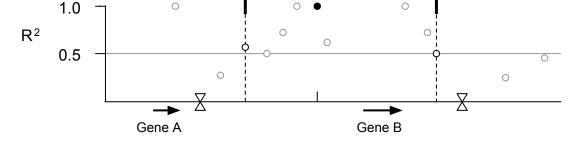
1. For each SNP, find neighbors with R^2 >= 0.5 within a 1 Mb window.



2. Extend to nearest recombination hotspots with rate > 3 cM / Mb.

