	10000 SNPs	1000 SNPs	10000 SNPs	100000bp	10000bp
MDS1	2 PCs	2 PCs	5 PCs	2 PCs	2 PCs
10000 SNPs, 2 PCs	1.00	0.87	0.96	0.90	0.88
1000 SNPs, 2 PCs	0.68	1.00	0.73	0.68	0.94
10000 SNPs, 5 PCs	0.96	0.92	1.00	0.88	0.93
100000bp, 2 PCs	0.90	0.87	0.88	1.00	0.87
10000bp, 2 PCs	0.68	0.93	0.72	0.67	1.00
MDS2					
10000 SNPs, 2 PCs	1.00	0.54	0.93	0.87	0.56
1000 SNPs, 2 PCs	0.82	1.00	0.76	0.83	0.92
10000 SNPs, 5 PCs	0.93	0.50	1.00	0.83	0.52
100000bp, 2 PCs	0.87	0.59	0.84	1.00	0.58
10000bp, 2 PCs	0.83	0.92	0.77	0.84	1.00

Table S2: Correlations between MDS coordinates of genomic regions between runs with different parameter values. To produce these, we first ran the algorithm with the specified window size and number of PCs (k in equation (1)) on the full *Medicago truncatula* dataset. Then to obtain the correlation between results obtained from parameters A in the row of the matrix above and parameters B in the column of the matrix above, we mapped the windows of B to those of A by averaging MDS coordinates of any windows of B whose midpoints lay in the corresponding window of A; we then computed the correlation between the MDS coordinates of A and the averaged MDS coordinates of B. This is not a symmetric operation, so these matrices are not symmetric. As expected, parameter values with smaller windows produce noisier estimates, but plots of MDS values along the genome are visually very similar.