

Table S5. Allelic imbalance of deleterious nsSNPs, stop-gained variants, and control sites across tissues

	Control	Deleterious nsSNPs		Stop-gained	
	mean	mean	p-value	mean	p-value
Cerebellum	0.481	0.415	0.016	0.391	0.059
Colon	0.474	0.430	0.068	0.392	0.057
Frontal Lobe	0.465	0.428	0.084	0.363	0.007
Heart	0.449	0.432	0.277	0.343	0.016
Small Intestine	0.479	0.440	0.065	0.364	0.011
Liver	0.460	0.413	0.053	0.343	0.008
Lung	0.485	0.412	0.007	0.386	0.025
Skeletal Muscle	0.441	0.439	0.463	0.337	0.014
Pancreas	0.452	0.394	0.028	0.346	0.031
Stomach	0.469	0.438	0.125	0.359	0.015

We tested if deleterious nsSNPs and stop-gained variants have a statistically significant reduction in expression across all tissues compared to control sites. We calculated the mean allelic ratio for each variant group and used the student's t-test to determine if there is a significant difference between the control sites and the corresponding variant group (deleterious nsSNPs or stop-gained variants). The mean allelic ratios for each variant group and the calculated p-values are shown in the table.