

Table S1. Characterization of the T-DNA insertions in activation tagging lines with improved biomass traits. All insertions were mapped in the <i>Populus genome</i> using BLAST analysis tool in Phytozone v1.0 data base (https://phytozone.jgi.doe.gov).											Arabidopsis Homolog	Feature	Distance to gene (Kbp)
Identifier #	Position (BLAST hit)	Identity (bp)	E-value	Left flanking loci / Distance from left border to start codon [insertion = 6.7Kbp]	Right flanking loci / Distance from left border to start codon in Kbp [insertion = 6.7Kbp]	Putative Gene function	Activated/Most likely activated loci						
A630-7	Chr14:4,719,725_4,720,217	459,494	0.0E+00	PxXaTreH.14G052500	12.6	PxXaTreH.14G052600	0.6	PxXaTreH.14G052600	GROWTH-REGULATING FACTOR 9		AT2G45480.1	Intron	0.6
A541-1	Chr05:19,283,082_19,283,351	264,270	4.0E-127	PxXaAbH.05G161200	24.3	PxXaAbH.05G161300	5.4	PxXaAbH.05G161300	TIC-LIKE PROTEIN		AT3G22380.1	Upstream region	5.4
A689-4	Chr10:17,990,503_17,991,103	589,601	0.0E+00	PxXaAbH.10G146700	0.9	PxXaAbH.10G146800	13.6	PxXaAbH.10G146700	RIBONUCLEASE P SUBUNIT P38		AT1G13790.2	5' untranslated region (UTR)	0.9
A726-3	Chr14:9,913,312_9,913,644	327,333	2.0E-162	PxXaTreH.14G114700	17.3	PxXaTreH.14G114800	9.3	PxXaTreH.14G114800	ACTIN-LIKE ATPASE SUPERFAMILY PROTEIN		AT1G30540.1	Intron	9.3
A842-3	Chr10:10,630,097_10,630,565	460,470	0.0E+00	PxXaAbH.10G086100	1.7	PxXaAbH.10G086200	9.2	PxXaAbH.10G086100	NO FUNCTIONAL ANNOTATION		AT3G07100.1	Upstream region	1.7
A82-2	Chr06:18,933,087_18,933,370	284,284	4.0E-144	PxXaTreH.06G160100	16.4	PxXaTreH.06G160200	3.8	PxXaTreH.06G160200	LARGE SUBUNIT RIBOSOMAL PROTEIN L21E (RP-L21E, RPL21)		AT5G78601.1	Upstream region	3.8
A835-3	Chr15:11,424,623_11,425,039	398,419	0.0E+00	PxXaTreH.15G090100	5.9	PxXaTreH.15G090200	6.9	PxXaTreH.15G090100	UNCHARACTERIZED		AT5G51120.1	Downstream region	5.9
A771-3	Chr08:711,508_711,709	201,202	4.0E-98	PxXaAbH.08G018000	0.8	PxXaAbH.08G019000	10.9	PxXaAbH.08G018000	GLUTARODEXIN FAMILY PROTEIN		AT5G01420.1	Upstream region	0.8
A826-3	Chr01:1,396,275_1,396,440	128,168	1.00E-22	PxXaTreH.01G014500	9.4	PxXaTreH.01G014600	20.8	PxXaTreH.01G014500	HELIX-LOOP-HELIX DNA-BINDING DOMAIN (HLH)		AT1G51140.1	Upstream region	9.4
A927-3	Chr06:7,439,340_7,439,974	477,581	2.0E-159	PxXaTreH.06G072700	0.6	PxXaTreH.06G072800	12.7	PxXaTreH.06G072700	ACYL-COA N-ACYLTRANSFERASE WITH RING-FYVE/PHD-TYPE ZINC FINGER DOMAIN-CONTAINING PROTEIN		AT2G37520.1	5' UTR	0.6
A972-5	Chr06:909,369_909,805	290,349	1.0E-99	PxXaTreH.06G019900	8.5	PxXaTreH.06G011000	11.2	PxXaTreH.06G019900	F-BOX PROTEIN CPR30		AT4G12560.1	Upstream region	8.5
A634-2	Chr08:4,458,012_4,458,561	550,550	0.0E+00	PxXaTreH.08G059200	0.0	PxXaTreH.08G059300	11.4	PxXaTreH.08G059200	GZ-GAMMA-BISBOLENE SYNTHASE 1-RELATED		AT5G05350.1	Exon	0.0
A635-1	Chr13:1,946,091_1,946,362	260,276	1.0E-113	PxXaTreH.13G026900	17.4	PxXaTreH.13G027000	0.2	PxXaTreH.13G027000	TRANSPORT PROTEIN PARTICLE (TRAPP) COMPLEX SUBUNIT		AT6G08000.1	5' UTR	0.2
A822-3	Chr06:25,176,034_25,176,909	839,880	0.0E+00	PxXaAbH.06G217500	9.8	PxXaAbH.06G217600	8.1	PxXaAbH.06G217600	SHN SHINE_1 DNA BINDING / TRANSCRIPTION FACTOR // ETHYLENE-RESPONSIVE TRANSCRIPTION FACTOR ERF003		AT5G25190.1	Upstream region	8.1
A862-1	Chr06:11,011,939_11,012,043	105,105	4.0E-47	PxXaAbH.06G097000	11.9	PxXaAbH.06G098000	0.6	PxXaAbH.06G098000	NO FUNCTIONAL ANNOTATION		N/A	Upstream region	0.6
A863-3	Chr08:1,237,541_1,237,795	253,255	1.0E-125	PxXaAbH.08G019100	0.2	PxXaAbH.08G019200	13.2	PxXaAbH.08G019100	GTU DOMAIN CONTAINING PROTEIN		AT3G57810.4	5' UTR	0.2
A836-1	Chr18:9,569,679_9,570,034	350,359	1.0E-170	PxXaAbH.18G066300	19.0	PxXaAbH.18G066400	2.0	PxXaAbH.18G066400	HOMOGENITISATE PHYTYLTRANSFERASE / HPT		AT2G18950.1	Intron	2.0
A857-2	Chr01:36,423,209_36,423,290	74,82	8.0E-23	PxXaAbH.01G282600	1.3	PxXaAbH.01G282700	27.8	PxXaAbH.01G282600	E3 UBIQUITIN-PROTEIN LIGASE RGL-G1-RELATED		AT5G14420.1	Exon	1.3
A885-1	Chr10:17,452,998_17,453,190	193,193	7.0E-95	PxXaAbH.10G139600	6.3	PxXaAbH.10G139700	7.7	PxXaAbH.10G139600	ZINC FINGER CCH3 DOMAIN-CONTAINING PROTEIN 37-RELATED		AT3G12680.1	3' UTR	6.3
A934-2	Chr18:142,446_142,543	96,998	7.0E-41	PxXaAbH.18G001300	0.2	PxXaAbH.18G001400	18.0	PxXaAbH.18G001300	SERINE PROTEASE FAMILY SIC HTRA-RELATED		AT5G27660.2	Exon	0.2
A943-1	Chr04:2,205,837_2,205,924	82,88	7.0E-30	PxXaAbH.04G022700	6.5	PxXaAbH.04G022800	11.7	PxXaAbH.04G022700	KINESIN-1 RELATED		AT4G08180.1	Upstream region	6.5
A991-1	Chr01:38,788,885_38,739,199	312,315	3.0E-156	PxXaTreH.01G300500	0.1	PxXaTreH.01G300600	11.8	PxXaTreH.01G300500	MEIOTIC RECOMBINATION PROTEIN SPO11		AT3G13170.1	5' UTR	0.1
B21-1	Chr11:15,661,025_15,661,305	247,281	1.7E-88	PxXaAbH.11G081800	5.8	PxXaAbH.11G081900	8.7	PxXaAbH.11G081800	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 3642		AT3G14400.1	Downstream region	5.8
A613-2	Chr01:48,013,773_48,014,052	229,281	2.0E-68	PxXaAbH.01G351100	12.2	PxXaAbH.01G351200	12.8	PxXaAbH.01G351100	BOI-RELATED E3 UBIQUITIN-PROTEIN LIGASE 3-RELATED		AT1G12920.1	Upstream region	12.2
A874-9	Chr02:17,294,793_17,294,986	193,194	2.0E-93	PxXaTreH.02G173800	8.5	PxXaTreH.02G173900	16.3	PxXaTreH.02G173800	DIMETHYLANILINE MONOOXYGENASE		AT1G48910.1	Upstream region	9.6
A901-5	Chr12:8,571,009_8,571,304	239,298	1.0E-66	PxXaTreH.12G059500	25.1	PxXaTreH.12G059600	1.8	PxXaTreH.12G059600	GDSL-MOTIF LIPASE/HYDROLASE FAMILY PROTEIN		AT5G62930.1	Intron	1.8
B0-4	Chr04:811,140_811,512	373,373	0.0E+00	PxXaTreH.04G008500	2.6	PxXaTreH.04G008600	12.7	PxXaTreH.04G008500	GLYOXALASE I HOMOLOG		AT3G53700.1	Upstream region	2.6
A915-2	Chr14:5,531,694_5,531,727	31,34	1.6E-03	PxXaAbH.14G064200	0.2	PxXaAbH.14G064300	22.1	PxXaAbH.14G064200	PHOSPHATIDYLINOSITOL N-ACETYLGUCOSAMINYTRANSFERASE SUBUNIT P-LIKE PROTEIN		AT4G00440.3	Intron	0.2
A975-4	Chr10:7,703,668_7,704,334	388,388	0.0E+00	PxXaAbH.10G054200	0.3	PxXaAbH.10G054300	28.9	PxXaAbH.10G054200	TOPPA_4 TYPE ONE SERINE/THREONINE PROTEIN PHOSPHATASE 4		AT2G39840.1	Upstream region	0.3
A955-1	Chr07:881,027_881,480	445,454	0.0E+00	PxXaTreH.07G010100	14.1	PxXaTreH.07G010200	1.4	PxXaTreH.07G010200	U-BOX DOMAIN-CONTAINING PROTEIN 50-RELATED		AT5G65500.1	Exon	1.4
A979-4	Chr01:17,597,610_17,597,872	263,263	8.9E-133	PxXaAbH.01G162300	65.1	PxXaAbH.01G162400	1.2	PxXaAbH.01G162400	ABC TRANSPORTER G FAMILY MEMBER 35-RELATED		AT1G59870.1	Exon	1.2
1999-5	Chr12:10,989,445_10,989,698	226,254	1.4E-85	PxXaAbH.12G082300	7.1	PxXaAbH.12G082400	9.2	PxXaAbH.12G082300	PROTEIN MEI2-LIKE 1-RELATED		AT5G61960.3	3' UTR	7.1
795L-6	Chr06:3,283_1_3,340.4	140,149	1.9E-58	PxXaTreH.06G000100	0.0	PxXaTreH.06G000200	13.2	PxXaTreH.06G000100	PENTATRICOPEPTIDE REPEAT-CONTAINING PROTEIN		AT5G01560.4	Exon	0.0
826L-3	Chr08:3,531,725_3,531,969	245,245	5.3E-123	PxXaAbH.08G048500	13.0	PxXaAbH.08G048600	3.0	PxXaAbH.08G048600	WALL-ASSOCIATED RECEPTOR KINASE GALACTURONAN-BINDING DOMAIN		AT5G02070.1	Upstream region	3.0
345L-1	Chr10:16,317,536_16,317,975	440,440	0.0E+00	PxXaAbH.10G123500	17.4	PxXaAbH.10G123600	3.8	PxXaAbH.10G123600	NUCLEAR TRANSPORT FACTOR 2 (NTF2) FAMILY PROTEIN		AT1G13730.2	3' UTR	3.8
501L-5	Chr14:1,957,182_1,957,297	114,125	8.6E-44	PxXaTreH.14G021900	17.7	PxXaTreH.14G022000	0.0	PxXaTreH.14G022000	MEMBRANE PROTEIN YCF1-RELATED		ATMG000370.1	Exon	0.0
575L-1	Chr01:34,466,030_34,466,136	107,107	2.5E-48	PxXaAbH.01G268000	2.0	PxXaAbH.01G268100	16.6	PxXaAbH.01G268000	DOUBLE-STRANDED RNA-BINDING PROTEIN 3		AT3G26932.1	3' UTR	2.0
659L-1	Chr06:23,150,863_23,151,505	642,643	0.0E+00	PxXaTreH.06G205900	3.5	PxXaTreH.06G206000	9.1	PxXaTreH.06G205900	HISTONE H2A (H2A)		AT1G52740.1	Upstream region	3.5
707L-1	Chr01:33,916,483_33,916,815	331,333	5.5E-168	PxXaTreH.01G268700	24.4	PxXaTreH.01G268800	7.2	PxXaTreH.01G268800	HYPOTHETICAL PROTEIN		AT3G01960.1	Upstream region	7.2
994L-1	Chr14:4,373,677_4,374,201	482,553	1.8E-172	PxXaTreH.14G048000	26.7	PxXaTreH.14G048100	3.8	PxXaTreH.14G048100	AUXIN-REGULATED PROTEIN-RELATED		AT3G60690.1	Upstream region	3.8