

labels	snpnames	Lin kage	Genetic_ Distances. cM.	Marker_ID	Description	Scientific Name	Max Score	Total Score	Query Cover	E value
S1	384	lg1	198.33	lm_ll_9859	PREDICTED: <i>Populus trichocarpa</i>					
S2	388	lg1	200.51	lm_ll_10319	transcription factor MYB83 (LOC7463851), mRNA	<i>Populus trichocarpa</i>	126	126	61%	5.00E-25
S3	539	lg1	266.27	lm_ll_8813						
S4	654	lg1	319.71	lm_ll_7100	PREDICTED: <i>Populus euphratica</i> putative glucose-6-phosphate 1-epimerase (LOC105127368), mRNA					
S5	825	lg1	408.58	lm_ll_10880		<i>Populus euphratica</i>	198	198	100%	1.00E-46
S6	849	lg1	423.84	nn_np_11246	PREDICTED: <i>Populus alba</i> protein ARABIDILLO 1-like (LOC118036755), transcript variant X3, mRNA	<i>Populus alba</i>	158	158	80%	2.00E-34
S7	850	lg1	423.84	nn_np_8244	PREDICTED: <i>Populus trichocarpa</i> endoglucanase 25 (LOC7491486), mRNA	<i>Populus trichocarpa</i>	198	198	100%	1.00E-46
S8	854	lg1	425.13	nn_np_3325	PREDICTED: <i>Populus euphratica</i> pentatricopeptide repeat-containing protein At3g57430, chloroplastic (LOC105113669), mRNA	<i>Populus euphratica</i>	198	198	100%	1.00E-46
S9	855	lg1	426.17	nn_np_11515	PREDICTED: <i>Populus alba</i> peptidyl-prolyl cis-trans isomerase					
S10	856	lg1	426.17	nn_np_9847	FKBP13, chloroplastic-like (LOC118036805), mRNA	<i>Populus alba</i>	87.9	87.9	42%	2.00E-13
S11	859	lg1	428.55	nn_np_9695	PREDICTED: <i>Populus</i>	<i>Populus alba</i>	198	198	100%	1.00E-46

					<i>alba</i> esterase-like (LOC118042355), mRNA					
S12	860	lg1	428.55	nn_np_12543	PREDICTED: <i>Populus euphratica</i>					
S13	863	lg1	430.46	nn_np_174	uncharacterized LOC105113656 (LOC105113656), ncRNA	<i>Populus euphratica</i>	198	198	100%	1.00E-46
S14	864	lg1	430.46	nn_np_8580						
S15	868	lg1	433.61	nn_np_10165	PREDICTED: <i>Populus euphratica</i>					
S16	869	lg1	436.65	nn_np_10694	uncharacterized LOC105133751 (LOC105133751), ncRNA	<i>Populus euphratica</i>	204	204	100%	2.00E-48
S17	870	lg1	436.77	nn_np_3042						
S18	871	lg1	436.85	nn_np_10269						
S19	872	lg1	436.86	nn_np_5995	PREDICTED: <i>Populus euphratica</i> protein					
S20	875	lg1	438.51	nn_np_12747	NRT1/ PTR FAMILY 6.1 (LOC105133784), transcript variant X5, mRNA	<i>Populus euphratica</i>	198	198	100%	1.00E-46
S21	877	lg1	438.51	nn_np_11694						
S22	881	lg1	441.33	nn_np_10893						
S23	882	lg1	441.49	nn_np_9467	PREDICTED: <i>Populus euphratica</i> histidine					
S24	889	lg1	442.75	nn_np_5989	kinase 3-like (LOC105133705), transcript variant X1, misc_RNA	<i>Populus euphratica</i>	204	204	100%	2.00E-48
S25	890	lg1	442.75	nn_np_11954	PREDICTED: <i>Populus euphratica</i> probable					
S26	910	lg1	450.82	nn_np_11836	leucine-rich repeat receptor-like protein kinase At2g33170 (LOC105116523), mRNA	<i>Populus euphratica</i>	198	198	100%	1.00E-46

S27	1491	lg2	244.2	hk_hk_2444						
S28	1660	lg3	12.51	lm_ll_10836						
					PREDICTED: <i>Populus euphratica</i> E3					
S29	1765	lg3	64.9	hk_hk_2098	ubiquitin-protein ligase HERC2 (LOC105138450), mRNA	<i>Populus euphratica</i>	204	204	100%	2.00E-48
					PREDICTED: <i>Populus alba</i> aspartic proteinase-like protein 1 (LOC118049145), transcript variant X2, mRNA	<i>Populus alba</i>	130	130	66%	4.00E-26
S31	2258	lg4	21.34	hk_hk_1961	<i>Populus trichocarpa</i> clone POP120-A02, complete sequence	<i>Populus trichocarpa</i>	176	176	100%	5.00E-40
					PREDICTED: <i>Phalaenopsis equestris</i> uncharacterized LOC110037592 (LOC110037592), partial mRNA	<i>Phalaenopsis equestris</i>	159	159	100%	5.00E-35
S33	2532	lg4	158.78	hk_hk_2687						
S34	2535	lg4	159.43	hk_hk_1366	<i>Populus trichocarpa</i> clone POP043-I07, complete sequence	<i>Populus trichocarpa</i>	156	156	98%	7.00E-34
S35	2537	lg4	160.27	hk_hk_2271	<i>Populus trichocarpa</i> clone POP043-I07, complete sequence	<i>Populus trichocarpa</i>	159	159	100%	5.00E-35
S36	2538	lg4	160.93	hk_hk_2206	<i>Populus trichocarpa</i> clone POP004-I13, complete sequence	<i>Populus trichocarpa</i>	73.1	73.1	81%	7.00E-09
S37	2541	lg4	163.44	hk_hk_2608	<i>Jasminum sambac</i> cultivar Hutoumoli linkage group Lg10	<i>Jasminum sambac</i>	80.5	80.5	81%	4.00E-11
					PREDICTED: <i>Populus trichocarpa</i> uncharacterized LOC112325761 (LOC112325761), mRNA	<i>Populus trichocarpa</i>	182	182	100%	1.00E-41
S39	2545	lg4	165.37	hk_hk_2306	<i>Populus trichocarpa</i>	<i>Populus trichocarpa</i>	106	106	98%	7.00E-19

					clone POP007-E06, complete sequence <i>Populus trichocarpa</i>					
S40	2546	lg4	165.65	hk_hk_1449	clone POP074-L11, complete sequence	<i>Populus trichocarpa</i>	159	240	100%	5.00E-35
S41	2548	lg4	165.87	hk_hk_2945						
S42	2550	lg4	166	hk_hk_1057	<i>Populus trichocarpa</i> clone POP006-H09, complete sequence	<i>Populus trichocarpa</i>	171	171	100%	2.00E-38
S43	2551	lg4	166.31	hk_hk_2952	<i>Populus trichocarpa</i> clone POP108-P17, complete sequence	<i>Populus trichocarpa</i>	148	411	100%	1.00E-31
S44	2552	lg4	167	hk_hk_1457	<i>Populus trichocarpa</i> clone POP091-F21, complete sequence	<i>Populus trichocarpa</i>	187	187	100%	2.00E-43
S45	2593	lg4	185.12	nn_np_5996						
S46	2762	lg4	270.86	nn_np_3833	PREDICTED: <i>Populus trichocarpa</i> putative F-box/kelch-repeat protein At1g20790 (LOC7494715), mRNA	<i>Populus trichocarpa</i>	191	191	99%	2.00E-44
S47	3035	lg5	130.52	nn_np_5908						
S48	3046	lg5	138.77	hk_hk_1933						
S49	3136	lg5	197.17	nn_np_10756	PREDICTED: <i>Populus trichocarpa</i> protease Do-like 10, mitochondrial (LOC18102668), partial mRNA	<i>Populus trichocarpa</i>	122	122	81%	7.00E-24
S50	3361	lg6	47.74	lm_ll_11231	<i>Populus trichocarpa</i> clone POP017-N07, complete sequence	<i>Populus trichocarpa</i>	148	148	100%	1.00E-31
S51	3562	lg6	144.19	lm_ll_5238	PREDICTED: <i>Populus euphratica</i> putative DNA-binding protein ESCAROLA (LOC105132215), mRNA	<i>Populus euphratica</i>	204	204	100%	2.00E-48
S52	3566	lg6	146.48	lm_ll_10915	PREDICTED: <i>Populus euphratica</i> protein FIZZY-RELATED 2-like (LOC105132191), mRNA	<i>Populus euphratica</i>	185	185	90%	8.00E-43

S53	3574	lg6	147.85	lm_ll_7994						
S54	3580	lg6	151.15	hk_hk_3039						
S55	3591	lg6	155.62	hk_hk_3195						
S56	4216	lg7	286.52	nn_np_10799						
S57	4227	lg7	286.99	nn_np_12765						
					PREDICTED: <i>Populus</i> <i>trichocarpa</i> uncharacterized LOC7463304 (LOC7463304), transcript variant X2, mRNA	<i>Populus trichocarpa</i>	198	198	100%	1.00E-46
S58	5479	lg11	29.93	lm_ll_5723						
					PREDICTED: <i>Populus</i> <i>euphratica</i> uncharacterized LOC105112383 (LOC105112383), mRNA	<i>Populus euphratica</i>	176	176	100%	5.00E-40
S59	5485	lg11	30.09	lm_ll_11763						
					<i>Populus trichocarpa</i> clone ACSB2753-D09, complete sequence	<i>Populus trichocarpa</i>	169	169	99%	8.00E-38
S60	5491	lg11	30.09	lm_ll_7120						
					PREDICTED: <i>Populus</i> <i>alba</i> uncharacterized LOC118051271 (LOC118051271), mRNA	<i>Populus alba</i>	80.5	80.5	39%	4.00E-11
S61	5750	lg12	0	hk_hk_2068						
S62	5751	lg12	0	hk_hk_2300						
S63	5754	lg12	2.04	hk_hk_2654						
S64	5787	lg12	36.81	lm_ll_8004						
S65	6085	lg12	169.67	lm_ll_6968						
					PREDICTED: <i>Populus</i> <i>euphratica</i> wall-associated receptor kinase-like 10 (LOC105120890), mRNA	<i>Populus euphratica</i>	204	204	100%	2.00E-48
S66	6115	lg12	192.69	lm_ll_7771						
S67	6117	lg12	192.7	lm_ll_5873						
					PREDICTED: <i>Populus</i> <i>euphratica</i> 5'-3' exoribonuclease 4-like (LOC105110438), transcript variant X5, misc_RNA	<i>Populus euphratica</i>	165	165	80%	1.00E-36
S68	6209	lg13	78.72	hk_hk_1264						
S69	6556	lg14	79.98	hk_hk_3108	<i>Populus trichocarpa</i>	<i>Populus trichocarpa</i>	182	182	100%	1.00E-41

S70	6606	lg14	86.35	lm_ll_7240	clone 13838686 integrase mRNA, complete cds					
S71	7186	lg16	0	lm_ll_7848	PREDICTED: <i>Populus euphratica</i> probable inactive receptor kinase At5g58300 (LOC105108877), transcript variant X4, mRNA	<i>Populus euphratica</i>	204	204	100%	2.00E-48
S72	7491	lg17	0.49	nn_np_7356	PREDICTED: <i>Populus euphratica</i> uncharacterized GPI-anchored protein At1g61900-like (LOC105142180), transcript variant X2, mRNA	<i>Populus euphratica</i>	204	204	100%	2.00E-48
S73	7492	lg17	1.1	nn_np_10281	<i>Populus trichocarpa</i> clone POP050-O20, complete sequence	<i>Populus trichocarpa</i>	117	117	100%	3.00E-22
S74	7639	lg17	64.81	hk_hk_1498						
S75	7660	lg17	74.28	hk_hk_2528						
S76	7701	lg17	91.42	hk_hk_2354	PREDICTED: <i>Populus euphratica</i> pentatricopeptide repeat-containing protein At4g21705, mitochondrial-like (LOC105129198), transcript variant X1, mRNA	<i>Populus euphratica</i>	204	204	100%	2.00E-48
S77	7816	lg18	19.32	nn_np_5502						
S78	7843	lg18	34.43	lm_ll_12799						
S79	7866	lg18	51.27	hk_hk_3130	PREDICTED: <i>Populus alba</i> protein SUPPRESSOR OF K(+) TRANSPORT GROWTH DEFECT 1-like (LOC118060148), transcript variant X3, mRNA	<i>Populus alba</i>	204	204	100%	2.00E-48

S80	7990	lg18	127.73	nn_np_11657	PREDICTED: <i>Populus alba</i> UBP1-associated protein 2C-like (LOC118062572), mRNA	<i>Populus alba</i>	198	198	100%	1.00E-46
S81	7993	lg18	133.97	nn_np_9127						
S82	7999	lg18	135.97	nn_np_8633						
S83	8003	lg18	140.51	nn_np_381						
S84	8004	lg18	144.34	hk_hk_1414						
S85	8009	lg18	150.12	nn_np_10664	PREDICTED: <i>Populus euphratica</i> pentatricopeptide repeat-containing protein At2g33760-like (LOC105128035), mRNA	<i>Populus euphratica</i>	204	204	100%	2.00E-48
S86	8011	lg18	150.59	nn_np_6308						
S87	8016	lg18	153.52	hk_hk_1488	<i>Populus trichocarpa</i> clone Pop1-49O2, complete sequence	<i>Populus trichocarpa</i>	119	119	99%	9.00E-23
S88	8020	lg18	154.4	hk_hk_3089	<i>Populus trichocarpa</i> clone Pop1-49O2, complete sequence	<i>Populus trichocarpa</i>	119	119	99%	9.00E-23
S89	8245	lg19	84.22	hk_hk_2795	PREDICTED: <i>Populus alba</i> uncharacterized LOC118056755 (LOC118056755), ncRNA	<i>Populus alba</i>	156	156	90%	7.00E-34
S90	8246	lg19	84.22	hk_hk_861	<i>Populus trichocarpa</i> clone POP024-G19, complete sequence	<i>Populus trichocarpa</i>	102	272	55%	9.00E-18
S91	8293	lg19	119.22	lm_ll_11569	<i>Populus trichocarpa</i> clone POP002-A24, complete sequence	<i>Populus trichocarpa</i>	176	176	100%	5.00E-40