

Transcriptomic and connectomic correlates of differential spatial patterning among gliomas

SUPPLEMENTAL MATERIAL

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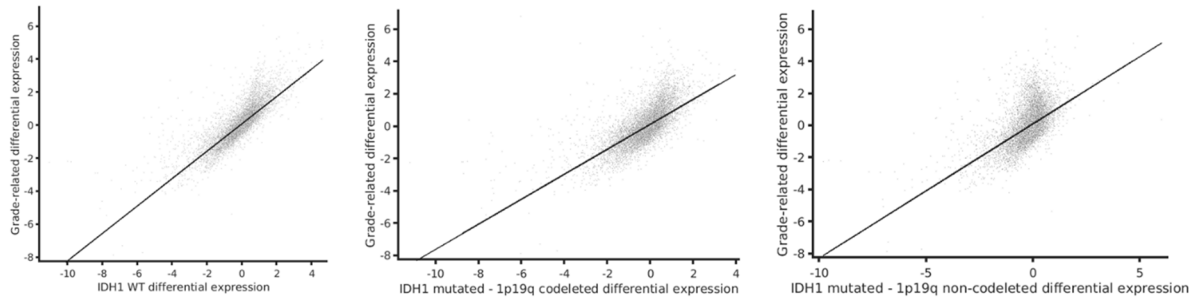


Figure S1. Association between expression values in bulk tissue (each point representing a gene) comparing GBM vs. LGG (grade-related) and IDH Wild Type vs. IDH1 Mutated (left), IDH mutated and 1p19q codeleted vs. all other cases (middle) and IDH mutated and 1p19q non-codeleted vs. all other cases (right).

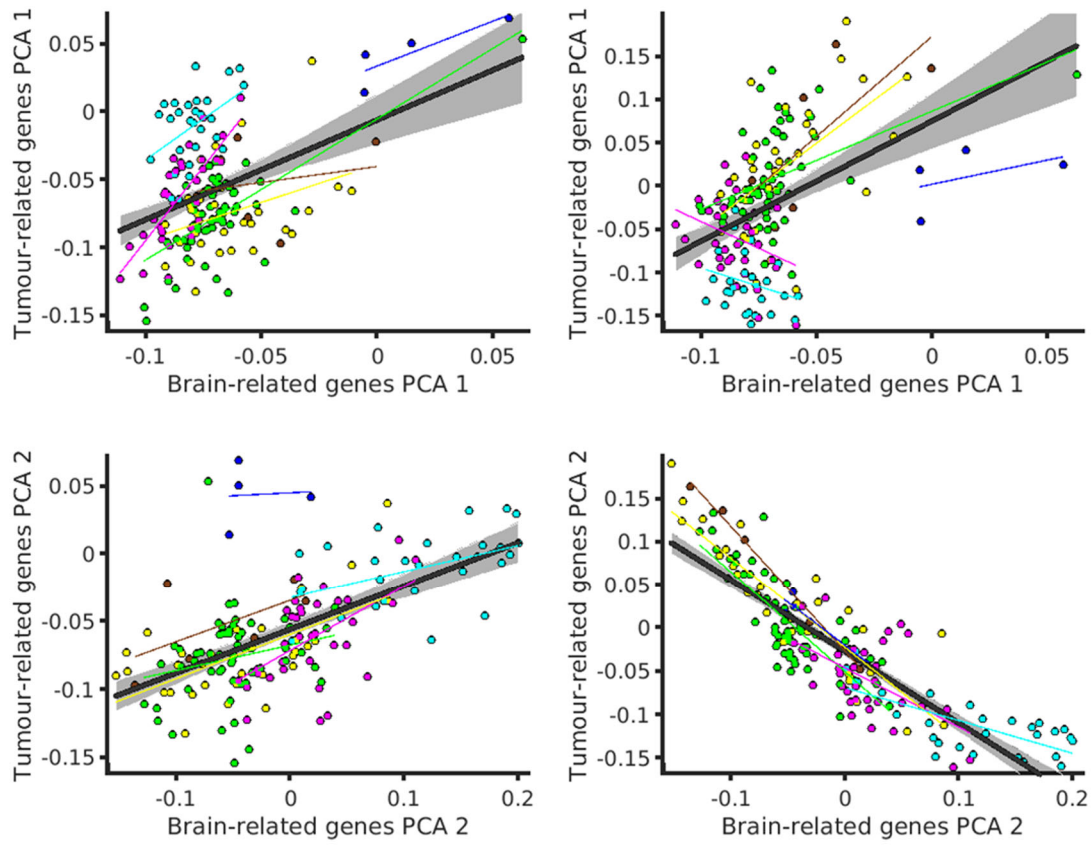


Figure S2. PCA components of brain-related gene expression are associated with PCA components of tumour-related gene expression.

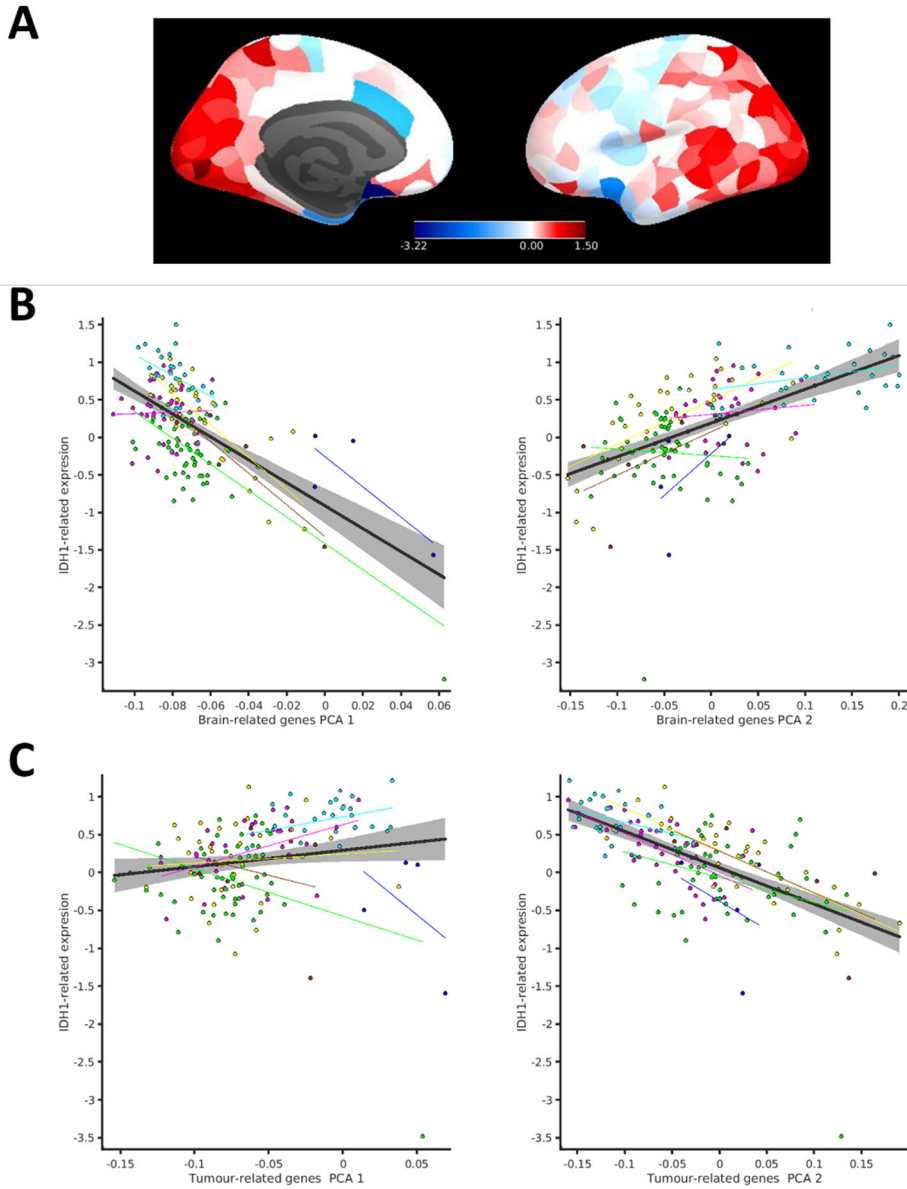


Figure S3. Regional pattern of genes differentially expressed in IDH1 wild-type and mutated tumour tissues. **A)** Regional expression of brain-related genes in controls weighted by differential expression in IDH1 Wild Type and IDH1 mutated tissues (z-scored). **B)** Association between IDH1-related expression (shown in A) and the first and second principal components of brain-related genes from the ABHA. **C)** Association between IDH1-related expression and the first and second principal components of tumour-related genes from the ABHA.

Modular decomposition

Functional networks
(Yeo et al. 2011)

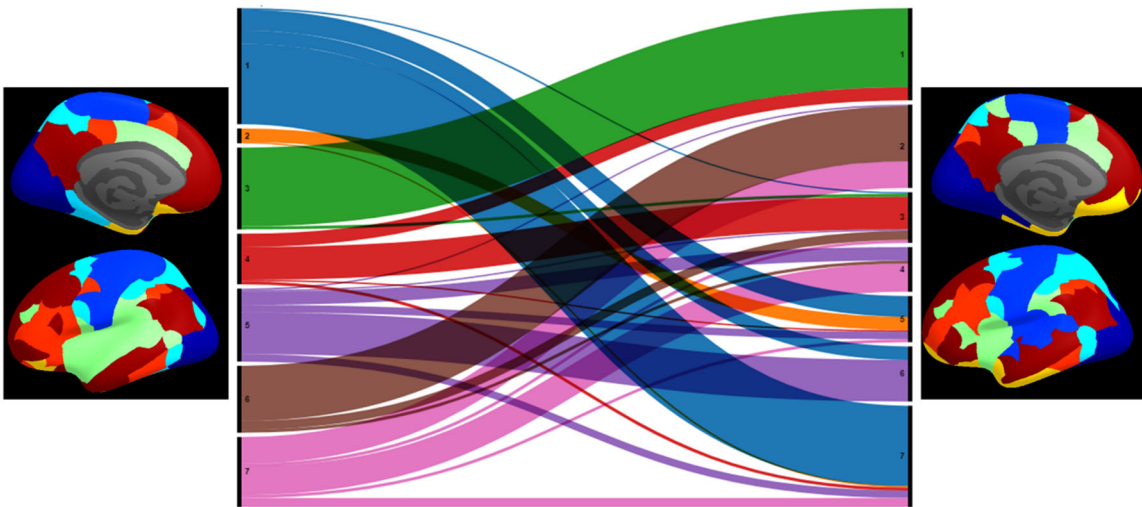


Figure S4. Modular decomposition of functional connectivity from UKBiobank individuals resembles functional networks from Yeo *et al.* (2011).¹

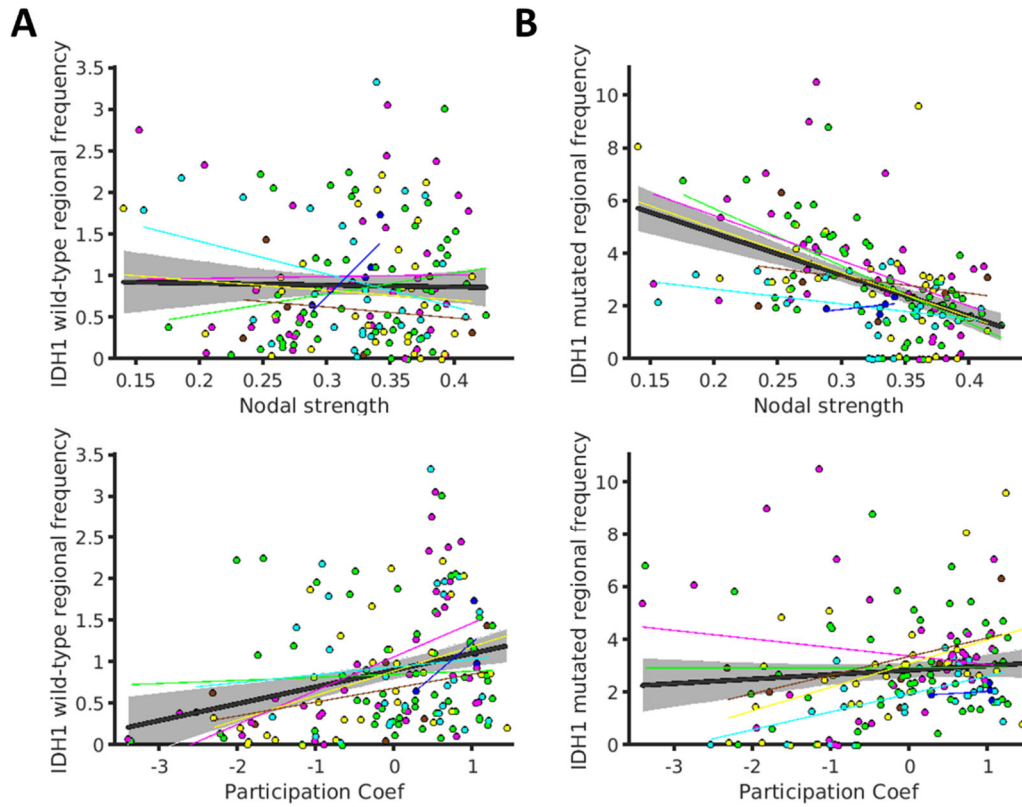


Figure S5. The regional distributions of IDH1 wild-type and mutated tumours are associated with brain network features. **A)** Association between IDH1 wild-type tumour regional frequency and nodal strength ($\rho = -0.04$, $P_{spin} = 0.58$) and participation coefficient ($\rho = 0.31$, $P_{spin} = 0.0002$). **B)** Association between IDH1 mutated tumour regional frequency and nodal strength ($\rho = -0.51$, $P_{spin} = 0.0001$) and participation coefficient ($\rho = 0.22$, $P_{spin} = 0.061$).

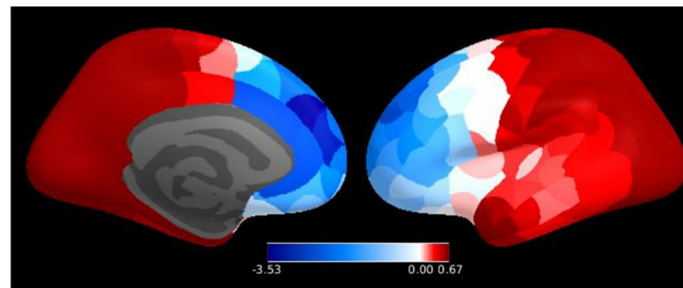
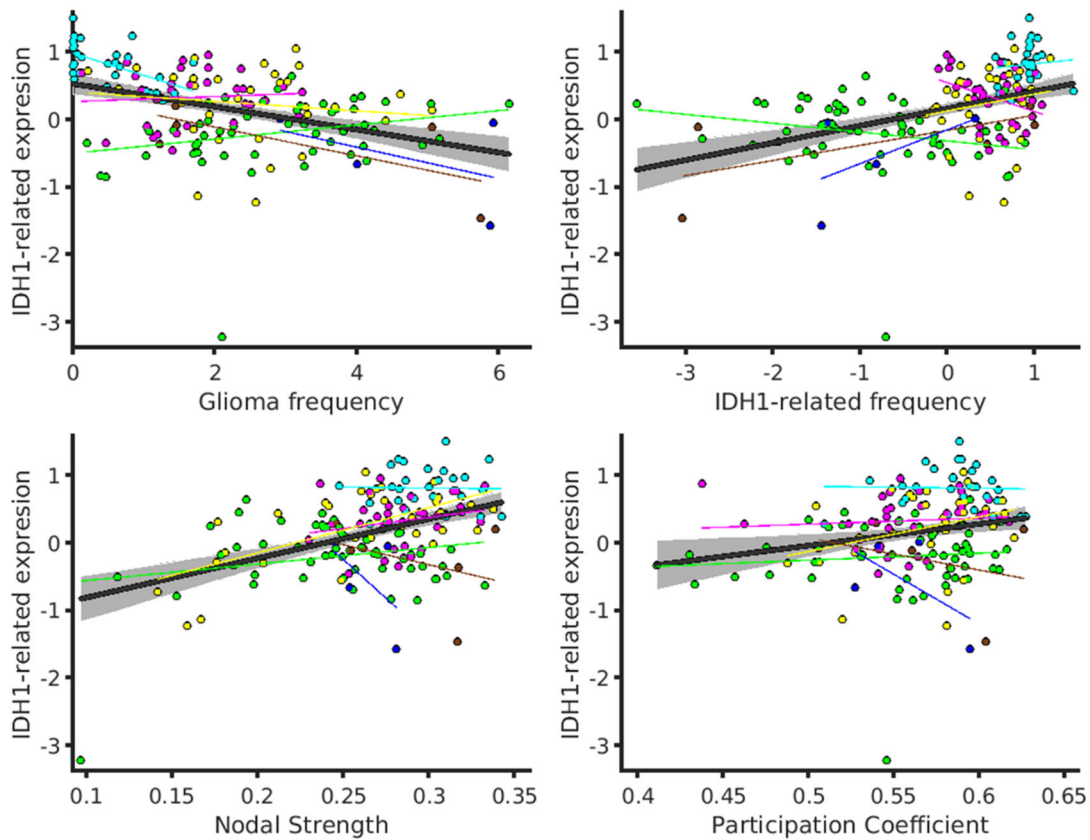
A**IDH1-related frequency****B**

Figure S6. Genes differentially expressed in IDH1 wild-type vs. mutated tissue are associated with imaging markers. **A)** IDH1-related frequency map created from subtracting and z-scoring the IDH1 wild-type and mutated tumour frequencies (i.e., occurrences) across brain regions. **B)** IDH1 differential expression association with glioma frequency (i.e., all tumour occurrences combined), IDH1-related expression, brain network nodal strength and participation coefficient.

Gene name	logCPM	P-value (FDR corrected)
IDH1	-0.96	2.04E-14
ATRX	0.56	0.00164
TERT	-	-
MGMT	-0.95	1.72E-06
EGFR	-0.62	0.08395
PDGFRA1	-	-
TP53	-0.65	1.67E-05
NF1	1.15	3.03E-25
MDM2	-3.29	5.05E-29
CDKN2A	-2.31	1.33E-10
CDKN2B	0.32	3.58E-01
PTEN	0.32	4.24E-04
PIK3CA	0.59	1.25E-05
MYCN	0.69	1.39E-02
CIC	0.12	2.64E-01
FUBP1	-0.08	0.5621
NOTCH1	0.70	0.00011
PI3K	-	-

Table S1. Differential expression between GBM and LGG bulk tissue of tumour-related genes. – indicates genes where expression values were not available. logCPM represents log counts per million with positive values indicating higher expression in GBM compared to LGG.

References

1. Yeo BT, Krienen FM, Sepulcre J, et al. The organization of the human cerebral cortex estimated by intrinsic functional connectivity. *J Neurophysiol.* 2011;106(3):1125-1165. doi:10.1152/jn.00338.2011