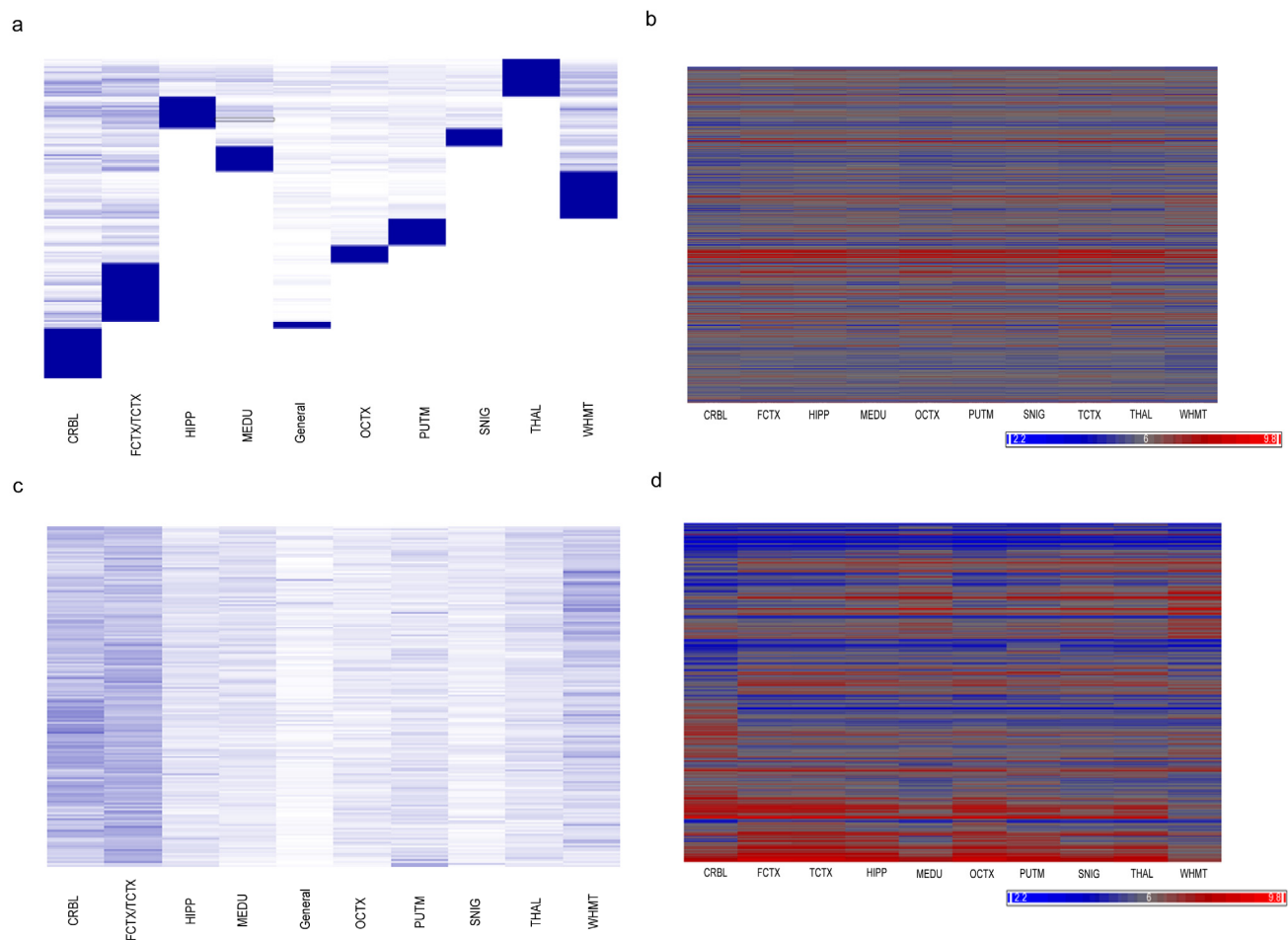


## Supplementary Figure 1

Summary of sample features and analyses.

(a) Summary of sample characteristics and demographic information. (b) Plots of principal component axes 1 and 3 of gene expression with each sample coloured on the basis of brain region of origin or individual of origin. Given the number of individuals (N=134) no key is provided within the figure. CRBL: cerebellar cortex; FCTX: frontal cortex; HIPP: hippocampus; MEDU: the inferior olivary nucleus (sub-dissected from the medulla); OCTX: occipital cortex; PUTM: putamen (at the level of the anterior commissure); SNIG: substantia nigra; TCTX: temporal cortex; THAL: thalamus (at the level of the lateral geniculate nucleus); WHMT: intralobular white matter. (c) Outline of the methods and analyses performed in this study.

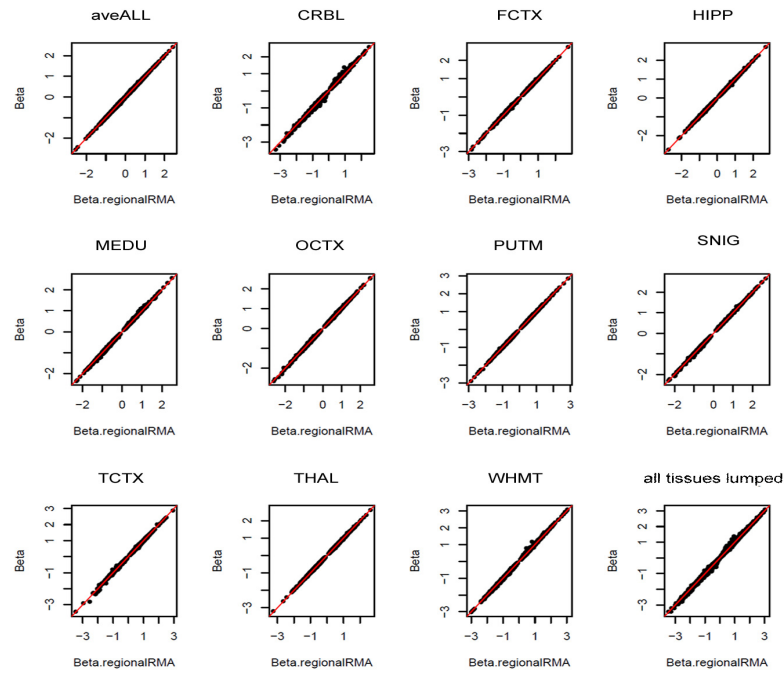


## Supplementary Figure 2

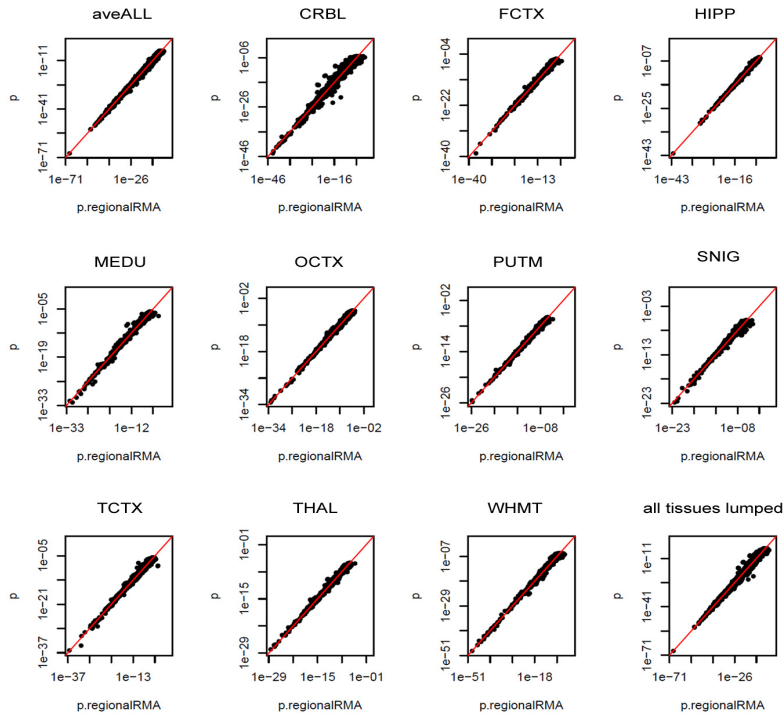
Comparison of *cis*-eQTL-based and expression-based clustering of gene expression

Rows relate to expression IDs in all panels. (a) Heatplot depicting membership of each expression ID within each of the ten *cis*-eQTL clusters identified in Figure 1a (labelled according to the brain region it is most associated with). Expression IDs are ordered according to *cis*-eQTL-based clustering (as depicted in Figure 1a). (b) Heatplot depicting gene expression in all ten brain regions. Expression IDs are ordered according to *cis*-eQTL-based clustering (as depicted in Figure 1a). (c) Heatplot depicting membership of each expression ID within each of the ten *cis*-eQTL clusters identified in Figure 1a (labelled according to the brain region it is most associated with). Expression IDs are ordered according to expression-based clustering (as depicted in Figure 1b). (d) Heatplot depicting gene expression in all ten brain regions. Expression IDs are ordered according to expression-based clustering (as depicted in Figure 1b). CRBL: cerebellar cortex; FCTX: frontal cortex; TCTX: temporal cortex; HIPP: hippocampus; MEDU: the inferior olivary nucleus (sub-dissected from the medulla); OCTX: occipital cortex; PUTM: putamen (at the level of the anterior commissure); SNIG: substantia nigra; THAL: thalamus (at the level of the lateral geniculate nucleus); WHMT: intralobular white matter.

a



b



### Supplementary Figure 3

The effect of normalization approaches on *cis*-eQTL signals.

(a) Comparison of the regression coefficients for *cis*-eQTL analysis when all tissues are normalized together vs. when each tissue is normalized separately. (b) Comparison of the p-value of regression coefficients for *cis*-eQTL analysis when all tissues are normalized together vs. when each tissue is normalized separately.