

Repeat types	37°C			40°C - 24h			Rec		
	Number of elements	Length occupied (bp)	Sequence (%)	Number of elements	Length occupied (bp)	Sequence (%)	Number of elements	Length occupied (bp)	Sequence (%)
SINEs:	1142	125687	7.28	2163	292474	9.6	2609	347859	10.96
ALUs	1067	119247	6.91	1992	276179	9.07	2462	334884	10.55
MIRs	74	6380	0.37	170	16141	0.53	146	12895	0.41
LINEs:	4093	700490	40.57	5046	800672	26.29	6567	1045142	32.93
LINE1	4025	694278	40.21	4928	788116	25.87	6404	1028639	32.41
LINE2	63	5770	0.33	105	11391	0.37	150	15266	0.48
L3/CR1	4	396	0.02	9	827	0.03	11	1067	0.03
LTR elements:	710	105263	6.1	1203	164224	5.39	1260	168221	5.3
ERV_L	54	6570	0.38	149	17028	0.56	129	14192	0.45
ERV_L-MaLRs	166	18397	1.07	397	47752	1.57	406	45705	1.44
ERV_classI	337	54013	3.13	510	75581	2.48	550	81453	2.57
ERV_classII	153	26283	1.52	139	23087	0.76	164	25964	0.82
DNA elements:	149	16608	0.96	330	35943	1.18	343	33572	1.06
hAT-Charlie	62	6633	0.38	126	12964	0.43	161	15661	0.49
TcMar-Tigger	58	6732	0.39	142	16926	0.56	133	13436	0.42
Unclassified:	384	51035	2.96	387	41448	1.36	501	55290	1.74
Total interspersed repeats:		999083	57.86		1334761	43.82		1650084	51.99
Small RNA:	174	11219	0.65	261	20524	0.67	266	14829	0.47
Satellites:	604	104211	6.04	1319	223112	7.32	1179	198216	6.25
Simple repeats:	571	23838	1.38	1087	64160	2.11	908	38319	1.21
Low complexity:	56	2872	0.17	128	7715	0.25	105	5887	0.19
% of bases masked			66.1			54.18			60.1
% of bases unmasked			33.9			45.82			39.9