Is there any sense in antisense editing?

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Table 1. Human mismatch clusters distribution for antisense and non-antisense regions[a]

Cluster type	Mismatch type	Antisense regions		Antisense regions excluding *Alu* repeats		Non-antisense regions		Non-antisense regions excluding *Alu* repeats	
		Number	Percent (%)	Number	Percent (%)	Number	Percent (%)	Number	Percent (%)
Cluster of	A to G	1731	34%	1286	29%	3382	37%	2113	29%
one	G to A	1029	20%	945	21%	1816	20%	1643	23%
mismatch	T to C	1317	25%	1191	27%	2007	22%	1783	24%
	C to T	1076	21%	1002	23%	1980	21%	1751	24%
Cluster of	A to G	100	78%	18	46%	340	75%	56	38%
three	G to A	9	7%	7	18%	37	8%	32	21%
mismatches	T to C	10	8%	8	21%	37	8%	30	20%
	C to T	9	7%	6	15%	39	9%	31	21%
Cluster of	A to G	37	95%	3	60%	135	96%	8	73%
five	G to A	0	0%	0	0%	1	1%	1	9%
mismatches	T to C	2	5%	2	40%	2	1%	1	9%
	C to T	0	0%	0	0%	3	2%	1	9%

[a]The mismatch clusters distributions for RNA sequences that have an antisense counterpart, comparing their antisense region to other parts of the RNA sequence. Antisense sequences show the same mismatch distribution in the antisense regions and in non-antisense regions. Before filtering *Alu* repeat elements, there is a preference for A-to-G mismatches over other common mismatches, whereas after filtering *Alu* repeats the preference is gone.

Table 2. Mismatch clusters in all mouse RNAs and antisense regions[a]

Cluster type	Mismatch type	All RNA (94 858)		Antisense regions only		Antisense regions excluding B1 repeats	
		Number	Percent (%)	Number	Percent (%)	Number	Percent (%)
Cluster of one	A to G	38 910	27%	1030	26%	952	25%
mismatch	G to A	35 876	25%	1045	26%	993	26%
	T to C	31 630	22%	850	21%	811	21%
	C to T	36 750	26%	1106	27%	1038	28%
Cluster of three	A to G	1112	31%	11	20%	4	8%
mismatches	G to A	748	21%	13	22%	11	23%
	T to C	742	20%	10	17%	10	21%
	C to T	1033	28%	24	41%	23	28%
Cluster of five	A to G	181	46%	2	33%	0	0%
mismatches	G to A	64	16%	0	0%	0	0%
	T to C	49	13%	0	0%	0	0%
	C to T	98	25%	4	67%	4	100%

[a]The number of a single or a cluster of consecutive mismatches, for the most common mismatches. Although in all mouse RNAs there is a slight preference for A-to-G mismatches over other mismatches, when focusing on antisense regions there is no preference.