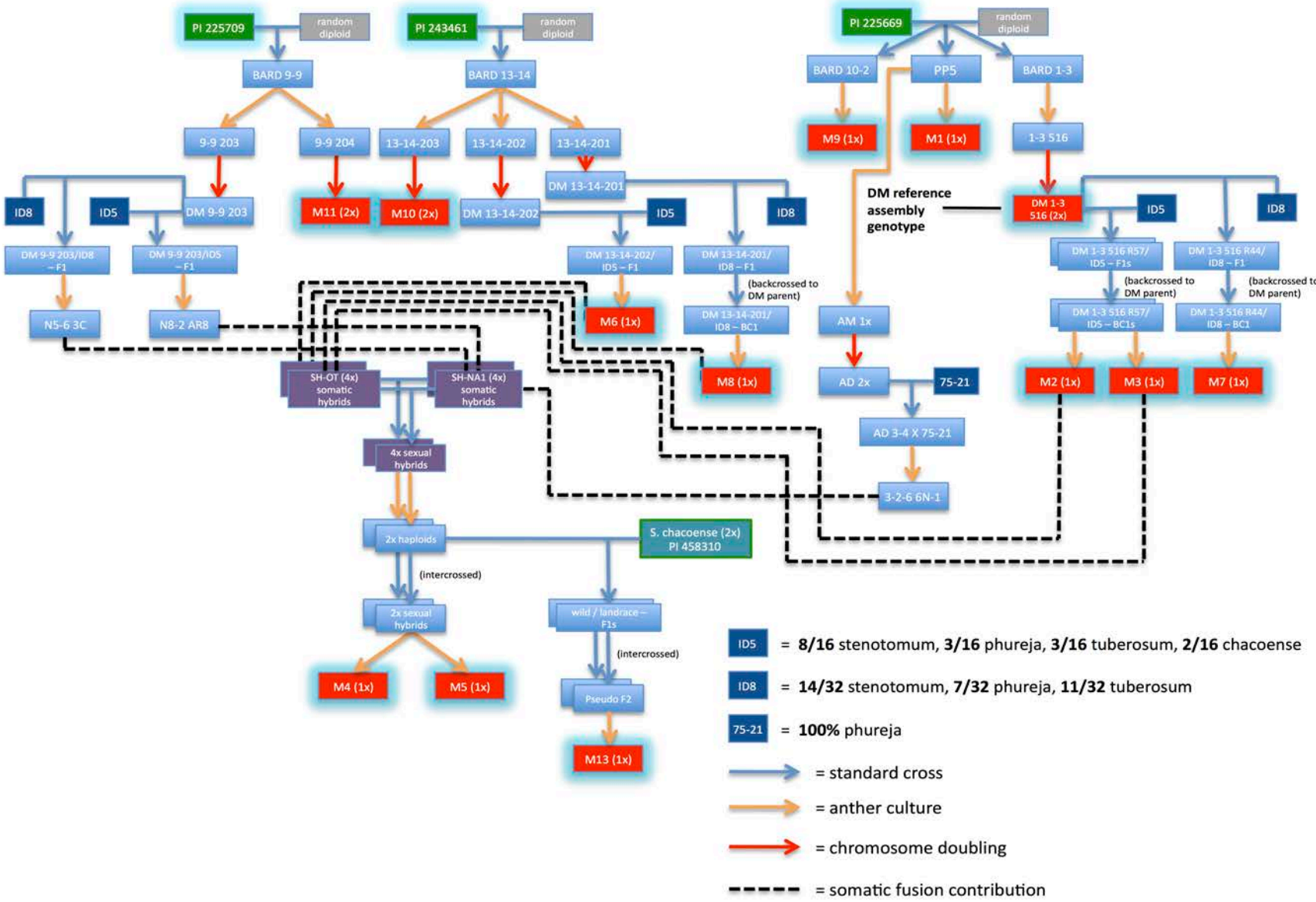
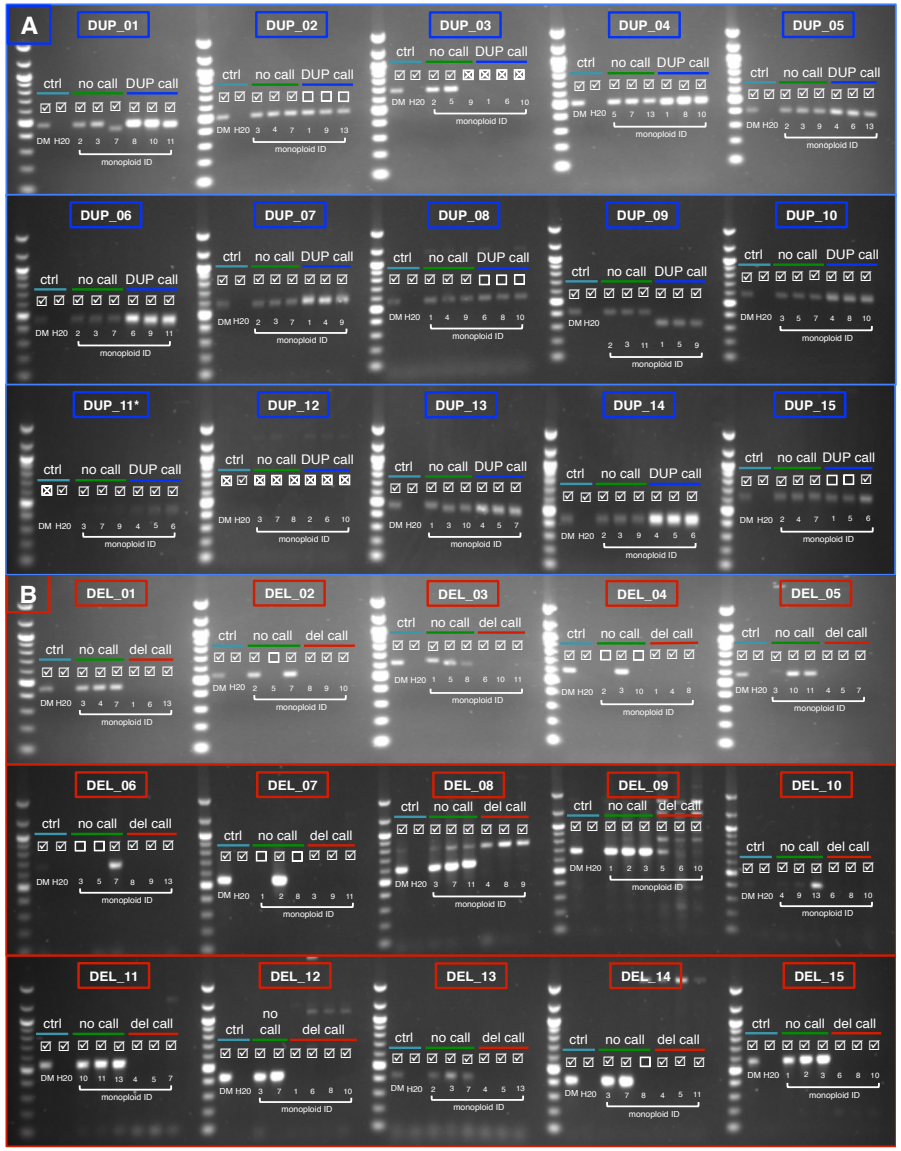
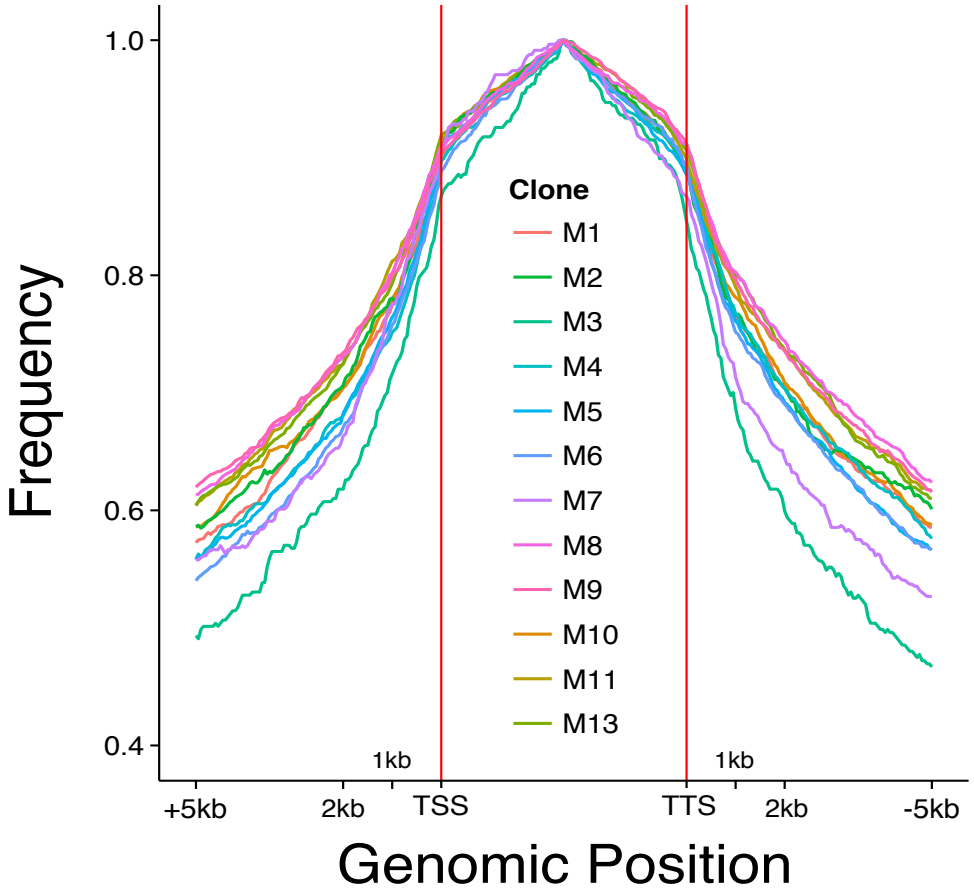


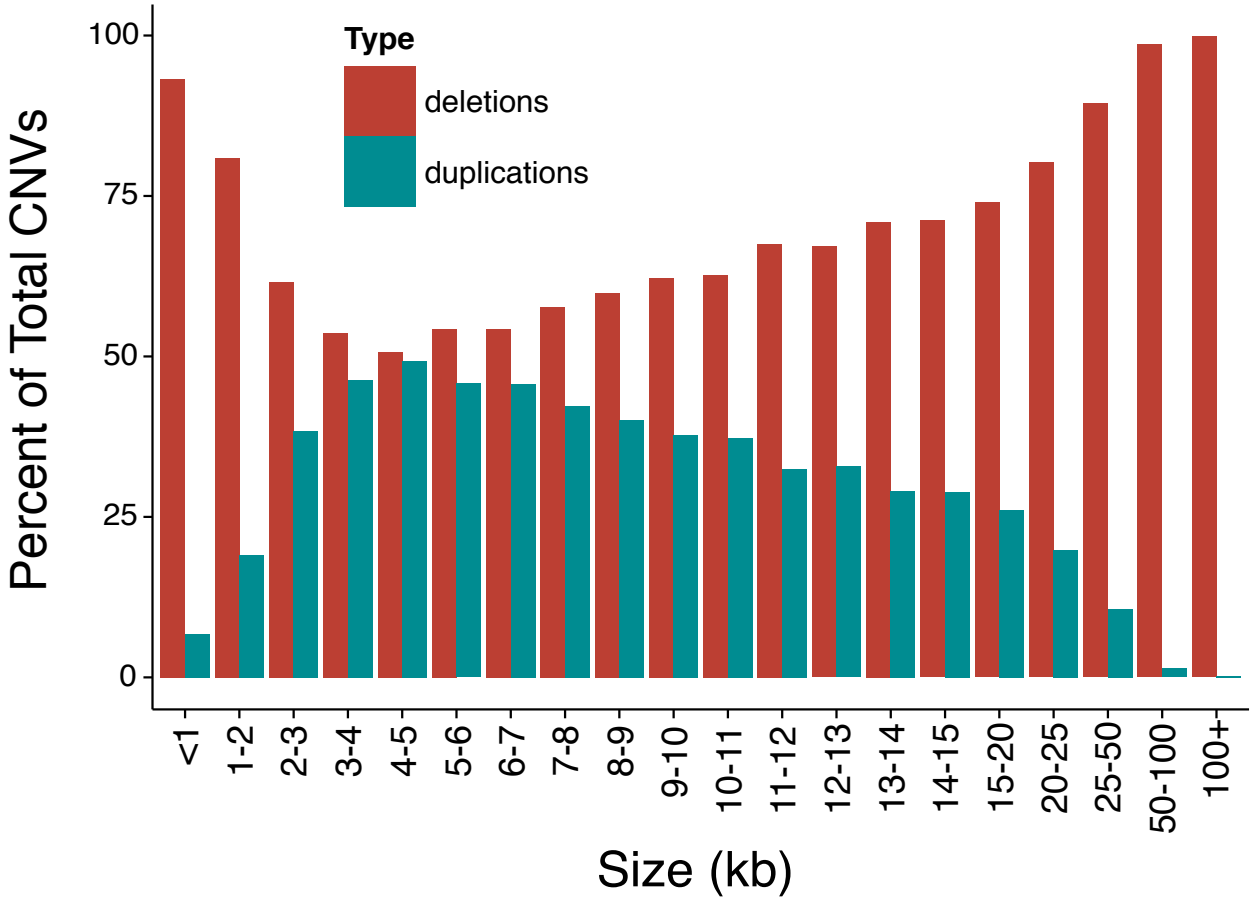
Supplemental Figure 1. (Best viewed in original PDF file at 125% magnification). Pedigree information for the monoploid panel clones (red). Germplasm is primarily derived from three native diploid *Solanum tuberosum* Group Phureja landrace populations (green) crossed to unknown random diploid landrace pollen parents from a photoperiod adapted landrace population (gray) (M1, M9, M10, M11), in some cases with further introgressions (M2, M3, M6, M7, M8) from heterogeneous diploid stocks (dark blue). Several accessions are descended from intercrossed tetraploid somatic hybrids (M4, M5) derived from other panel clones, and in the case of M13 an interspecies hybridization. Generations: blue) standard cross; orange) anther culture event; red) chromosome doubling event; black) somatic fusion event.



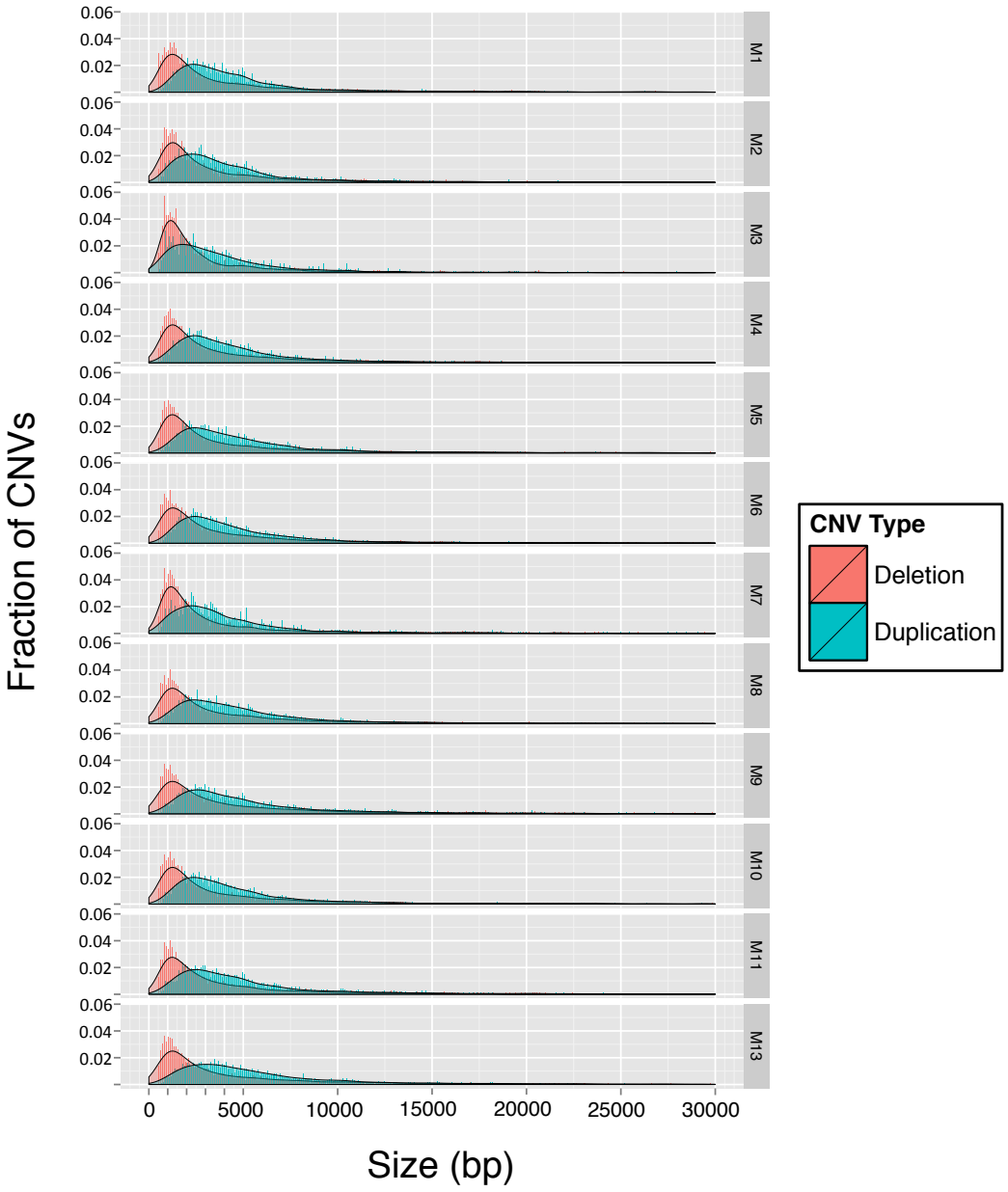
Supplemental Figure 2. (Best viewed in original PDF file at 250% magnification). Experimental PCR validation of 15 randomly selected duplication (A) and deletion (B) loci. A) Two assays (DUP_03, DUP_12) failed to amplify a product in any duplicate sample, indicating uncalled variants at primer binding sites preventing effective amplification. Assay DUP_11 yielded bands visible only at a higher exposure. For primers designed to duplicated loci, PCR assays confirmed 97.6% of the targets in single copy clones and 74% of targets in CNVnator-predicted duplications. B) Deletions were scored relative to the reference control (DM). PCR assays confirmed 82% of the targets in single copy clones and 100% of CNVnator-predicted deletions in the analysis. A check mark indicates validation of CNVnator-predicted copy status or lack of bank in the water control, an “x” indicates failed reaction, and an empty box indicates inability to validate predicted copy status.



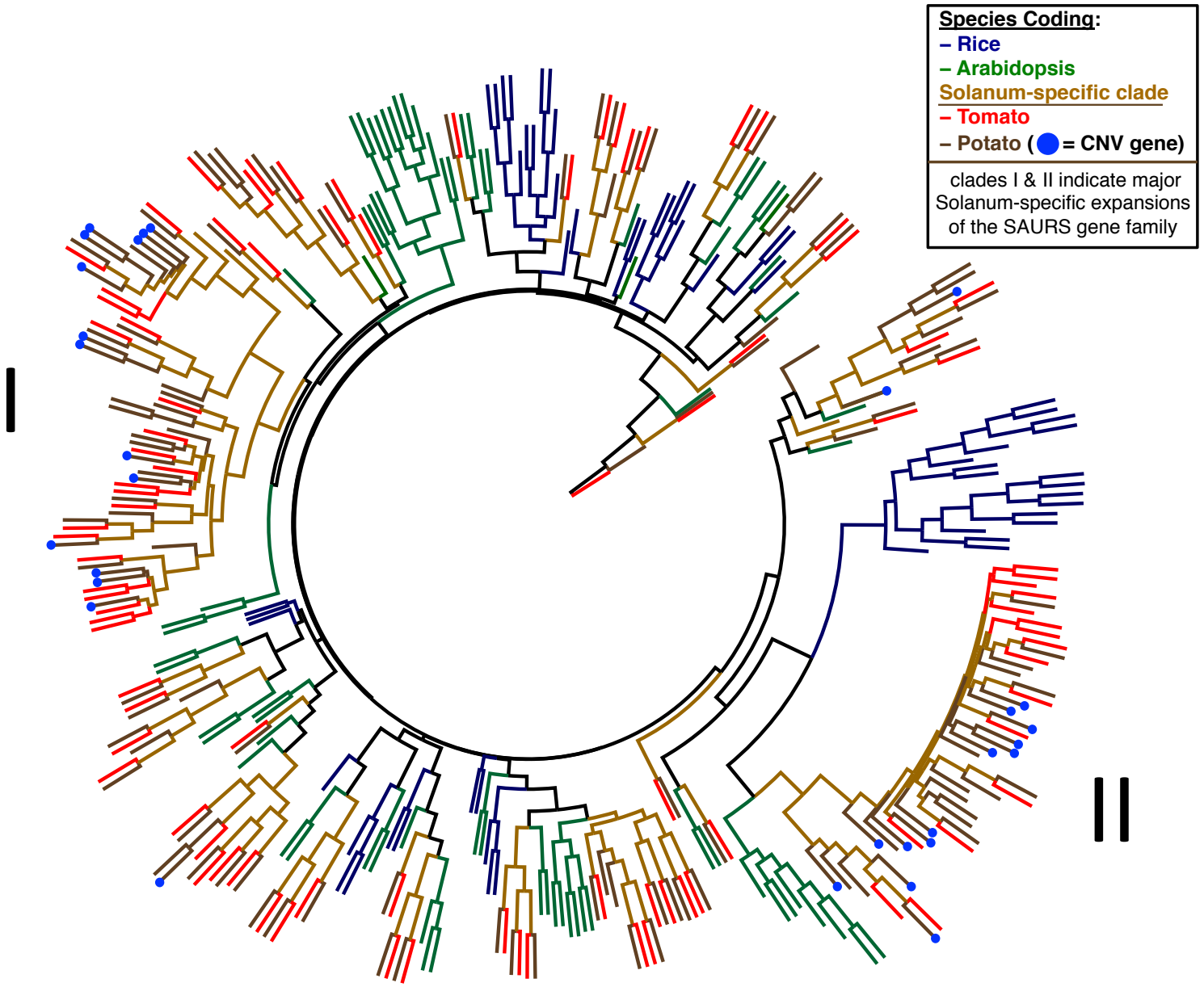
Supplemental Figure 3. Distribution of copy number variation (CNV) frequency (per clone) relative to the position of genes impacted by deletion (required minimum 50% gene model overlap with a deleted sequence).



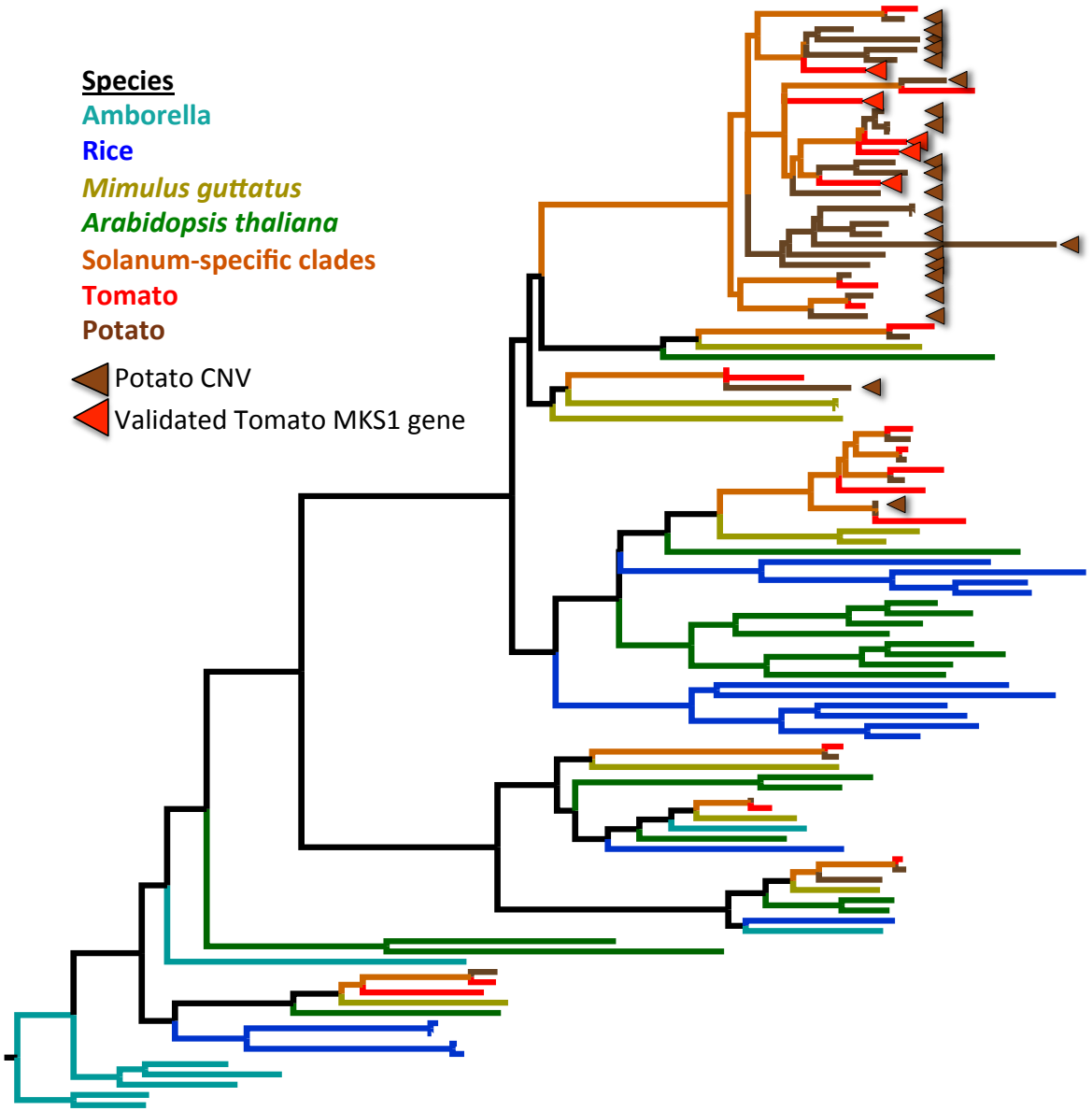
Supplemental Figure 4. Fraction of copy number variants represented by duplication and deletion binned by size.



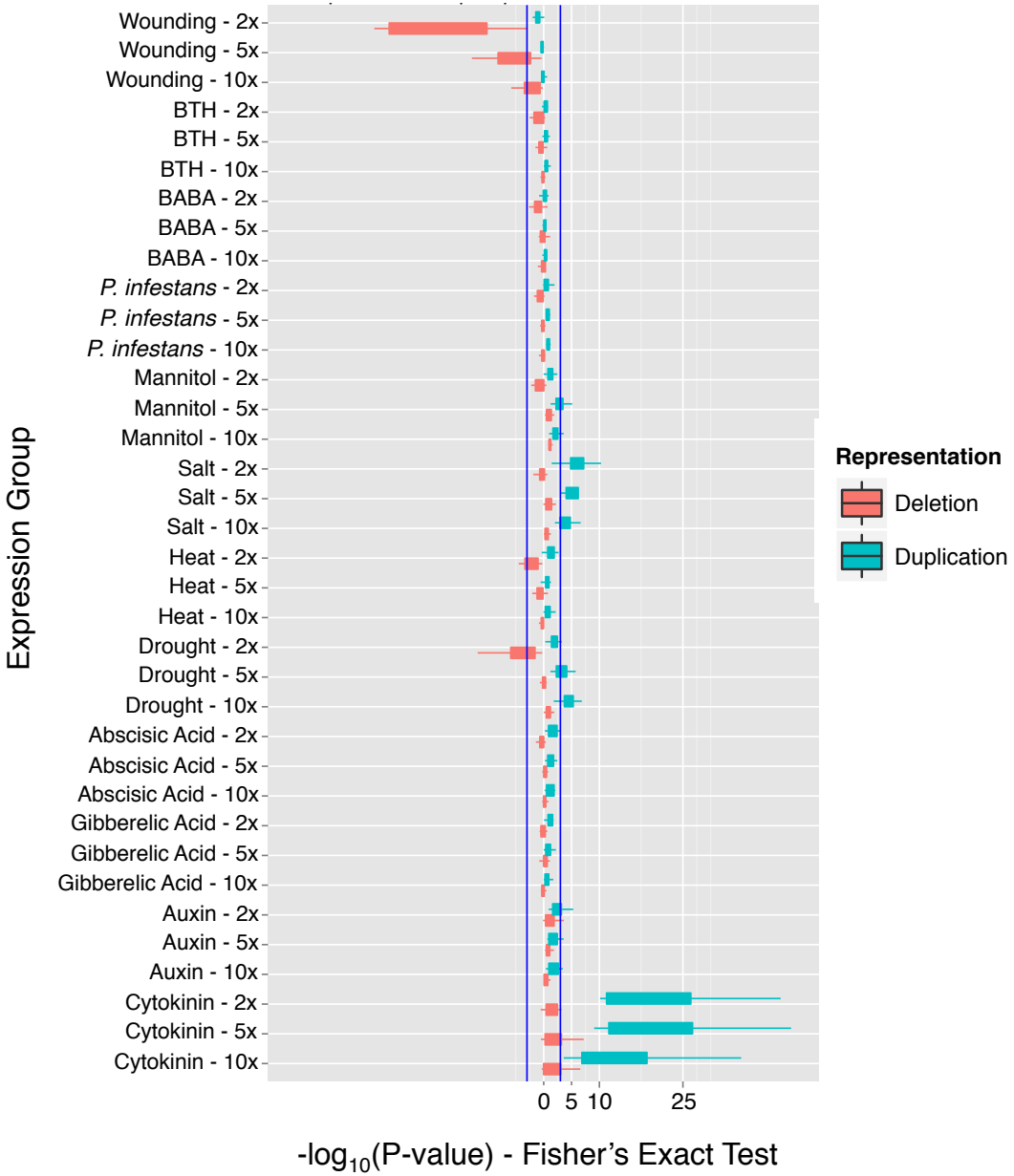
Supplemental Figure 5. Copy number variation (CNV) size distribution by clone up to 30-kb for each clone in the monoploid panel.



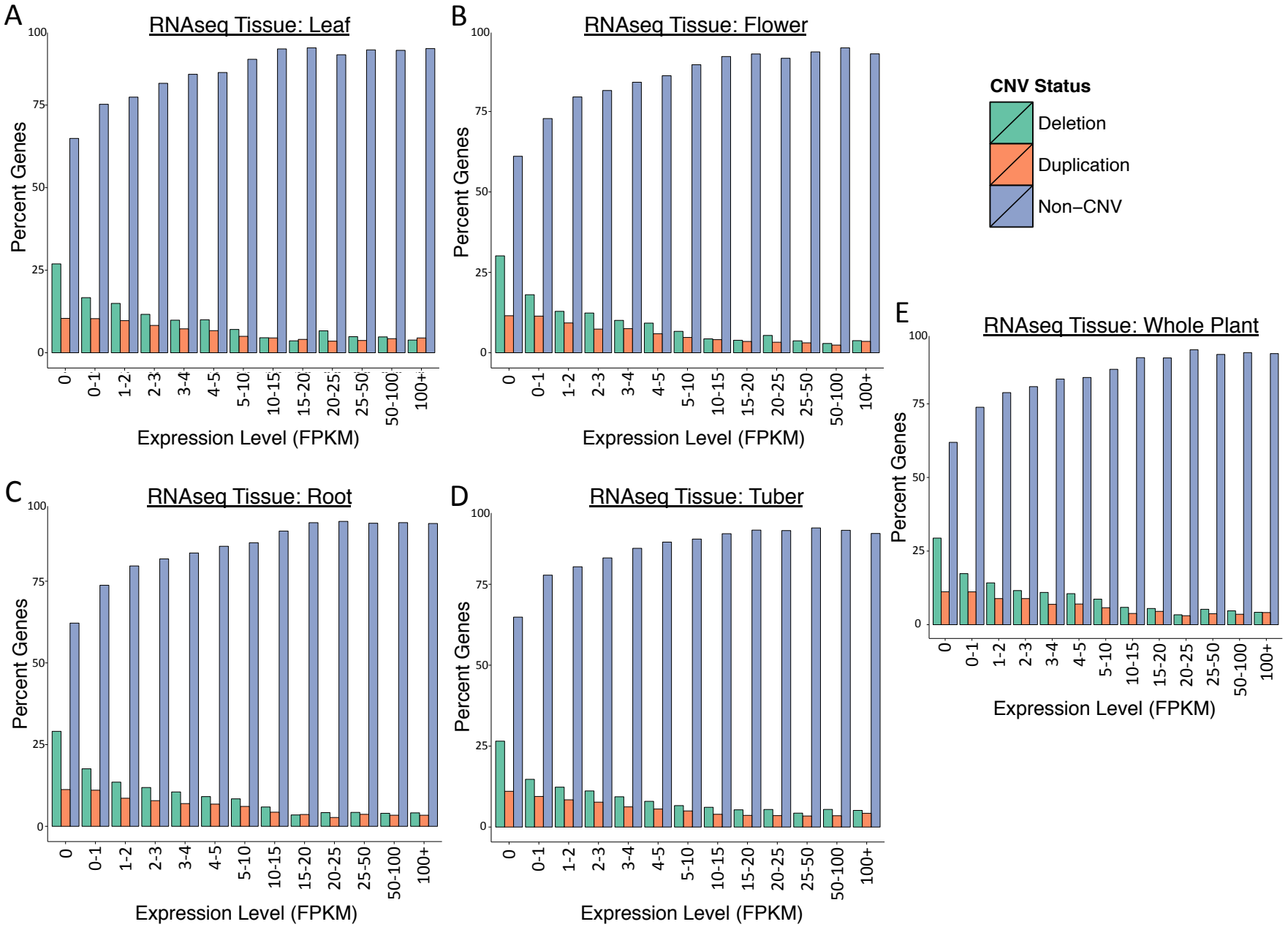
Supplemental Figure 6. Phylogenetic tree based on protein alignment of annotated small auxin up-regulated RNA (SAUR) genes from rice (blue), Arabidopsis (green), tomato (red), and potato (brown) proteomes. Clades I & II indicated major Solanum-specific expansions of the SAURs gene family. Blue circles indicated potato genes showing copy number variation in the monoploid panel. Specific potato SAUR genes with CNV can be found in Supplemental Dataset 5.



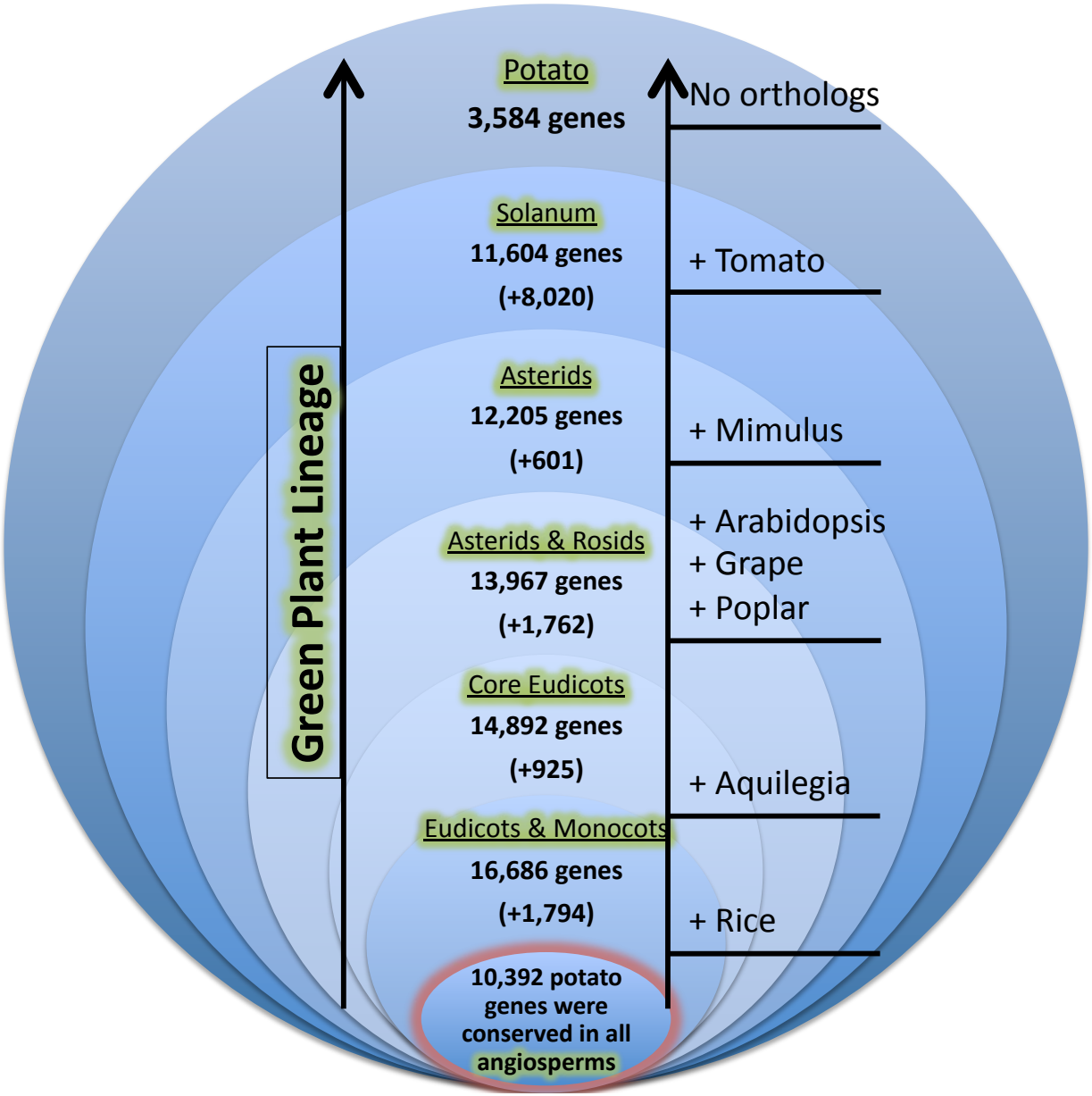
Supplemental Figure 7. Phylogenetic tree based on protein alignment of genes with sequence homology to five tomato methylketone synthase 1 (MKS1) genes from Amborella (turquoise), rice (blue), Arabidopsis (green), *Mimulus guttatus* (yellow), tomato (red) and potato (brown). Orange branches indicated *Solanum*-specific clades. Brown triangles indicate potato genes showing copy number variation in the monoploid panel. Genes highlighted with red triangles indicated the five annotated tomato MKS1 genes. Specific potato MKS1 homologs with CNV can be found in Supplemental Dataset 5.



Supplemental Figure 8. Boxplot of copy number variation enrichment for individual stress and hormone response expression classes.



Supplemental Figure 9. Summary of copy number variation rates in genes with different expression levels based on fragments per kilobase per million mapped reads (FPKM) values from leaf (A), flower (B), root (C), tuber (D), and whole *in vitro* plants tissues (E).



Supplemental Figure 10. Overview of potato gene lineage categories generated based on orthologous gene clustering.

Supplemental Table 1. Whole genome resequencing data generated for the monoploid panel.

Library ID	Library SRA Accession No.	Clone	Library Insert Size (bp)	Total # reads	# reads mapped	% reads mapped	Overall Coverage
NPV_FN	SRX1060643	DM	300	313,380,049	312,905,950	99.85	35
NPV_AH	SRX1060631	M1	200	337,950,033	334,797,446	99.07	
NPV_AH	SRX1060631	M1	600-700	261,620,303	258,537,516	98.82	62
NPV_AI	SRX1060632	M2	200	298,793,893	296,606,355	99.27	
NPV_AI	SRX1060632	M2	600-700	319,373,505	316,412,887	99.07	69
NPV_AJ	SRX1060633	M3	200	298,442,626	297,361,266	99.64	
NPV_AJ	SRX1060633	M3	600-700	258,409,721	257,151,360	99.51	62
NPV_BD	SRX1060634	M4	200	167,806,255	166,203,217	99.04	
NPV_BD	SRX1060634	M4	600-700	262,272,410	259,298,458	98.87	48
NPV_BE	SRX1060635	M5	200	194,820,693	192,767,485	98.95	
NPV_BE	SRX1060635	M5	600-700	227,641,242	224,860,805	98.78	47
NPV_GQ_1	SRX1060637	M6	200	109,085,479	108,228,516	99.21	
NPV_GQ_1	SRX1060637	M6	200	20,879,807	20,710,034	99.19	
NPV_GQ_2	SRX1060637	M6	600-700	116,847,681	115,697,215	99.02	
NPV_GQ_2	SRX1060637	M6	600-700	20,239,784	20,004,607	98.84	30
NPV_AK	SRX1060638	M7	200	270,697,520	269,538,247	99.57	
NPV_AK	SRX1060638	M7	600-700	241,147,483	239,741,768	99.42	57
NPV_AL	SRX1060639	M8	200	211,294,041	209,674,869	99.23	
NPV_AL	SRX1060639	M8	600-700	275,220,134	272,524,257	99.02	54
NPV_BG	SRX1060640	M9	200	279,983,384	278,526,757	99.48	
NPV_BG	SRX1060640	M9	600-700	140,012,009	138,122,135	98.65	47
NPV_AO	SRX1060641	M10	200	231,360,207	229,557,169	99.22	
NPV_AO	SRX1060641	M10	600-700	259,883,198	257,297,930	99.01	55
NPV_AP	SRX1060642	M11	200	338,160,694	335,346,760	99.17	
NPV_AP	SRX1060642	M11	600-700	218,179,498	215,938,171	98.97	62
NPV_AN	SRX1060946	M13	200	254,491,943	251,747,073	98.92	
NPV_AN	SRX1060946	M13	600-700	278,513,799	274,689,840	98.63	59

Supplemental Table 2. Information on single nucleotide polymorphisms identified in the monoploid panel.

Sample	Total SNPs	Intergenic	1kb Upstream /Down-stream	UTR	Intron	Splicing	Exon	Coding synon-ymous	Coding non-synon-ymous	Stop Gain	Stop Loss
M1	3,433,063	2,539,108	465,825	67,232	271,029	451	89,418	35,706	52,027	1,262	423
M2	1,557,476	1,179,533	185,994	27,875	122,272	198	41,604	16,787	24,041	602	174
M3	800,333	582,514	110,577	17,826	67,435	111	21,870	9,535	11,978	261	96
M4	3,242,070	2,304,768	460,132	80,190	286,236	415	110,329	48,747	59,927	1,228	427
M5	3,664,157	2,605,542	507,524	90,288	332,693	473	127,637	56,404	69,340	1,416	477
M6	3,632,667	2,544,889	473,958	98,808	357,201	491	157,320	70,883	84,156	1,687	594
M7	1,186,135	842,979	176,651	28,786	104,062	124	33,533	14,135	18,843	395	160
M8	3,625,031	2,644,080	510,149	74,759	300,706	442	94,895	38,336	54,796	1,292	471
M9	3,989,158	2,968,254	474,675	80,713	327,627	617	137,272	57,531	77,272	1,841	628
M10	3,718,500	2,732,463	504,737	74,133	301,235	494	105,438	43,085	60,405	1,453	495
M11	3,648,940	2,740,365	478,165	65,986	276,628	431	87,365	34,511	51,107	1,321	426
M13	4,764,182	3,449,119	667,678	107,513	408,093	571	131,208	54,047	74,810	1,782	569

Supplemental Table 3. Number of copy number variants identified in the monoploid panel.

Clone	CNV Type	chr00	chr01	chr02	chr03	chr04	chr05	chr06	chr07	chr08	chr09	chr10	chr11	chr12	chr-Unk	Total
M1	DEL	465	889	318	405	666	456	341	501	232	706	434	435	366	46	6,260
M2	DEL	330	988	56	85	81	505	64	153	388	290	67	63	327	34	3,431
M3	DEL	140	99	116	468	93	86	69	490	242	69	58	55	67	29	2,081
M4	DEL	381	596	770	902	187	427	459	623	72	306	381	265	419	64	5,852
M5	DEL	393	473	411	882	1261	470	467	587	66	386	121	337	403	50	6,307
M6	DEL	431	589	266	649	490	379	491	496	258	556	413	318	347	80	5,763
M7	DEL	238	188	57	604	78	761	68	90	121	71	68	393	75	28	2,840
M8	DEL	423	785	294	651	568	392	472	513	243	529	317	475	384	53	6,099
M9	DEL	406	696	257	264	744	375	448	521	383	527	368	454	301	49	5,793
M10	DEL	404	597	403	665	588	394	494	511	282	524	371	371	348	43	5,995
M11	DEL	450	850	432	358	588	433	489	585	239	533	415	274	621	56	6,323
M13	DEL	422	374	432	384	1130	445	1035	530	208	286	1069	343	367	39	7,064
M1	DUP	201	285	171	170	277	188	164	185	154	234	185	126	215	22	2,577
M2	DUP	128	277	93	93	108	117	92	80	122	135	86	54	156	24	1,565
M3	DUP	117	70	44	96	66	48	56	89	66	57	47	26	60	55	897
M4	DUP	220	303	138	210	212	176	228	193	170	177	173	132	216	24	2,572
M5	DUP	217	302	160	217	321	235	252	221	181	218	166	133	239	25	2,887
M6	DUP	237	332	163	226	244	195	225	202	197	251	214	141	217	20	2,864
M7	DUP	113	111	69	104	70	177	71	82	77	68	75	107	74	24	1,222
M8	DUP	182	287	154	191	245	179	211	193	177	227	185	161	200	25	2,617
M9	DUP	220	307	135	185	308	195	195	183	198	213	178	157	194	35	2,703
M10	DUP	197	262	173	198	242	187	205	165	183	236	201	134	201	61	2,645
M11	DUP	211	306	148	171	254	185	212	178	176	237	184	113	237	27	2,639
M13	DUP	257	383	179	240	360	247	215	220	268	269	242	195	338	55	3,468

Supplemental Table 4. Comparison of structural variation identified by CNVnator and through read depth analyses.

Sample	CNV Type	No. CNVnator Calls	No. CNVnator Calls Validated	% CNVnator Calls Validated	Total Sequence (Mb) - CNVnator Validated	Total Sequence (Mb) - Unique to CNVnator	Total Sequence (Mb) - Unique to Read Depth Analysis
M1	deletion	6,260	5,969	95.35	45.984	0.937	127.479
M2	deletion	3,431	3,130	91.23	22.989	1.004	130.949
M3	deletion	2,081	1,842	88.52	10.000	0.848	150.671
M4	deletion	5,852	5,551	94.86	41.871	1.000	120.759
M5	deletion	6,307	6,037	95.72	46.117	0.805	121.879
M6	deletion	5,763	5,530	95.96	43.285	0.736	79.435
M7	deletion	2,840	2,589	91.16	15.080	0.656	146.038
M8	deletion	6,099	5,830	95.59	52.344	1.016	123.404
M9	deletion	5,793	5,574	96.22	52.676	0.877	81.499
M10	deletion	5,995	5,731	95.6	45.412	0.924	124.536
M11	deletion	6,323	6,032	95.4	52.464	0.898	127.511
M13	deletion	7,064	6,833	96.73	63.246	0.819	122.382
ALL	deletion	63,808	60648	**95.05**			
M1	duplication	2,577	2,212	85.84	11.013	1.540	67.694
M2	duplication	1,565	1,169	74.7	5.368	1.455	38.382
M3	duplication	897	521	58.08	2.315	1.344	38.943
M4	duplication	2,572	2,130	82.81	10.534	2.067	67.223
M5	duplication	2,887	2,461	85.24	12.971	2.060	66.933
M6	duplication	2,864	2,441	85.23	12.234	1.912	49.536
M7	duplication	1,222	783	64.08	3.751	1.829	37.067
M8	duplication	2,617	2,306	88.12	12.206	1.490	119.794
M9	duplication	2,703	2,328	86.13	13.205	2.147	59.831
M10	duplication	2,645	2,288	86.5	11.419	1.760	74.526
M11	duplication	2,639	2,285	86.59	12.131	1.550	97.259
M13	duplication	3,468	3,099	89.36	19.089	2.503	115.770
ALL	duplication	28,656	24,023	**83.83**			

Supplemental Table 5. Gene expression categories assessed for enrichment in the CNV gene set.

Expression Class	Criteria
Highly Expressed - Root	FPKM >= 10 in at least one root tissue library
Highly Expressed - Tuber	FPKM >= 10 in at least one tuber tissue library
Highly Expressed - Vegetative	FPKM >= 10 in at least one aboveground vegetative tissue library
Highly Expressed - Reproductive	FPKM >= 10 in at least one aboveground reproductive tissue library
Low Expression	FPKM < 1 in all tissue libraries
Wounding - induced	[x]assessed 2-.5-.10-fold FPKM increase under wounding treatment
BTH - induced	[x]assessed 2-.5-.10-fold FPKM increase under BTH treatment
BABA - induced	[x]assessed 2-,5-,10-fold FPKM increase under BABA treatment
P.infestans - induced	[x]assessed 2-,5-,10-fold FPKM increase under P.infestans treatment
Biotic - induced	[x]assessed 2-.5-.10-fold FPKM increase under BTH. BABA. or P.infestans treatment
Mannitol - induced	[x]assessed 2-,5-,10-fold FPKM increase under mannitol treatment
Salt - induced	[x]assessed 2-,5-,10-fold FPKM increase under salt treatment
Heat - induced	[x]assessed 2-.5-.10-fold FPKM increase under heat treatment
Drought - induced	[x]assessed 2-,5-,10-fold FPKM increase under drought treatment
Abiotic - induced	[x]assessed 2-,5-,10-fold FPKM increase under mannitol, salt, heat, drought, or ABA treatment
ABA - induced	[x]assessed 2-.5-.10-fold FPKM increase under ABA treatment
GA3 - induced	[x]assessed 2-,5-,10-fold FPKM increase under GA3 treatment
Auxin - induced	[x]assessed 2-,5-,10-fold FPKM increase under auxin treatment
Cytokinin - induced	[x]assessed 2-.5-.10-fold FPKM increase under cytokinin treatment
Hormone - induced	[x]assessed 2-.5-.10-fold FPKM increase under ABA. GA3.auxin. or cytokinin treatment

[x]Genes reported as in-text induced were based on a 5-fold FPKM induction threshold