

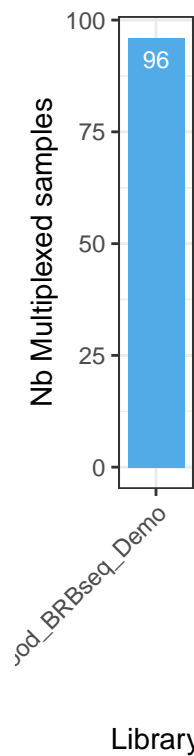
Library preparation and sequencing data analysis report

2023-08-03

Project name (ID): **HS_Blood_BRBseq_Demo**

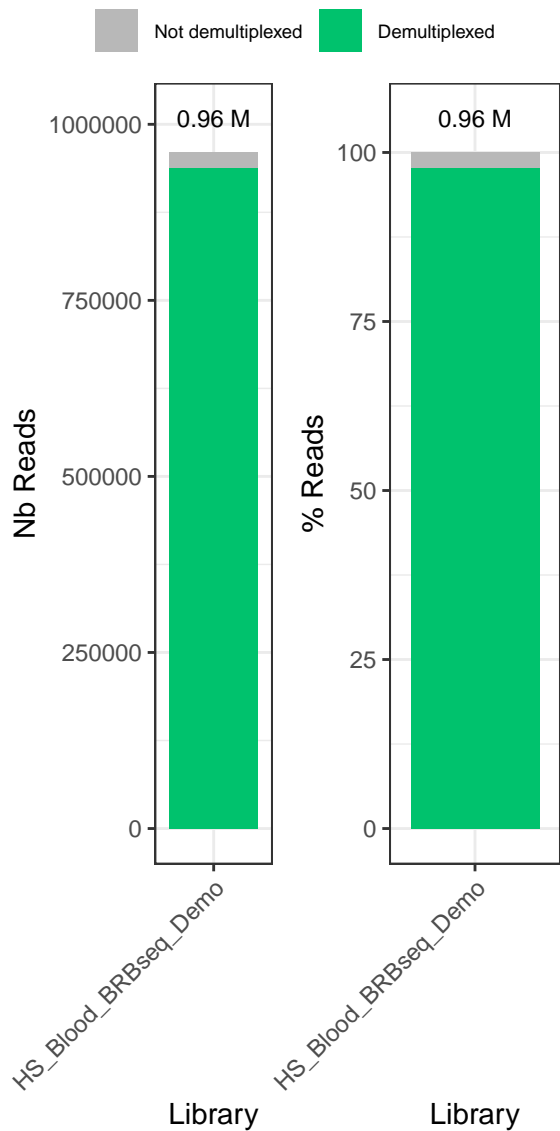
Library preparation summary

Library	Nb of samples	Avg RNA/sample, ng
HS_Blood_BRBseq_Demo	96	NA



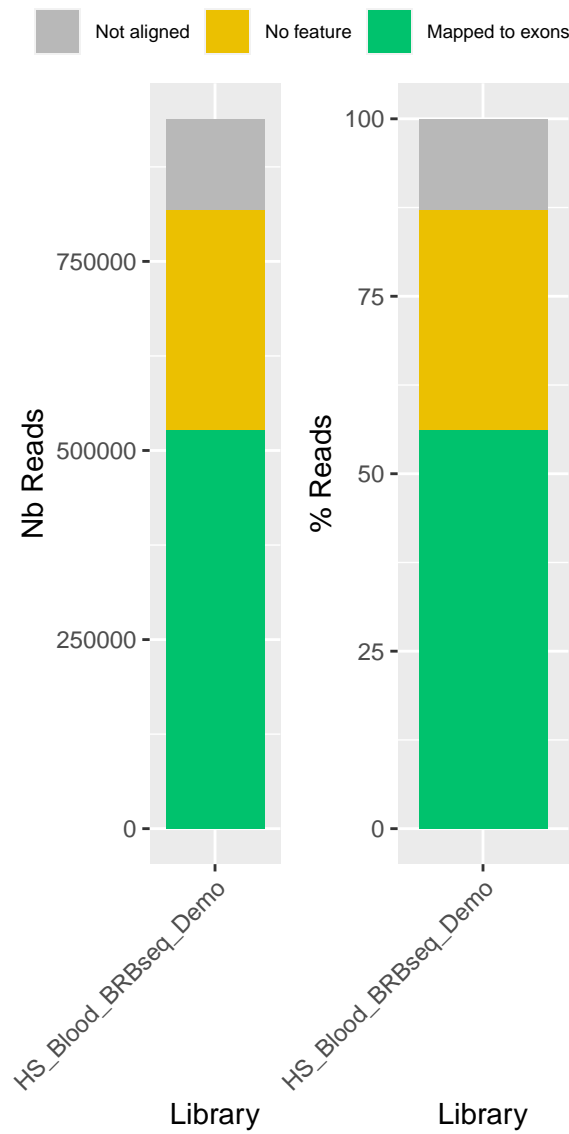
Library sequencing summary

Library	PF_reads	Demultiplexed reads	% Demultiplexed	Avg. demultiplexed reads/sample
HS_Blood_BRBseq_Demo	960,000	938,549	97.77	9,776.6



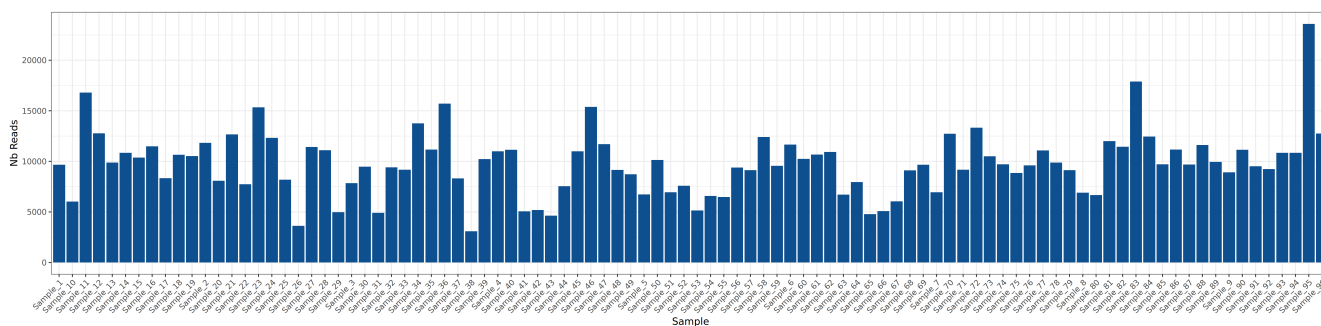
Library alignment summary

Library	Genome assembly	% Mapped to genome (from demultiplexed)	% Mapped to exons (from demultiplexed)
HS_Blood_BRBseq_Demo	homo_sapiens hg38 (GRCh38) (Ensembl release 104)	87.13	56.17

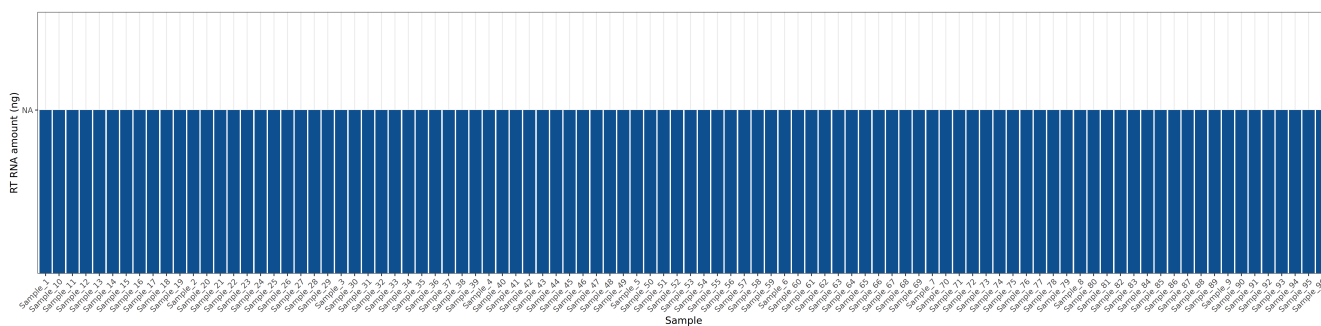


Library HS_Blood_BRBseq_Demo, per sample summary

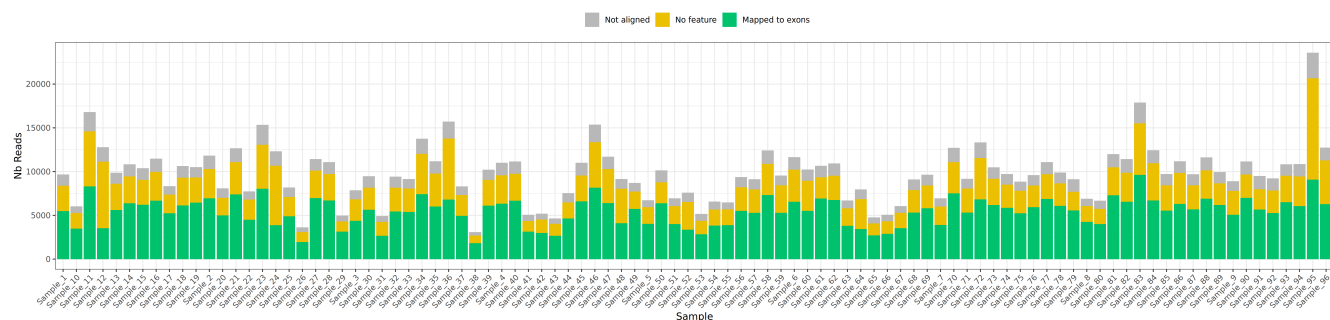
1. Number of sequencing reads per sample



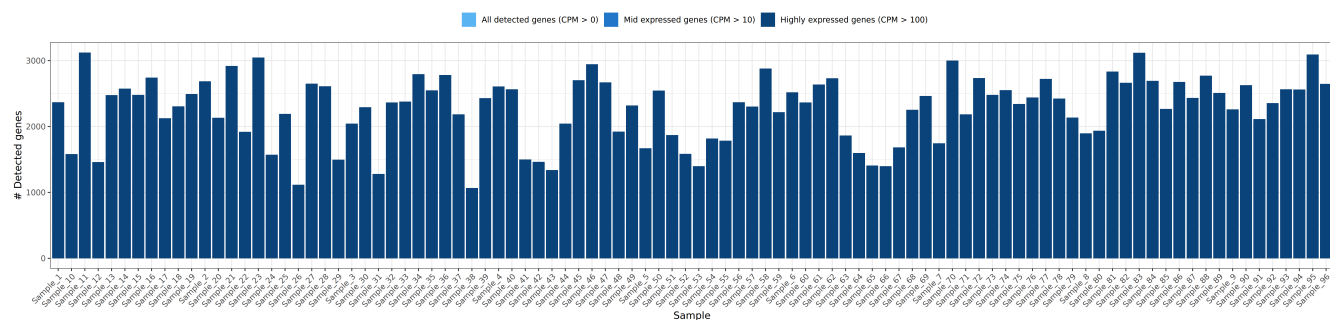
2. RT RNA amount (ng), per sample



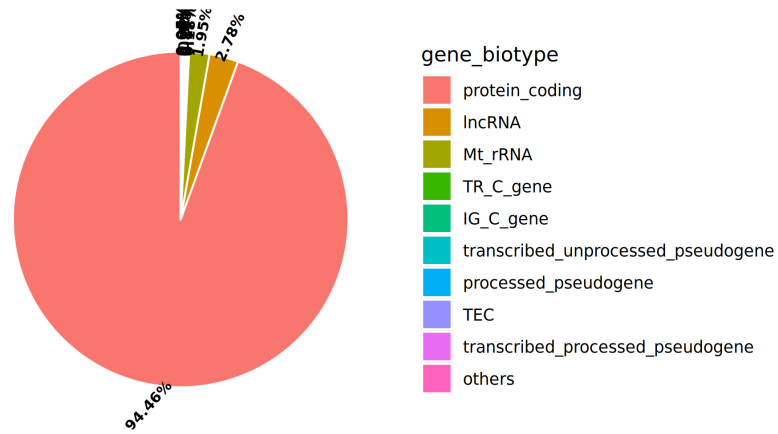
3. Alignment stats, per sample



4. Detected genes, per sample



5. Biotypes, across samples



6. Most expressed genes, across samples

