

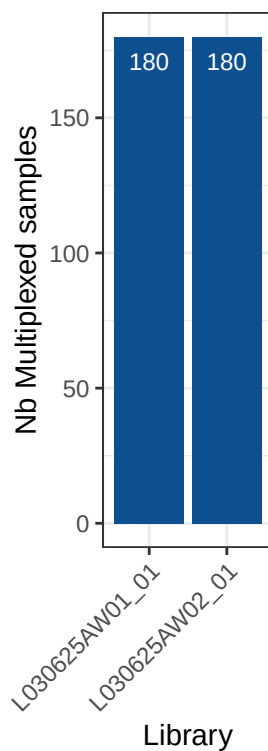
Library preparation and sequencing data analysis report

2025-06-18

Project name (ID): **AMP0435**

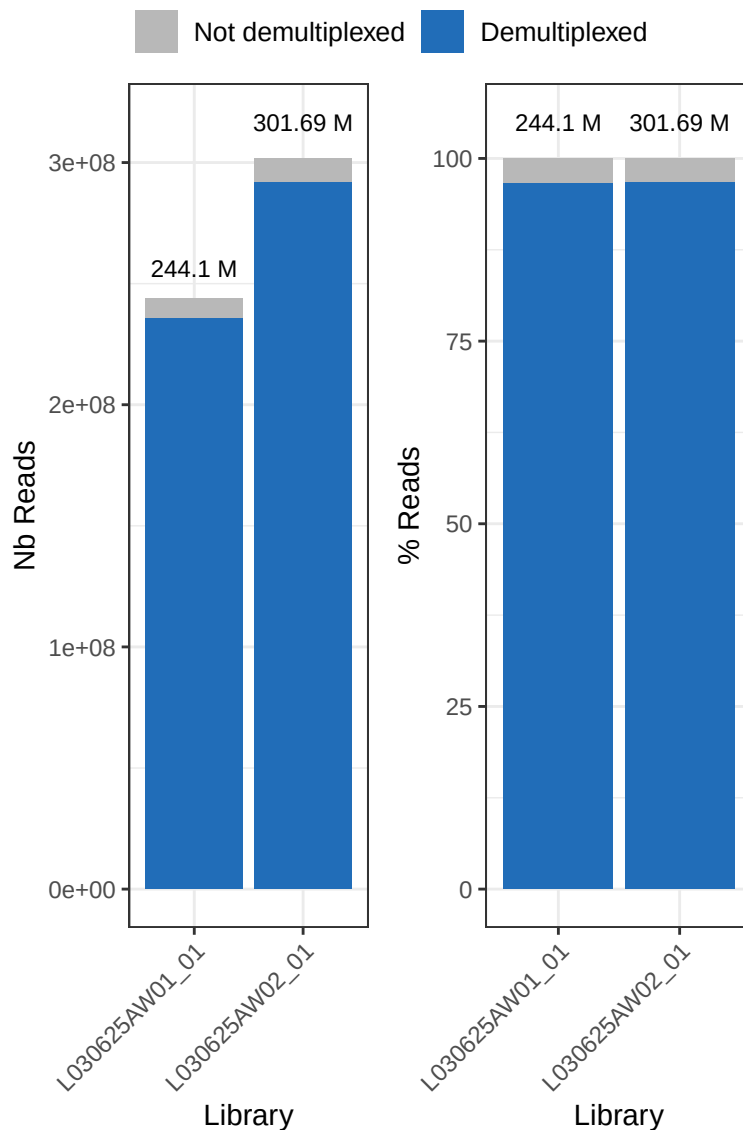
Library preparation summary

Library	Nb of samples	Avg RNA/sample, ng
L030625AW01_01	180	NA
L030625AW02_01	180	NA



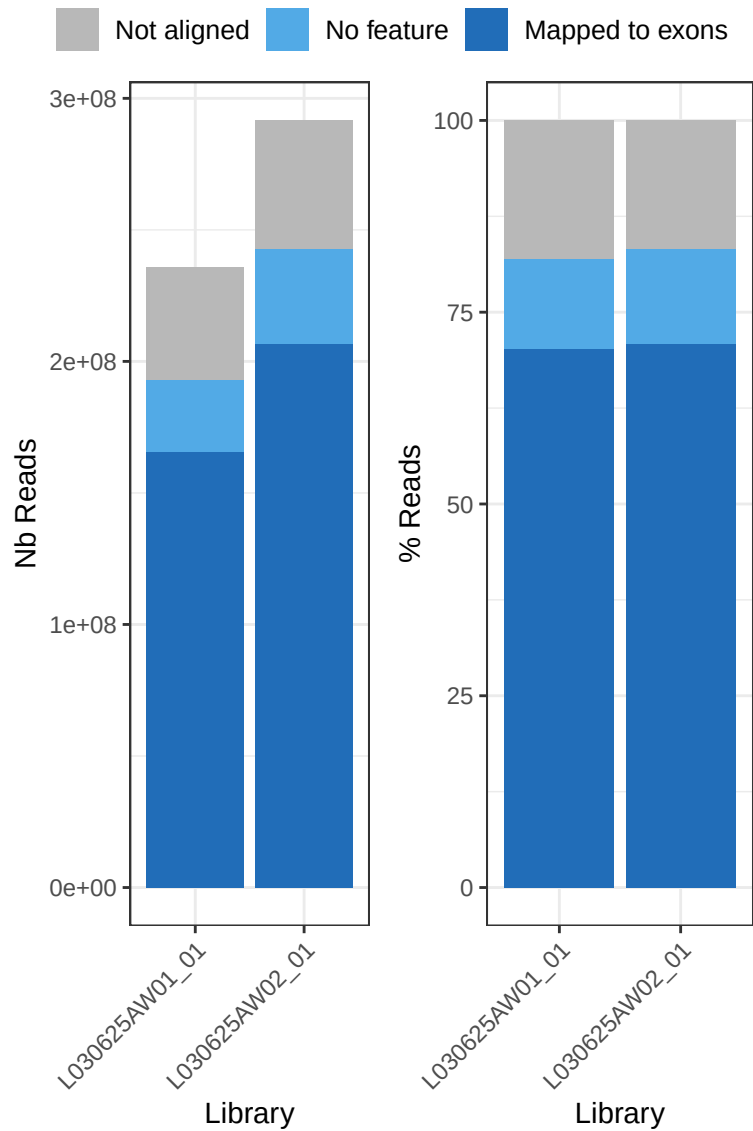
Library sequencing summary

Library	PF_reads	Demultiplexed reads	% Demultiplexed	Avg. demultiplexed reads/sample
L030625AW01_01	244,102,044	235,637,965	96.53	1,309,100
L030625AW02_01	301,692,560	291,632,999	96.67	1,620,183



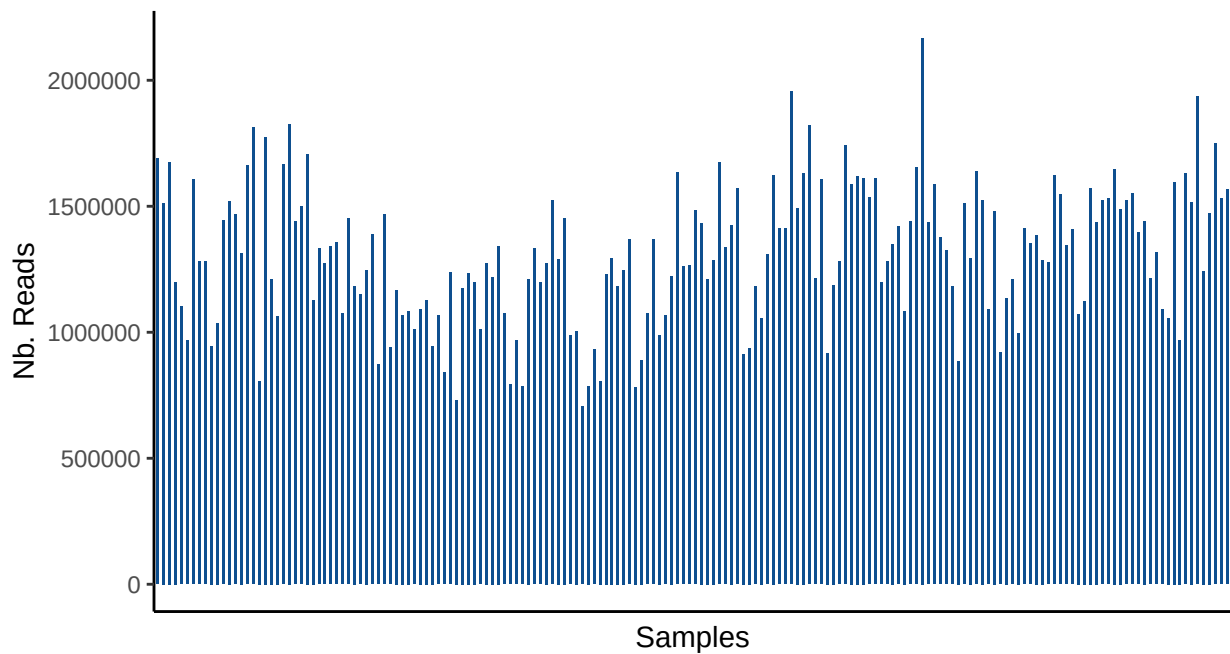
Library alignment summary

Library	Genome assembly	% Mapped to genome (from demultiplexed)	% Mapped to exons (from demultiplexed)
L030625AW01_01	homo_sapiens hg38 (GRCh38) with ERCC (Ensembl release 104)	81.86	70.19
L030625AW02_01	homo_sapiens hg38 (GRCh38) with ERCC (Ensembl release 104)	83.15	70.87



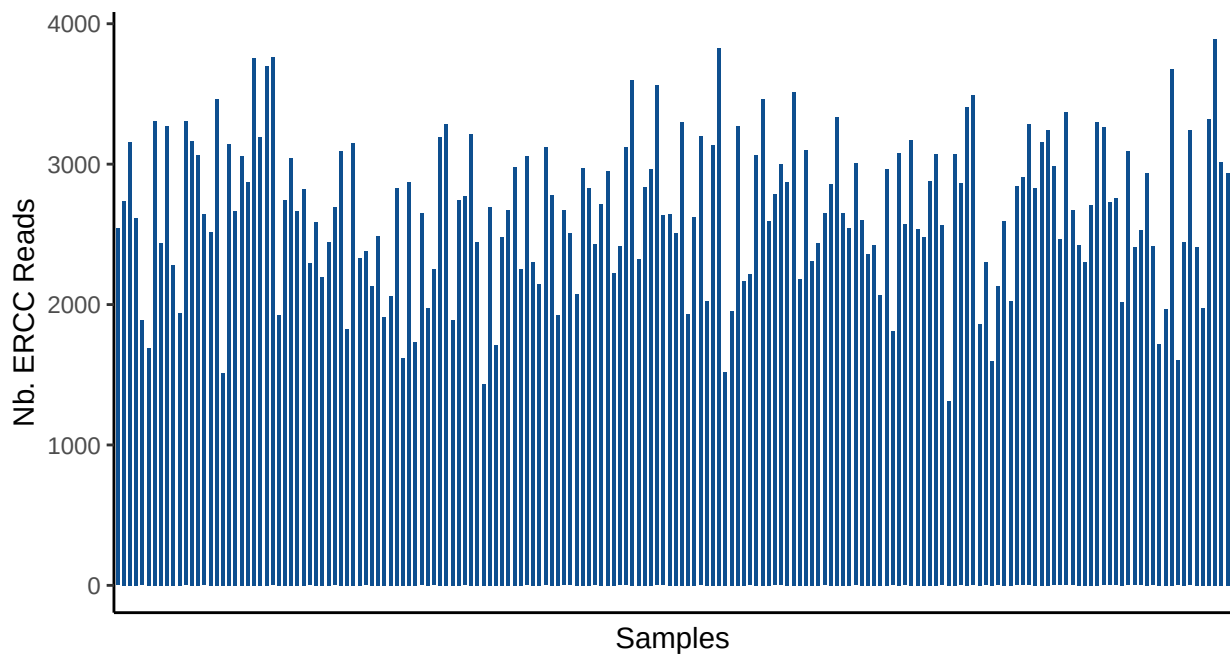
Library L030625AW01_01, per sample summary

Number of sequencing reads per sample

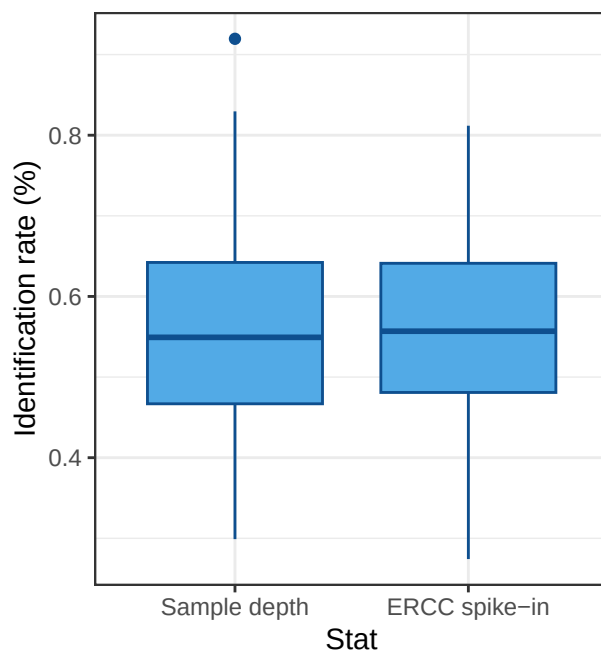
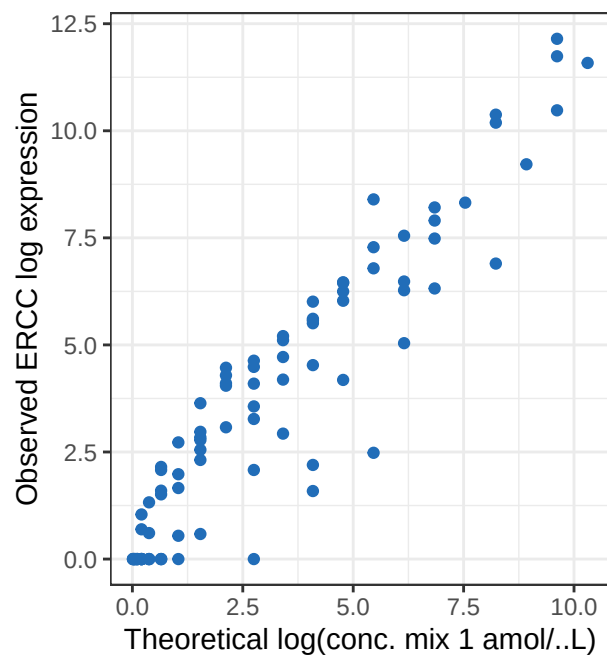


A	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM
B	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM
C	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM
D	OM	OM	OM	1.7M	1.5M	1.7M	1.4M	1.6M	1.7M	1.5M	1.3M	1.6M	1M	1.2M	1.3M	1.7M	1.4M	1.1M	1.1M	1M	0.8M	OM	OM	OM
E	OM	OM	OM	1.2M	1.4M	1.3M	2M	1.6M	2.2M	1.1M	1.6M	1.5M	1.6M	1.1M	1.7M	1.1M	0.9M	0.8M	0.8M	1M	0.9M	OM	OM	OM
F	OM	OM	OM	1.6M	1.2M	1.4M	1.5M	1.6M	1.4M	1.5M	1.5M	1.5M	1.5M	1M	1.8M	1.3M	1.5M	1.2M	1M	0.7M	1.1M	OM	OM	OM
G	OM	OM	OM	1.3M	1.1M	1.6M	1.6M	1.5M	1.6M	0.9M	1.3M	1.6M	1.9M	1.6M	0.8M	1.3M	0.9M	0.7M	0.8M	0.8M	1.4M	OM	OM	OM
H	OM	OM	OM	1.1M	1.2M	0.9M	1.8M	1.6M	1.4M	1.1M	1.4M	1.4M	1.2M	1.3M	1.8M	1.3M	1.2M	1.2M	1.2M	0.9M	1M	OM	OM	OM
I	OM	OM	OM	1.3M	1.3M	0.9M	1.2M	1.2M	1.3M	1.2M	1.1M	1.4M	1.5M	1.3M	1.2M	1.4M	1.1M	1.2M	1.3M	0.8M	1.1M	OM	OM	OM
J	OM	OM	OM	1.4M	1.2M	1.2M	1.6M	1.3M	1.2M	1M	1.1M	1.2M	1.7M	0.9M	1.1M	1.1M	1.1M	1.2M	1.2M	1.2M	1.2M	OM	OM	OM
K	OM	OM	OM	1.5M	1.3M	1.1M	0.9M	1.4M	0.9M	1.4M	1.6M	1.3M	1.5M	1M	1.7M	1.5M	1M	1M	1.3M	1.3M	1.6M	OM	OM	OM
L	OM	OM	OM	1.1M	1.4M	1.3M	1.2M	1.4M	1.5M	1.4M	1.4M	1.1M	1.6M	1.4M	1.8M	1.2M	1.1M	1.3M	1.5M	1.2M	1.3M	OM	OM	OM
M	OM	OM	OM	1.5M	1.3M	1.4M	1.7M	1.4M	1.6M	1.3M	1.5M	1.6M	1.7M	1.5M	1.5M	1.2M	0.9M	1.3M	1.5M	1.4M	1.5M	OM	OM	OM
N	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM
O	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM
P	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

Number of RNA spike-in read counts, per sample

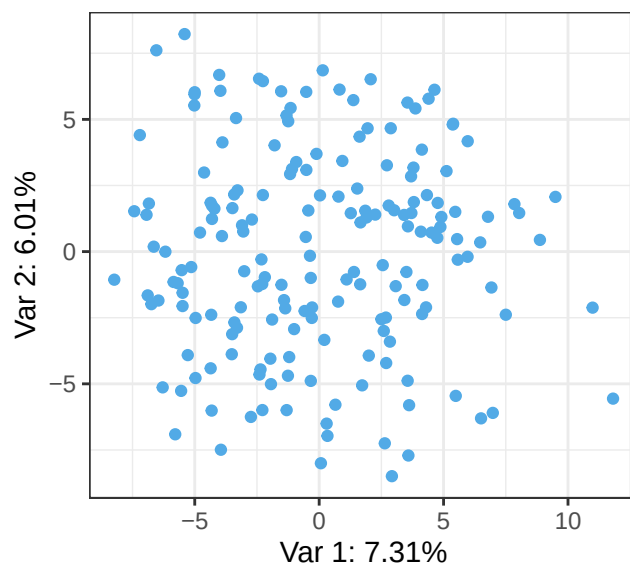
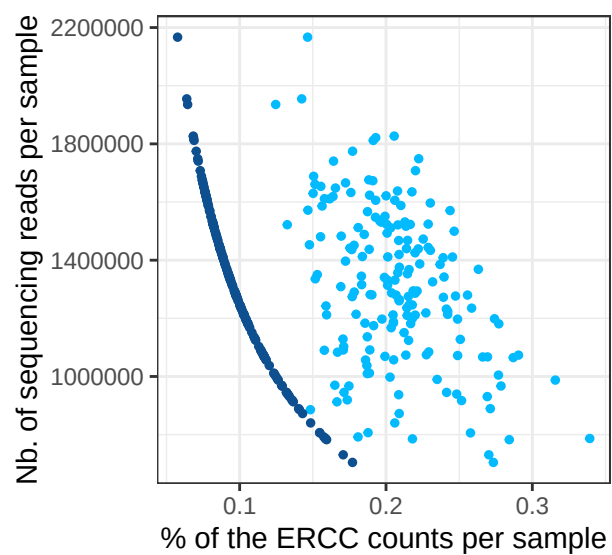


A	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	
B	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	
C	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	
D	OK	OK	OK	2.5K	3.2K	3.2K	2.6K	3.3K	2.6K	3.5K	3.2K	2.7K	1.6K	2.6K	2.6K	3.8K	3.1K	2.9K	2.4K	3.1K	2.2K	OK	OK	OK
E	OK	OK	OK	1.9K	3.2K	2K	2.8K	2.7K	3.2K	1.9K	3.2K	2.8K	2.4K	1.9K	2.5K	1.9K	1.8K	1.7K	1.4K	2.8K	2.4K	OK	OK	OK
F	OK	OK	OK	3.1K	2.4K	3.1K	3K	2.5K	2.5K	2.3K	3K	2K	3.2K	1.7K	3.5K	2.7K	3.2K	2.6K	2.7K	1.9K	3.1K	OK	OK	OK
G	OK	OK	OK	2.6K	2.8K	3.8K	2.9K	3K	2.5K	1.6K	2.5K	3.1K	2.4K	3.3K	1.5K	3K	2.3K	2K	1.7K	2.7K	3.6K	OK	OK	OK
H	OK	OK	OK	1.8K	2.8K	1.5K	3.5K	2.6K	2.9K	2.1K	3.4K	2.4K	2K	2.4K	3.1K	2.7K	2.4K	2.2K	2.5K	2.5K	2.3K	OK	OK	OK
I	OK	OK	OK	2.9K	2.3K	2K	2.2K	2.4K	3.1K	2.6K	2.7K	2.5K	3.3K	3.3K	2.7K	2.8K	2.1K	3.2K	2.7K	2.1K	2.8K	OK	OK	OK
J	OK	OK	OK	3.3K	2.7K	3.3K	3.1K	2.4K	2.6K	2K	2.4K	2.9K	3.9K	2.3K	3.1K	2.3K	2.5K	3.3K	3K	3K	3K	OK	OK	OK
K	OK	OK	OK	3.3K	2.6K	2.2K	2.3K	2.1K	1.3K	2.8K	2.3K	2.4K	3K	1.9K	2.9K	2.6K	1.9K	1.9K	2.3K	2.8K	3.6K	OK	OK	OK
L	OK	OK	OK	2K	3.3K	2.2K	2.4K	3K	3.1K	2.9K	2.7K	1.7K	2.9K	3.3K	3.8K	2.2K	2.1K	2.7K	3.1K	2.4K	2.6K	OK	OK	OK
M	OK	OK	OK	2.7K	2.6K	3.5K	2.9K	3.1K	3.4K	2.8K	3.3K	3.7K	3.2K	3.1K	3.7K	2.7K	1.6K	3.2K	2.1K	3K	2.5K	OK	OK	OK
N	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	
O	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	
P	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	
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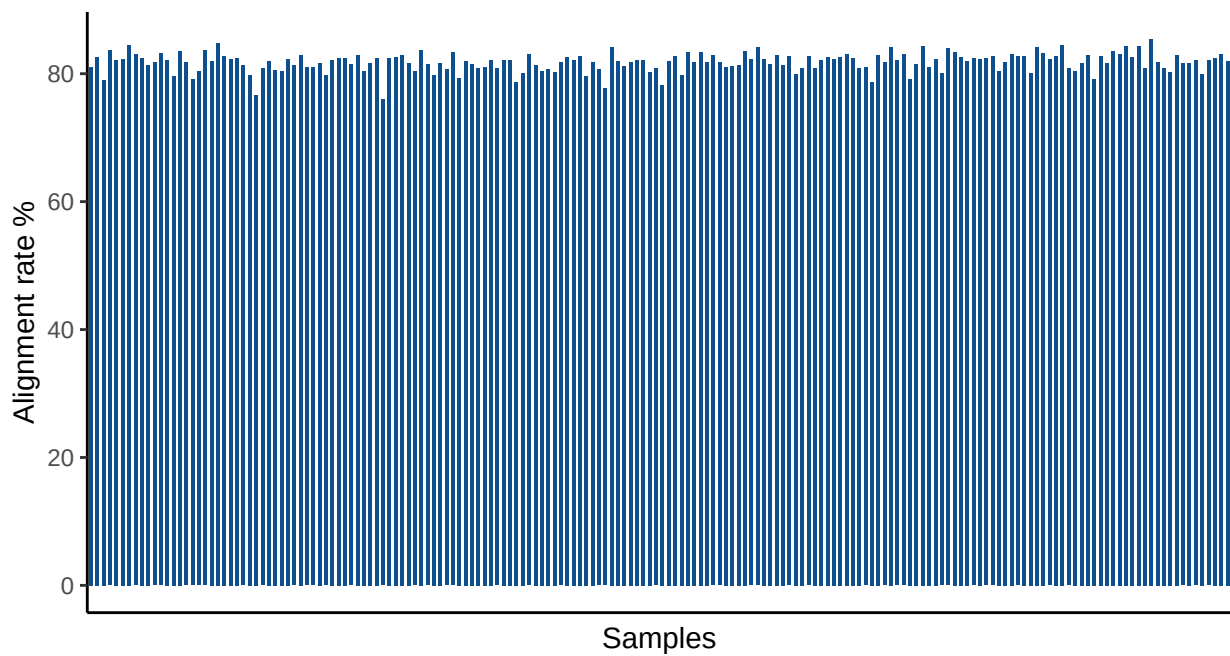


• Observed • Theoretical

Sample clusterization by ERCC

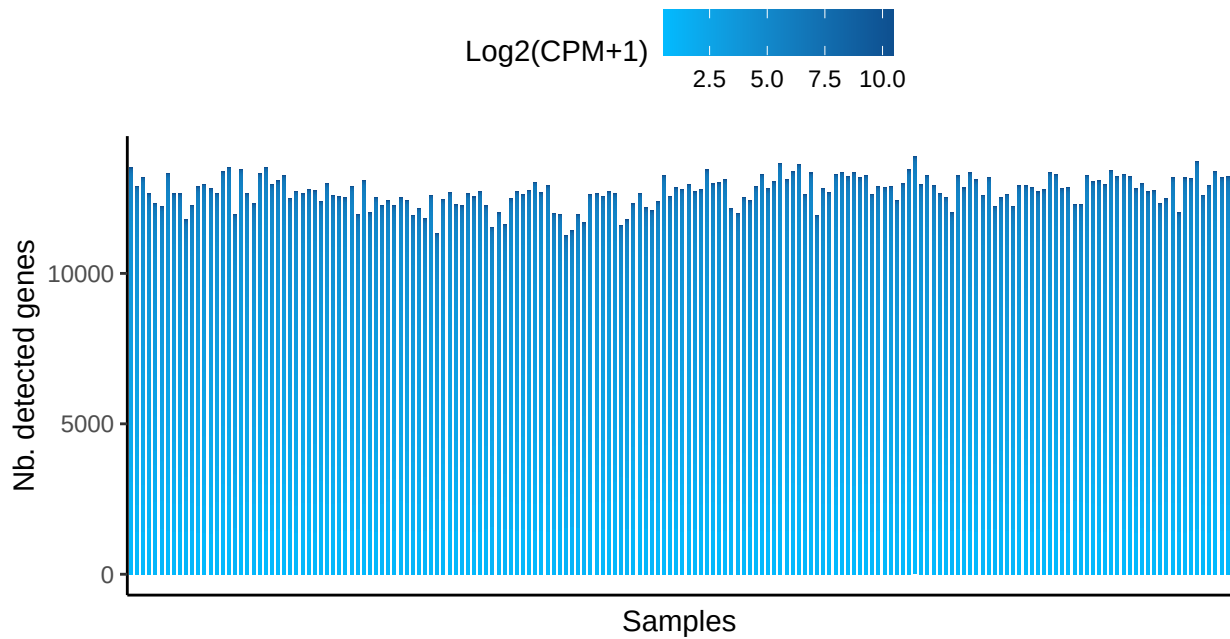


Alignment stats, per sample



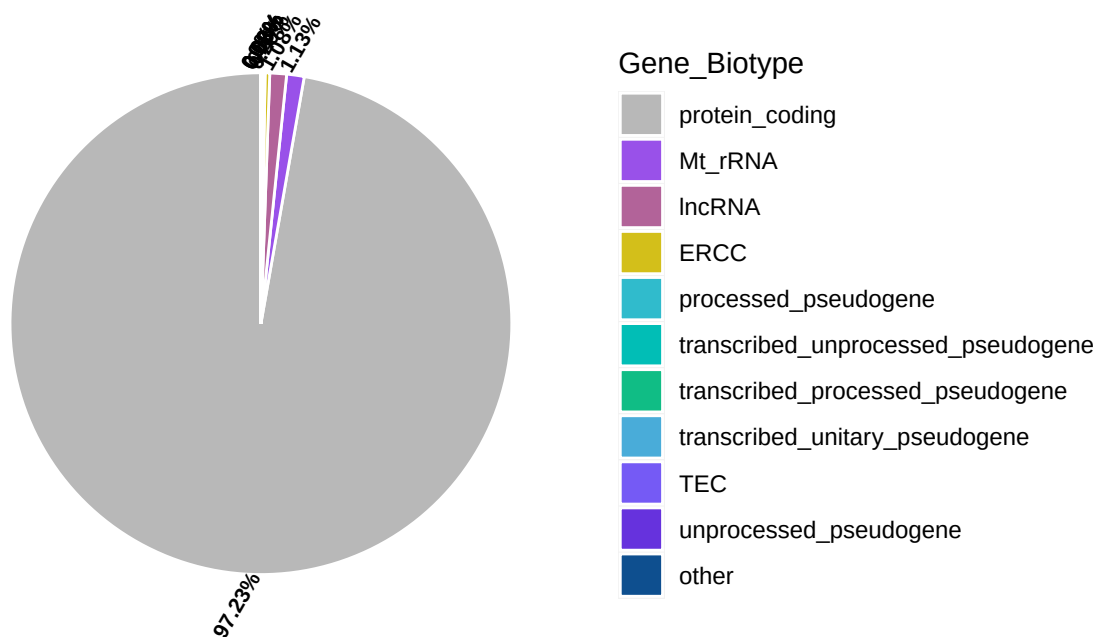
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B	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
D	NA	NA	NA	81.1%	82.2%	83.4%	84.1%	82.6%	82.1%	82%	84.2%	81.6%	83%	83.6%	83.5%	79.8%	81.7%	82.5%	79.3%	83%	80.7%	NA	NA	NA
E	NA	NA	NA	82.8%	82.4%	81.8%	82.3%	82.3%	83%	82.4%	83.2%	83.5%	81.6%	82.2%	81.8%	76.7%	79.7%	82.6%	82%	81.3%	77.7%	NA	NA	NA
F	NA	NA	NA	83.6%	81%	83.4%	81.5%	82.7%	79.1%	82.3%	82.2%	83.1%	81.6%	82.3%	79.1%	80.8%	82.1%	82.9%	81.5%	80.5%	84.2%	NA	NA	NA
G	NA	NA	NA	80.9%	82.5%	81.8%	83%	83.1%	81.5%	82.4%	82.8%	84.3%	82.1%	84.4%	80.3%	82%	82.4%	81.6%	80.9%	80.7%	82%	NA	NA	NA
H	NA	NA	NA	81.8%	80.7%	82.9%	81.3%	82.5%	84.3%	82.7%	84.4%	82.6%	80%	83%	83.6%	80.6%	82.5%	80.4%	81.1%	80.3%	81.2%	NA	NA	NA
I	NA	NA	NA	83.3%	78.7%	81.8%	82.7%	80.8%	81%	80.4%	80.8%	84.3%	82.1%	82.4%	81.9%	80.4%	81.4%	83.7%	82.1%	81.7%	81.9%	NA	NA	NA
J	NA	NA	NA	82.8%	79.6%	81.1%	79.9%	81%	82.3%	81.9%	80.4%	80.9%	82.5%	81.4%	84.9%	82.3%	83%	81.5%	80.8%	82.6%	82.2%	NA	NA	NA
K	NA	NA	NA	79.2%	80.8%	81.2%	80.9%	78.7%	80%	83.1%	81.6%	85.4%	83.1%	81.8%	82.7%	81.3%	80.4%	79.8%	82.2%	82.1%	82.1%	NA	NA	NA
L	NA	NA	NA	80.9%	82%	81.4%	82.7%	82.9%	83.9%	82.7%	83%	81.8%	81.9%	83.2%	82.3%	82.9%	81.7%	81.6%	82.1%	82.7%	80.2%	NA	NA	NA
M	NA	NA	NA	82.6%	79.8%	82.2%	82.2%	84.1%	82.6%	80.1%	82.8%	80.2%	79.1%	79.6%	81.3%	80.9%	76%	83.3%	80.1%	81.8%	78.2%	NA	NA	NA
N	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
O	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
P	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

Detected genes, per sample

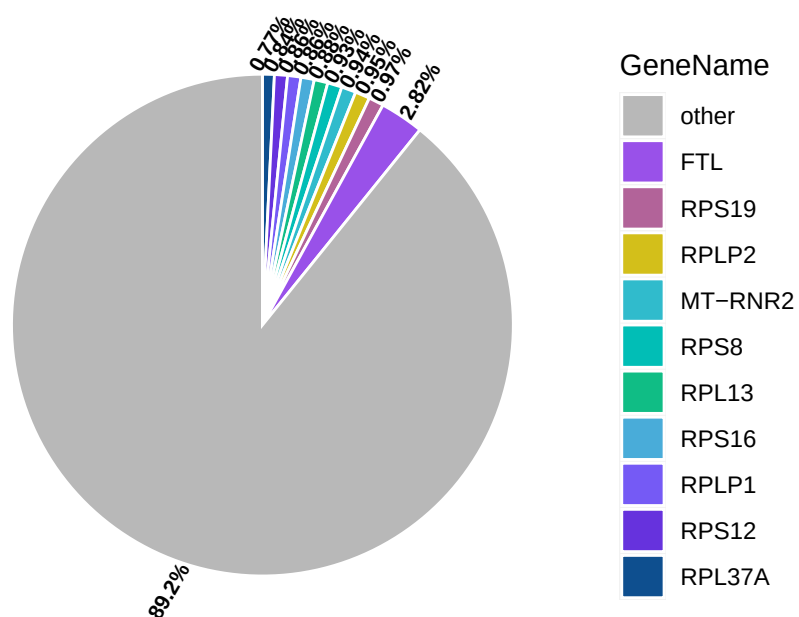


A	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK
B	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK
C	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK
D	NAK	NAK	NAK	13.5K	13K	13.4K	13K	13.4K	13.4K	13.1K	12.8K	13.4K	12K	12.6K	12.7K	13.2K	12.9K	12.2K	12.2K	12K	11.6K	NAK	NAK	NAK
E	NAK	NAK	NAK	12.7K	13K	13K	13.7K	13.2K	13.9K	12.6K	13.4K	13.2K	13.2K	12.3K	13.4K	12.5K	12K	11.8K	11.5K	12K	11.8K	NAK	NAK	NAK
F	NAK	NAK	NAK	13.3K	12.6K	13K	13.1K	13.3K	12.9K	13.2K	13.3K	13.3K	13.2K	12.2K	13.5K	12.7K	13.1K	12.6K	12K	11.3K	12.3K	NAK	NAK	NAK
G	NAK	NAK	NAK	12.7K	12.4K	13.1K	13.4K	13.2K	13.3K	12.2K	12.8K	13.2K	13.7K	13.3K	12K	12.6K	12K	11.3K	11.6K	11.4K	12.7K	NAK	NAK	NAK
H	NAK	NAK	NAK	12.4K	12.5K	12.2K	13.6K	13.3K	12.9K	12.5K	12.9K	12.8K	12.6K	12.6K	13.5K	12.8K	12.5K	12.5K	12.5K	12K	12.2K	NAK	NAK	NAK
I	NAK	NAK	NAK	12.8K	12.7K	12K	12.6K	12.6K	12.7K	12.6K	12.3K	13K	12.9K	12.6K	12.7K	12.7K	12.3K	12.7K	12.7K	11.7K	12.1K	NAK	NAK	NAK
J	NAK	NAK	NAK	12.9K	12.7K	12.5K	13.3K	12.9K	12.5K	12.2K	12.3K	12.7K	13.4K	11.8K	12.3K	12.4K	12.4K	12.3K	12.6K	12.6K	12.4K	NAK	NAK	NAK
K	NAK	NAK	NAK	13.1K	12.8K	12.4K	11.9K	12.9K	12K	12.9K	13.3K	12.8K	13.2K	12.3K	13.3K	13K	12.2K	12.2K	12.8K	12.7K	13.2K	NAK	NAK	NAK
L	NAK	NAK	NAK	12.5K	13K	12.9K	12.8K	12.9K	13.2K	12.9K	13K	12.3K	13.2K	12.9K	13.5K	12.6K	12.5K	12.6K	13K	12.6K	12.6K	NAK	NAK	NAK
M	NAK	NAK	NAK	12.9K	12.8K	12.8K	13.3K	13K	13.3K	12.7K	13K	13.2K	13.2K	12.8K	13.1K	12.5K	11.9K	12.7K	12.9K	12.7K	12.8K	NAK	NAK	NAK
N	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	
O	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	
P	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

Biotypes, across samples

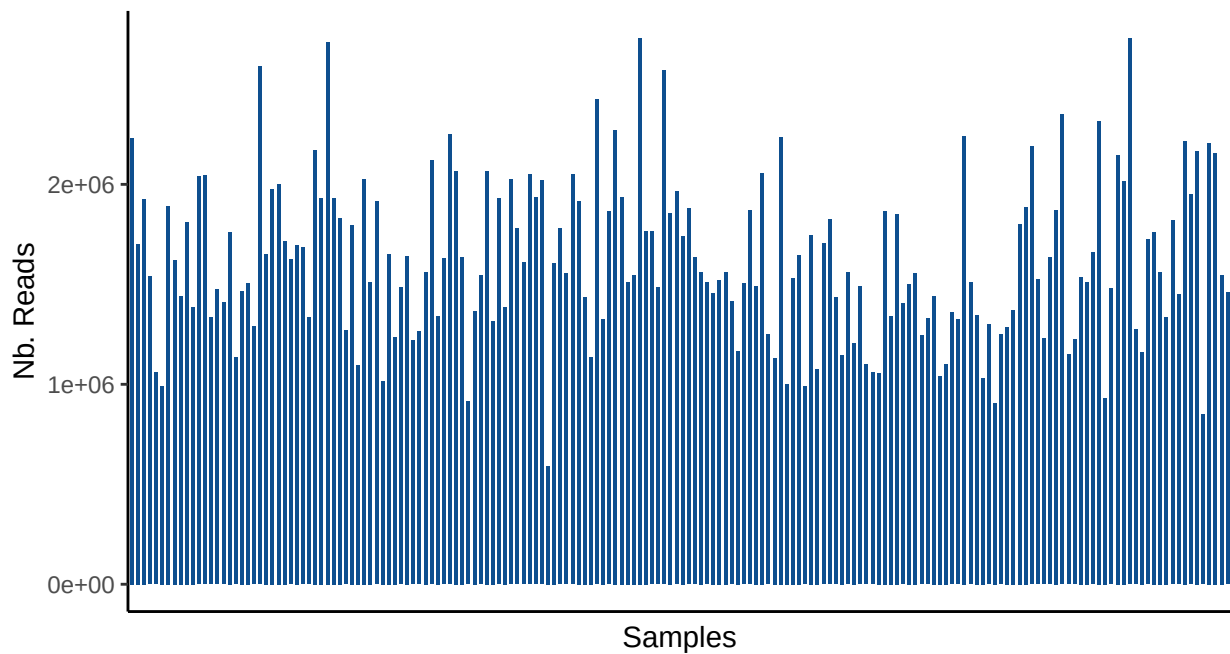


Most expressed genes, across samples



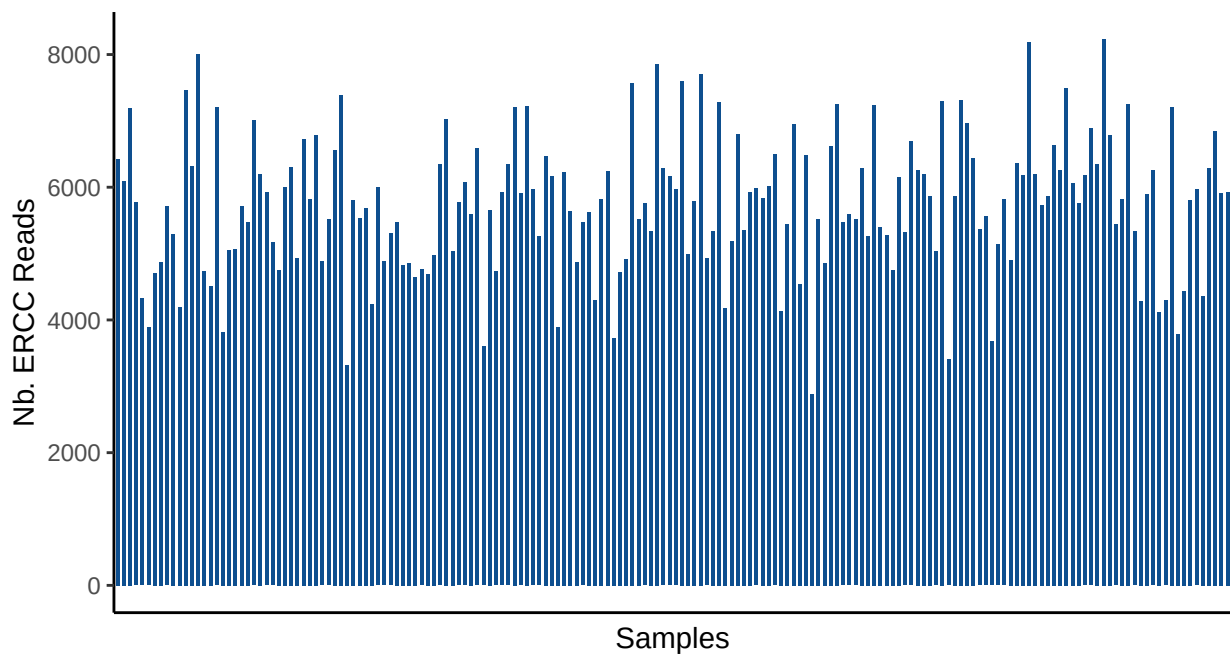
Library L030625AW02_01, per sample summary

Number of sequencing reads per sample

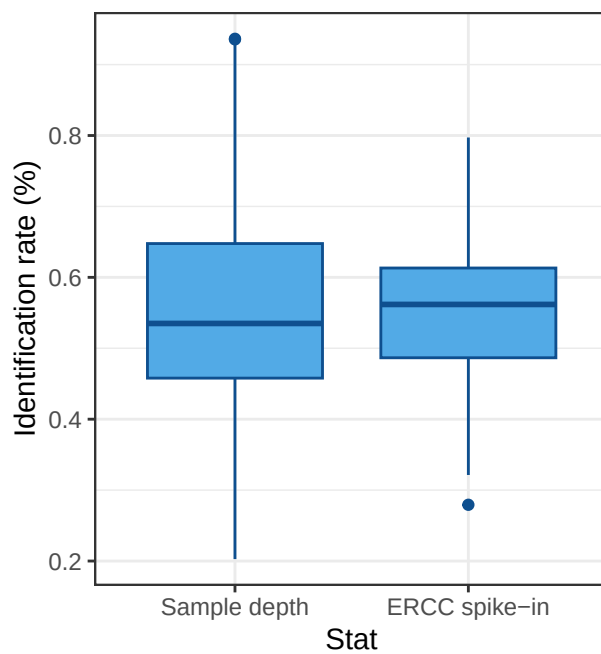
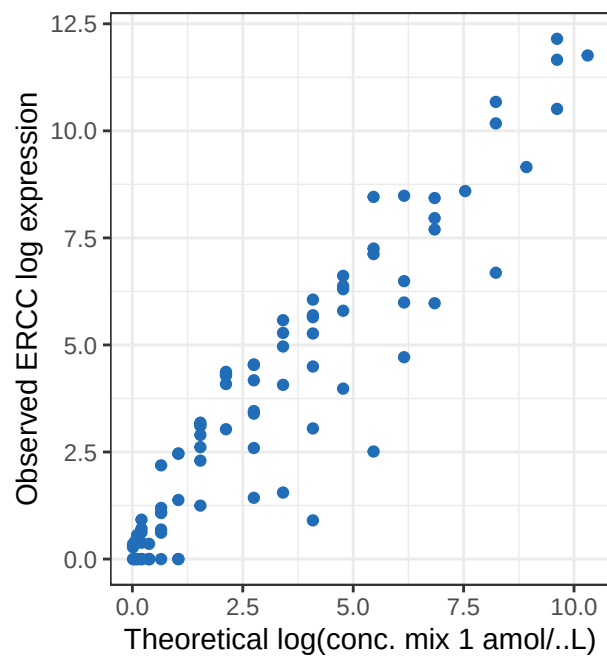


A	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM
B	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM
C	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM
D	OM	OM	OM	2.2M	2M	1.5M	1.1M	1.1M	1.5M	1.3M	1.2M	1.5M	1.4M	1.5M	1.5M	1.7M	1.8M	1.3M	2.1M	1.6M	1.9M	OM	OM	OM
E	OM	OM	OM	1.6M	2M	1.5M	2.2M	1.6M	1.6M	1M	1.6M	2.1M	2.2M	1.1M	1.4M	1.6M	1.1M	1.6M	1.3M	1.8M	1.5M	OM	OM	OM
F	OM	OM	OM	2.1M	1.8M	1.5M	1M	1.2M	1.2M	1.3M	1.9M	2M	1.9M	1M	1.8M	1.7M	2M	2.1M	1.9M	1.6M	1.5M	OM	OM	OM
G	OM	OM	OM	1.8M	1.6M	1.6M	1.5M	1.5M	1.3M	0.9M	2.3M	2.7M	2.2M	1.9M	1.1M	1.7M	1.5M	1.3M	1.4M	2M	2.7M	OM	OM	OM
H	OM	OM	OM	1.9M	1.4M	1.4M	1.6M	1.1M	1.4M	1.2M	1.1M	1.3M	0.8M	1.6M	1.5M	1.3M	1.9M	1.6M	2M	1.9M	1.8M	OM	OM	OM
I	OM	OM	OM	2.2M	2M	1.2M	1M	1.1M	1M	1.3M	1.2M	1.2M	2.2M	1.4M	1.5M	2.2M	1M	2.3M	1.8M	1.4M	1.8M	OM	OM	OM
J	OM	OM	OM	2.2M	1.9M	1.5M	1.7M	1.1M	1.1M	1.4M	1.5M	1.7M	2.2M	1.8M	1.3M	1.9M	1.7M	2.1M	1.6M	1.1M	1.5M	OM	OM	OM
K	OM	OM	OM	2.3M	2M	1.9M	1.1M	1.9M	1.4M	1.8M	1.5M	1.8M	1.5M	1.4M	2.6M	2.7M	1.2M	1.6M	2M	2.4M	2.6M	OM	OM	OM
L	OM	OM	OM	1.3M	1.9M	1.5M	1.7M	1.3M	1.3M	1.9M	1.7M	1.6M	1.5M	2M	1.7M	1.9M	1.5M	0.9M	1.9M	1.3M	1.9M	OM	OM	OM
M	OM	OM	OM	1.7M	1.6M	1.2M	1.4M	1.4M	1.5M	1.5M	0.9M	1.8M	1.9M	1.3M	2M	1.3M	1.2M	1.5M	0.6M	2.3M	1.7M	OM	OM	OM
N	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM
O	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM
P	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM	OM
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

Number of RNA spike-in read counts, per sample

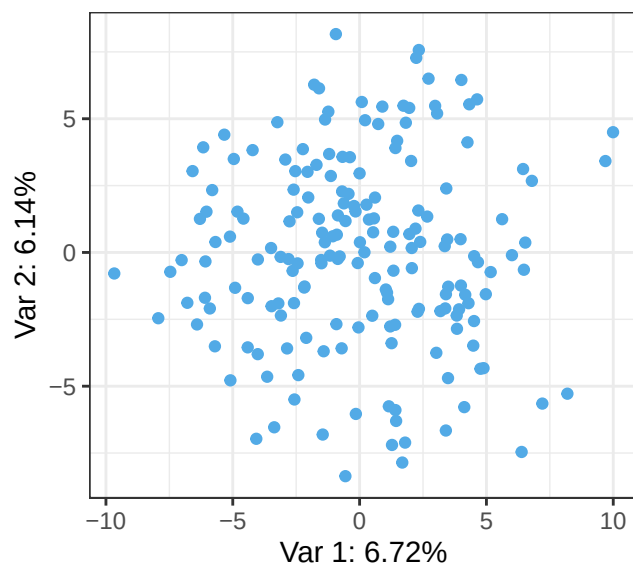
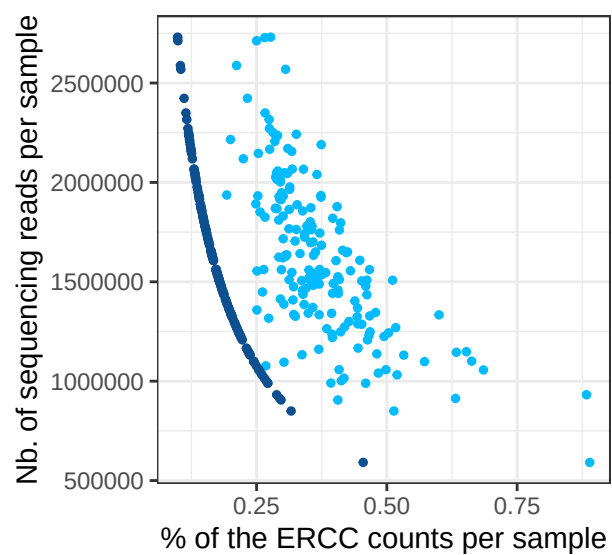


A	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	
B	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	
C	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	
D	OK	OK	OK	6.4K	6.3K	7.7K	6K	7.3K	5.3K	6.4K	5.7K	6.8K	3.8K	5.8K	4.7K	5.2K	7.4K	4.9K	6.6K	6.5K	3.7K	OK	OK	OK
E	OK	OK	OK	5K	6.2K	4.9K	6.5K	5.5K	6.7K	5.4K	5.9K	5.4K	4.4K	4.3K	4.5K	4.8K	3.3K	4.6K	3.6K	6.2K	4.7K	OK	OK	OK
F	OK	OK	OK	6K	5.5K	5.3K	4.1K	5.6K	6.3K	5.6K	6.6K	5.8K	5.8K	3.9K	7.2K	6K	5.8K	4.8K	5.7K	3.9K	4.9K	OK	OK	OK
G	OK	OK	OK	4.9K	5.5K	7.3K	5.4K	5.5K	6.2K	3.7K	6.3K	7.3K	6K	4.7K	3.8K	6.3K	5.5K	4.7K	4.7K	6.2K	7.6K	OK	OK	OK
H	OK	OK	OK	4.8K	6.1K	4.2K	7K	6.3K	5.9K	5.1K	7.5K	5.3K	4.4K	4.9K	5.1K	4.9K	5.7K	5K	5.9K	5.6K	5.5K	OK	OK	OK
I	OK	OK	OK	7.3K	6K	5.2K	4.5K	5.3K	5K	5.8K	6.1K	4.3K	6.3K	5.7K	5.1K	6.7K	4.2K	6.3K	6.3K	4.9K	5.8K	OK	OK	OK
J	OK	OK	OK	8.2K	5.8K	6.8K	6.5K	7.2K	7.3K	4.9K	5.8K	5.9K	6.8K	5.3K	5.7K	5.8K	6K	7K	7.2K	5.5K	5.3K	OK	OK	OK
K	OK	OK	OK	6.3K	6.2K	5.3K	2.9K	5.4K	3.4K	6.4K	6.2K	6.3K	5.9K	4.2K	5.5K	6.8K	4.9K	5K	5.9K	5.6K	7.9K	OK	OK	OK
L	OK	OK	OK	4.3K	7.6K	5.9K	5.5K	5.3K	5.9K	6.2K	6.9K	4.1K	5.9K	7.5K	7K	4.9K	5.3K	5.8K	7.2K	4.3K	6.3K	OK	OK	OK
M	OK	OK	OK	6.1K	5.8K	5.8K	6.6K	6.2K	7K	6.2K	8.2K	7.2K	7.2K	8K	5.9K	6.6K	4.8K	5.6K	5.3K	6.2K	6K	OK	OK	OK
N	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	
O	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	
P	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

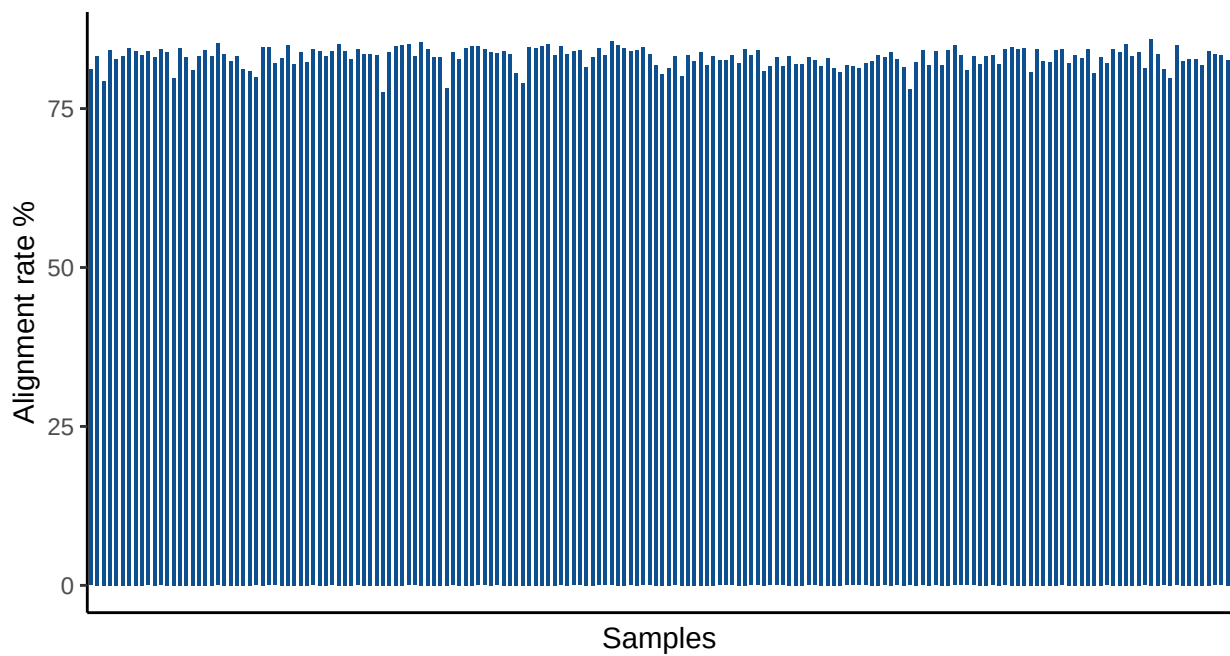


• Observed • Theoretical

Sample clusterization by ERCC

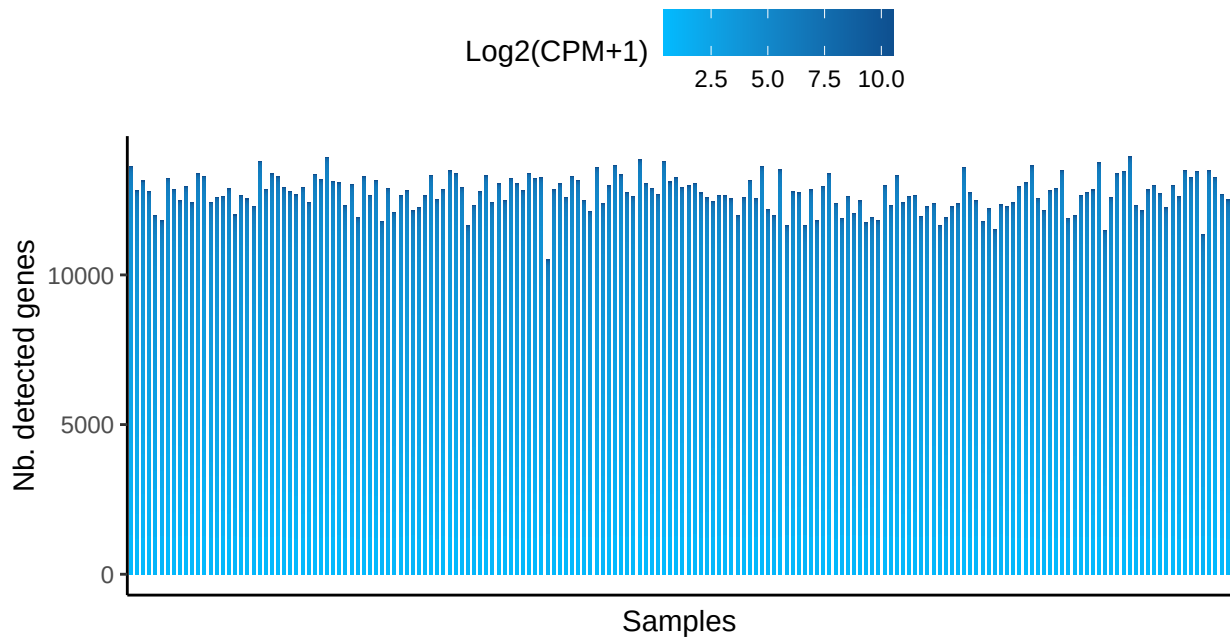


Alignment stats, per sample



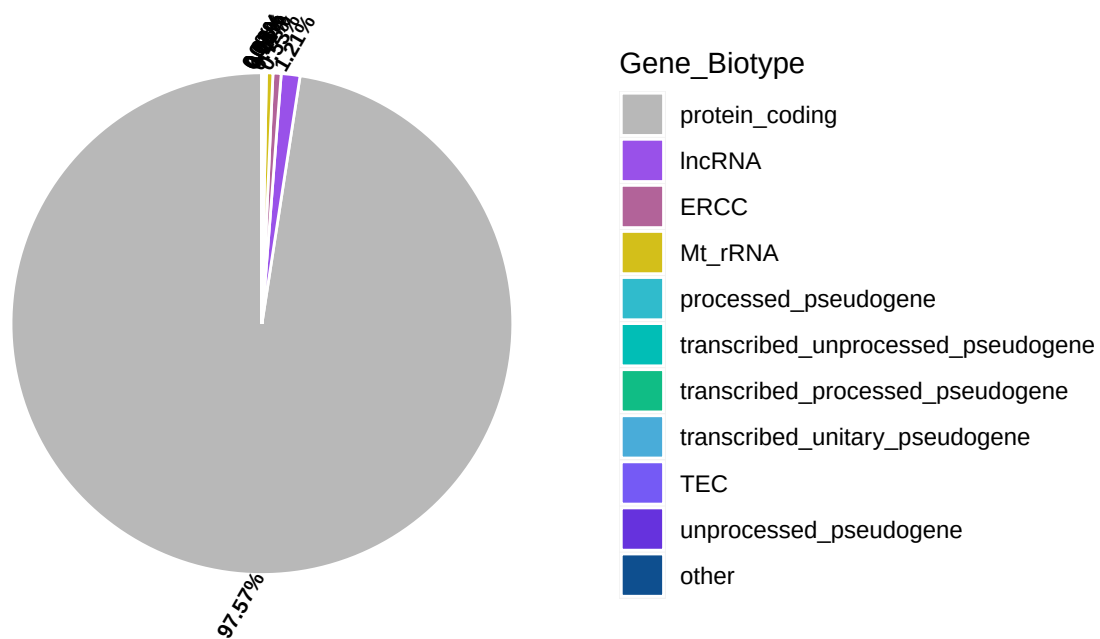
A	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
B	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
D	NA	NA	NA	81.1%	83.9%	83.5%	84.1%	83%	82.7%	81%	84.3%	82.1%	84.9%	84.2%	84.5%	80.9%	84.1%	83.9%	82.8%	84.7%	84.5%	NA	NA	NA
E	NA	NA	NA	83.2%	83.3%	82.5%	80.9%	81.4%	81.5%	83.2%	82.5%	84.4%	82.5%	82.8%	83.1%	79.9%	83.3%	84.8%	84.6%	84.6%	83.3%	NA	NA	NA
F	NA	NA	NA	84.4%	82.3%	83.9%	81.6%	80.8%	78%	82%	82.3%	83.9%	82.8%	83.3%	81%	84.7%	84%	85%	84.9%	84.8%	85.6%	NA	NA	NA
G	NA	NA	NA	82.6%	83.4%	81.9%	83%	81.8%	82.3%	83.3%	84.3%	85.1%	82.8%	84.5%	83.3%	84.6%	85.2%	85.1%	84.8%	85.1%	85%	NA	NA	NA
H	NA	NA	NA	83%	78.3%	83.2%	81.6%	81.6%	84.1%	83.4%	84.3%	83.3%	81.8%	84%	84.2%	82.1%	84.1%	83.2%	84.3%	83.5%	84.5%	NA	NA	NA
I	NA	NA	NA	84.9%	80.6%	82.6%	83.3%	81.3%	81.9%	82%	82.2%	83.8%	84.1%	83.4%	83.3%	83%	82.8%	85.5%	83.9%	84.7%	84%	NA	NA	NA
J	NA	NA	NA	84.5%	81.6%	82.6%	82%	82.1%	84%	84.3%	83.4%	81.3%	83.5%	84%	85.2%	85%	84.3%	84.4%	83.6%	83.5%	84.2%	NA	NA	NA
K	NA	NA	NA	80.6%	81.8%	83.3%	82%	82.5%	81.9%	84.7%	83%	85.9%	83.3%	83.1%	83.6%	82%	83.6%	83.1%	84.1%	84%	84.6%	NA	NA	NA
L	NA	NA	NA	81.2%	81.3%	82.2%	83%	83.4%	84.2%	84.4%	84.3%	83.6%	82.6%	84.3%	82.4%	83.9%	83.6%	83.1%	83.6%	84.1%	83.5%	NA	NA	NA
M	NA	NA	NA	83.2%	80.1%	83.3%	81.7%	83.8%	83.3%	80.8%	83.2%	79.8%	79.3%	79.8%	81.2%	84.3%	77.6%	83.8%	79%	83.1%	80.4%	NA	NA	NA
N	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
O	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
P	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

Detected genes, per sample



A	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK
B	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK
C	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK
D	NAK	NAK	NAK	13.6K	13.3K	12.6K	12K	11.9K	12.6K	12.5K	12.2K	12.6K	12.6K	12.8K	12.6K	12.9K	13K	12.2K	13.3K	12.8K	13.3K	NAK	NAK	NAK
E	NAK	NAK	NAK	13.1K	13.4K	12.5K	13.5K	12.6K	12.7K	11.8K	12.8K	13.4K	13.5K	12K	12.6K	12.8K	11.9K	12.6K	12.4K	13K	12.8K	NAK	NAK	NAK
F	NAK	NAK	NAK	13.6K	13.1K	12.7K	11.6K	12.1K	12K	12.2K	12.9K	13.5K	13.3K	11.8K	12.9K	12.7K	13.3K	13.3K	13K	12.6K	12.6K	NAK	NAK	NAK
G	NAK	NAK	NAK	13.4K	12.8K	12.6K	12.8K	12.5K	12.3K	11.5K	13.5K	13.9K	13.5K	13.2K	12K	12.9K	12.7K	12.5K	12.5K	13.3K	13.8K	NAK	NAK	NAK
H	NAK	NAK	NAK	13.3K	12.3K	12.5K	12.7K	11.7K	12.4K	12.3K	11.9K	12.3K	11.3K	12.9K	12.6K	12.4K	13.2K	12.9K	13.2K	13.2K	13.1K	NAK	NAK	NAK
I	NAK	NAK	NAK	13.6K	13.3K	12K	11.7K	11.9K	11.7K	12.3K	12K	12.1K	13.5K	12.5K	12.5K	13.4K	11.8K	13.5K	13K	12.5K	12.9K	NAK	NAK	NAK
J	NAK	NAK	NAK	13.6K	13K	12.6K	12.8K	11.8K	11.9K	12.4K	12.7K	12.8K	13.3K	12.9K	12.3K	13.2K	12.9K	13.4K	12.8K	12.1K	12.7K	NAK	NAK	NAK
K	NAK	NAK	NAK	13.7K	13.2K	13.2K	11.8K	13K	12.3K	12.9K	12.8K	13K	12.7K	12.4K	13.8K	13.9K	12.1K	12.9K	13.4K	13.6K	13.8K	NAK	NAK	NAK
L	NAK	NAK	NAK	12.2K	13K	12.5K	12.9K	12.3K	12.4K	13.1K	12.8K	12.7K	12.5K	13.4K	12.9K	13.1K	12.7K	11.6K	13.2K	12.4K	13.1K	NAK	NAK	NAK
M	NAK	NAK	NAK	12.8K	12.7K	12.2K	12.4K	12.4K	12.7K	12.6K	11.5K	13K	13.1K	12.4K	13.3K	12.3K	12.1K	12.8K	10.5K	13.7K	12.9K	NAK	NAK	NAK
N	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	
O	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	
P	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	NAK	
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

Biotypes, across samples



Most expressed genes, across samples

