

Table S3. Total fragments and unique sequences in the partially edited RPS12 sequence libraries.

(A) The breakdown of the number of fragments (decollapsed) in each sample (uninduced (-) and induced (+)) for the MRB7260 RNAi deep sequencing samples. Standard alignment (i.e. no non-T insertions, deletions or SNPs) and non-standard (i.e. with non-T errors) with a breakdown of the number of mismatches within the non-standard sequences (1, 2, >3) are shown. (B) The number of unique (collapsed) sequences represented in each category for the data set.

A) RPS12: Fragments

RNAi	Replicate	Induction	Standard Alignments	Non-Standard	1-Mismatch	2-Mismatch	>3-Mismatch	Indels	Total
MRB7260	1	-	1182819 (69.66%)	515286 (30.34%)	50250 (2.96%)	3869 (0.23%)	1053 (0.06%)	460114 (27.10%)	1698105
MRB7260	1	+	1223935 (69.89%)	527413 (30.11%)	56903 (3.25%)	4538 (0.26%)	1334 (0.08%)	464638 (26.53%)	1751348
MRB7260	2	-	897353 (63.69%)	511543 (36.31%)	40147 (2.85%)	2976 (0.21%)	752 (0.05%)	467668 (33.19%)	1408896
MRB7260	2	+	909999 (68.04%)	427483 (31.96%)	40885 (3.06%)	3162 (0.24%)	859 (0.06%)	382577 (28.60%)	1337482
		Total	4214106	1981725	188185	14545	3998	1774997	6195831

B) RPS12: Unique Sequences

RNAi	Replicate	Induction	Standard Alignments	Non-Standard	1-Mismatch	2-Mismatch	>3-Mismatch	Indels	Total
MRB7260	1	-	303704 (41.35%)	430773 (58.65%)	34444 (4.69%)	3687 (0.50%)	1052 (0.14%)	391590 (53.32%)	734477
MRB7260	1	+	232070 (35.09%)	429256 (64.91%)	35499 (5.37%)	4247 (0.64%)	1329 (0.20%)	388181 (58.70%)	661326
MRB7260	2	-	351464 (43.23%)	461588 (56.77%)	33107 (4.07%)	2940 (0.36%)	748 (0.09%)	424793 (52.25%)	813052
MRB7260	2	+	275948 (42.56%)	372399 (57.44%)	31327 (4.85%)	3060 (0.47%)	856 (0.13%)	337156 (52.00%)	648347
		Total	1163186	1694016	134377	13934	3985	1541720	2857202