

Dataset stats RNA (incorrect human-only alignments)

Library	Read Length	Mapping	Species	Raw fragments	Complexity	Unique	Unique Splices	Multi	Multi Splices	Fraction mapped	Cells >500 UMIs
SK-L247-K562_3T3_gRNAs_RNA_10k_1	1x50	STAR-2.5.3a	hg38	216,880,522	0.56	65,905,643	3,926,075	12,284,729	2,565,917	0.39	7,773
SK-L247-K562_3T3_gRNAs_RNA_10k_1	1x50	STAR-2.5.3a	mm10	216,880,522	0.67	8,675,051	594,101	2,286,788	220,694	0.05	941
SK-L248-K562_3T3_gRNAs_RNA_10k_2	1x50	STAR-2.5.3a	hg38	193,560,973	0.56	59,727,886	3,198,224	11,116,867	2,257,628	0.39	7,702
SK-L248-K562_3T3_gRNAs_RNA_10k_2	1x50	STAR-2.5.3a	mm10	193,560,973	0.65	7,853,072	496,337	2,075,290	183,584	0.05	959

SK-L247

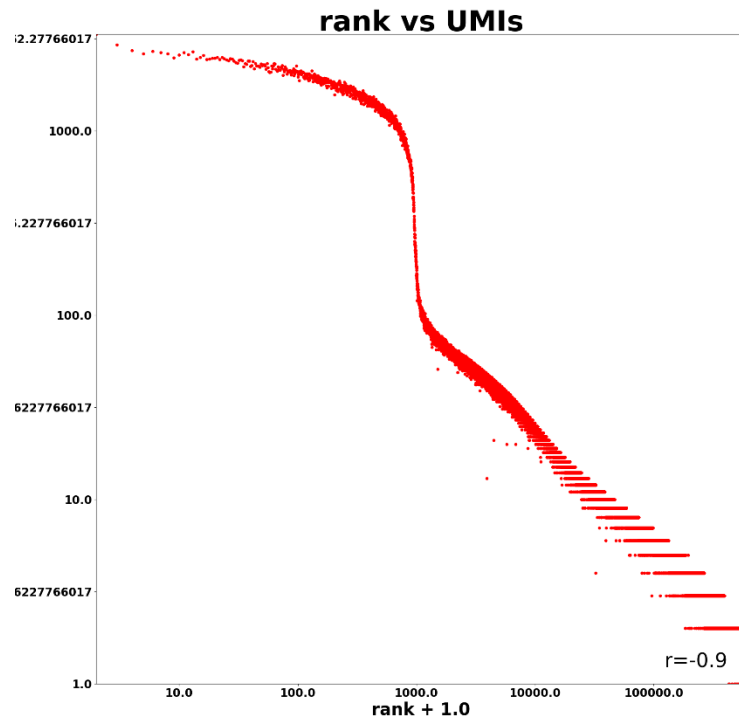
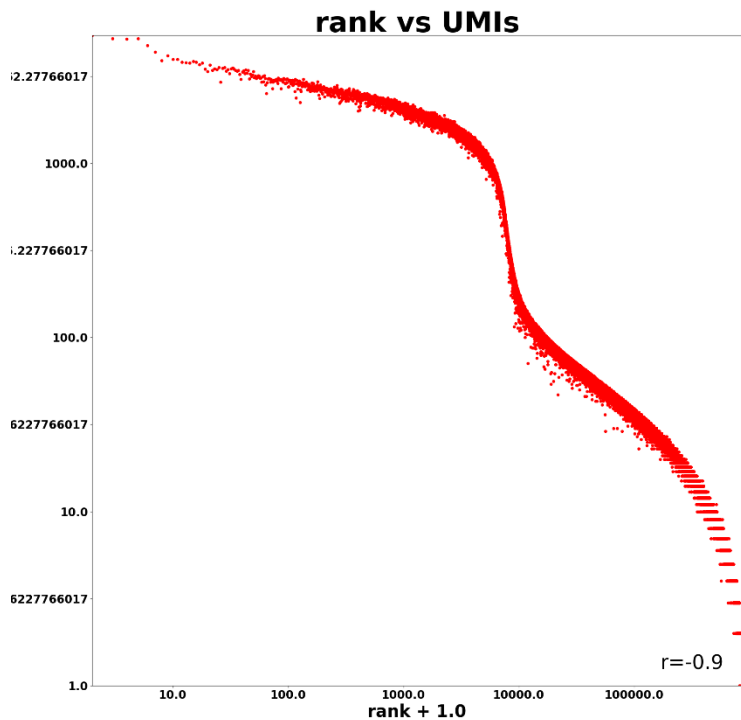
	mm10	hg38
0	557,177	374,680
10	25,387	227,747
20	9,500	196,668
50	2,378	43,105
100	199	7,865
200	53	1,913
500	85	1,217
1000	856	6,556

SK-L248

	mm10	hg38
0	539,611	400,188
10	21,944	220,984
20	8,443	179,592
50	2,424	37,558
100	267	6,605
200	57	1,851
500	80	1,363
1000	879	6,339

hg38

mm10

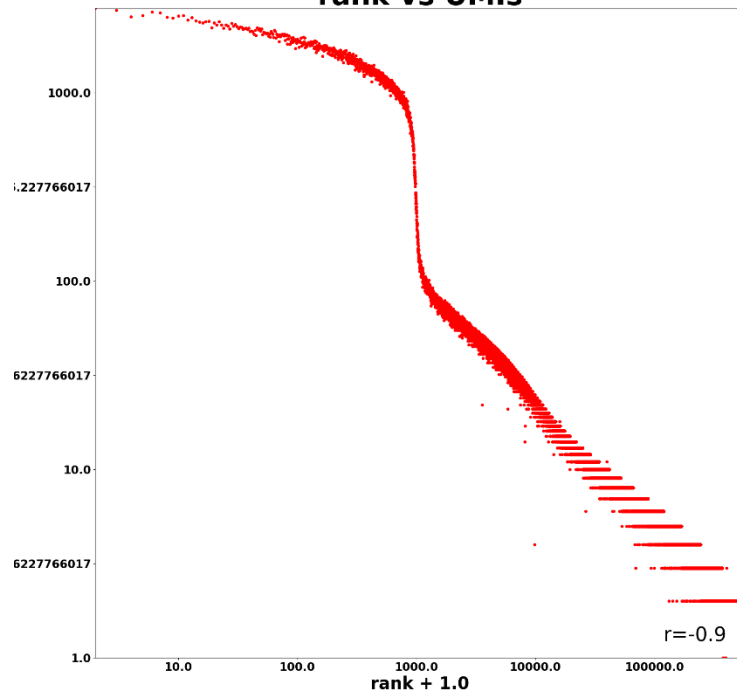
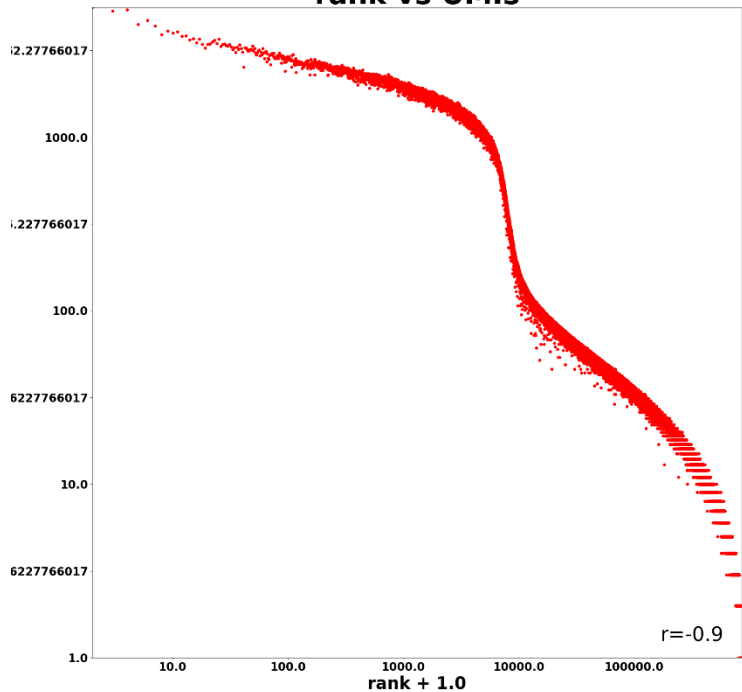


hg38

mm10

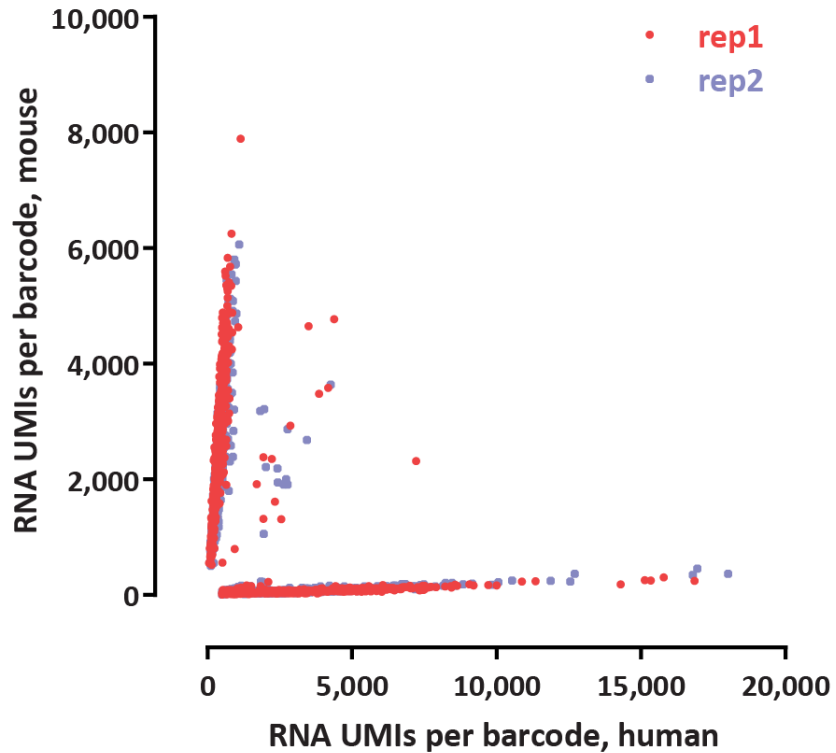
rank vs UMIs

rank vs UMIs

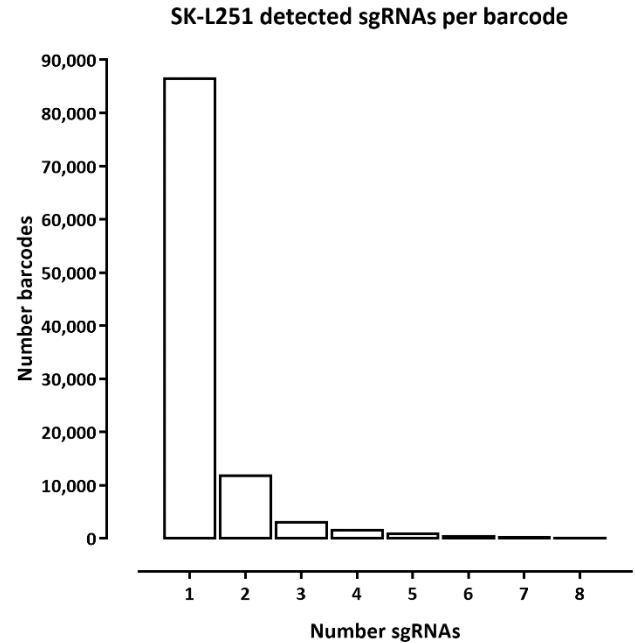
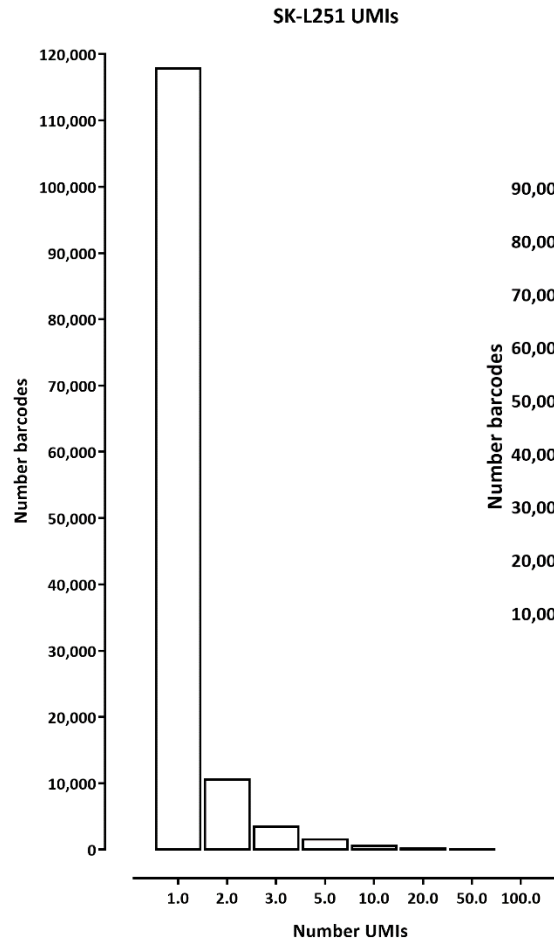
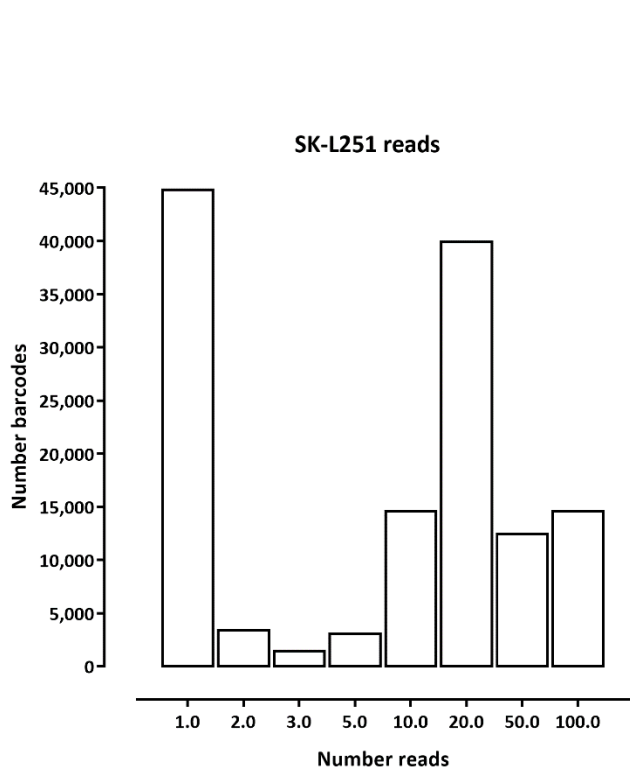


RNA

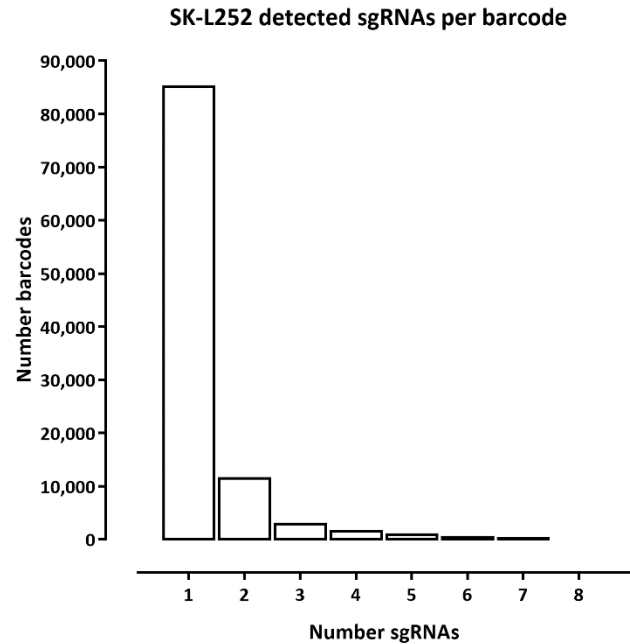
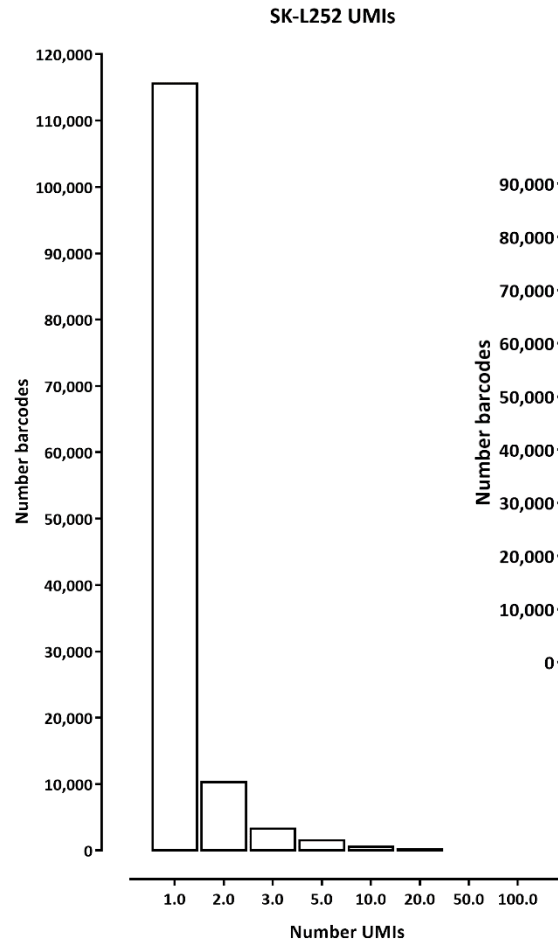
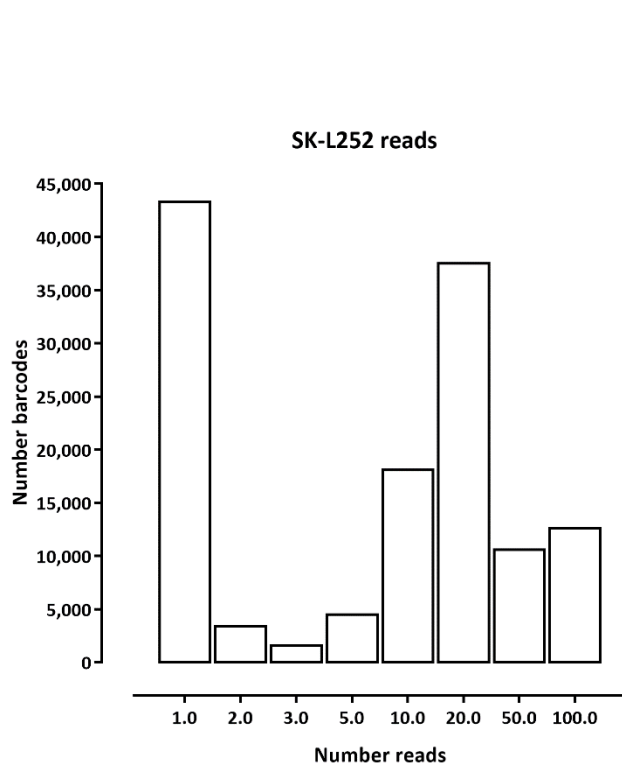
species mixing, RNA



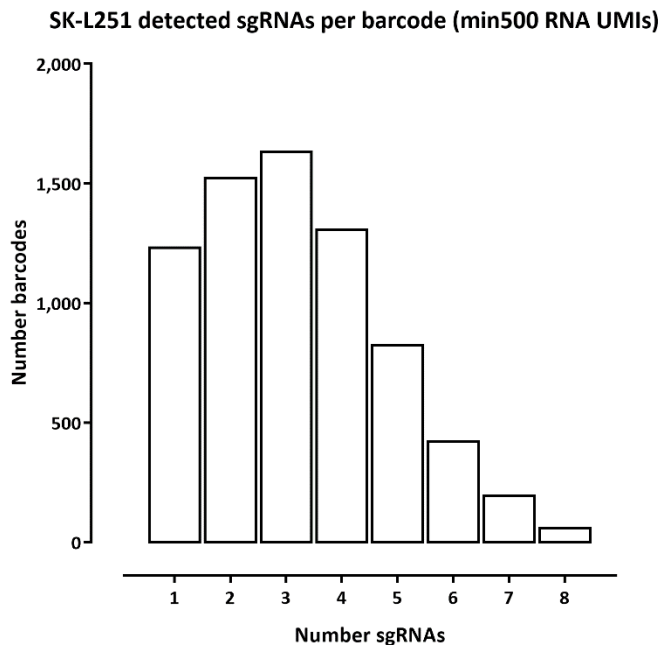
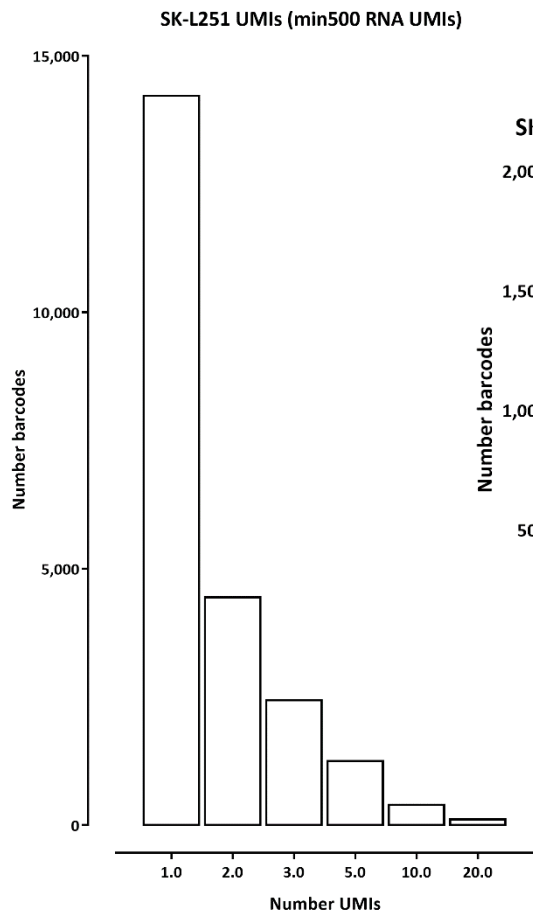
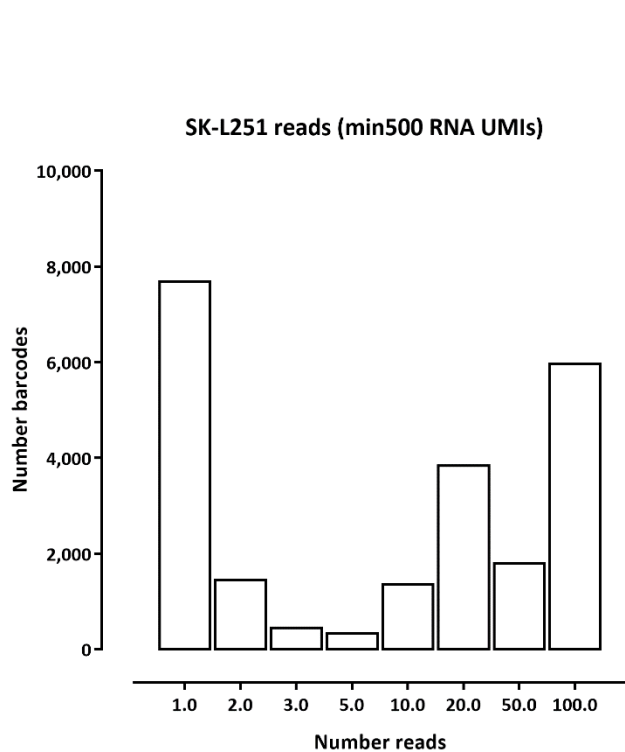
sgRNAs UMIs vs reads, all BCs



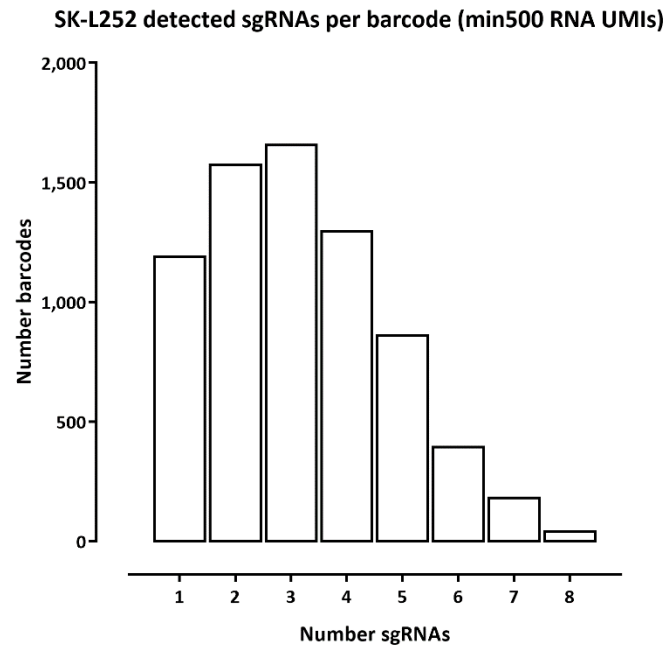
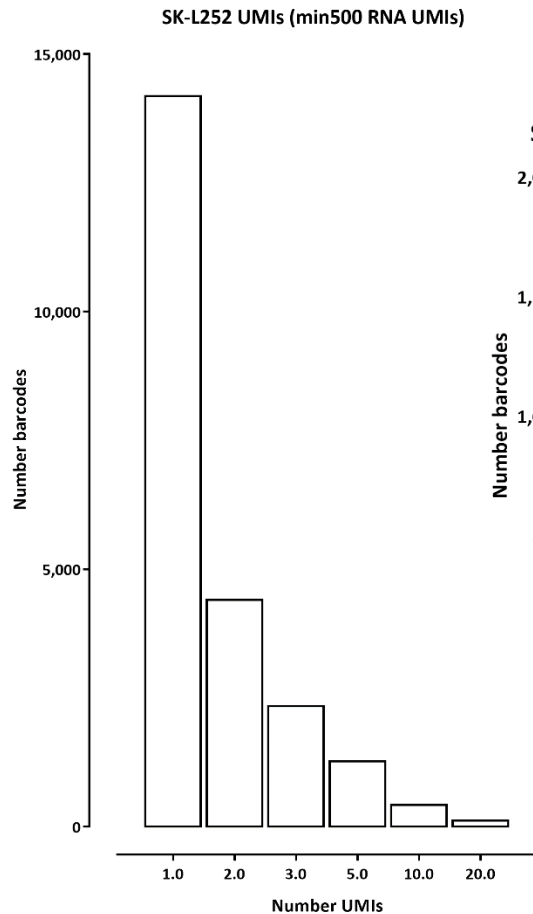
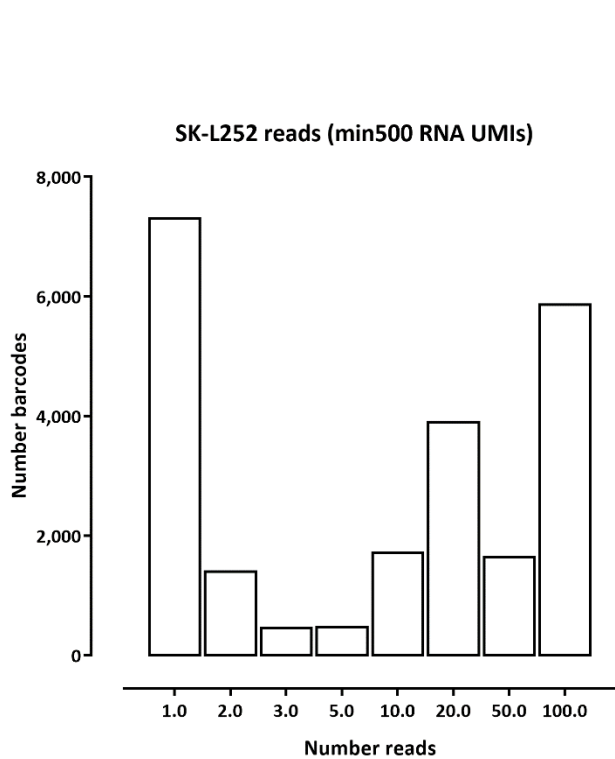
sgRNAs UMIs vs reads, all BCs



sgRNAs UMIs vs reads, >500 RNA UMIs BCs

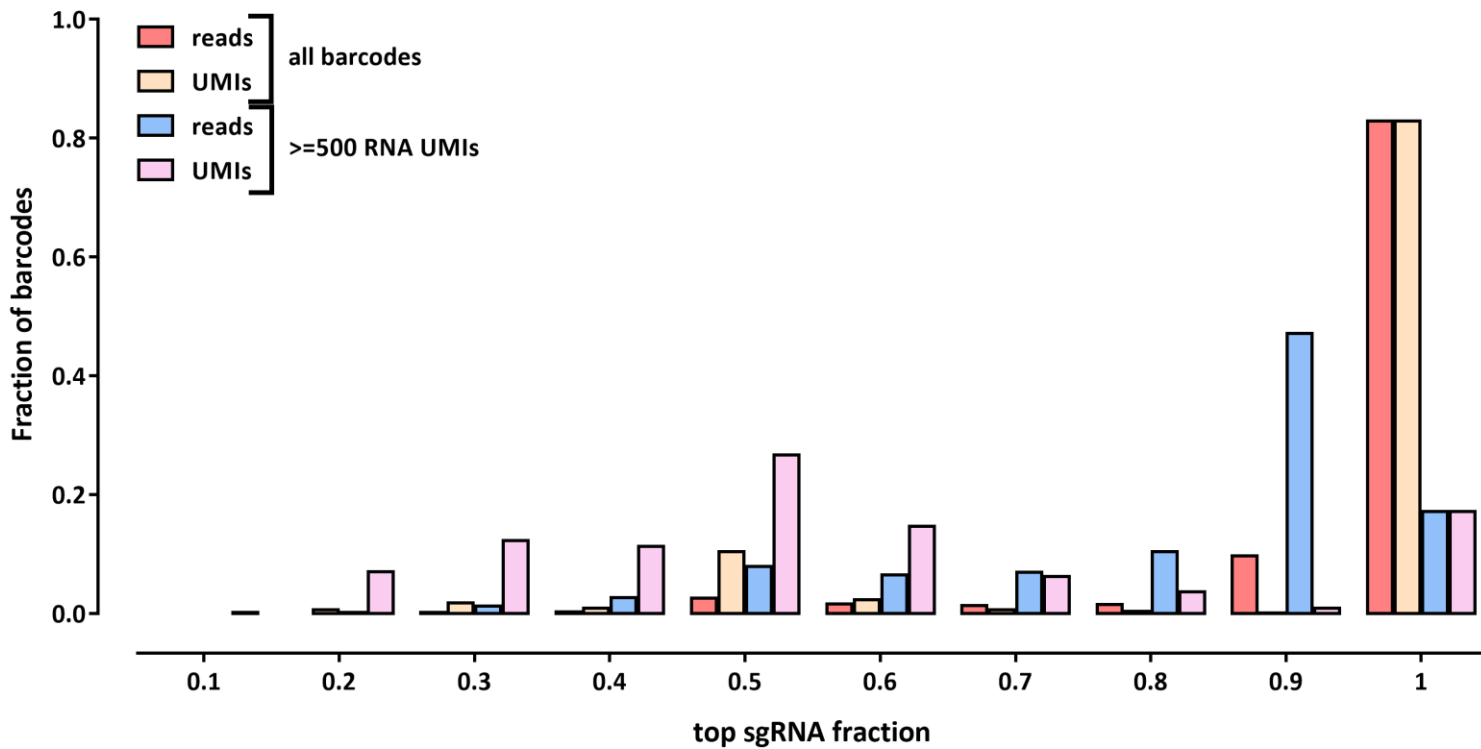


sgRNAs UMIs vs reads, >500 RNA UMIs BCs



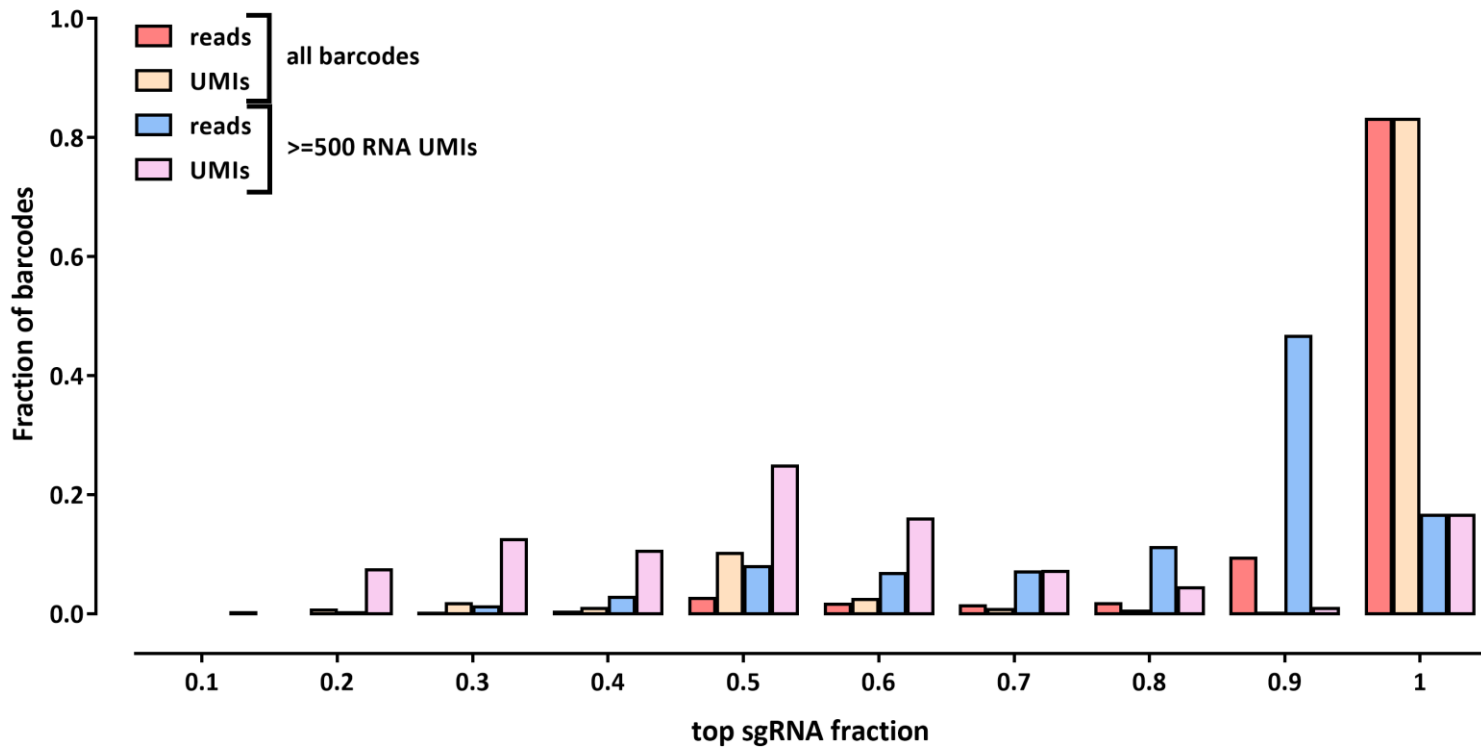
sgRNAs reads per barcode SK-L251

top sgRNA fraction SK-L251



sgRNAs reads per barcode SK-L252

top sgRNA fraction SK-L252



sgRNAs reads per barcode, min500 RNA UMI, SK-L251

top sgRNA fraction per barcode, min 500 RNA UMIs

#	0	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1
1	0	0	0	0	0	0	0	0	0	0	365
2	0	0	0	0	0	109	0	0	0	0	36
3	0	0	3	30	0	14	24	7	0	0	7
5	0	0	2	2	4	5	3	4	15	0	29
10	0	0	0	0	0	0	2	12	26	68	97
20	0	0	0	0	8	54	51	28	46	291	257
50	0	0	1	20	42	103	92	65	34	147	111
100	0	0	5	40	139	284	292	381	625	2,882	329

top sgRNA fraction per barcode, min 500 RNA UMIs

#	0	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1
1	0	0	0	0	0	0	0	0	0	0	892
2	0	0	0	0	0	707	0	0	0	0	201
3	0	0	169	403	0	432	357	132	0	0	100
5	0	9	216	358	566	452	402	135	166	0	32
10	0	4	79	139	206	260	226	129	61	25	3
20	0	0	2	20	40	64	69	49	32	17	2
50	0	0	0	0	0	0	0	2	6	16	0
100	0	0	0	0	0	0	0	1	0	9	1

sgRNAs reads per barcode, min500 RNA UMI, SK-L252

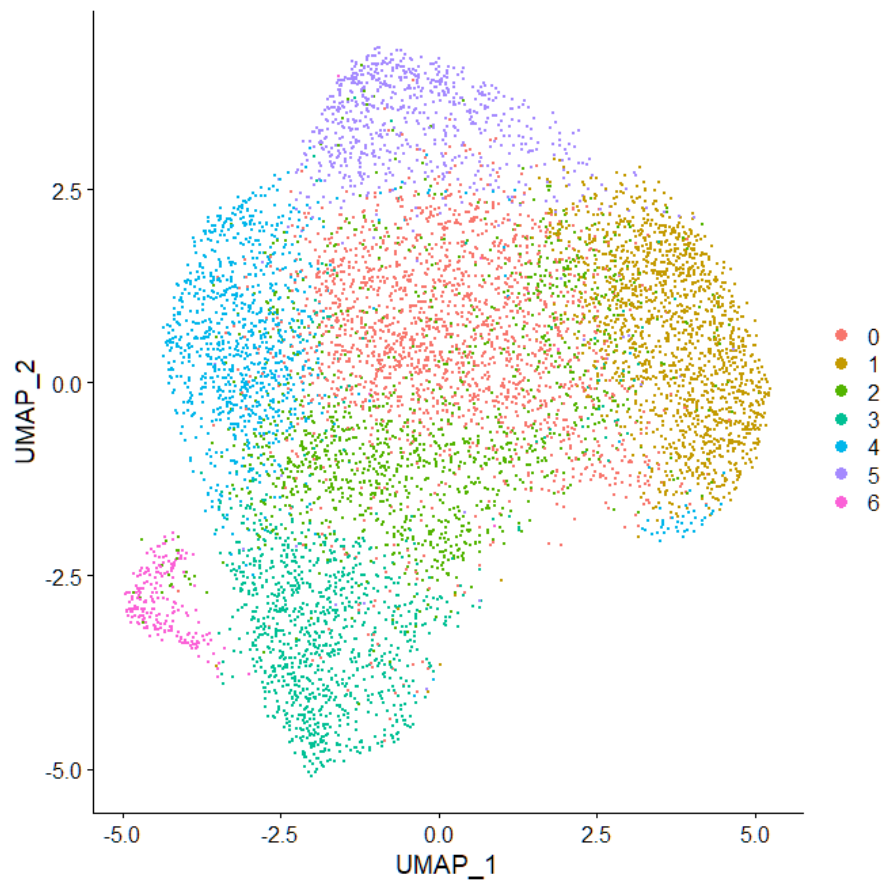
top sgRNA fraction per barcode, min 500 RNA UMIs

#	0	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1
1	0	0	0	0	0	0	0	0	0	0	324
2	0	0	0	0	0	114	0	0	0	0	49
3	0	0	4	18	0	12	30	12	0	0	20
5	0	0	1	5	3	8	6	5	16	0	27
10	0	0	0	1	0	3	3	12	42	80	106
20	0	0	0	0	13	57	61	52	54	267	231
50	0	0	2	21	44	94	72	55	33	170	96
100	0	0	4	35	138	279	316	371	657	2,832	336

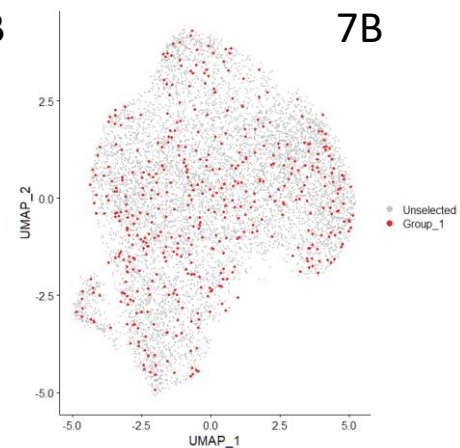
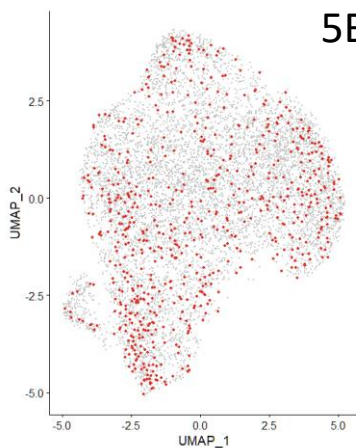
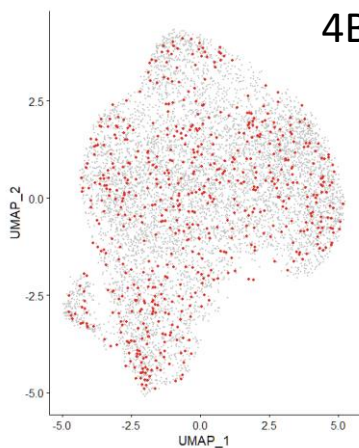
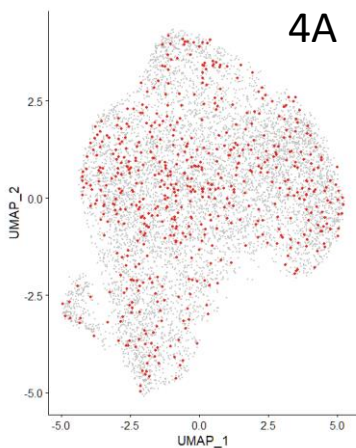
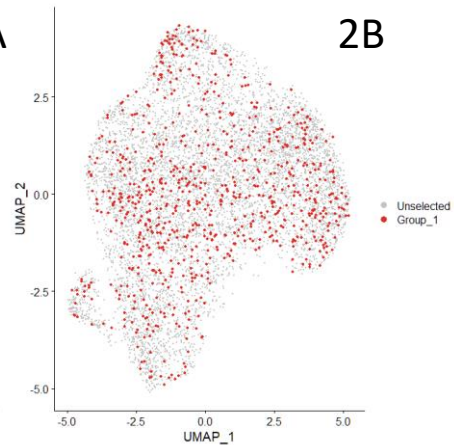
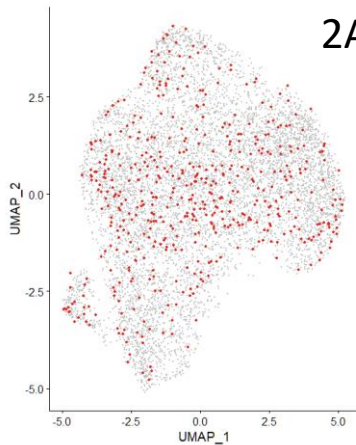
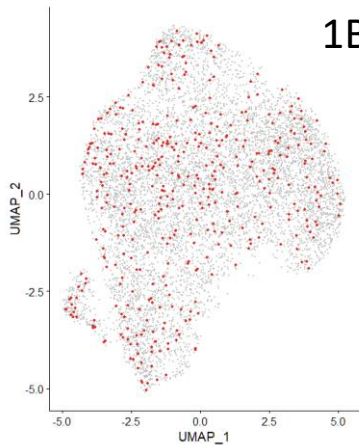
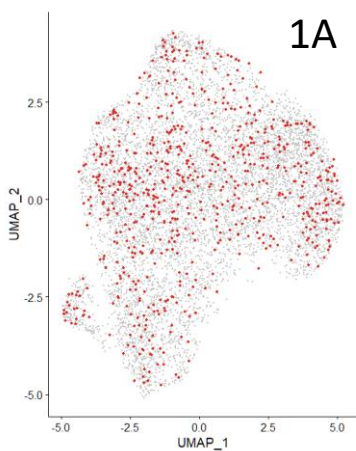
top sgRNA fraction per barcode, min 500 RNA UMIs

#	0	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1
1	0	0	0	0	0	0	0	0	0	0	828
2	0	0	0	0	0	680	0	0	0	0	194
3	0	0	166	419	0	426	373	145	0	0	118
5	0	12	255	357	545	414	434	150	189	0	41
10	0	1	63	144	184	229	243	164	86	21	8
20	0	0	4	13	24	35	92	48	36	16	0
50	0	0	0	0	0	1	2	4	3	17	0
100	0	0	0	0	0	0	0	0	0	7	0

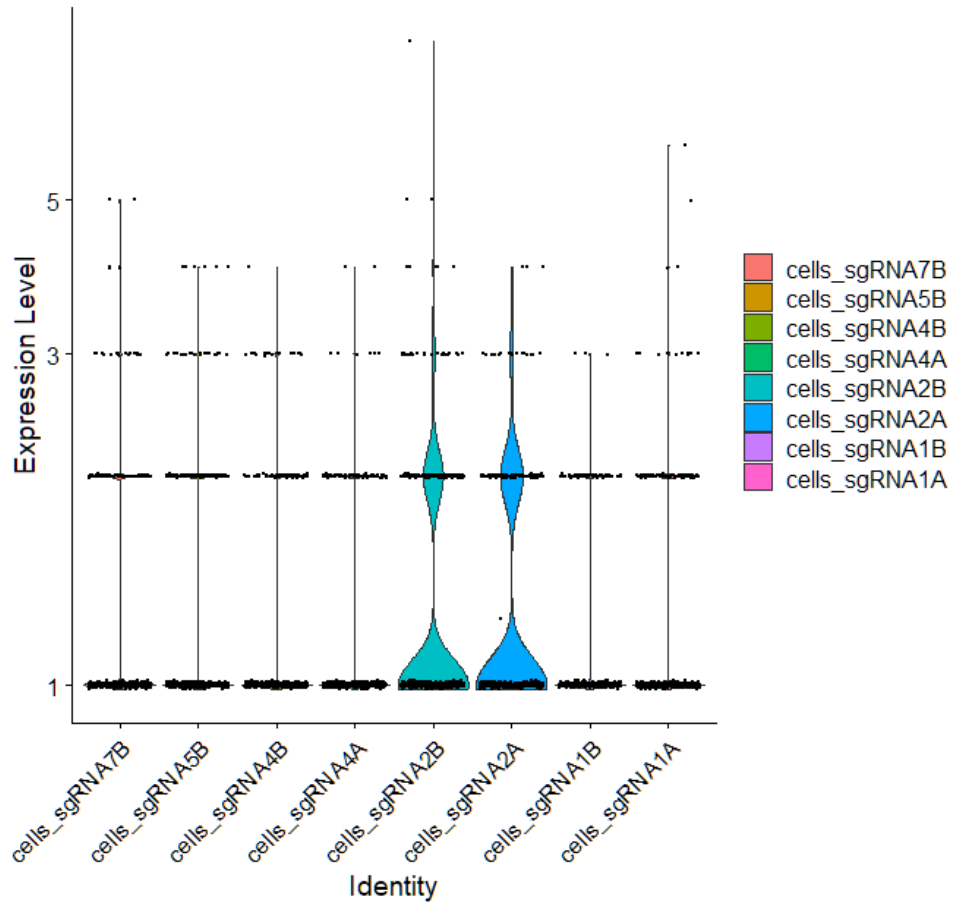
RNA UMAP SK-L247



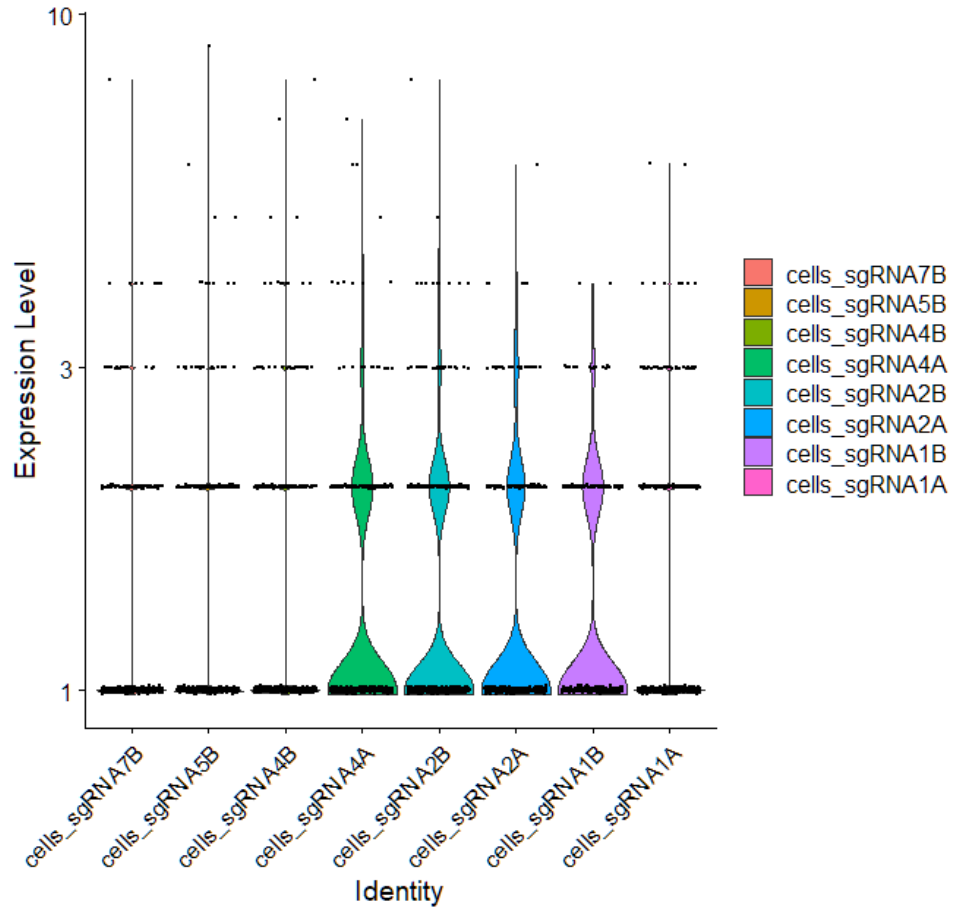
RNA UMAP SK-L247



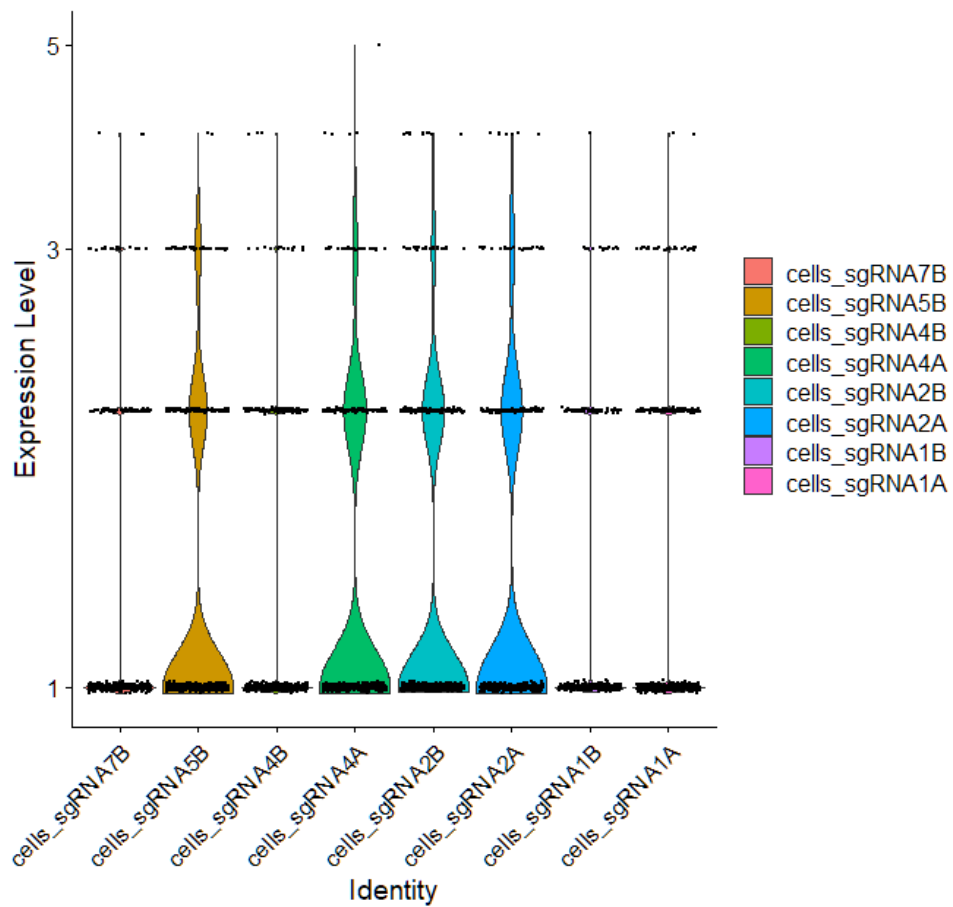
CBFA2T3



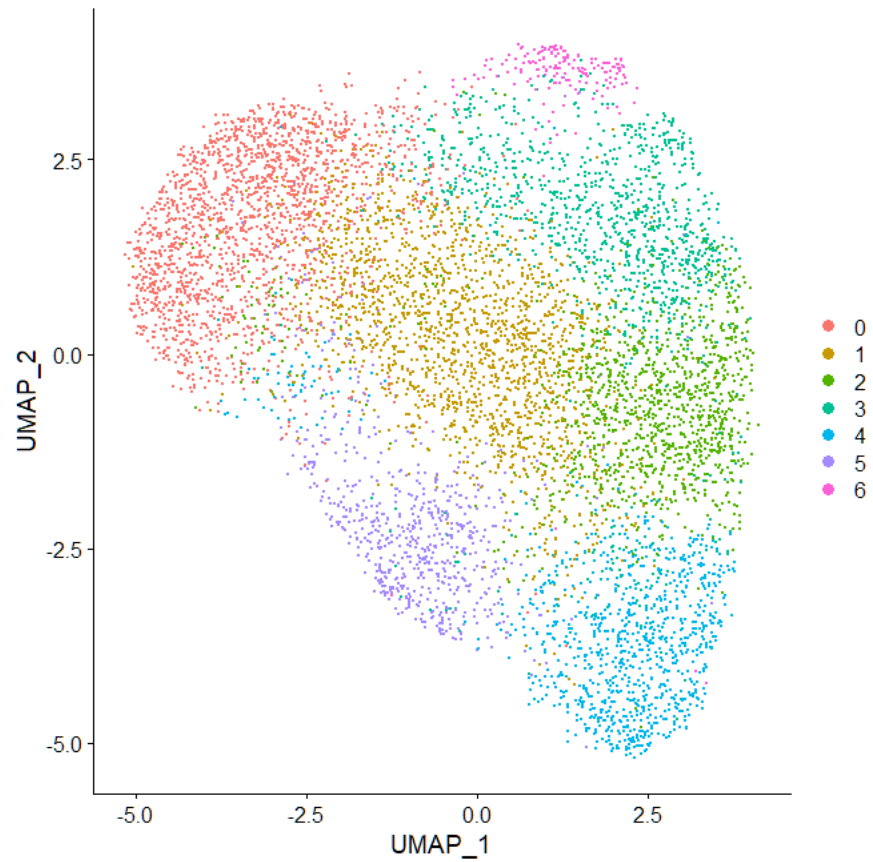
NR2F2-AS1



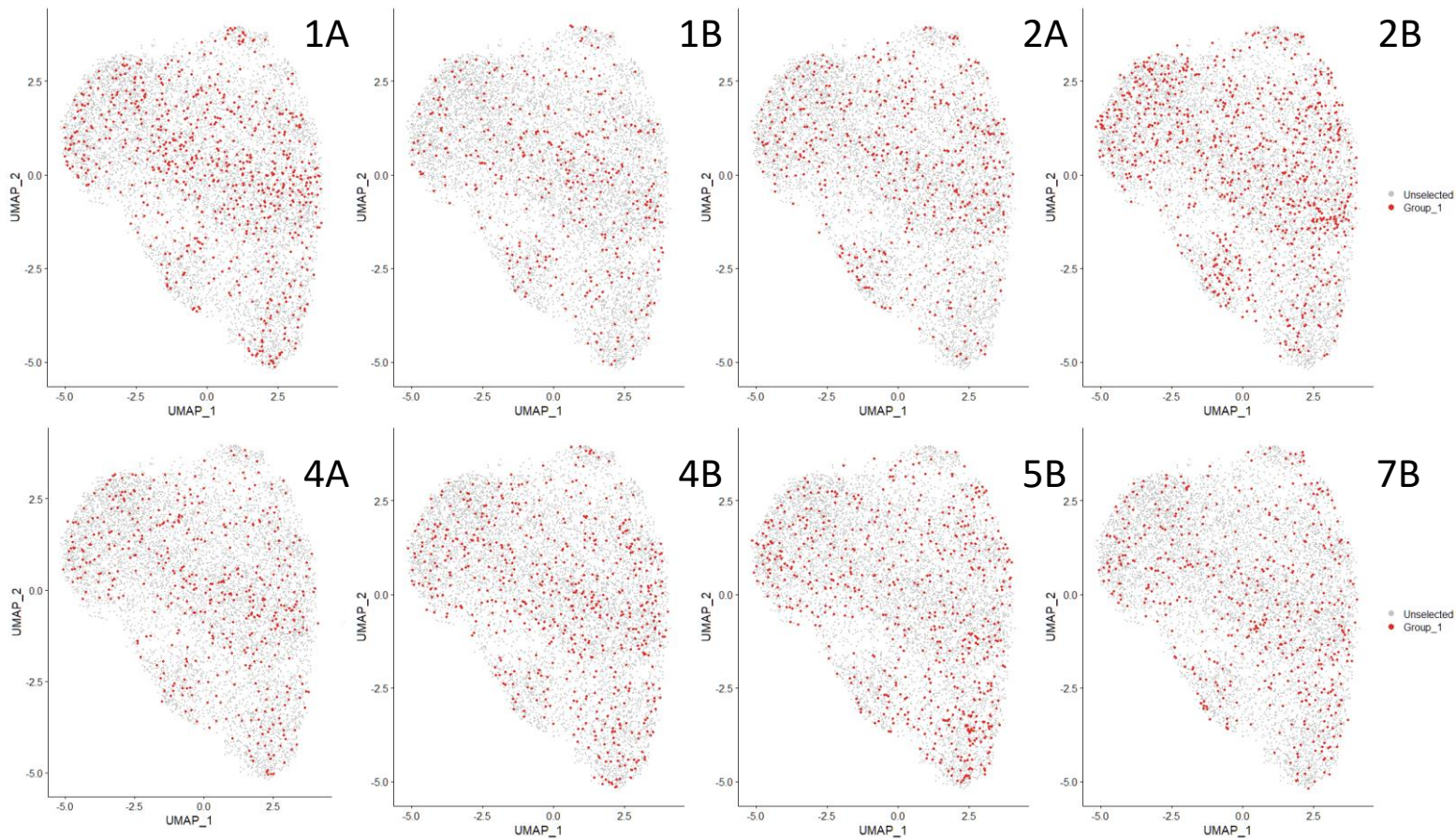
PIEZO1



RNA UMAP SK-L248



RNA UMAP SK-L248



CBFA2T3

