



**Figure S1: Relationship between likelihood ratios of a pair of SNPs 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 number of 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

Table S2: In section 2.3.2, we assume that the effect of SNP  $v$  on  $g$  in  $T$  tissues takes the form  $\lambda_{vg} \sim N(\mu_{vg}\mathbf{1}, c_{vg}\mathbf{U}_{vg})$ . When estimating  $\mathbf{U}_{vg}$ , we use SNPs which are far from  $v$ . In this scheme, we hope that SNPs in strong LD with  $v$  are removed. In this experiment, we sample a subset of genes, and divide their cis-SNPs into 10 segments. We pick a random SNP  $v$  in a random segment, and compute its LD with respect to all other SNPs. The table shows that when excluding the segment containing SNP  $v$ , we have fewer SNPs with  $LD \geq 0.9$  with respect to  $v$ .

Gene Ensembl	Number <i>cis</i> -SNPs	Physical location of SNP $v$	Segment index containing $v$	SNPs in LD $\geq 0.9$ in all segments	SNPs in LD $\geq 0.9$ excluding segment
ENSG00000000938.8	1897	28442747	7	11	0
ENSG000000035928.10	4610	40030473	9	25	0
ENSG000000072401.10	4441	59903016	6	2	0
ENSG000000100003.13	3319	31175009	8	8	0
ENSG000000100749.3	3773	96827247	4	30	4
ENSG000000105193.4	3813	39104375	1	14	0
ENSG000000105379.5	5433	52837937	10	7	0
ENSG000000105538.4	5051	50205234	10	0	0
ENSG000000124787.9	4975	5109592	6	14	8
ENSG000000125388.15	4505	3839996	9	5	0
ENSG000000142684.7	2604	27168188	10	46	13
ENSG000000143771.7	3354	223860210	2	20	0
ENSG000000154059.5	3369	22796580	10	0	0
ENSG000000156502.9	4574	69949234	1	11	0
ENSG000000157613.6	2072	45998186	5	2	0
ENSG000000158874.7	3766	161940014	9	12	0
ENSG000000160993.3	3120	102416493	8	4	0
ENSG000000163535.13	2768	202246493	10	53	0
ENSG000000173599.9	2618	67530795	8	1	0
ENSG000000203583.2	3468	38680870	3	5	0
ENSG000000213088.5	4358	159536458	8	5	0
ENSG000000236364.2	4644	166211818	7	30	0
ENSG000000267282.1	4297	46163948	9	3	0