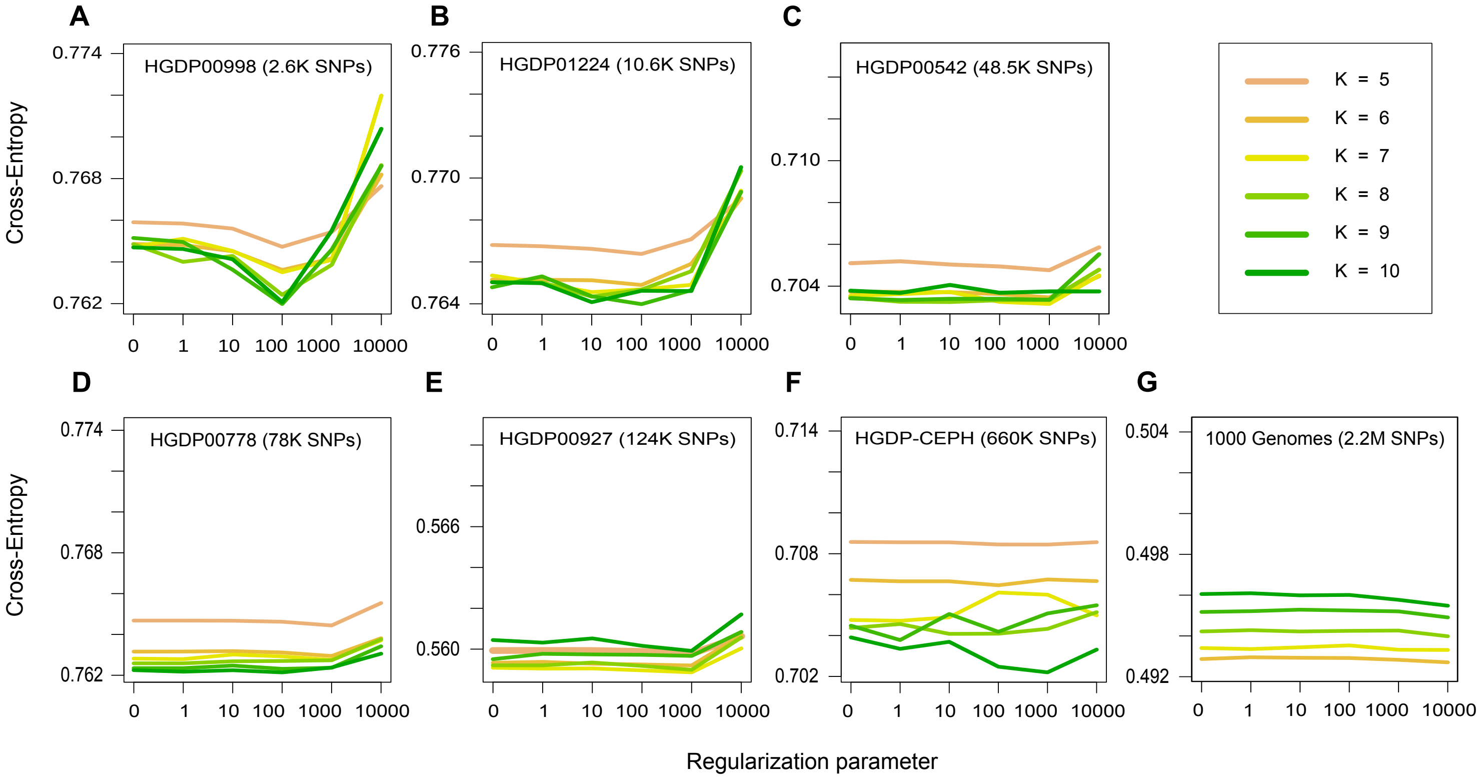

Figure S2. Values of the cross-entropy criterion for `sNMF` algorithms. Minimal values of the cross-entropy criterion over 5 runs of the `sNMF` program for A-E) 5 Harvard HGDP panel, F) the HGDP-CEPH data, and G) The 1000 Genomes Project data set. The number of clusters ranged from 5 to 10, and the values of the regularization parameter ranged from 0 to 10,000.