

Worksheet - 3

1. The most frequently used CTSSs in the PMA time course are typically around 450 bp from an H3K9 AC island.
2. Gata1 forms a complex with Ldb1 and Tal1 proteins in hematopoietic transcription.
3. The relationship between gene expression patterns and morphology shapes evolution through development constraints and channels.
4. Natural selection scrutinizes exons more than intron sequences due to their explicit encoding of molecular function.
5. A phylogenetic tree based on gene expression differences mirrors the known phylogeny of species.
6. Changes in the trichome pattern in insects, whether induced in the laboratory or occurring through evolutionary diversification, are solely linked to variations in the expression of *svb*.
7. Later discussions hinge on the fact that each block can only contain one row.
8. These sequences, typically less constrained in the genome, serve as a credible neutral standard, reflecting regional variation in mutation and recombination rates.
9. Differences in *Sn* among datasets are of significant interest. Recent studies indicate that genes related to developmental and transcriptional regulation have tightly constrained CRMs, while the HBB gene complex has been extensively studied.