

Len. (bp)	Homopolymer classes		Dinucleotide repeat classes				Trinucleotide repeat classes										
	101	102	201	202	203	204	301	302	303	304	305	306	307	308	309	310	
1	3200535	2909952															
2	1082377	644594															
3	377969	110227															
4	138707	19708	82509	82741	98187	15849											
5	49191	3571	24561	20063	29223	2367											
6	16408	648	7806	4115	6277	453	24909	24760	17143	16907	9371	8971	8454	7220	4467	2745	
7	6918	143	2584	1197	1741	90	7837	8215	5598	5103	2789	2864	2774	2006	1180	798	
8	2668	23	918	246	399	23	2654	3474	2094	1876	904	896	1006	691	465	146	
9	1290	13	400	127	147	13	983	1192	775	662	217	256	251	176	90	41	
10	788	6	164	31	34	4	344	441	261	212	76	155	120	70	33	10	
11	489	4	93	23	16	1	144	285	146	128	22	48	99	37	28	6	
12	343	0	55	7	1	0	60	93	51	45	12	15	30	12	12	1	
13	246	0	56	14	1	0	47	36	19	22	2	13	11	8	1	0	
14	124	2	32	3	2	0	25	38	19	24	3	6	14	5	7	0	
15	93	0	32	6	3	0	8	22	6	9	3	2	9	2	1	0	
16	63	1	20	2	1	0	13	12	9	10	0	0	7	2	3	0	
17	51	0	21	5	2	0	7	11	8	20	0	1	13	3	1	0	
18	28	0	23	2	0	0	6	9	4	5	1	0	2	1	0	0	
19	33	1	12	1	0	0	3	2	1	3	0	0	1	0	1	0	
20	22	0	18	1	0	0	4	7	6	10	0	1	4	1	2	0	
21	15	0	14	1	4	0	4	1	2	5	1	1	0	0	1	0	
22	18	0	14	2	0	0	1	2	1	0	0	0	0	0	0	0	
23	13	0	16	1	0	0	5	3	1	3	1	0	4	1	0	0	
24	18	0	12	0	0	0	3	3	3	0	1	1	4	0	1	0	
25	9	0	3	1	0	0	2	2	0	1	0	0	1	0	1	0	
26	9	0	8	2	0	0	1	1	1	5	0	0	3	1	0	0	
27	5	0	9	1	0	0	1	5	2	3	0	0	1	0	0	0	
28	4	0	2	0	0	0	1	1	1	3	0	0	0	0	0	0	
29	4	0	5	0	0	0	3	0	0	1	0	0	1	0	0	0	
30	1	0	6	0	0	0	2	0	2	0	1	0	0	0	0	0	
31	4	0	2	0	0	0	1	2	1	0	1	0	0	0	0	0	
32	1	0	7	0	0	0	0	1	0	0	0	0	1	0	0	0	
33	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	
34	1	0	1	1	0	0	1	0	1	0	0	0	0	0	0	0	
35	2	0	2	1	0	0	2	0	0	1	0	0	0	0	0	0	
36	1	0	3	0	0	0	0	0	1	0	0	0	0	0	0	0	
37	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	
38	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	
39	0	0	1	1	0	0	0	1	0	1	0	0	0	0	0	0	
40	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	
>40	1	0	1	2	1	0	7	1	1	3	0	0	1	0	2	0	

Table S1. Number of repeats of various classes in the yeast genome. "Len." = length of repeat tract.

Class	Type	Reference	Mutation	Chrom.	Position	5'-Flank	3'-Flank	Feature	Data Set (all mmmr-)
101a	Deletion	AAAA	----	5	267229	GATCATCGAG	AAAAAAAAAAA		<i>pol2-M644G</i> TAK217
101a	Deletion	AAAA	----	12	723078	AACGAAAAAC	AAAAAAAAAAA		<i>pol2-M644G</i> TAK206
101a	Deletion	TTTT	----	15	214947	CATTCTAGTA	TTTTTTTTTT		<i>pol2-M644G</i> TAK180
102	Deletion	CC	--	4	411724	ATATTGTACA	CCCCCCCCCT		<i>pol2-M644G</i> TAK206
102	Deletion	CCCC	----	15	94816	CAACGAAATA	CCCCCCCCCT		<i>pol2-M644G</i> TAK217
102	Deletion	CCCC	----	15	94816	CAACGAAATA	CCCCCCCCCT		<i>pol1-L868M</i> TAK269
102	Deletion	GGGGGG	-----	5	544032	AGGGGAAAAA	GGGGGGGGGG		<i>WT pols</i> TAK258
201b	Deletion	ATATATAT	-----	2	133861	TCTTGGTCAC	ATATATATAT		<i>pol2-M644G</i> TAK206
202b	Deletion	CACA	----	10	701336	CCAATACAAT	CACACACACA		<i>pol2-M644G</i> TAK068
202b	Deletion	ACAC	----	1	17291	ACCGTTTTTA	ACACACACCA		<i>WT pols</i> TAK258
202b	Deletion	ACAC	----	1	17291	ACCGTTTTTA	ACACACACCA		<i>WT pols</i> TAK260
202b	Deletion	ACAC	----	1	17291	ACCGTTTTTA	ACACACACCA		<i>WT pols</i> TAK266
301	Deletion	TAA	---	10	469784	GCAATAATAG	TAATAATAAT		<i>WT pols</i> TAK266
303	Deletion	TCA	---	3	267305	GTCTCAGTTT	TCATCATCAT	FIG2	<i>WT pols</i> TAK258
304	Deletion	GTT	---	1	112763	TTCACCGCC	GTTGTTGTTG	CCR4	<i>WT pols</i> TAK258
N/A	Deletion	AT	--	4	1054665	AAAAAAAAAAA	TTTTGTAC		<i>pol2-M644G</i> TAK217
N/A	Deletion	CTAG	----	4	233743	TGTCATGTCT	CTATGTATAT	VCX1	<i>pol2-M644G</i> TAK206
101	Insertion	--	TT	2	71821	AATAATTTTC	TTTTTTTTTT		<i>pol1-L868M</i> TAK269
101	Insertion	--	TT	3	6292	TTTTGCTTTC	TTTTTTTTTT		<i>WT pols</i> TAK259
101	Insertion	---	TTT	9	142349	ACTTCATCAA	TTTTTTTTTT		<i>pol2-M644G</i> TAK068
101	Insertion	--	TT	9	355450	TGTTGAAGTG	TTTTTTTTGG	SGN1	<i>pol3-L612M</i> TAK281
101	Insertion	--	AA	10	574851	AAGAATGAAG	AAAAAAAAAAA		<i>pol2-M644G</i> TAK206
101	Insertion	--	TT	12	130828	AATCCCAGAC	TTTTTTTTTT		<i>pol2-M644G</i> TAK206
101	Insertion	--	TT	13	49837	CACTTATTC	TTTTTTTTTT		<i>WT pols</i> TAK258
101	Insertion	--	TT	13	49837	CACTTATTC	TTTTTTTTTT		<i>WT pols</i> TAK259
101	Insertion	--	TT	13	920840	TCTTGTTCC	TTTTTTTTTT		<i>WT pols</i> TAK260
102	Insertion	---	GGG	12	327626	ATGAAAAGGT	GGGGGGTCTA		<i>pol2-M644G</i> TAK166
102	Insertion	---	GGG	12	327626	ATGAAAAGGT	GGGGGGTCTA		<i>pol2-M644G</i> TAK180
202	Insertion	--	CA	6	11242	GAATGAATTT	CACACACACA		<i>pol1-L868M</i> TAK269
305	Insertion	---	TAC	1	192003	ATATTATTTT	TACTACTACT		<i>WT pols</i> TAK260
N/A	Insertion	--	AG	8	529365	TCAAAAAAAAA	AAAAAATTAT		<i>pol2-M644G</i> TAK206
N/A	Insertion	--	TA	3	9012	GAAGCGAATT	TTTTTTTTTT		<i>pol1-L868M</i> TAK175
N/A	Insertion	--	TA	3	9012	GAAGCGAATT	TTTTTTTTTT		<i>pol1-L868M</i> TAK264

Table S2. List of notable multi-base indels. Full mutation lists may be found in (11). “Chrom.” = Chromosome number.

Indel Type	Δ	+	Δ	+	Δ	+	Δ	+	Δ	Δ	Δ	+	Δ	+
Repeat Class	101	101	102	102	201	201	202	202	301	303	304	305	Other	Other
Indel Length	A/T	A/T	G/C	G/C	TA	TA	CA	CA	ATT	ATC	GTT	ACT		
1	4646	571	322	77										
2	276	8	1		47	16	9	1					1	3
3	25	1		2					1	1	1	1		
4	3						4						1	
5			2											
6			1											
7														
8					1									

Table S3. Indel counts by repeat class and length.

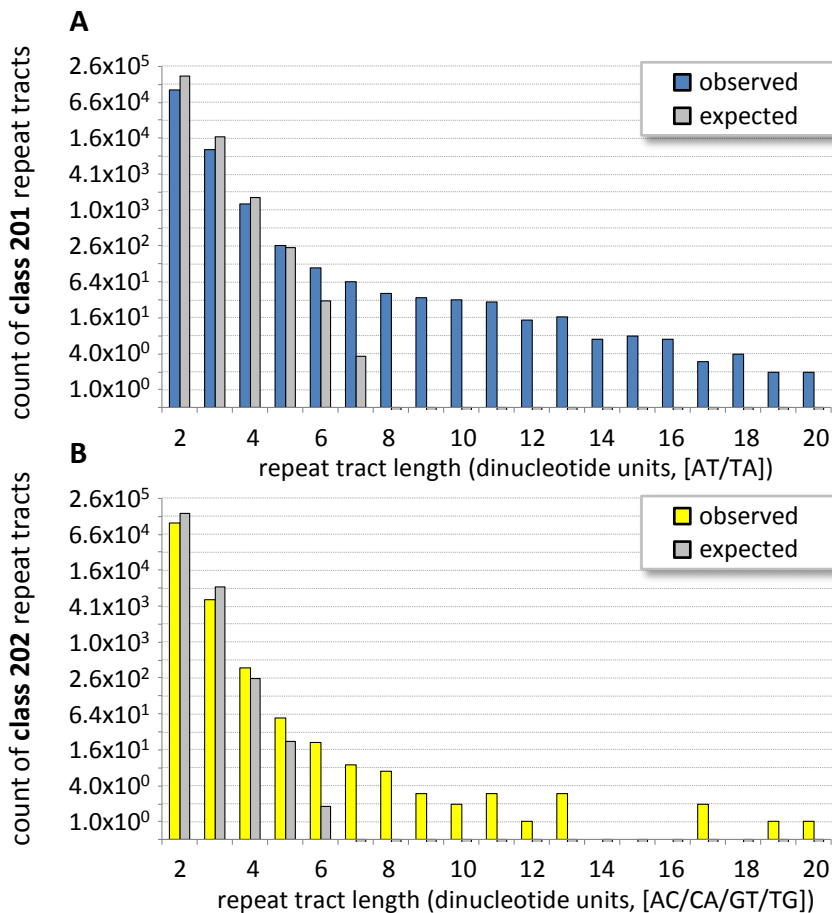


Figure S1. Dinucleotide repeat classes and counts. As per Figure 1 A-B, but for (A) AT/TA and (B) AC/CA/GT/TG dinucleotide repeat tracts.