

Table S5. Details of the different annotated categories of transposable elements in the ESM015 genome assembly

Reference	Number of Tes copies	Tes load in kb	% genome	cumulative size	Name ref fasta
ESM015					
Tes_db1	1659	3280	7.47		
Tes_db3	1915	4375	9.97		
LTR (class I) Gypsy invader	924	2640	6.01	2,639,789	>Gypsy_invader_from_XIM
LTR (class I) Gypsy missing GAG AP	58	69	0.16	68,591	>RL_GYPSY_like_missing_GAG_AP
LTR (class I) COPYA	113	66	0.15	65,604	>RLC_COPYA_clean
LTR (class I) COPYA Missing AP	48	121	0.27	120,558	>RL_COPYA_like_Missing_AP
LARD (large retrotransposon derivatives) (class I)	24	37	0.08	37,025	>RXX_LARD_onlyIntegrase
LARD (class I)	40	57	0.13	57,023	>RXX-LARD_NomoreInformation
LARD (class I) (from Tes_db2)	88	101	0.23	101,304	>RXX_LARD_EP155denovo_B_R154_Map3
LARD (class I) (from Tes_db2)	228	1047	2.38	1,046,869	>RXX_LARD_EP155denovo_B_R79_Map13
LARD (class I) (from Tes_db2)	83	27	0.06	26,848	>RXX-LARD_EP155denovo-B-R32-Map13
TIR (class II) Mariner	48	44	0.10	44,393	>DT_Supposed_Mariner_With_Endonuclease
TIR (class II) Mariner	55	67	0.15	66,595	>DT_Supposed_Mariner_With_Endonuclease_CLEAN
TIR (class II) Mariner	17	24	0.05	23,980	>DT_Supposed_Mariner_NoClearTransposase_With_Endonuclease
TIR (class II) Mariner	5	4	0.01	4,143	>DTX_comp_Mariner_Like
TIR (class II) Mariner Without Transposase	37	7	0.02	7,315	>DTX_Mariner_Like_No_Transposase
Crypton (class II) Crypt1	34	27	0.06	27,470	>Crypt1_Transposon_Verif_Blast
Helitron (class II)	49	13	0.03	12,831	>DH_Helitron_like_remooved_repeat
Chimeric LTR TIR (class I / class II)	18	7	0.02	6,996	>Doubt_LTR_TIR_RNA_DNA
PotentialHostGene	46	18	0.04	17,581	>PotentialHostGene_ESMdenovo-B-G64-Map3
EP155					
Tes_db2	2510	4980	11.34		
Tes_db3	2116	4991	11.37		
LTR (class I) Gypsy invader	1027	3008	6.85	3,007,549	>Gypsy_invader_from_XIM
LTR (class I) Gypsy missing GAG AP	72	132	0.30	132,202	>RL_GYPSY_like_missing_GAG_AP
LTR (class I) COPYA	116	58	0.13	57,637	>RLC_COPYA_clean
LTR (class I) COPYA Missing AP	57	161	0.37	160,734	>RL_COPYA_like_Missing_AP
LARD (large retrotransposon derivatives) (class I)	21	24	0.05	23,884	>RXX_LARD_onlyIntegrase
LARD (class I)	71	138	0.31	138,164	>RXX-LARD_NomoreInformation
LARD (class I) (from Tes_db2)	109	215	0.49	214,543	>RXX_LARD_EP155denovo_B_R154_Map3
LARD (class I) (from Tes_db2)	217	944	2.15	944,334	>RXX_LARD_EP155denovo_B_R79_Map13
LARD (class I) (from Tes_db2)	87	58	0.13	57,783	>RXX-LARD_EP155denovo-B-R32-Map13
TIR (class II) Mariner	43	44	0.10	43,844	>DT_Supposed_Mariner_With_Endonuclease
TIR (class II) Mariner	61	76	0.17	76,410	>DT_Supposed_Mariner_With_Endonuclease_CLEAN
TIR (class II) Mariner	22	39	0.09	39,242	>DT_Supposed_Mariner_NoClearTransposase_With_Endonuclease
TIR (class II) Mariner	6	4	0.01	4,261	>DTX_comp_Mariner_Like
TIR (class II) Mariner Without Transposase	38	7	0.02	7,380	>DTX_Mariner_Like_No_Transposase
Crypton (class II) Crypt1	46	43	0.10	43,021	>Crypt1_Transposon_Verif_Blast
Helitron (class II)	53	12	0.03	11,634	>DH_Helitron_like_remooved_repeat
Chimeric LTR TIR (class I / class II)	20	9	0.02	9,213	>Doubt_LTR_TIR_RNA_DNA
PotentialHostGene	50	19	0.04	18,690	>PotentialHostGene_ESMdenovo-B-G64-Map3