

Table S5 Statistics of repeat sequences

Type	Number	Length	Rate (%)
ClassI	903,203	275,112,366	48.28
ClassI/DIRS	20,909	11,117,466	1.95
ClassI/LARD	554,788	125,896,714	22.09
ClassI/LINE	49,672	14,128,907	2.48
ClassI/LTR/Copis	119,256	50,355,392	8.84
ClassI/LTR/Gypsy	143,643	91,328,457	16.03
ClassI/LTR/Unknown	4,024	993,093	0.17
ClassI/PLE	1,932	687,941	0.12
ClassI/SINE	4,098	786,956	0.14
ClassI/TRIM	4,073	1,595,467	0.28
ClassI/Unknown	808	260,812	0.05
ClassII	101,405	29,949,385	5.26
ClassII/Crypton	9	431	0.00
ClassII/Helitron	12,126	3,062,586	0.54
ClassII/MITE	4,744	1,093,163	0.19
ClassII/Maverick	386	280,146	0.05
ClassII/TIR	80,909	25,136,064	4.41
ClassII/Unknown	3,231	571,772	0.10
PotentialHostGene	42,706	8,897,896	1.56
SSR	789	232,804	0.04
Unknown	188,876	40,444,159	7.10
Total	1,236,979	329,228,711	57.78

Note: Type: type of repeat sequence; Number: number of repeats obtained; Length: total length of predicted repetitive sequence; Rate (%): proportion of repetitive sequence in total genome.