Expression dynamics of repetitive DNA in early human embryonic development

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SUPPLEMENTARY FIGURES

Figure S1

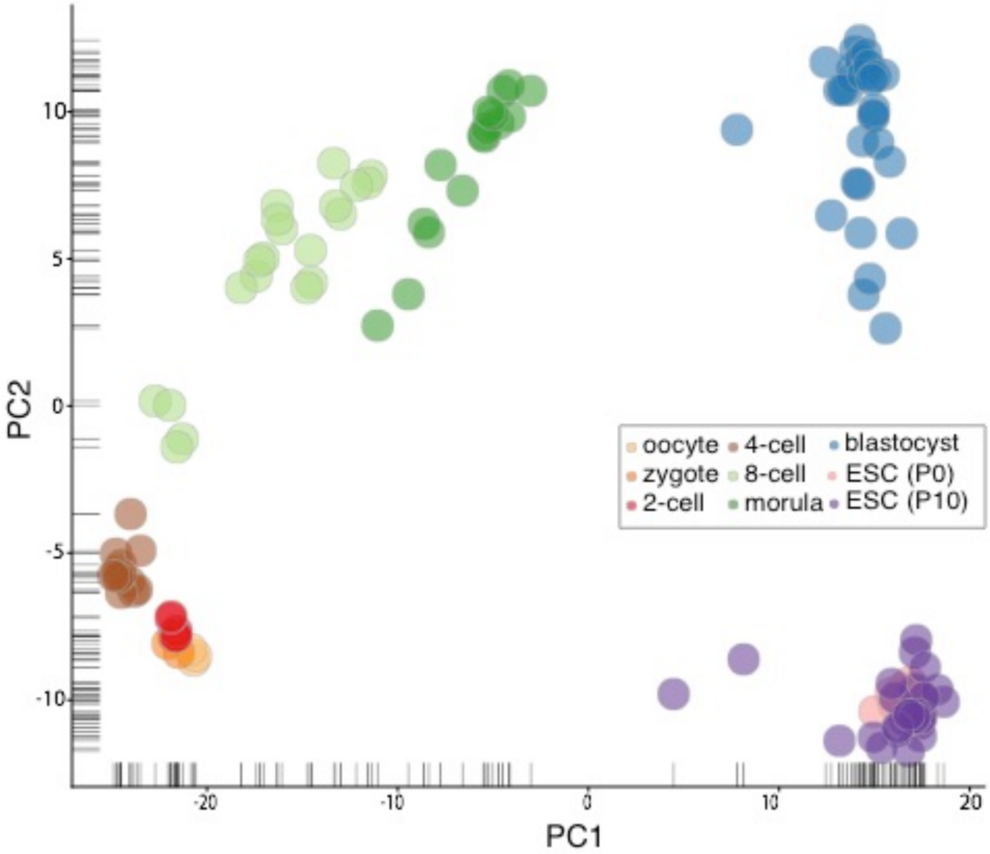


Figure S1. Principal component (PCA) analysis of gene expression. Each circle represents a single cell in the corresponding developmental stage.

Figure S2

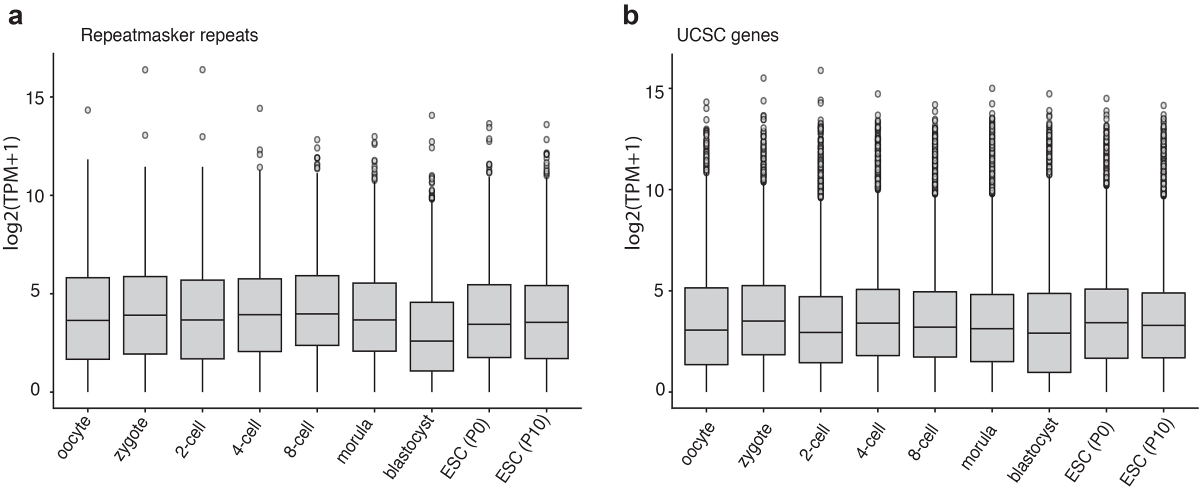


Figure S2. Box-plot representations of repeat and gene expressions obtained from single cells across stages of human pre-implantation and different passages (P0 and P10) of embryonic stem cells (ESC). **a** Expression levels of 1116 repeat elements. **b** Expression levels of UCSC annotated genes.

Figure S3

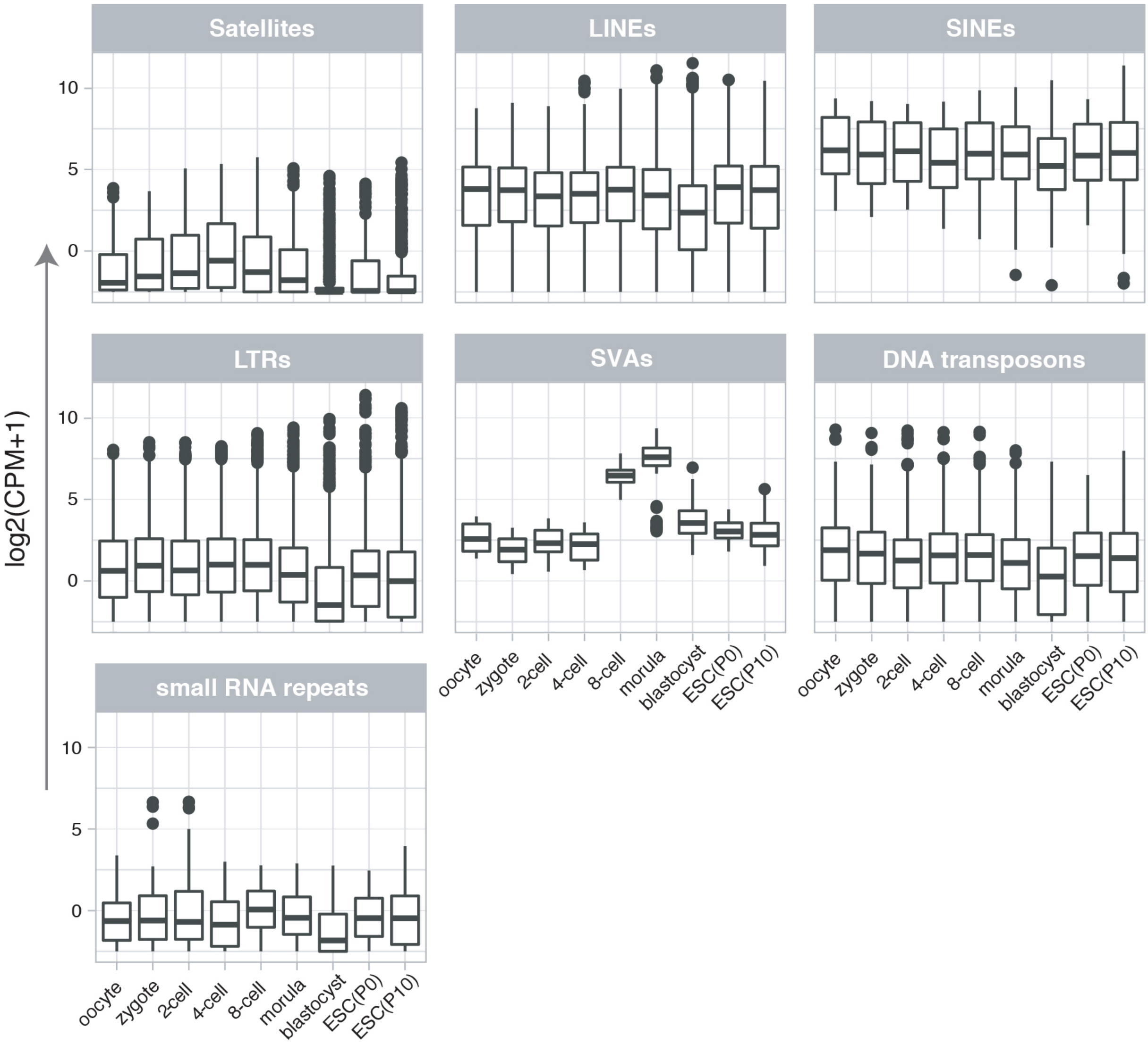


Figure S3. Box-plot representations of expression levels of all members of each major repeat class across stages of human pre-implantation and different passages (P0 and P10) of embryonic stem cells (ESC).

Figure S4

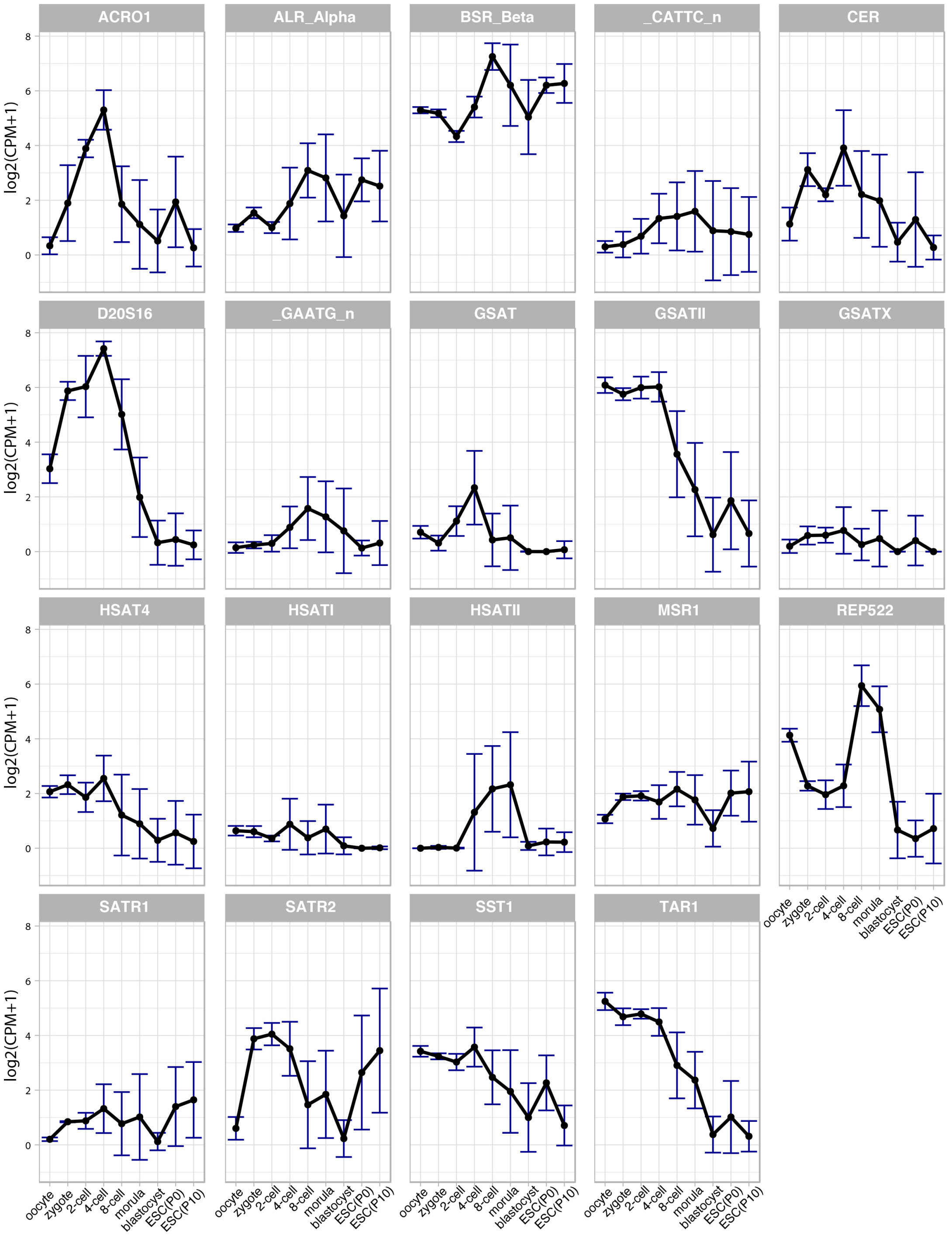
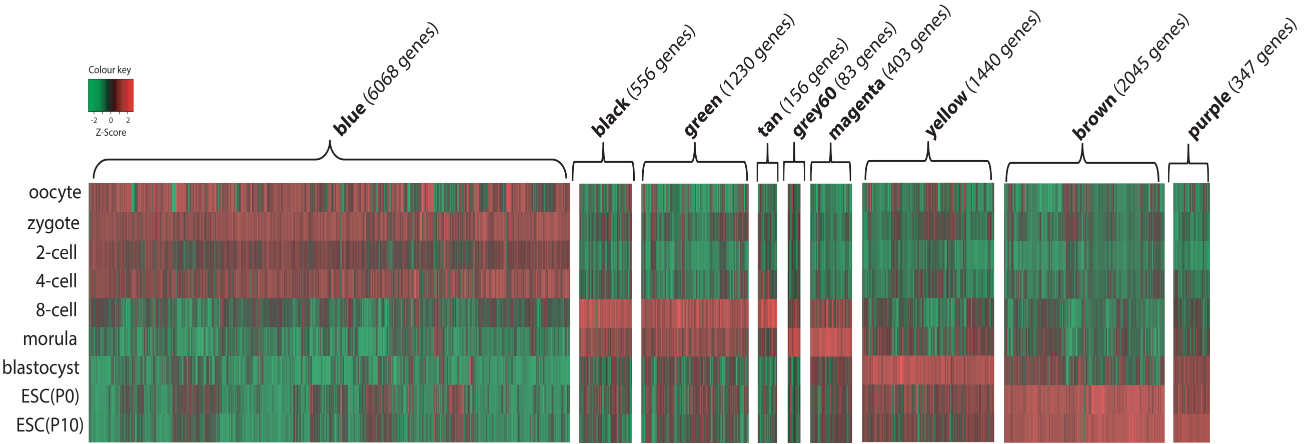


Figure S4. Line plots representing the expression levels of each member of satellite repeat family. Error bars indicate standard errors of the mean. Repeats that are expressed below the 1-CPM threshold are not shown.

Figure S5



oogenesis (GO:0048477) 6.67E-04
cell cycle checkpoint (GO:0000075) 6.01E-05
DNA damage checkpoint (GO:0000077) 3.17E-04
organelle localization by membrane tethering (GO:0140056) 1.00E-04
microtubule-based movement (GO:0007018) 2.54E-07

RNA splicing (GO:0008380) 1.85E-06
transcription, DNA-templated (GO:0006351) 5.22E-06
chromatin organization (GO:0006325) 6.15E-06

dosage compensation by inactivation of X chromosome (GO:0009048) 1.87E-04
selective autophagy (GO:0061912) 3.23E-04
ribosome biogenesis (GO:0042254) 1.88E-29

methylation-dependent chromatin silencing (GO:0006346) 1.06E-04
organ induction (GO:0001759) 1.54E-04
protein targeting to ER (GO:0045047) 9.97E-11

no statistically significant GOTERM enrichment

ribonucleoprotein complex biogenesis (GO:0022613) 1.32E-09
RNA processing (GO:0006396) 1.05E-09
cellular metabolic process (GO:0044237) 3.09E-05

mitochondrial translation (GO:0032543) 1.64E-29
mitochondrial gene expression (GO:0140053) 1.43E-26
mitochondrial respiratory chain complex assembly (GO:0033108) 1.69E-05
TP metabolic process (GO:0046034) 7.05E-07

somatic stem cell population maintenance (GO:0035019) 1.23E-09
DNA damage response, detection of DNA damage (GO:0042769) 7.95E-04
Wnt signaling pathway, planar cell polarity pathway (GO:0060071) 5.24E-04
maintenance of cell number (GO:0098727) 1.45E-07
placenta development (GO:0001890) 4.48E-04

ATP synthesis coupled electron transport (GO:0042773) 3.79E-26
oxidative phosphorylation (GO:0006119) 3.94E-31
protein targeting to ER (GO:0045047) 2.20E-38
protein targeting to membrane (GO:0006612) 7.02E-32
ncRNA processing (GO:0034470) 3.86E-06

Figure S5. Heat-map representing the expression levels of genes in stage specific modules as analysed with weighted gene co-expression network analysis (WGCNA). GO terms enriched in these modules and their corresponding p-values are listed next to them.

Figure S6

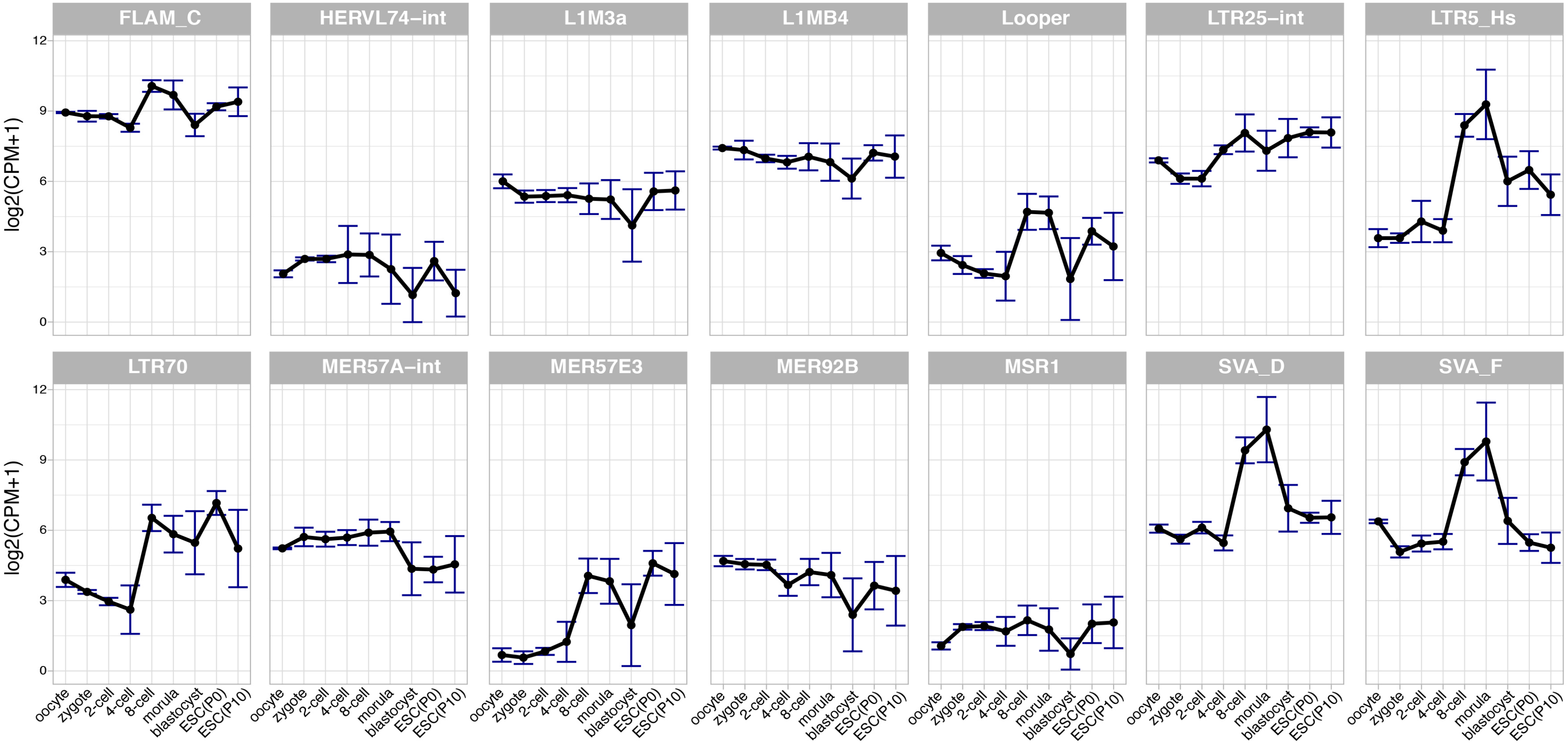


Figure S6. Line plots representing mean expression levels of repeats that exhibit higher than 3.5 fold enrichment in any WGCNA module. In addition to 11 repeats which are above the 3.5 threshold; FLAM_C, SVA_D and SVA_F levels are also shown. Error bars indicate the standard error of the mean.

Figure S7

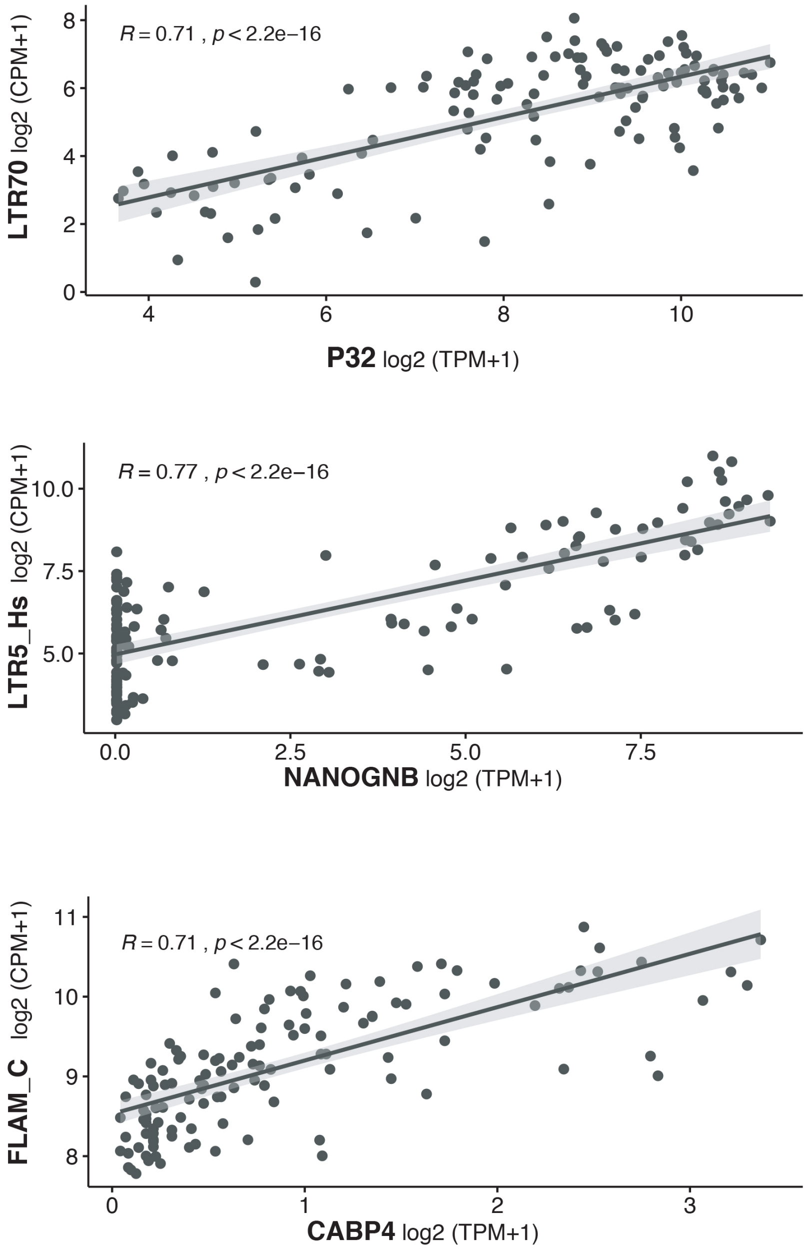


Figure S7. Scatter plots representing the correlation between developmentally vital genes and the relevant repeats.

Figure S8

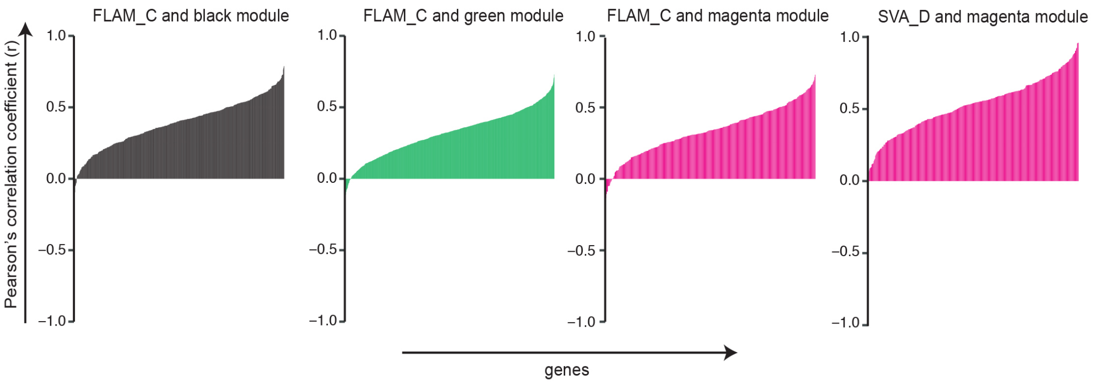


Figure S8. Additional module-repeat correlations for repeats that are below the 3.5 enrichment threshold.

Figure S9

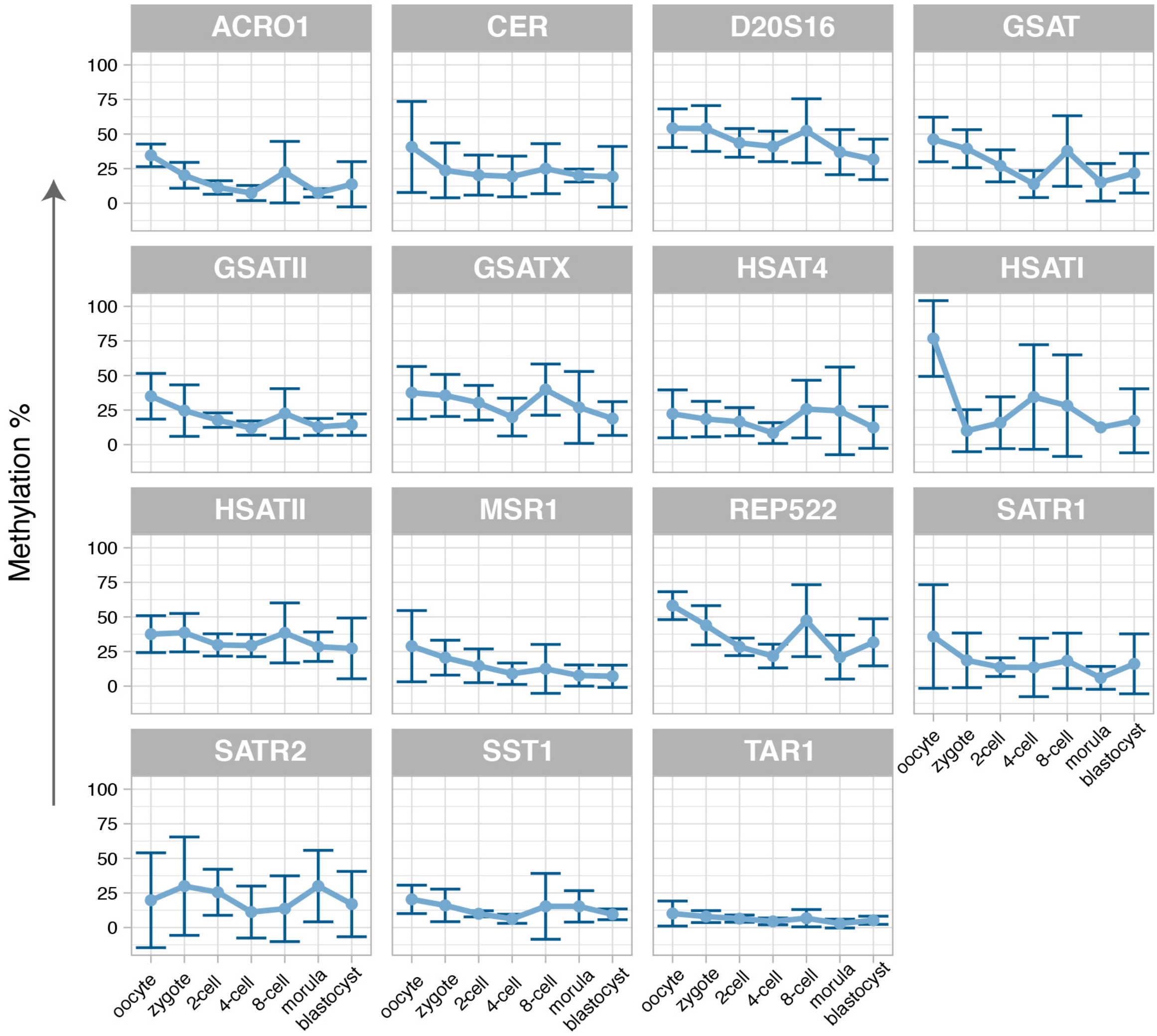


Figure S9. Line plots representing mean DNA methylation levels of different members of satellite repeat family. Error bars indicate the standard error of the mean.