



Figure S3: **ProPCA is computationally efficient relative to other methods:** We compute the total time taken to estimate the top five principal components as a function of a measure of accuracy (MEV) for ProPCA compared to FastPCA and FlashPCA2. We performed these comparisons on simulated genotype data containing 50,000 SNPs, 10,000 individuals, six subpopulations, and  $F_{st} \in \{0.001, 0.005, 0.01\}$ .