

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Locations in the human genome version GRCh38 of the 2,621,118 four-fold degenerate sites analysed in this study, in BED format.

File Name: Supplementary Data 2

Description: Summary statistics for 16,602 transcripts containing four-fold degenerate sites across mammals.

File Name: Supplementary Data 3

Description: Gene ontology enrichment results for genes enriched with conserved four-fold degenerate sites. Fisher's exact test with false discovery rate correction for multiple testing.

File Name: Supplementary Data 4

Description: Gene ontology enrichment results for genes enriched with conserved four-fold degenerate sites in CpG sites. Fisher's exact test with false discovery rate correction for multiple testing.

File Name: Supplementary Data 5

Description: Summary statistics of genes enriched for Polycomb Group transcription factor binding sites at conserved four-fold degenerate sites.

File Name: Supplementary Data 6

Description: Gene ontology enrichment results for genes enriched for Polycomb Group transcription factor binding sites at conserved four-fold degenerate sites. Fisher's exact test with false discovery rate correction for multiple testing.

File Name: Supplementary Data 7

Description: Summary statistics of genes absent of Polycomb Group transcription factor binding sites at conserved four-fold degenerate sites.

File Name: Supplementary Data 8

Description: Gene ontology enrichment results for genes absent of Polycomb Group transcription factor binding sites at conserved four-fold degenerate sites. Fisher's exact test with false discovery rate correction for multiple testing.

File Name: Supplementary Data 9

Description: Results from a general linear model of gene expression against overlap of four-fold degenerate sites with genomic features.