

Supplementary Figure 1. Concordance indices from Hou data analysis. Gene expression trajectories were inferred by providing (a) genetic ancestry annotation using DNA sequences and (b and c) annotations using RNA sequences. SNV filtering cutoffs of 60% (b) and 70% (c) were used. Genetic ancestry annotations were presented in Figures. 2a and 2b.



Supplementary Figure 2. MGH26 data analysis with MOCA. Four phylogenies were reconstructed using different computational tools (BEAM and SCITE) and SNV filtering cutoffs (60% and 70%). (**a**-**c**) The phylogeny was reconstructed using BEAM on the dataset, where 70% SNV filtering cutoff was applied (BEAM7). (**a**) The inferred phylogeny. (**b**) The *Sub-concordance index* (*SCI*) for each ancestry. (**c**) The *Overall concordance index* (*OCI*). These indices were calculated using expression trajectories that were inferred from 200 to 1,000 genes. (**d-f**) The results using BEAM on a dataset with a 60% SNV filtering cutoff, (**g-i**) SCITE with a 70% SNV filtering cutoff. (**d**, **g**, and **j**) Cellular phylogenies. The genetic ancestry annotation using BEAM with 70% SNV filtering cutoff (BEAM7) is mapped onto the phylogeny via the heatmap.



Supplementary Figure 3. Genetic ancestry annotation comparison. Four phylogenies were reconstructed for both the MGH26 (**a**) and MGH31 (**b**) datasets. Rows of each heatmap represent cells in their respective position in the phylogeny reconstructed. Each column represents the genetic ancestries identified from a phylogeny inferred using a different combination of reconstruction method (BEAM and SCITE) and SNV filtering cutoff (60% and 70%). The final column represents a consensus annotation (an aggregated annotation). A cell is assigned to whichever genetic ancestry it is most commonly assigned to across all four phylogenies. (**a**) Cells are ordered based on their respective position in the phylogeny reconstructed using BEAM on the dataset with a 70% SNV filtering cutoff. Ancestries 1 and 3 largely agree across both cutoffs and reconstructed using BEAM on the dataset with a 60% SNV filtering cutoff. Across cutoffs and reconstruction methods there show little agreement in the genetic ancestry annotation. (**c** and **d**) The significance of the relationship (agreement) between each pair of genetic ancestry annotations is measured using a p-value from a chi-square test, denoted by the red text, and Cramer's V-measure of association (effect size), denoted in the black text.