

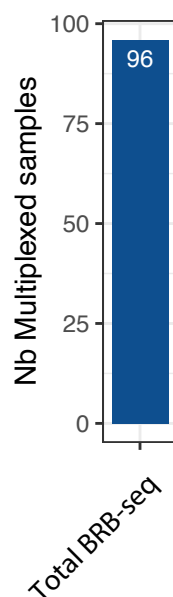
Library preparation and sequencing data analysis report

2025-11-07

Project name (ID): Total BRB-seq

Library preparation summary

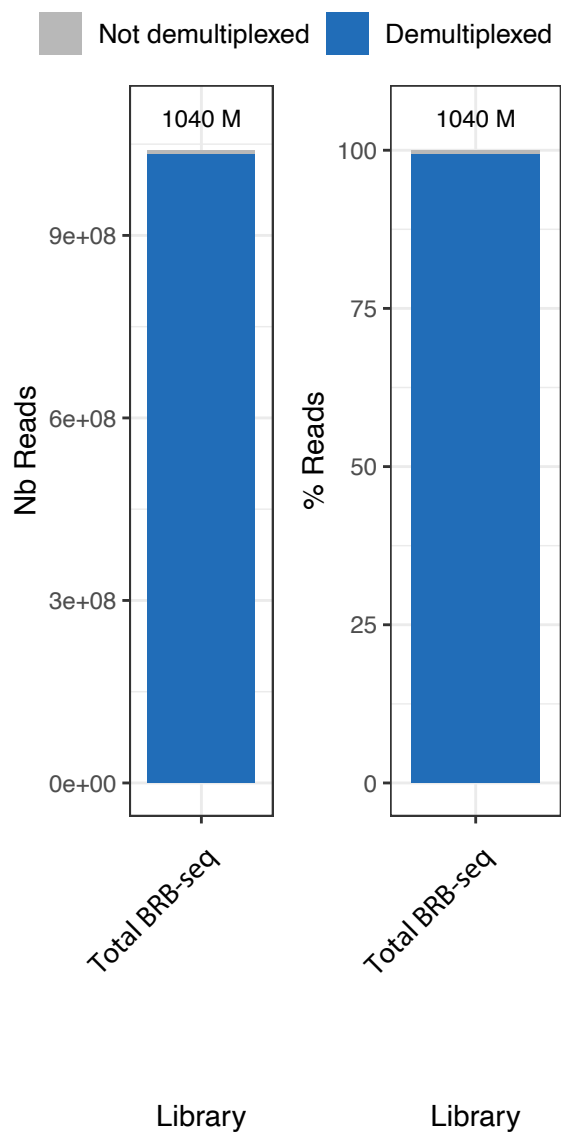
Library	Nb of samples	Avg RNA/sample, ng
Total BRB-seq	96	NA



Library

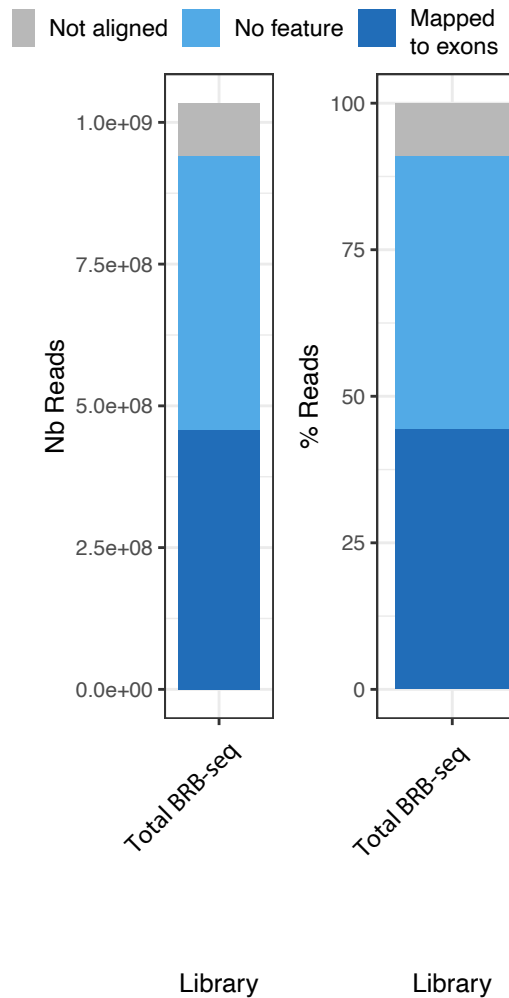
Library sequencing summary

Library	PF_reads	Demultiplexed reads	% Demultiplexed	Avg. demultiplexed reads/sample
Total BRB-seq	1,039,998,526	1,033,797,486	99.4	10,768,724



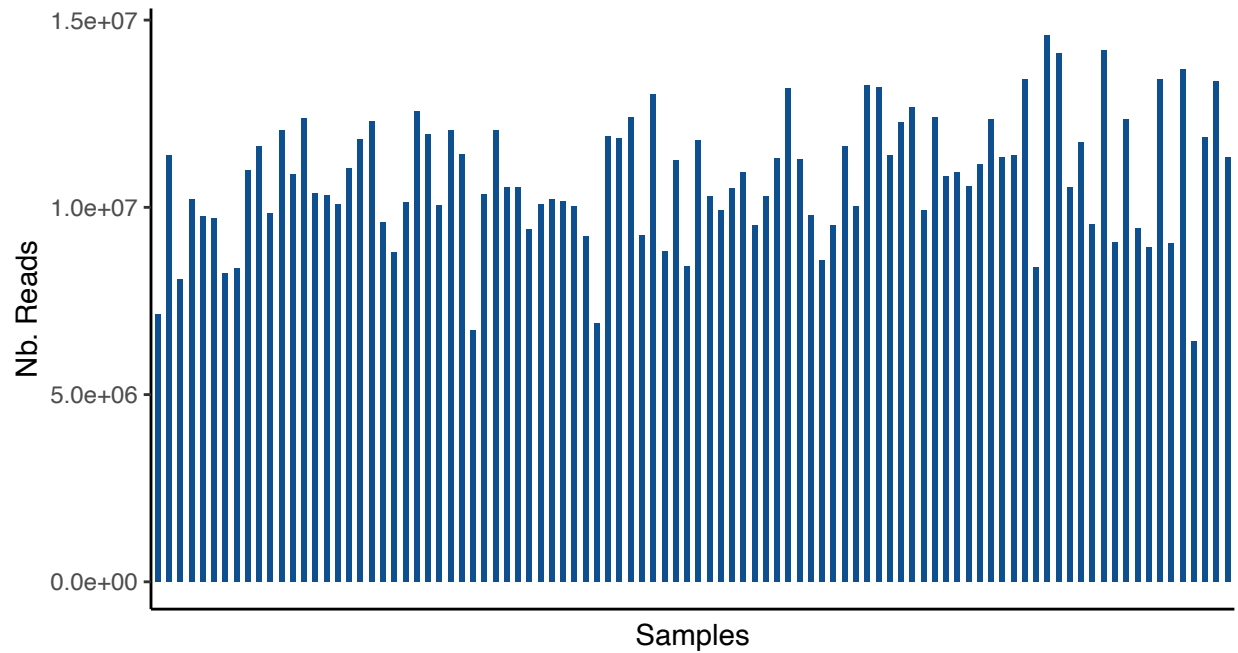
Library alignment summary

Library	Genome assembly	% Mapped to genome (from demultiplexed)	% Mapped to exons (from demultiplexed)
Total BRB-seq	homo_sapiens GRCh38 114	91.03	44.31



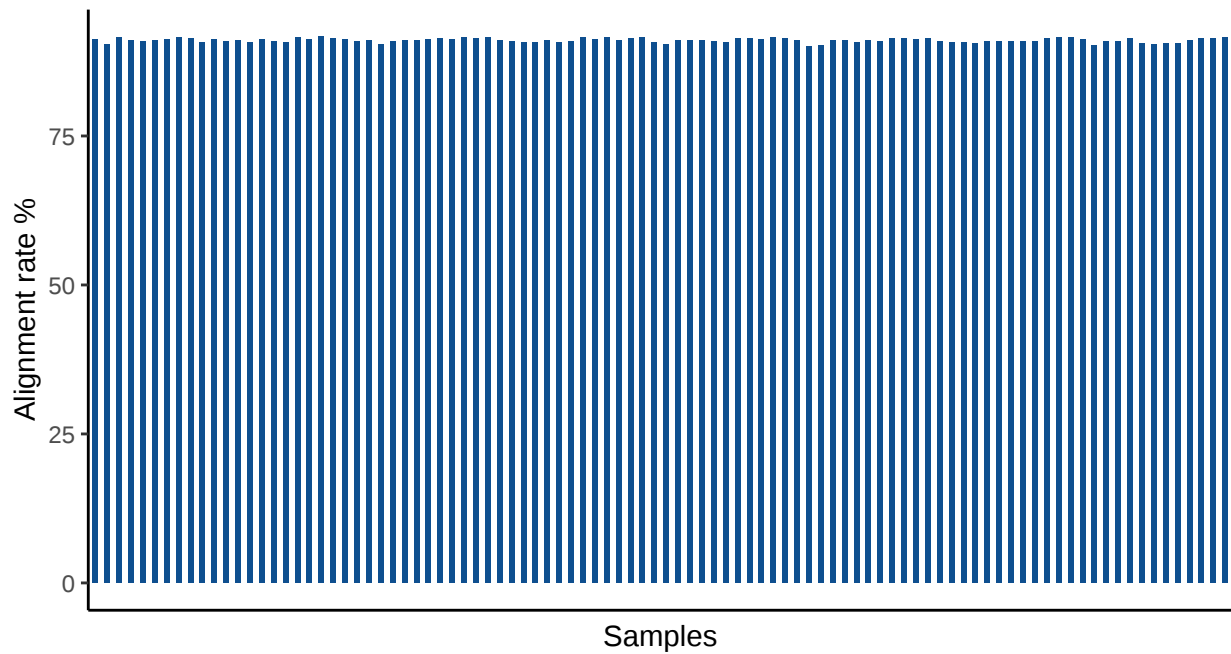
Library Total BRB-seq, per sample summary

Number of sequencing reads per sample



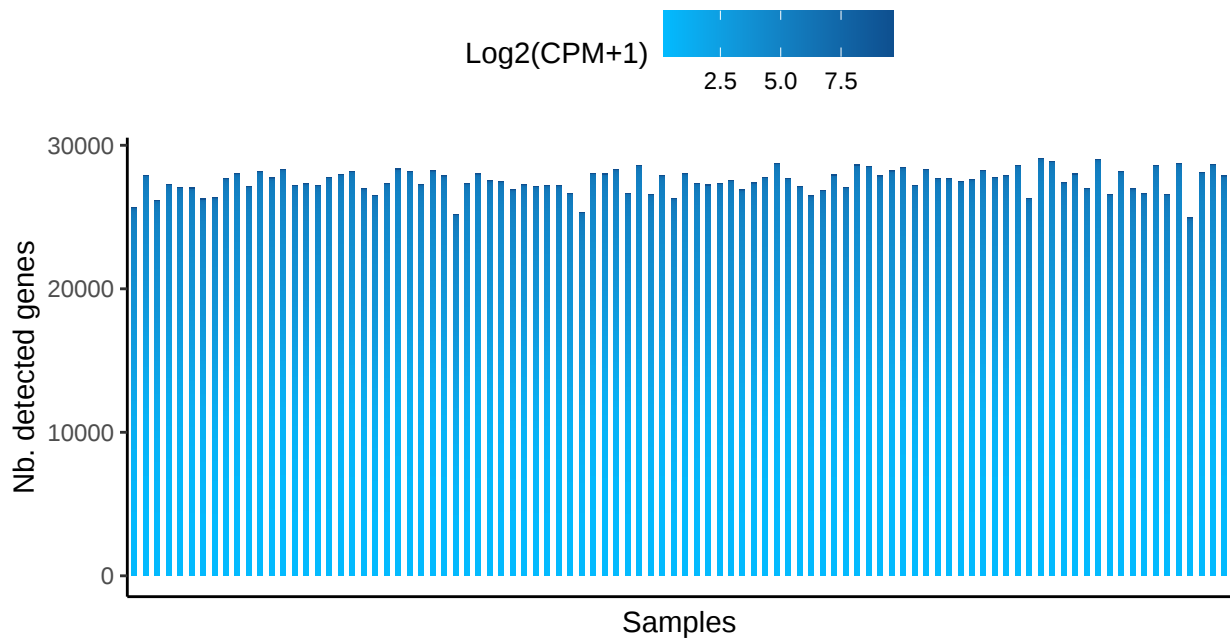
A	7.1M	11.4M	8.1M	10.2M	9.8M	9.7M	8.3M	8.4M	11M	11.6M	9.8M	12M
B	10.9M	12.4M	10.4M	10.3M	10.1M	11M	11.8M	12.3M	9.6M	8.8M	10.1M	12.6M
C	11.9M	10.1M	12.1M	11.4M	6.7M	10.3M	12.1M	10.5M	10.5M	9.4M	10.1M	10.2M
D	10.2M	10M	9.2M	6.9M	11.9M	11.8M	12.4M	9.2M	13M	8.8M	11.2M	8.4M
E	11.8M	10.3M	9.9M	10.5M	10.9M	9.5M	10.3M	11.3M	13.2M	11.3M	9.8M	8.6M
F	9.5M	11.6M	10M	13.3M	13.2M	11.4M	12.3M	12.7M	9.9M	12.4M	10.8M	10.9M
G	10.6M	11.1M	12.3M	11.3M	11.4M	13.4M	8.4M	14.6M	14.1M	10.5M	11.7M	9.5M
H	14.2M	9.1M	12.4M	9.4M	8.9M	13.4M	9M	13.7M	6.4M	11.9M	13.4M	11.3M
	1	2	3	4	5	6	7	8	9	10	11	12

Alignment stats, per sample



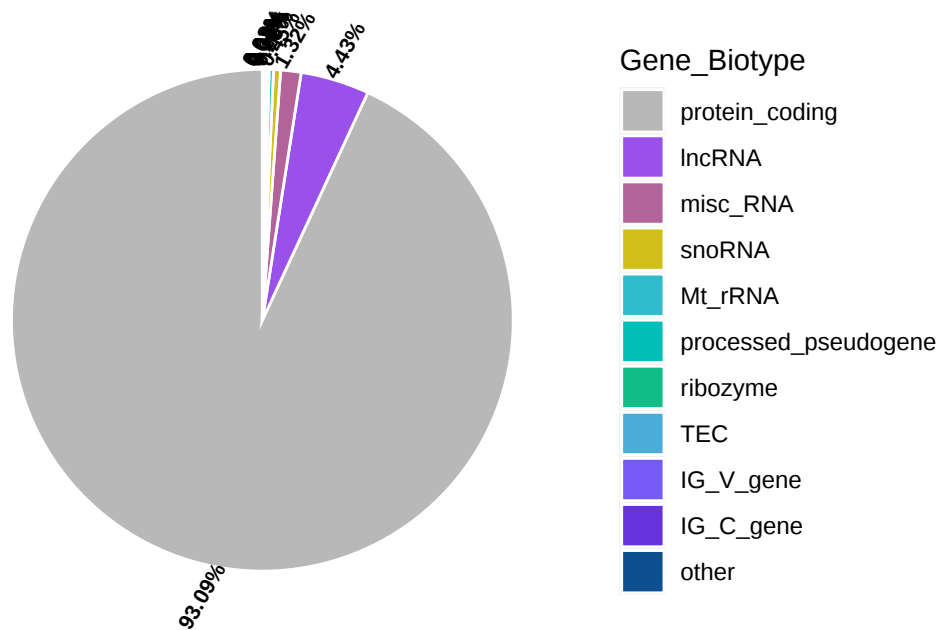
A	91.2%	90.4%	91.5%	91%	90.9%	91%	91.2%	91.5%	91.4%	90.8%	91.2%	90.8%
B	91.1%	90.7%	91.2%	90.8%	90.7%	91.6%	91.2%	91.6%	91.4%	91.2%	90.8%	91%
C	90.4%	90.9%	91.1%	91%	91.2%	91.4%	91.1%	91.5%	91.3%	91.6%	91.1%	90.9%
D	90.6%	90.7%	91.1%	90.8%	90.9%	91.5%	91.2%	91.6%	91.1%	91.4%	91.5%	90.7%
E	90.4%	91.1%	91.1%	91%	90.9%	90.6%	91.4%	91.4%	91.3%	91.5%	91.4%	91%
F	90.1%	90.3%	91%	91%	90.7%	91%	90.8%	91.4%	91.4%	91.3%	91.4%	90.9%
G	90.7%	90.7%	90.6%	90.8%	90.9%	90.8%	90.8%	90.9%	91.3%	91.5%	91.6%	91.2%
H	90.1%	90.9%	90.9%	91.3%	90.5%	90.4%	90.5%	90.5%	91%	91.4%	91.4%	91.6%
	1	2	3	4	5	6	7	8	9	10	11	12

Detected genes, per sample



A	25.7K	27.9K	26.2K	27.3K	27.1K	27K	26.3K	26.3K	27.7K	28K	27.1K	28.2K
B	27.7K	28.3K	27.2K	27.3K	27.2K	27.8K	28K	28.2K	27K	26.5K	27.3K	28.3K
C	28.2K	27.3K	28.2K	27.9K	25.2K	27.3K	28K	27.5K	27.5K	26.9K	27.2K	27.1K
D	27.2K	27.2K	26.7K	25.3K	28.1K	28K	28.3K	26.7K	28.6K	26.6K	27.9K	26.3K
E	28K	27.4K	27.2K	27.4K	27.6K	26.9K	27.4K	27.8K	28.7K	27.7K	27.1K	26.5K
F	26.9K	27.9K	27.1K	28.6K	28.5K	27.9K	28.2K	28.4K	27.2K	28.3K	27.7K	27.7K
G	27.5K	27.6K	28.3K	27.8K	27.9K	28.6K	26.3K	29.1K	28.9K	27.4K	28K	27K
H	29K	26.6K	28.2K	27K	26.6K	28.6K	26.6K	28.7K	24.9K	28.1K	28.7K	27.9K
	1	2	3	4	5	6	7	8	9	10	11	12

Biotypes, across samples



Most expressed genes, across samples

