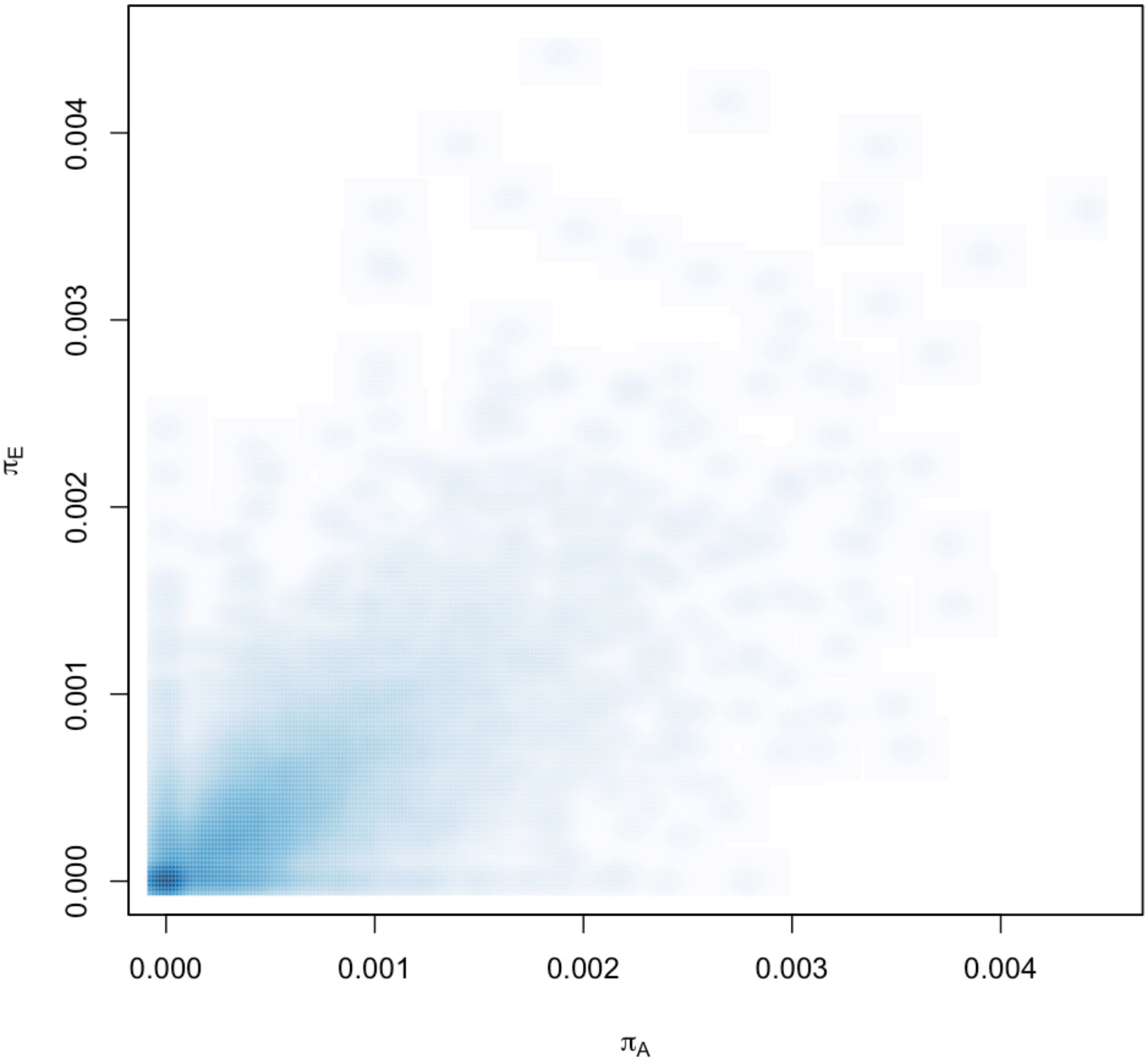
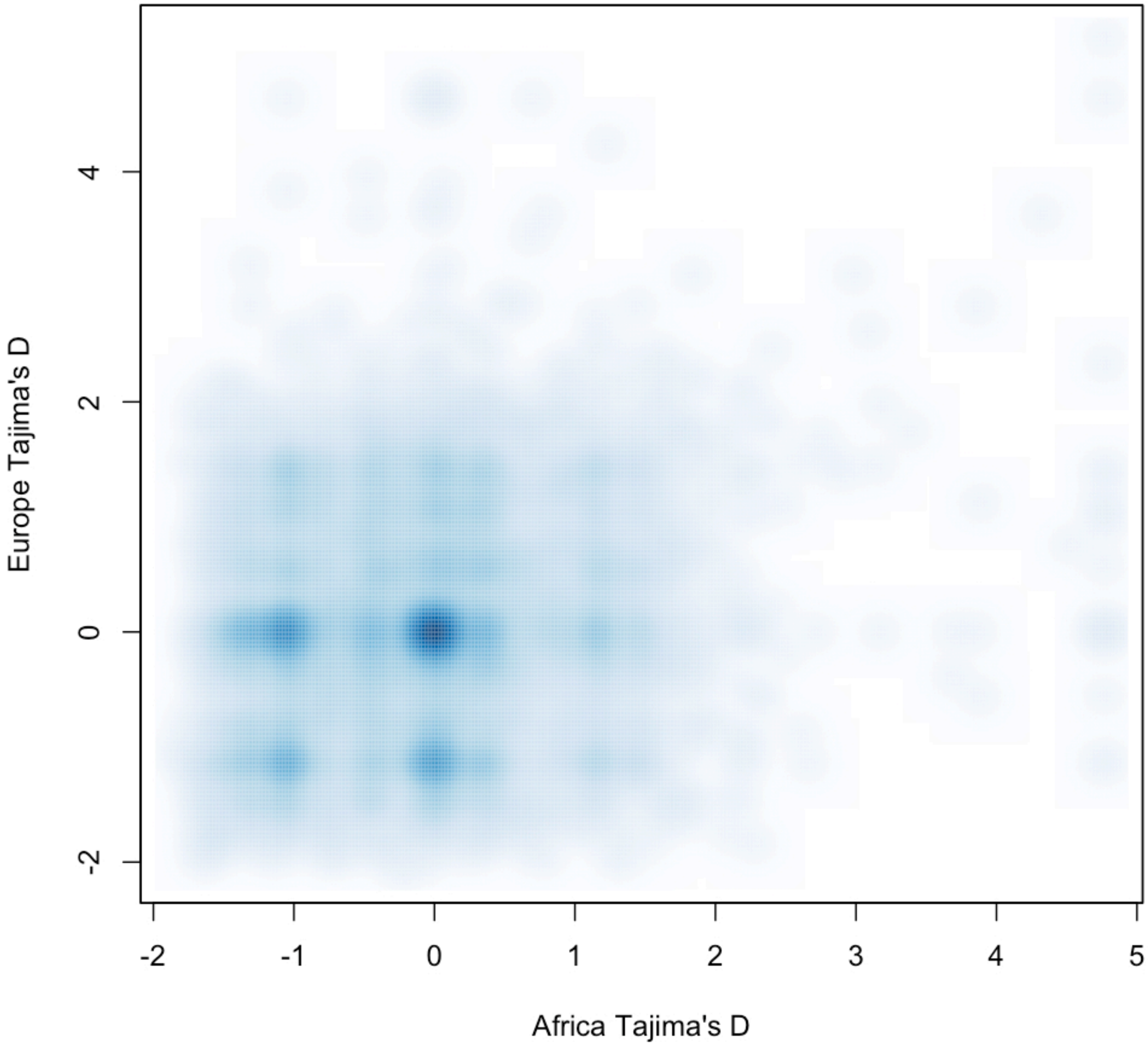
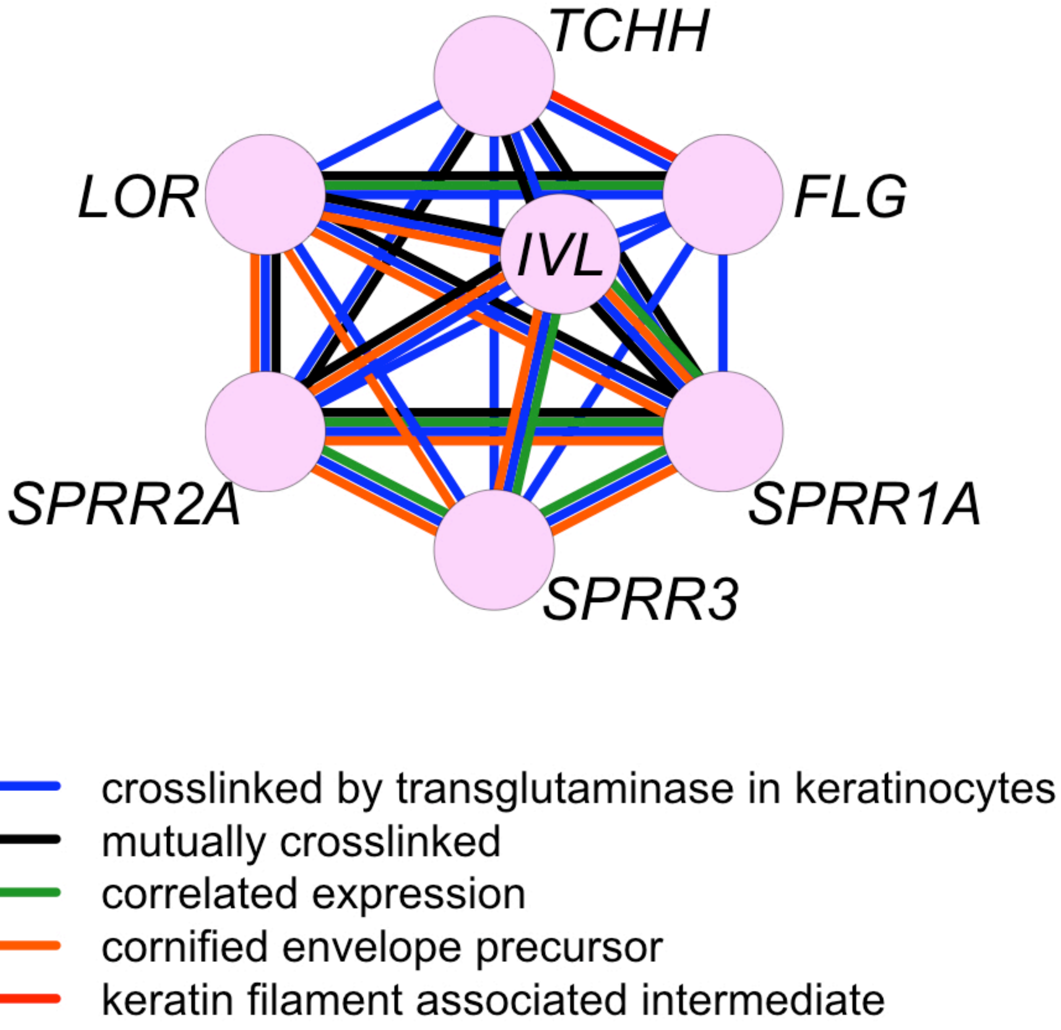
Supplementary Figure 1. Polymorphism in Europe versus Africa. The axes show π for each continent. Color darkness is proportional to the density of 100-kb regions in that vicinity. Polymorphism is positively correlated among continents ($R^2 = 0.55$). Approximately 15% of regions show no polymorphism on either continent (large dark spot in lower left corner).



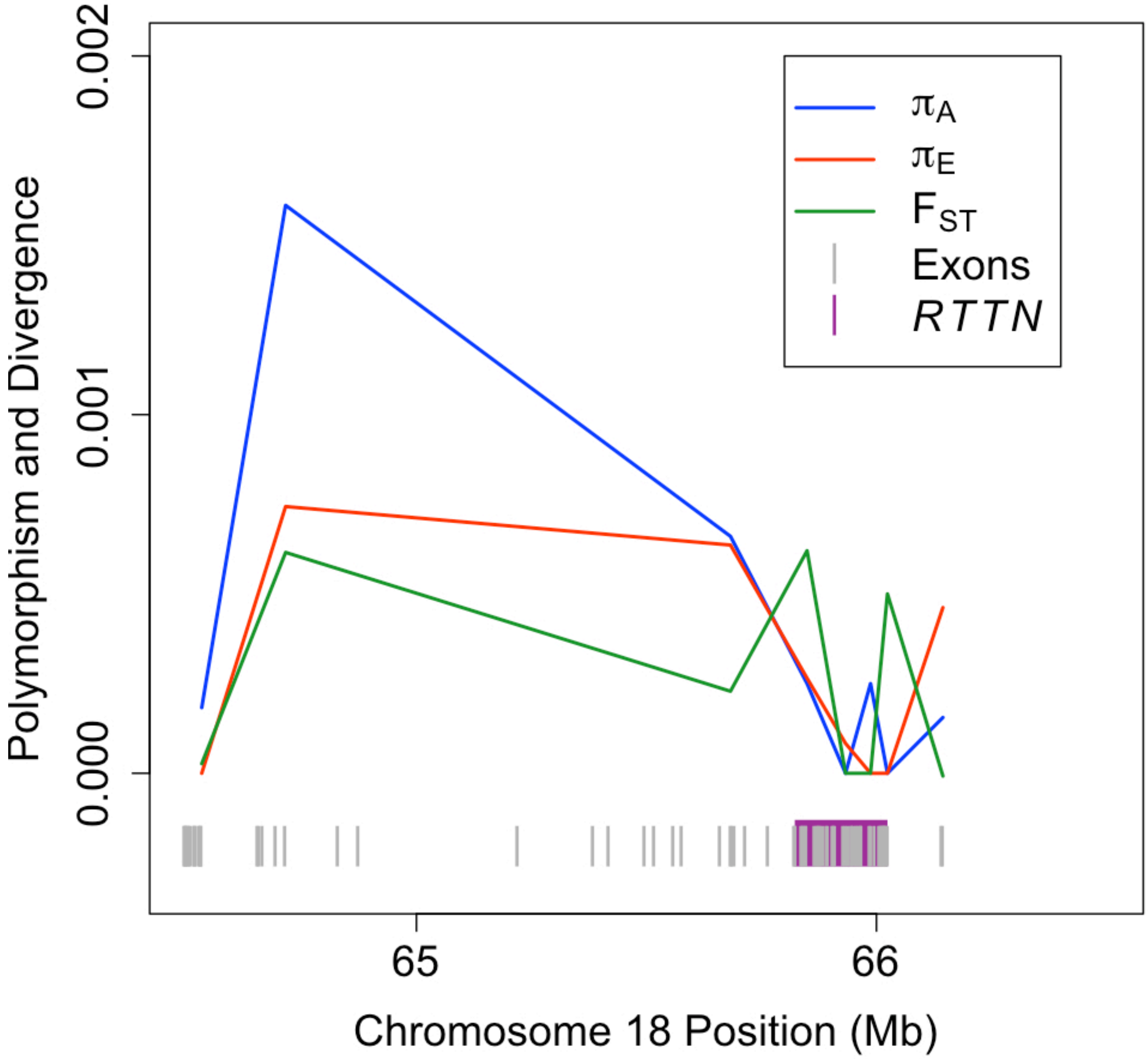
Supplementary Figure 2. Distribution of Tajima's D in Europe and Africa. Color darkness is proportional to the density of 100-kb regions in that vicinity. This statistic is slightly lower in Africa and is weakly positively correlated between continents ($R^2 = 0.01$). Approximately 15% of regions show no polymorphism on either continent, and thus have a D value of zero (large central dark spot).



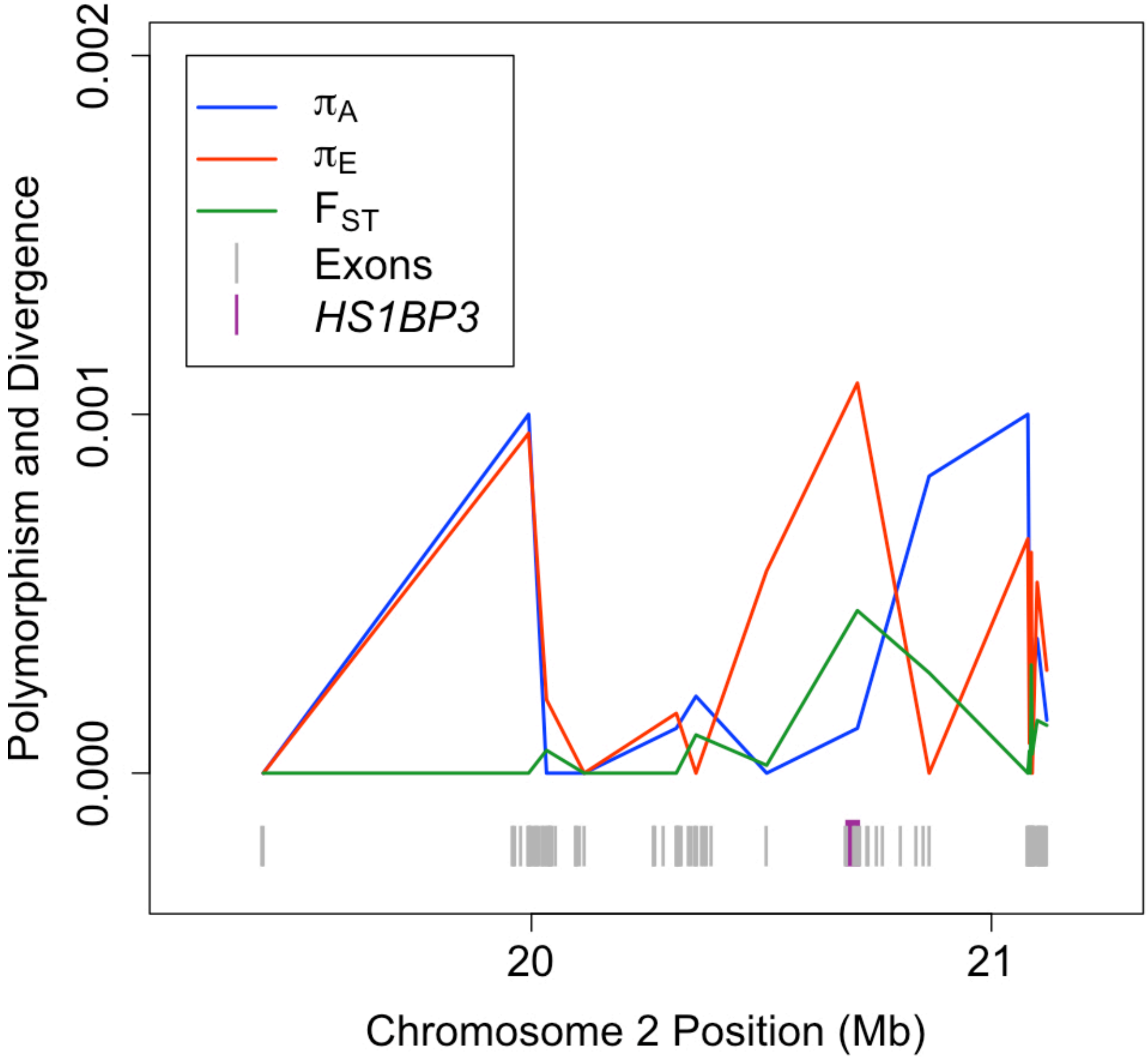
Supplementary Figure 3. Interaction network of the epidermal differentiation complex proteins encoded by the genes indicated in Figure 3A, showing correlated expression patterns, mutual crosslinking, and functional roles.



Supplementary Figure 4. Sliding window graph of exome polymorphism and divergence in the vicinity of *RTTN*. There are two independent spikes of high F_{ST} on either end of the gene, each associated with a high-frequency derived SNP on a different continent, making *RTTN* a candidate on both continents. *RTTN* is thought to help to maintain the cilia that provide the leftward nodal flow of extra-embryonic fluid, resulting in left-right asymmetry.



Supplementary Figure 5. Sliding window graph of exome polymorphism and divergence in the vicinity of *HS1BP3*, a motor neuron gene that may be linked to essential tremor or Parkinson disease. This locus is a novel candidate target of selection that does not appear on the evaluated candidate lists. It shows an unusually low ratio of π_A to π_E, coupled with high F_{ST}.



Supplementary Figure 6. Polymorphism versus sequence length for all included regions. The y-axis shows global π. The x-axis shows the log of the total length of exon sequence in each region, in bp. Color darkness is proportional to the density of 100-kb regions in that vicinity. Regions with less than 500 bp exon sequence have been excluded. The effect of lengths over 500 bp on the mean and variance of π is not substantial, and we have ignored it in our analyses.