Supplementary Materials

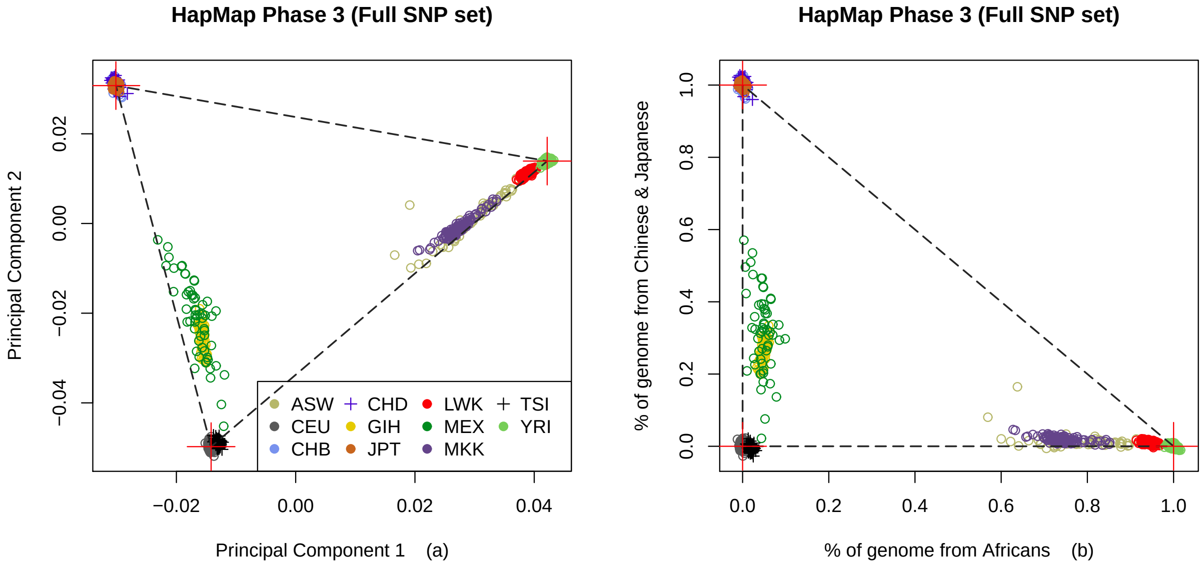


Figure S1: The principal component analysis on HapMap Phase 3 data, using the full set of 1,423,833 SNPs and 1,198 founders consisting of 11 populations: a) the first and second eigenvectors; b) a linear transformation of coordinate from a) followed by a translation, assuming three ancestral populations with surrogate samples: CEU, YRI and CHB+JPT. The average positions of three surrogate samples are masked by a red plus sign.

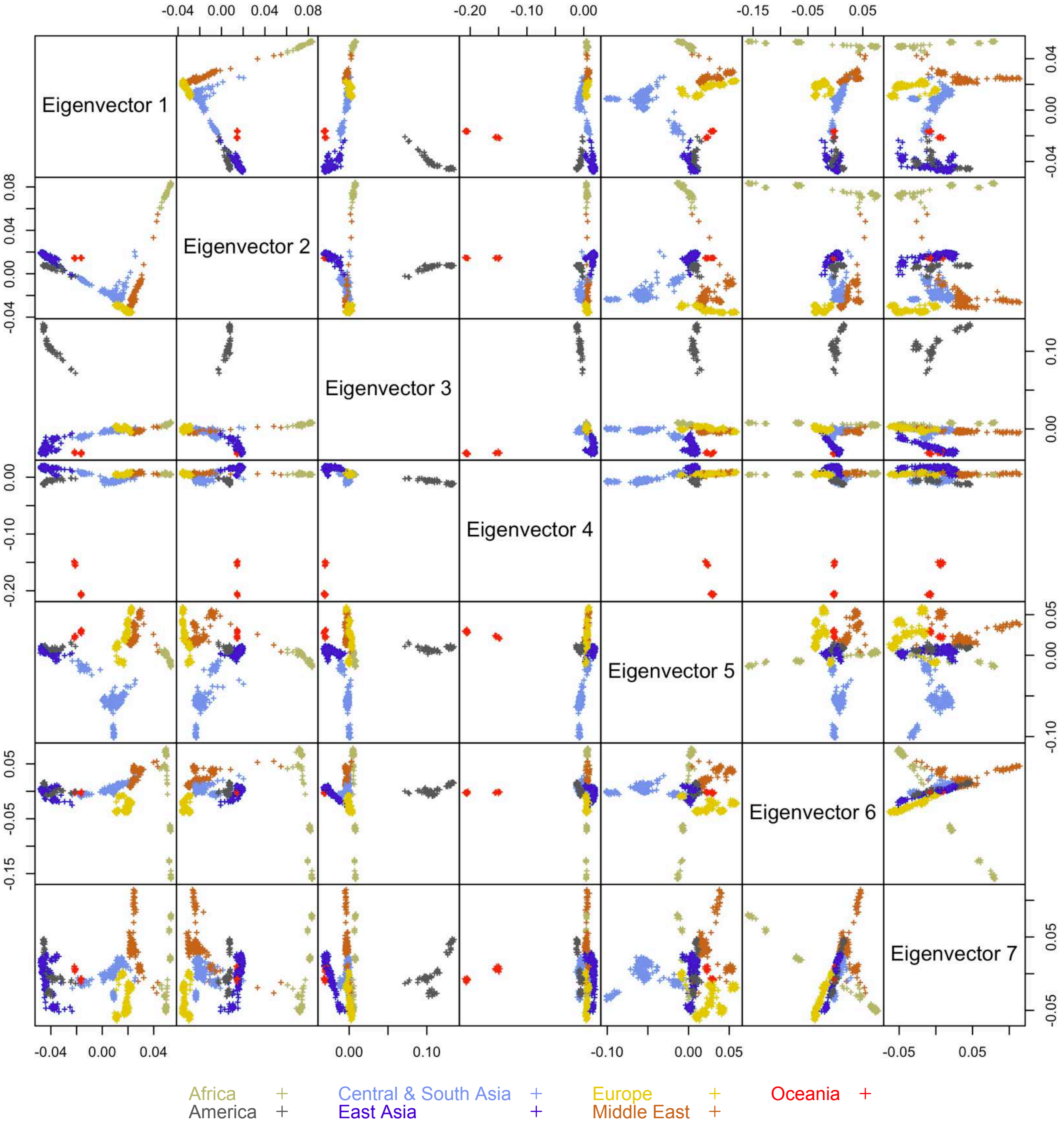


Figure S2: The eigenanalysis of EIGMIX on HGDP data using a full set of 644,258 SNPs.

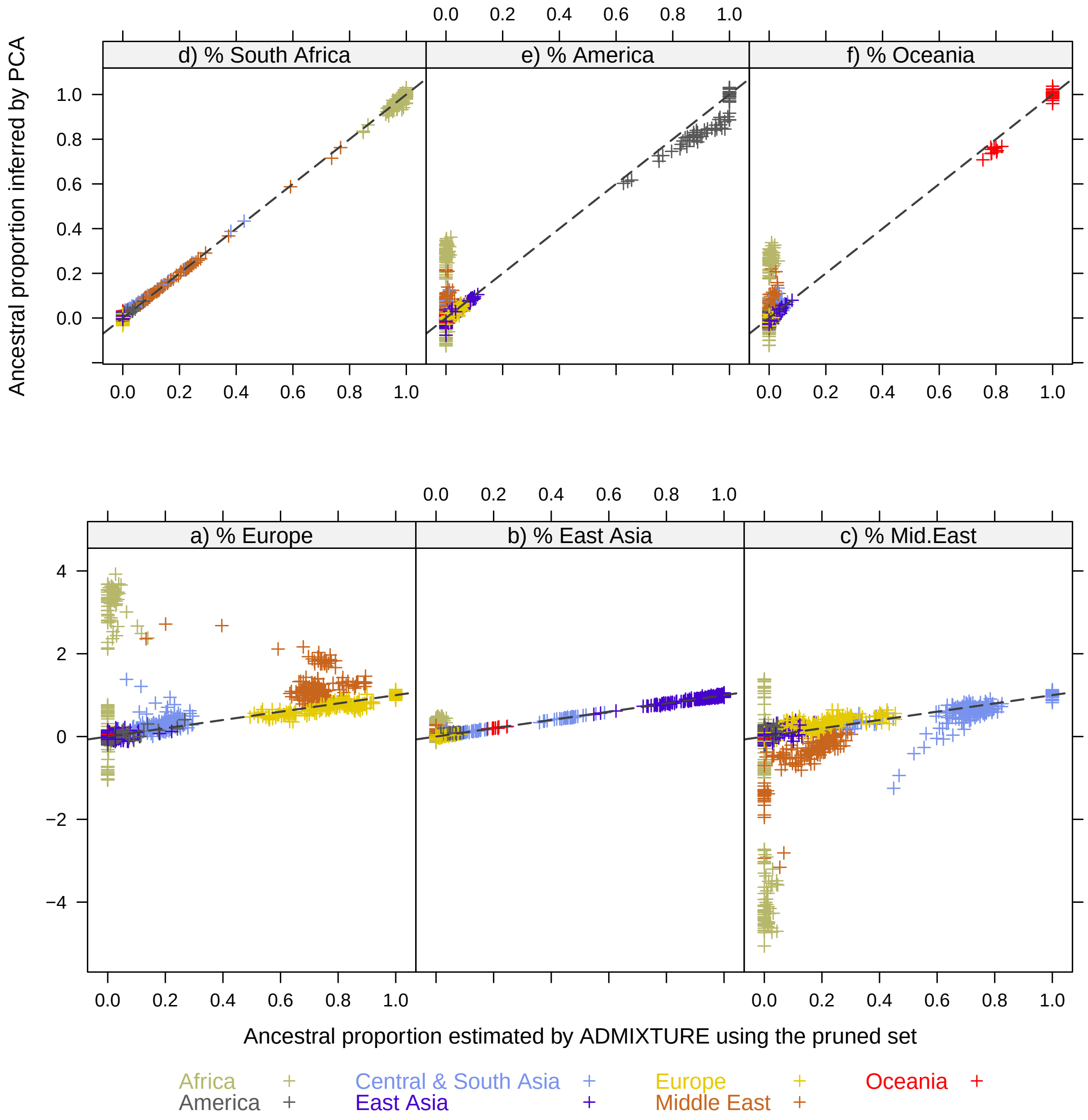
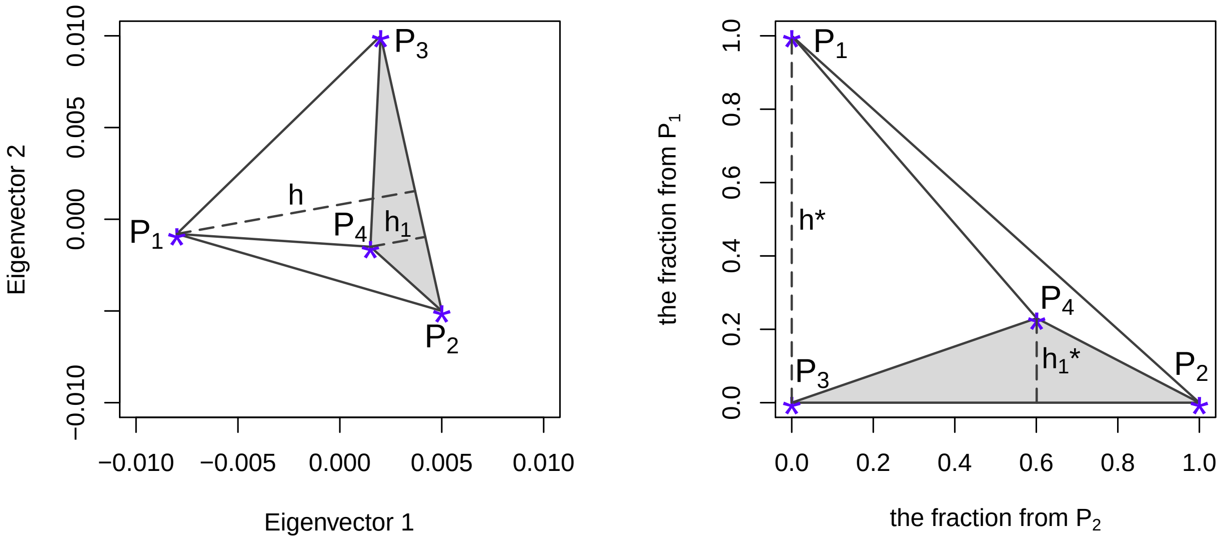


Figure S3: A comparison of ancestral proportions between PCA and supervised ADMIXTURE with six ancestral populations with a pruned set of 9,790 SNPs.



$$h_1/h = h_1^*/h^*$$

(a) (b)

Figure S4: The eigenvectors of the four hypothetical populations for three-way admixture. Ma and Amos (2012) observed that a three-way admixed population P_4 could divide the triangle of parental populations (P_1, P_2 and P_3) into three small triangles with areas according to their admixture proportions, i.e., the area ratio ($\triangle P_2P_3P_4 : \triangle P_1P_2P_3$) is the genome fraction of P_4 from P_1. This area ratio equals to the ratio of heights of the base P_2P_3, h_1/h. The mapping from the two-dimensional coordinate in (a) to that of (b) is an affine transformation, which is a linear transformation followed by a translation. Sets of parallel lines remain parallel after an affine transformation, and it also preserves ratios of distances between points lying on a straight line. Therefore, the ratio of new heights h_1^*/h^* in the coordinate of (b), equals to h_1/h in (a). Ma and Amos's observation can be confirmed under their theoretical framework with our proof of linear transformation.