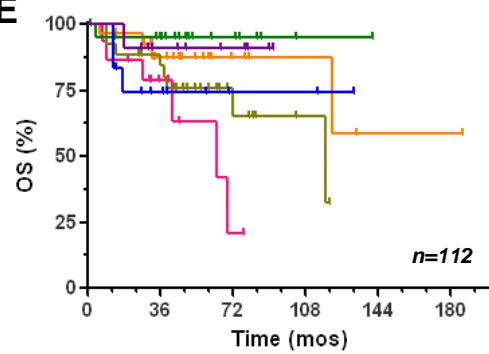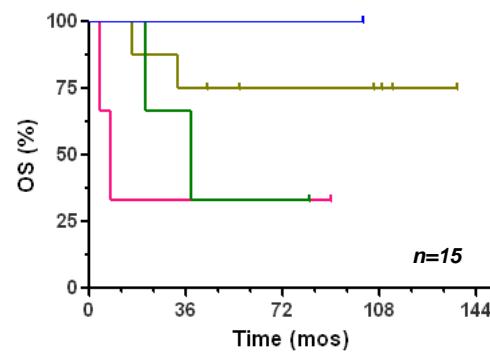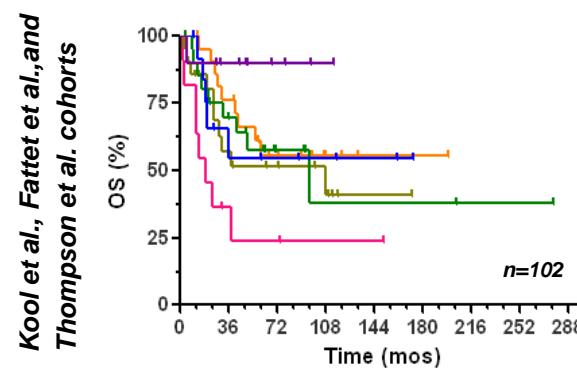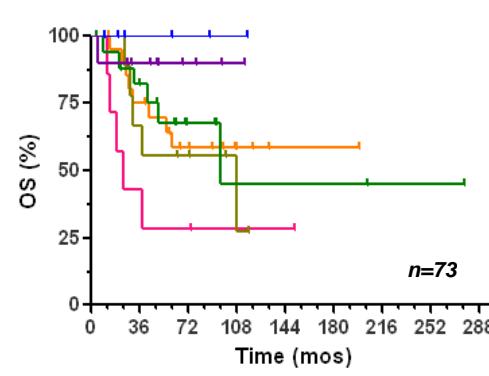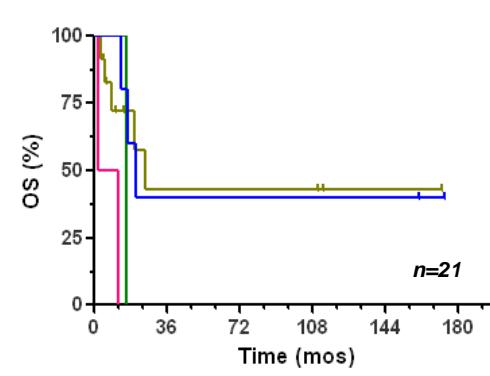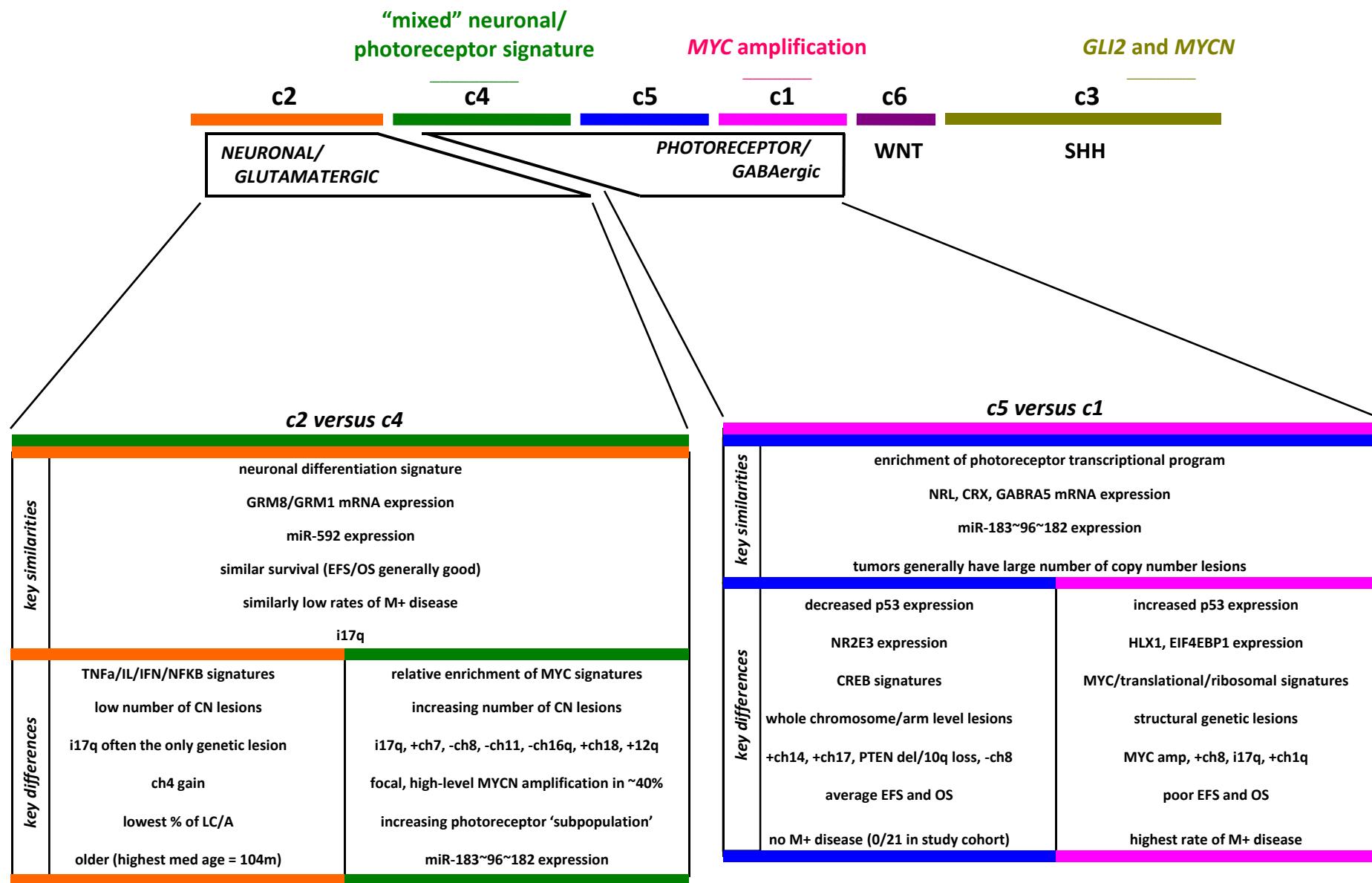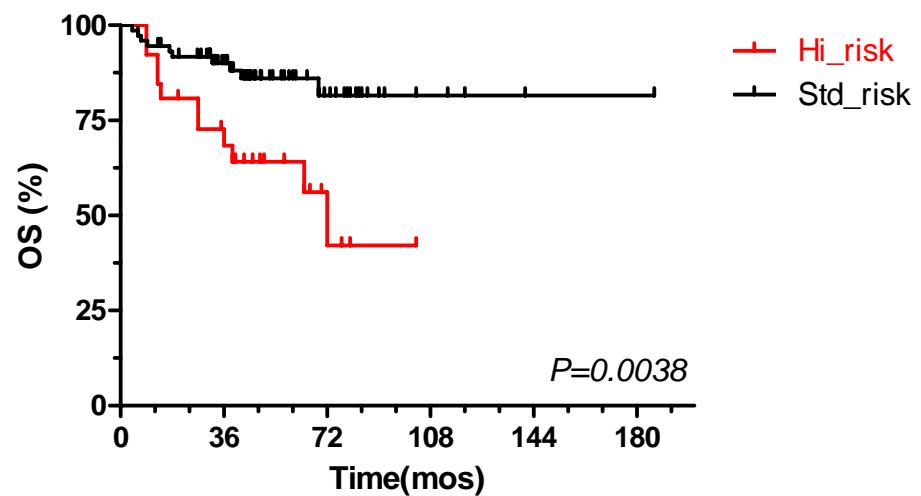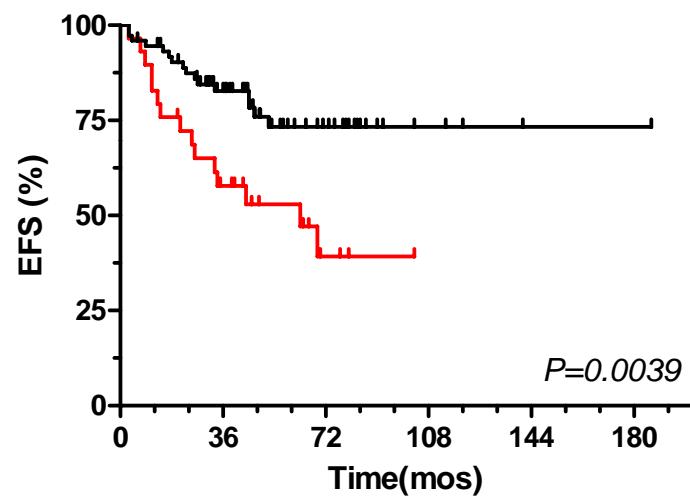
*patients >3years of age who did not receive radiation therapy excluded

Supplementary Figure S11

"mixed" neuronal/ photoreceptor signature

MYC amplification

GLI2 and *MYCN*

c2 **c4** **c5** **c1** **c6** **c3**

NEURONAL/ GLUTAMERGIC

PHOTORECEPTOR/ GABAergic

WNT

SHH

c2 versus c4

key similarities

neuronal differentiation signature

GRM8/GRM1 mRNA expression

miR-592 expression

similar survival (EFS/OS generally good)

similarly low rates of M+ disease

i17q

key differences

TNFa/IL/IFN/NFKB signatures	relative enrichment of MYC signatures
low number of CN lesions	increasing number of CN lesions
i17q often the only genetic lesion	i17q, +ch7, -ch8, -ch11, -ch16q, +ch18, +12q
ch4 gain	focal, high-level MYCN amplification in ~40%
lowest % of LC/A	increasing photoreceptor 'subpopulation'
older (highest med age = 104m)	miR-183~96~182 expression

c5 versus c1

key similarities

enrichment of photoreceptor transcriptional program

NRL, CRX, GABRA5 mRNA expression

miR-183~96~182 expression

tumors generally have large number of copy number lesions

key differences

decreased p53 expression	increased p53 expression
NR2E3 expression	HLX1, EIF4EBP1 expression
CREB signatures	MYC/translational/ribosomal signatures
whole chromosome/arm level lesions	structural genetic lesions
+ch14, +ch17, PTEN del/10q loss, -ch8	MYC amp, +ch8, i17q, +ch1q
average EFS and OS	poor EFS and OS
no M+ disease (0/21 in study cohort)	highest rate of M+ disease

Survival analysis (EFS and OS) of patients categorized as 'Hi-risk'* or 'standard-risk'*
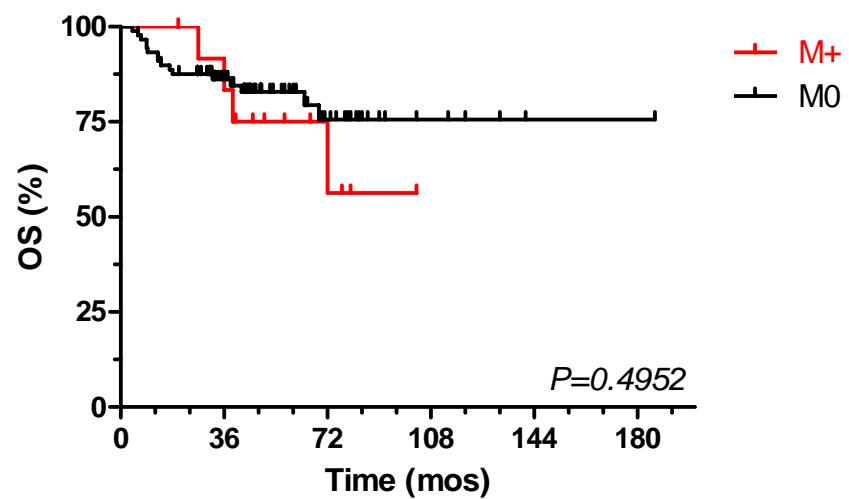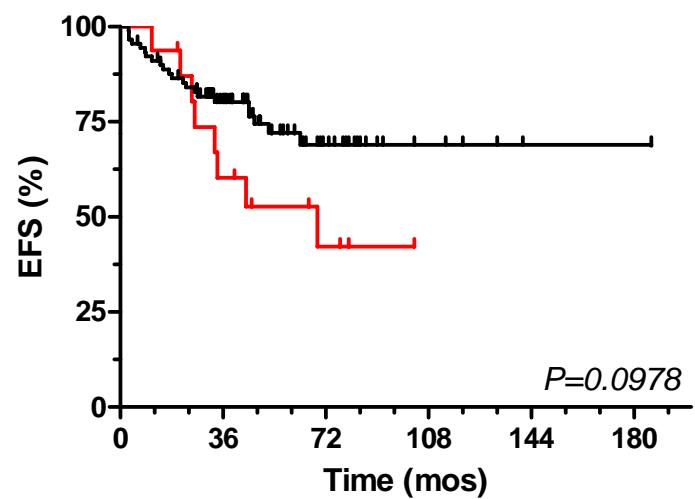
*'Hi-risk' defined as <3 years of age or >3 years of age with M+ disease, LC/A histology or bulk residual tumor after resection greater than 1.5 cm3
**'standard-risk' defined as >3 years of age with M0 disease, no evidence of large cell or anaplastic features on histology and residual disease less than 1.5 cm3
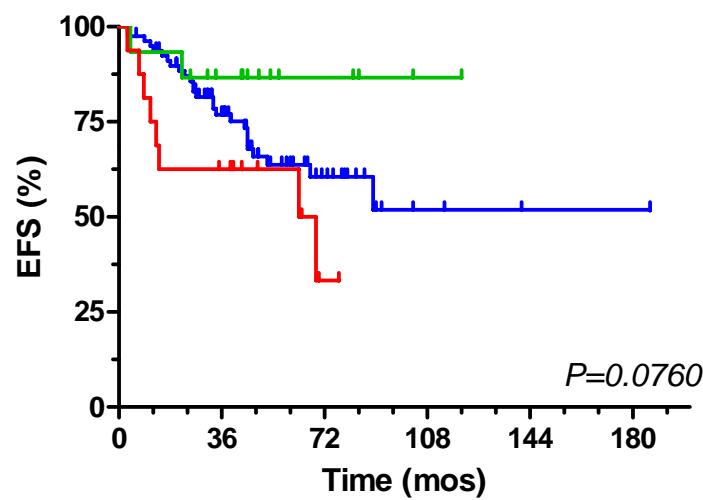
Survival analysis (EFS and OS) of patients categorized by 'M+' versus 'M0' disease
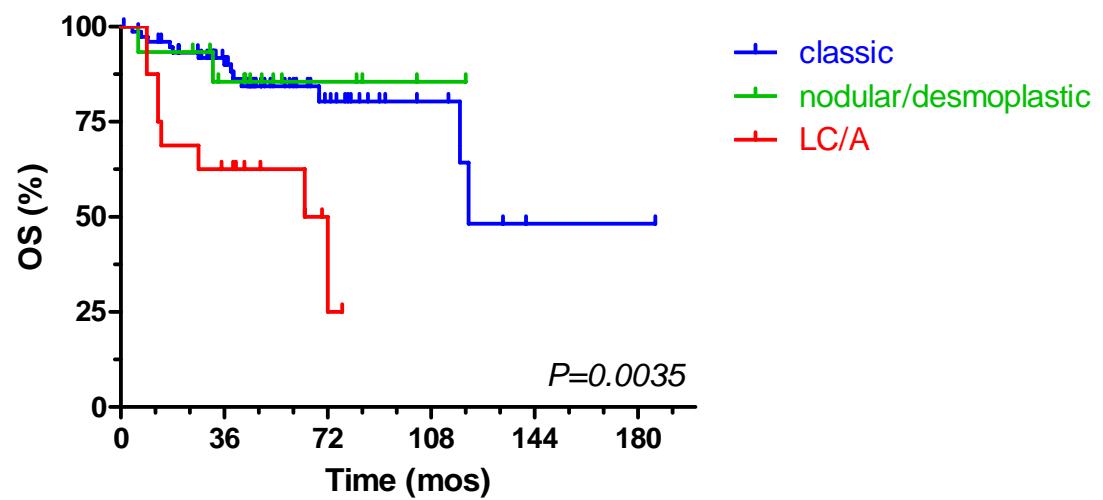
Survival analysis (EFS and OS) of patients categorized by histological subtype

Table S1

|	Gene set name	Description	Database	NES*	nom P-value*
c1	MYC_TARGETS	Myc-responsive genes (39) reported in multiple systems.	MSigDB v2.5/C2	2.2470677	<0.0001
c1	ZELLER_MYC_UP	Genes (23) upregulated by MYC in >3 papers.	MSigDB v2.5/C2	2.0984483	<0.0001
c1	HAS00970_AMINOACYL_TRNA_BIOSYNTHESIS	Genes (38) involved in aminoacyl-tRNA biosynthesis. KEGG	MSigDB v2.5/C2	1.986022	<0.0001
c1	TRANSLATION_FACTORS	Translation factor genes (52) GenMAPP	MSigDB v2.5/C2	1.9820051	0.0020202
c1	PENG_RAPAMYCIN_DN	Genes (229) downregulated in response to rapamycin starvation	MSigDB v2.5/C2	1.9357171	0.0021786
c1	BRCA_BRCA1_POS	Genes (107) whose expression is consistently positively correlated with brca1 germline status.	MSigDB v2.5/C2	1.9152514	<0.0001
c2	CREBPATHWAY	BIOCARTA (27 genes)	MSigDB v2.5/C2	1.9477868	0.0044248
c2	IL22BPPATHWAY	IL-22 (13) is produced by T cells and induces the acute phase inflammatory response in hepatocytes.	MSigDB v2.5/C2	1.7755636	0.010661
c2	PTENPATHWAY	BIOCARTA (18 genes)	MSigDB v2.5/C2	1.6823599	0.0331126
c2	P21_ANY_UP	Genes (8) upregulated at any timepoint after ectopic expression of CDKN1A in OvCa cells.	MSigDB v2.5/C2	1.6680897	0.0296128
c2	STAT3PATHWAY	BIOCARTA (8 genes)	MSigDB v2.5/C2	1.5071098	0.0566038
c2	IFNGPATHWAY	BIOCARTA (6 genes)	MSigDB v2.5/C2	1.5038848	0.0566038
c3	POMEROY_DESMOPLASIC_VS_CLASSIC_MD_UP	Genes (47) upregualted in desmoplastic medulloblastomas relative to classic medulloblastomas	MSigDB v2.5/C2	2.1249564	<0.0001
c3	HAS03010_RIBOSOME	Genes (98) involved in ribosome. KEGG	MSigDB v2.5/C2	1.7778438	0.0116959
c3	LEE_MYC_UP	Genes (54) upregulated in hepatoma tissue of Myc transgenic mice.	MSigDB v2.5/C2	1.6206341	0.0239651
c3	VANASSE_BCL2_TARGETS	Genes (113) differentially expressed after ectopic expression of Bcl-2 in murine CD19+ B-cells.	MSigDB v2.5/C2	1.5597178	0.0141844
c3	P53PATHWAY	BIOCARTA (16 genes)	MSigDB v2.5/C2	1.5274951	0.0453515
c3	GCNP_SHH_LATE.V1_UP	Genes (148) upregulated with activation of the SHH pathway .	OPAM.v3	1.3524649	0.1141649
c4	CREBPATHWAY	BIOCARTA (27 genes)	MSigDB v2.5/C2	1.9587663	<0.0001
c4	AGEING_BRAIN_DN	Genes (122) downregulated in the ageing frontal cortex.	MSigDB v2.5/C2	1.883448	<0.0001
c4	AGED_MOUSE_HIPPOCAMPUS_ANY_DN	Genes (42) downregulated in hippocampus of 16 month aged mice compared to 3 month young controls	MSigDB v2.5/C2	1.7113705	0.0098039
c4	GPCRS_CLASS_C_METABOTROPIC_GLUTAMATE	Genes (14) associated with G-protein coupled receptors related to metabotropic glutamate receptors.	MSigDB v2.5/C2	1.627873	0.0401891
c4	CAHOY_NEURONAL	Genes (70) up and down-regulated in P7 and P16 neurons compared to astrocytes or oligodendrocytes. Cahoy et al. 2008	OPAM.v3	1.5009767	0.0466472
c4	has04360_AXON_GUIDANCE	Genes (128) involved in axon guidance.	MSigDB v2.5/C2	1.455076	0.0218579
c5	POMEROY_DESMOPLASTIC_VS_CLASSIC_MD_DN	Genes (41) expressed in classic medulloblastomas.	MSigDB v2.5/C2	1.900318	0.0022173
c5	PHOTO_DN.V1_UP	Genes upregulated (150) in retina of wt mice compared to retinae of Nr2e3 -/-, Nrl -/-, and Crx -/- mice. Hsiau et al. 2007	OPAM.v3	1.5292192	0.0351438
c5	CRX_DN.V1_UP	Genes (150) upregulated in retinae of wt mice compared to retinae of Crx -/- mice. Hsiau et al. 2007	OPAM.v3	1.3321834	0.1
c5	NRL_DN.V1_UP	Genes (150) upregulated in retinae of wt mice compared to retinae of Nrl -/- mice. Hsiau et al. 2007	OPAM.v3	1.1607616	0.2096774
c5	IGLESIAS_ESFMINUS_DN	Genes (17) that decrease in the absence of E2F1 and E2F2.	MSigDB v2.5/C2	1.7437446	0.0169492
c5	CREBPATHWAY	BIOCARTA (27 genes)	MSigDB v2.5/C2	1.6355608	0.0286344
c6	TGFBETA_LATE_UP	Genes (33) upregulated by TGF-beta treatment of skin fibroblasts only at 1-4 hrs (clusters 4-6)	MSigDB v2.5/C2	2.077431	0.0027701
c6	LEF1_UP.V1_UP	Genes (200) upregulated by Lef1. (GEO dataset GSE3229) Medici et al. 2005	OPAM.v3	2.0324185	<0.0001
c6	BCAT_UP.V1_UP	Genes (200) upregulated by expression of mutant beta-catenin (S37A) in 293T cells.(GEO dataset GDS748) Chamorro et al. 2007	OPAM.v3	2.031653	<0.0001
c6	ST_WNT_BETA_CATENIN_PATHWAY	Genes (34) associated with Wnt/Beta-catenin signaling.	MSigDB v2.5/C2	1.7606045	<0.0001
c6	EMT_UP	Genes (62) upregulated during TGF-beta induced epithelial to mesenchymal transition of Eph4 cells	MSigDB v2.5/C2	1.75	0.019
c6	JECHLINGER_EMT_UP	Genes (57) upregulated for epithelial plasticity in tumor progression	MSigDB v2.5/C2	1.71	0.027

*NES = normalized enrichment score; nom P-value = nominal P-value; for full details of each gene set, please refer to www.broadinstitute.org/gsea/msigdb/index.jsp;

Table S2

Pair-wise GSEA of NMF c1 versus c5

Enriched in c1 versus c5

Gene set	NES*	nom P-val*
MYC_TARGETS	2.089566	0
BRCA_BRCA1_POS	2.071055	0
RIBOSOMAL_PROTEINS	2.030252	0
AGUIRRE_PANCREAS_CHR8	1.96373	0.001953
MENSSEN_MYC_UP	1.955444	0
TRANSLATION_FACTORS	1.933928	0.001927
ZELLER_MYC_UP	1.909006	0
LEE_MYC_UP	1.908047	0
POMEROY_MD_TREATMENT_GOOD_VS_POOR_DN	1.904966	0
MYC_ONCOGENIC_SIGNATURE	1.855839	0.003781

Enriched in c5 versus c1

Gene set	NES	nom P-val
CREBPATHWAY	-2.00536	0
ERK5PATHWAY	-1.87296	0
BADPATHWAY	-1.86171	0.002016
PPARGPATHWAY	-1.80103	0.003984
BRCA2_BRCA1_DN	-1.77599	0.006452
GATA3PATHWAY	-1.69993	0.005952
CORTEX_ENRICHMENT_EARLY_UP	-1.65546	0.020243
YU_CMYC_DN	-1.62335	0.032854
MITOCHONDRIAL_FATTY_ACID_BETAOXIDATION	-1.61145	0.018947
POMEROY_DESMOPLASIC_VS_CLASSIC_MD_DN	-1.52065	0.063241

*NES = normalized enrichment score; nom P-value = nominal P-value; for full details of each gene set, please refer to www.broadinstitute.org/gsea/msigdb/index.jsp;

Table S3

Pair-wise GSEA of NMF c2 versus c4

Enriched in c2 versus c4

Gene set	NES*	nom P-val*
SCHUMACHER_MYC_DN	1.7234862	0.007952286
IL22BPPATHWAY	1.6883659	0.011881189
IL10PATHWAY	1.6877216	0.0113852
TNFALPHA_ADIP_UP	1.6708775	0.003960396
ST_INTERLEUKIN_13_PATHWAY	1.6621488	0.009746589
ST_IL_13_PATHWAY	1.6621488	0.009746589
IL6_SCAR_FIBRO_DN	1.6235157	0.022044089
ST_INTERFERON_GAMMA_PATHWAY	1.6108645	0.035785288
HINATA_NFKB_IMMU_INF	1.5191829	0.042145595
IL4PATHWAY	1.5032254	0.051526718

Enriched in c4 versus c2

Gene set	NES	nom P-val
BADPATHWAY	-1.8262955	<0.0001
AGUIRRE_PANCREAS_CHR7	-1.810225	0.012269938
DSRNA_DN	-1.7628983	0.002028398
PENG_RAPAMYCIN_DN	-1.7483155	0.005847953
SCHUMACHER_MYC_UP	-1.7414796	0.009881423
CORTEX_ENRICHMENT_EARLY_UP	-1.7160639	0.011673152
O6BG_RESIST_MEDULLOBLASTOMA_DN	-1.7124412	0.001930502
CREB_BRAIN_2WKS_UP	-1.6516688	0.014
AGUIRRE_PANCREAS_CHR18	-1.6227533	0.045009784
HIPPOCAMPUS_DEVELOPMENT_NEONATAL	-1.5581534	0.053892214

*NES = normalized enrichment score; nom P-value = nominal P-value; for full details of each gene set, please refer to www.broadinstitute.org/gsea/msigdb/index.jsp;

Table S4

Average (avg) and median (med) number of copy number lesions per tumor

	avg	med
c1	11.72222	11.5
c2	4.352941	4
c3	4.275862	3
c4	8.35	9
c5	10.77778	10.5
c6	1	1

Table S5

NMF subgroup	Positional gene set enriched in NMF cluster (inferred copy number gain)			Positional gene set enriched in 'rest' (inferred copy number loss)		
	Name	*NES**	*nom P-value*	*Name*	*NES**	*nom P-value*
c1	CHR8Q24	2.250693	<0.0001	CHR16Q22	-1.8994529	<0.0001
	CHR8Q22	1.8838278	0.011210762	CHR4Q32	-1.8823338	0.003565062
	CHR1Q44	1.8084368	0.019027485	CHR16Q12	-1.8816221	0.001788909
	CHR8P12	1.7958734	0.011013215	CHR4Q26	-1.8400798	0.001828154
	CHR8Q21	1.7795274	0.022573363	CHRXQ22	-1.7713392	0.012681159
	CHR8Q11	1.7591428	0.023529412	CHR16Q23	-1.7443051	0.02131783
	CHR5Q11	1.7206597	0.014117647	CHR16Q24	-1.733623	0.017921148
	CHR1Q42	1.7040539	0.034883723	CHR15Q23	-1.7335428	0.01559792
	CHR1Q41	1.6782655	0.03773585	CHR15Q26	-1.7154063	0.012068966
	CHR8P22	1.673351	0.030162413	CHR16Q13	-1.6919621	0.017667845
c2	CHR17Q11	2.2727506	<0.0001	CHR2Q33	-1.798832	0.001845019
	CHR17Q23	1.9115108	0.006342495	CHR13Q31	-1.7907692	0.001886793
	CHR17Q21	1.8920196	0.004464286	CHR2P15	-1.7516466	0.003787879
	CHR17Q12	1.7936867	0.009456265	CHR2P16	-1.7333654	0.011450382
	CHR6Q23	1.6651441	0.017316017	CHR2P21	-1.7122612	0.007272727
	CHR16Q12	1.6614091	0.04454343	CHR8Q22	-1.6705288	0.03954802
	CHR17Q25	1.6593256	0.03803132	CHR13Q32	-1.6509	0.02108963
	CHR4Q11	1.621779	0.043933053	CHR19Q12	-1.6303024	0.017509727
	CHR17Q22	1.616684	0.02832244	CHR6Q16	-1.6221133	0.020797227
	CHRXQ27	1.5914041	0.05543237	CHR1P12	-1.6174711	0.01953125
c3	CHR3Q25	1.8654408	0.008247423	CHR17Q21	-2.0879242	<0.0001
	CHR2Q13	1.8499793	0.002141328	CHR17Q11	-2.010558	0.001949318
	CHR13Q34	1.8450608	0.006550218	CHR17Q23	-1.9643952	<0.0001
	CHR6P	1.7768651	0.002105263	CHR9Q34	-1.8872199	0.015594542
	CHR2P15	1.7106773	0.014285714	CHR9Q33	-1.8626797	0.011406845
	CHR11Q22	1.700544	0.01814059	CHR17Q25	-1.8237622	0.01509434
	CHR6Q16	1.6800518	0.02173913	CHR17Q12	-1.812055	0.003610108
	CHRXQ21	1.652775	0.036170214	CHR17Q22	-1.7396696	0.011342155
	CHR13Q33	1.6301136	0.038854804	CHR7Q35	-1.7206488	0.03460838
	CHR2Q33	1.6180238	0.03640257	CHR5Q31	-1.6284627	0.012939001
c4	CHR6Q22	1.7428397	0.016913319	CHR3Q25	-1.8193414	0.00754717
	CHR17Q22	1.714105	0.015283843	CHR2Q33	-1.788349	0.009107468
	CHR9Q34	1.7051464	0.038724374	CHR1P22	-1.7239883	0.010948905
	CHR17Q21	1.6321447	0.03409091	CHR4Q23	-1.7061654	0.011363637
	CHR17Q25	1.6220071	0.06535948	CHR5Q33	-1.6863109	0.013833992
	CHR12Q24	1.6184632	0.045045044	CHR8Q22	-1.6586181	0.02578269
	CHR7Q36	1.6101096	0.06323185	CHR8P11	-1.5795851	0.032478634
	CHR17Q12	1.5809617	0.028503563	CHR4Q24	-1.5779066	0.036900368
	CHR7P22	1.5797045	0.06666667	CHR8P23	-1.5572784	0.05204461
	CHR7P21	1.5715357	0.029279279	CHR3P13	-1.5539203	0.038674034
c5	CHR14Q32	2.0876608	0.002544529	CHRXP22	-1.9556537	0.001626016
	CHR14Q24	1.9171987	0.004545454	CHR8P12	-1.9321878	0.001703578
	CHR14Q11	1.775132	0.013921114	CHR11P13	-1.8926054	0.005172414
	CHR14Q31	1.7649634	0.012077294	CHR10Q26	-1.8618424	0.01598579
	CHR14Q13	1.7562042	0.014989293	CHR8P21	-1.8327014	<0.0001
	CHR2Q24	1.6065754	0.022792023	CHR3P26	-1.8028281	<0.0001
	CHR2Q34	1.5862199	0.038043477	CHR10Q25	-1.7746584	0.014336918
	CHR14Q22	1.574708	0.058252428	CHR8Q12	-1.7634267	<0.0001
	CHR7Q35	1.5559679	0.058536585	CHR4Q22	-1.7520354	0.010471204
	CHR1P21	1.5431106	0.049222797	CHR10Q23	-1.7463275	0.024911031
c6	CHR3P13	1.8980178	0.002237137	CHR6Q22	-2.2793353	<0.0001
	CHR11P15	1.7522583	0.012406948	CHR6P21	-2.2377422	<0.0001
	CHR2Q35	1.7156441	0.007853403	CHR6Q15	-2.1716144	<0.0001
	CHR3Q13	1.6826246	0.01843318	CHR6Q25	-2.1706293	<0.0001
	CHR9Q13	1.6807413	0.019662922	CHR6P25	-2.1333554	<0.0001
	CHR10Q26	1.675763	0.022727273	CHR6Q21	-2.1095939	<0.0001
	CHR7Q33	1.6698258	0.015228426	CHR6Q23	-2.1007936	<0.0001
	CHR20Q12	1.6457286	0.04197531	CHR6Q24	-2.0889313	<0.0001
	CHR9Q32	1.6413147	0.025700934	CHR6P12	-2.05087	<0.0001
	CHR20P12	1.6410226	0.022332506	CHR6Q27	-2.0433245	<0.0001

*NES = normalized enrichment score; nom P-value = nominal P-value

Table S6

Kool_Fattet NMF subgroup	Positional gene set enriched in NMF cluster (inferred copy number gain)			Positional gene set enriched in 'rest' (inferred copy number loss)		
	Name	NES*	nom P-value	Name	NES*	nom P-value
c1	CHR8Q24	1.9828601	0.009661836	CHRXQ22	-1.8025601	0.009191177
	CHR1Q44	1.7771809	0.008810572	CHR13Q33	-1.7078948	0.01610018
	CHR8Q13	1.7499149	0.020512821	CHRXQ11	-1.6046345	0.019097222
	CHR1Q42	1.7119223	0.01754386	CHR15Q12	-1.5706607	0.008787346
	CHR8Q22	1.6704329	0.04405286	CHR13Q22	-1.5528166	0.042662118
	CHR1Q31	1.621693	0.022222223	CHR9P22	-1.5370772	0.05226481
	CHR1Q23	1.6081628	0.012345679	CHR3Q24	-1.5269535	0.053333335
	CHR13Q21	1.6054857	0.035897437	CHR12P	-1.5187151	0.0227704
	CHR19Q12	1.5940264	0.042	CHR4Q32	-1.4804995	0.06788991
	CHR1Q22	1.5616021	0.06772009	CHR4Q12	-1.4598036	0.09515571
c2	CHR4Q28	1.797571	0.004385965	CHR17P13	-1.9933875	0.001862197
	CHR17Q11	1.7896708	0.01590909	CHR2Q36	-1.9730184	<0.0001
	CHR17Q21	1.7661254	0.030162413	CHR7P15	-1.8575606	0.002928258
	CHR19P12	1.7564334	0.012847966	CHR2P15	-1.7039444	0.017475728
	CHR17Q12	1.7506748	0.013452915	CHR2P21	-1.6798258	0.017793594
	CHR13Q22	1.7433089	0.004576659	CHR7P12	-1.6624299	0.0237691
	CHR6P23	1.7380869	0.006696429	CHR7Q34	-1.6124617	0.032667875
	CHR4Q11	1.6651118	0.040449437	CHR17P12	-1.5938015	0.041884817
	CHR17Q25	1.6650832	0.050458714	CHR4Q24	-1.577857	0.040139616
	CHR16Q21	1.6555468	0.033407573	CHR13Q31	-1.5622524	0.034146342
c3	CHR13Q33	2.1709802	<0.0001	CHR17Q12	-2.1061225	<0.0001
	CHR3Q25	1.8920418	0.004149378	CHR17Q22	-1.9359707	0.001838235
	CHR13Q34	1.7260286	0.019027485	CHR17Q11	-1.9034747	0.001782531
	CHR4Q22	1.6536411	0.008908686	CHR9Q34	-1.8854921	0.011764706
	CHRXQ21	1.6211768	0.042283297	CHR17Q25	-1.8831774	0.005524862
	CHR13Q31	1.598058	0.04077253	CHR17Q21	-1.8753396	0.001831502
	CHR6Q14	1.5834956	0.03521127	CHR17Q23	-1.8173074	0.005357143
	CHR11Q22	1.5631658	0.05394191	CHR9Q33	-1.8119558	0.015009381
	CHR11P13	1.5556105	0.05102041	CHR5Q31	-1.7957602	0.001697793
	CHR3Q	1.5201668	0.03422053	CHR9Q32	-1.704091	0.035984848
c4	CHR7Q11	1.9260644	0.003929273	CHR8Q22	-1.914215	0.001883239
	CHR7Q36	1.8374237	0.006122449	CHR11Q13	-1.7689819	0.011627907
	CHR17Q24	1.7720046	0.023655914	CHR11Q14	-1.7012067	0.020952381
	CHR7Q22	1.7590142	0.03448276	CHR11Q12	-1.692987	0.008179959
	CHR7P14	1.7144943	0.024948025	CHR8Q24	-1.6879599	0.017142856
	CHR7Q21	1.6942682	0.025586354	CHR11Q22	-1.6815585	0.026070764
	CHR7Q31	1.6694566	0.033333335	CHR4Q23	-1.6689975	0.018281536
	CHR6Q22	1.6611366	0.037199125	CHR13Q32	-1.660491	0.034798536
	CHR6Q15	1.6017267	0.06198347	CHR22Q13	-1.6480018	0.0251938
	CHR7Q34	1.5934799	0.05367793	CHR2P11	-1.604739	0.031835206
c5	CHR1P32	2.0414867	<0.0001	CHR10Q23	-1.949841	<0.0001
	CHR14Q13	1.8828543	0.004597701	CHR8Q12	-1.8347867	0.009107468
	CHR2Q34	1.8395232	0.004889976	CHR16Q21	-1.8036907	0.003676471
	CHR11Q23	1.7919259	0.023622047	CHR16Q24	-1.788946	0.02247191
	CHR14Q32	1.7415793	0.01907357	CHR10Q25	-1.7084578	0.025773196
	CHR1P21	1.7131884	0.016172506	CHR10Q24	-1.7044622	0.014897579
	CHR1P33	1.6790125	0.010443864	CHR16Q22	-1.7025235	0.039923955
	CHR14Q12	1.6774906	0.014619883	CHR16Q13	-1.6934845	0.02020202
	CHR1P34	1.6760565	0.030303031	CHR8P22	-1.6701384	0.01244168
	CHR7Q35	1.6308197	0.032863848	CHRXQ13	-1.6107678	0.03327787
c6	CHR4Q23	2.0127268	<0.0001	CHR6Q22	-2.2793353	<0.0001
	CHR3Q13	1.9271897	0.002392344	CHR6P21	-2.2377422	<0.0001
	CHR2Q31	1.8882152	0.005025126	CHR6Q15	-2.1716144	<0.0001
	CHR2Q35	1.8676988	0.004555809	CHR6Q25	-2.1706293	<0.0001
	CHR16Q12	1.7909206	0.010869565	CHR6P25	-2.1333554	<0.0001
	CHR4Q24	1.7797402	0.00954654	CHR6Q21	-2.1095939	<0.0001
	CHR3P11	1.7734421	0.004065041	CHR6Q23	-2.1007936	<0.0001
	CHR12Q	1.770975	0.010460251	CHR6Q24	-2.0889313	<0.0001
	CHR8Q22	1.7211294	0.02173913	CHR6P12	-2.05087	<0.0001
	CHR2P13	1.7018371	0.01330377	CHR6Q27	-2.0433245	<0.0001

*NES = normalized enrichment score; nom P-value = nominal P-value