Supplement 2

The figures indicate the mean values for a given feature in various tissues plotted according to different EV percentiles. The x-axis starts from 5% most hypo-variable and increments 5% upto 50%. This is followed by 50% most hyper-variable decrementing by 5% down to 5%. The names of tissues where a significant linear regression correlation was observed are colored red (positive) and blue (negative).

For DHS, histone marks, and intrinsic disorder, values are transformed using ln(x/(1-x)), where x is the fraction of base pairs in the given region that exhibit the feature. Conservation values are mean PhastCons scores. Values for gene and transcript size are base pairs. CNV and disease genes are shown as fractions of their percentile. Protein–protein interaction is quantified as mean node degree.

FEATURES

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Figure 1. DHS 2kb upstream 1.1 airway_epithelial_cells 1.2 astrocytes 1.3 breast_epithelial_cells 1.4 breast_stroma 0000000000 00000000 000000000 -2.0 -2.0 -2.0 00000000 0000000 0000000 -3.0 001 -3.0 -3.0 0 4.0 4.0 4.0 4.0 1.5 cd4+_t_cells 1.6 cerebellum 1.7 hippocampus 1.8 prostate_gland 000000000 00000000 0000000000 000000000 -2.0 -2.0 000000000 00000 -3.0 -3.0 -3.0 -3.0 -4.0 4.0 4.0 4.0 1.9 skeletal_muscle 1.10 skin 000000000 -2.0 -2.0 000000000 000000000000 00000000 -3.0 4.0 4.0

Figure 2. DHS 5kb upstream 2.1 airway_epithelial_cells 2.2 astrocytes 2.3 breast_epithelial_cells 2.4 breast_stroma 000000000 000000 -2.5 00000000 -2.5 -2.500000000 00000000 -3.0 -3.0 -3.0 0 001 -3.5 -3.5 -3.5 4.0 -4.0 0.4 4.0 2.7 hippocampus 2.5 cd4+_t_cells 2.6 cerebellum 2.8 prostate_gland +00000000 000000000 -2.5 -2.5 -2.5 00000000 -3.0 00000 -3.5 -3.5 -3.5 -3.5 4.0 -4.0 -4.0 -4.0 2.9 skeletal_muscle 2.10 skin -2.5 -2.5 000000000 000000000 -3.0 -3.0-3.5

-4.0

-4.0

Figure 3. DHS gene body 3.1 airway_epithelial_cells 3.2 astrocytes 3.3 breast_epithelial_cells 3.4 breast_stroma -2.5 -2.5 -2.5 -2.5 00000000 -3.0 -3.0 -3.0 0 -3.5 -3.5 -3.5 -3.5 3.5 cd4+_t_cells 3.6 cerebellum 3.7 hippocampus 3.8 prostate_gland 000000000 -2.5 -2.5 -2.5 -2.5 00000000 000000000 -3.0 -3.0 00000000000000 -3.5 -3.5 -3.5 -3.5 3.10 skin 3.9 skeletal_muscle 0000000000 -2.5 -2.5 0000000 -3.0 0000000 000000000

0

-3.5

Figure 4. DHS gene + flanks
2 astrocytes 4.3 breast_epithelial_cells 4.1 airway_epithelial_cells 4.2 astrocytes 4.4 breast_stroma -2.6 -2.6 -2.6 -2.6 00000000 -3.0 -3.0 -3.0 0 -3.4 -3.4 3.4 4.5 cd4+_t_cells 4.6 cerebellum 4.7 hippocampus 4.8 prostate_gland 00000000 -2.6 -2.6 -2.6 -2.6 000000000 0000000 °00000000 00000000 -3.0 -3.0 -3.0 000000000 0 -3.4 -3.4 3.4 4.9 skeletal_muscle 4.10 skin 0000000000 -2.6 -2.6 -3.0 -3.4 -3.4

Figure 5. H3K4me3 2kb upstream 5.3 breast_stroma 5.1 airway_epithelial_cells 5.2 breast_epithelial_cells 5.4 cerebellum 5.5 skeletal_muscle 5.6 skin ī က

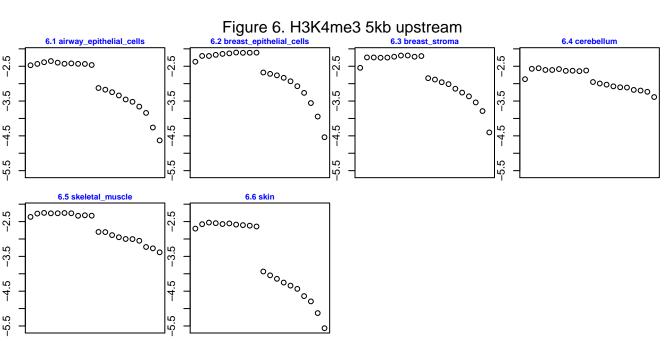
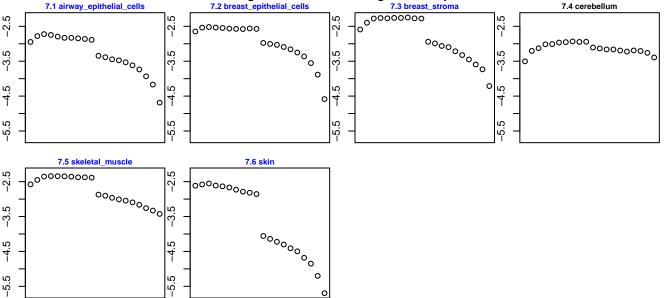
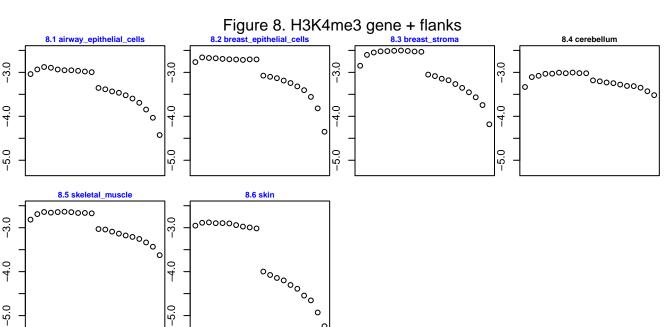
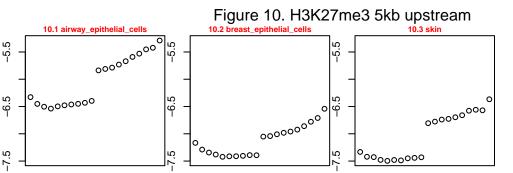


Figure 7. H3K4me3 gene body 7.2 breast_epithelial_cells 7.3 breast_strom







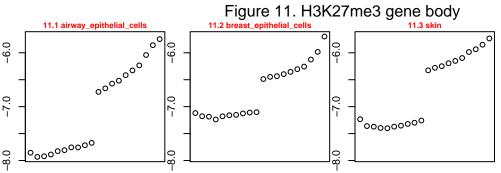


Figure 12. H3K27me3 gene + flanks 12.2 breast_epithelial_cells 12.3 skin

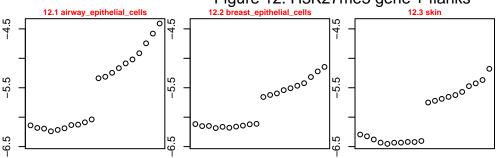


Figure 13. H3K36me3 2kb upstream

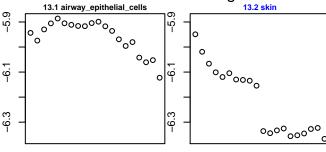


Figure 14. H3K36me3 5kb upstream

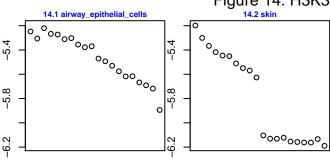


Figure 15. H3K36me3 gene body

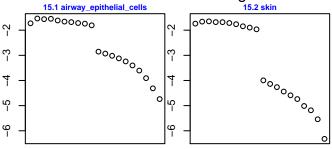
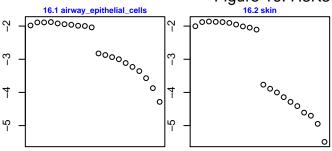
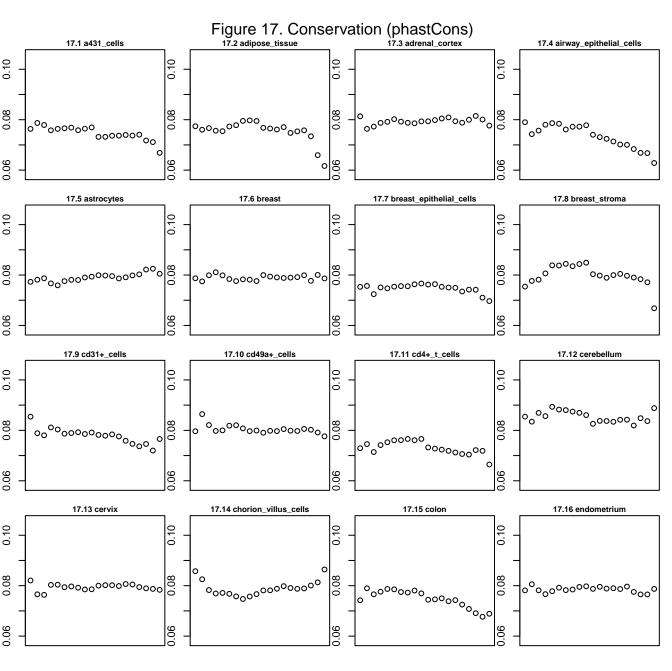
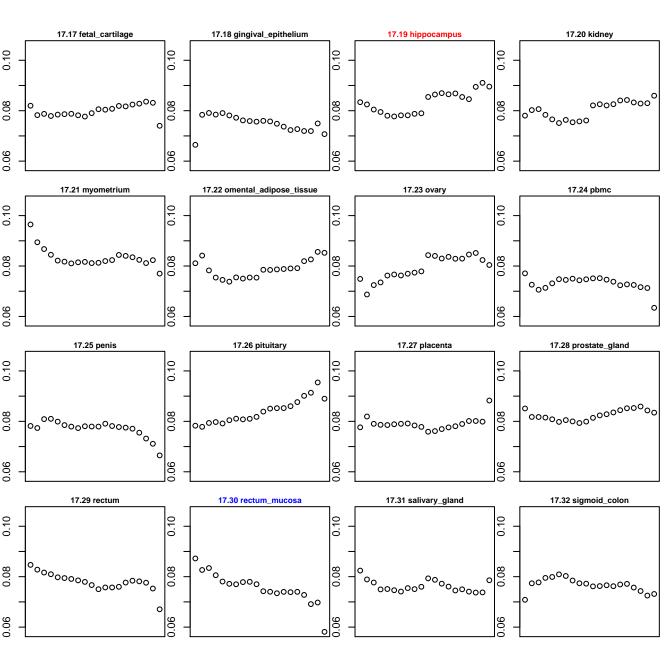


Figure 16. H3K36me3 gene + flanks







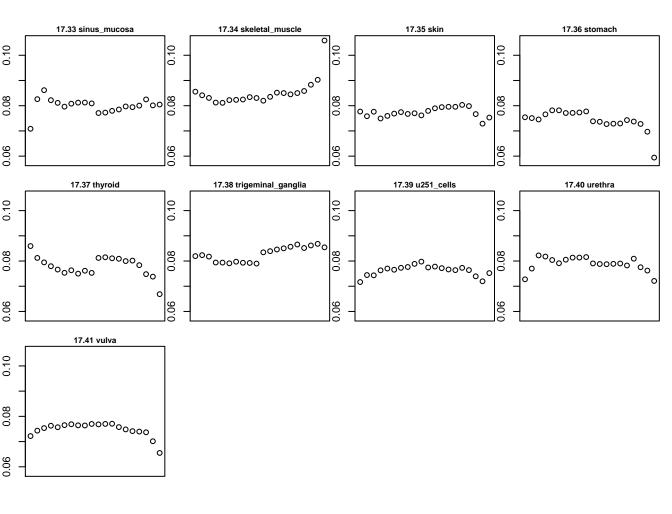
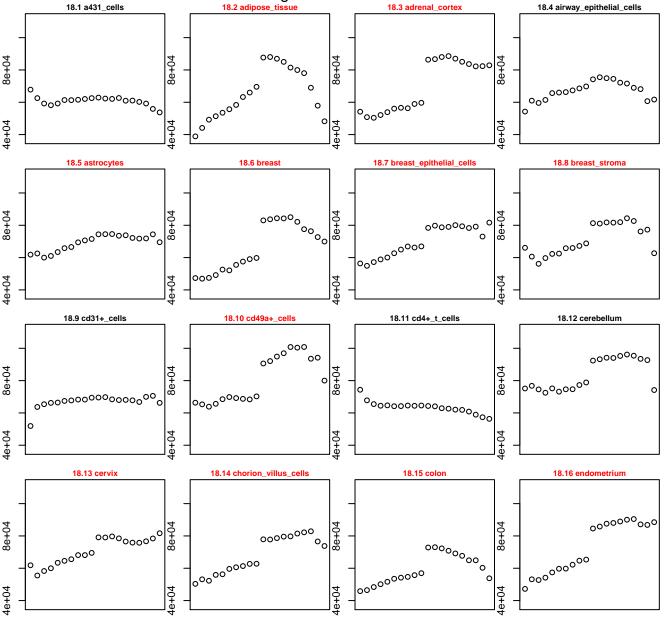
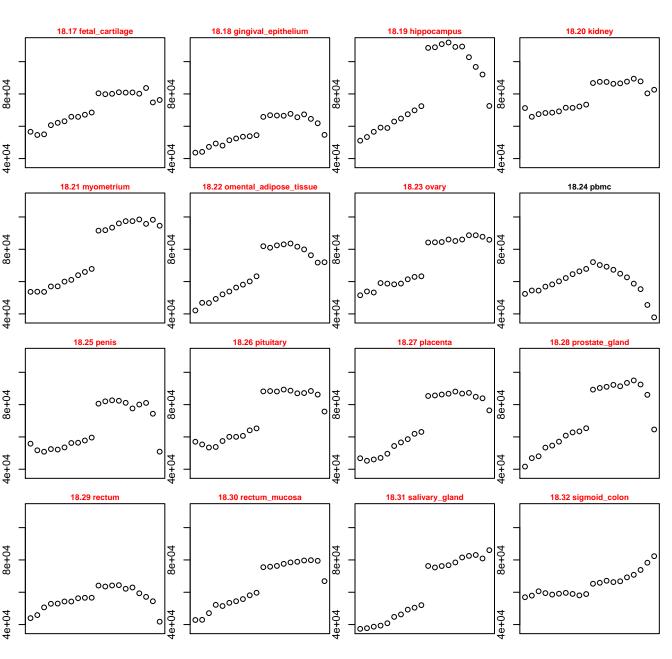


Figure 18. Gene Size





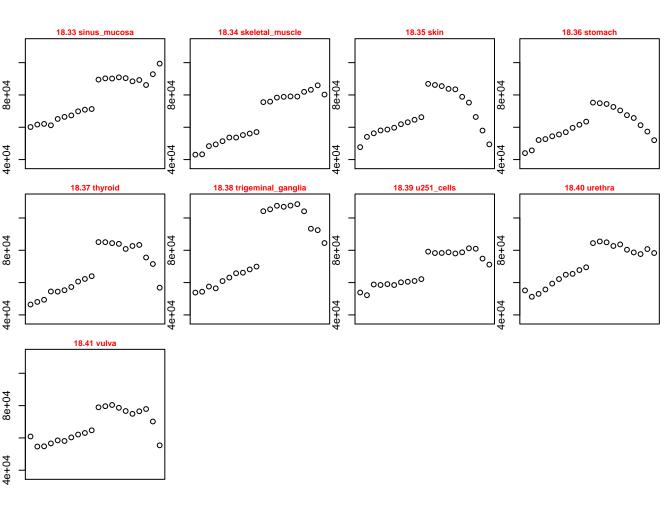
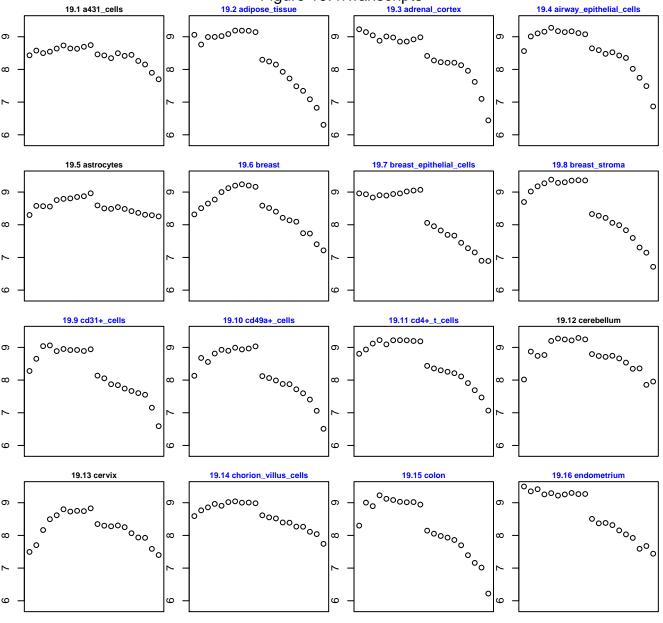
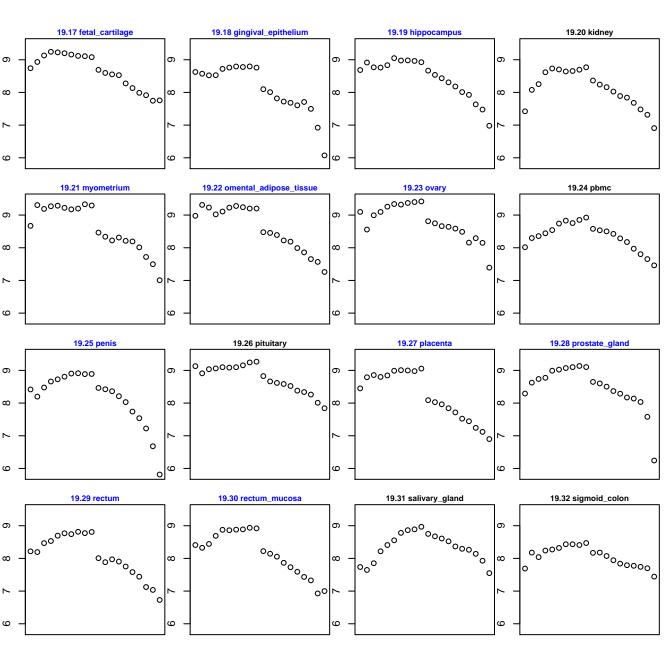


Figure 19. nTranscripts





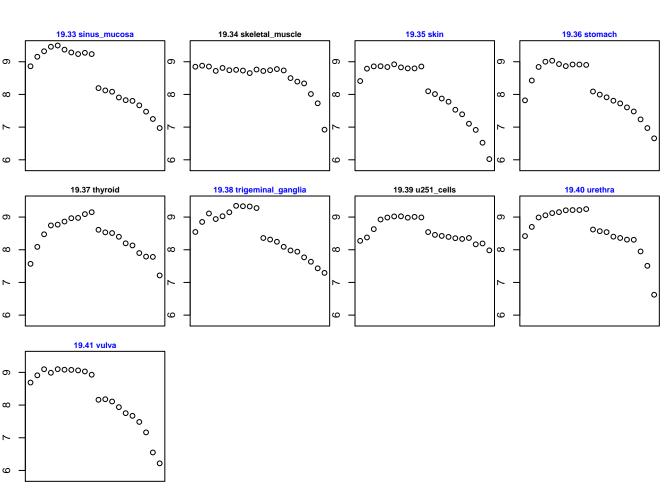
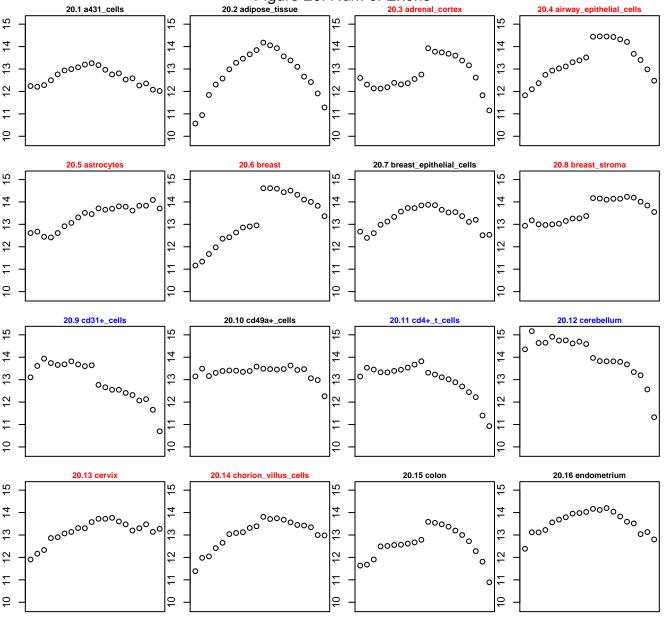
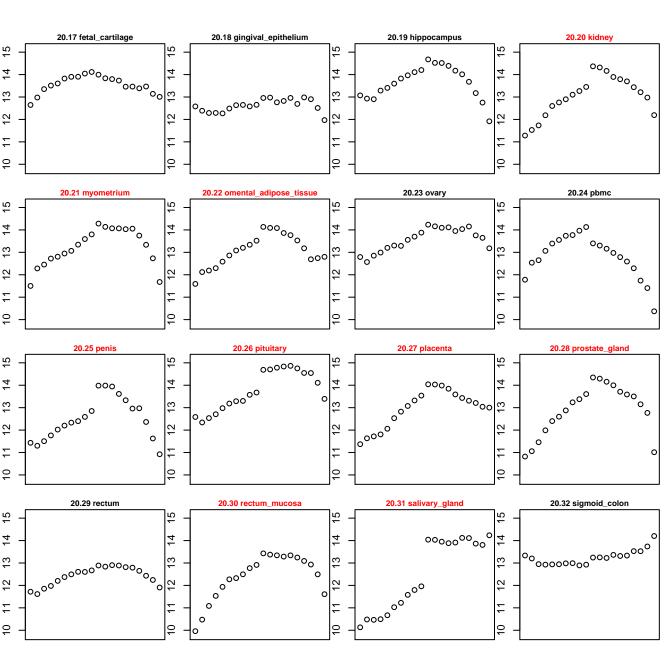


Figure 20. Num of Exons





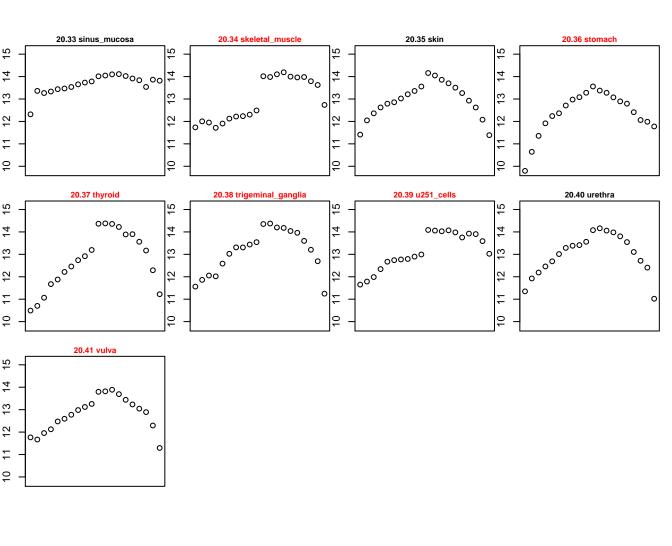
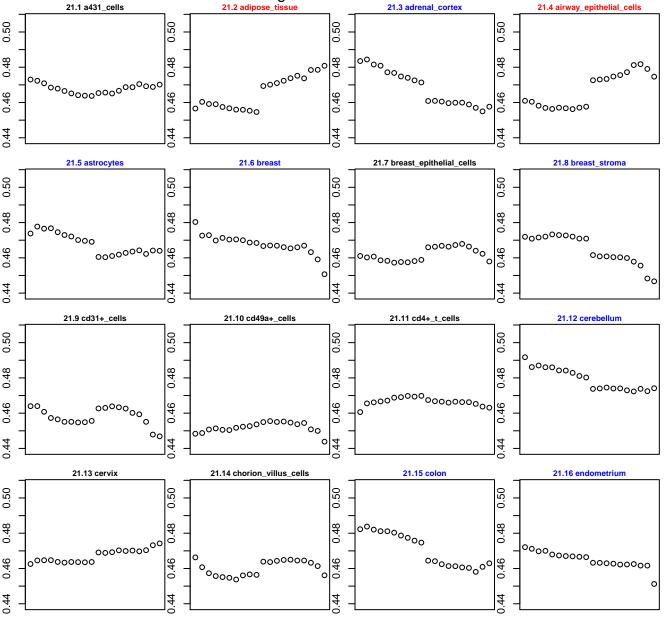
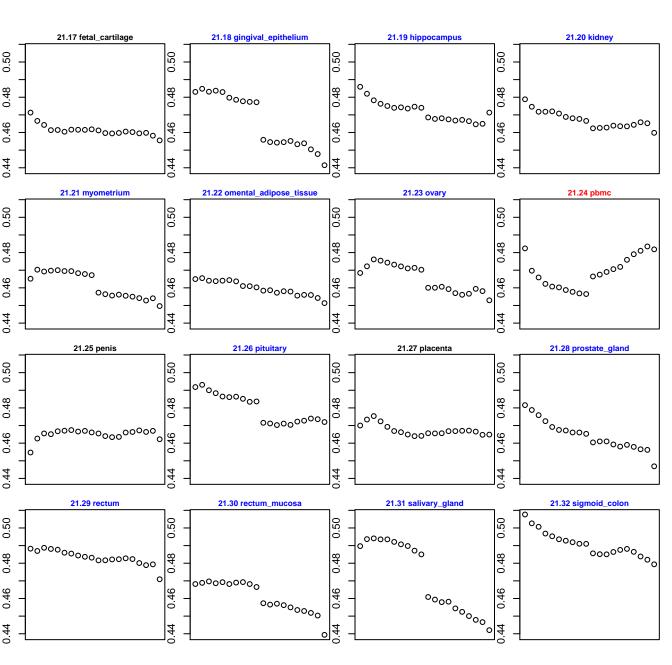


Figure 21. GC fraction





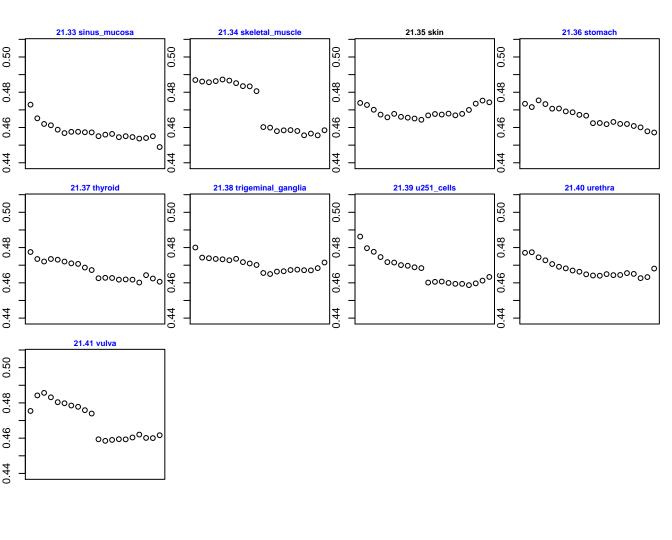
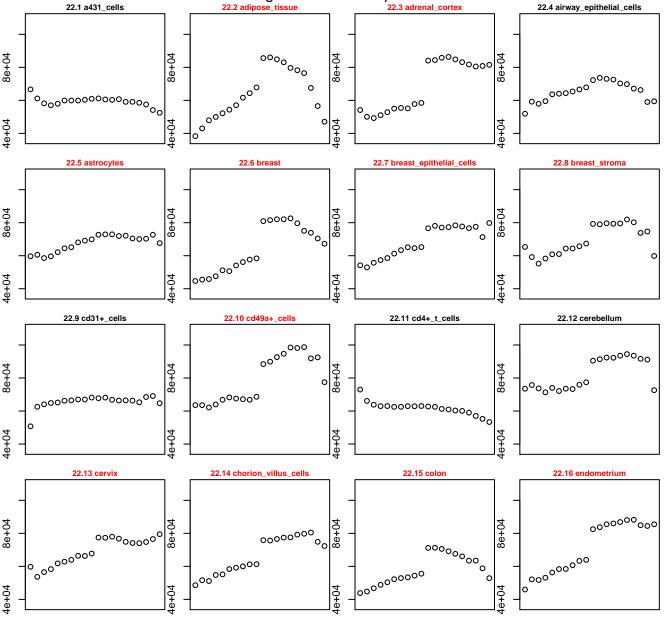
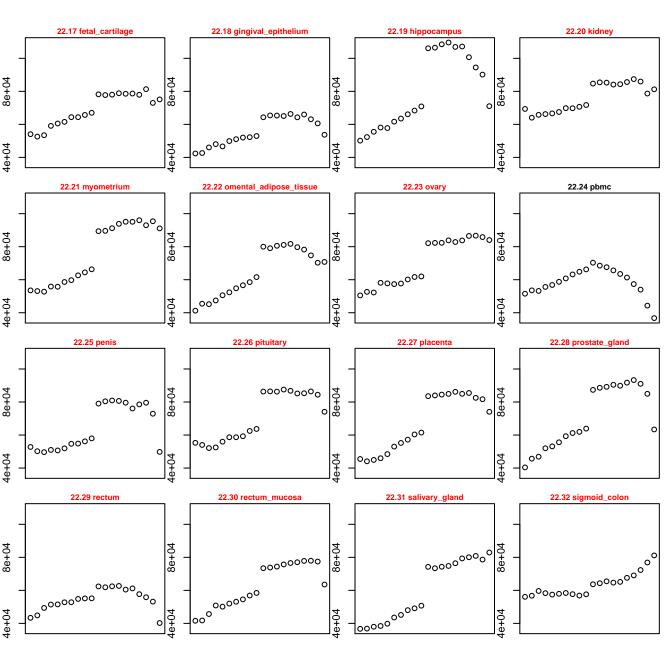
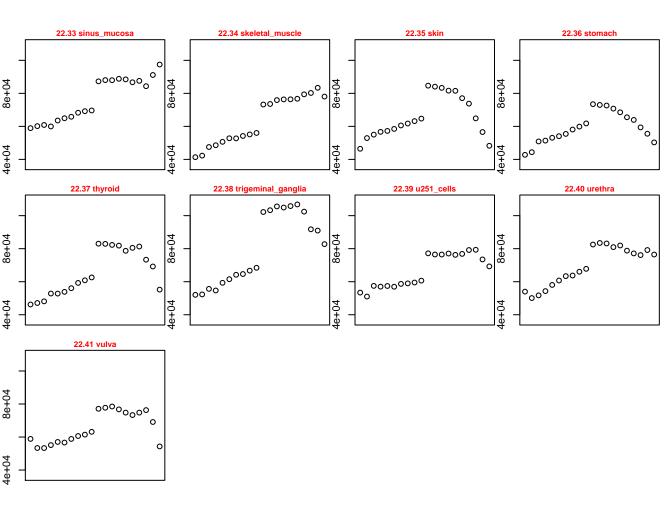
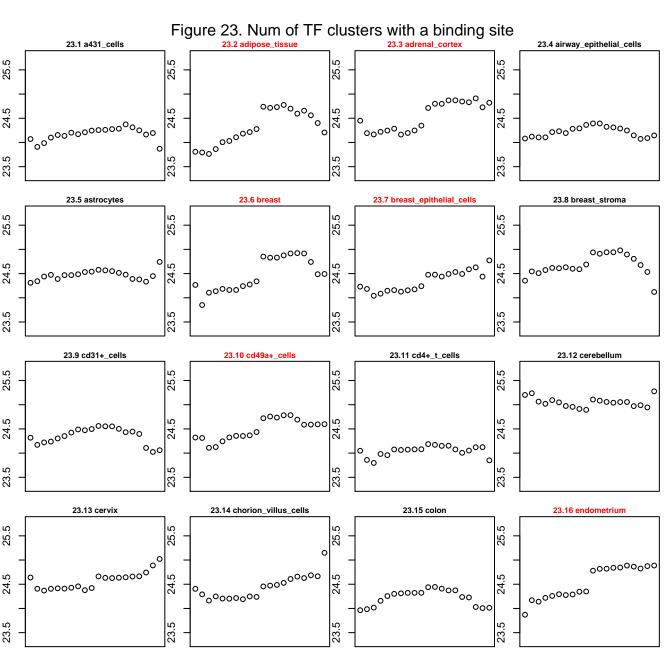


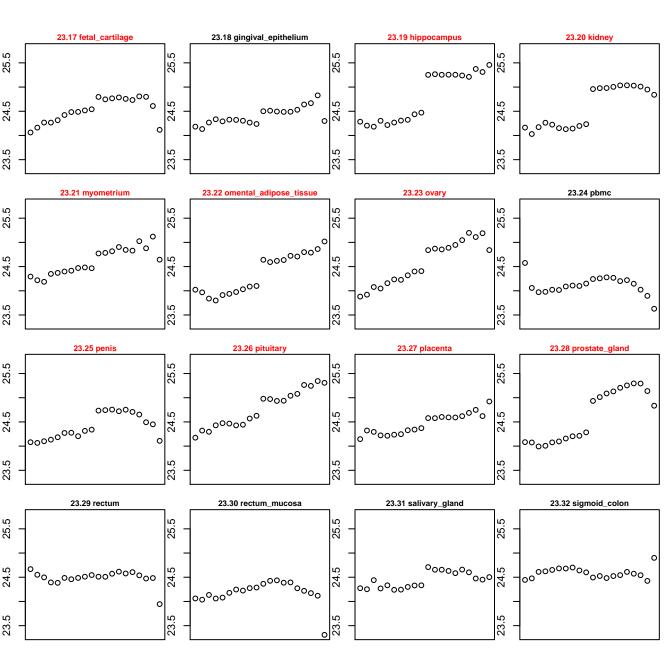
Figure 22. Transcript Size











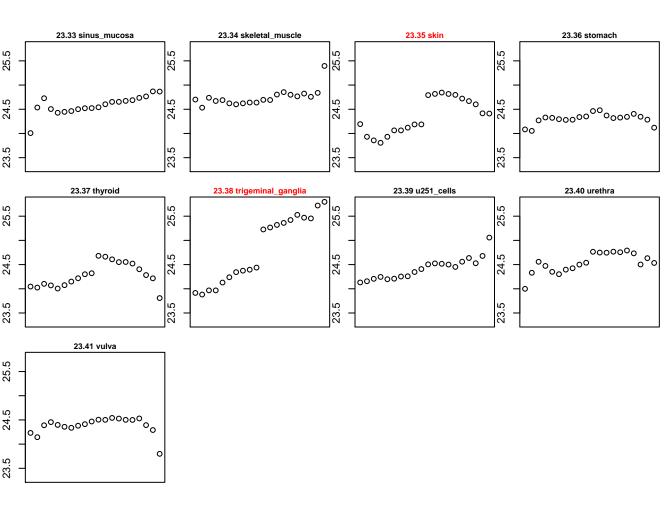
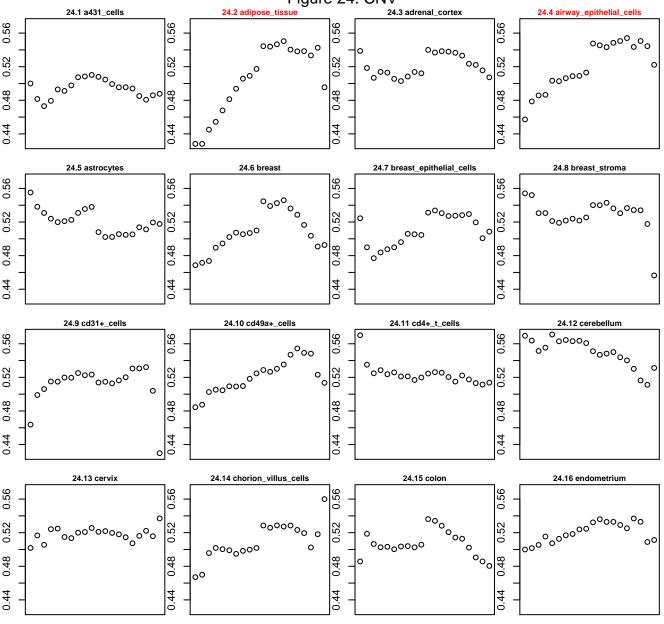
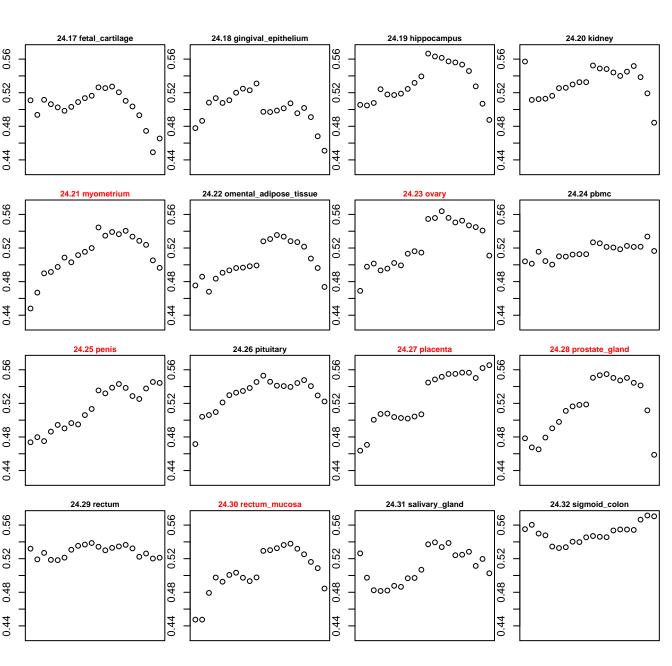


Figure 24. CNV





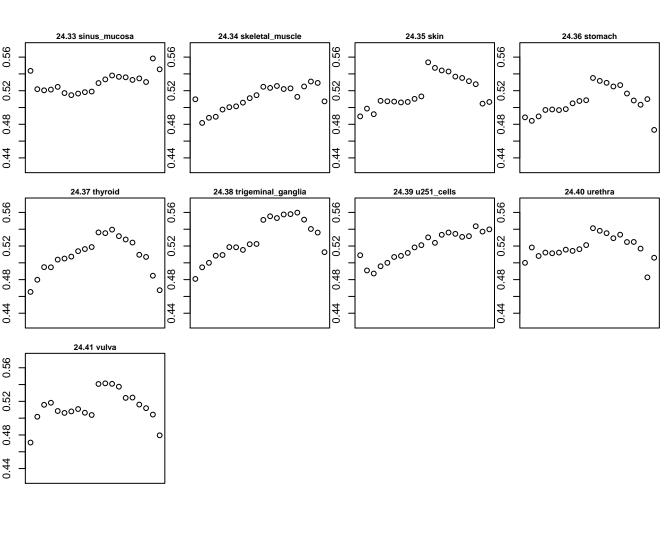
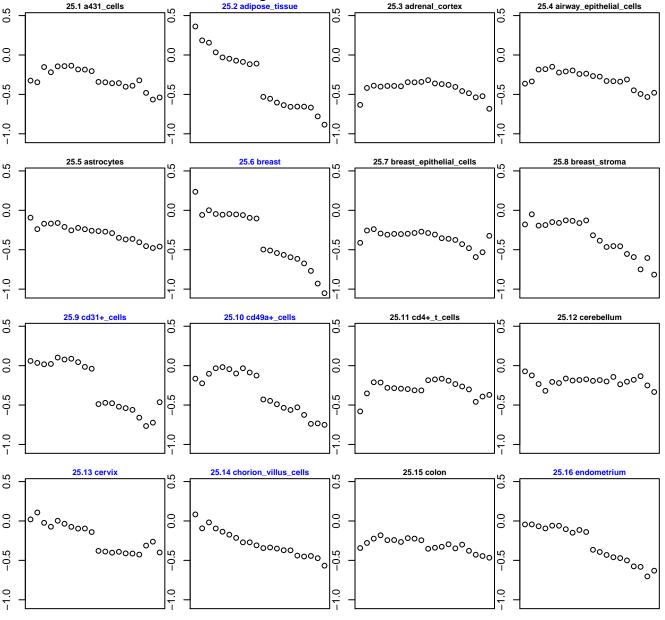
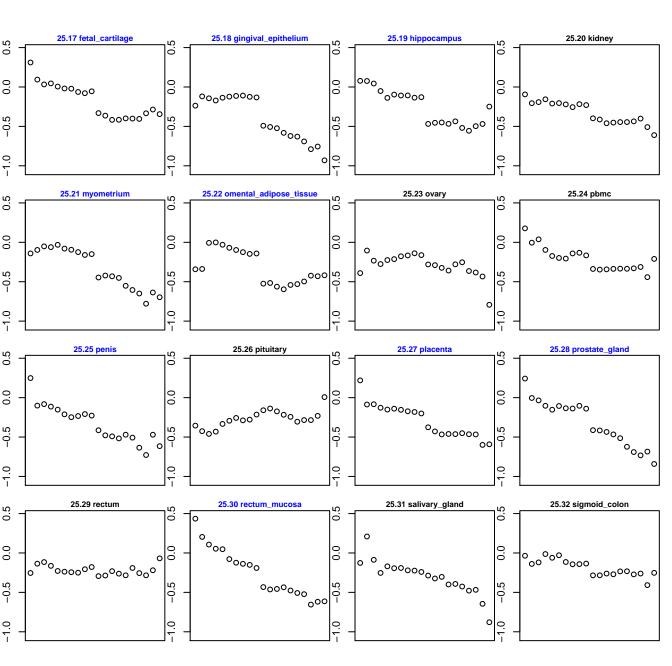
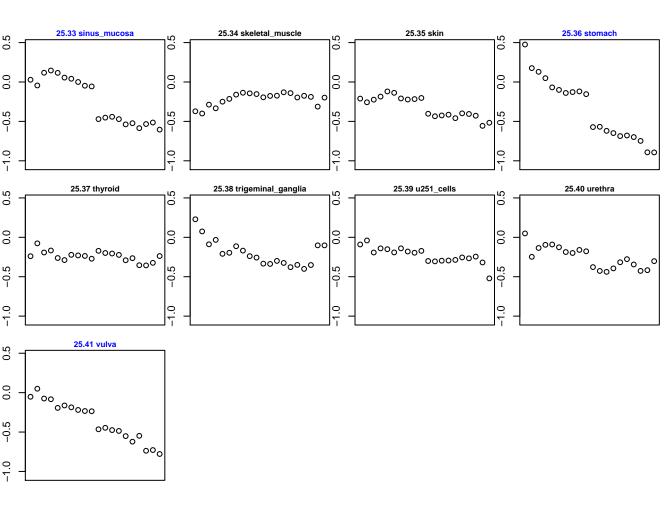
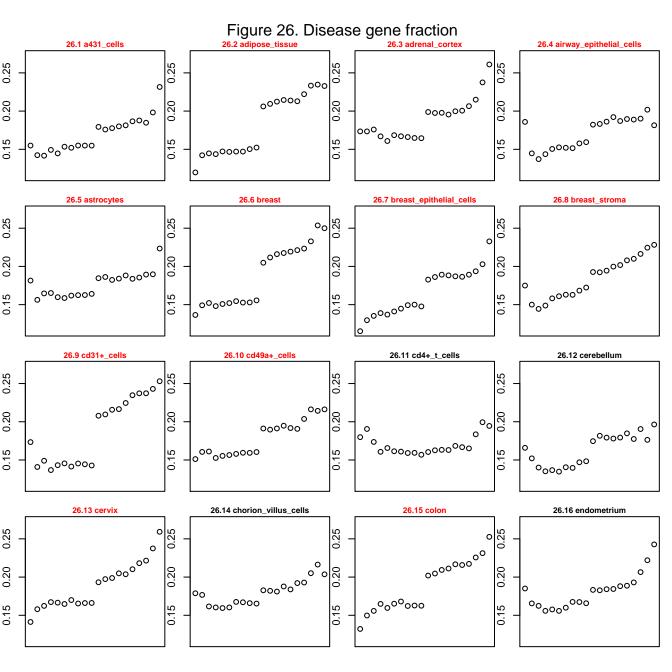


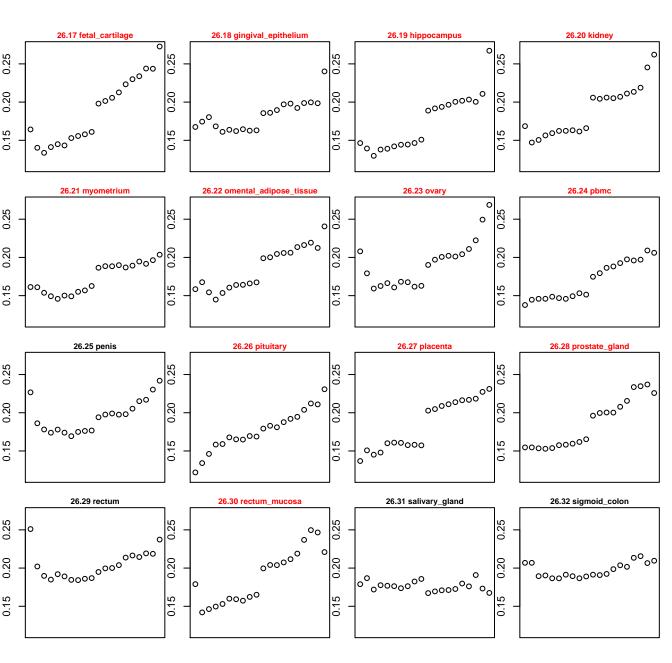
Figure 25. Intrinsic disorder











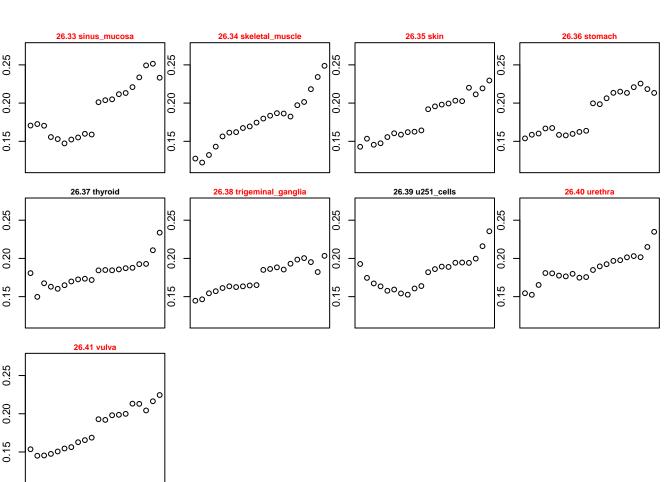
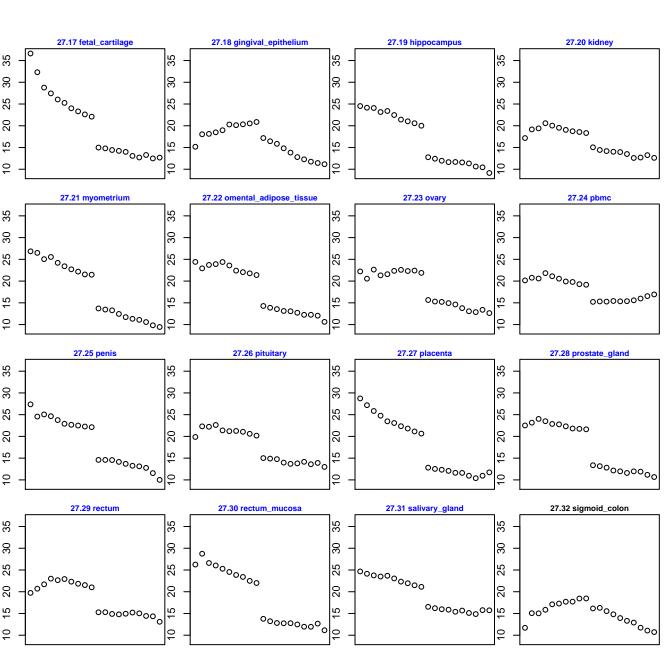


Figure 27. Protein-protein interactions 27.1 a431_cells 27.2 adipose_tissue 27.3 adrenal_cortex 27.4 airway_epithelial_cells ဗ္က ဗြ 27.8 breast_stroma 27.5 astrocytes 27.6 breast 27.7 breast_epithelial_cells ဗ္က ဗြ ကြ 27.10 cd49a+_cells 27.9 cd31+_cells 27.11 cd4+_t_cells 27.12 cerebellum ဗ္က 0000000 ^{′000}00000 ကြ 27.13 cervix 27.14 chorion_villus_cells 27.15 colon 27.16 endometrium ဗြ ဗြ 10⁰⁰000000



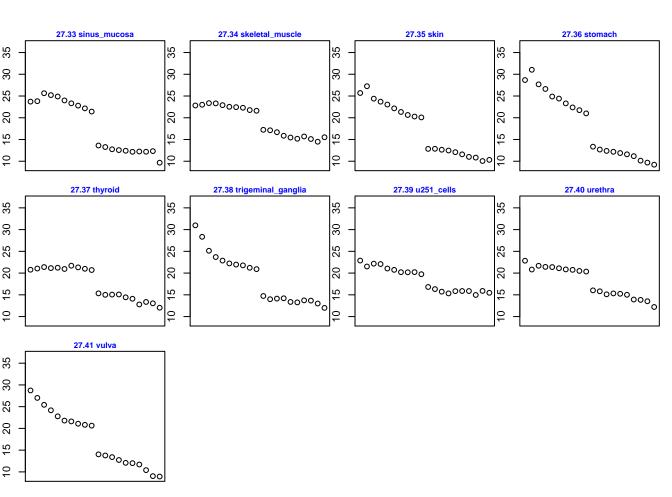


Figure 28. miRNA

