Supplementary Tables

Supplementary Table 1 - Number of gene expression probes associated with copy number in HapMap data. Significance threshold for uncorrected p-values was used as 0.001, for comparability with Stranger et al (2007).

Population	Gene-set model	Stranger	Overlap
CEU	61	85	8
CHB	48	44	6
JPT	96	58	6
YRI	112	96	8

Supplementary Table 2 - Parameter values used in simulation

Definition	Notation	Values		
Region length	I	250	500	1000
Sample size	N	25	50	100
Proportion affected samples	π	0.10	0.25	0.50