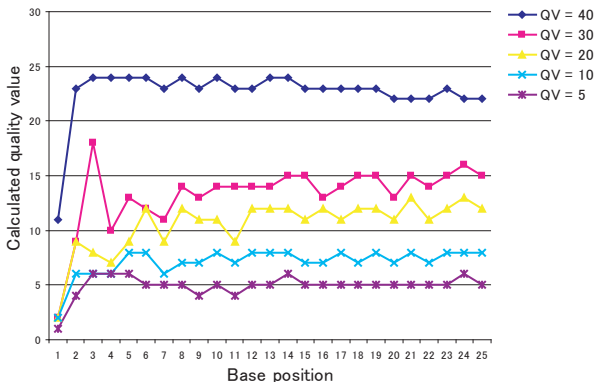
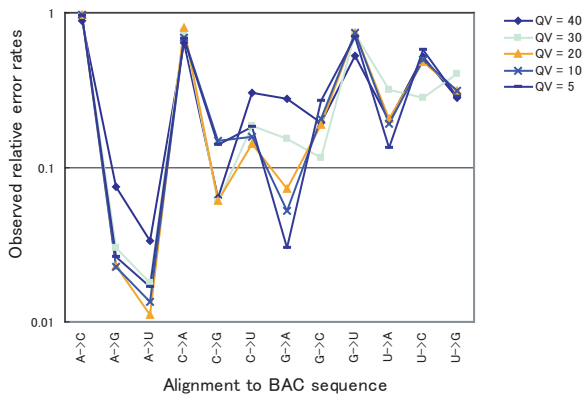




Supplementary Figure 1. Position-specific dependence of actual Illumina base-calling accuracy for the small RNAs sample.



Supplementary Figure 2. Relative error rates of error patterns normalized to the total number of error patterns. The horizontal axis shows observed error patterns, e.g., “A→C” indicates a cytosine substitution for adenine in the observed BAC reads, and its rate is normalized by the total number of “A→C,” “A→G” and “A→T” substitutions.

Table S1. Quality values at individual positions calculated from observed data. Because QVs after the 26th base were not collected, the median value of 15th~25th bases was used instead as the observed QV.

A. Small RNAs from HT-29

Calculated QV Illumina QV	1st base	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26~
40	11	23	24	24	24	24	23	24	23	24	23	23	24	24	23	23	23	23	23	22	22	22	23	22	22	23
39	3	11	12	11	14	14	13	15	14	16	14	16	15	16	16	17	16	17	19	16	17	16	17	17	18	17
38	2	11	12	12	16	15	14	14	13	15	14	14	17	16	15	16	16	16	16	16	17	15	18	18	16	16
37	3	10	11	11	12	14	13	13	14	16	14	16	15	16	14	15	16	15	17	16	17	15	17	17	16	16
36	2	10	12	13	14	13	14	14	14	17	14	15	17	16	17	15	15	16	16	15	15	15	17	17	16	16
35	3	11	11	13	15	13	14	16	15	16	14	16	15	14	15	16	16	15	16	15	16	15	16	17	16	16
34	3	10	11	10	14	14	13	16	13	14	14	16	15	16	15	15	16	15	16	15	16	15	17	16	16	16
33	4	11	10	10	13	14	13	14	12	16	13	15	14	16	15	14	16	15	15	15	14	16	17	16	15	15
32	3	11	14	10	11	14	14	14	12	15	13	14	16	15	14	15	14	15	16	15	17	15	17	16	17	15
31	2	10	10	10	14	14	14	14	14	14	13	14	15	17	16	14	14	16	14	16	14	16	16	15	15	15
30	2	9	18	10	13	12	11	14	13	14	14	14	14	15	15	13	14	15	15	13	15	14	15	16	15	15
29	3	9	11	9	12	13	12	13	12	12	12	14	14	14	14	13	14	14	16	13	16	14	14	15	15	14
28	2	11	10	12	11	11	12	12	12	14	12	14	14	15	14	13	13	15	14	14	14	15	13	15	15	14
27	3	9	10	9	10	11	11	12	12	12	12	13	15	14	15	13	13	14	14	13	14	13	15	15	14	14
26	3	11	10	11	10	11	10	12	12	13	12	13	14	14	14	13	13	13	14	13	14	13	14	14	14	14
25	3	9	10	8	11	13	11	13	11	13	11	12	14	15	13	13	13	13	15	12	14	12	13	14	14	13
24	3	8	10	9	12	13	11	12	12	12	10	13	13	13	12	13	12	13	14	12	13	12	14	14	14	13
23	3	8	9	8	10	12	11	12	11	12	11	12	13	13	12	13	12	13	13	12	13	12	13	13	13	13
22	2	8	9	9	11	11	9	13	11	12	11	12	13	13	13	11	11	12	13	11	13	12	13	13	13	13
21	2	8	10	10	11	11	11	10	12	10	11	12	13	12	12	11	12	12	11	12	11	12	13	13	12	12
20	2	9	8	7	9	12	9	12	11	11	9	12	12	12	11	12	11	12	12	11	13	11	12	13	12	12
19	2	8	9	8	10	11	10	11	10	11	10	11	11	12	12	11	11	11	12	10	12	11	12	12	11	11
18	2	9	9	9	10	9	10	10	10	9	10	9	11	10	12	11	11	10	11	12	10	11	12	12	11	11
17	2	8	8	8	10	10	9	10	10	10	9	11	10	11	11	10	10	11	11	10	11	10	11	12	11	11
16	2	9	9	9	8	10	10	11	9	10	9	10	10	10	11	10	10	11	11	10	10	11	11	11	11	11
15	2	7	7	8	8	10	8	9	8	9	9	10	9	10	10	10	10	10	10	9	10	10	10	10	10	10
14	2	8	9	8	8	9	10	8	8	9	9	10	9	9	9	9	10	9	10	9	10	9	10	10	9	9
13	2	8	7	6	7	7	7	9	8	9	8	9	9	10	9	9	9	9	9	9	10	9	9	10	9	9
12	2	6	8	7	7	9	8	8	8	8	8	8	9	8	9	8	8	8	9	8	9	8	9	10	9	9
11	2	6	8	5	7	8	8	8	8	8	8	7	8	8	9	8	8	8	8	8	8	8	9	9	8	8
10	2	6	6	6	8	8	6	7	7	8	7	8	8	8	7	7	8	7	8	7	8	7	8	8	8	8
9	1	5	6	6	7	8	7	7	7	7	6	7	7	8	7	7	7	8	8	7	8	7	8	7	7	7
8	2	7	6	5	6	8	7	7	6	7	6	7	7	7	7	7	6	7	7	6	7	6	7	7	7	7
7	2	6	7	5	7	6	7	6	6	7	6	7	6	6	6	6	6	6	6	7	6	6	6	7	6	6
6	1	5	6	6	7	6	6	6	5	5	6	6	6	6	6	6	6	6	6	5	6	5	6	6	6	6
5	1	4	6	6	6	5	5	5	4	5	4	5	5	6	5	5	5	5	5	5	5	5	5	6	5	5
4	1	4	7	5	5	6	4	5	4	5	4	5	4	5	4	5	4	5	4	5	5	4	5	5	5	5
3	1	5	4	4	6	5	4	4	4	4	3	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4
2	2	6	4	4	4	4	4	4	3	4	4	3	4	4	3	3	3	4	3	4	3	4	4	4	4	4
1	1	2	4	4	4	4	4	4	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
0	1	4	3	4	3	3	3	3	2	3	3	3	2	3	3	2	2	3	2	3	2	2	3	3	3	2
minus	0	4	5	0	0	2	1	0	1	1	2	2	3	2	2	2	2	2	2	2	1	2	1	1	2	1

B. 5'-end SAGE from *dmel*

Calculated Illumina QV	1st base	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26~
40	10	23	24	23	23	23	23	23	23	23	22	22	22	21	22	21	21	21	21	21	21	21	20	19	21	
39	3	8	10	11	10	10	12	12	12	11	12	12	11	13	11	12	11	12	12	12	12	12	13	12	12	12
38	2	11	11	11	9	12	10	10	12	12	12	12	11	12	12	11	11	12	12	11	12	11	11	12	12	12
37	2	9	10	10	10	11	14	11	12	11	13	12	11	12	12	11	11	11	12	12	12	11	12	11	11	11
36	2	7	8	10	9	11	11	10	12	11	12	11	11	12	11	12	11	12	12	12	11	12	12	11	11	12
35	3	9	10	10	10	12	11	12	11	11	12	13	11	12	12	12	10	11	11	11	11	12	11	12	11	11
34	2	9	9	11	9	10	9	10	11	10	12	11	12	12	11	12	11	11	11	11	11	11	12	11	11	11
33	3	9	13	8	9	10	10	11	12	10	11	10	11	11	11	10	11	11	10	11	11	11	12	11	11	11
32	3	9	11	12	9	10	10	11	13	11	11	12	11	11	11	12	11	12	11	11	11	11	12	11	10	11
31	2	8	10	10	8	11	9	8	11	11	11	11	11	11	10	11	11	11	11	11	11	11	10	11	11	11
30	2	9	9	9	10	10	9	11	10	12	11	11	12	11	11	11	11	11	11	11	10	10	10	11	11	11
29	2	11	8	7	11	11	9	10	10	9	10	12	10	9	10	10	10	11	9	11	10	10	11	11	10	10
28	3	9	9	8	11	10	9	11	10	9	11	11	10	10	10	11	11	10	11	11	10	10	10	10	10	10
27	2	8	11	8	9	9	9	8	10	11	11	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
26	2	10	9	11	9	8	9	9	11	11	11	10	10	10	9	10	10	10	10	10	10	10	10	10	10	10
25	2	7	9	8	10	9	9	9	9	10	10	10	10	11	10	10	9	10	10	9	9	10	10	9	10	10
24	2	8	7	8	8	9	10	10	12	10	10	10	10	11	9	10	9	9	10	10	9	9	10	10	9	9
23	2	8	8	8	8	9	9	9	10	9	11	10	10	10	10	10	8	9	9	10	9	9	9	10	9	9
22	2	7	8	9	9	9	8	9	8	10	11	10	10	9	9	9	10	9	9	9	9	9	9	10	9	9
21	2	6	9	7	9	10	9	9	10	10	9	9	9	9	10	10	9	9	9	9	9	9	9	9	9	9
20	2	7	8	7	8	8	11	9	8	10	10	9	9	9	8	9	8	9	9	9	9	9	9	9	9	9
19	2	7	9	8	6	8	9	9	8	10	10	9	9	8	9	8	9	8	9	8	9	9	9	8	8	9
18	2	6	6	7	7	8	8	8	8	10	9	8	8	10	8	9	8	8	9	8	8	8	8	8	8	8
17	2	6	8	7	7	8	8	8	9	9	8	9	8	9	9	8	8	8	8	8	8	8	8	8	8	8
16	1	7	8	7	7	8	8	8	9	8	9	9	8	8	8	8	7	8	8	8	8	8	8	8	7	8
15	2	7	8	8	7	7	8	8	8	8	8	8	8	8	7	8	8	8	8	7	7	7	7	7	7	7
14	2	7	7	5	6	7	8	8	8	8	8	8	8	8	7	7	7	8	7	8	7	7	7	7	7	7
13	1	5	7	7	6	7	7	7	7	7	7	7	7	8	8	7	7	7	7	7	7	7	7	7	7	7
12	1	7	6	6	6	8	7	7	7	7	8	8	7	7	7	7	7	7	7	7	6	7	7	7	7	7
11	1	5	6	5	6	6	7	7	7	6	7	8	7	7	6	6	6	6	6	6	6	6	6	6	6	6
10	1	5	5	5	5	7	6	6	8	7	7	5	7	6	6	6	6	6	6	6	6	6	6	6	6	6
9	1	5	7	5	4	7	6	6	7	6	6	7	6	7	6	5	6	6	6	6	6	6	6	6	6	6
8	1	5	4	5	4	6	6	6	6	5	7	6	6	6	6	5	5	5	6	5	5	5	5	5	5	5
7	2	4	5	5	5	4	5	5	5	6	5	5	6	5	5	5	5	5	5	5	5	5	5	5	5	5
6	1	4	3	4	4	5	5	5	5	5	5	5	5	4	4	4	4	5	5	4	4	4	4	4	4	4
5	1	4	4	4	4	4	5	4	4	4	5	4	4	5	4	4	4	4	4	4	3	4	4	4	4	4
4	1	2	5	4	3	4	4	4	5	4	4	4	4	4	3	4	3	4	3	3	3	3	3	3	3	3
3	1	3	2	3	3	4	3	4	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
2	1	3	3	2	3	3	3	3	3	4	2	3	3	3	2	3	2	3	2	3	2	3	2	3	2	3
1	1	2	2	3	3	3	3	2	3	3	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
0	0	3	3	3	3	3	2	2	3	4	2	1	3	2	2	2	2	1	2	2	2	1	2	2	2	2
minus	-1	0	1	1	3	2	1	3	3	3	2	2	3	2	3	2	2	3	2	2	1	2	2	2	2	2

Table S2. Substitution patterns according to quality value. Observed numbers of bases are shown in the table.
A. Small RNAs from HT-29

Basepair Substitution		40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	0-mism			
A-A	2313190	14878	15000	15288	15829	15877	16367	16844	17187	17619	18233	18268	18811	19281	19713	20444	21175	21732	22365	22971	23487	24218	25018	25827	26828	27904	29042	30243	31497	32798	34133	35493	36948	38448	39948	41448	42948	44448	45948	47448	48948	50448			
A-C	35046	746	808	874	930	980	1034	1092	1150	1208	1274	1345	1392	1465	1522	1600	1716	1812	1914	2044	2212	2461	2806	3247	3844	4544	5344	6244	7244	8344	9544	10844	12244	13844	15544	17444	19444	21444	23444	25444	27444	29444	31444		
A-G	1779	17	20	18	18	12	12	23	17	21	18	26	18	27	28	30	26	25	31	48	37	34	42	44	55	61	64	80	90	114	132	148	174	213	234	269	275	304	308	348	368	398	438		
A-U	3735389	886	881	881	880	880	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	878	
C-A	1429	8	6	7	9	8	12	12	12	8	11	9	8	10	16	17	17	18	16	16	11	23	13	28	34	30	38	21	34	44	52	42	35	64	58	50	80	67	118	90	132	153	182	184	510
C-C	2525	17	23	20	18	26	27	21	19	20	27	32	24	32	24	42	29	25	37	31	27	42	24	42	24	42	35	42	41	57	64	58	50	80	67	118	90	132	153	182	184	510			
C-G	20108	9794	9607	9624	9631	9680	10243	10259	10264	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490		
C-U	2298	23	13	16	22	31	18	23	25	22	19	21	34	39	33	41	50	50	47	63	67	71	88	100	107	127	119	133	162	208	245	302	355	382	520	621	709	875	954	1061	629	342			
G-A	20718	9794	9607	9624	9631	9680	10243	10259	10264	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	
G-C	2298	23	13	16	22	31	18	23	25	22	19	21	34	39	33	41	50	50	47	63	67	71	88	100	107	127	119	133	162	208	245	302	355	382	520	621	709	875	954	1061	629	342			
G-G	20108	9794	9607	9624	9631	9680	10243	10259	10264	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	10490	
G-U	2109	17	24	23	28	18	23	19	31	32	19	31	32	24	27	38	32	23	47	38	37	42	41	39	64	45	48	55	63	65	77	78	133	123	102	88	117	122	127	144	181	189	209	100	558
U-A	401628	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392
U-C	5212	37	30	29	30	29	30	39	32	41	31	42	47	43	47	53	64	50	70	61	60	76	94	107	115	120	142	174	200	256	244	251	353	372	461	546	637	751	919	1017	948	1201	1		
U-G	401628	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392	392

B. 5'-end SAGE from deml

Basepair Substitution		40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	0-mism																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
A-A	455804	12095	11900	12444	12550	12735	12701	13248	12898	12797	12871	12891	12899	13149	13138	13517	13289	13719	13798	13913	13992	14459	14843	15294	15844	16459	16944	17459	17944	18459	18944	19459	19944	20459	20944	21459	21944	22459	22944	23459	23944	24459	24944	25459	25944	26459	26944	27459	27944	28459	28944	29459	29944	30459	30944	31459	31944	32459	32944	33459	33944	34459	34944	35459	35944	36459	36944	37459	37944	38459	38944	39459	39944	40459	40944	41459	41944	42459	42944	43459	43944	44459	44944	45459	45944	46459	46944	47459	47944	48459	48944	49459	49944	50459	50944	51459	51944	52459	52944	53459	53944	54459	54944	55459	55944	56459	56944	57459	57944	58459	58944	59459	59944	60459	60944	61459	61944	62459	62944	63459	63944	64459	64944	65459	65944	66459	66944	67459	67944	68459	68944	69459	69944	70459	70944	71459	71944	72459	72944	73459	73944	74459	74944	75459	75944	76459	76944	77459	77944	78459	78944	79459	79944	80459	80944	81459	81944	82459	82944	83459	83944	84459	84944	85459	85944	86459	86944	87459	87944	88459	88944	89459	89944	90459	90944	91459	91944	92459	92944	93459	93944	94459	94944	95459	95944	96459	96944	97459	97944	98459	98944	99459	99944	100459	100944	101459	101944	102459	102944	103459	103944	104459	104944	105459	105944	106459	106944	107459	107944	108459	108944	109459	109944	110459	110944	111459	111944	112459	112944	113459	113944	114459	114944	115459	115944	116459	116944	117459	117944	118459	118944	119459	119944	120459	120944	121459	121944	122459	122944	123459	123944	124459	124944	125459	125944	126459	126944	127459	127944	128459	128944	129459	129944	130459	130944	131459	131944	132459	132944	133459	133944	134459	134944	135459	135944	136459	136944	137459	137944	138459	138944	139459	139944	140459	140944	141459	141944	142459	142944	143459	143944	144459	144944	145459	145944	146459	146944	147459	147944	148459	148944	149459	149944	150459	150944	151459	151944	152459	152944	153459	153944	154459	154944	155459	155944	156459	156944	157459	157944	158459	158944	159459	159944	160459	160944	161459	161944	162459	162944	163459	163944	164459	164944	165459	165944	166459	166944	167459	167944	168459	168944	169459	169944	170459	170944	171459	171944	172459	172944	173459	173944	174459	174944	175459	175944	176459	176944	177459	177944	178459	178944	179459	179944	180459	180944	181459	181944	182459	182944	183459	183944	184459	184944	185459	185944	186459	186944	187459	187944	188459	188944	189459	189944	190459	190944	191459	191944	192459	192944	193459	193944	194459	194944	195459	195944	196459	196944	197459	197944	198459	198944	199459	199944	200459	200944	201459	201944	202459	202944	203459	203944	204459	204944	205459	205944	206459	206944	207459	207944	208459	208944	209459	209944	210459	210944	211459	211944	212459	212944	213459	213944	214459	214944	215459	215944	216459	216944	217459	217944	218459	218944	219459	219944	220459	220944	221459	221944	222459	222944	223459	223944	224459	224944	225459	225944	226459	226944	227459	227944	228459	228944	229459	229944	230459	230944	231459	231944	232459	232944	233459	233944	234459	234944	235459	235944	236459	236944	237459	237944	238459	238944	239459	239944	240459	240944	241459	241944	242459	242944	243459	243944	244459	244944	245459	245944	246459	246944	247459	247944	248459	248944	249459	249944	250459	250944	251459	251944	252459	252944	253459	253944	254459	254944	255459	255944	256459	256944	257459	257944	258459	258944	259459	259944	260459	260944	261459	261944	262459	262944	263459	263944	264459	264944	265459	265944	266459	266944	267459	267944	268459	268944	269459	269944	270459	270944	271459	271944	272459	272944	273459	273944	274459	274944	275459	275944	276459	276944	277459	277944	278459	278944	279459	279944	280459	280944	281459	281944	282459	282944

Table S3. Substitution rates according to quality value. Observed relative error rates are shown in the table

A. Small RNAs from HT-29

Year	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2433	2434	2435	2436	2437	2438	2439	2440	2441	2442	2443	2444	2445	2446	2447	2448	2449	2450	2451	2452	2453	2454	2455	2456	2457	2458	2459	2460	2461	2462	2463	2464	2465	2466	2467	2468	2469	2470	2471	2472	2473	2474	2475	2476	2477	2478	2479	2480	2481	2482	2483	2484	2485	2486	2487	2488	2489	2490	2491	2492	2493	2494	2495	2496	2497	2498	2499	2500	2501	2502	2503	2504	2505	2506	2507	2508	2509	2510	2511	2512	2513	2514	2515	2516	2517	2518	2519	2520	2521	2522	2523	2524	2525	2526	2527	2528	2529	2530	2531	2532	2533	2534	2535	2536	2537	2538	2539	2540	2541	2542	2543	2544	2545	2546	2547	2548	2549	2550	2551	2552	2553	2554	2555	2556	2557	2558	2559	2560	2561	2562	2563	2564	2565	2566	2567	2568	2569	2570	2571	2572	2573	2574	2575	2576	2577	2578	2579	2580	2581	2582	2583	2584	2585	2586	2587	2588	2589	2590	2591	2592	2593	2594	2595	2596	2597	2598	2599	2600	2601	2602	2603	2604	2605	2606	2607	2608	2609	2610	2611	2612	2613	2614	2615	2616	2617	2618	2619	2620	2621	2622	2623	2624	2625	2626	2627	2628	2629	2630	2631	2632	2633	2634	2635	2636	2637	2638	2639	2640	2641	2642	2643	2644	2645	2646	2647	2648	2649	2650	2651	2652	2653	2654	2655	2656	2657	2658	2659	2660	2661	2662	2663	2664	2665	2666	2667	2668	2669	2670	2671	2672	2673	2674	2675	2676	2677	2678	2679	2680	2681	2682	2683	2684	2685	2686	2687	2688	2689	2690	2691	2692	2693	2694	2695	2696	2697	2698	2699	2700	2701	2702	2703	2704	2705	2706	2707	2708	2709	2710	2711	2712	2713	2714	2715	2716	2717	2718	2719	2720	2721	2722	2723	2724	2725	2726	2727	2728	2729	2730	2731	2732	2733	2734	2735	2736	2737	2738	2739	2740	2741	2742	2743	2744	2745	2746	2747	2748	2749	2750	2751	2752	2753	2754	2755	2756	2757	2758	2759	2760	2761	2762	2763	2764	2765	2766	2767	2768	2769	2770	2771	2772	2773	2774	2775	2776	2777	2778	2779	2780	2781	2782	2783	2784	2785	2786	2787	2788	2789	2790	2791	2792	2793	2794	2795	2796	2797	2798	2799	2800	2801	2802	2803	2804	2805	2806	2807	2808	2809	2810	2811	2812	2813	2814	2815	2816	2817	2818	2819	2820	2821	2822	2823	2824	2825	2826	2827	2828	2829	2830	2831	2832	2833	2834	2835	2836	2837	2838	2839	2840	2841	2842	2843	2844	2845	2846	2847	2848	2849	2850	2851	2852	2853	2854	2855	2856	2857	2858	2859	2860	2861	2862	2863	2864	2865	2866	2867	2868	2869	2870	2871	2872	2873	2874	2875	2876	2877	2878	2879	2880	2881	2882	2883	2884	2885	2886	2887	2888	2889	2890	2891	2892	2893	2894	2895	2896	2897	2898	2899	2900	2901	2902	2903	2904	2905	2906	2907	2908	2909	2910	2911	2912	2913	2914	2915	2916	2917	2918	2919	2920	2921	2922	2923	2924	2925	2926	2927	2928	2929	2930	2931	2932	2933	2934	2935	2936	2937	2938	2939	2940	2941	2942	2943	2944	2945	2946	2947	2948	2949	2950	2951	2952	2953	2954	2955	2956	2957	2958	2959	2960	2961	2962	2963	2964	2965	2966	2967	2968	2969	2970	2971	2972	2973	2974	2975	2976	2977	2978	2979	2980	2981	2982	2983	2984	2985	2986	2987	2988	2989	2990	2991	2992	2993	2994	2995	2996	2997	2998	2999	3000
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B. 5'-end SAGE from *dem1*[illegible]

Table S4. Illumina data processing results for 5'-end SAGE reads

Short RNA	Total raw reads	QV filtered reads
Redundant reads	8,275,008	7,093,539
Non-redundant Sequences	4,575,275	3,513,538

Table S5. ELAND alignment of 5'-end SAGE short reads to reference *Drosophila melanogaste* (*dmel*) genome.

	Unique			Non-unique			Non-aligned
	Perfect match	One mismatch	Two mismatches	Perfect match	One mismatch	Two mismatches	
Redundant	833,259	961,492	974,067	905,493	1,038,590	1,090,609	4,058,847
--Percent	11.7%	13.6%	13.7%	12.8%	14.6%	15.4%	57.2%
Non-redundant Sequences	141,926	234,987	345,102	150,439	257,222	401,684	2,704,193
--Percent	4.0%	6.7%	9.8%	4.3%	7.3%	11.4%	77.0%

Table S6. All-against-all pair-wise ELAND alignment of 5'-end SAGE reads.

	Non-unique		Non-aligned
	One mismatch	Two mismatches	
Redundant	4,921,467	678,601	1,493,471
--Percent	69.4%	9.6%	21.1%
Non-redundant Sequences	1,395,932	658,672	1,458,934
--Percent	39.7%	18.7%	41.5%

Table S7. ELAND alignment of small RNAs reads to the reference genome after clustering.

	Unique			Non-unique			Non-aligned
	perfect match	one mismatch	two mismatches	Perfect match	One mismatch	Two mismatches	
Redundant reads	2,714,525	452,179	294,408	2,816,897	564,446	456,206	428,689
--Percent	63.6%	10.6%	6.9%	66.0%	13.2%	10.7%	10.0%
Non-redundant Sequences	179,599	96,002	122,165	207,812	145,597	213,125	270,969
--Percent	21.4%	11.5%	14.6%	24.8%	17.4%	25.4%	32.4%

Table S8. ELAND alignments of 5'-end SAGE reads to the reference genome before clustering.

	Unique			Non-unique			Non-aligned
	Perfect match	One mismatch	Two mismatches	Perfect match	One mismatch	Two mismatches	
Redundant	833,259	961,492	974,067	905,493	1,038,590	1,090,609	4,058,847
--Percent	11.7%	13.6%	13.7%	12.8%	14.6%	15.4%	57.2%
Non-redundant Sequences	141,926	234,987	345,102	150,439	257,222	401,684	2,704,193
--Percent	4.0%	6.7%	9.8%	4.3%	7.3%	11.4%	77.0%

Table S9. ELAND alignments of 5'-end SAGE reads to the reference genome after clustering.

	Unique			Non-unique			Non-aligned
	Perfect match	One mismatch	Two mismatches	Perfect match	One mismatch	Two mismatches	
Redundant	1,227,736	954,777	891,090	1,334,982	1,024,966	999,236	3,734,355
—Percent	17.3%	13.5%	12.6%	18.8%	14.4%	14.1%	52.6%
Non-redundant Sequences	301,947	257,189	322,559	326,598	279,293	376,381	2,531,266
—Percent	8.6%	7.3%	9.2%	9.3%	7.9%	10.7%	72.0%

Table S10. BAC sequencing data.

Sample	Raw reads	Reads without uncalled base	QV filtered reads	Reads with perfect or unique match (≤ 2 mismatches) && without polyN
Small RNAs	2,358,411	2,290,849	1,937,999	623,969
5'-end SAGE	3,214,493	2,960,318	2,839,995	1,217,785