**RNA-seq data processing and analysis**

Except where otherwise indicated, all analyses were carried out using custom-written Python scripts (available from https://github.com/georgimarinov/GeorgiScripts).

For visualization and quality control purposes, paired-end (2 x 100bp) RNA-seq reads were aligned against the hg38 version of the human genome using TopHat2 (Kim et al. 2013; version 2.0.8), run with Bowtie (Langmead et al. 2009; version 0.12.9) and the GENCODE V25 annotation (Harrow et al. 2012) with default parameters. Read coverage tracks were then generated using custom written python scripts. Read mapping statistics can be found in Supplementary Table XXX.

For quantification and differential expression analysis, reads were aligned against the GENCODE V25 transcriptome with unlimited numbers of multimapping locations using Bowtie, and then quantified using eXpress (Roberts & Pachter 2009; version 1.5.1). The resulting TPM values were used for clustering and visualization, while estimated read counts were supplied as input for differential expression analysis using DESeq2 (Love et al. 2014).

**Analysis of repetitive element expression**

For the purposes of repetitive element expression analysis, a separate transcriptome index containing both the GENCODE V25 annotation and the RepBase (Bao et al. 2015; version 16.03) humrep sequences. Quantification and differential expression was then carried out as described above.

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