

**Table 1.** Total number of extracted gene flanking regions and total number of hits to predicted LTRs.

Genome and gene set		Flanking region from the gene start/end coordinates									
		5'	3'	5'	3'	5'	3'	5'	3'	5'	3'
		0-1kb	0-1kb	1-2 kb	1-2 kb	2-3kb	2-3kb	3-4kb	3-4kb	4-5kb	4-5kb
<i>P. taeda</i> v.2.0. all genes	Nb of extr.seq.	36726	36728	34711	34063	33184	32310	31767	30838	30349	29479
	Nb of hah to LTRs	5851	6450	4362	3901	3750	3628	3310	3069	3202	2924
	ratio	0.16	0.18	0.13	0.11	0.11	0.11	0.10	0.10	0.11	0.10
	>50	17	22	10	10	4	2	1	0	0	0
	>100	8	9	1	0	0	0	0	0	0	0
<i>P. taeda</i> v.2.0. annotated genes	Nb of extr.seq.	15084	15057	14114	13793	13371	12912	12713	12192	11985	11569
	Nb of hah to LTRs	816	773	800	732	875	968	1161	991	901	1000
	ratio	0.05	0.05	0.06	0.05	0.07	0.07	0.09	0.08	0.08	0.09
	>50	0	0	0	0	0	0	0	0	0	0
	>100	0	0	0	0	0	0	0	0	0	0
<i>P. taeda</i> v.1.0. HQ genes	Nb of extr.seq.	4298	4239	4177	4128	4130	4091	4081	4028	4023	3967
	Nb of hah to LRs	784	779	2258	1890	3151	2693	3593	3222	3816	3539
	ratio	0.18	0.18	0.54	0.46	0.76	0.66	0.88	0.80	0.95	0.89
	>50	1	1	1	0	0	0	0	0	0	0
	>100	0	0	0	0	0	0	0	0	0	0
<i>P. taeda</i> v.1.0. LQ genes	Nb of extr.seq.	75425	75459	72840	72797	71554	71470	70002	69836	68237	68017
	Nb of hah to LTRs	2317	2540	4188	4243	4979	5070	5256	5387	5645	5382
	ratio	0.03	0.03	0.06	0.06	0.07	0.07	0.08	0.08	0.08	0.08
	>50	2	2	5	5	6	5	4	7	7	6
	>100	1	1	3	4	1	1	0	1	0	0
<i>P. lambertiana</i> v.1.0 HQ genes	Nb of extr.seq.	8779	8778	8746	8742	8719	8708	8692	8673	8660	8640
	Nb of hah to LTR	71	55	163	187	278	277	315	296	355	357
	ratio	0.01	0.01	0.02	0.02	0.03	0.03	0.04	0.03	0.04	0.04
	>50	0	0	0	0	0	0	0	0	0	0
	>100	0	0	0	0	0	0	0	0	0	0
<i>P. lambertiana</i> v.1.0 LQ genes	Nb of extr.seq.	71162	71157	70386	70475	69773	69909	69217	69344	68660	68836
	Nb of hah to LTRs	470	466	1063	1011	1556	1508	1789	1368	2038	1999
	ratio	0.01	0.01	0.02	0.01	0.02	0.15	0.03	0.02	0.03	0.03
	>50	0	0	1	0	4	3	6	1	7	7
	>100	0	0	0	0	0	0	0	0	0	0

\* >50 or >100 indicate count of TE families that hits greater than 50 or greater than 100 gene flanking regions;

**Table 2.** *P. taeda* v.2.0 and *P. lambertiana* v.1.01 genes carrying several *MITE3321* insertions.

Species	Genes ID with multiple <i>3321MITEs</i>	Nb	Description	qq, %	e-value	ID, %	Accession
<i>P. taeda</i> v.2.0.	PITA_12742	7	uncharacterized protein with domain of phosphoglucosamine mutase family protein	88	0.00E+00	65	PLN02371
	PITA_21987	4	subtilisin-like protease SBT5.3	96	0.0	47	XP_012083905.1
	PITA_00114	3	metal tolerance protein 11	99	0.0	72	XP_006857671.1
	PITA_24114	2	probable xyloglucan endotransglucosylase/hydrolase protein B	93	3.00E-153	72	XP_030961064.1
	PITA_21327	2	60S ribosomal protein L8-1-like	95	2.00E-169	90	XP_022936671.1
	PITA_17959	2	TMV resistance protein N-like	93	8.00E-165	31	XP_023886681.1
	PITA_34859	2	3-oxoacyl-[acyl-carrier-protein] synthase I, chloroplastic-like isoform X1	95	0.0	74	XP_028101593.1
	PITA_28894	2	L-gulonolactone oxidase 2 isoform X2	95	0.0	54	XP_011621860.1
	PITA_00539	2	probable potassium transporter 11	99	0.0	67	XP_006830082.1
	PITA_33316	2	plasma membrane intrinsic protein 2;8	95	5.00E-141	74	NP_179277.1
	PITA_09881	2	cytokinin hydroxylase	93	0.0	52	XP_011099558.1
<i>P. lambertiana</i> v.1.01. HQ genes	S/hiseq/c38458_g1_i1 m.23006	2	bifunctional phosphatase IMPL2, chloroplastic	75	7.00E-147	73	XP_011088446.1
	PILAhq_048992	2	putative clathrin assembly protein At4g40080	80	2.00E-40	36	XP_027337607.1
	PILAhm_002002	2	histone deacetylase 15 isoform X3	69	4.00E-179	63.89	XP_010265267.1

**Table 3.** Node genes containing several TE insertions and found to be homologous or carrying identical domains between *P. taeda* (*pita*) and *P. lambertiana* (*pila*).

LTR Nb. <i>pita</i>	LTR Nb. <i>pila</i>	Description	Accession, <sup>h</sup> -homologous genes	Conserved domain name	Accession	GO terms
24	19	plastidial pyruvate kinase 2	XP_006843356.1 <sup>h</sup>	PLN02623	PLN02623	reproduction; ATP generation from ADP; seed maturation;
23	26	DEAD-box ATP-dependent RNA helicase 20 isoform X2/helicase 58, chloroplastic isoform X3	XP_025888827.1	SrmB	COG0513	RNA secondary structure unwinding
21	21	phospholipid:diacylglycerol acyltransferase 1	XP_006849611.1 <sup>h</sup>	PLN02517	PLN02517	acylglycerol biosynthetic process
18	20	nuclear pore complex protein NUP62-like/GPCR-type G protein 1 isoform X2	XP_024396806.1	SMC_prok_B super family	cl37069	RNA export from nucleus; protein import/export into/from nucleus; nucleocytoplasmic transport, localization
13	23	WD repeat-containing protein WRAP73	XP_008798782.1	WD40 super family	COG2319	-
	19	protein RAE1	XP_028076289.1		cl29593	
	24	actin-related protein 2/3 complex subunit 1A	XP_011627051.1		cl29593	
12	19	uncharacterized protein LOC109715170/probable E3 ubiquitin-protein ligase HERC4 isoform X1	XP_020095639.1	ATS1 super family	cl34932	-
11	31	peroxisomal adenine nucleotide carrier 1/mitochondrial substrate carrier family protein C-like	XP_006841423.1	Mito_carr	pfam00153	Establishment of localization; transmembrane transport; amide biosynthetic process; translation; nitrogen compound metabolic process.