Table S1. The numbers of TRs in the three populations (A) before and after upper thresholding; (B) separated by motif size and repeat number after upper thresholding.

Α.

	Number of TRs		
Population	Before upper cut-off	After upper cut-off *	
YRI	453,854,766	453,500,758	
CEU	473,350,569	472,996,810	
JPTCHB	473,361,805	473,009,688	

\* In this column, only mono-, di-, tri-, and tetranucleotide TRs under 10-bp, 18-bp, 24-bp, and 28-bp were considered.

	Repeat		Number of TR	S
IR CIASS	Number	YRI	CEU	JPTCHB
	2	246493315	246494715	246495135
	3	82682392	82684184	82684723
	4	28102544	28103294	28104008
	5	9466463	9467098	9467380
Mono	6	2580344	2580726	2580806
	7	996553	996750	996774
	8	357577	356944	356799
	9	142710	143814	144061
	10	87945	88612	89031
	2	51119753	62970957	62975747
	3	4294322	5291957	5292472
	4	560433	688397	688420
Di -	5	75393	75398	75357
	6	26218	26164	26030
	7	12616	12676	12576
	8	6929	6939	6904
	9	4367	4364	4365
	2	19270525	24136549	24139464
	3	616995	772052	772051
	4	47164	47121	47147
Tri	5	12949	12917	12938
	6	5358	5389	5353
	7	2527	2472	2466
	8	1327	1327	1290
	2	6322125	7776436	7778707
	3	165519	203244	203470
Tetra	4	27514	27461	27448
	5	11249	11284	11236
	6	5057	5007	4998
	7	2575	2562	2532

В.

Table S2. Proportion of TRs in intergenic+intronic vs. exonic+regulatory regions.

	Intergenic and	Exonic and
	Intronic	Regulatory
	regions (%)	regions (%)
Genomic	93.2%	6.8%
coverage		
Coverage by	92.8%	7.2%
TRs		

The proportions of all (polymorphic and non-polymorphic) microsatellites in putatively neutral regions (intergenic+intronic, 92.8%) vs. those in regions under selective constraints (exonic+regulatory comprising coding exons, UTR exons, and regulatory regions defined as 5 kb upstream and downstream from transcript boundaries, 7.2%) were found to be consistent with the genomic coverage of the two regions (intergenic+intronic: 2,896,745,931 bp (93.2%), exonic+regulatory: 210,598,511 bp (6.8%)).

Table S3. Linear regression model for (A) log polymorphism incidence (using CEU population data), (B) log polEF as a function of repeat number.

#### Α.

TR class	log(Polymorphi	sm incidence) ~ Repeat	number
	Intercept (P value)	Slope (P value)	R <sup>2</sup>
Mono	-3.347 (1.4E-07)	0.4056 (6.7E-07)	97.55%
Di	-2.872 (4.4E-04)	0.5438 (2.3E-04)	91.13%
Tri	-2.723 (8.3E-03)	0.5874 (4.5E-03)	82.77%
Tetra	-3.050 (0.0194)	0.7095 (0.0134)	81.74%

## В.

TR class	log(Po	IEF) ~ Repeat number	
	Intercept (P value)	Slope ( <i>P</i> value)	R <sup>2</sup>
Mono	-5.025 (0.00071)	0.3485 (0.00825)	92.88%
Di	-4.608 (3.3E-06)	0.1973 (0.00260)	86.05%

Table S4. Segmented regression model for log polymorphism incidence as a function of repeat number for mono-, di-, tri-, and tetranucleotide TRs in (A) YRI, (B) JPTCHB.

1	١.
-	٦.

TR		log(Polym	orphism incide	nce) ~ Repeat ı	number	
class	Change-	Intercept	Slope below	Slope above	P value	R <sup>2</sup>
	point	(P value)	change-	change-	for	
			point	point	difference	
					in slope	
Mono	8.373	-3.986	0.512	0.295	0.0561	99.54%
		(0.00023)				
Di	4.519	-4.231	1.014	0.282	2.2E-16	99.69%
		(3.8E-05)				
Tri	3.327	-6.204	1.921	0.297	2.2E-16	99.83%
		(0.00021)				
Tetra	3.321	-5.176	1.656	0.310	2.2E-16	99.78%
		(0.0040)				

#### Β.

TR		log(Polym	orphism incide	nce) ~ Repeat ı	number	
class	Change-	Intercept	Slope below	Slope above	P value	R <sup>2</sup>
	point	(P value)	change-	change-	for	
			point	point	difference	
					in slope	
Mono	8.308	-4.120	0.515	0.268	0.0160	99.56%
		(0.00019)				
Di	4.653	-4.490	1.027	0.292	2.2E-16	99.75%
		(2.5E-05)				
Tri	3.391	-6.488	1.952	0.293	2.2E-16	99.88%
		(0.00012)				
Tetra	3.356	-5.425	1.672	0.326	2.2E-16	99.82%
		(0.0032)				

Table S5. (A) Polymorphism Incidence and (B) Theta values for the four TR classes

Α.

	Repeat	Polyr	norphism Incid	lence	
TR class	Number	YRI     CEU     JPTCHB       0     0.245     0.2     4.925     0.2			
	2	6.34E-03	5.34E-03	4.82E-03	
•	3	9.44E-03	8.21E-03	7.35E-03	
•	4	1.28E-02	1.07E-02	9.76E-03	
•	5	0.035350423	0.030015425	0.027013951	
Mono	6	0.121840212	0.103627062	0.092005076	
	7	0.295175867	0.264246267	0.232497578	
•	8	1.601941086	1.352809271	1.248049496	
•	9	3.033424427	2.457340732	2.204621653	
•	10	5.976462562	4.637069471	4.087340365	
	2	6.00E-03	3.87E-03	3.48E-03	
•	3	0.070371994	0.046863571	0.042985584	
•	4	0.639148658	0.423592781	0.394090817	
- Di -	5	2.356982744	2.080957055	1.924174264	
	6	7.243115417	6.413392448	5.758739915	
	7	13.10240964	12.14105396	10.98918575	
•	8	23.56761437	22.19339963	20.32155272	
	9	33.40966338	32.14940422	29.43871707	
	2	4.35E-03	2.93E-03	2.61E-03	
•	3	0.362563716	0.251148886	0.23392237	
•	4	2.149944873	1.878143503	1.832566229	
Tri	5	4.849795351	4.157312069	3.988251662	
•	6	11.83277342	10.68843941	9.770222305	
	7	20.8547685	17.43527508	15.85563666	
•	8	31.80105501	29.5403165	26.82170543	
	2	1.37E-02	2.69E-03	8.29E-03	
•	3	0.621076734	0.42559682	0.389246572	
Totra	4	2.940321291	2.47623903	2.142232585	
Tetra -	5	8.285180905	7.328961361	6.247775009	
	6	16.13604904	14.04034352	12.36494598	
•	7	25.32038835	24.59016393	20.85308057	

В.

TR class	Repeat		Theta	
	Number	YRI	CEU	JPTCHB
Mono	2	4.36E-05	3.97E-05	3.60E-05
	3	6.65E-05	6.12E-05	5.38E-05
	4	8.15E-05	7.58E-05	6.90E-05
	5	0.00012055	0.000110074	0.000100938
	6	0.000254181	0.000233861	0.000208288
	7	0.00051213	0.000487145	0.000424778
	8	0.00754285	0.006346304	0.006117739
	9	0.021942723	0.018798028	0.016817317
	10	0.036968009	0.033156261	0.029456925
Di	2	3.68E-05	2.70E-05	2.53E-05
	3	0.000470231	0.000337183	0.000308566
	4	0.004371223	0.003131246	0.002841724
	5	0.01679632	0.015591007	0.014215596
	6	0.05042812	0.04691796	0.043438378
	7	0.089110952	0.081329464	0.074679148
	8	0.161969691	0.15080808	0.138290547
	9	0.244308932	0.231465493	0.212395294
Tri	2	2.66E-05	2.06E-05	1.85E-05
	3	0.00272718	0.002005706	0.001851005
	4	0.016372411	0.015149574	0.013980667
	5	0.035023233	0.030721388	0.030328081
	6	0.088289466	0.086815074	0.076652748
	7	0.158221961	0.147703061	0.128793494
	8	0.269163378	0.249760058	0.233731846
Tetra	2	8.94E-05	7.20E-05	5.97E-05
	3	0.004107482	0.003237235	0.002892039
	4	0.021232175	0.018739421	0.01628053
	5	0.064202797	0.056401373	0.050804832
	6	0.120160074	0.102670138	0.09661464
	7	0.224981115	0.210602773	0.183994594

TR			log(theta) ~	Repeat num	ber	
class	Change	Intercept	Slope	Slope	P value for	$R^2$
	point	(P value)	below	above	difference	
			change	change	in slope	
			point	point		
Mono	8.761	-8.0644	0.7168	0.2465	0.4348	97.12%
		(0.126)				
Di	4.658	-6.6106	1.032	0.285	2.2E-16	99.78%
		(3.9E-06)				
Tri	3.356	-8.664	1.989	0.312	2.2E-16	99.86%
		(6.9E-05)				
Tetra	3.363	-7.448	1.653	0.341	2.2E-16	99.87%
		(0.0012)				

Table S6. Segmented regression model for log theta as a function of repeat number for mono-, di-, tri-, and tetranucleotide TRs in the CEU population.

Table S7. Primary Pol EF data for (A) mono-, and (B) dinucleotide TRs A.

2 41111 11101103	Target Location	TP mutante	Dol EE
A A	107 100		FULEF
AA	127-128	4	ა.90E-Uპ
	161-162	1	
	164-165	0	
TT	94-95	2	
	111-112	62	
	142 142	16	
	142-143	16	
CC	99-100	3	
	120-121	5	
	129-130	1	
	152 154	12	
	103-104	12	
	167-168	63	
GG	102-103	0	
	118-119	1	
	138-139	3	
	150-155	7	
	155-156	1	
2 unit monos	Target Location	TR mutants	Pol EF
TT	127-128	8	5.17E-03
	161-162	9	
	164 165	55	
	104 100	00	
AA	94-95	0	
	111-112	2	
	142-143	1	
GG	99-100	0	
	120-121	6	
	120-121	0	<u> </u>
	129-130	0	
	153-154	0	
	167-168	0	
00	102-103	60	
50	110 110	44	└───┤
	118-119	11	
	138-139	18	
	155-156	21	
total all mutants			1134
total TP mutanta		371	1134
	l	3/1	
avg Pol EF		L	5.57E-03
TR EF			1.82E-03
TR EF per site	İ	İ	6.07E-05
3 unit monoo	Target Leastien	TP mutanta	Pol 55
3 unit monos	Target Location	TR mutants	POLEL
CCC	147-149	18	7.98E-03
	180-182	6	
	196-198	1	
	269.271	0	
063	200-211	0	<u> </u>
GGG	209-211	1	
	232-234	1	
	273-275	0	
TTT	212.214	2	
	212-214	2	
3 unit monos	Target Location	TR mutants	Pol EF
3 unit monos GGG	Target Location 147-149	TR mutants 0	Pol EF 1.34E-02
3 unit monos GGG	Target Location 147-149 180-182	TR mutants 0 1	Pol EF 1.34E-02
3 unit monos GGG	Target Location 147-149 180-182 196-198	TR mutants           0           1           0	Pol EF 1.34E-02
3 unit monos GGG	Target Location 147-149 180-182 196-198	TR mutants           0           1           0	Pol EF 1.34E-02
3 unit monos GGG	Target Location           147-149           180-182           196-198           269-271	TR mutants           0           1           0           0           0	Pol EF 1.34E-02
3 unit monos GGG CCC	Target Location           147-149           180-182           196-198           269-271           209-211	TR mutants           0           1           0           0           0           0           0	Pol EF 1.34E-02
3 unit monos GGG CCC	Target Location           147-149           180-182           196-198           269-271           209-211           232-234	TR mutants           0           1           0           0           0           0           1	Pol EF 1.34E-02
3 unit monos GGG CCC	Target Location           147-149           180-182           196-198           269-271           209-211           232-234           273-275	TR mutants           0           1           0           0           0           0           1           0           1           3	Pol EF 1.34E-02
3 unit monos GGG CCC	Target Location           147-149           180-182           196-198           269-271           209-211           232-234           273-275           2014	TR mutants           0           1           0           0           0           1           3	Pol EF 1.34E-02
3 unit monos GGG CCC AAA	Target Location           147-149           180-182           196-198           269-271           209-211           232-234           273-275           212-214	TR mutants           0           1           0           0           0           1           3           0	Pol EF 1.34E-02
3 unit monos GGG CCC AAA avg Pol EF	Target Location           147-149           180-182           196-198           269-271           209-211           232-234           273-275           212-214	TR mutants           0           1           0           0           0           1           0           1           3           0	Pol EF 1.34E-02
3 unit monos GGG CCC AAA avg Pol EF totai all mutants	Target Location           147-149           180-182           196-198           269-271           209-211           232-234           273-275           212-214	TR mutants           0           1           0           0           1           3           0	Pol EF 1.34E-02
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STP mutants	Target Location           147-149           180-182           196-198           269-271           209-211           232-234           273-275           212-214	TR mutants           0           1           0           0           1           3           0	Pol EF 1.34E-02 
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants TTR Pol TT	Target Location           147-149           180-182           196-198           269-271           232-234           273-275           212-214	TR mutants           0           1           0           1           3           0	Pol EF 1.34E-02 
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants TR Pol EF	Target Location           147-149           180-182           196-198           269-271           209-211           232-234           273-275           212-214	TR mutants           0           1           0           0           1           3           0	Pol EF 1.34E-02 
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants TR Pol EF TR Pol EF per site	Target Location 147-149 180-182 196-198 299-271 209-211 232-234 273-275 212-214	TR mutants           0           1           0           0           1           3           0	Pol EF 1.34E-02 1.07E-02 414 34 8.76E-04 5.47E-05
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants TR Pol EF TR Pol EF TR Pol EF per site 4 unit monos	Target Location           147-149           180-182           196-198           269-271           209-211           232-234           273-275           212-214           Target Location	TR mutants 0 1 1 0 0 0 1 1 3 0 1 TR mutants	Pol EF 1.34E-02 1.34E-02 1.07E-02 414 34 8.76E-04 5.47E-05 Pol EF
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants TR Pol EF TR Pol EF per site 4 unit monos AAAA	Target Location           147-149           180-182           196-198           299-271           209-211           232-234           273-275           212-214	TR mutants           0           1           0           0           1           0           1           3           0           TR mutants           2	Pol EF 1.34E-02 1.07E-02 414 34 8.76E-04 5.47E-05 Pol EF 7.98E-03
3 unit monos GGG CCC AAA avg Poi EF total all mutants total STR mutants TR Poi EF TR Poi EF TR Poi EF per site 4 unit monos AAAA	Target Location           147-149           180-182           196-198           269-271           209-211           232-234           273-275           212-214           Target Location           190-194           201-194	TR mutants           0           1           0           0           0           1           0           0           1           0           0           1           3           0	Pol EF 1.34E-02 
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants TR Pol EF TR Pol EF per site 4 unit monos AAAA	Target Location           147-149           180-182           196-198           209-271           209-211           232-234           273-275           212-214	TR mutants           0           1           0           0           1           0           0           1           0           0           1           0           1           0           1           1           0           1	Pol EF 1.34E-02 1.34E-02 1.07E-02 414 34 8.76E-04 5.47E-05 Pol EF 7.98E-03
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants TR Pol EF TR Pol EF TR Pol EF Por STR 4 unit monos AAAA CCCC CCC	Target Location           147-149           180-182           196-198           269-271           232-234           273-275           212-214           Target Location           190-194           201-244           228-229           2026-229           2027-2012	TR mutants           0           1           0           0           0           0           1           0           0           1           0           0           1           3           0	Pol EF 1.34E-02 1.07E-02 414 34 8.76E-04 5.47E-05 Pol EF 7.98E-03
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants TR Pol EF TR Pol EF per site 4 unit monos AAAA CCCC GGGG	Target Location 147-149 180-182 196-198 269-271 209-211 232-234 273-275 212-214 Target Location 190-194 241-244 226-229 237-240	TR mutants 0 1 0 0 0 0 1 0 0 TR mutants 2 6 2 9 9 9 0 0 0 0 0 0 0 0 0 0 0	Pol EF 1.34E-02 1.07E-02 414 34 8.76E-04 5.47E-05 Pol EF 7.98E-03
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants TR Pol EF TR Pol EF TR Pol EF F per site 4 unit monos AAAA CCCC GGGG 4 unit monos	Target Location           147-149           180-182           196-198           269-271           232-234           273-275           212-214	TR mutants           0           1           0           0           1           0           0           1           3           0           TR mutants           2           6           2           9           TR mutants	Pol EF 1.34E-02 1.07E-02 414 34 8.76E-04 5.47E-05 Pol EF 7.98E-03 Pol EF
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants TR Pol EF TR Pol EF per site 4 unit monos AAAA CCCC GGGG 4 unit monos TTTT	Target Location           147-149           180-182           196-198           269-271           209-211           232-234           273-275           212-214	TR mutants 0 1 0 0 0 0 1 3 0 0 TR mutants 2 6 2 9 TR mutants 6 6	Pol EF 1.34E-02 1.07E-02 414 34 8.76E-04 5.47E-05 Pol EF 1.34E-02 Pol EF 1.34E-02
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants TR Pol EF TR Pol EF TR Pol EF F per site 4 unit monos AAAA CCCC GGGG 4 unit monos TTTT	Target Location 147-149 180-182 196-198 269-271 209-211 232-234 273-275 212-214 Target Location 190-194 241-244 226-229 237-240 Target Location 190-194 241-244	TR mutants           0           1           0           0           1           0           0           1           3           0           1           3           0           1           3           0           1           3           0           1           1           1           1	Pol EF 1.34E-02 1.34E-02 1.07E-02 414 34 8.76E-04 5.47E-05 Pol EF 1.34E-02
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants TR Pol EF TR Pol EF per site 4 unit monos TTTT CCCC GGGG 4 unit monos TTTT	Target Location           147-149           180-182           196-198           269-271           209-211           232-234           273-275           212-214           190-194           241-244           226-229           237-240           Target Location           190-194           241-244           226-229           237-240           Target Location           190-194           241-244           270-270	TR mutants 0 1 1 0 0 0 1 1 0 0 1 1 3 0 0 1 TR mutants 2 6 2 9 TR mutants 6 12 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Pol EF 1.34E-02 1.07E-02 414 34 8.76E-04 5.47E-05 Pol EF 1.34E-02
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants TR Pol EF TR Pol EF TR Pol EF per site 4 unit monos AAAA CCCC GGGG 4 unit monos TTTT GGGGG	Target Location 147-149 180-182 196-198 269-271 232-234 273-275 212-214 Target Location 190-194 241-244 226-229 237-240 Target Location 190-194 241-244 226-229 237-240	TR mutants 0 1 0 0 0 0 0 1 3 0 0 1 TR mutants 2 6 2 9 TR mutants 6 12 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Pol EF 1.34E-02 1.34E-02 1.07E-02 4.14 3.4 8.76E-04 5.47E-05 Pol EF 1.34E-02 Pol EF
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants TR Pol EF per site 4 unit monos AAAA CCCC GGGG 4 unit monos TTTT GGGG CCCC	Target Location           147-149           180-182           196-198           269-271           209-211           232-234           273-275           212-214           190-194           241-244           226-229           237-240	TR mutants           0           1           0           0           0           1           0           0           1           3           0           TR mutants           2           6           2           6           12           0           1	Pol EF 1.34E-02 1.07E-02 414 34 8.76E-04 5.47E-05 Pol EF 1.34E-02 Pol EF 1.34E-02
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants TR Pol EF TR Pol EF TR Pol EF For Site 4 unit monos AAAA CCCC GGGG 4 unit monos TTTT GGGG CCCC avg EF	Target Location           147-149           180-182           196-198           269-271           232-234           273-275           212-214	TR mutants 0 1 0 0 0 0 1 3 0 0 1 TR mutants 2 6 2 9 TR mutants 6 12 0 1 1 0 1 1 0 0 1 0 0 0 0 0 0 0 0 0	Pol EF 1.34E-02 1.34E-02 1.07E-02 4.14 3.4 8.76E-04 5.47E-05 Pol EF 1.34E-02 1.07E-02 1.07E-02
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants TR Pol EF per site 4 unit monos AAAA CCCC GGGG 4 unit monos TTTT GGGG CCCC avg EF total TR mutants	Target Location           147-149           180-182           196-198           269-271           209-211           232-234           273-275           212-214	TR mutants           0           1           0           0           0           1           0           0           1           0           0           1           3           0           1           3           0           1           2           6           2           9           TR mutants           6           12           0           1	Pol EF 1.34E-02 1.07E-02 414 34 8.76E-04 5.47E-05 Pol EF 1.34E-02 1.07E-02 38
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants TR Pol EF TR Pol EF TR Pol EF per site 4 unit monos AAAA CCCC GGGG 4 unit monos TTTT GGGG CCCC avg EF total TR mutants total TR mutants	Target Location           147-149           180-182           196-198           209-211           232-234           273-275           212-214	TR mutants           0           1           0           0           1           0           0           1           3           0           TR mutants           2           6           2           9           TR mutants           6           12           0           1	Pol EF 1.34E-02 1.34E-02 1.07E-02 4.14 3.74E-04 Pol EF 1.34E-02 1.07E-02 38 4.14
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants TR Pol EF TR Pol EF per site 4 unit monos AAAA CCCC GGGG 4 unit monos TTTT GGGG CCCC avg EF total IR mutants total all mutants total all mutants total all mutants	Target Location           147-149           180-182           196-198           269-271           209-211           232-234           273-275           212-214           Target Location           190-194           241-244           226-229           237-240           Target Location           190-194           241-244           226-229           237-240	TR mutants           0           1           0           0           0           1           0           0           1           3           0           1           3           0           1           3           0           1           3           0           1           2           6           2           9           TR mutants           6           12           0           1	Pol EF 1.34E-02 1.07E-02 414 34 8.76E-04 5.47E-05 Pol EF 1.34E-02 Pol EF 1.34E-02 1.07E-02 0.0
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants TR Pol EF TR Pol EF per site 4 unit monos AAAA CCCC GGGG 4 unit monos TTTT GGGG CCCC avg EF total TR mutants total Mathematics total all mutants	Target Location           147-149           180-182           196-198           299-271           209-211           232-234           273-275           212-214	TR mutants           0           1           0           0           1           3           0           3           0           TR mutants           2           6           2           9           TR mutants           6           2           12           0           1	Pol EF 1.34E-02 1.34E-02 1.07E-02 414 3.76E-04 5.47E-03 Pol EF 1.34E-02 1.07E-02 38 414 9.79E-04 1.07E-02
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants total STR mutants TR Pol EF per site 4 unit monos AAAA CCCC GGGG 4 unit monos TTTT GGGG CCCC avg EF total TR mutants total all mutants TR Pol EF per site	Target Location 147-149 180-182 196-198 269-271 209-211 232-234 273-275 212-214  Target Location 190-194 241-244 226-229 237-240 Target Location 190-194 241-244 226-229 237-240	TR mutants 0 1 0 0 0 0 1 3 0 0 TR mutants 2 6 2 9 TR mutants 6 12 0 1 1	Pol EF 1.34E-02 1.34E-02 1.07E-02 414 34 8.76E-04 5.47E-05 Pol EF 1.34E-02 1.07E-02 38 414 9.79E-04 1.07E-02 38 414
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants TR Pol EF TR Pol EF per site 4 unit monos AAAA CCCC GGGG 4 unit monos TTTT GGGG CCCC avg EF total TR mutants total all mutants total all mutants TR Pol EF TR Pol EF TR Pol EF TR Pol EF	Target Location           147-149           180-182           196-198           209-211           232-234           273-275           212-214	TR mutants 0 1 0 0 0 0 1 0 0 1 3 0 0 TR mutants 2 6 6 2 9 TR mutants 6 12 0 1 1 1 TR mutants	Pol EF 1.34E-02 1.34E-02 1.07E-02 414 3.76E-04 5.47E-05 Pol EF 1.34E-02 1.07E-02 38 1.07E-02 38 414 9.79E-04 1.22E-04 Pol EF Pol EF 1.34E-02
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants total STR mutants TR Pol EF per site 4 unit monos AAAA CCCC GGGG 4 unit monos TTTT GGGG CCCC avg EF total TR mutants total all mutants TR Pol EF TR Pol EF per site 8 unit monos T8	Target Location           147-149           180-182           196-198           269-271           209-211           232-234           273-275           212-214	TR mutants           0           1           0           0           1           0           0           1           3           0           TR mutants           2           6           2           9           TR mutants           0           12           0           1	Pol EF 1.34E-02 1.34E-02 1.07E-02 414 34 8.76E-04 5.47E-05 Pol EF 1.34E-02 1.07E-02 38 414 1.07E-02 38 414 1.07E-02 1.07E-02 38 414 1.07E-02 38 414 1.07E-02 38 414 1.07E-02 38 414 1.07E-02 38 414 1.07E-02 38 414 1.07E-02 38 414 1.07E-02 38 414 1.07E-02 38 414 1.07E-02 38 414 1.07E-02 38 414 1.07E-02 1.07
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants tr Pol EF TR Pol EF per site 4 unit monos AAAA CCCC GGGG 4 unit monos TTTT GGGG CCCC avg EF total TR mutants total TR mutants total TR Pol EF TR Pol EF TR Pol EF TR Pol EF TR Pol EF TR Pol EF Stalt monos TB AR	Target Location           147-149           180-182           196-198           209-211           232-234           273-275           212-214	TR mutants           0           1           0           0           1           3           0           1           3           0           1           3           0           7           7           7           7           12           0           12           1           1           26           33	Pol EF 1.34E-02 1.34E-02 1.107E-02 414 3.4 8.76E-04 Pol EF 1.34E-02 1.07E-02 38 Pol EF 1.34E-02 1.07E-02 38 414 9.79E-04 1.22E-04 Pol EF 1.34E-02
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants total STR mutants TR Pol EF TR Pol EF per site 4 unit monos AAAA CCCC GGGG CCCC GGGG CCCC avg EF total TR mutants TTTT GGGG CCCC avg EF total TR mutants TR Pol EF per site 8 unit monos TB A8 A8	Target Location           147-149           180-182           196-198           269-271           209-211           232-234           273-275           212-214	TR mutants 0 1 1 0 0 1 0 0 1 1 3 0 0 1 TR mutants 2 6 2 9 TR mutants 6 12 0 1 1 TR mutants 2 6 12 0 TR mutants 6 12 0 1 TR mutants 2 6 33	Pol EF 1.34E-02 1.34E-02 1.07E-02 414 34 8.76E-04 5.47E-05 Pol EF 1.34E-02 1.07E-02 38 414 9.79E-04 1.07E-02 38 414 9.79E-04 1.07E-02 38 414 9.79E-04 1.07E-02 38 414 9.79E-04 1.07E-02 38 414 9.79E-04 1.07E-02 38 414 9.79E-04 1.07E-02 38 414 9.79E-04 1.07E-02 38 414 9.79E-04 1.07E-02 38 414 9.79E-04 1.07E-02 38 414 9.79E-04 1.07E-02 38 414 1.07E-02 4.72E-04 1.07E-02 4.72E-04 1.07E-02 4.72E-02 4
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants TR Pol EF per site 4 unit monos AAAA CCCC GGGG 4 unit monos TTTT GGGG CCCC avg EF total TR mutants total TR mutants total all mutants TR Pol EF TR Pol EF per site 8 unit monos T8 A8 avg pol EF	Target Location           147-149           180-182           196-198           209-211           209-211           232-234           273-275           212-214	TR mutants 0 1 1 0 0 0 1 1 3 0 0 1 TR mutants 2 6 2 9 TR mutants 6 12 0 1 1 TR mutants 2 6 3 3 3	Pol EF 1.34E-02 1.34E-02 4.14 3.46 5.47E-02 4.14 3.46 5.47E-02 Pol EF 1.34E-02 1.07E-02 38 1.07E-02 38 1.07E-02 38 1.07E-02 3.10
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants total STR mutants TR Pol EF TR Pol EF CCCC GGGG CCCC GGGG CCCC avg EF total TR mutants total all mutants TTTT GGGG CCCC avg EF total TR mutants total all mutants TR Pol EF TR Pol EF per site 8 unit monos TR A8 avg pol EF total TR A8 avg pol EF total TR	Target Location           147-149           180-182           196-198           269-271           232-234           273-275           212-214	TR mutants 0 1 0 0 1 0 0 1 3 0 0 1 3 0 0 TR mutants 2 6 2 9 TR mutants 6 1 2 0 TR mutants 6 1 2 0 TR mutants 2 6 3 3 3	Pol EF 1.34E-02 1.34E-02 1.07E-02 414 34 8.76E-04 5.47E-05 Pol EF 1.34E-02 1.07E-02 38 414 9.79E-04 1.22E-04 9.79E-04 1.22E-04 3.10E-02 3.10E-02 3.10E-02 3.10E-02 55
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants total STR mutants TR Pol EF per site 4 unit monos AAAA CCCC GGGG 4 unit monos TTTT GGGG CCCC avg EF total TR mutants total all mutants TR Pol EF per site 8 unit monos TB A8 avg pol EF total TR mutants total all mutants	Target Location           147-149           180-182           196-198           209-271           209-211           232-234           273-275           212-214	TR mutants           0           1           0           0           1           3           0           1           3           0           1           3           0           1           3           0           1           2           6           2           9           TR mutants           6           12           0           1           1           26           33	Pol EF 1.34E-02 1.34E-02 4.14 3.46 3.76-03 Pol EF 1.34E-02 1.07E-02 38 Pol EF 1.34E-02 1.07E-02 38 4.14 9.79E-04 1.22E-04 4.14 9.79E-04 1.22E-04 4.14 9.79E-02 3.8 4.14 1.22E-04 4.14 9.79E-02 3.91E-02
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants TR Pol EF TR Pol EF per site 4 unit monos AAAA CCCCC GGGG 4 unit monos TTTT GGGG CCCC avg EF total TR mutants total all mutants TR Pol EF per site 8 unit monos TR A8 avg pol EF total TR mutants total all mutants TR Pol EF per site 1 nt pol EF TR Pol EF per site 1 nt pol EF 1 nt pol EF	Target Location           147-149           180-182           196-198           269-271           232-234           273-275           212-214	TR mutants 0 1 0 1 0 0 1 0 0 1 3 0 0 1 3 0 0 TR mutants 2 6 2 9 TR mutants 6 12 0 1 TR mutants 2 6 33	Pol EF 1.34E-02 1.34E-02 1.07E-02 4.14 3.4 3.76E-04 5.47E-05 Pol EF 1.34E-02 1.07E-02 3.8 4.14 9.79E-04 1.22E-04 Pol EF 1.34E-02 3.10E-02
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants total STR mutants TR Pol EF per site 4 unit monos TTTT GGGG 4 unit monos TTTT GGGG CCCC avg EF total TR mutants total all mutants TR Pol EF per site 8 unit monos TB A8 avg pol EF total TR mutants total all mutants TR Pol EF TR Pol EF per site 8 unit monos T8 A8 avg pol EF total TR mutants total all mutants TR Pol EF TR Pol EF per site 8 unit monos T8 A8 avg pol EF total TR mutants total all mutants TR Pol EF TR Pol EF TR Pol EF TR Pol EF TB Pol EF TR Pol EF TR Pol EF TB Pol EF TR Pol EF TR Pol EF TB Pol EF TR Pol EF TR Pol EF TB Pol EF TR Pol EF TR Pol EF TB Pol EF TR Pol EF TR Pol EF TB Pol EF TR Pol EF TR Pol EF TB Pol EF TR Pol EF TB Pol EF TR Pol EF TB Pol EF TB Pol EF TR Pol EF TB Pol EF TB Pol EF TB Pol EF TB Pol EF TB Pol EF TR Pol EF TB Pol EF TB Pol EF TR Pol EF TB Pol EF TB Pol EF TB Pol EF TB Pol EF TB Pol EF TB Pol EF TB Pol EF TB Pol EF TB Pol EF TB Pol EF TB Pol EF TB Pol EF TB Pol EF TB Pol EF TB Pol EF TB Pol EF TB Pol EF TB POL FB TB POL FB TB POL FB TB POL FB TB POL FB TB P	Target Location           147-149           180-182           196-193           209-271           209-211           232-234           273-275           212-214	TR mutants 0 1 1 0 0 1 0 1 3 0 0 1 1 3 0 0 1 TR mutants 2 6 2 9 TR mutants 6 12 0 1 1 1 TR mutants 26 33 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Pol EF 1.34E-02 1.34E-02 4.14 3.46 4.14 3.76-02 4.14 3.76-02 Pol EF 1.34E-02 1.07E-02 38 4.14 9.79E-04 1.07E-02 3.01E-02 3.02E-02
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants TR Pol EF TR Pol EF per site 4 unit monos AAAA CCCCC GGGG 4 unit monos TTTT GGGG CCCC avg EF total TR mutants total all mutants total all mutants TR Pol EF per site 8 unit monos TB A8 avg pol EF total TR mutants total all mutants TR Pol EF TR Pol EF per site 7 R Pol EF TR Pol EF	Target Location           147-149           180-182           196-198           269-271           232-234           273-275           212-214	TR mutants 0 1 0 1 0 0 1 0 0 1 3 0 0 1 3 0 0 TR mutants 2 6 2 9 TR mutants 6 12 0 1 1 TR mutants 2 6 33 0	Pol EF 1.34E-02 1.34E-02 1.07E-02 4.14 3.4 3.76E-04 5.47E-05 Pol EF 1.34E-02 1.07E-02 3.8 4.14 9.79E-04 1.22E-04 Pol EF 1.34E-02 3.10E-02
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants total STR mutants TR Pol EF per site 4 unit monos AAAA CCCC GGGG 4 unit monos TTTT GGGG CCCC avg EF total TR mutants total all mutants TR Pol EF per site 8 unit monos T8 Aa avg pol EF total TR mutants total all mutants total all mutants TR Pol EF TR Pol EF per site 10 unit monos	Target Location           147-149           180-182           196-193           209-271           209-211           232-234           273-275           212-214	TR mutants 0 1 1 0 0 1 0 1 3 0 0 1 1 3 0 0 1 TR mutants 2 6 2 9 TR mutants 6 12 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Pol EF 1.34E-02 1.34E-02 4.14 3.46 4.14 3.76-03 Pol EF 1.34E-02 Pol EF 1.34E-02 3.79E-04 1.07E-02 3.8 4.14 9.79E-04 1.22E-04 4.14 9.79E-02 3.91E-02
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants TR Pol EF TR Pol EF per site 4 unit monos AAAA CCCC GGGG 4 unit monos TTTT GGGG CCCC avg EF total TR mutants total all mutants total all mutants total all mutants total all mutants total all mutants TR Pol EF per site 8 unit monos T8 A8 avg pol EF total TR mutants total all mutants TR Pol EF TR Pol EF	Target Location           147-149           180-182           196-198           269-271           232-234           273-275           212-214	TR mutants 0 1 0 1 0 0 1 0 0 1 3 0 0 1 3 0 0 1 TR mutants 2 6 1 2 0 TR mutants 6 1 2 0 1 TR mutants 2 6 3 3 0 N mutants 57	Pol EF 1.34E-02 1.34E-02 1.07E-02 4.14 3.4 3.76E-04 5.47E-05 Pol EF 1.34E-02 1.07E-02 3.8 4.14 9.79E-04 1.22E-04 Pol EF 1.34E-02 3.10E-02 3.10E-02 3.10E-02 3.10E-02 3.10E-02 1.22E-04 Pol EF 1.34E-02 1.22E-04 Pol EF 1.34E-02 1.22E-04 1.22E-04 Pol EF 1.34E-02 1.22E-04 1.22E-04 Pol EF 1.34E-02 1.22E-04 Pol EF 1.34E-02 1.22E-04 1.22E-04 Pol EF 1.34E-02 1.34
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants TR Pol EF per site 4 unit monos AAAA CCCC GGGG 4 unit monos TTTT GGGG CCCC avg EF total TR mutants total all mutants TR Pol EF per site 8 unit monos TR Pol EF s unit monos TR Pol EF total TR mutants total all mutants total all mutants TR Pol EF TR Pol EF per site 8 unit monos TR A8 avg pol EF total TR mutants total all mutants total all mutants TR Pol EF TR Pol EF per site 10 unit monos G10 C10	Target Location           147-149           180-182           196-193           209-271           209-211           232-234           273-275           212-214	TR mutants 0 1 1 0 0 1 0 1 3 0 0 1 1 3 0 0 1 TR mutants 2 6 2 9 TR mutants 6 12 0 1 1 1 TR mutants 26 33 3 1 N mutants 57 22	Pol EF 1.34E-02 1.34E-02 4.14 3.46 4.14 3.76-03 Pol EF 1.34E-02 Pol EF 1.34E-02 3.79E-03 1.07E-02 3.8 4.14 9.79E-04 1.22E-04 4.14 9.79E-02 3.91E-02
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants TR Pol EF TR Pol EF per site 4 unit monos AAAA CCCC GGGG CCCC GGGG CCCC avg EF total TR mutants total all mutants total all mutants total all mutants total all mutants total all mutants total all mutants total all mutants total all mutants total all mutants total all mutants total all mutants total all mutants TR Pol EF per site 8 unit monos T8 A8 avg pol EF total TR mutants total all mutants TR Pol EF per site 10 unit monos G10 C10 avo EF	Target Location           147-149           180-182           196-198           269-271           232-234           273-275           212-214	TR mutants 0 1 0 1 0 0 1 0 0 1 3 0 0 1 3 0 0 1 TR mutants 2 6 1 2 9 TR mutants 6 1 2 0 1 TR mutants 2 6 3 3 0 N mutants 5 7 2 2	Pol EF 1.34E-02 1.34E-02 1.07E-02 1.07E-02 1.07E-04 1.34 34 3.76E-04 5.47E-05 Pol EF 1.34E-02 1.07E-02 38 Pol EF 1.34E-02 1.07E-02 38 414 9.79E-04 1.22E-04 Pol EF 3.10E-02 4.72E-02 3.91E-02 59 62 2.97E-02 3.91E-02 2.47E-02 3.94E-02 3.94E
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants total STR mutants total STR mutants total STR mutants CCCC GGGG 4 unit monos TTTT GGGG CCCC avg EF total TR mutants total all mutants TR Pol EF TR Pol EF per site 8 unit monos T8 A8 avg pol EF total TR mutants total all mutants TR Pol EF T8 A8 avg pol EF total TR mutants total all mutants TR Pol EF T8 A9 A9 A9 GIE total TR mutants total all mutants T8 A8 avg pol EF total TR mutants total all mutants TR Pol EF T8 A9 A9 A9 CCCC A9 CCC A9 CCC A9 CCC A9 CCC A9 CCC A9 CCC A9 CCC A9 CCC A9 CCC A9 CCC A9 CCCC A9 CCCC A9 CCCC A9 CCCC A9 CCCC A9 CCCC A9 CCCCC A9 CCCC A9 CCCCC A9 CCCCCCCCC A9 CCCCCCCCCC	Target Location           147-149           180-182           196-198           209-211           209-211           232-234           273-275           212-214	TR mutants 0 1 1 0 0 1 1 0 0 1 1 3 0 0 1 TR mutants 2 6 2 9 TR mutants 6 12 0 1 1 1 TR mutants 26 33 3 3	Pol EF 1.34E-02 1.07E-02 414 3.46 414 3.76-03 Pol EF 1.34E-03 Pol EF 1.34E-02 1.07E-02 3.8 414 9.79E-04 1.07E-02 3.91E-02 3.92E-0
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants TR Pol EF TR Pol EF per site 4 unit monos AAAA CCCC GGGG 4 unit monos TTTT GGGG CCCC avg EF total all mutants total all mutants total all mutants total all mutants TR Pol EF per site 8 unit monos T8 A8 avg pol EF total TR mutants total all mutants total all mutants TR Pol EF TR Pol EF per site 10 unit monos G10 C10 avg EF total TR mutants	Target Location           147-149           180-182           196-198           269-271           232-234           273-275           212-214	TR mutants           0           1           0           0           1           3           0           1           3           0           1           3           0           1           3           0           1           2           9           TR mutants           6           12           0           12           0           12           0           12           0           12           0           12           0           12           0           13           26           33           1           1           1           1           1           1           1           1           1           1           1           1           1           1	Pol EF 1.34E-02 1.34E-02 1.07E-02 4.14 34 3.76E-04 5.47E-05 Pol EF 1.34E-02 1.07E-02 38 Pol EF 1.34E-02 1.07E-02 38 4.14 9.79E-04 1.22E-04 Pol EF 3.10E-02 3.31E-02 5.95 6.2 3.72E-02 3.54E-02 2.47E-02 3.54E-02 7.9 7.9 7.9 7.9 7.9 7.9 7.9 7.9
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants total STR mutants total STR mutants TR Pol EF TR Pol EF per site 4 unit monos AAAA CCCC GGGG 4 unit monos TTTT GGGG CCCC avg EF total TR mutants total all mutants TR Pol EF TR Pol EF per site 8 unit monos T T8 A8 avg pol EF total TR mutants total all mutants total all mutants total all mutants total all mutants total all mutants total all mutants total all mutants total all mutants total all mutants total all mutants total all mutants C10 avg EF total TR mutants total all mutants total all mutants total all mutants total all mutants total all mutants total all mutants total all mutants total all mutants total all mutants total all mutants total all mutants	Target Location           147-149           180-182           196-198           209-211           209-211           232-234           273-275           212-214	TR mutants 0 1 1 0 0 1 1 0 0 1 1 3 0 0 1 TR mutants 2 6 2 9 TR mutants 6 12 0 1 TR mutants 26 33 33	Pol EF 1.34E-02 1.34E-02 4.14 3.4 3.76E-04 4.14 3.76E-04 Pol EF 1.34E-05 Pol EF 1.34E-02 Pol EF 1.34E-02 1.07E-02 3.8 4.14 9.79E-04 1.07E-02 3.91E-
3 unit monos GGG CCC AAA avg Pol EF total all mutants total STR mutants TR Pol EF total all mutants total STR mutants TR Pol EF 4 unit monos AAAA CCCC GGGG 4 unit monos TTTT GGGG CCCC avg EF total TR mutants total all mutants total all mutants TR Pol EF per site 8 unit monos T8 A8 avg pol EF total TR mutants total all mutants total all mutants TR Pol EF per site 10 unit monos G10 C10 avg EF total TR mutants total all mutants total all mutants total all mutants total all mutants total all mutants total all mutants total all mutants total all mutants TR Pol EF per site 10 unit monos G10 C10 avg EF total TR mutants total all mutants TR Pol EF per site 10 unit monos G10 C10 avg EF total TR mutants total all mutants TR Pol EF	Target Location           147-149           180-182           196-198           269-271           232-234           273-275           212-214	TR mutants 0 1 0 1 0 0 1 0 0 1 3 0 0 1 1 3 0 0 1 TR mutants 2 6 2 9 TR mutants 6 12 0 1 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Pol EF 1.34E-02 1.34E-02 1.07E-02 4.14 3.76E-04 5.47E-05 Pol EF 1.34E-02 Pol EF 1.34E-02 1.07E-02 38 Pol EF 1.34E-02 1.07E-02 38 4.14 9.79E-04 1.22E-04 Pol EF 3.10E-02 59 62 3.72E-02 1.86E-02 Pol EF 3.10E-02 59 62 3.72E-02 1.86E-02 Pol EF 3.10E-02 59 62 3.72E-02 1.86E-02 Pol EF 3.10E-02 59 62 3.72E-02 1.86E-02 Pol EF 3.10E-02 59 62 3.72E-02 3.81E-02 59 62 3.72E-02 59 9 52 2.47E-02 3.54E-02 59 9 9 52 2.94E-02 2.94E-02 1.94E-02 1.95 1.9

В.

2 unit dinucleotides	Pol EF	TR mutants	Total mutants
GCGC	2.90E-03	1	61
CGCG avg EE	4.10E-03	1	
sum	0.00L-00	2	61
STR EF			1.15E-04
per site			5.74E-05
3 unit dinucleotides	Pol EF	TR mutants	Total mutants
TA	7.99E-03 3.10E-03	6	19
TC	3.00E-03	0	18
TC	1.80E-03	0	17
AG	2.40E-03	0	12
AG	2.80E-03	0	12
avy Er	3.52E-03	8	89
avg STR EF		0	3.16E-04
avg STR EF per site			1.05E-04
4 unit dinucleotides	Pol EF	TR mutants	Total mutants
TC	3.70E-03	5	20
AG	2.90E-03	3	13
AG	3.30E-03	1	15
GT	2.90E-03	0	40
GT	4.10E-03	2	21
CA	1.60E-03	1	11
CA	1.80E-03	1	13
TA	1.20E-02	14	19
avg EF	3.63E-03	0	
TOTAL		37	185
avg STR EF			7.27E-04
avg STR EF per site	D. 1 55		1.45E-04
5 unit dinucleotides	1 20E-02	IR mutants	10tal mutants
TA	4.68E-03	18	22
TC	5.40E-03	2	23
TC	3.80E-03	5	20
AG	4.00E-03	2	16
AG	5.00E-03	2	18
GT	2.10E-03	1	20
CA	3.50E-04	5	10
CA	2.00E-03	0	14
avg EF	4.21E-03		
sum		41	1/4
avg STR EF per site			1.99E-04
6 unit dinucleotides		TR mutants	Total mutants
TA	1.99E-02	10	12
TA	9.69E-03	16	18
GI	4.10E-03	6	21
CA	5.10E-03	5	24
CA	5.20E-03	4	20
avg EF	8.02E-03		
sum		48	116
avg STR EF			3.32E-03
8 unit dinucleotides	Pol EF	TR mutants	Total mutants
GT	2.60E-03	8	27
GT	3.30E-03	1	21
CA	3.30E-03	9	14
TC UA	4.70E-03	3	13
TC	8.30E-02	2	17
AG	2.00E-03	15	16
AG	3.20E-03	16	19
TA	2.12E-02	26	31
IA ave FF	7.30E-03	35	40
avyEr	6 79 -02		
sum	6.79E-03	120	209
sum avg STR EF	6.79E-03	120	209 3.90E-03
sum avg STR EF avg STR EF per site	6.79E-03	120	209 3.90E-03 7.80E-04
sum avg STR EF avg STR EF per site 9 unit dinucleotides	6.79E-03	120 TR mutants	209 3.90E-03 7.80E-04 Total mutants
sum avg STR EF avg STR EF per site 9 unit dinucleotides GT CT	6.79E-03 Pol EF 5.40E-03	120 TR mutants 10	209 3.90E-03 7.80E-04 Total mutants 29
sum avg STR EF avg STR EF per site 9 unit dinucleotides GT GT CA	6.79E-03 Pol EF 5.40E-03 5.90E-03 3.30E-03	120 TR mutants 10 11 15	209 3.90E-03 7.80E-04 Total mutants 29 19 19
sum avg STR EF avg STR EF per site 9 unit dinucleotides GT GT CA CA	6.79E-03 Pol EF 5.40E-03 5.90E-03 3.30E-03 3.60E-03	120 TR mutants 10 11 15 12	209 3.90E-03 7.80E-04 Total mutants 29 19 19 20
sum avg STR EF avg STR EF per site 9 unit dinucleotides GT GT CA CA avg EF	6.79E-03 Pol EF 5.40E-03 5.90E-03 3.30E-03 3.60E-03 4.55E-03	120 TR mutants 10 11 15 12	209 3.90E-03 7.80E-04 Total mutants 29 19 19 20
sum avg STR EF <b>9 unit dinucleotides</b> GT GT CA CA avg EF sum 	6.79E-03 Pol EF 5.40E-03 5.90E-03 3.30E-03 3.60E-03 4.55E-03	120 TR mutants 10 11 15 12 48	209 3.90E-03 7.80E-04 Total mutants 29 19 19 20 87 87
sum avg STR EF avg STR EF per site 9 unit dinucleotides GT GT CA CA CA avg EF sum avg STR EF avg STR EF	6.79E-03 <b>Pol EF</b> 5.40E-03 5.90E-03 3.30E-03 3.60E-03 4.55E-03	120 TR mutants 10 11 15 12 48	209 3.90E-03 7.80E-04 Total mutants 29 19 19 19 20 87 2.51E-03 1.26E-02

TR class	Polymorphism incidence ~ Recombination rate					
	Intercept (P value)	Slope (P value)	R <sup>2</sup>			
Mono	-0.0139 (0.517)	0.3891 (<2E-16)	4.62%			
Di	-0.0058 (0.79)	0.1626 (4.0E-05)	0.81%			
Tri	8E-04 (<2E-16)	7.2E-05 (2.3E-08)	1.48%			
Tetra	0.0015 (<2E-16)	1.4E-04 (7.7E-07)	1.17%			

Table S8. Linear regression models for polymorphism incidence as a function of recombination rate for mono-, di-, tri-, and tetranucleotide TRs.

TR class	Mean recor	P value for	
	Polymorphic (P)	Non-polymorphic (NP)	difference in mean recombination rate between P and NP > 0
Mono	0.977778	0.959090	2.2E-16
Di	0.983590	0.968106	1.409E-07
Tri	0.990975	0.966578	8.358E-09
Tetra	0.999976	0.968900	2.076E-08

Table S9. Two sample mean t-test for recombination rate of polymorphic and non-polymorphic mono-, di-, tri-, and tetranucleotide TRs

Table S10. Segmented regression model for log polymorphism incidence as a function of repeat number for motif-composition/structure based sub-classes of mono-, di-, tri-, and tetranucleotide TRs in the CEU population.

TR	Motif-		log(Polymorphism incidence) ~ Repeat number					
class	composit ion/struct ure sub- class	Change point	Intercept ( <i>P</i> value)	Slope below change point	Slope above change point	<i>P</i> value for difference in slope	R <sup>2</sup>	
Mono	A	n.s.	-3.362 (0.292)	0.317	n.s.	0.792 (n.s.)	96.53%	
	G	n.s.	-5.740 (0.015)	0.7562	n.s.	0.1351 (n.s.)	98.46%	
Di	AC	4.532	-4.414 (1.3E-05)	1.003	0.3187	2.2E-16	99.82%	
	AG	4.483	-4.6681 (1.9E-06)	1.093	0.2851	2.2E-16	99.76%	
	AT	5.491	-4.0730 (1.2E-06)	0.9166	0.2005	2.2E-16	99.92%	
	GC	NA						
Tri	No secondary structure	3.467	-5.839 (9.8E-05)	1.736	0.289	2.2E-16	99.91%	
	Triplex	3.423	-6.359 (8.7E-05)	1.915	0.406	2.2E-16	99.94%	
	Hairpin	3.288	-6.729 (0.0472)	2.051	0.319	2.2E-16	99.82%	
Tetra	No secondary structure	3.390	-5.050 (0.00528)	1.654	0.295	2.2E-16	99.69%	
	Triplex	3.481	-4.507 (0.00304)	1.385	0.346	1.2E-14	99.86%	
	Hairpin	3.505	-6.188 (0.00176)	1.821	0.341	2.2E-16	99.90%	

NA = data not available at all repeat numbers

n.s.: no statistical significance

# Figure S1. Proportion of polymorphic TRs by Tract length with proposed upper cut-offs

#### A. Dinucleotide TRs



**Dinucleotide TRs** 

## B. Trinucleotide TRs



### **Trinucleotide TRs**

Repeat Number

## C. Tetranucleotide TRs



#### **Tetranucleotide TRs**