

Table S6 Lack of overlap between types of genomic response.

	Total	HS SNP	LS SNP	G×D Txt	TG RNAi	eQTL
HF SNP Genes^a	571	287	208	34	22	25
HS SNP Genes^a	661		222	28	21	24
LS SNP Genes^a	484			28	15	14
G×D Transcripts^b	697				38	22
TG RNAi Genes^c	505					19
eQTL Genes^d	486					

Cells show number of genes out of the Total listed for each of 6 genomic responses that are found in the indicated pair of responses. With 13,394 CG entries in the genome, and an average of 495 genes for each type of genomic response (3.7% of all genes), expected values are ~18 overlaps per pair. There may be an enrichment for the transcripts that show a significant G×D interaction and genes that affect Triglyceride content after RNAi-knockdown.

^a Gene nearest to a SNP that shows significant change in frequency of both replicates of the High Sugar (HS) or Low Sugar (LS) diets at $p < 10^{-5}$.

Fat (HF), High

^b Transcripts that show a significant Genotype×Diet interaction term in the microarray analyses.

^c Genes that influence total adult triglyceride content when knocked down by RNAi (Pospisilik et al, 2010)

^d regulatory eQTL detected in adults of both sexes (Massouras et al, 2012)