File Name: Supplementary Data 1

Description: Alignment and QC metrics for ATAC-seq, RNA-seq, WGBS, and Hi-C assays. Processed using hg38, CHM13, the individual's Maternal assembly, or the individual's Paternal assembly. For RNA-seq and ATAC-seq the draft pangenome was also applied.

File Name: Supplementary Data 2

Description: Partial eta squared estimates for partitioning variance across principle components of alignment/QC metrics, and Functional outputs. Using hg38, CHM13, the individual's Maternal assembly, or the individual's Paternal assembly. For RNA-seq and ATAC-seq the draft pangenome was also applied.

File Name: Supplementary Data 3

Description: Unfiltered chromatin accessibility peak calls and cluster assignments derived from ATAC-seq analysis using hg38, CHM13, the individual's Maternal assembly, the individual's Paternal assembly, or the draft pangenome. Available at: https://doi.org/10.5281/zenodo.19655874

File Name: Supplementary Data 4

Description: Unfiltered transcript abundance estimates derived from RNA-seq analysis using hg38, CHM13, the individual's Maternal assembly, the individual's Paternal assembly, or the draft pangenome. Using RSEM to estimate abundances for linear assemblies and RPVG to estimate abundances for the draft pangenome.

File Name: Supplementary Data 5

Description: Unfiltered differentially methylated regions (DMR) derived from WGBS analysis using hg38, CHM13, the individual's Maternal assembly, or the individual's Paternal assembly. Using DSS to call DMRs from CpG methylation values genome-wide.

File Name: Supplementary Data 6

Description: Chromatin topology annotations derived from Hi-C analysis using hg38, CHM13, the individual's Maternal assembly, or the individual's Paternal assembly. Using HiCCUPs and DELTA to call chromatin loops and ArrowHead to call domains.

File Name: Supplementary Data 7

Description: Genome choice affected gene sets used to perform overrepresentation analysis using WebGestalt and results of overrepresentation analysis. Statistical significance was assessed using one-sided hypergeometric enrichment tests. P-values were adjusted for multiple comparisons using false discovery rate correction.

File Name: Supplementary Data 8

Description: Unfiltered variant counts, positions, and count enrichment per 24 kb interval for SNVs, indels, and structural variants. Enrichment was assessed using a one-tailed randomization test based on chromosome-constrained permutation of variant positions. P-values were adjusted for multiple comparisons using the Benjamini-Hochberg procedure.

File Name: Supplementary Data 9

Description: Lengths of individual assemblies' number annotations produced via LiftOff.

File Name: Supplementary Data 10

Description: Genomic features showing differential chromatin accessibility between linear and pangenomic analyses. Differential categories reflect peak presence or absence after peak quality filtering and thresholding and were not assigned a statistical significance test. The table includes coordinates for peaks that were consistently missing, partially missing, or gained when aligning ATAC-seq Data to the draft human pangenome, as well as the corresponding genes whose promoters overlap these regions. HOMER results are provided for each peak class, summarizing enrichment and depletion across genomic annotations including promoters, CpG islands, exons, introns, transcription termination sites, intergenic regions, and repetitive elements. HOMER enrichment and depletion statistics were calculated using the default one-sided cumulative hypergeometric test implemented in HOMER. No adjustment for multiple comparisons was applied.