

Sup - Simulating L1HS reads, aligning w diff. aligners

Bowtie

+STAR

+BWA

Sup - Effect of read length on mapping signature

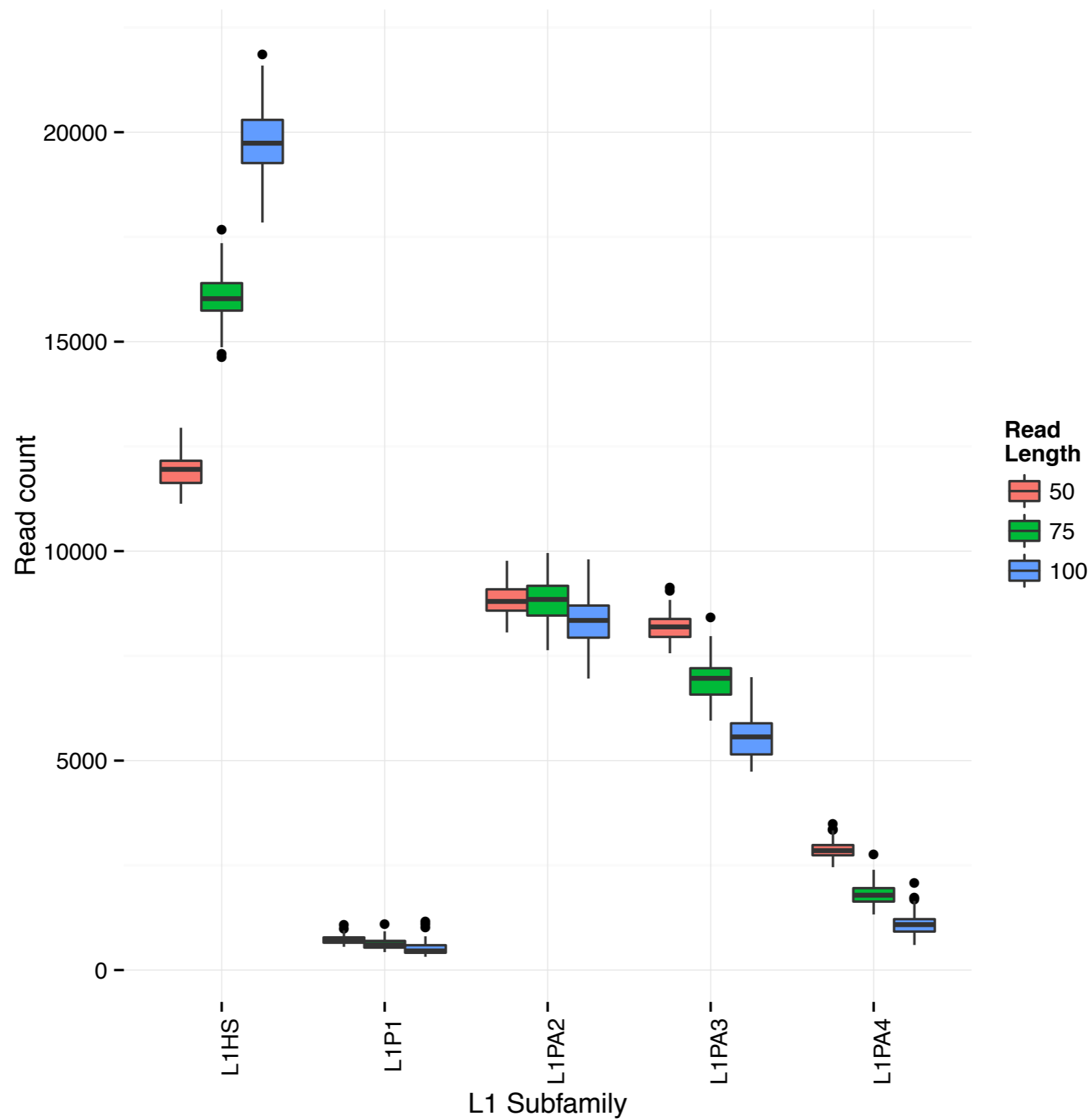
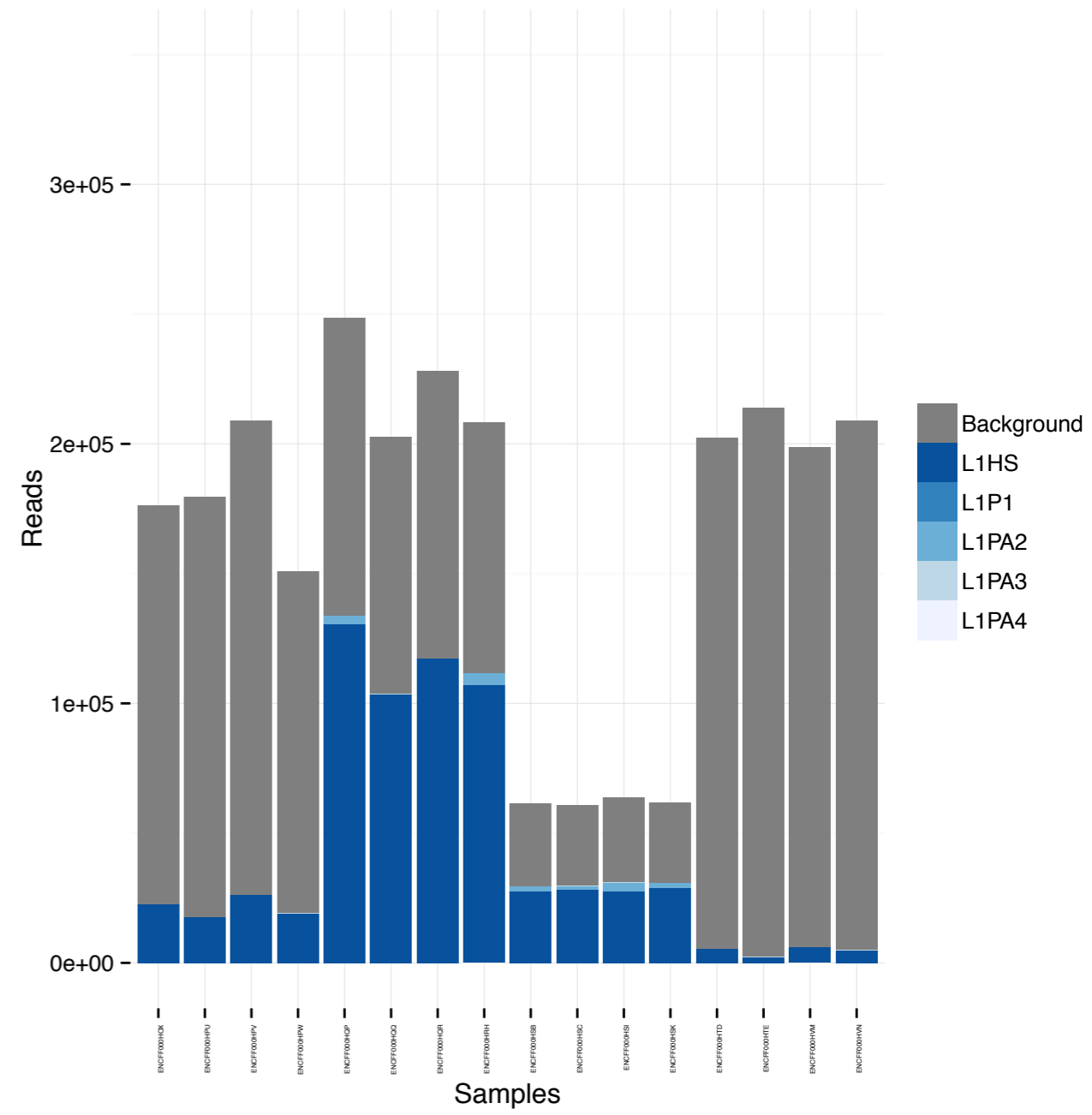
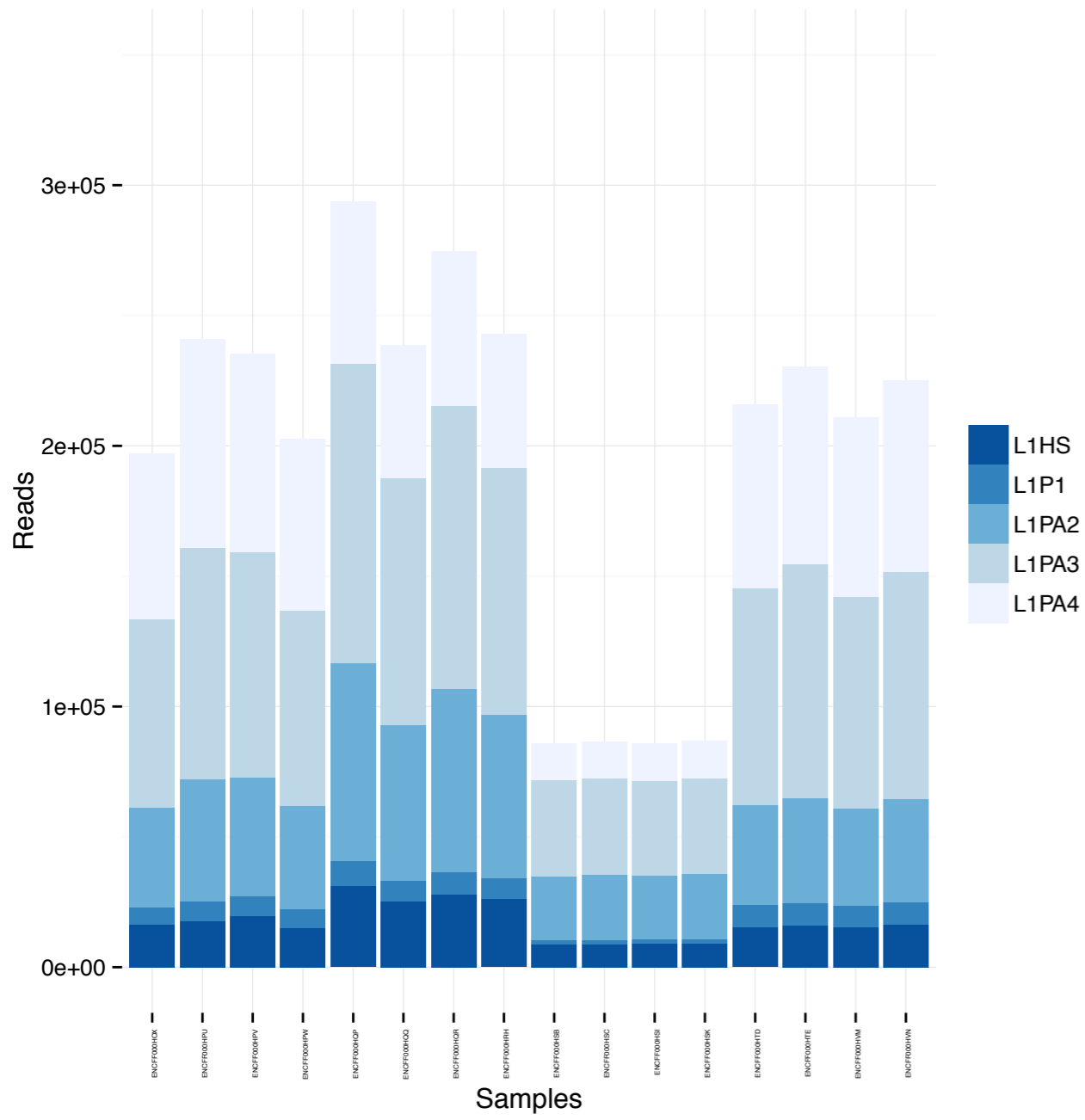
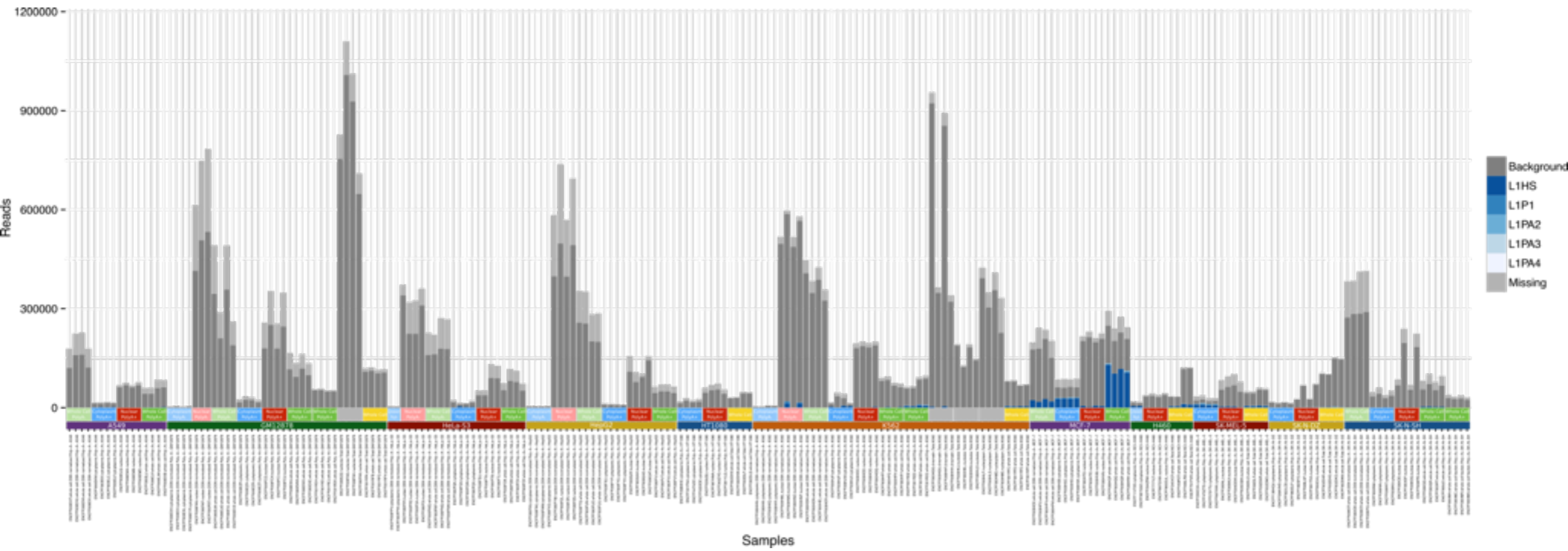


Fig1B - MCF7 after/before



Sup - All analyzed Cell Lines

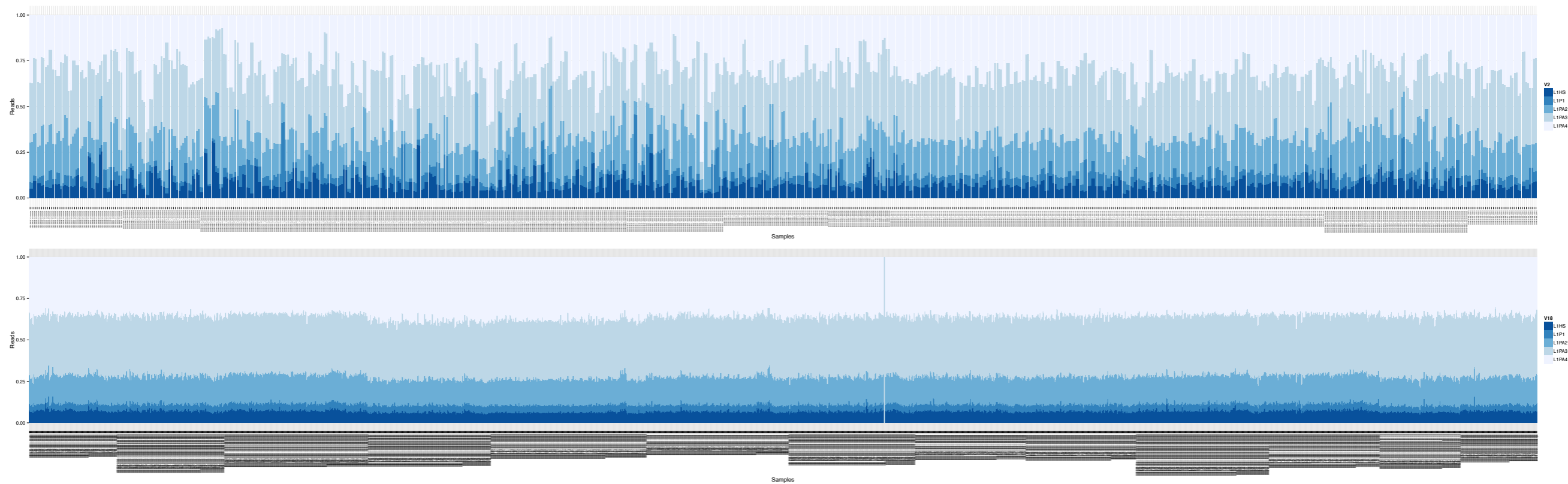


Sup - Before/After other cell lines

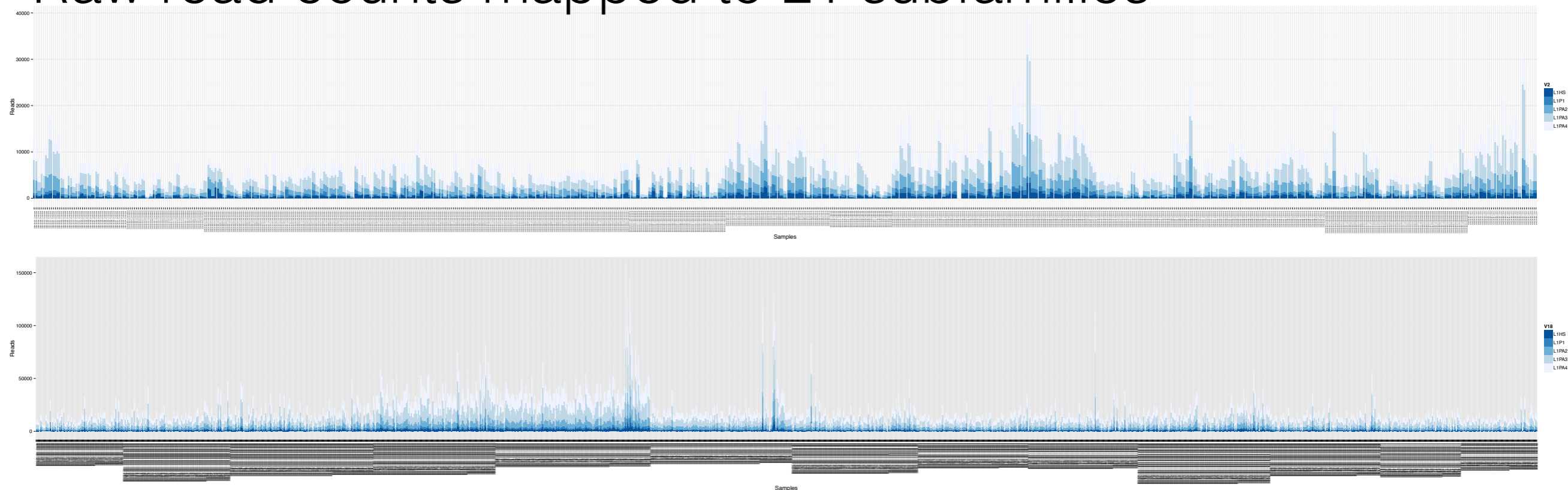
Sup3 - Comparing with available methods

Sup - L1HS raw counts in GTex_brain vs Single_cell

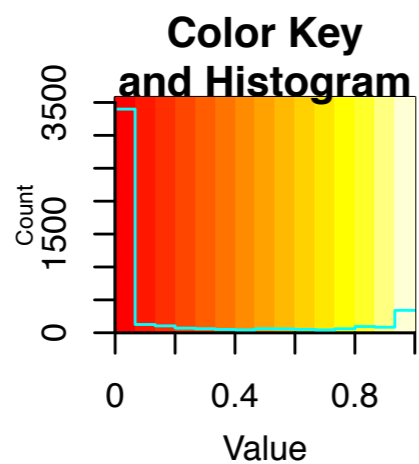
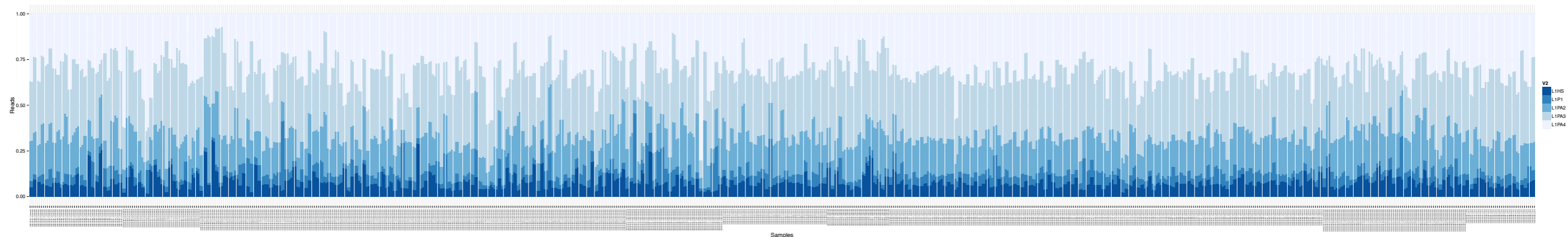
% of reads mapped to L1 subfamilies



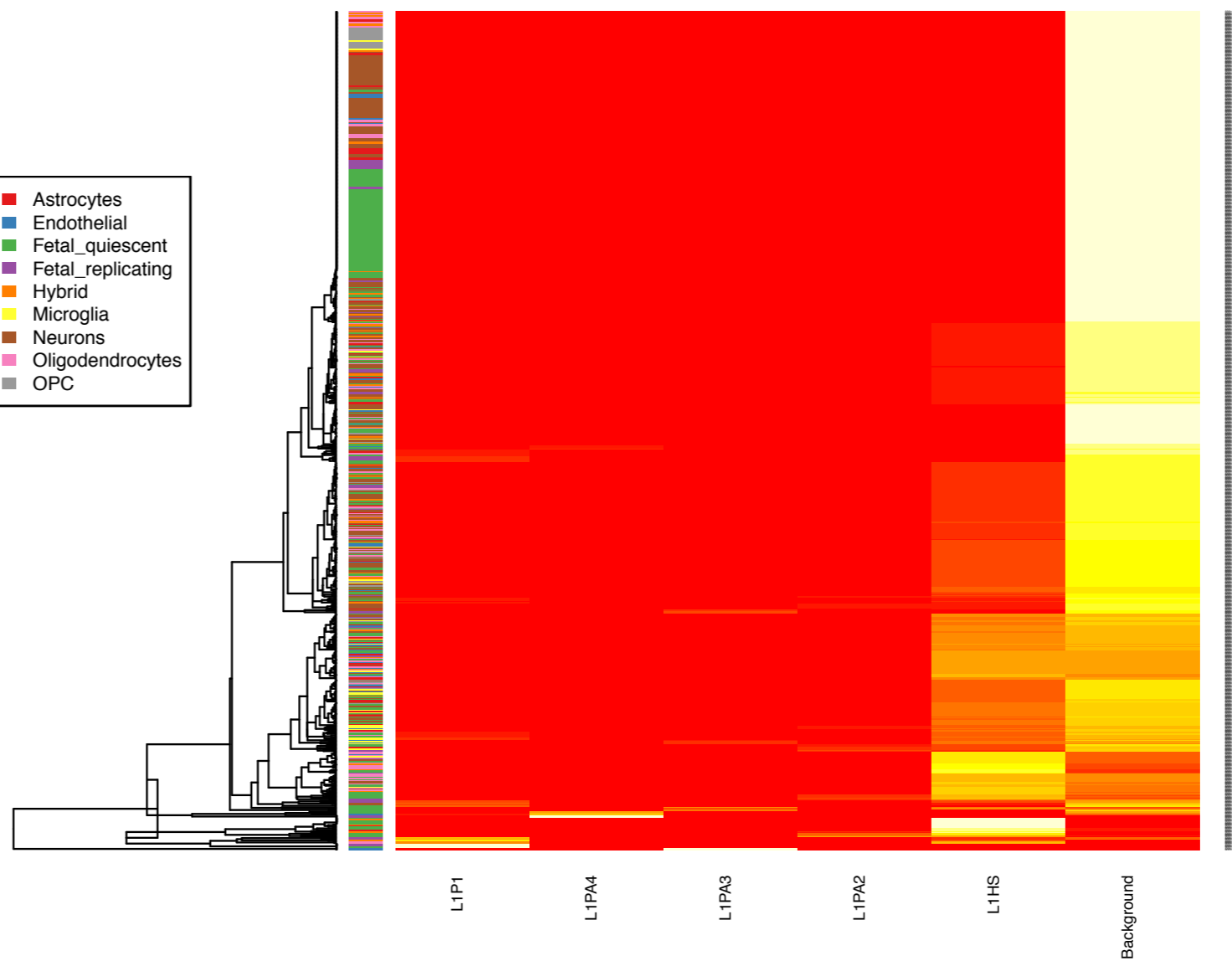
Raw read counts mapped to L1 subfamilies



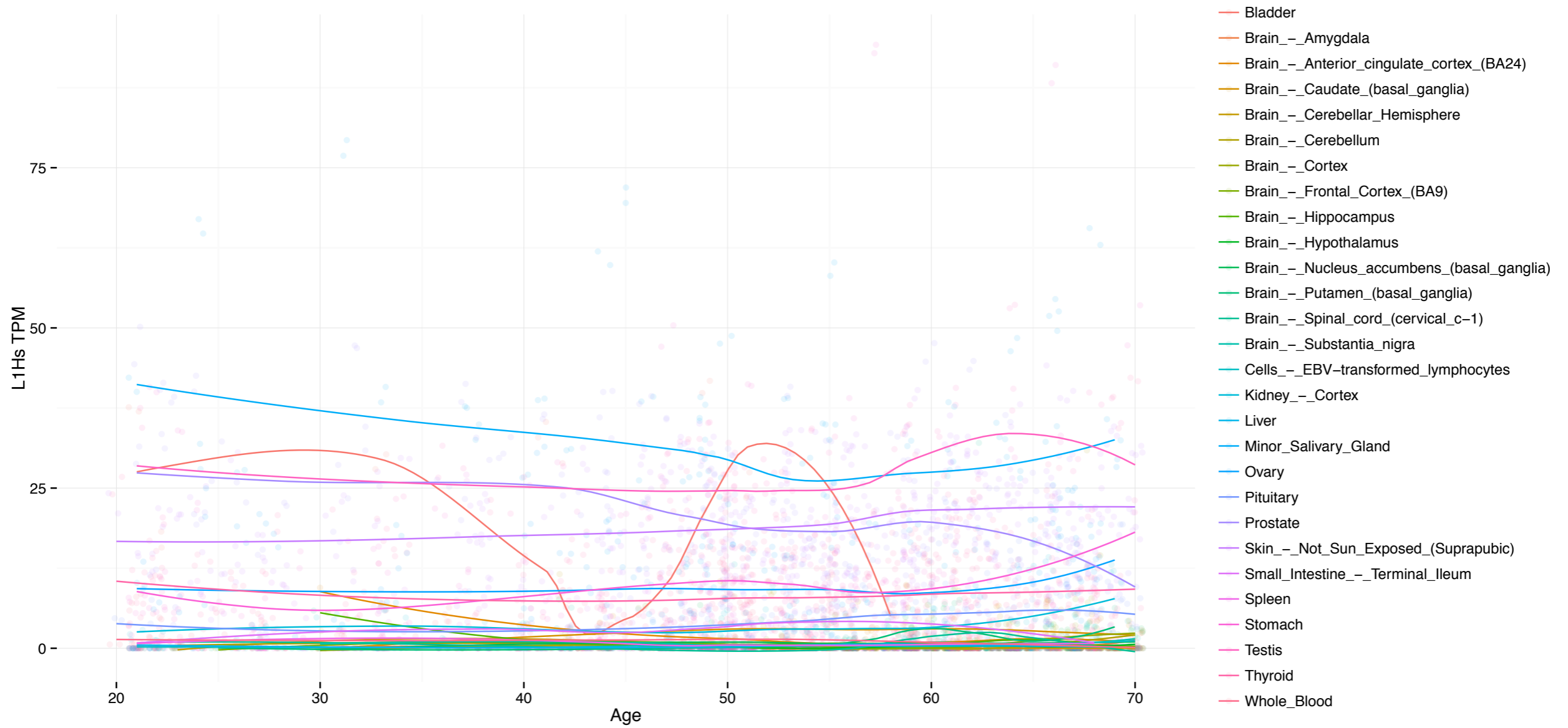
??Sup?? - Single cell data - Clustering by cell type



- Astrocytes
- Endothelial
- Fetal_quiescent
- Fetal_replicating
- Hybrid
- Microglia
- Neurons
- Oligodendrocytes
- OPC



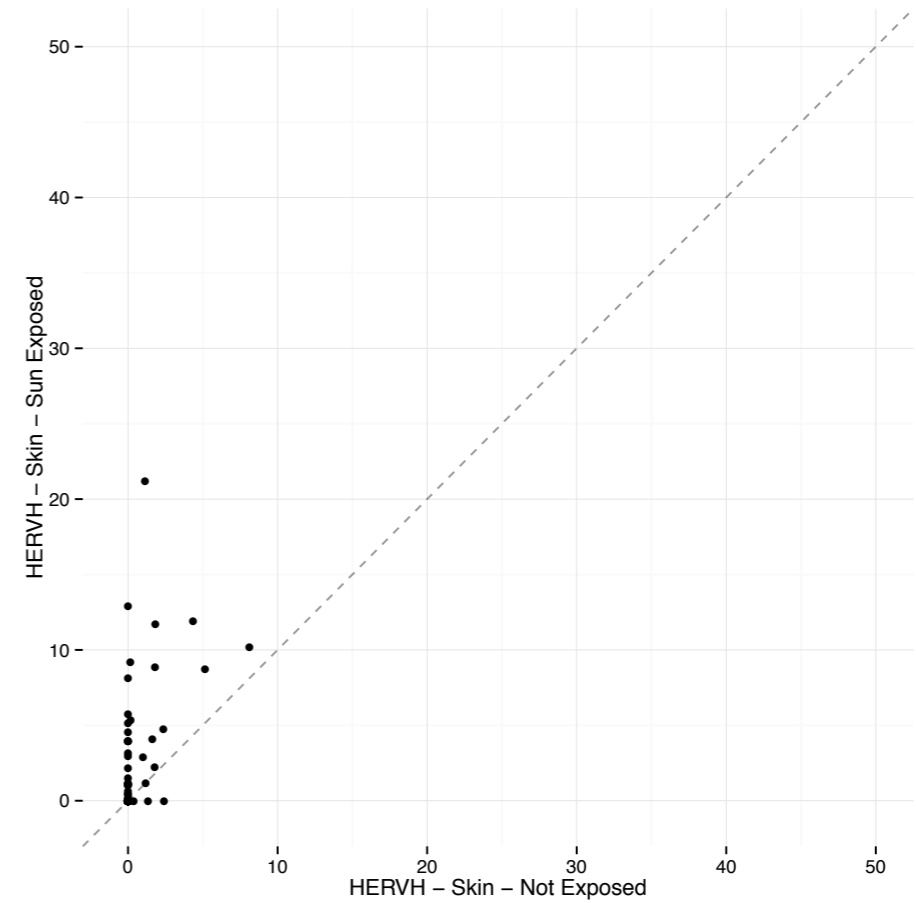
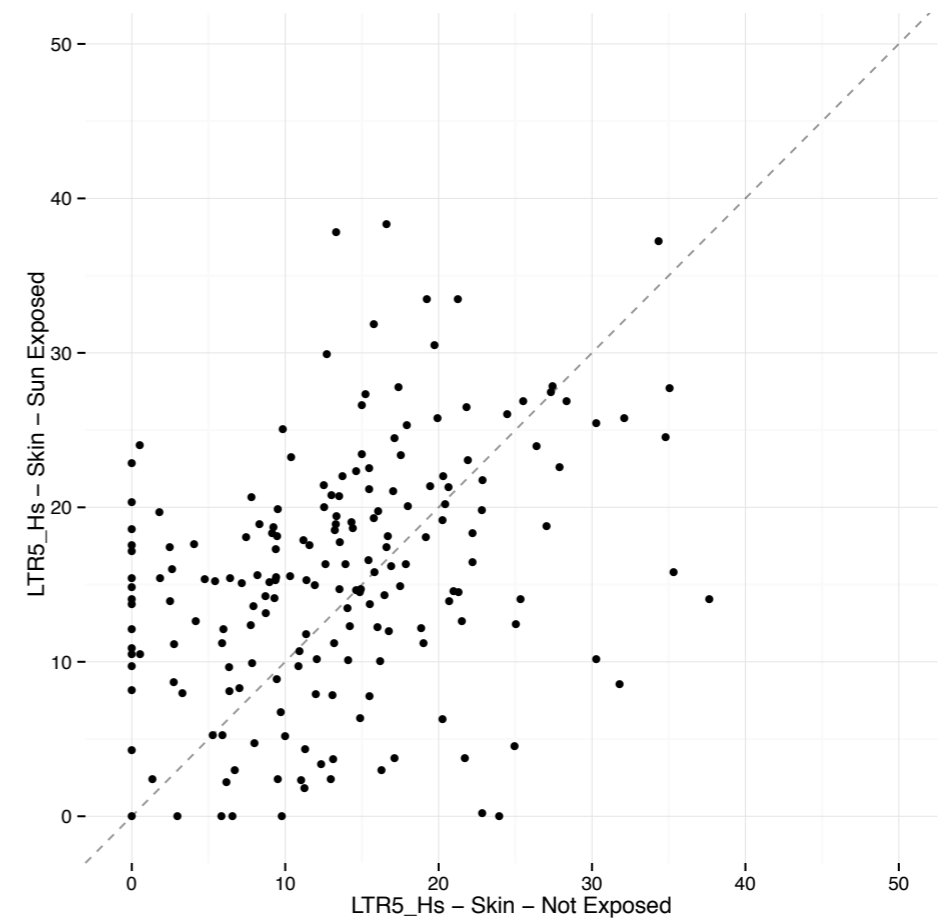
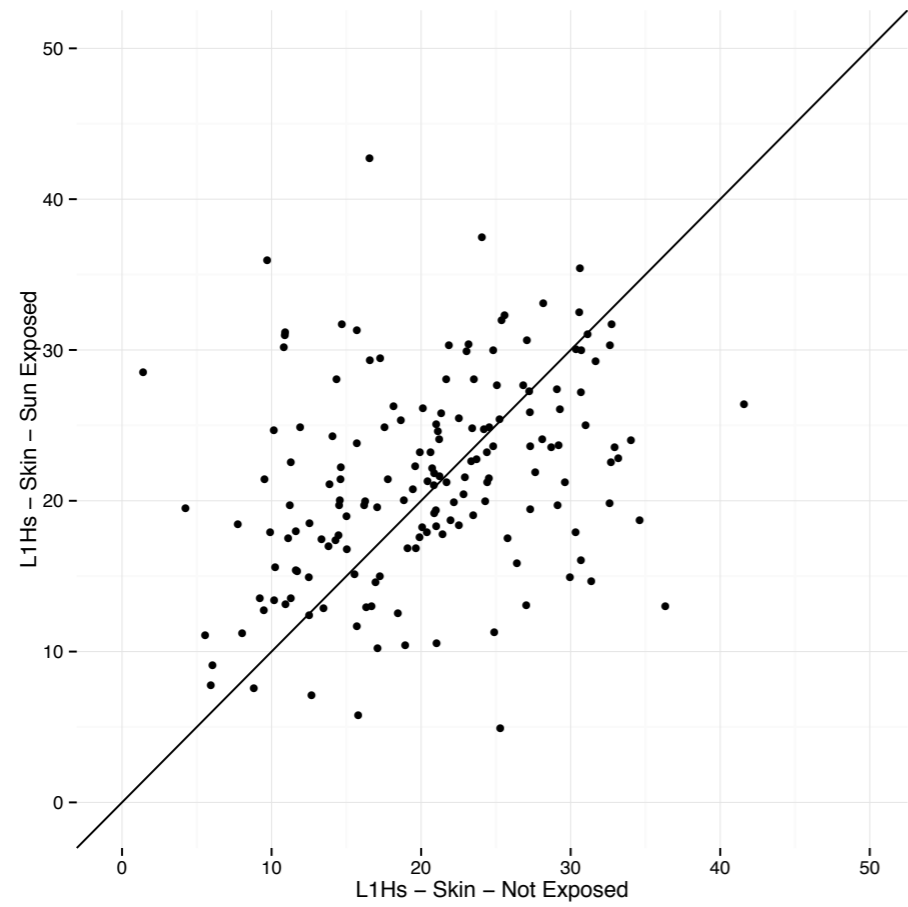
FigSup2B - L1Hs and age



FigSup2B - L1Hs and age



FigSup - Sun exposure does not influence L1Hs expression



FigSup3 - L1 Subfamily % profile. Differences in the proportion of reads mapped to each subfamily alter value of L1Hs TPM

