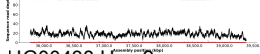
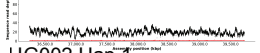


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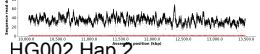
HG00438 Hap 1



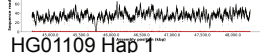
HG00438 Hap 2



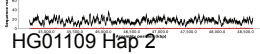
HG002 Hap 1



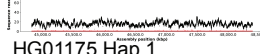
HG002 Hap 2



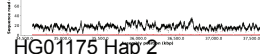
HG01109 Hap 1



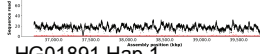
HG01109 Hap 2



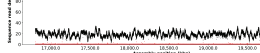
HG01175 Hap 1



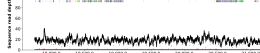
HG01175 Hap 2



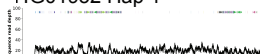
HG01891 Hap 1



HG01891 Hap 2



HG01952 Hap 1



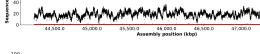
HG01952 Hap 2



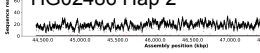
HG02486 Hap 1



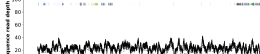
HG02486 Hap 2



HG02723 Hap 1



HG02723 Hap 2



HG00741 Hap 2



HG00741 Hap 1



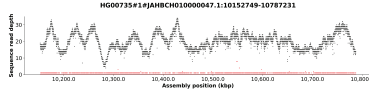
HG02717 Hap 2



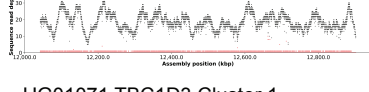
HG02717 Hap 1



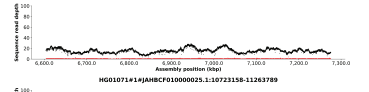
HG00735 TBC1D3 Cluster 1



HG00735 TBC1D3 Cluster 2



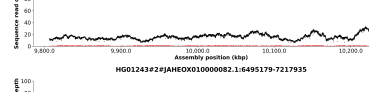
HG01071 TBC1D3 Cluster 1



HG01071 TBC1D3 Cluster 2



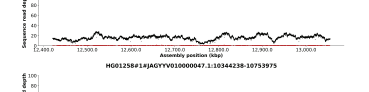
HG01243 TBC1D3 Cluster 1



HG01243 TBC1D3 Cluster 2



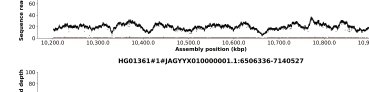
HG01258 TBC1D3 Cluster 1



HG01258 TBC1D3 Cluster 2



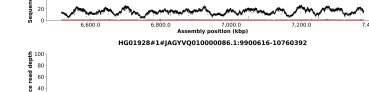
HG01361 TBC1D3 Cluster 1



HG01361 TBC1D3 Cluster 2



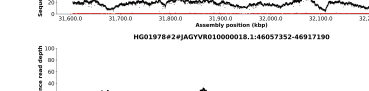
HG01928 TBC1D3 Cluster 1



HG01928 TBC1D3 Cluster 2



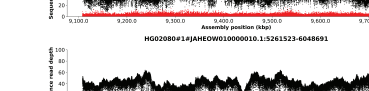
HG01978 TBC1D3 Cluster 1



HG01978 TBC1D3 Cluster 2



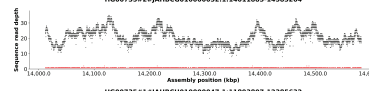
HG02080 TBC1D3 Cluster 1



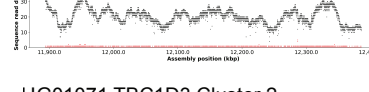
HG02080 TBC1D3 Cluster 2



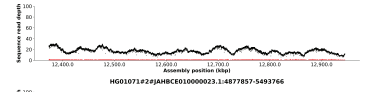
HG00735 TBC1D3 Cluster 1



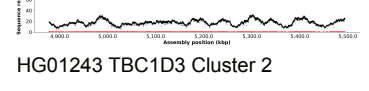
HG00735 TBC1D3 Cluster 2



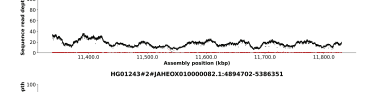
HG01071 TBC1D3 Cluster 1



HG01071 TBC1D3 Cluster 2



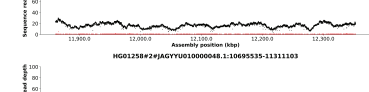
HG01243 TBC1D3 Cluster 1



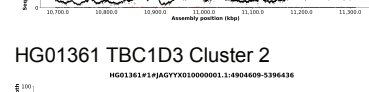
HG01243 TBC1D3 Cluster 2



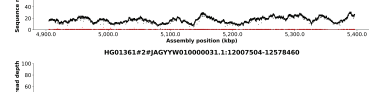
HG01258 TBC1D3 Cluster 1



HG01258 TBC1D3 Cluster 2



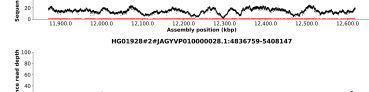
HG01361 TBC1D3 Cluster 1



HG01361 TBC1D3 Cluster 2



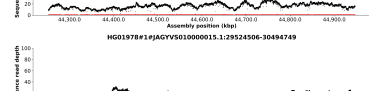
HG01928 TBC1D3 Cluster 1



HG01928 TBC1D3 Cluster 2



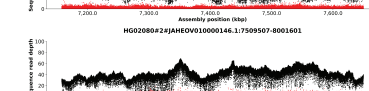
HG01978 TBC1D3 Cluster 1



HG01978 TBC1D3 Cluster 2



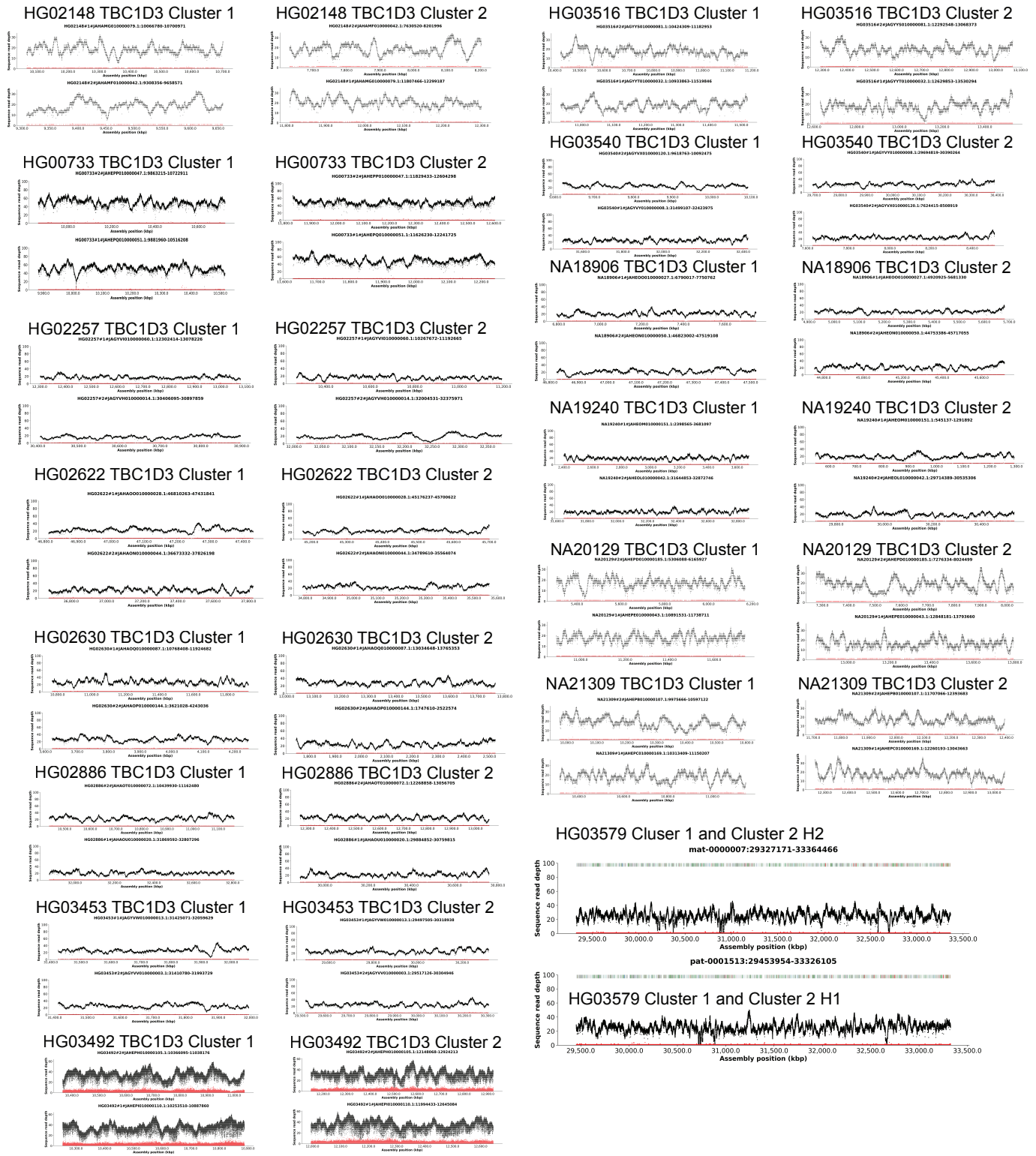
HG02080 TBC1D3 Cluster 1



HG02080 TBC1D3 Cluster 2



B



Supplemental Figure S1: NucFreq validation. Haplotype assembly accuracy was tested with NucFreq. Here, accuracy over each haplotype of *TBC1D3* cluster 1 and cluster 2 is demonstrated. Endogenous HiFi reads used to assemble respective phylogenies were mapped back onto the respective assemblies. We illustrated primary and secondary most prevalent base calls for reads aligned over a portion of an assembly in black and red, respectively. We expect primary base-call coverage to be relatively consistent, and consistently higher than the secondary base call, which should illustrate the sparse inaccuracies of HiFi sequencing.