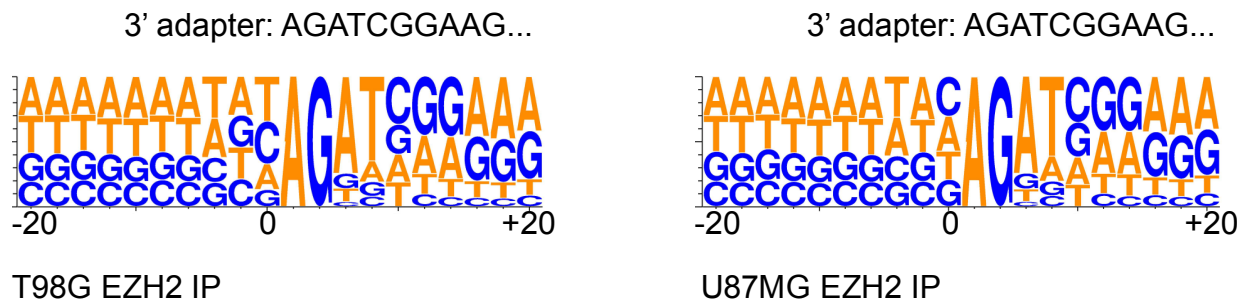
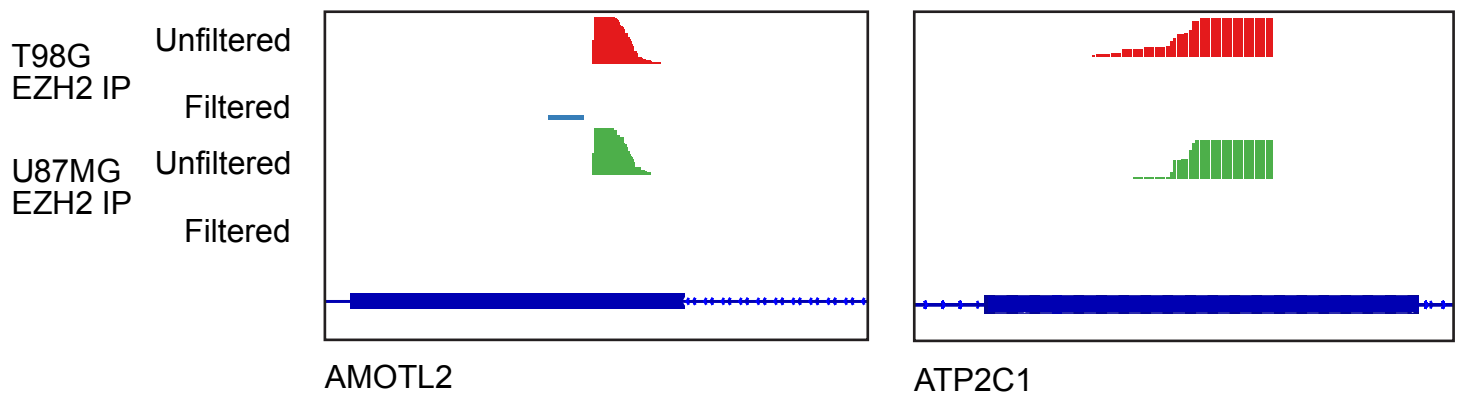


Figure S2

A



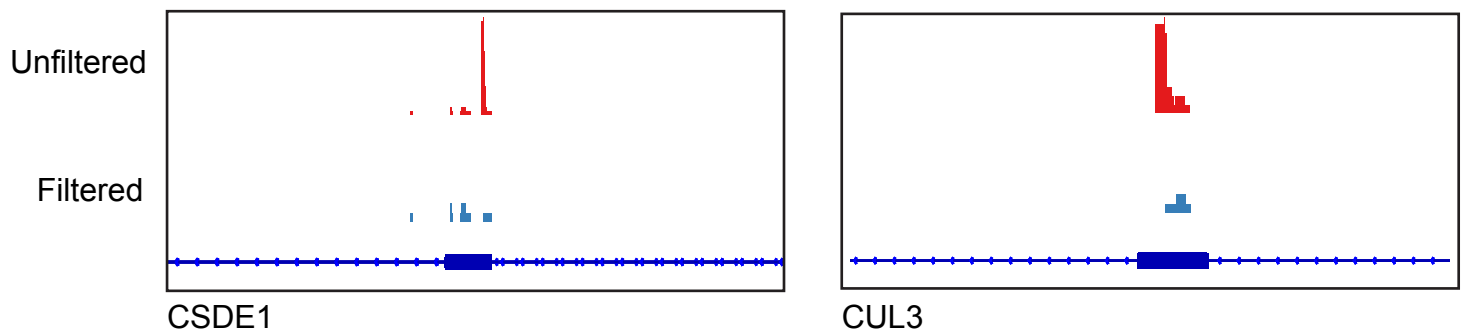
B



C



SRR1995349



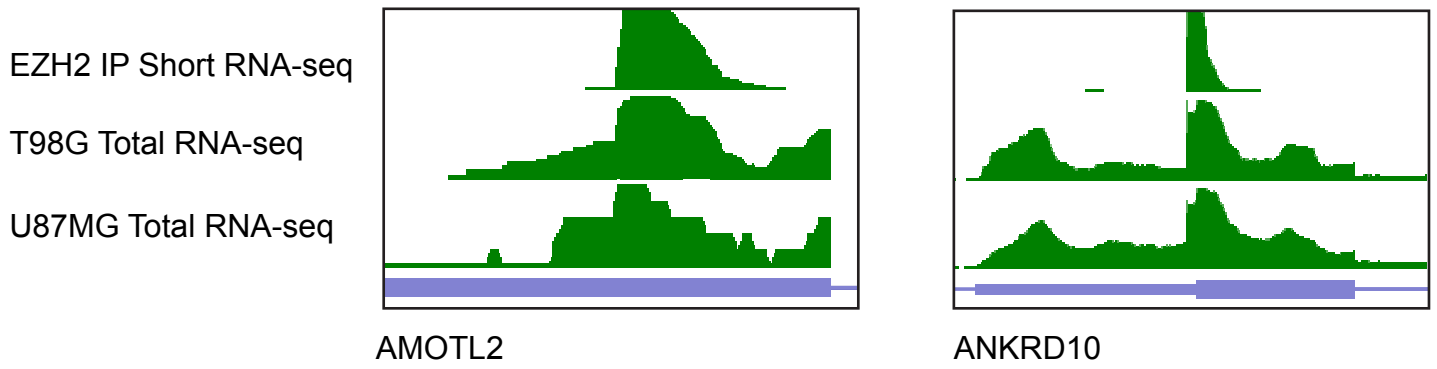
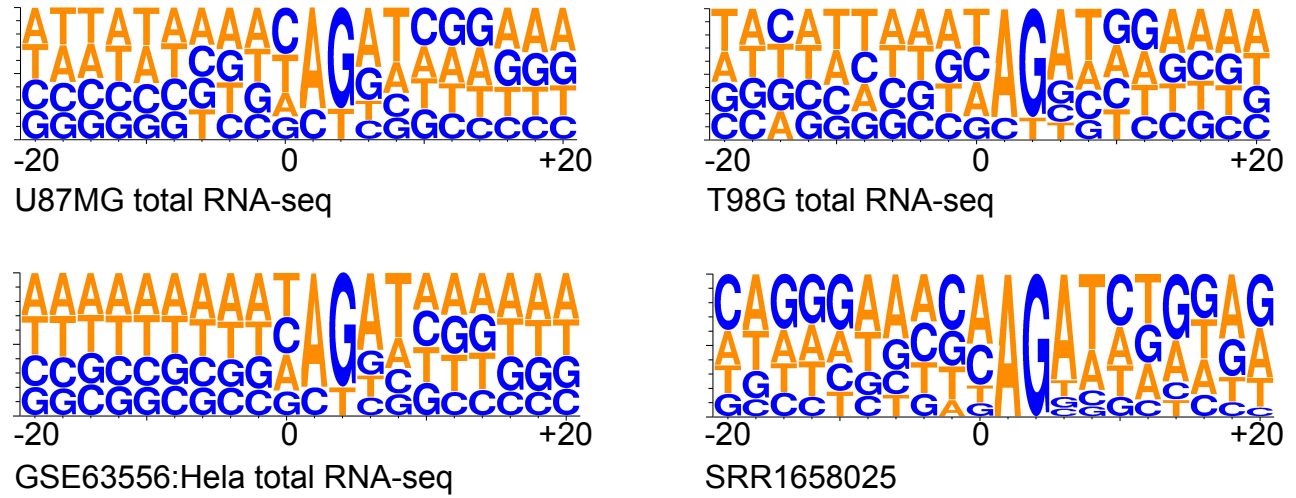
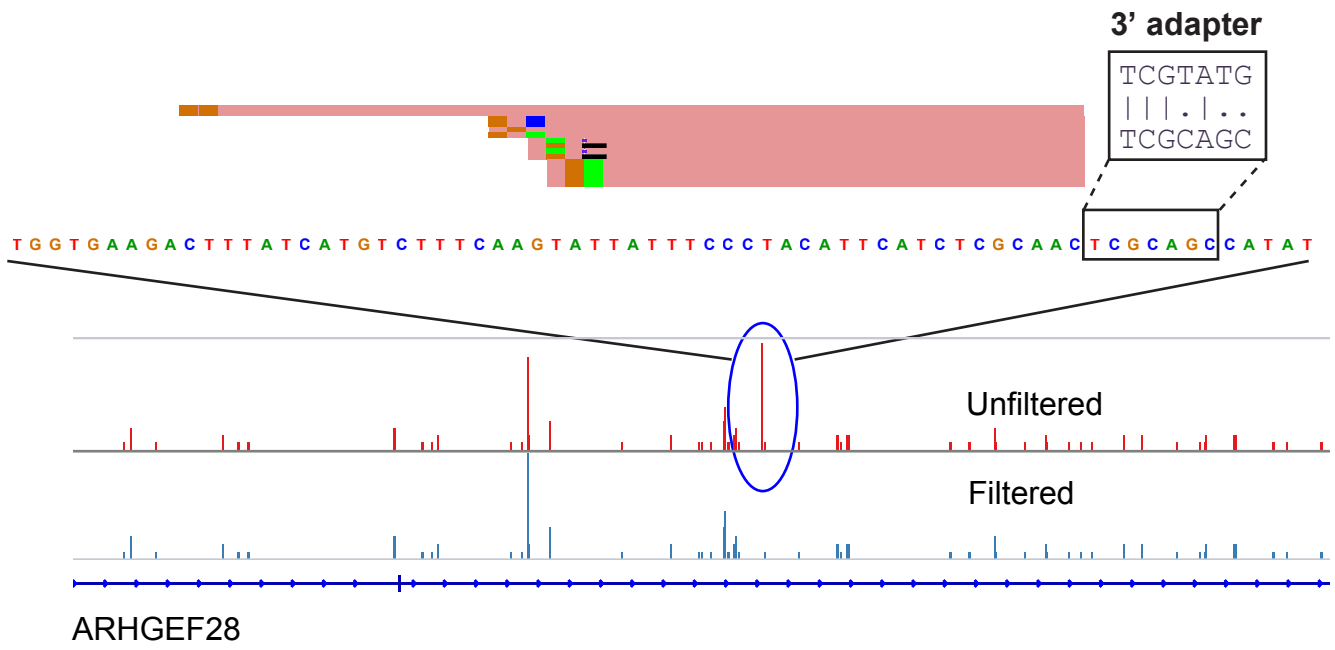
A**B**

Figure S4

A



B

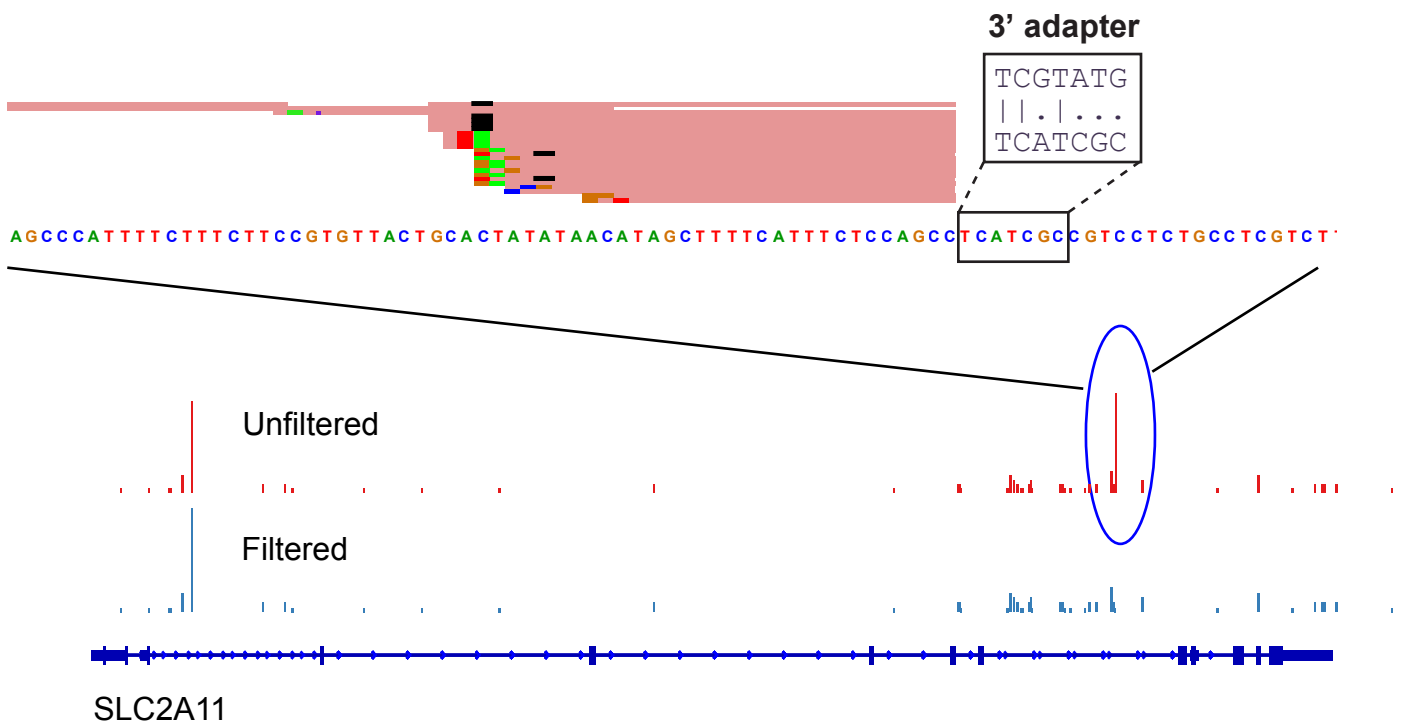
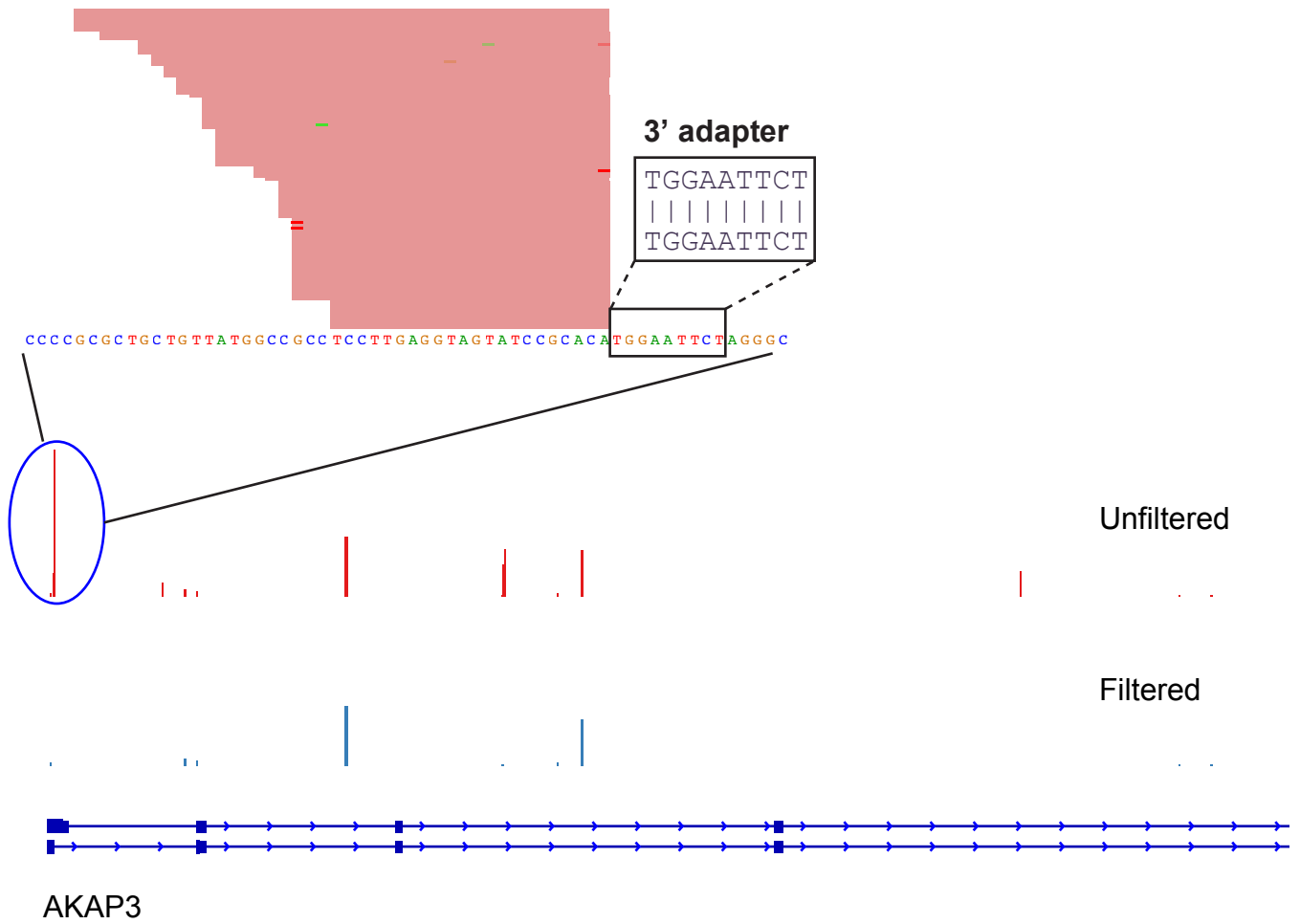
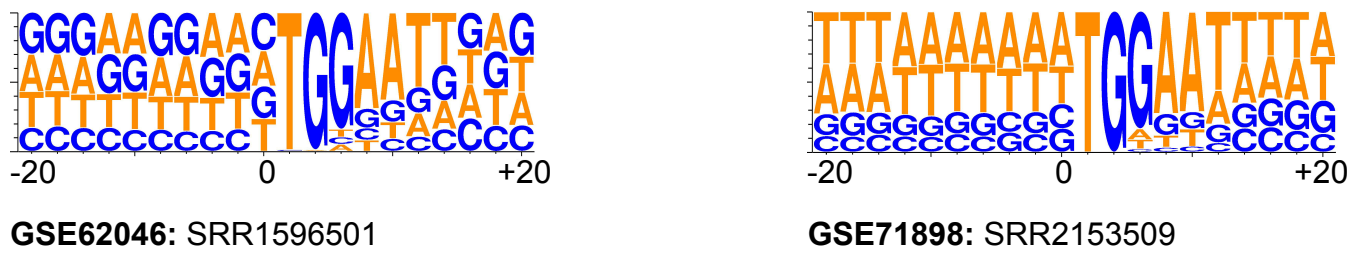


Figure S5

A



B



Supplementary Table 1: RT mispriming events identified by our pipeline in published datasets.

Study	Accession	Technique	Number of mispriming sites	Number of misprimed reads	Percent of reads misprimed
GSE68254	SRR1995349	Short RNA-seq	2773	75105	0.587
GSE63556	SRR1660042	RNA-seq	4004	55688	0.082
GSE63556	SRR1660043-45	RNA-seq	3858	44165	0.073
GSE63496	SRR1658024	RNA-seq	122	3145	0.020
GSE63496	SRR1658025	RNA-seq	136	3601	0.020
GSE62047	SRR1596500	GRO-seq	10496	236794	0.849
GSE62047	SRR1596501	GRO-seq	2926	44319	0.141
GSE71901	SRR2153508	GRO-seq	104293	4720754	5.098
GSE71901	SRR2153509	GRO-seq	109035	4866057	5.608
GSE71901	SRR2153510	GRO-seq	40897	4175377	4.167
GSE41357	SRR580356	HITS-CLIP	4305	514864	3.285
GSE41357	SRR580357	HITS-CLIP	2239	366095	2.898
GSE42701	SRR628446	HITS-CLIP	3241	69343	0.802

Supplementary Table 2: RT mispriming events identified by our pipeline in mRNA-seq and short RNA-seq datasets we generated.

Sample	Technique	Number of mispriming sites	Number of misprimed reads	Percent of reads misprimed
T98G EZH2 IP BR1	Short RNA-seq	36558	1531591	44.070
T98G EZH2 IP BR2	Short RNA-seq	37203	1704240	28.926
T98G IgG IP BR1	Short RNA-seq	10439	227480	2.766
T98G IgG IP BR2	Short RNA-seq	12968	302368	3.808
T98G Input BR1	Short RNA-seq	1318	32800	0.267
T98G Input BR2	Short RNA-seq	3009	91975	0.514
U87MG EZH2 IP BR1	Short RNA-seq	1878	49135	4.870
U87MG EZH2 IP BR2	Short RNA-seq	46293	2380088	54.748
U87MG IgG IP BR1	Short RNA-seq	591	11015	1.040
U87MG IgG IP BR2	Short RNA-seq	19981	535942	8.182
U87MG Input BR1	Short RNA-seq	67	1770	0.069
U87MG Input BR2	Short RNA-seq	1920	57762	0.593
U87MG Total RNA-seq BR1	RNA-seq	2890	37395	0.066
U87MG Total RNA-seq BR2	RNA-seq	3638	45185	0.064