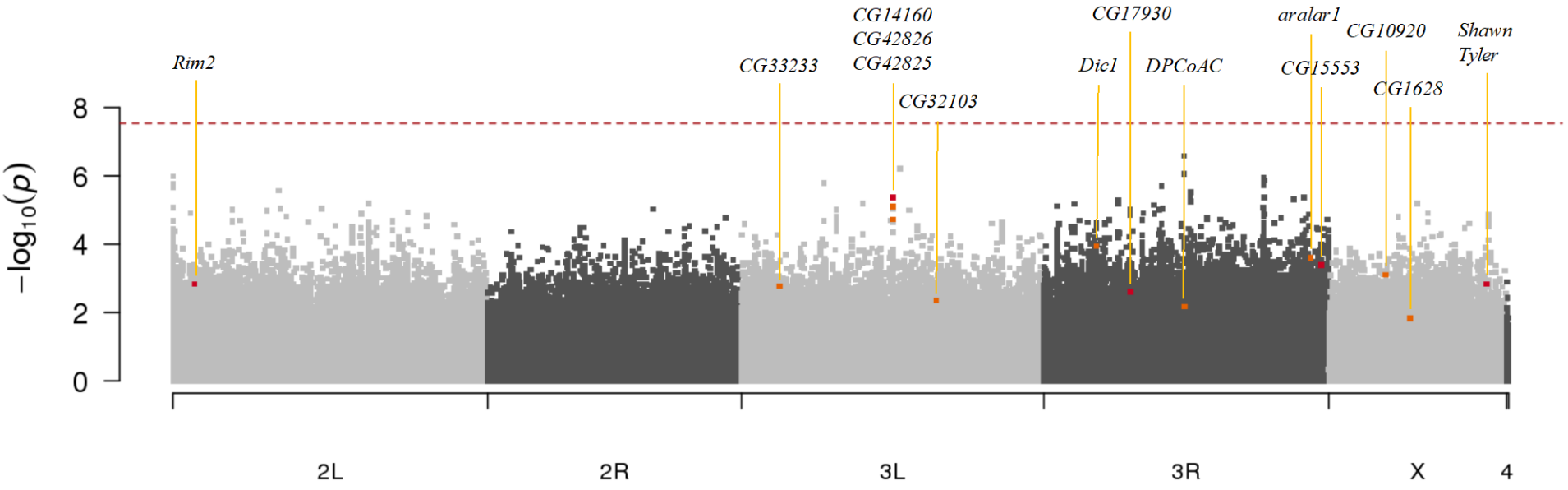

Figure S1 Manhattan plot of marginal SNP analysis of locomotor activity in the DGRP with CVAT associated genes highlighted in orange and red (indicate significant effect of gene expression knockdown). Each dot represents the $-\log_{10}(p\text{-value})$ of association between SNP variation and locomotor activity. Horizontal dashed line indicates genome-wide significance, *i.e.*, $-\log_{10}(p)=7.5$ (0.05/1.725.755 SNPs).