





Figure S1: **Relationship between likelihood ratios of a pair of variants and their LD for 20 genes.** We repeat the experiment in Figure 1 of the main text for 20 additional randomly selected genes. Again, we chose pairs of cis-SNPs from those genes that appear together in at least two other genes, then compared their LD against the correlation between the log likelihood ratios of the SNPs estimated by RECOV and RE2 in all genes where the pair appears together. The identity line is shown in red for each plot. We note that some genes have cis SNPs that only appeared in a few genes together, shown in the accompanying Table S1.

Table S1: Median number of genes shared per SNP pair, using cis-SNPs chosen from the genes in Figure S1 to create the pairs.

Gene	Median shared genes per SNP pair
ENSG00000009307.11	18
ENSG000000064989.8	7
ENSG000000070759.12	34
ENSG000000079263.14	7
ENSG000000090020.6	44
ENSG000000117054.9	8
ENSG000000119777.14	24
ENSG000000135951.10	14
ENSG000000144136.6	17
ENSG000000158019.16	40
ENSG000000162627.12	3
ENSG000000163082.9	3
ENSG000000174514.8	20
ENSG000000180198.11	40
ENSG000000183682.7	20
ENSG000000217702.1	25
ENSG000000228794.4	74
ENSG000000229994.1	11
ENSG000000238009.2	74
ENSG000000271427.1	10