



Figure S4 The presence of inversions can be captured in the leading principal components (PCs) in an unstructured population. The loadings of the SNPs on the top six PCs across 15 pseudo-chromosomes simulated as being from a population with no structure (as described in the text), with the addition of a simulated 4 Mb inversion locus with inverted sequence at 20% frequency (black squares) at position 'A'. The variation attributed to the inverted region is captured in the 1st PC in this unstructured population, whereas the variation in loadings across the rest of the genome and the other PCs is uniform.