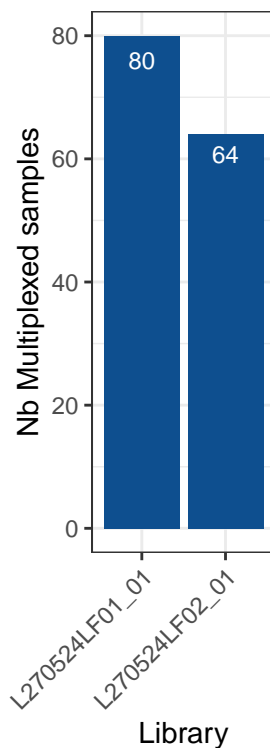


Library preparation and sequencing data analysis report 2024-06-11

Project name (ID): **AMP0211**

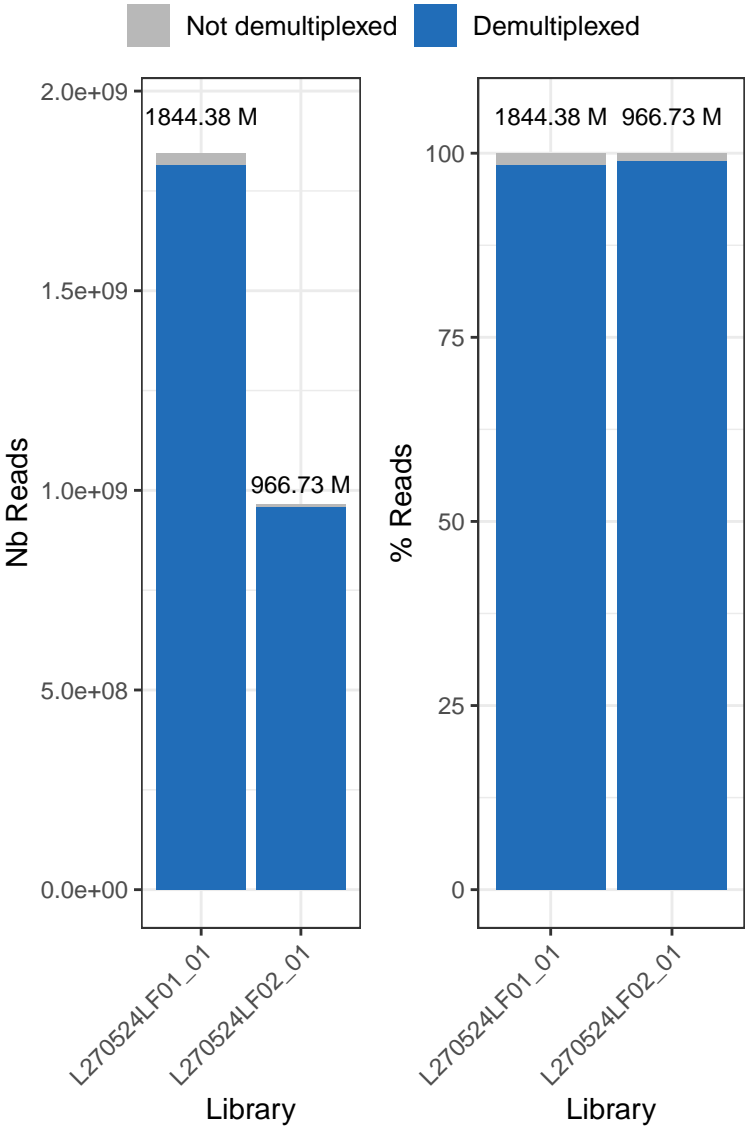
Library preparation summary

Library	Nb of samples	Avg RNA/sample, ng
L270524LF01_01	80	NA
L270524LF02_01	64	NA



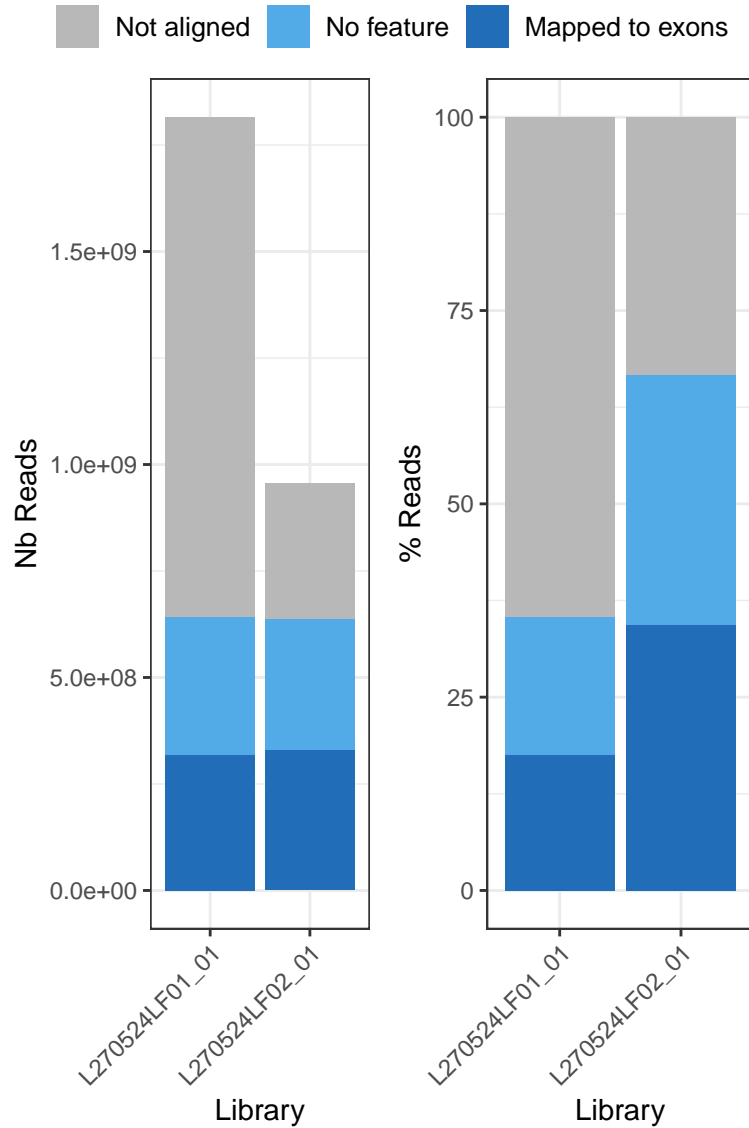
Library sequencing summary

Library	PF_reads	Demultiplexed reads	% Demultiplexed	Avg. demultiplexed reads/sample
L270524LF01_01	1,844,384,795	1,815,334,854	98.42	22,691,686
L270524LF02_01	966,725,484	956,845,294	98.98	14,950,708



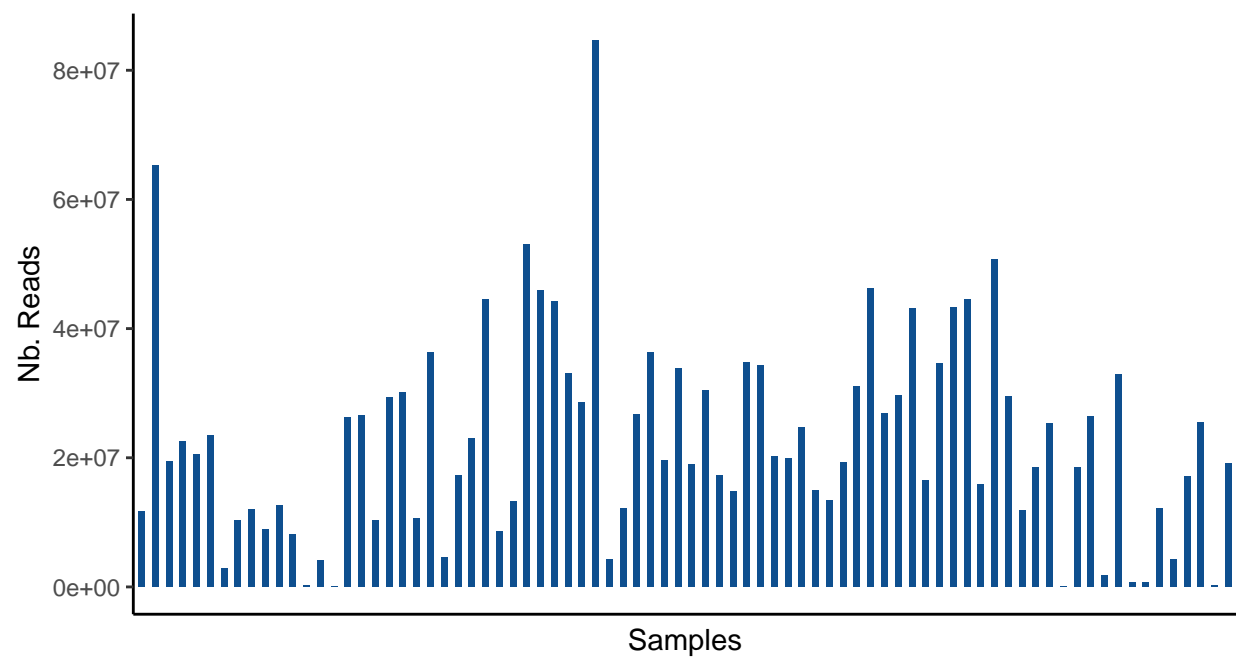
Library alignment summary

Library	Genome assembly	% Mapped to genome (from demultiplexed)	% Mapped to exons (from demultiplexed)
L270524LF01_01	homo_sapiens hg38 (GRCh38) (Ensembl release 104)	35.38	17.46
L270524LF02_01	homo_sapiens hg38 (GRCh38) (Ensembl release 104)	66.66	34.34



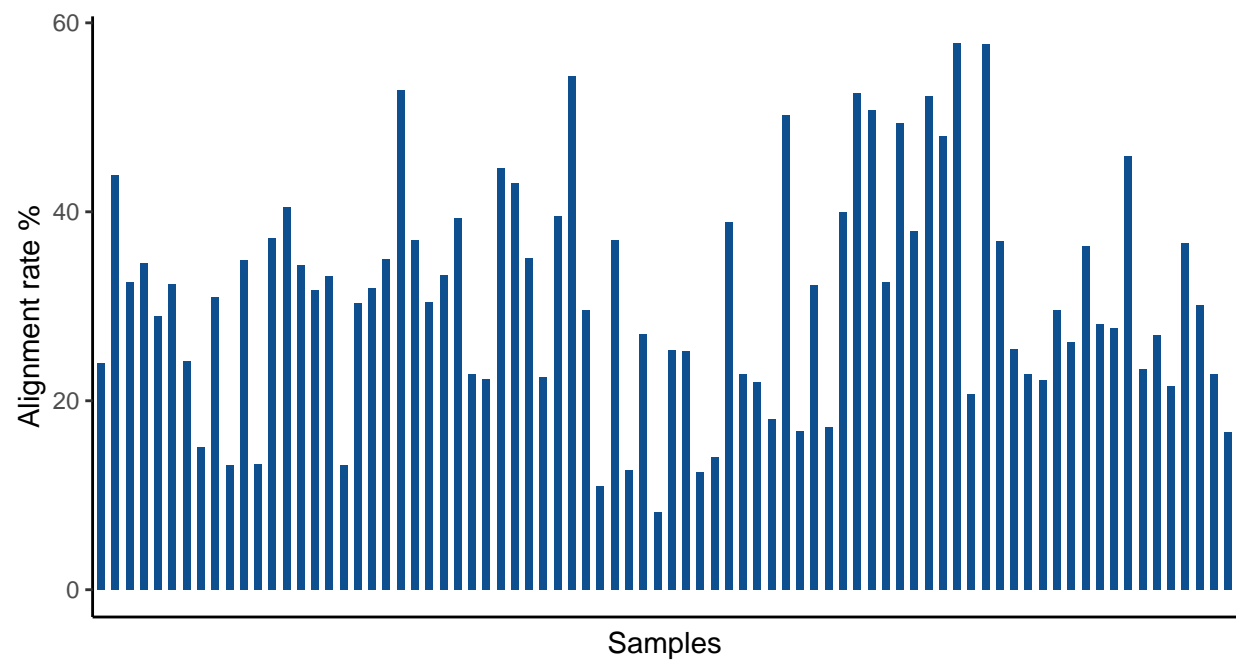
Library L270524LF01_01, per sample summary

Number of sequencing reads per sample



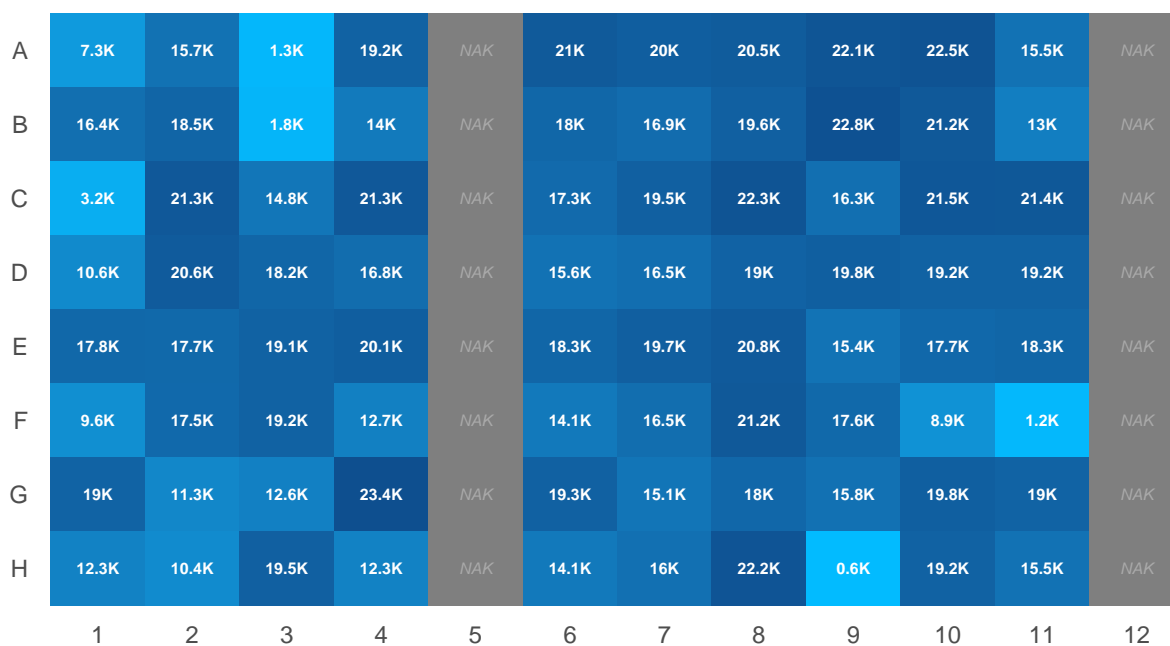
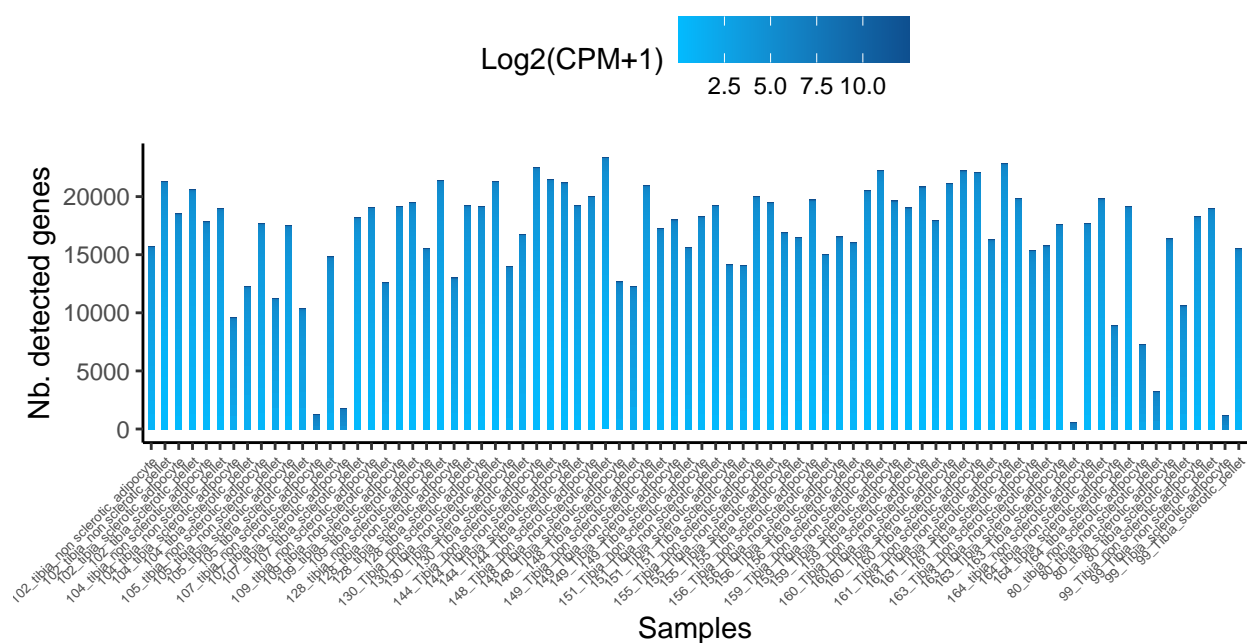
A	0.7M	11.7M	0.2M	23M	OM	26.7M	34.8M	31M	44.5M	53M	10.6M	OM
B	12.2M	19.4M	0.1M	8.6M	OM	19.6M	20.2M	26.8M	50.7M	44.2M	4.6M	OM
C	0.6M	65.3M	4.2M	44.5M	OM	36.4M	34.4M	46.2M	15.9M	46M	36.3M	OM
D	4.2M	22.5M	26.3M	13.2M	OM	33.9M	19.9M	29.7M	29.5M	33.1M	17.3M	OM
E	20.5M	12M	26.6M	28.6M	OM	19M	24.8M	43.1M	11.9M	18.6M	17.1M	OM
F	2.9M	12.6M	29.4M	4.3M	OM	17.2M	13.4M	34.5M	25.3M	1.8M	0.2M	OM
G	23.5M	8.9M	10.3M	84.6M	OM	30.4M	15M	16.4M	18.5M	26.4M	25.5M	OM
H	10.3M	8.1M	30.1M	12.2M	OM	14.7M	19.3M	43.2M	0.1M	32.9M	19.1M	OM
	1	2	3	4	5	6	7	8	9	10	11	12

Alignment stats, per sample

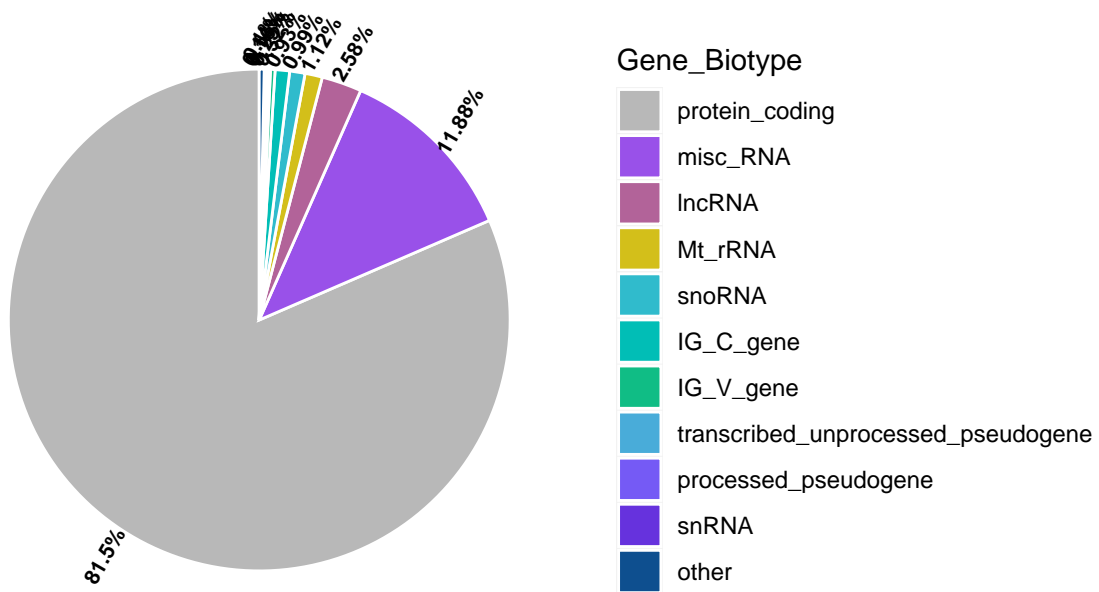


A	45.9%	24%	37.2%	33.3%	NA	37%	38.9%	39.9%	57.8%	44.6%	35%	NA
B	26.9%	32.6%	34.3%	22.8%	NA	27%	21.9%	50.7%	57.7%	35%	37%	NA
C	23.3%	43.9%	40.4%	39.3%	NA	12.7%	22.8%	52.6%	20.7%	43%	52.9%	NA
D	21.6%	34.6%	31.7%	22.3%	NA	8.2%	18.1%	32.6%	36.9%	22.5%	30.4%	NA
E	29%	31%	33.1%	39.6%	NA	25.3%	50.3%	49.3%	25.5%	26.2%	36.7%	NA
F	24.2%	34.9%	30.3%	29.6%	NA	12.4%	32.2%	52.2%	22.2%	28.1%	22.8%	NA
G	32.3%	13.1%	13.2%	54.4%	NA	25.2%	16.8%	38%	22.8%	36.4%	30.1%	NA
H	15%	13.3%	31.9%	11%	NA	14%	17.2%	48%	29.5%	27.7%	16.7%	NA
	1	2	3	4	5	6	7	8	9	10	11	12

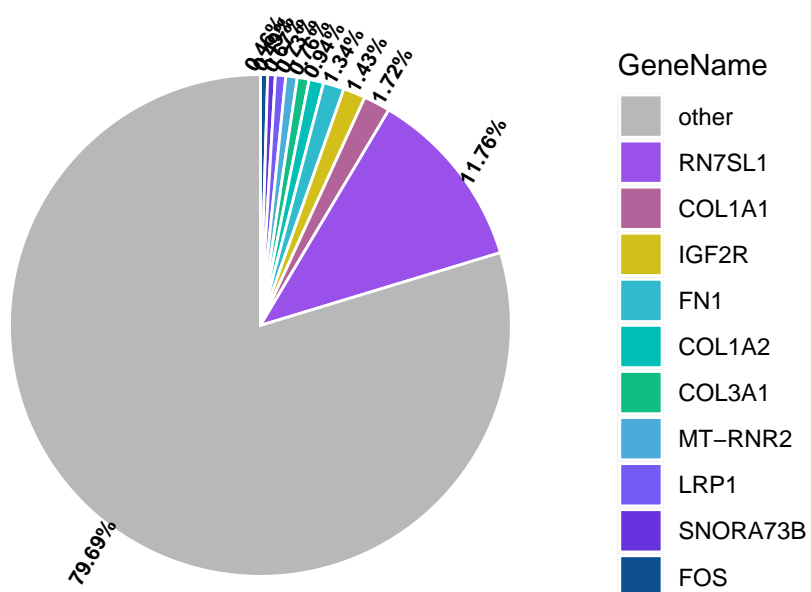
Detected genes, per sample



Biotypes, across samples

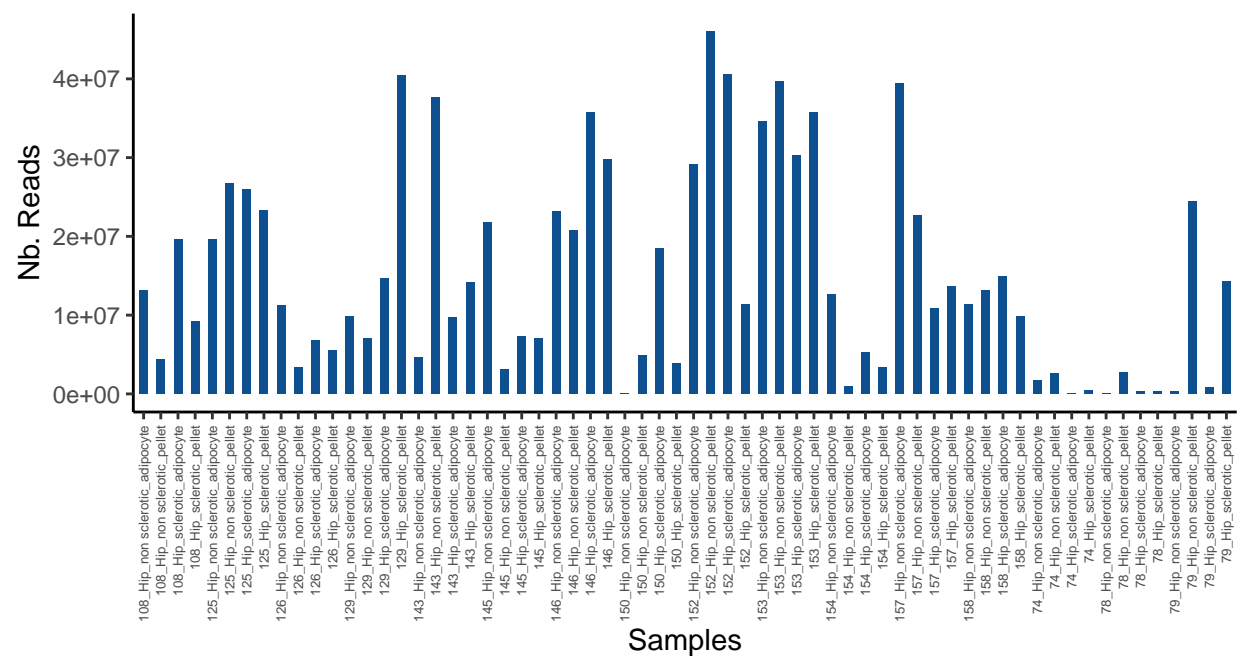


Most expressed genes, across samples



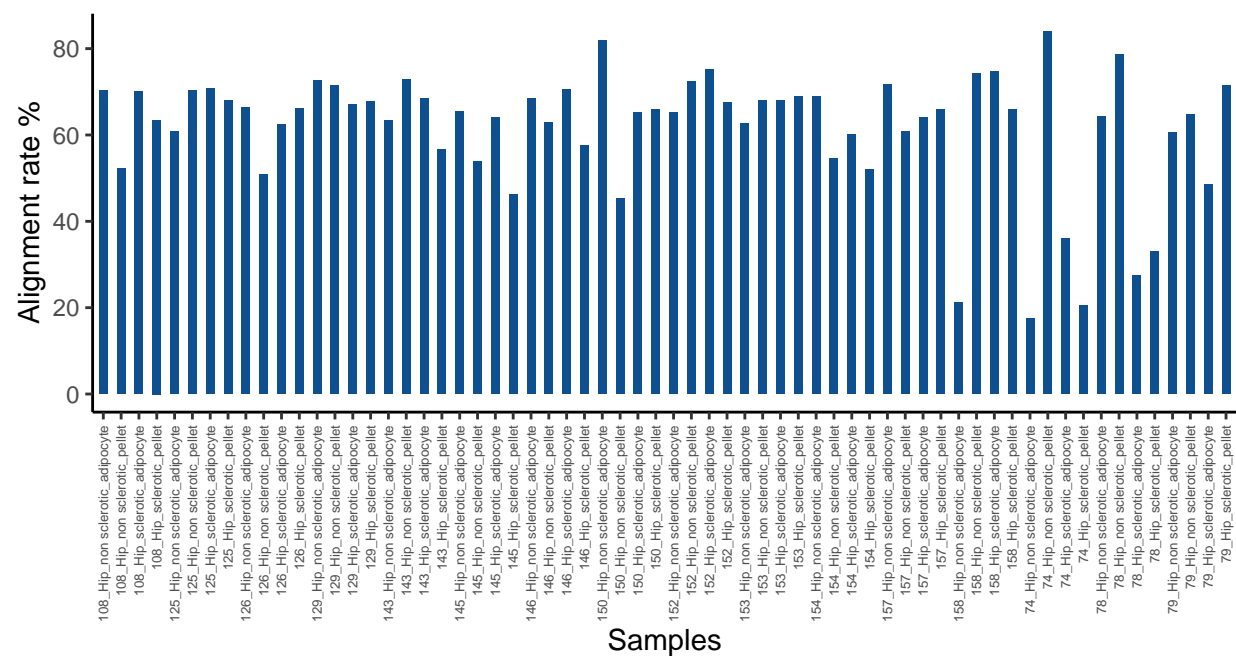
Library L270524LF02_01, per sample summary

Number of sequencing reads per sample



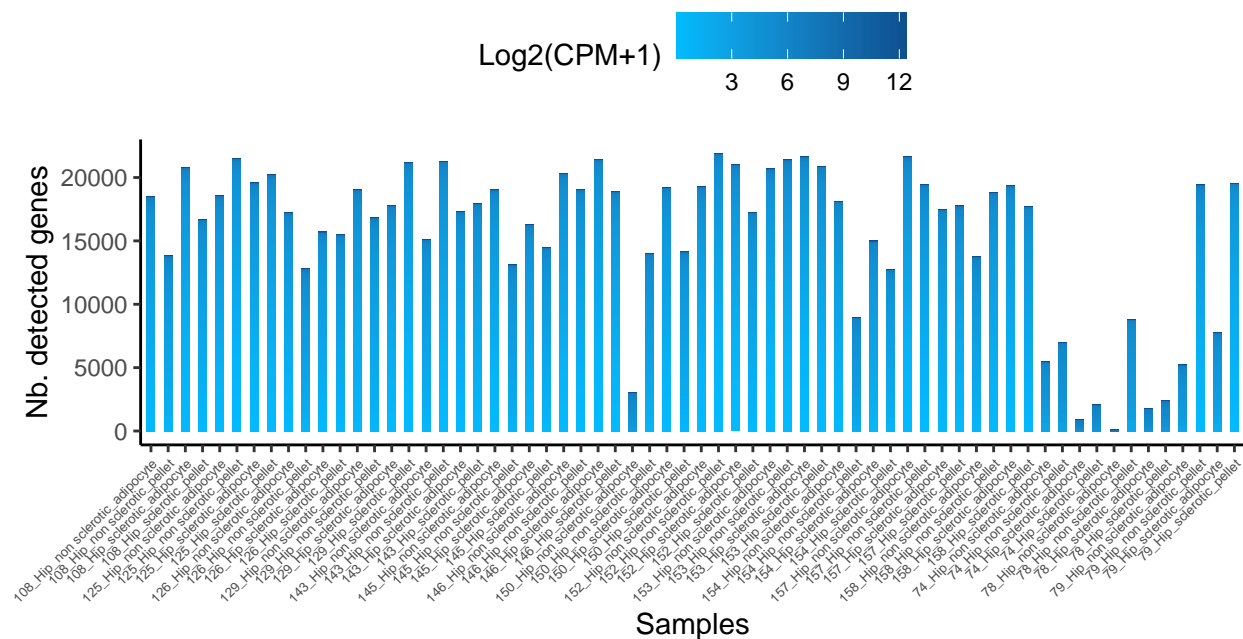
A	1.7M	0.3M	19.6M	9.9M	21.8M	0.1M	34.6M	39.4M	0M	0M	0M	0M
B	0.1M	0.9M	26M	14.6M	7.3M	18.5M	30.3M	10.9M	0M	0M	0M	0M
C	2.6M	24.4M	26.8M	7M	3.1M	4.9M	39.7M	22.6M	0M	0M	0M	0M
D	0.5M	14.3M	23.3M	40.5M	7M	3.9M	35.7M	13.7M	0M	0M	0M	0M
E	0M	13.1M	11.2M	4.6M	23.2M	29.1M	12.7M	11.4M	0M	0M	0M	0M
F	0.4M	19.7M	6.8M	9.7M	35.8M	40.5M	5.3M	14.9M	0M	0M	0M	0M
G	2.7M	4.4M	3.4M	37.6M	20.8M	46M	1M	13.2M	0M	0M	0M	0M
H	0.4M	9.1M	5.6M	14.1M	29.7M	11.3M	3.4M	9.9M	0M	0M	0M	0M
	1	2	3	4	5	6	7	8	9	10	11	12

Alignment stats, per sample



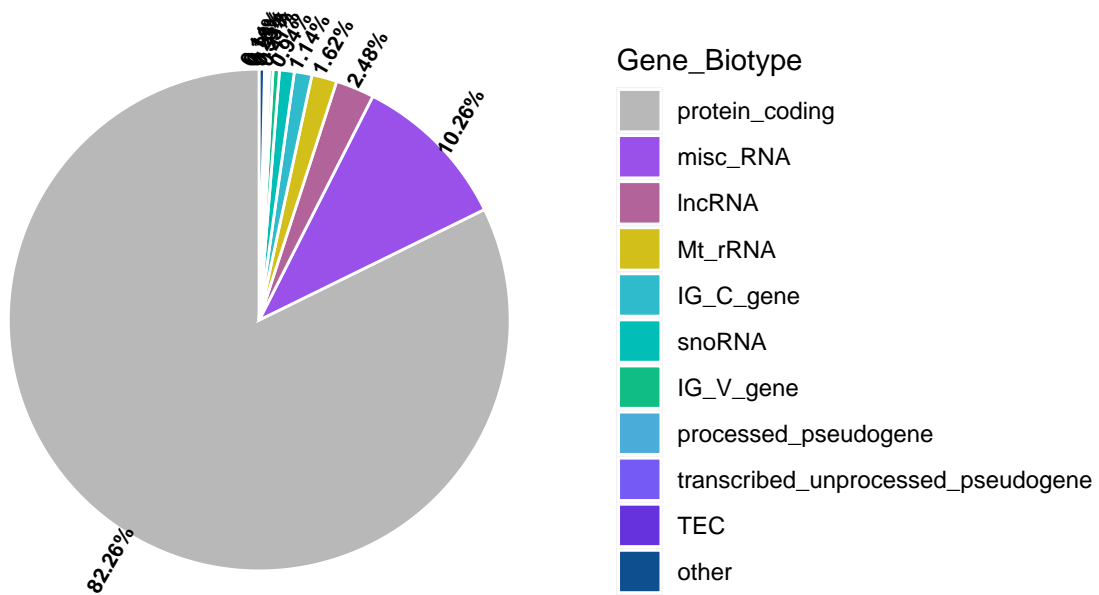
A	17.4%	60.6%	60.8%	72.6%	65.5%	81.8%	62.7%	71.7%	NA	NA	NA	NA
B	36%	48.5%	70.9%	67%	64%	65.2%	68.1%	64.1%	NA	NA	NA	NA
C	83.9%	64.7%	70.3%	71.5%	53.8%	45.3%	68.1%	60.9%	NA	NA	NA	NA
D	20.5%	71.5%	68%	67.8%	46.2%	65.9%	68.9%	66%	NA	NA	NA	NA
E	64.2%	70.4%	66.3%	63.4%	68.5%	65.2%	68.9%	21.3%	NA	NA	NA	NA
F	27.4%	70.2%	62.5%	68.5%	70.6%	75.2%	60.1%	74.8%	NA	NA	NA	NA
G	78.6%	52.3%	50.9%	72.7%	62.9%	72.4%	54.6%	74.1%	NA	NA	NA	NA
H	33%	63.5%	66.1%	56.6%	57.6%	67.5%	51.9%	66%	NA	NA	NA	NA
	1	2	3	4	5	6	7	8	9	10	11	12

Detected genes, per sample



A	5.5K	5.2K	18.6K	19K	19K	3.1K	20.7K	21.6K	NAK	NAK	NAK	NAK
B	0.9K	7.8K	19.6K	17.8K	16.3K	19.2K	21.7K	17.5K	NAK	NAK	NAK	NAK
C	7K	19.4K	21.5K	16.8K	13.1K	14K	21.4K	19.4K	NAK	NAK	NAK	NAK
D	2.1K	19.6K	20.2K	21.2K	14.5K	14.2K	20.9K	17.8K	NAK	NAK	NAK	NAK
E	0.2K	18.5K	17.2K	15.1K	20.4K	19.3K	18.1K	13.7K	NAK	NAK	NAK	NAK
F	1.8K	20.8K	15.7K	17.3K	21.4K	21.1K	15K	19.4K	NAK	NAK	NAK	NAK
G	8.8K	13.8K	12.8K	21.3K	19.1K	21.9K	9K	18.8K	NAK	NAK	NAK	NAK
H	2.4K	16.7K	15.5K	18K	18.9K	17.3K	12.8K	17.8K	NAK	NAK	NAK	NAK
	1	2	3	4	5	6	7	8	9	10	11	12

Biotypes, across samples



Most expressed genes, across samples

