Fig S1. The genes Brawand et al found to have changed their expression significantly in human also have high Z score. Genes listed with significant lineage-specific expression switches in human in Brawand et al. are divided in two groups: Brawand's significant genes which are Z score positive (in blue) and the ones with negative Z scores (in yellow). These two subsets are then plotted against the rest of the genes, shown in green, across different tissues. There was no Z score negative gene in 4 genes Brawand found to have significantly changed their expression in human brain. Please also note that genes found to have extremely high or low Z score have been removed from this plot to improve clarity of comparison between our method and Brawand et al's method.

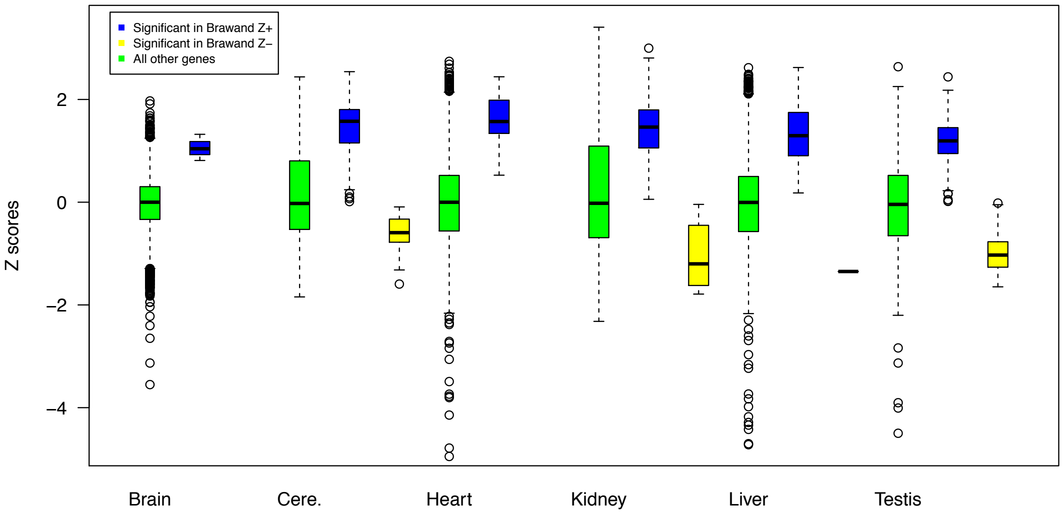
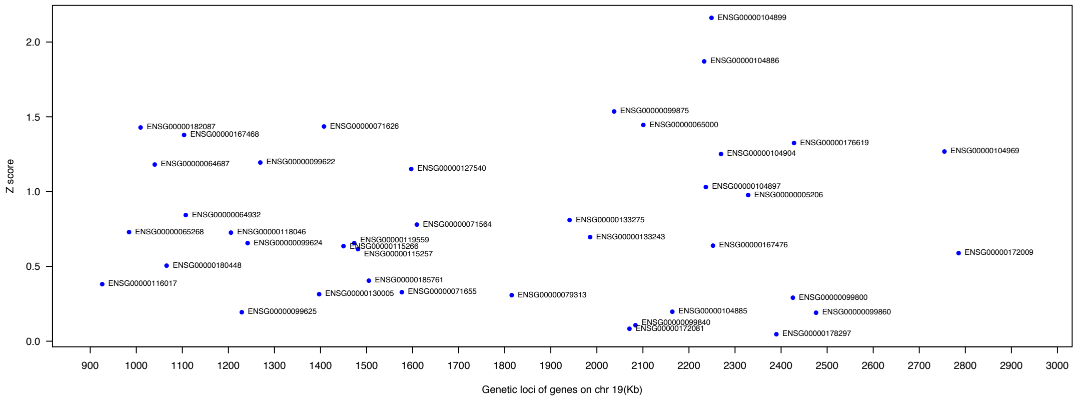
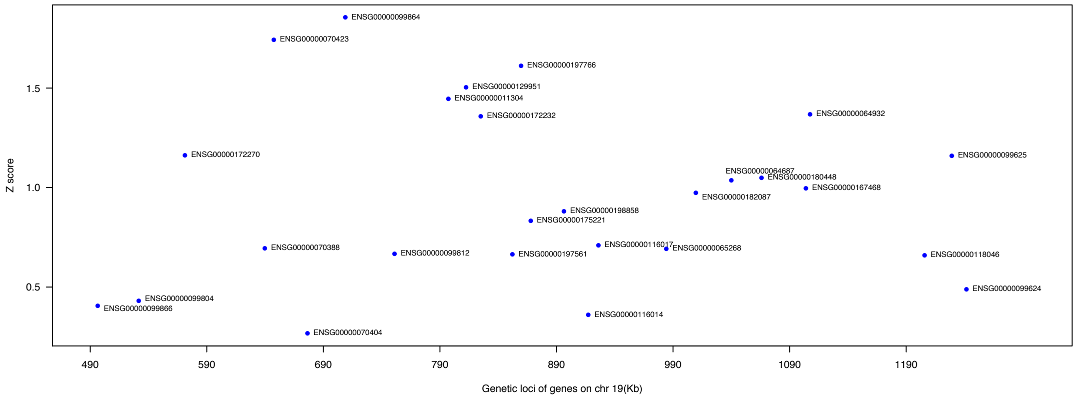


Fig S2a. Examples of large positive Z clusters

Male Kidney – Positive Z Cluster Example



Testis – Positive Z Cluster Example 1



Testis – Positive Z Cluster Example 2

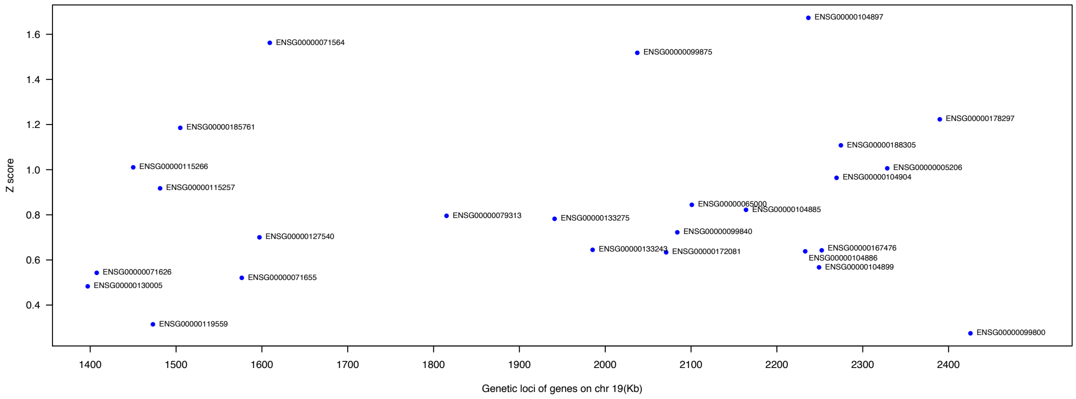
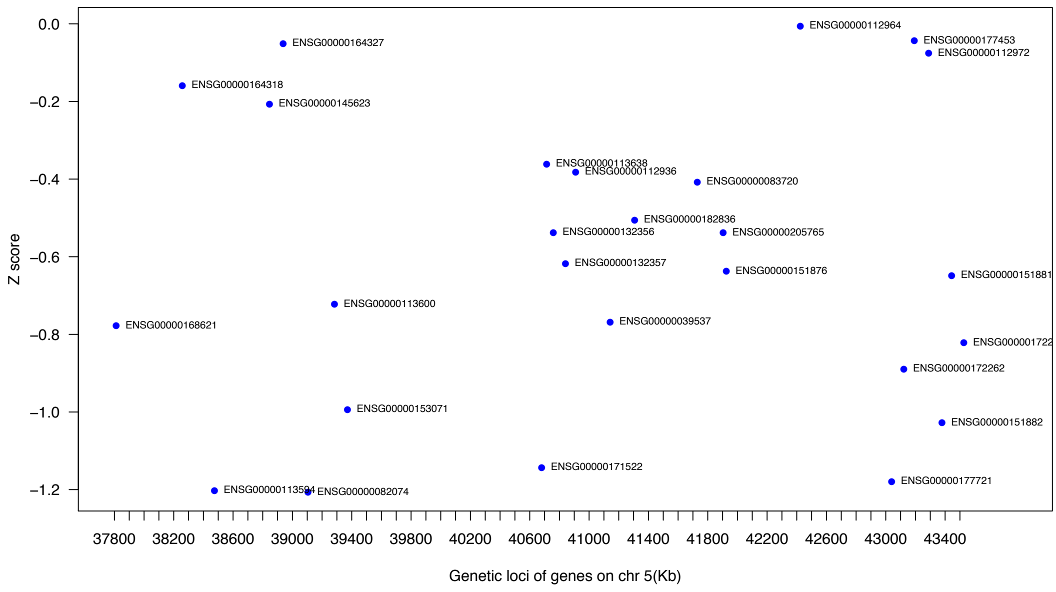


Fig S2b. Examples of large negative Z clusters


Male Cerebellum – Negative Z Cluster Example

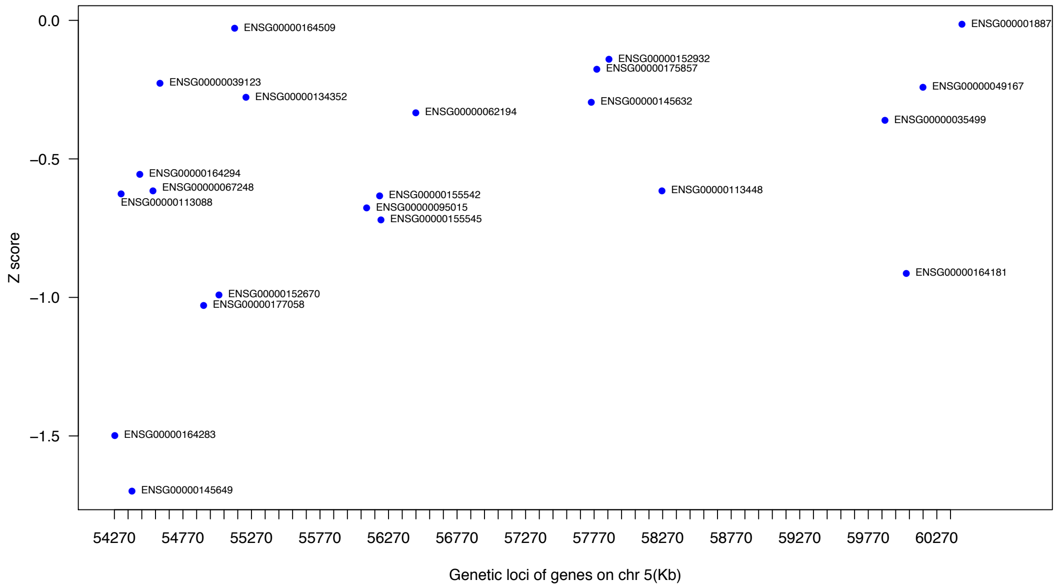

Male Heart – Negative Z Cluster Example

Fig S3. Genes showing increase in expression across all tissues or decrease in expression across all tissues are more common than expected by chance. The sign of Z score indicates the direction of change in gene expression across time (from common ancestor to human). One may represent Z positive genes with +1 and Z negative with -1, keeping zero Z scores unchanged, and calculate for each gene their sum across 6 male tissues. Genes with sums equal to +6 (or -6) have gone up (or down) across all 6 tissues. The number of concerted up-regulated genes is shown by the right-most bar in histogram and the number of concerted down-regulated genes is shown by the left-most bar. Null expectations are shown in blue. Null is derived from randomizations in which the number of Z+, Z- and Z=0 genes are kept the same as observed, but the gene order is randomised across tissues. Errors bars are +/-SD from 1000 simulations.

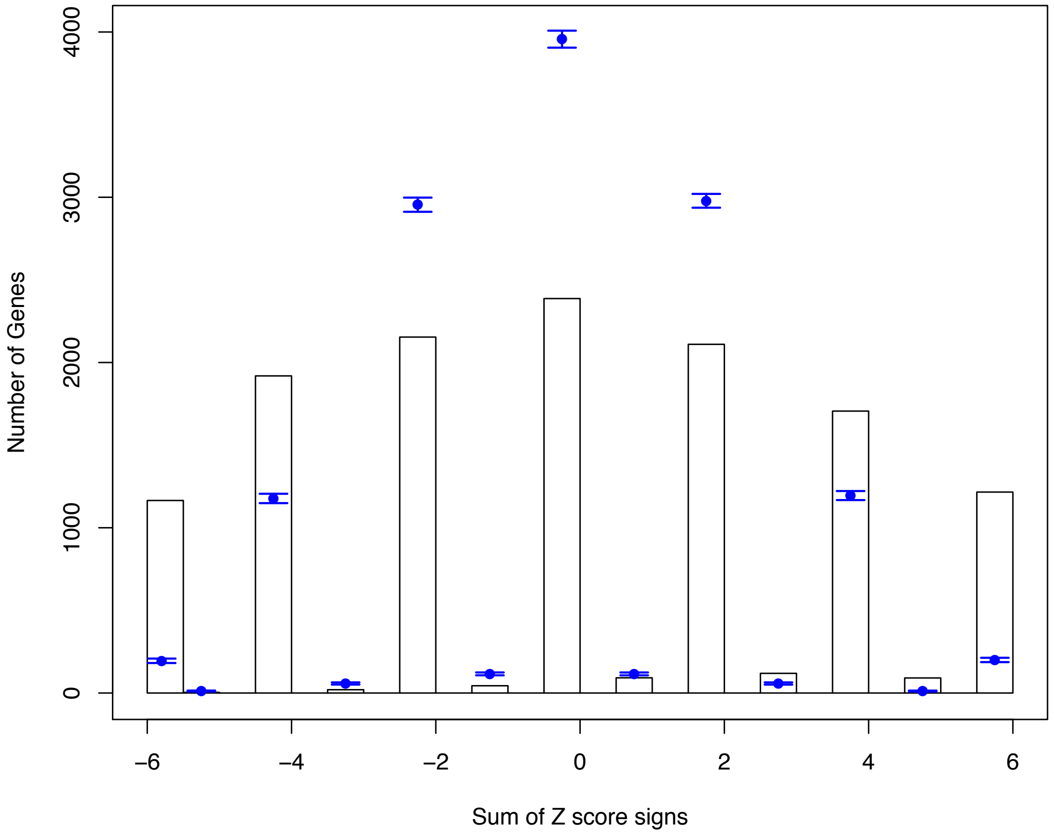


Fig S4. Positive Z score clusters are denser in most tissues except in brain. Positive Z score clusters are shown in green and negative ones in red. The effect is most pronounced in male kidney.

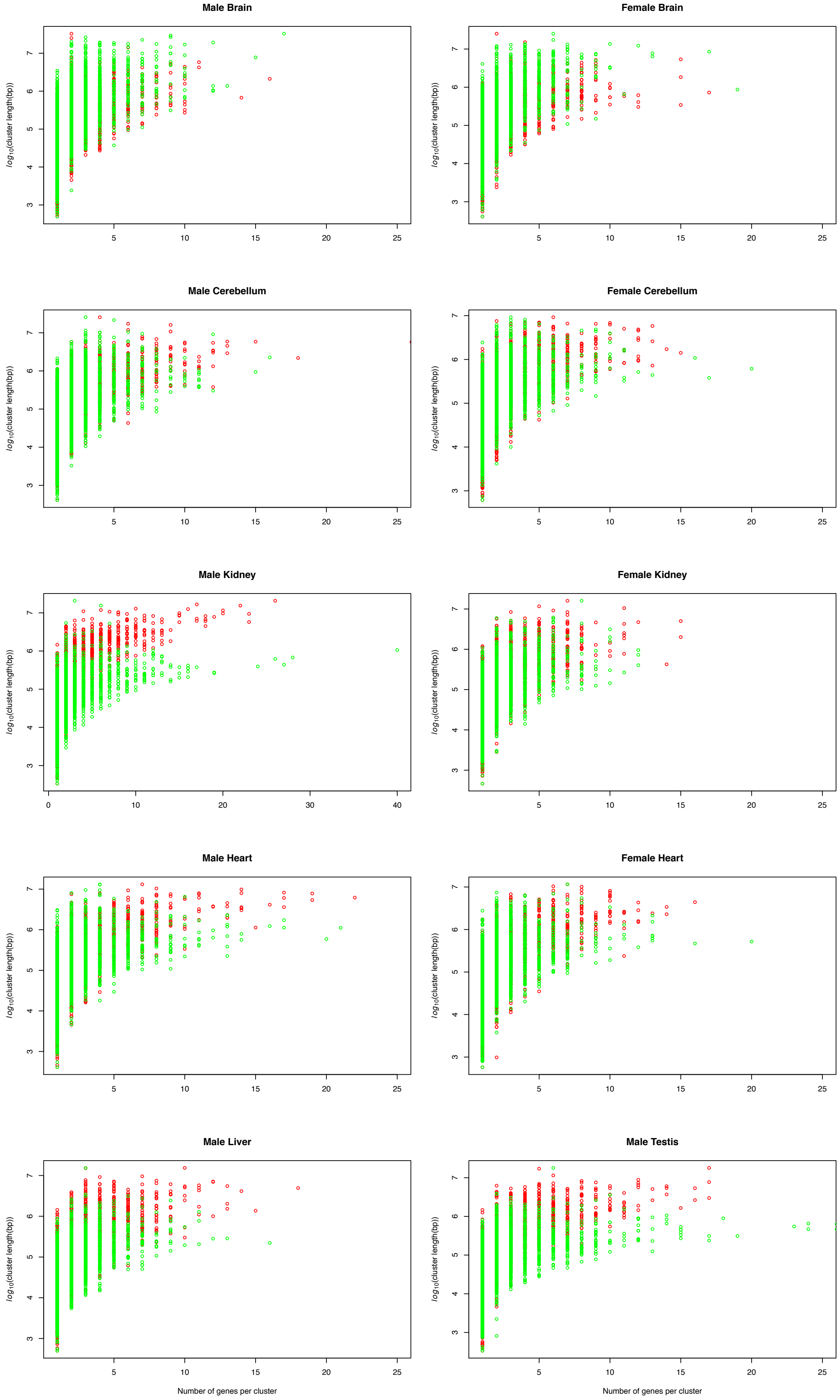


Fig S5. The longest concerted Z score positive cluster based on expression profile in males

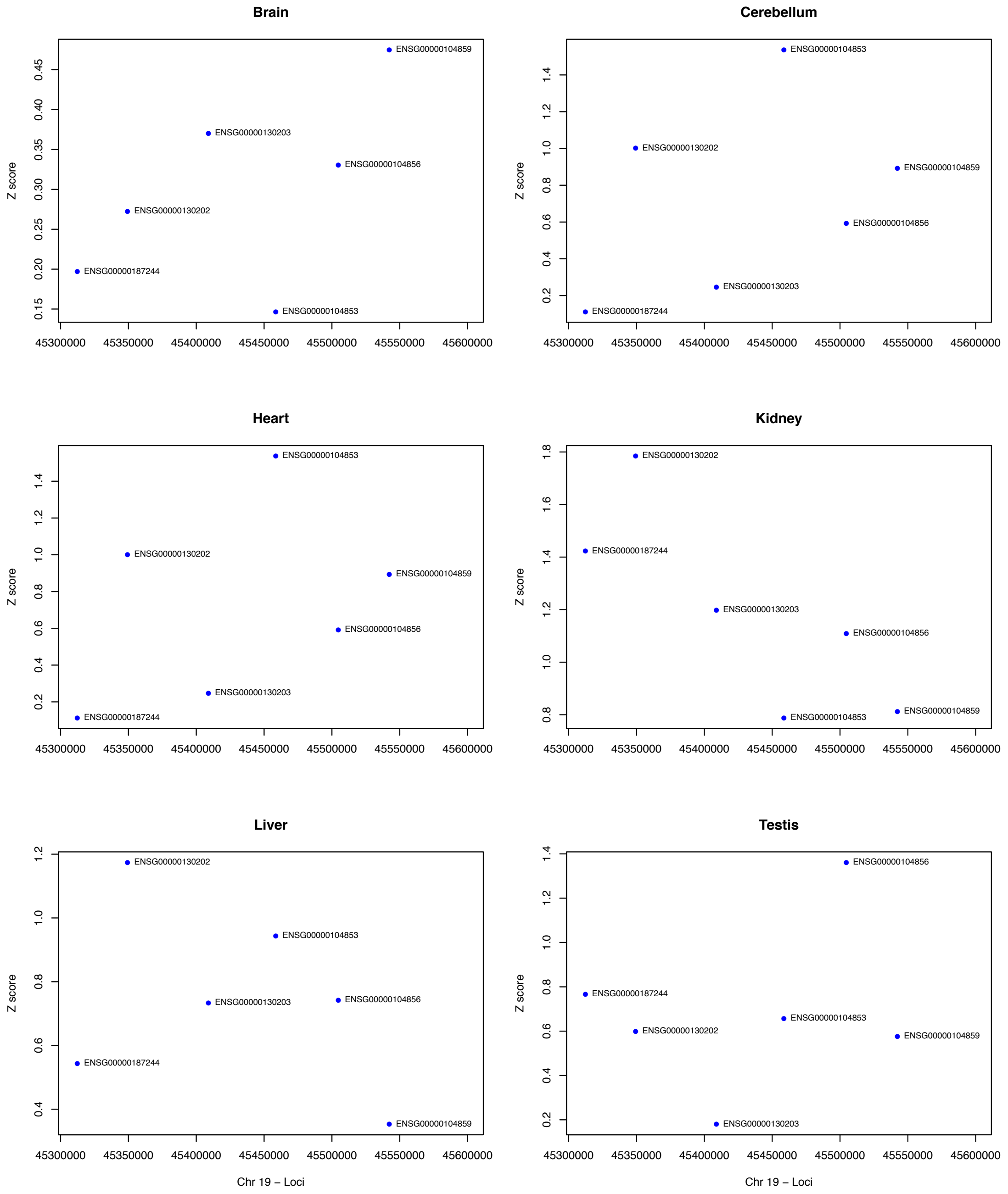


Fig S6. Tissue-specific up-regulated genes tend to be in domains of low gene density compared to genes with concerted change in expression across all 6 tissues. Number of genes in ±100Kb window around the tissue-specific up-regulated and concerted genes are shown below. There is a significant difference between number of genes in ±100Kb of focal genes is tissue-specific genes compared to concerted ones, Mann-Whitney U test *P-value* = 1.26e-43.

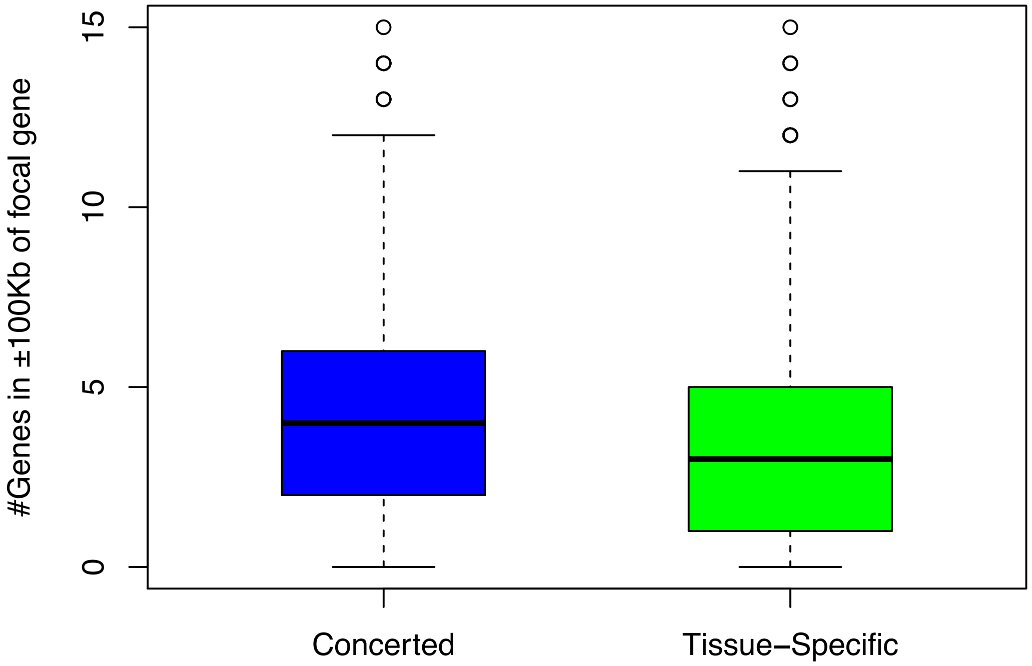


Fig S7. Mean of Z scores of genes across 6 tissues in the vicinity of fusion point on human chromosome 2. Means are averages across all tissues. Error bars indicate SEM. The vertical line indicates the approximate location of the fusion zone.