

labels	snpnames	Linkage	Genetic_Distances.cM.	Marker_ID	Description	Scientific Name	Max_Score	Total_Score	Query_Cover	E_value
S1	183	lg1	105.78	lm_ll_10323	PREDICTED: <i>Populus trichocarpa</i> asparagine synthetase					
S2	369	lg1	187.97	lm_ll_11582	[glutamine-hydrolyzing] 1 (LOC7496783), transcript variant X1, mRNA	<i>Populus trichocarpa</i>	126	126	61%	5.00E-25
S3	667	lg1	327.97	hk_hk_1180	PREDICTED: <i>Populus euphratica</i> uncharacterized					
S4	720	lg1	356.2	hk_hk_1683	LOC105121580 (LOC105121580), transcript variant X1, mRNA	<i>Populus euphratica</i>	204	204	100%	2.00E-48
S5	1024	lg2	12.84	nn_np_5659	<i>Populus trichocarpa</i> clone POP073-O22, complete sequence	<i>Populus trichocarpa</i>	187	344	100%	2.00E-43
S6	1050	lg2	32.28	nn_np_9026	PREDICTED: <i>Populus euphratica</i> agamous-like MADS-box protein AGL6 (LOC105136119), mRNA	<i>Populus euphratica</i>	204	204	100%	2.00E-48
S7	1051	lg2	32.28	nn_np_10254	<i>Populus alba</i> mitochondrion, complete sequence	<i>Populus alba</i>	154	154	78%	2.00E-33
S8	1072	lg2	43.96	nn_np_4242						
S9	1078	lg2	48.94	nn_np_10480	PREDICTED: <i>Populus alba</i> nuclear poly(A) polymerase 4-like (LOC118030661), transcript variant X2, misc_RNA	<i>Populus alba</i>	178	178	100%	1.00E-40
S10	1083	lg2	51.56	nn_np_8109	<i>Populus trichocarpa</i> clone POP051-N24, complete sequence	<i>Populus trichocarpa</i>	154	154	100%	2.00E-33
S11	1538	lg2	268.17	hk_hk_1218	PREDICTED: <i>Populus euphratica</i>	<i>Populus euphratica</i>	163	163	82%	4.00E-36
S12	1738	lg3	48.99	lm_ll_6748						

					pentatricopeptide repeat-containing protein At2g42920, chloroplastic-like (LOC105126976), mRNA					
S13	1753	lg3	58.05	lm_ll_1118 2						
S14	1755	lg3	58.05	lm_ll_6387						
S15	1756	lg3	58.05	lm_ll_8169						
					PREDICTED: <i>Populus trichocarpa</i> nuclear speckle RNA-binding protein B (LOC7466409), mRNA	<i>Populus trichocarpa</i>	198	198	100%	1.00E-46
S16	1764	lg3	62.67	lm_ll_1092 6						
					PREDICTED: <i>Populus euphratica</i> uncharacterized LOC105120648 (LOC105120648), mRNA	<i>Populus euphratica</i>	204	204	100%	2.00E-48
S17	1905	lg3	141.37	nn_np_261 7						
					PREDICTED: <i>Phalaenopsis equestris</i> uncharacterized LOC110037592 (LOC110037592), partial mRNA	<i>Phalaenopsis equestris</i>	159	159	100%	5.00E-35
S18	2434	lg4	131.52	hk_hk_399						
S19	3061	lg5	146.07	hk_hk_866						
S20	3863	lg7	69.45	lm_ll_1237 3						
					PREDICTED: <i>Populus trichocarpa</i> uncharacterized LOC7472443 (LOC7472443), transcript variant X3, misc_RNA	<i>Populus trichocarpa</i>	100	100	49%	3.00E-17
S21	3865	lg7	71.24	lm_ll_8640						
					PREDICTED: <i>Populus euphratica</i> probable enoyl-CoA hydratase, mitochondrial (LOC105122438), mRNA	<i>Populus euphratica</i>	113	113	58%	4.00E-21
S22	3913	lg7	106.76	lm_ll_1102 3						
S23	4608	lg8	155.07	lm_ll_1245 5						
					PREDICTED: <i>Populus euphratica</i> probable RNA-dependent RNA polymerase 5 (LOC105126434), transcript variant X2,	<i>Populus euphratica</i>	161	161	81%	1.00E-35
S24	4757	lg9	84.26	hk_hk_113 5						

					mRNA						
					PREDICTED: <i>Populus</i>						
S25	5065	lg10	19.13	hk_hk_211	<i>trichocarpa</i> peroxisomal						
				3	2,4-dienoyl-CoA reductase						
					(LOC7482193), mRNA	<i>Populus trichocarpa</i>	204	204	100%	2.00E-48	
					PREDICTED: <i>Populus</i>						
					<i>euphratica</i> COMM						
S26	5128	lg10	48.49	hk_hk_139	domain-containing						
				1	protein 9-like						
					(LOC105139428),						
					transcript variant X2,						
					misc_RNA	<i>Populus euphratica</i>	174	174	88%	2.00E-39	
					<i>Populus trichocarpa</i> clone						
S27	5132	lg10	48.95	hk_hk_269	POP033-D24, complete						
				5	sequence	<i>Populus trichocarpa</i>	124	124	100%	2.00E-24	
S28	6050	lg12	142.29	lm_ll_7965							
S29	6237	lg13	95.91	lm_ll_1307							
				6							
					PREDICTED: <i>Populus</i>						
S30	6238	lg13	95.91	lm_ll_4077	<i>euphratica</i> uncharacterized						
					LOC105132545						
					(LOC105132545), ncRNA	<i>Populus euphratica</i>	204	204	100%	2.00E-48	
S31	6241	lg13	98.81	lm_ll_7261							
					PREDICTED: <i>Populus</i>						
					<i>euphratica</i> random slug						
S32	6260	lg13	108.35	lm_ll_1007	protein 5-like						
				9	(LOC105141521),						
					transcript variant X3,						
					mRNA	<i>Populus euphratica</i>	204	204	100%	2.00E-48	
					<i>Populus trichocarpa</i> clone						
S33	6298	lg13	118.81	lm_ll_6984	POP024-G19, complete						
					sequence	<i>Populus trichocarpa</i>	182	340	100%	1.00E-41	
S34	6309	lg13	118.81	lm_ll_6982							
					<i>Populus trichocarpa</i> clone						
S35	6322	lg13	122.06	lm_ll_931	JGIACSB21-D15, complete						
					sequence	<i>Populus trichocarpa</i>	154	154	100%	2.00E-33	
					PREDICTED: <i>Populus</i>						
S36	6330	lg13	124.43	lm_ll_4594	<i>euphratica</i> uncharacterized						
					LOC105112383						
					(LOC105112383), mRNA	<i>Populus euphratica</i>	128	128	81%	1.00E-25	
					PREDICTED: <i>Populus</i>						
S37	6369	lg13	131	lm_ll_6031	<i>trichocarpa</i>						
					uncharacterized						
					LOC18104421	<i>Populus trichocarpa</i>	198	198	100%	1.00E-46	

S38	6377	lg13	132	lm_ll_7344	(LOC18104421), mRNA					
S39	7043	lg15	72.12	lm_ll_12024	PREDICTED: <i>Populus euphratica</i> uncharacterized LOC105111429 (LOC105111429), mRNA	<i>Populus euphratica</i>	204	204	100%	2.00E-48
S40	8011	lg18	150.59	nn_np_6308	PREDICTED: <i>Populus euphratica</i> pentatricopeptide repeat-containing protein At2g33760-like (LOC105128035), mRNA	<i>Populus euphratica</i>	204	204	100%	2.00E-48
S41	8044	lg18	168.11	nn_np_8035	PREDICTED: <i>Populus trichocarpa</i> probable pyruvate, phosphate dikinase regulatory protein, chloroplastic (LOC7458550), mRNA	<i>Populus trichocarpa</i>	198	198	100%	1.00E-46
S42	8057	lg18	177.14	nn_np_10502						
S43	8062	lg18	180.14	nn_np_4862	PREDICTED: <i>Populus euphratica</i> cytochrome b561 and DOMON domain-containing protein At5g35735-like (LOC105141447), mRNA	<i>Populus euphratica</i>	198	198	100%	1.00E-46
S44	8072	lg18	184.27	nn_np_2539	<i>Populus trichocarpa</i> clone POP106-O02, complete sequence	<i>Populus trichocarpa</i>	174	174	99%	2.00E-39