Supplementary Table S1: Gene pairs with significant tendency for co-occurrence by association.

| geneA	geneB	p-Value	Log Odds Ratio	Association
ZH2	KMT2C	**<0.001**	2.084	Tendency towards co-occurrence(**Significant**)
ZH2	CDKN2A	**<0.001**	1.506	Tendency towards co-occurrence(**Significant**)
EZH2	CIC	0.055	-0.954	Tendency towards mutual exclusivity
EZH2	EGFR	0.049	0.889	Tendency towards co-occurrence(**Significant**)
EZH2	PIK3CA	0.095	0.707	Tendency towards co-occurrence
EZH2	TP53	0.028	0.893	Tendency towards co-occurrence(**Significant**)
CHD4	TFPT	0.003	1.571	Tendency towards co-occurrence(**Significant**)
CHD4	KDM5A	**<0.001**	2.612	Tendency towards co-occurrence(**Significant**)
CHD4	ATRX	0.015	0.821	Tendency towards co-occurrence(**Significant**)
CHD4	EGFR	0.031	-1.379	Tendency towards mutual exclusivity(**Significant**)
CHD4	MYC	0.017	1.023	Tendency towards co-occurrence(**Significant**)
CHD4	TP53	0.005	0.994	Tendency towards co-occurrence(**Significant**)
KMT2C	KDM5A	0.056	0.851	Tendency towards co-occurrence
KMT2C	ATRX	0.019	0.918	Tendency towards co-occurrence(Significant)
KMT2C	CIC	0.09	-0.764	Tendency towards mutual exclusivity
SMARCA4	DOT1L	**<0.001**	2.903	Tendency towards co-occurrence(Significant)
ARID1A	CIC	0.0172	0.828	Tendency towards co-occurrence(**Significant**)
ARID1A	FUBP1	0.064	0.762	Tendency towards co-occurrence
ARID1A	NOTCH1	0.093	0.635	Tendency towards co-occurrence
TFPT	KDM5A	0.057	0.994	Tendency towards co-occurrence
TFPT	ATRX	0.057	0.885	Tendency towards co-occurrence
TFPT	CIC	0.03	0.995	Tendency towards co-occurrence(**Significant**)
TFPT	EGFR	0.03	-Infinity	Tendency towards mutual exclusivity(**Significant**)
TFPT	FUBP1	0.308	0.455	Tendency towards co-occurrence
TFPT	MYC	0.093	0.914	Tendency towards co-occurrence
TFPT	TP53	0.009	1.363	Tendency towards co-occurrence(**Significant**)
KDM5A	ATRX	**<0.001**	1.638	Tendency towards co-occurrence(**Significant**)
KDM5A	MYC	0.024	0.949	Tendency towards co-occurrence(**Significant**)
KDM5A	TP53	**<0.001**	1.374	Tendency towards co-occurrence(**Significant**)
HDAC4	ATRX	0.013	1.069	Tendency towards co-occurrence(**Significant**)
DOT1L	CIC	0.04	0.986	Tendency towards co-occurrence(**Significant**)
DOT1L	MYC	0.062	1.066	Tendency towards co-occurrence
DOT1L	TP53	0.073	-0.852	Tendency towards mutual exclusivity
ATRX	CDKN2A	0.008	-0.879	Tendency towards mutual exclusivity(**Significant**)

ATRX	CIC	0.013	-0.625	Tendency towards mutual exclusivity(**Significant**)	
ATRX	EGFR	0.005	-0.921	Tendency towards mutual exclusivity(**Significant**)	
ATRX	FUBP1	0.025	-0.743	Tendency towards mutual exclusivity(**Significant**)	
ATRX	MYC	0.062	0.627	Tendency towards co-occurrence	
ATRX	TP53	**<0.001**	2.72	Tendency towards co-occurrence(**Significant**)	
CDKN2A	CIC	0.004	-1.259	Tendency towards mutual exclusivity(**Significant**)	
CDKN2A	EGFR	**<0.001**	2.198	Tendency towards co-occurrence(**Significant**)	
CDKN2A	TP53	0.044	-0.626	Tendency towards mutual exclusivity(**Significant**)	
CIC	FUBP1	**<0.001**	1.338	Tendency towards co-occurrence(**Significant**)	
CIC	NOTCH1	**<0.001**	1.092	Tendency towards co-occurrence(**Significant**)	
CIC	PIK3CA	0.018	0.736	Tendency towards co-occurrence(**Significant**)	
CIC	TP53	**<0.001**	-1.774	Tendency towards mutual exclusivity(**Significant**)	
EGFR	TP53	**<0.001**	-1.553	Tendency towards mutual exclusivity(**Significant**)	
FUBP1	NOTCH1	0.024	0.87	Tendency towards co-occurrence(**Significant**)	
FUBP1	PIK3CA	0.003	1.13	Tendency towards co-occurrence(**Significant**)	
FUBP1	TP53	0.002	-1.104	Tendency towards mutual exclusivity(**Significant**)	
MYC	TP53	0.023	0.813	Tendency towards co-occurrence(**Significant**)	
NOTCH1	PIK3CA	0.06	0.654	Tendency towards co-occurrence	
NOTCH1	TP53	0.004	-0.89	Tendency towards mutual exclusivity(**Significant**)	
PIK3CA	TP53	0.007	-0.826	Tendency towards mutual exclusivity(**Significant**)	

**Supplementary Table S2:** Epigenetic regulators analyzed.

Gene	Gene	Gene	Gene	Gene	Gene
ACTL6A	HDAC1	JMJD7	KMT2C	PRMT8	SMARCA4
ACTL6B	HDAC10	JMJD8	KMT2D	PRMT9	SMARCA5
ACTR5	HDAC11	KAT2A	KMT2E	RBBP4	SMARCC1
ACTR8	HDAC2	KAT2B	MBD1	RBBP7	SMARCC2
ARID1A	HDAC3	KAT5	MBD2	RING1	SMARCD1
ARID1B	HDAC4	KAT6A	MBD3	RIOX1	SMARCD2
ASH1L	HDAC5	KAT6B	MBD4	RUVBL1	SMARCD3
ASH2L	HDAC6	KAT7	MCRS1	RUVBL2	SMYD1
ASXL1	HDAC7	KAT8	MECP2	SETD1A	SMYD2
CARM1	HDAC8	KDM1A	MGEA5	SETD1B	SMYD3
CDY1	HDAC9	KDM1B	MINA	SETD2	SMYD4
CDYL	HIF1AN	KDM2A	MTA1	SETD3	SMYD5
CHD3	HINFP	KDM2B	MTA2	SETD4	SUV39H1
CHD4	HR	KDM3A	MTA3	SETD5	SUV39H2

|					
CHRAC1	HSPBAP1	KDM3B	NAT10	SETD6	KMT5A
CREBBP	ING1	KDM4A	NCOA1	SETD7	KMT5B
DNMT1	ING2	KDM4B	NCOA3	SETD8	KMT5C
DNMT3A	ING3	KDM4C	NFRKB	SETD9	TAF1
DNMT3B	ING4	KDM4D	NSD1	SETDB1	TET1
DOT1L	ING5	KDM5A	PHF2	SETDB2	TET2
EHMT1	INO80	KDM5B	PHF8	SETMAR	TFPT
EHMT2	INO80B	KDM5C	PRDM2	SIRT1	UCHL5
ELP3	INO80C	KDM5D	PRDM9	SIRT2	UTY
EP300	INO80D	KDM6A	PRMT1	SIRT3	NSD2
EZH1	INO80E	KDM6B	PRMT2	SIRT4	NSD3
EZH2	JARID2	KDM7A	PRMT3	SIRT5	YY1
FBXO10	JMJD1C	KDM8	PRMT5	SIRT6	
GTF3C4	JMJD4	KMT2A	PRMT6	SIRT7	
HAT1	JMJD6	KMT2B	PRMT7	SMARCA1	

Footnote: Total = 171 genes.
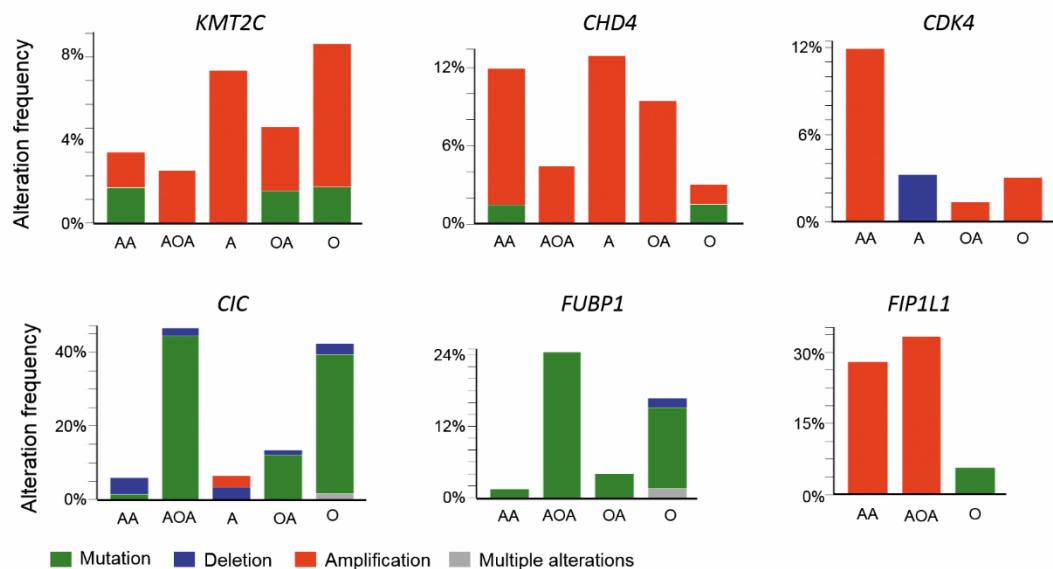
Supplementary Figure S1. Frequency of alterations (mutation in green, deletion in blue, amplification in red, and multiple alterations in gray) of genes in glioma subtypes. From left: Anaplastic astrocytoma (AA), Anaplastic oligoastrocytoma (AOA), Astrocytoma (A), Oligoastrocytoma (OA), Oligodendroglioma (O). Database: Brain Lower Grade Glioma (TCGA, provisional). N= 283.
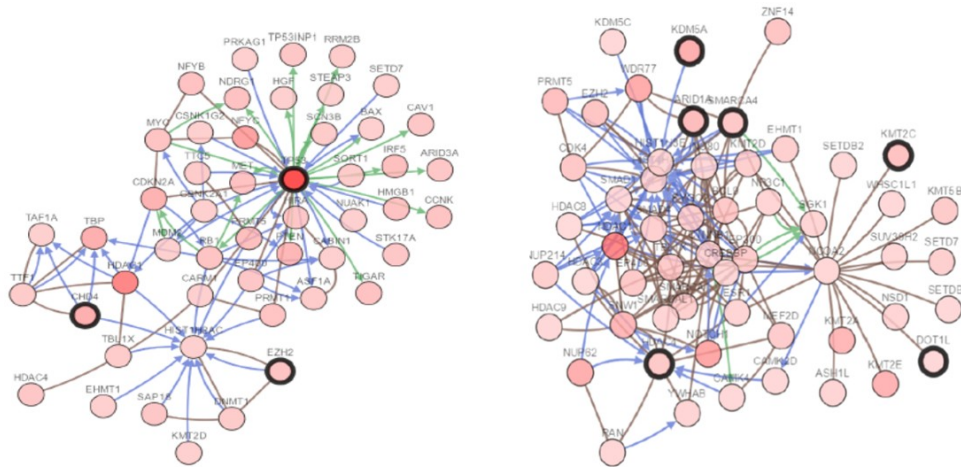
Supplementary Figure S2. Network of epigenetic modifiers and neighbors. Left panel:EZH2、CHD4 and TP53 network. Right panel: Epigentic modifiers KMT2C、SMARCA4、ARID1A、TFPT、KDM5A、HDAC4 and DOT1L networking. Blue line: Controls state change of; Green line: Controls expression of; Brown line: In complex with.
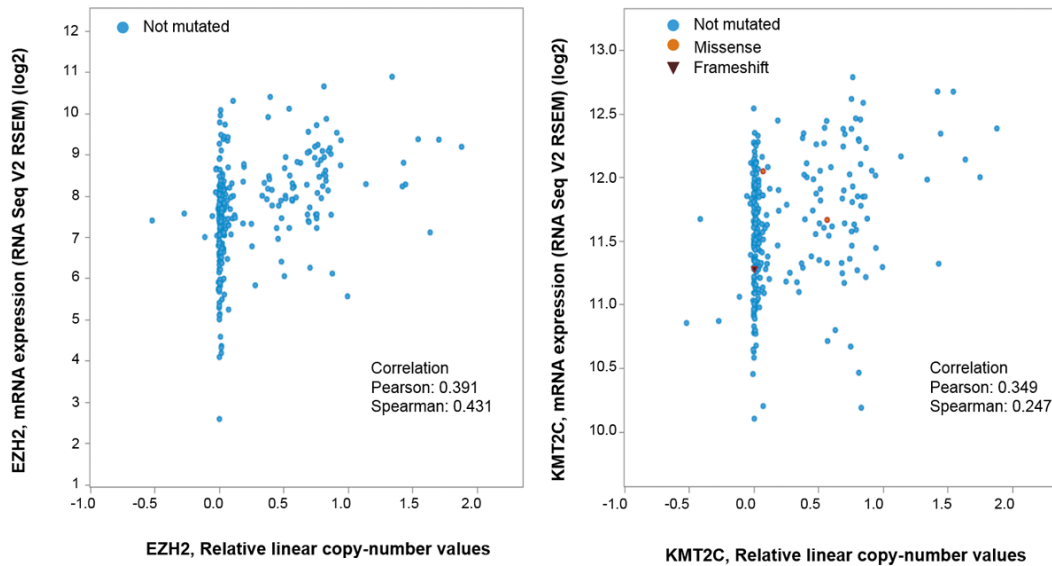
Supplementary Figure S3. Copy number alteration (CNA) versus mRNA expression plot. X-axis: relative linear copy-number values. Y-axis: mRNA expression (RNAseq V2 RSEM) (log 2). Blue dots: not mutated. Red dots: missense mutation. Red triangle: Frame shift. Left panel: EZH2 CNA vs EZH2 mRNA. Right panel: KMT2C CNA vs mRNA.
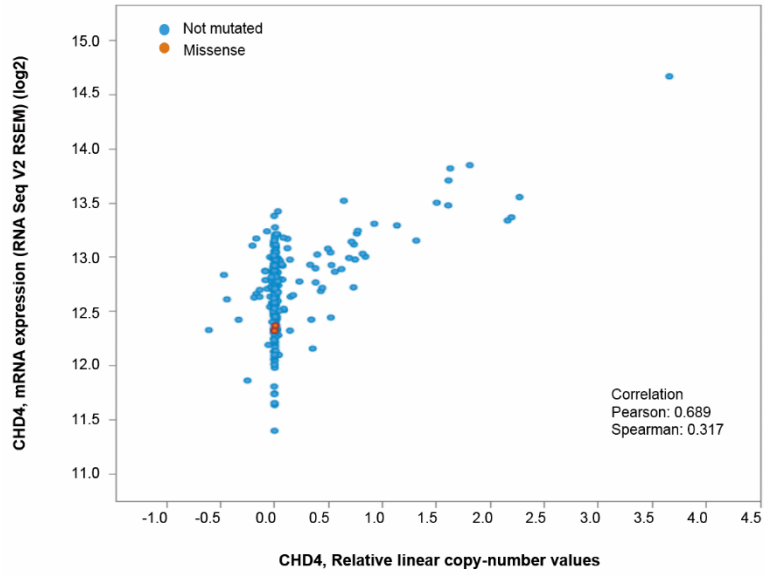
Supplementary Figure S4. CHD4 Copy number alteration (CNA) versus mRNA expression plot. X-axis: relative linear copy-number values. Y-axis: mRNA expression (RNAseq V2 RSEM) (log 2). Blue dots: not mutated. Red dots: missense mutation.