Cell Line	A6 Mapped Reads	COII Mapped Reads	CYb Mapped Reads	MURF2 Mapped Reads	ND7 Mapped Reads	Total Number of Mapped Reads	Unmapped Reads Excluded from analysis	Total Reads in Sample	% of Mapped Reads
427wt	66,513	204,222	287,122	300,691	252,105	1,110,653	353,574	1,464,227	75.9
MGA	29,984	106,824	142,268	169,248	136,959	585,283	179,268	764,551	76.6
KREN2 null	220,567	631,677	863,295	1,076,317	692,339	3,484,195	859,029	4,343,224	80.2
KREN3 null	57,028	81,897	172,841	153,394	85,745	550,905	247,288	798,193	69.0
KREN1 only	136,160	228,734	299,137	418,238	289,855	1,372,124	296,590	1,668,714	82.2
KREN2 only	133,800	417,694	468,452	527,111	455,485	2,002,542	737,825	2,740,367	73.1
KREN3 only	141,482	262,820	414,425	401,130	308,994	1,528,851	420,566	1,949,417	78.4
Triple null	77,114	132,076	170,174	188,131	142,762	710,257	199,634	909,891	78.1
sum:	862,648	2,065,944	2,817,714	3,234,260	2,364,244	11,344,810	3,293,774	14,638,584	77.5

Table S1. Read counts mapped to target mitochondrial transcripts by cell line. Total number of reads identified for target amplicons analysed by Illumina sequencing.

Cell Line	A6 Unique Reads	COII Unique Reads	CYb Unique Reads	MURF2 Unique Reads	ND7 Unique Reads
427wt	167	47	1546	1929	1166
MGA	95	37	1592	2108	1012
KREN2 null	419	48	701	5480	3288
KREN3 null	118	21	586	4426	729
KREN1 only	103	21	103	573	335
KREN2 only	1397	34	1605	3392	7775
KREN3 only	1238	34	732	3678	3521
Triple null	49	19	85	90	141

Table S2. Unique read sequence counts mapped to target mitochondrial transcripts by cell line. Numbers of unique read sequences identified for target amplicons analysed by Illumina sequencing.

	A6 (ED)	A6 (Partial)	A6 (PRE)	COII (ED)	COII (Partial)	COII (PRE)	CYb (ED)	CYb (Partial)	CYb (PRE)	MURF2 (ED)	MURF2 (Partial)	MURF2 (PRE)	ND7 (ED)	ND7 (Partial)	ND7 (PRE)	Total Mapped
427wt	-	1,955	64,558	1,567	956	201,699	45,099	42,903	199,120	132,879	89,365	78,447	58,582	50,031	143,492	**1,110,653**
MGA	-	808	29,176	496	323	106,005	1	22,198	120,069	52,265	61,339	55,644	26,880	27,756	82,323	**585,283**
KREN2 null	9	67,091	153,467	1,055	1,211	629,411	2	32,788	830,505	9,184	934,361	132,772	128,889	237,778	325,672	**3,484,195**
KREN3 null	-	1,397	55,631	1	144	81,752	2,510	6,020	164,311	23,153	81,580	48,661	26,261	13,575	45,909	**550,905**
KREN1 only	-	43,005	93,155	-	442	228,292	1	2,595	296,541	6	311,566	106,666	6	131,654	158,195	**1,372,124**
KREN2 only	-	19,291	114,509	-	797	416,897	8,472	42,217	417,763	450	391,937	134,724	30	339,395	116,060	**2,002,542**
KREN3 only	-	22,555	118,927	249	588	261,983	-	14,576	399,849	22,778	315,805	62,547	22	173,702	135,270	**1,528,851**
Triple Null	-	7,454	69,660	-	248	131,828	-	1,587	168,587	1	1,843	186,287	4	16,470	126,288	**710,257**
sum:	***9***	***163,556***	***699,083***	***3,368***	***4,709***	***2,057,867***	***56,085***	***164,884***	***2,596,745***	***240,716***	***2,187,796***	***805,748***	***240,674***	***990,361***	***1,133,209***	***11,344,810***

Table S3. Read counts identified as pre-edited, partially edited, or fully edited by PARERS for each mRNA target and cell line. Numbers of reads identified for each mRNA from each cell line after classification as pre-edited (PRE), partially edited (Partial), or fully edited (ED).

INSERTION

	1U	*2U*	*3U*	*4U*	*5U*	*6U*	*7U*	*8U*
427wt	4740	2371	174	3	78	16	7	0
MGA	6392	2454	222	25	102	20	1	1
KREN2 null	3904	1429	159	29	228	42	9	2
KREN3 null	4677	1220	39	4	105	1	6	0
KREN1 only	192	7	1	0	46	0	2	0
KREN2 only	5540	12236	1003	98	108	38	45	0
KREN3 only	4149	18049	4115	266	354	165	57	29
Triple null	763	59	2	2	51	5	4	0
	30358	**37825**	**5715**	**426**	**1072**	**288**	**132**	**33**

DELETION

	1U	*2U*	*3U*	*4U*	*5U*
427wt	790	334	128	1	0
MGA	1125	386	183	0	0
KREN2 null	1478	949	429	0	0
KREN3 null	2404	895	194	4	0
KREN1 only	6050	76896	12657	154	0
KREN2 only	599	15	4	0	0
KREN3 only	331	23	2	0	0
Triple null	24612	1354	191	9	0
	37389	**80851**	**13789**	**168**	**0**

Table S4. Normalized read counts (reads per million reads) identified within reads that contained a single edited site. Data for Figure 5 in tabular form, showing read numbers normalized to the total number of reads for each cell line (Column 6 in Table S1). Columns show the number of Us either deleted or inserted at a single editing site.

Normalized Number of Reads with Only a Single Insertion Edited Site by Position in the Read (Reads per Million Reads)

		G 303	G 304	A 305	G 306	G 307	A 308	G 309	A 310	G 311	A 312	A 313	G 314	A 315	A 316	A 317	G 318	G 319	G 320	A 321	A 322	A 323	G 324	G 327	G 329	A 330	G 335	
		ES18	ES17		ES16	ES15	ES14		ES13		ES12		ES11	ES10	ES9	ES8	ES7	ES6				ES5	ES4	ES3	ES2	ES1	sum
A6	427wt	0	0	0	0	180	0	0	15	15	0	0	0	0	0	0	0	150	0	737	30	0	15	0	391	391	1924
A6	MGA	0	0	0	0	334	0	0	0	0	0	0	0	0	0	0	0	0	0	1067	0	0	0	0	267	667	2335
A6	KREN2 null	0	0	0	0	199	0	0	0	0	0	0	0	0	0	0	517	0	0	1215	0	0	0	0	449	236	2616
A6	KREN3 null	0	0	0	0	70	0	0	0	18	0	0	0	0	0	0	18	35	0	333	53	0	0	0	123	1368	2017
A6	KREN1 only	0	0	0	0	118	0	0	0	0	0	0	0	0	0	51	22	0	88	0	0	0	0	0	0	15	294
A6	KREN2 only	0	0	0	0	75	0	0	0	0	0	0	0	0	0	0	164	7	0	3169	0	478	157	82	4111	6846	15090
A6	KREN3 only	0	0	0	0	113	0	7	0	14	0	0	0	0	0	0	212	42	21	3633	262	0	0	0	8340	177	12821
A6	Triple null	0	0	0	0	117	0	0	0	0	0	0	0	0	0	0	195	39	584	246	13	0	0	52	0	726	1971
	sum	0	0	0	0	422	0	7	0	14	0	0	0	0	0	0	51	593	89	693	7048	274	478	157	134	12451	7764	30176
	% of reads	0%	0%	0%	0%	1%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	2%	0%	2%	23%	1%	2%	1%	0%	41%	26%	100%

		A 4	A 5	A 6	G 7	G 8	G 9	G 10	A 11	A 16	A 17	G 18	A 19	G 22	G 23	C 24	G 28	A 29	G 32	A 33	G 34	
		ES11		ES10	ES9		ES8	ES7	ES6	ES5		ES4	ES3	ES2						ES1		sum
MURF2	427wt	0	0	319	33	3	3	3	17	17	0	0	50	53	47	0	0	0	14826	110	15481
MURF2	MGA	0	0	142	0	0	0	0	41	30	6	0	41	278	24	0	12	0	21034	47	21655
MURF2	KREN2 null	0	0	38	0	0	0	4	4	9	10	15	84	171	0	7	20	0	10795	0	11157
MURF2	KREN3 null	0	0	169	0	0	0	7	13	26	33	33	104	1004	111	13	33	0	15268	39	16852
MURF2	KREN1 only	0	0	84	0	5	2	0	7	0	2	0	29	5	0	0	0	2	2	0	139
MURF2	KREN2 only	0	2	782	21	34	0	2	2	19	51	288	592	2588	116	13	27	11	10990	85	15623
MURF2	KREN3 only	0	0	42	0	0	0	0	0	0	45	30	160	833	0	50	17	10	11627	25	12839
MURF2	Triple null	0	0	255	5	5	5	11	43	27	64	101	181	80	16	5	0	0	223	43	1063
	sum	0	2	1370	26	44	8	23	68	81	205	467	1149	4680	242	88	97	24	48906	192	57672
	% of reads	0%	0%	2%	0%	0%	0%	0%	0%	0%	0%	1%	2%	8%	0%	0%	0%	0%	85%	0%	100%

		A 474	A 478	C 479	A 480	A 481	A 483	C 485	A 486	A 487	G 488	A 492	G 493	G 494	A 496	A 498	A 499	A 500	A 501	G 502	A 504	G 505	A 506	G 507	A 508	A 509	C 510	
																							ES3	ES2	ES1			sum
COII	427wt	0	0	5	191	88	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	24	10	0	656	29	1009
COII	MGA	0	0	0	56	103	0	0	0	0	19	0	0	0	0	0	0	37	0	0	0	75	28	0	749	0	1067
COII	KREN2 null	0	0	3	92	79	2	0	0	0	2	0	0	0	0	0	0	0	11	0	0	0	0	0	70	0	258
COII	KREN3 null	0	0	0	37	98	12	0	0	0	24	0	0	0	0	0	0	0	0	0	0	0	12	0	0	0	183
COII	KREN1 only	0	0	0	83	39	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	127
COII	KREN2 only	0	0	0	84	74	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	158
COII	KREN3 only	0	0	0	68	76	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	0	0	114	0	266
COII	Triple null	0	0	0	61	106	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	174
	sum	0	0	3	424	472	21	0	0	0	30	0	0	0	0	0	0	0	11	0	0	8	12	0	184	0	1166
	% of reads	0%	0%	0%	36%	41%	2%	0%	0%	0%	3%	0%	0%	0%	0%	0%	0%	0%	1%	0%	0%	1%	1%	0%	16%	0%	100%

		A -7	A -5	A -3	A -2	A -1	A 1	G 2	C 3	G 4	G 5	A 6	G 7	A 8	A 9	A 10	A 11	A 12	A 13	G 14	A 15	A 16	A 17	G 18	G 19	G 20	
						ES13	ES12	ES11		ES10	ES9			ES8	ES7	ES6	ES5	ES4					ES3	ES2	ES1		sum
CYb	427wt	293	21	0	0	0	0	42	0	0	56	0	28	0	28	0	205	0	188	543	136	181	387	1853	1449	5409
CYb	MGA	155	21	21	0	0	0	0	0	35	77	0	21	28	21	0	0	49	232	998	218	457	738	1582	1307	5961
CYb	KREN2 null	219	8	5	0	0	2	15	0	0	0	10	0	14	0	5	3	0	10	36	60	95	1098	2101	1161	4843
CYb	KREN3 null	266	29	12	0	23	0	0	0	12	29	0	0	35	0	0	0	0	98	191	93	1209	526	949	764	4235
CYb	KREN1 only	257	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	20	27	0	40	33	7	23	418
CYb	KREN2 only	194	15	6	0	0	0	4	0	21	30	0	77	13	64	0	2	41	145	401	45	4551	636	1725	1955	9926
CYb	KREN3 only	227	19	7	0	0	0	14	5	5	5	0	19	19	22	0	22	0	19	77	63	229	883	2097	1894	5627
CYb	Triple null	270	18	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	41	0	335
	sum	1434	99	36	0	23	2	34	5	38	64	10	96	81	86	5	27	41	293	732	260	6125	3177	6920	5797	25384
	% of reads	6%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	1%	3%	1%	24%	13%	27%	23%	100%

		A 49	G 50	G 51	A 52	G 53	A 54	G 55	G 56	G 57	G 58	A 59	A 61	A 62	G 63	A 64	A 68	G 71	A 72	G 74	A 75	A 76	A 77	G 81	G 83	A 84	G 88	
		ES20	ES19	ES18	ES17	ES16	ES15	ES14		ES13		ES12	ES11	ES10	ES9	ES8			ES7	ES6	ES5	ES4	ES3	ES2	ES1			sum
ND7-5'	427wt	0	0	0	0	0	0	0	0	0	365	0	20	452	0	0	0	0	0	0	8	28	405	44	14970	131	16422
ND7-5'	MGA	0	0	0	0	0	0	0	0	0	263	0	22	920	0	0	0	0	15	0	0	7	277	29	15486	44	17064
ND7-5'	KREN2 null	0	0	0	0	0	0	0	0	0	144	3	6	1648	12	0	0	0	0	0	0	4	248	235	9254	130	11685
ND7-5'	KREN3 null	0	0	0	0	0	0	0	0	12	222	0	0	198	0	0	12	0	0	0	0	128	105	58	14776	70	15581
ND7-5'	KREN1 only	0	0	0	0	0	0	0	0	0	252	7	0	28	0	0	0	0	0	0	0	0	0	3	3	7	300
ND7-5'	KREN2 only	0	0	0	0	0	0	0	0	0	127	0	13	318	2	4	0	0	0	0	13	79	114	59	80784	151	81667
ND7-5'	KREN3 only	0	0	0	0	0	0	0	0	0	259	0	6	2906	0	3	10	0	0	0	0	10	485	2165	133598	1670	141113
ND7-5'	Triple null	0	0	0	0	0	0	0	0	0	301	0	7	7	0	21	0	0	0	0	21	28	385	757	665	42	2234
	sum	0	0	0	0	0	0	0	0	12	1305	10	32	5105	14	29	21	0	0	0	34	249	1338	3278	239082	2070	252580
	% of reads	0%	0%	0%	0%	0%	0%	0%	0%	0%	1%	0%	0%	2%	0%	0%	0%	0%	0%	0%	0%	0%	1%	1%	95%	1%	100%

Table S5. Normalized number of reads with only a single insertion edited site by position in the read (reads per million reads). Table shows distribution of reads that contain some amount of insertion editing at a single site, and demonstrates that a noticeable proportion of editing events are not at ES1. Columns show position of edited site within the read sequence, with the number of reads normalized to the total number of reads corresponding to each mRNA in each cell line (Columns 1-5 in Table S1). The position is indicated by the non-U nucleotide mRNA sequence, with numbering starting at the first base of the start codon in the pre-edited sequence. Canonical insertion editing sites (ES#) have red column labels, and deletion sites have blue labels, with numbering starting at the 3' end relative to mRNA; unlabeled columns are non-canonical sites. Data in this table are also analysed in Figure 5A and Table S4. ES1 is a canonical deletion site for A6, and 26% of A6 reads with a single edited site contain insertion editing at this site. Other transcripts have canonical insertion sites at ES1, with MURF2, COII, CYb, and ND7-5' having 85%, 16%, 23%, and 95% of their reads with a single edited site containing insertion editing at this site, respectively. The lower percentages observed for COII and CYb may reflect the developmental down-regulation of editing of these transcripts in BF parasites. Because these reads have editing at only a single site, these results are an approximate report of the first editing event, which is not exclusive to ES1 for any transcript.

Normalized Number of Reads with Only a Single Deletion Edited Site by Position in the Read (Reads per Million Reads)

		G 303	G 304	A 305	G 306	G 307	A 308	G 309	A 310	G 311	A 312	A 313	G 314	A 315	A 316	A 317	G 318	G 319	G 320	A 321	A 322	A 323	G 324	G 327	G 329	A 330	G 335	
		ES18	ES17		ES16	ES15	ES14		ES13		ES12			ES11	ES10	ES9	ES8	ES7	ES6				ES5	ES4	ES3	ES2	ES1	sum
A6	427wt	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	15	15	0	2060	2090
A6	MGA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1601	1601
A6	KREN2 null	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	494	0	0	3953	4448
A6	KREN3 null	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3735	3735
A6	KREN1 only	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1843	0	0	46746	48590
A6	KREN2 only	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	0	1756	1764
A6	KREN3 only	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	368	375
A6	Triple null	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	39	1206	0	88739	89984
	sum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1889	1213	0	137609	140712
	% of reads	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	1%	1%	0%	98%	100%

		A 4	A 5	A 6	G 7	G 8	G 9	G 10	A 11	A 16	A 17	G 18	A 19	G 22	G 23	C 24	G 28	A 29	G 32	A 33	G 34	
		ES11		ES10	ES9		ES8	ES7	ES6	ES5		ES4	ES3	ES2					ES1			sum
MURF2	427wt	0	0	0	0	0	0	0	80	0	0	0	3346	0	0	482	0	40	0	0		3948
MURF2	MGA	0	0	0	0	0	0	0	124	0	0	0	4892	0	0	384	0	24	0	0		5424
MURF2	KREN2 null	0	0	0	0	0	0	0	66	0	0	0	6302	0	0	738	0	13	0	0		7119
MURF2	KREN3 null	0	0	0	0	0	0	0	137	0	0	0	12315	0	0	1806	0	46	0	0		14303
MURF2	KREN1 only	0	0	0	0	0	0	0	316	0	0	0	289273	0	0	5722	0	6735	0	0		302046
MURF2	KREN2 only	0	0	0	0	0	0	0	101	0	0	0	1965	0	0	59	0	0	0	0		2125
MURF2	KREN3 only	0	0	0	0	0	0	0	42	0	0	0	439	0	0	60	0	10	0	0		551
MURF2	Triple null	0	0	0	0	0	0	0	3078	0	0	0	547	0	0	1265	0	983	0	0		5874
	sum	0	0	0	0	0	0	0	3739	0	0	0	310842	0	0	9649	0	7787	0	0		332017
	% of reads	0%	0%	0%	0%	0%	0%	0%	1%	0%	0%	0%	94%	0%	0%	3%	0%	2%	0%	0%		100%

		A 474	A 478	C 479	A 480	A 481	A 483	C 485	A 486	A 487	G 488	A 492	G 493	G 494	A 496	A 498	A 499	A 500	A 501	G 502	A 504	G 505	A 506	G 507	A 508	A 509	C 510	
																							ES3	ES2	ES1			sum
COII	427wt	0	0	0	0	0	0	0	0	0	211	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	211
COII	MGA	9	0	0	0	0	0	0	0	0	84	0	0	0	9	0	0	0	0	0	0	0	0	0	0	0	0	103
COII	KREN2 null	5	0	0	0	2	0	0	0	0	127	0	0	2	0	0	0	0	0	3	0	0	0	0	0	0	0	138
COII	KREN3 null	0	0	0	0	0	0	0	0	0	183	0	0	0	12	0	0	0	0	0	0	0	0	0	0	0	0	195
COII	KREN1 only	0	0	0	0	0	0	0	0	0	219	0	0	9	9	0	0	0	0	0	0	0	0	0	0	0	0	236
COII	KREN2 only	5	0	0	0	2	0	0	0	0	132	0	0	0	12	0	0	0	0	2	0	0	0	0	0	0	0	153
COII	KREN3 only	0	0	0	0	4	0	0	0	0	171	0	0	0	8	0	0	0	0	4	0	0	0	0	0	0	0	186
COII	Triple null	8	0	0	0	0	0	0	0	0	129	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	136
	sum	17	0	0	0	8	0	0	0	0	960	0	0	10	41	0	0	0	0	9	0	0	0	0	0	0	0	1045
	% of reads	2%	0%	0%	0%	1%	0%	0%	0%	0%	92%	0%	0%	1%	4%	0%	0%	0%	0%	1%	0%	0%	0%	0%	0%	0%	0%	100%

		A -7	A -5	A -3	A -2	A -1	A 1	G 2	C 3	G 4	G 5	A 6	G 7	A 8	A 9	A 10	A 11	A 12	A 13	G 14	A 15	A 16	A 17	G 18	G 19	G 20	
						ES13	ES12	ES11		ES10	ES9			ES8	ES7	ES6	ES5	ES4						ES3	ES2	ES1	sum
CYb	427wt		0	21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	21
CYb	MGA		0	35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	35
CYb	KREN2 null		2	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13
CYb	KREN3 null		0	35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	35
CYb	KREN1 only		0	20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	20
CYb	KREN2 only		4	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	19
CYb	KREN3 only		2	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	12
CYb	Triple null		0	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6
	sum		9	96	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	105
	% of reads		9%	91%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	100%

		A 49	G 50	G 51	A 52	G 53	A 54	G 55	G 56	G 57	G 58	A 59	A 61	A 62	G 63	A 64	A 68	G 71	A 72	G 74	A 75	A 76	A 77	G 81	G 83	A 84	G 88	
		ES20	ES19	ES18	ES17	ES16	ES15	ES14		ES13		ES12	ES11	ES10	ES9	ES8			ES7	ES6	ES5	ES4	ES3	ES2	ES1			sum
ND7-5'	427wt	0	0	0	0	0	0	0	0	0	0	4	0	0	0	75	242	0	4	0	0	0	877	59	0	123		1384
ND7-5'	MGA	0	0	0	0	0	0	0	0	0	0	29	0	0	0	139	131	0	0	0	0	0	1409	37	0	29		1774
ND7-5'	KREN2 null	0	0	0	0	0	0	0	0	0	0	17	0	0	0	58	140	0	23	0	0	0	4153	188	0	85		4664
ND7-5'	KREN3 null	0	0	0	0	0	0	0	0	0	0	23	0	0	0	93	47	0	0	0	0	0	2321	47	0	93		2624
ND7-5'	KREN1 only	0	0	0	0	0	0	0	0	0	0	148	0	0	0	366	914	0	52	0	0	0	82907	7231	0	269		91887
ND7-5'	KREN2 only	0	0	0	0	0	0	0	0	0	0	7	0	0	0	18	0	0	0	0	0	0	26	2	0	40		92
ND7-5'	KREN3 only	0	0	0	0	0	0	0	0	0	0	3	0	0	0	94	6	0	0	0	0	0	32	6	0	146		288
ND7-5'	Triple null	0	0	0	0	0	0	0	0	0	0	56	0	0	0	939	7	0	0	0	0	0	1786	105532	0	1107		109427
	sum	0	0	0	0	0	0	0	0	0	0	255	0	0	0	1567	1114	0	75	0	0	0	91225	113007	0	1740		208982
	% of reads	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	1%	1%	0%	0%	0%	0%	0%	44%	54%	0%	1%		100%

Table S6. Normalized number of reads with only a single deletion edited site by position in the read (reads per million reads). Table shows distribution of reads that contain some amount of deletion editing at a single site, and demonstrates that a noticeable proportion of editing events are not at ES1, or the 3' most (relative to mRNA) site capable of U deletion. Data in this table are also analysed in Figure 5B and Table S4. ES1 is a canonical deletion site for A6, and 98% of A6 reads with a single edited site contain deletion editing at this site. MURF2, COII, CYb, and ND7-5' transcripts lack Us at ES1, thereby preventing deletion editing at this site. In MURF2, non-canonical sites between ES1 and ES2 have deletion editing in some reads, but 94% occurs at ES3, which is a canonical insertion site. In COII, 92% of deletion editing occurs at a non-canonical site between G488 and A492, although a small amount occurs at three other non-canonical sites further 3'. In CYb, the only site within the read sequence that contains Us is a non-canonical site upstream of the start codon, between A-5 and A-3, where 92% of the limited amount of deletion editing is found. 98% of ND7-5' reads with a single edited site containing deletion editing have editing at either ES2 or ES3, which are canonical deletion sites. See description of Table S5 for additional chart information.

Oligo Name	Oligo Sequence
Oligos for knockout constructs	
KREN1 FOR long A	GAAACGGTTACCAGCGACG
KREN1 REV long H	TTGCTGAAGCACGCAAATTTTC
KREN1 FOR nested A	CTCACAAGGAATTGGATA
KREN1 FOR nested H	CGCAAAGATAAGTGACATATG
KREN1 REV B	ATACGAAGTTATAAGCTTATCAATGCTTTTTTACTCCTTTTC
KREN1 FOR C	ACCATGGTGTTGCTTAATTAC
KREN1 REV D	ATACGAAGTTATAAGCTTATCCTACCTTTAGCCACTTAGCAA
KREN1 FOR E	TTATGGATCCTAAGTGGGTCTAATTATTTGGATGATGAGGT
KREN1 REV F	TGTACATGAGTGGAGGACATTG
KREN1 FOR G	TTATGGATCCTAAGTGGGTCCAAGGATGGGGAATATGCAT
KREN2 FOR long A	TCTGGTGGAAATAGAGAAG
KREN2 REV long H	TTGTAGAGCTGAGACGCT
KREN2 FOR nested A	TCCTCTTCTTCTCTTACTCAC
KREN2 FOR nested H	AATACCAAAATTTAAGAAACG
KREN2 REV B	ATACGAAGTTATAAGCTTATCGAAGTTCGTGGTTCCTTGC
KREN2 FOR C	AGTGTTCACTTACCTCCCA
KREN2 REV D	ATACGAAGTTATAAGCTTATCATGGTAATGCCTTACTTCAA
KREN2 FOR E	TTATGGATCCTAAGTGGGTCTGATTACATTCCCTACTTTC
KREN2 REV F	CACATGAACATAAAGAAGAA
KREN2 FOR G	TTATGGATCCTAAGTGGGTCCACCGGGTGTGCATCCAT
KREN3 FOR long A	GGTAGTAGCAAACAATTGTGC
KREN3 REV long H	ATACGACAAGAAGTCTTGCTA
KREN3 FOR nested A	TTGTGGTCTTTTTCCCCATCT
KREN3 FOR nested H	CATGATAGGGAAAAGTAACAA
KREN3 REV B	ATACGAAGTTATAAGCTTATCGAGGTATAAAGCAACTAGGGAG
KREN3 FOR C	CCTGCGGCACTACGACTAC
KREN3 REV D	ATACGAAGTTATAAGCTTATCTTGGCGAATTTCACAAAGCT
KREN3 FOR E	TTATGGATCCTAAGTGGGTCATCGTCATTGGAGGTTTGC
KREN3 REV F	TGACAAAACGTGCGGAGC
KREN3 FOR G	TTATGGATCCTAAGTGGGTCCGCATAGGTGGTTATGGCG
Oligos for First Round RT-PCR for RNAseq analysis	
11209 ND7-5' FOR	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGATGACTACATGATAAGTA
11210 ND7-5' REV	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACTTTTCTGTACCACGATGC
11215 MURF2 FOR	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGATAGAAAGGTATATAATCTATAATG
11216 MURF2 REV	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCATAACAAATCAAAAACACGAC
11217 A6 FOR	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGAGCAGGAAAGGTTAG
11218 A6 REV	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTTTGATCTTATTCTATAACTCC
11211 CYb FOR	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGTTAAGAATAATGGTTATAAATT
11212 CYb REV	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCAACCTGACATTAAAAGAC
11213 COII FOR	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGATTACAGTGTAACCATGTATTGACATT

11214 COII REV	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGATTTCATTACACCTACCAGG
Oligos for Second Round PCR for RNAseq analysis	
P5-TAGATCGC-F1 (427wt)	AATGATACGGCGACCACCGAGATCTACACTAGATCGCTCGTCGGCAGCGTC
P5-CTCTCTAT-F2 (MGA)	AATGATACGGCGACCACCGAGATCTACACCTCTCTATTCGTCGGCAGCGTC
P5-TATCCTCT-F3 (N2null)	AATGATACGGCGACCACCGAGATCTACACTATCCTCTTCGTCGGCAGCGTC
P5-AGAGTAGA-F4 (N3null)	AATGATACGGCGACCACCGAGATCTACACAGAGTAGATCGTCGGCAGCGTC
P5-GTAAGGAG-F5 (N1only)	AATGATACGGCGACCACCGAGATCTACACGTAAGGAGTCGTCGGCAGCGTC
P5-ACTGCATA-F6 (N2only)	AATGATACGGCGACCACCGAGATCTACACACTGCATATCGTCGGCAGCGTC
P5-AAGGAGTA-F7 (N3only)	AATGATACGGCGACCACCGAGATCTACACAAGGAGTATCGTCGGCAGCGTC
P5-CTAAGCCT-F8 (Triple null)	AATGATACGGCGACCACCGAGATCTACACCTAAGCCTTCGTCGGCAGCGTC
P7-TCGCCTTA-R1 (427wt)	CAAGCAGAAGACGGCATACGAGATTCGCCTTAGTCTCGTGGGCTCGG
P7-CTAGTACG-R2 (MGA)	CAAGCAGAAGACGGCATACGAGATCTAGTACGGTCTCGTGGGCTCGG
P7-TTCTGCCT-R3 (N2null)	CAAGCAGAAGACGGCATACGAGATTTCTGCCTGTCTCGTGGGCTCGG
P7-GCTCAGGA-R4 (N3null)	CAAGCAGAAGACGGCATACGAGATGCTCAGGAGTCTCGTGGGCTCGG
P7-AGGAGTCC-R5 (N1only)	CAAGCAGAAGACGGCATACGAGATAGGAGTCCGTCTCGTGGGCTCGG
P7-CATGCCTA-R6 (N2only)	CAAGCAGAAGACGGCATACGAGATCATGCCTAGTCTCGTGGGCTCGG
P7-GTAGAGAG-R7 (N3only)	CAAGCAGAAGACGGCATACGAGATGTAGAGAGGTCTCGTGGGCTCGG
P7-CCTCTCTG-R8 (Triple null)	CAAGCAGAAGACGGCATACGAGATCCTCTCTGGTCTCGTGGGCTCGG

Table S7. Oligo sequences used in this study.

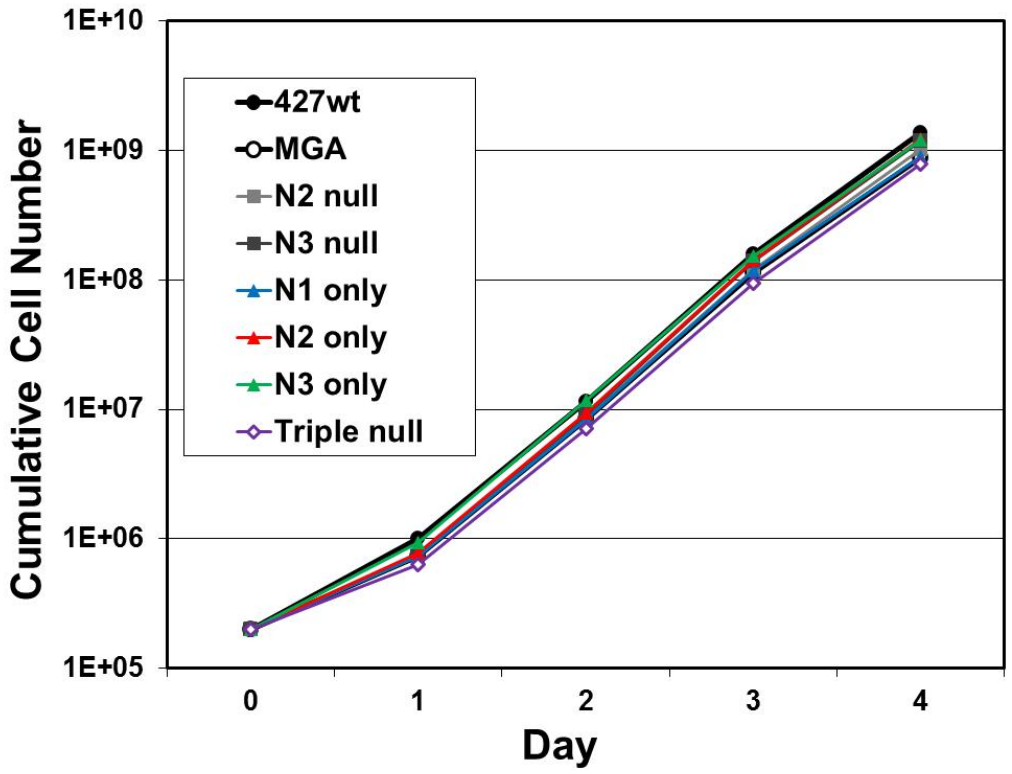
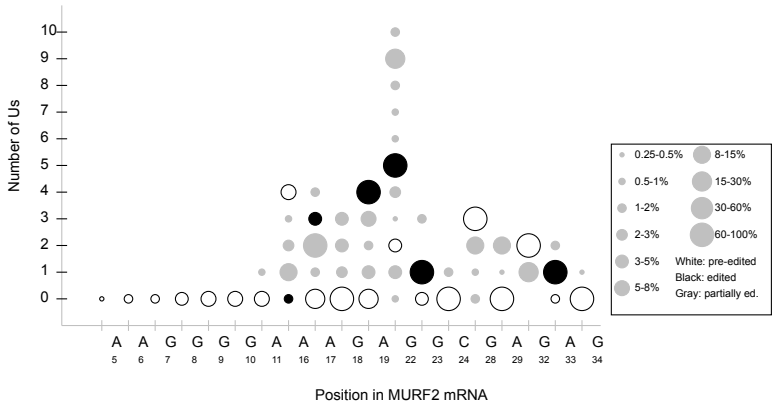


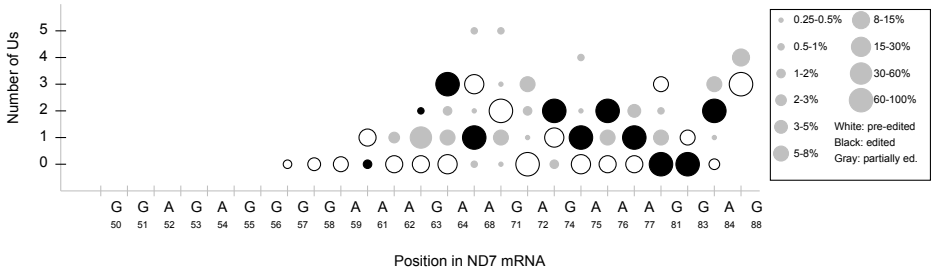
Figure S1. Cumulative growth curves of cell lines used in this study. No notable differences in growth among cell lines were observed.

427wt

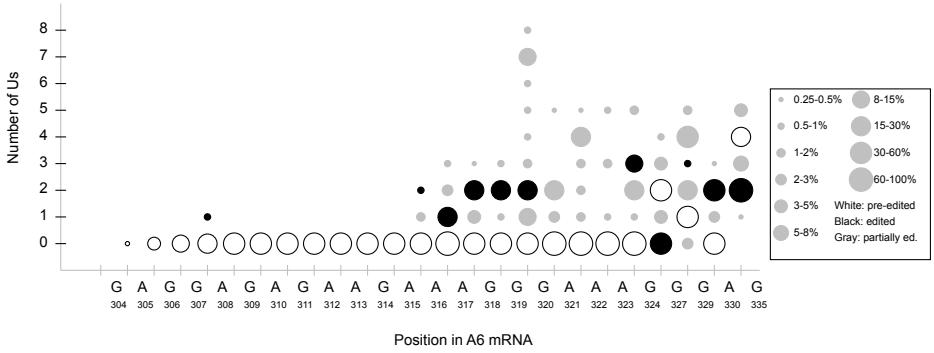
MURF2



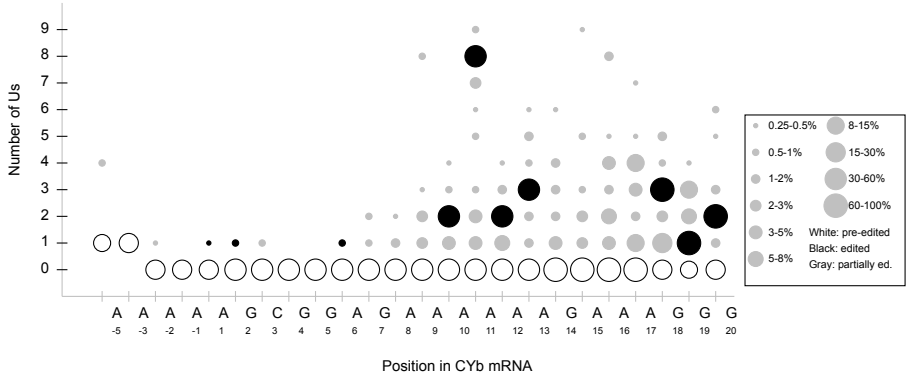
ND7



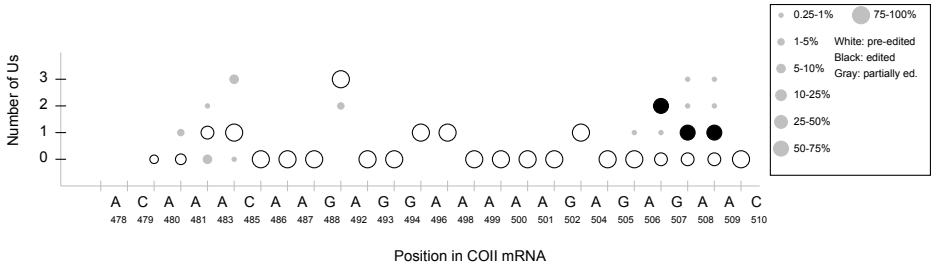
A6



CYb

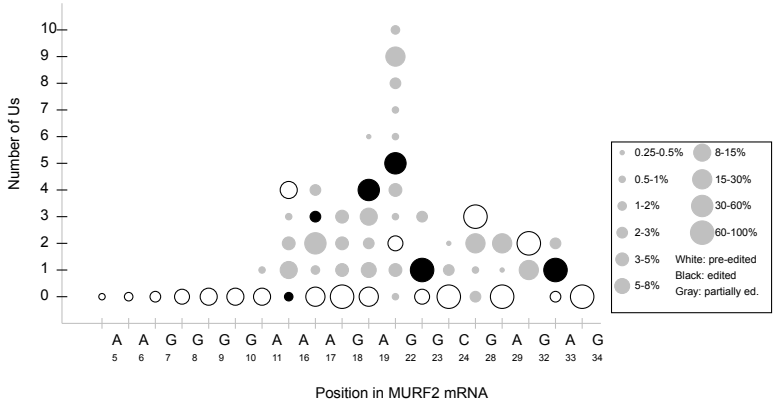


COII

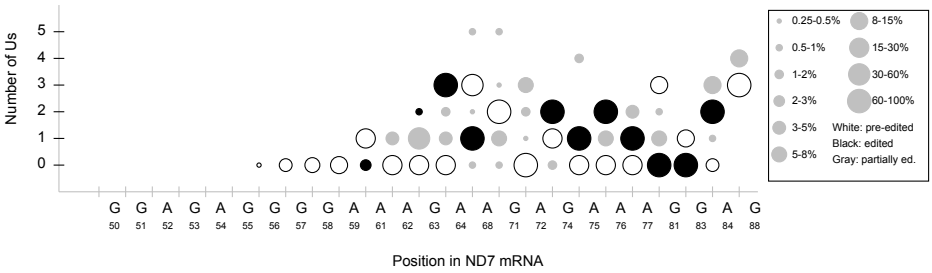


MGA

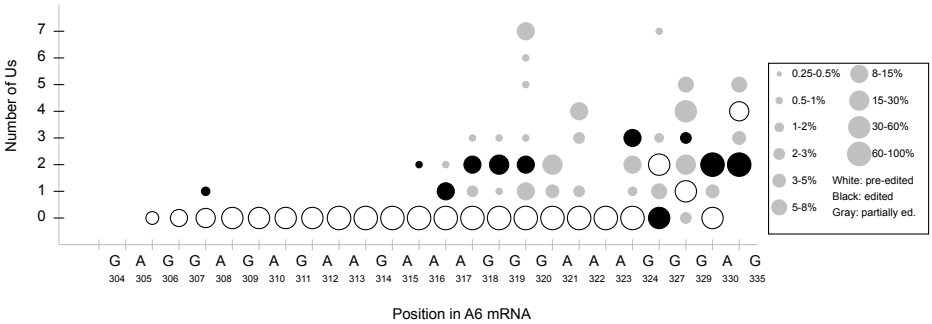
MURF2



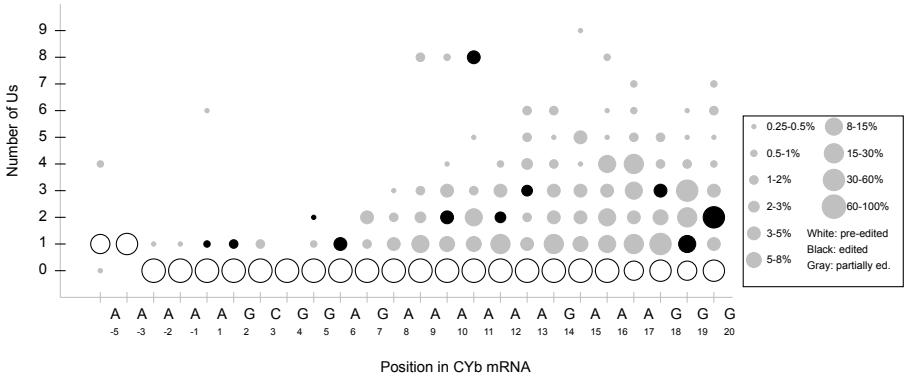
ND7



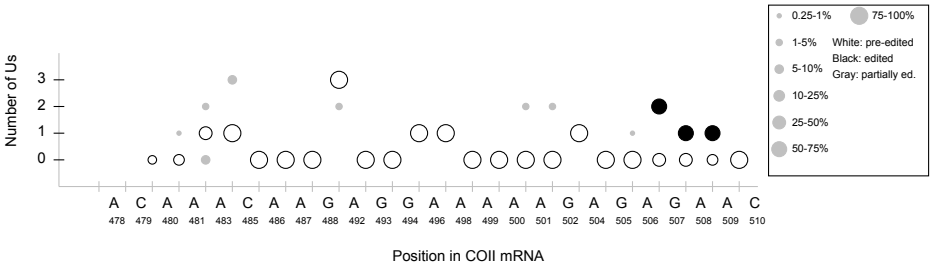
A6



CYb

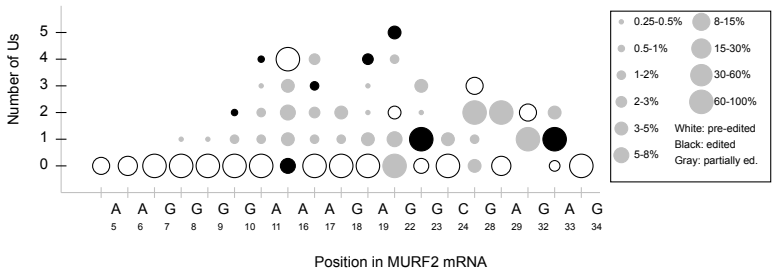


COII



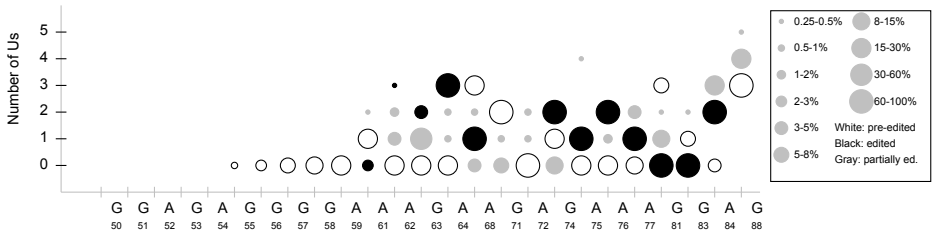
KREN2 null

MURF2



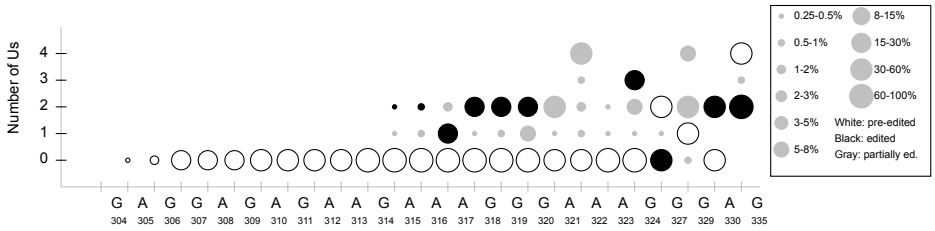
Position in MURF2 mRNA

ND7



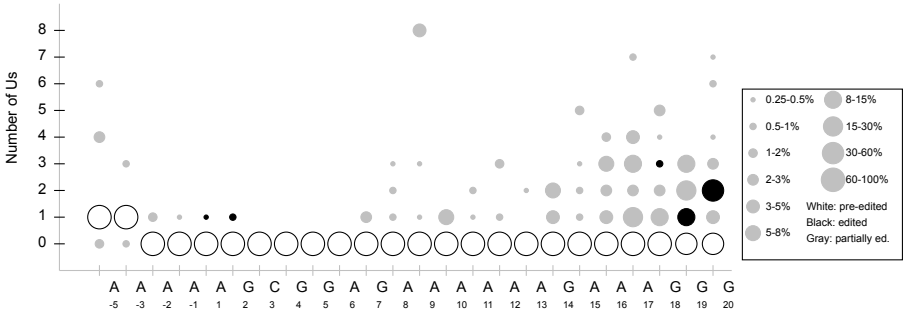
Position in ND7 mRNA

A6



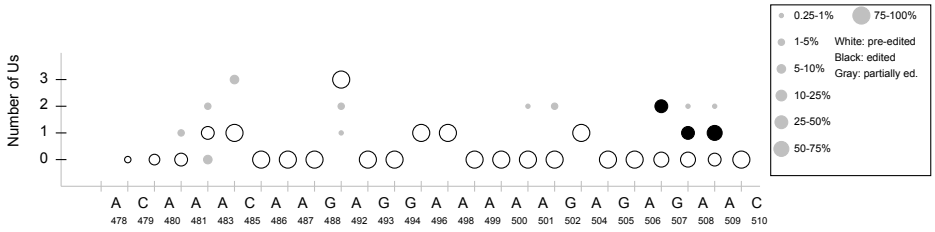
Position in A6 mRNA

CYb



Position in CYb mRNA

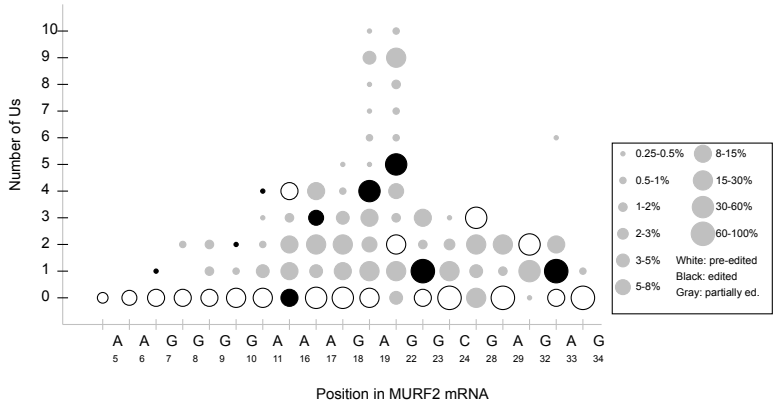
COII



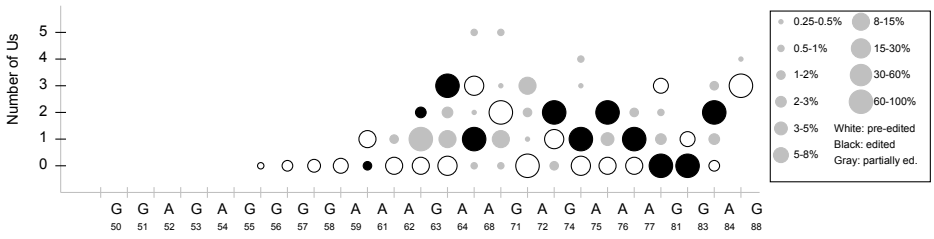
Position in COII mRNA

KREN3 null

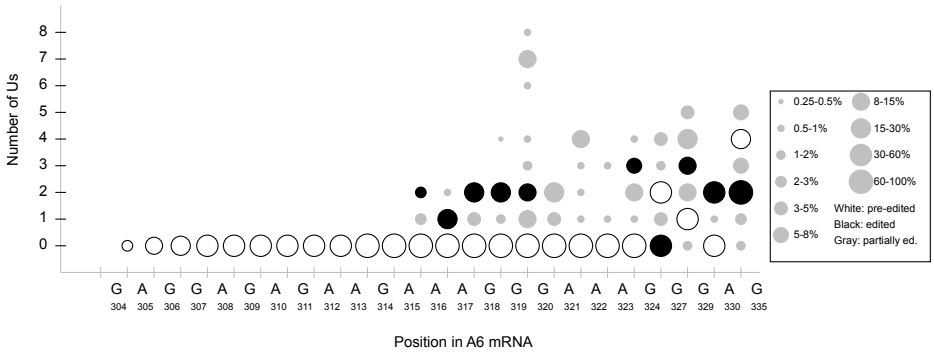
MURF2



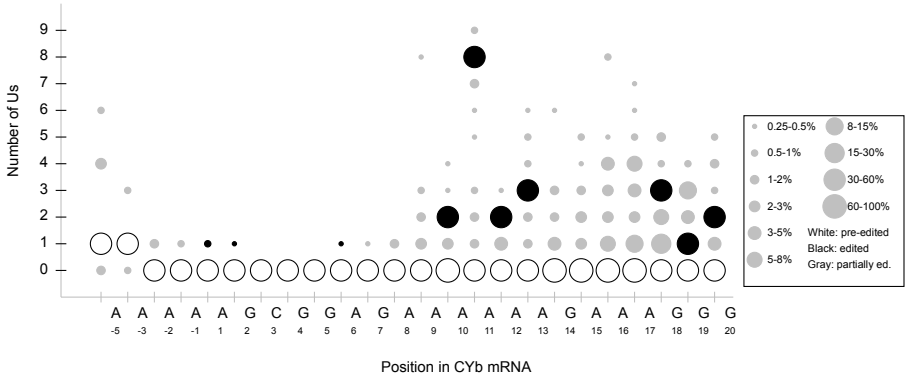
ND7



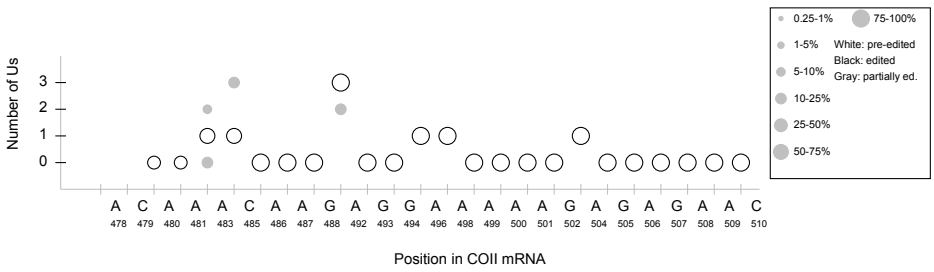
A6



CYb

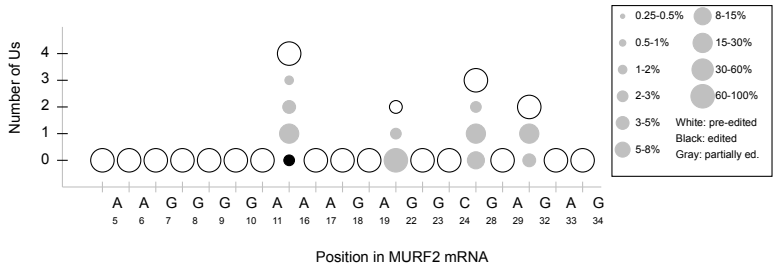


COII



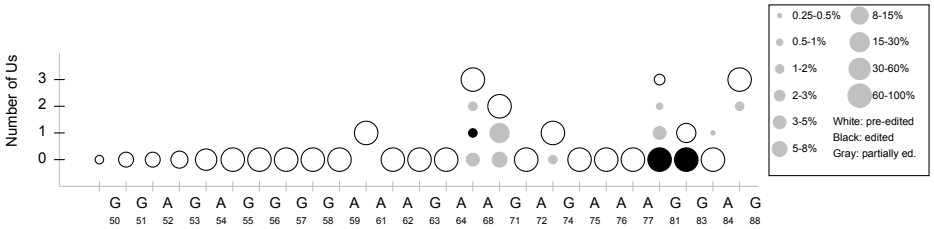
KREN1 only

MURF2



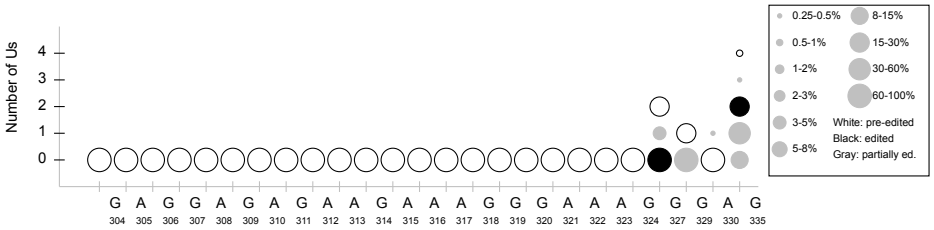
Position in MURF2 mRNA

ND7



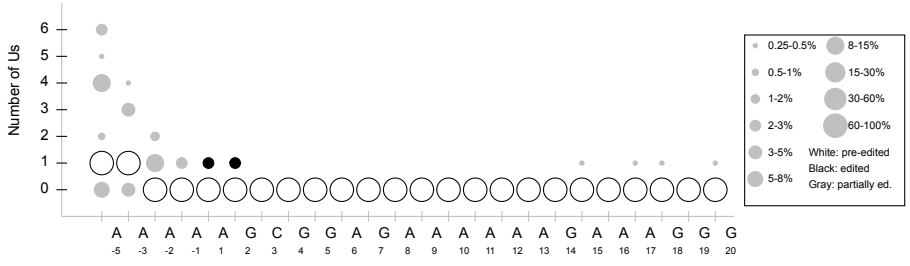
Position in ND7 mRNA

A6



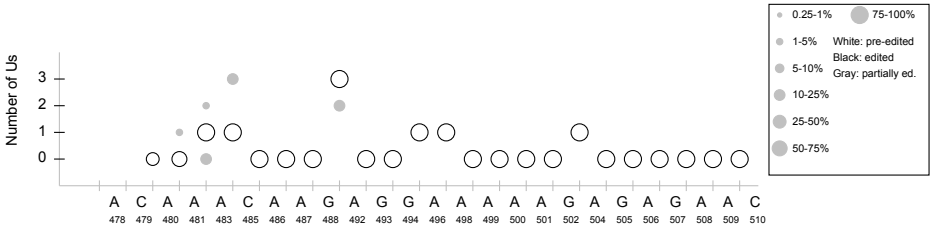
Position in A6 mRNA

CYb



Position in CYb mRNA

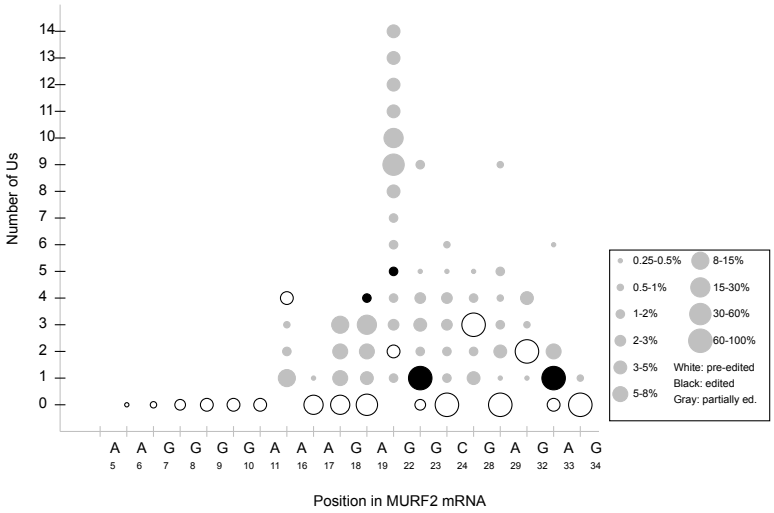
COII



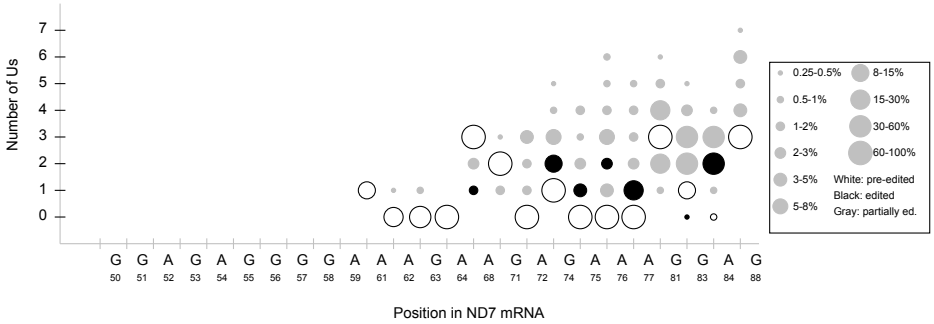
Position in COII mRNA

KREN2 only

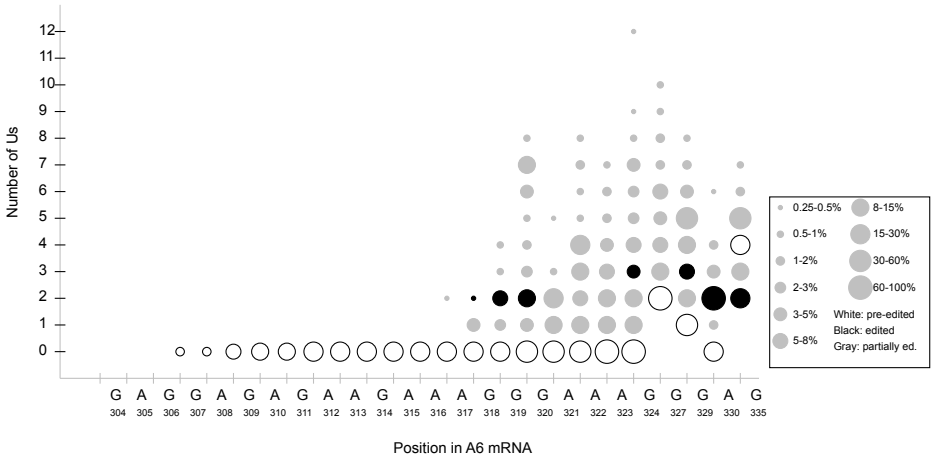
MURF2



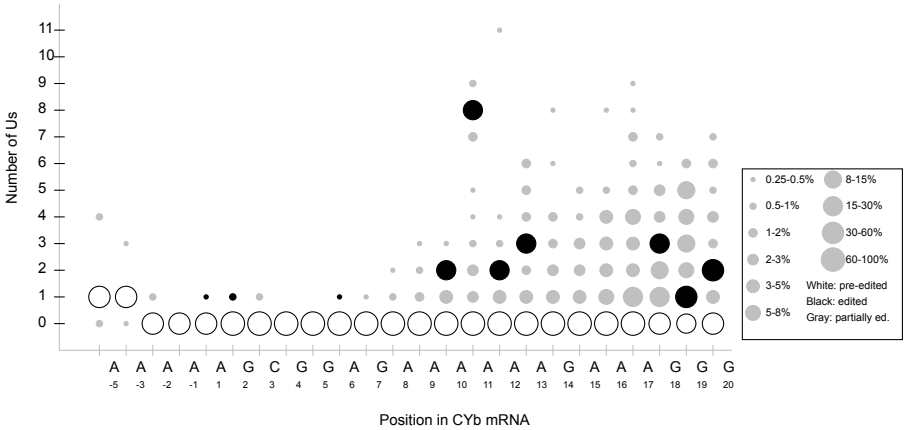
ND7



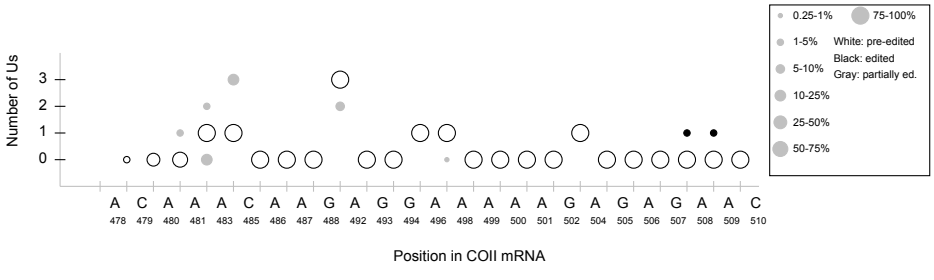
A6



CYb

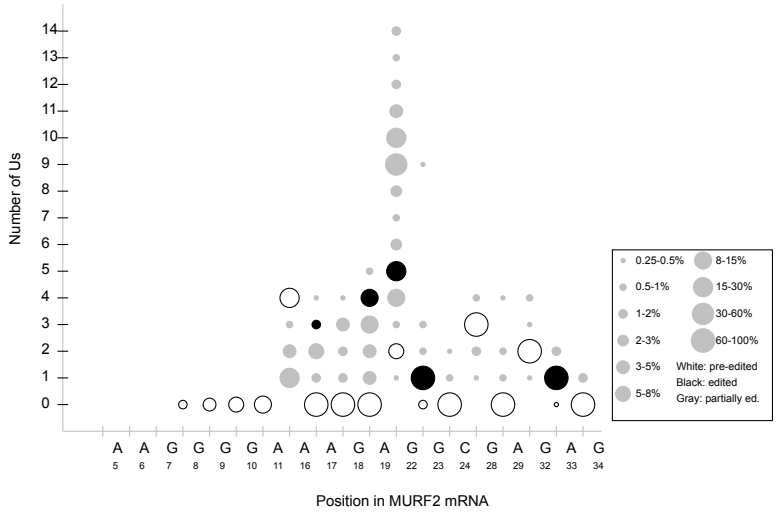


COII

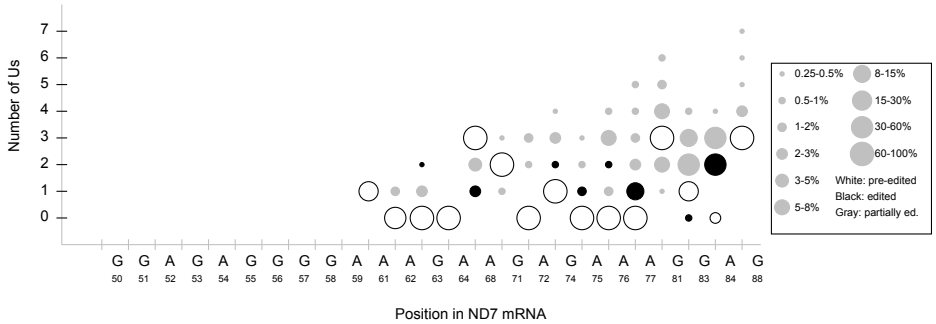


KREN3 only

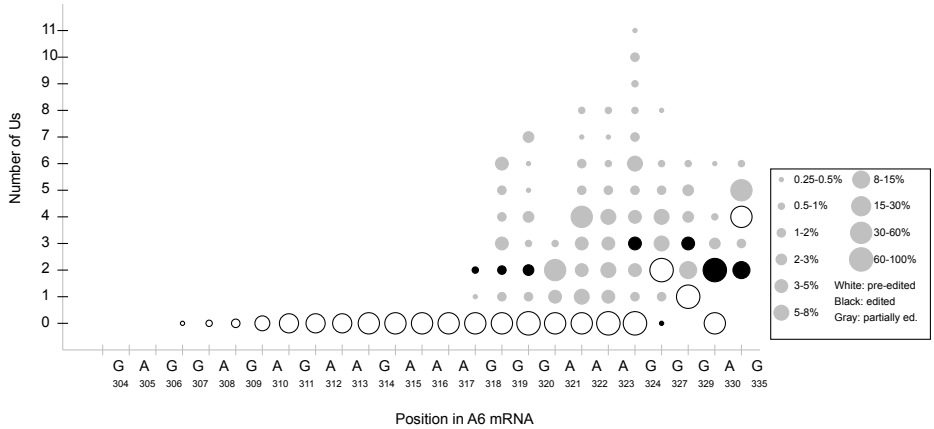
MURF2



ND7



A6



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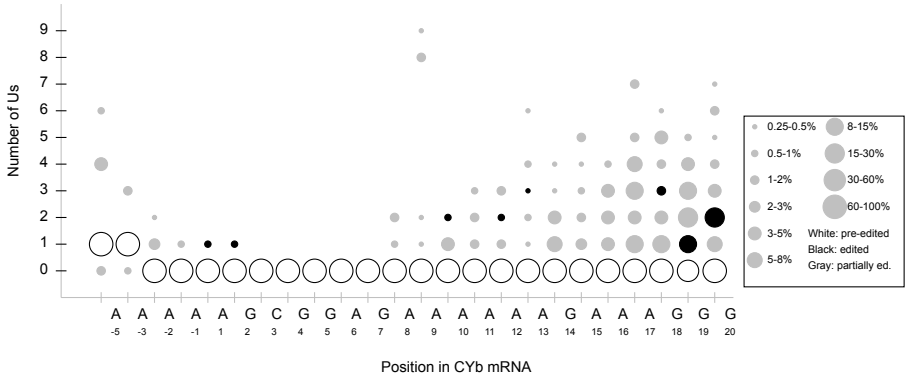

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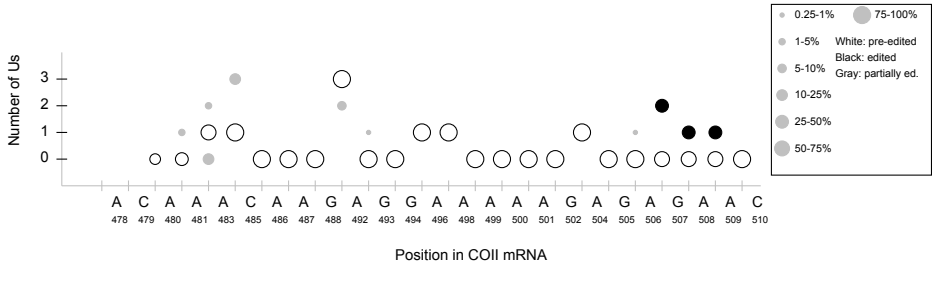
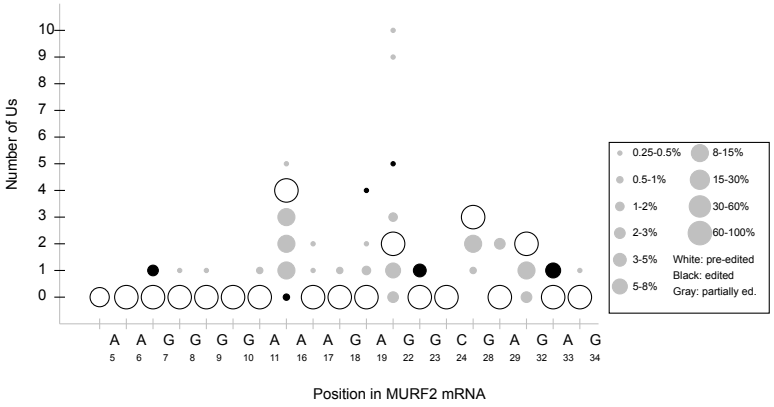


Triple null

MURF2



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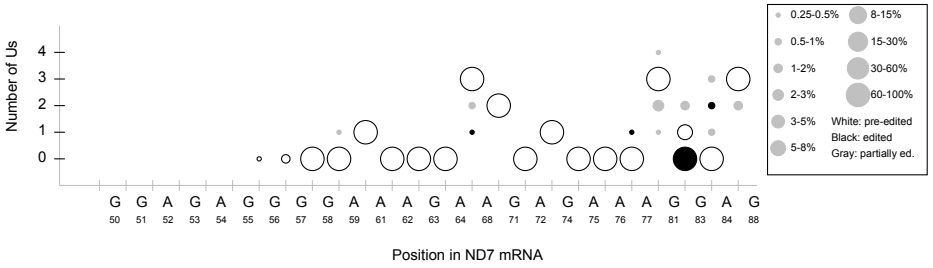

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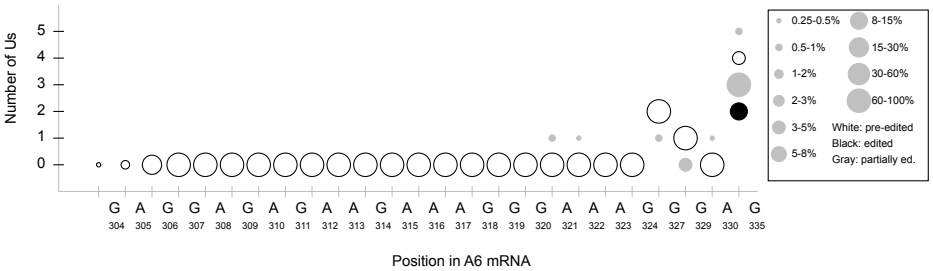

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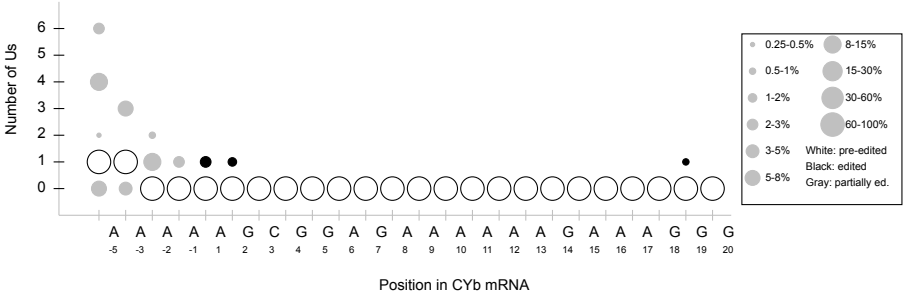

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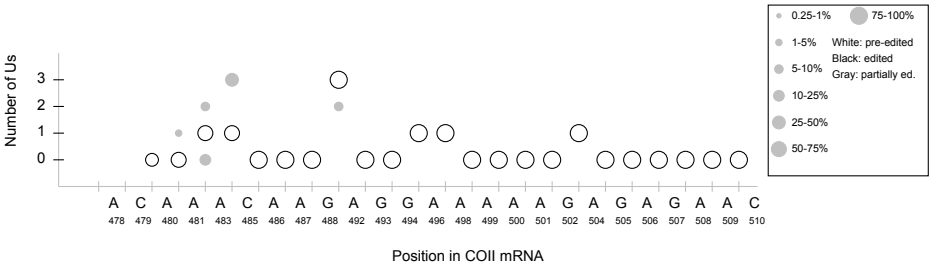

Figure S2. Bubble plot analyses of edited read sequences show the frequency of site-specific insertion and deletion activities. Bubble plots show number of Us inserted at potential editing sites at the 3' end of indicated transcripts for each cell line. In comparison to Figures 7-11, these plots include all of the sites in the dataset, not just the first 10 sites at the 3' end of the sequence. All mapped reads for each transcript are analyzed to determine the amount (number of Us, y-axis) and position (location within 3' end of edited region, x-axis) of editing events within each cell line. The x-axis shows the mRNA position using the non-U nucleotide sequence, with position numbering starting at the first base of the start codon in the pre-edited sequence. When the number of Us at a position matches the pre-edited number of Us, the bubble is white; when the number of Us is altered by editing, the number of Us matching a fully edited mRNA is colored black. When the number of Us at a position matches neither pre-edited nor fully edited sequence, bubbles are colored grey to denote partial editing. The size of the bubble correlates with the proportion of reads that have that number of Us at each position, with the legend giving the percent range for each size bubble. To decrease noise in these plots, data points that represent less than 0.25% of reads or fewer than 5 reads total are not shown.