

Additional file 4

File format: PDF

Title: Supplementary Table S3

Description:

Table S3. Proteins identified in poplar (*P. deltoides*) stem apoplast using 2-D PAGE MS/MS.

Poplar protein ID	Poplar transcript ID	Poplar new ID	<u>Spot number</u>	Mr/pl (theor.)	Number of matched peptides	Protein score	Protein identity/similarity	Sequence similarity	Accession number	Organism	Signal peptide (SP)	Non-classical SP
Cell wall metabolism												
255102*	gw1.XVI.1041.1	POPTR_0016s02620.2	<u>28</u>	73.3/5.5	14	213	Alpha-L-arabinofuranosidase	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.2	<u>29</u>	73.3/5.5	10	126	Alpha-L-arabinofuranosidase	74%	Q7X9G7	<i>Malus domestica</i>	yes	
718566	estExt_Genewise1_v1.C_LG_VII1401	POPTR_0007s04020.1	<u>44</u>	62.1/6.3	9	99	Pectin methylesterase 2	68%	A0ZNK0	<i>Pyrus communis</i>	yes	
816882	estExt_fgenesH4_pg.C_LG_II2363	POPTR_0002s23920.1	<u>55</u>	114.8/5.8	14	175	Alpha-mannosidase	71%	P94078	<i>Arabidopsis thaliana</i>	yes	
649422	grail3.0001045402	POPTR_0009s11830.2	<u>60</u>	39.8/6.6	3	94	Glucan endo-1,3-beta-glucosidase 7	73%	Q9M069	<i>Arabidopsis thaliana</i>	yes	
830063*	estExt_fgenesH4_pm.C_LG_II0164	POPTR_0002s03580.1	<u>12</u>	34.0/5.5	9	109	Phenylcoumaran benzylic ether reductase	100%	O65904	<i>Populus trichocarpa</i>	no	no
830063*	estExt_fgenesH4_pm.C_LG_II0164	POPTR_0002s03580.1	<u>22</u>	34.0/5.5	9	118	Phenylcoumaran benzylic ether reductase	100%	O65904	<i>Populus trichocarpa</i>	no	no
830063*	estExt_fgenesH4_pm.C_LG_II0164	POPTR_0002s03580.1	<u>47</u>	34.0/5.5	10	247	Phenylcoumaran benzylic ether reductase	100%	O65904	<i>Populus trichocarpa</i>	no	no
830063*	estExt_fgenesH4_pm.C_LG_II0164	POPTR_0002s03580.1	<u>46</u>	34.0/5.5	13	242	Phenylcoumaran benzylic ether reductase	100%	O65904	<i>Populus trichocarpa</i>	no	no
830063*	estExt_fgenesH4_pm.C_LG_II0164	POPTR_0002s03580.1	<u>49</u>	34.0/5.5	13	236	Phenylcoumaran benzylic ether reductase	100%	O65904	<i>Populus trichocarpa</i>	no	no
830063*	estExt_fgenesH4_pm.C_LG_II0164	POPTR_0002s03580.1	<u>1</u>	34.0/5.5	15	298	Phenylcoumaran benzylic ether reductase	100%	O65904	<i>Populus trichocarpa</i>	no	no
830063*	estExt_fgenesH4_pm.C_LG_II0164	POPTR_0002s03580.1	<u>50</u>	34.0/5.5	12	239	Phenylcoumaran benzylic ether reductase	100%	O65904	<i>Populus trichocarpa</i>	no	no
830063*	estExt_fgenesH4_pm.C_LG_II0164	POPTR_0002s03580.1	<u>48</u>	34.0/5.5	14	274	Phenylcoumaran benzylic ether reductase	100%	O65904	<i>Populus trichocarpa</i>	no	no
830063*	estExt_fgenesH4_pm.C_LG_II0164	POPTR_0002s03580.1	<u>21</u>	34.0/5.5	13	194	Phenylcoumaran benzylic ether reductase	100%	O65904	<i>Populus trichocarpa</i>	no	no
Cell wall and stress related												
547681*	eugene3.00010122	POPTR_0001s05050.1	<u>23</u>	36.8/4.5	4	292	Peroxidase	98%	Q43101	<i>Populus trichocarpa</i>	yes	
817692*	estExt_fgenesH4_pg.C_LG_III1871	POPTR_0003s21620.1	<u>37</u>	37.2/4.5	6	380	Peroxidase	95%	Q43049	<i>Populus kitakamiensis</i>	yes	
413562 [#] *	gw1.III.665.1	POPTR_0003s21640.1	<u>37</u>	32.8/4.7	6	356	Peroxidase	100%	Q43102	<i>Populus trichocarpa</i>	no	yes
817692*	estExt_fgenesH4_pg.C_LG_III1871	POPTR_0003s21620.1	<u>38</u>	37.2/4.5	6	94	Peroxidase	95%	Q43049	<i>Populus kitakamiensis</i>	yes	
413562 [#] *	gw1.III.665.1	POPTR_0003s21640.1	<u>38</u>	32.8/4.7	7	71	Peroxidase	100%	Q43102	<i>Populus trichocarpa</i>	no	yes
817694*	estExt_fgenesH4_pg.C_LG_III1873	POPTR_0003s21660.1	<u>58</u>	33.4/5.8	10	282	Peroxidase N	67%	Q42517	<i>Armoracia rusticana</i>	no	yes
800693*	fgenesH4_pm.C_LG_IV000380	POPTR_0004s14240.1	<u>73</u>	34.6/5.5	6	124	Peroxidase ATP17a like protein	68%	Q67XK7	<i>Arabidopsis thaliana</i>	yes	
589413*	eugene3.00280149	POPTR_0006s13190.1	<u>20</u>	36.9/5.7	8	75	Peroxidase 21	71%	Q42580	<i>Arabidopsis thaliana</i>	yes	
208491 [#] *	gw1.V.3892.1	POPTR_0005s14190.1	<u>57</u>	32.6/5.2	11	142	Peroxidase 10	66%	Q9FX85	<i>Arabidopsis thaliana</i>	no	yes
Stress/defense												
746640*	estExt_Genewise1_v1.C_1970084	POPTR_0015s05990.1	<u>18</u>	30.8/4.4	5	182	Acidic class III chitinase	71%	Q09Y38	<i>Citrullus lanatus</i>	yes	
290846 [#]	gw1.5405.1.1	POPTR_0001s26210.1	<u>79</u>	34.7/4.7	6	102	Beta-1,3-glucanase	69%	Q84RT6	<i>Fragaria ananassa</i>	no	yes
821619*	estExt_fgenesH4_pg.C_LG_IX1399	POPTR_0009s02070.1	<u>77</u>	27.3/5.5	9	291	Cytosolic ascorbate peroxidase 1	88%	A7KIX5	<i>Gossypium hirsutum</i>	no	no
821619*	estExt_fgenesH4_pg.C_LG_IX1399	POPTR_0009s02070.1	<u>105</u>	27.3/5.5	14	270	Cytosolic ascorbate peroxidase 1	88%	A7KIX5	<i>Gossypium hirsutum</i>	no	no
811643*	fgenesH4_pm.C_scaffold_163000009	POPTR_0011s01280.1	<u>90</u>	21.6/6.4	8	314	Cu-Zn superoxide dismutase	99%	A9PJW9	<i>Populus jackii</i>	no	yes
595511*	eugene3.00700152	POPTR_0005s04590.1	<u>11</u>	15.3/5.6	6	288	Superoxide dismutase [Cu-Zn]	100%	A3FM77	<i>Populus trichocarpa</i>	no	yes
595511*	eugene3.00700152	POPTR_0005s04590.1	<u>91</u>	15.3/5.6	4	93	Superoxide dismutase [Cu-Zn]	100%	A3FM77	<i>Populus trichocarpa</i>	no	yes
727757*	estExt_Genewise1_v1.C_LG_XI2337	POPTR_0011s03570.1	<u>7</u>	21.7/6.1	6	266	Benzoquinone reductase	85%	A3F7Q3	<i>Gossypium hirsutum</i>	no	no
663306*	grail3.0055008002	POPTR_0001s43940.1	<u>5</u>	21.6/5.8	8	283	Benzoquinone reductase	91%	A3F7Q3	<i>Gossypium hirsutum</i>	no	no

Table S3. continued

726993	estExt_Genewise1_v1.C_LG_XI0270	POPTR_0011s13310.1	<u>87</u>	21.7/6.0	7	371	Benzoquinone reductase	90%	A3F7Q3	<i>Gossypium hirsutum</i>	no	no
813818*	estExt_fgenes4_kg.C_LG_IV0063	POPTR_0004s17610.1	<u>39</u>	18.1/8.7	6	71	Peptidyl-prolyl <i>cis-trans</i> isomerase	100%	A9P8L4	<i>Populus trichocarpa</i>	no	no
813818*	estExt_fgenes4_kg.C_LG_IV0063	POPTR_0004s17610.1	<u>40</u>	18.1/8.7	10	234	Peptidyl-prolyl <i>cis-trans</i> isomerase	100%	A9P8L4	<i>Populus trichocarpa</i>	no	no
813818*	estExt_fgenes4_kg.C_LG_IV0063	POPTR_0004s17610.1	<u>13</u>	18.1/8.7	7	90	Peptidyl-prolyl <i>cis-trans</i> isomerase	100%	A9P8L4	<i>Populus trichocarpa</i>	no	no
179209 [#]	gw1.I.7809.1	POPTR_0001s13480.1	<u>99</u>	19.2/8.0	7	157	Peptidyl-prolyl <i>cis-trans</i> isomerase	91%	A7QUU7	<i>Vitis vinifera</i>	no	no
643603*	grail3.0003069401	POPTR_0002s08260.1	<u>45</u>	56.2/4.8	20	266	Protein disulfide-isomerase	76%	Q43116	<i>Ricinus communis</i>	yes	
832078	estExt_fgenes4_pm.C_LG_VI0650	POPTR_0006s24030.1	<u>98</u>	17.5/6.2	4	135	Cytosolic class II low molecular weight heat shock protein	88%	Q9XGS6	<i>Prunus dulcis</i>	no	no
563962	eugene3.00080557	POPTR_0008s06260.1	<u>100</u>	18.3/6.2	11	152	18.5 kDa class I heat shock protein	80%	P05478	<i>Glycine max</i>	no	yes
563887	eugene3.00080482	POPTR_0008s05410.1	<u>30</u>	71.2/5.1	14	110	DnaK-type molecular chaperone hsp70	95%	Q53NM9	<i>Oryza sativa subsp. japonica</i>	no	no
198984 [#] *	gw1.IV.4073.1	POPTR_0004s10240.1	<u>80</u>	26.6/9.1	8	112	Mangrin	73%	Q9AYT8	<i>Bruguiera sexangula</i>	no	no
729432*	estExt_Genewise1_v1.C_LG_XIII0635	POPTR_0013s01090.1	<u>51</u>	47.4/4.4	17	315	Calreticulin	86%	P93508	<i>Ricinus communis</i>	yes	
811231*	fgenes4_pm.C_scaffold_133000042	POPTR_0005s01850.1	<u>51</u>	43.8/4.6	9	111	Calreticulin-1	88%	O81919	<i>Beta vulgaris</i>	yes	
811231*	fgenes4_pm.C_scaffold_133000042	POPTR_0005s01850.1	<u>52</u>	43.8/4.6	12	260	Calreticulin-1	88%	O81919	<i>Beta vulgaris</i>	yes	
729432*	estExt_Genewise1_v1.C_LG_XIII0635	POPTR_0013s01090.1	<u>52</u>	47.4/4.4	7	64	Calreticulin	86%	P93508	<i>Ricinus communis</i>	yes	
729432*	estExt_Genewise1_v1.C_LG_XIII0635	POPTR_0013s01090.1	<u>53</u>	47.4/4.4	14	312	Calreticulin	86%	P93508	<i>Ricinus communis</i>	yes	
811231*	fgenes4_pm.C_scaffold_133000042	POPTR_0005s01850.1	<u>53</u>	43.8/4.6	7	141	Calreticulin-1	88%	O81919	<i>Beta vulgaris</i>	yes	
243514 [#]	gw1.XIV.257.1	POPTR_0483s00220.1	<u>53</u>	24.2/5.7	7	122	Glutathione S-transferase	63%	A0T2X7	<i>Vitis vinifera</i>	no	yes
665133	grail3.0104000601	POPTR_0002s20890.1	<u>8</u>	23.2/6.2	5	61	Glutathione S-transferase	63%	A0T2X7	<i>Vitis vinifera</i>	no	no
819386*	estExt_fgenes4_pg.C_LG_VI1270	POPTR_0006s19310.1	<u>106</u>	13.8/8.9	6	208	Blight-associated protein p12	49%	Q6K4C4	<i>Oryza sativa subsp. japonica</i>	yes	
573766	eugene3.00190240	POPTR_0019s04070.1	<u>101</u>	21.9/8.3	8	179	Peroxioredoxin	76%	Q5JBR7	<i>Ipomoea batatas</i>	no	yes
749645	fgenes4_kg.C_LG_IX000057	POPTR_0009s01280.1	<u>67</u>	20.8/5.6	13	159	Glyoxalase I	87%	A5A8J4	<i>Cucurbita maxima</i>	no	no
201272	gw1.IX.1737.1	POPTR_0009s12090.1	<u>49</u>	34.0/7.8	2	71	Isoflavone reductase related protein	80%	O81355	<i>Pyrus communis</i>	no	yes
201272	gw1.IX.1737.1	POPTR_0009s12090.1	<u>48</u>	34.1/7.8	2	79	Isoflavone reductase related protein	80%	O81355	<i>Pyrus communis</i>	no	yes
201272	gw1.IX.1737.1	POPTR_0009s12090.1	<u>1</u>	34.0/7.8	2	71	Isoflavone reductase related protein	80%	O81355	<i>Pyrus communis</i>	no	yes
Proteolysis												
551801*	eugene3.00021116	POPTR_0002s12130.1	<u>34</u>	82.0/6.6	12	132	Serine protease	98%	Q8RVJ7	<i>Populus canadensis</i>	yes	
781583*	fgenes4_pg.C_scaffold_40000333	POPTR_0014s02410.1	<u>78</u>	50.4/5.4	9	389	Cysteine protease CP1	82%	Q52QX8	<i>Manihot esculenta</i>	yes	
675847	grail3.0028002001	POPTR_0006s14400.1	<u>81</u>	39.3/6.3	5	124	Cysteine protease CP1	79%	A5HIJ1	<i>Actinia deliciosa</i>	yes	
675847	grail3.0028002001	POPTR_0006s14400.1	<u>82</u>	39.3/6.3	3	66	Cysteine protease CP1	79%	A5HIJ1	<i>Actinia deliciosa</i>	yes	
262677*	gw1.XVIII.3218.1	POPTR_0018s11600.1	<u>63</u>	55.1/5.9	14	214	Leucine aminopeptidase 1	77%	P30184	<i>Arabidopsis thaliana</i>	no	yes
708470*	estExt_Genewise1_v1.C_LG_I7028	POPTR_0001s06560.1	<u>54</u>	45.6/9.5	15	313	Nucleoid DNA-binding-like protein	66%	Q8L934	<i>Arabidopsis thaliana</i>	yes	
Carbohydrate metabolism												
656103*	grail3.0049021504	POPTR_0008s05640.1	<u>6</u>	27.2/6.0	15	480	Triosephosphate isomerase	100%	A9PE68	<i>Populus trichocarpa</i>	no	yes
656103*	grail3.0049021504	POPTR_0008s05640.1	<u>84</u>	27.2/6.0	14	382	Triosephosphate isomerase	100%	A9PE68	<i>Populus trichocarpa</i>	no	yes
724697*	estExt_Genewise1_v1.C_LG_X2172	POPTR_0010s21100.1	<u>86</u>	27.4/6.5	9	312	Triosephosphate isomerase	100%	A9P7V6	<i>Populus trichocarpa</i>	no	no
724697*	estExt_Genewise1_v1.C_LG_X2172	POPTR_0010s21100.1	<u>85</u>	27.4/6.5	8	171	Triosephosphate isomerase	100%	A9P7V6	<i>Populus trichocarpa</i>	no	no
822907	estExt_fgenes4_pg.C_LG_XI0680	POPTR_0011s09860.1	<u>10</u>	35.6/8.7	15	345	Malate dehydrogenase	100%	A9PCR0	<i>Populus trichocarpa</i>	no	no
564942*	eugene3.00081537	POPTR_0008s16670.1	<u>66</u>	35.7/6.1	11	117	Malate dehydrogenase	100%	A9P8R3	<i>Populus trichocarpa</i>	no	yes

Table S3. continued

564942*	eugene3.00081537	POPTR_0008s16670.1	<u>65</u>	35.7/6.1	18	308	Malate dehydrogenase	100%	A9P8R3	<i>Populus trichocarpa</i>	no	yes
707785	estExt_Genewise1_v1.C_LG_I4975	POPTR_0001s38560.1	<u>70</u>	35.5/8.0	11	266	Malate dehydrogenase	93%	A9PCR0	<i>Populus trichocarpa</i>	no	no
707785	estExt_Genewise1_v1.C_LG_I4975	POPTR_0001s38560.1	<u>68</u>	35.5/8.0	11	266	Malate dehydrogenase	93%	A9PCR0	<i>Populus trichocarpa</i>	no	no
575698*	eugene3.00151093	POPTR_0015s14380.1	<u>9</u>	47.9/5.7	18	192	Enolase	100%	A9PD49	<i>Populus trichocarpa</i>	no	yes
836259*	estExt_fgenesh4_pm.C_280132	POPTR_0006s11800.1	<u>61</u>	47.6/5.6	8	64	Enolase	100%	A9PIJ2	<i>Populus trichocarpa</i>	no	yes
575698*	eugene3.00151093	POPTR_0015s14380.1	<u>31</u>	47.9/5.7	11	136	Enolase	100%	A9PD49	<i>Populus trichocarpa</i>	no	yes
575698*	eugene3.00151093	POPTR_0015s14380.1	<u>32</u>	47.9/5.7	21	403	Enolase	100%	A9PD49	<i>Populus trichocarpa</i>	no	yes
836259*	estExt_fgenesh4_pm.C_280132	POPTR_0006s11800.1	<u>32</u>	47.6/5.6	6	133	Enolase	100%	A9PIJ2	<i>Populus trichocarpa</i>	no	yes
575698*	eugene3.00151093	POPTR_0015s14380.1	<u>2</u>	47.9/5.7	20	371	Enolase	100%	A9PD49	<i>Populus trichocarpa</i>	no	yes
836259*	estExt_fgenesh4_pm.C_280132	POPTR_0006s11800.1	<u>2</u>	47.6/5.6	6	133	Enolase	100%	A9PIJ2	<i>Populus trichocarpa</i>	no	yes
564181*	eugene3.00080776	POPTR_0008s08400.1	<u>64</u>	42.5/5.8	10	118	Phosphoglycerate kinase	99%	A9P828	<i>Populus trichocarpa</i>	no	no
564181*	eugene3.00080776	POPTR_0008s08400.1	<u>3</u>	42.5/5.8	13	184	Phosphoglycerate kinase	99%	A9P828	<i>Populus trichocarpa</i>	no	no
564181*	eugene3.00080776	POPTR_0008s08400.1	<u>24</u>	42.5/5.8	13	260	Phosphoglycerate kinase	99%	A9P828	<i>Populus trichocarpa</i>	no	no
659332*	grail3.0154005402	POPTR_0010s17870.1	<u>36</u>	42.7/5.7	8	75	Phosphoglycerate kinase	99%	O82159	<i>Populus nigra</i>	no	no
659332*	grail3.0154005402	POPTR_0010s17870.1	<u>104</u>	42.7/5.7	19	318	Phosphoglycerate kinase	99%	O82159	<i>Populus nigra</i>	no	no
825441*	estExt_fgenesh4_pg.C_LG_XVI1334	POPTR_0016s14950.1	<u>26</u>	61.1/5.4	29	496	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	90%	P35493	<i>Ricinus communis</i>	no	no
593790	eugene3.00570034	POPTR_0005s10990.1	<u>35</u>	98.2/5.9	18	99	Aconitate hydratase 1	90%	Q42560	<i>Arabidopsis thaliana</i>	no	no
592888	eugene3.00440223	POPTR_0017s01390.1	<u>74</u>	51.6/5.8	20	510	UDP-glucose pyrophosphorylase	98%	Q2V506	<i>Populus tremula x Populus tremuloides</i>	no	no
Other metabolic processes												
835828	estExt_fgenesh4_pm.C_LG_XVII10158	POPTR_0018s02250.1	<u>75</u>	50.9/8.7	20	183	Aspartate aminotransferase	89%	A5AZ93	<i>Vitis vinifera</i>	no	yes
720428	estExt_Genewise1_v1.C_LG_VIII1306	POPTR_0008s12550.1	<u>103</u>	59.9/5.9	11	66	ATP synthase subunit beta	88%	O82722	<i>Nicotiana sylvestris</i>	no	yes
720428	estExt_Genewise1_v1.C_LG_VIII1306	POPTR_0008s12550.1	<u>56</u>	59.9/5.9	14	116	ATP synthase subunit beta	88%	O82722	<i>Nicotiana sylvestris</i>	no	yes
644907	grail3.0050014702	POPTR_0002s19000.1	<u>62</u>	43.2/5.6	17	260	S-adenosylmethionine synthetase	98%	A9P822	<i>Populus trichocarpa</i>	no	no
823550	estExt_fgenesh4_pg.C_LG_XII1303	POPTR_0012s14980.1	<u>72</u>	25.6/5.5	8	122	Proteasome subunit alpha type	94%	A9PAG0	<i>Populus trichocarpa</i>	no	no
734681	estExt_Genewise1_v1.C_LG_XVI1054	POPTR_0016s02790.1	<u>59</u>	46.5/5.4	18	297	26S protease regulatory subunit 6B homolog	92%	Q9SEI4	<i>Arabidopsis thaliana</i>	no	yes
560773	eugene3.00060732	POPTR_0006s08710.1	<u>69</u>	27.0/5.7	11	277	3-beta hydroxysteroid dehydrogenase/isomerase protein	82%	Q94HJ5	<i>Oryza sativa</i>	no	yes
738638	estExt_Genewise1_v1.C_LG_XIX1453	POPTR_0019s08100.1	<u>88</u>	17.7/5.4	10	225	S-adenosylmethionine:2-demethylmenaquinone methyltransferase-like	89%	Q8W0C5	<i>Oryza sativa subsp. japonica</i>	no	no
816369*	estExt_fgenesh4_pg.C_LG_II0927	POPTR_0002s10150.1	<u>89</u>	18.8/5.6	1	108	Blue copper-like protein	55%	A3F8V0	<i>Gossypium hirsutum</i>	yes	
816369*	estExt_fgenesh4_pg.C_LG_II0927	POPTR_0002s10150.1	<u>93</u>	18.8/5.6	3	101	Blue copper-like protein	55%	A3F8V0	<i>Gossypium hirsutum</i>	yes	
816369*	estExt_fgenesh4_pg.C_LG_II0927	POPTR_0002s10150.1	<u>43</u>	18.8/5.6	1	153	Blue copper-like protein	55%	A3F8V0	<i>Gossypium hirsutum</i>	yes	
816369*	estExt_fgenesh4_pg.C_LG_II0927	POPTR_0002s10150.1	<u>42</u>	18.8/5.6	3	92	Blue copper-like protein	55%	A3F8V0	<i>Gossypium hirsutum</i>	yes	
816369*	estExt_fgenesh4_pg.C_LG_II0927	POPTR_0002s10150.1	<u>94</u>	18.8/5.6	2	117	Blue copper-like protein	55%	A3F8V0	<i>Gossypium hirsutum</i>	yes	
816369*	estExt_fgenesh4_pg.C_LG_II0927	POPTR_0002s10150.1	<u>92</u>	18.8/5.6	3	186	Blue copper-like protein	55%	A3F8V0	<i>Gossypium hirsutum</i>	yes	
816369*	estExt_fgenesh4_pg.C_LG_II0927	POPTR_0002s10150.1	<u>14</u>	18.8/5.6	3	126	Blue copper-like protein	55%	A3F8V0	<i>Gossypium hirsutum</i>	yes	
816369*	estExt_fgenesh4_pg.C_LG_II0927	POPTR_0002s10150.1	<u>17</u>	18.8/5.6	3	180	Blue copper-like protein	55%	A3F8V0	<i>Gossypium hirsutum</i>	yes	
816369*	estExt_fgenesh4_pg.C_LG_II0927	POPTR_0002s10150.1	<u>16</u>	18.8/5.6	3	136	Blue copper-like protein	55%	A3F8V0	<i>Gossypium hirsutum</i>	yes	
174402 [#] *	gw1.l.3002.1	POPTR_0001s33960.1	<u>95</u>	11.9/8.5	2	66	Blue copper protein	70%	Q8LED5	<i>Arabidopsis thaliana</i>	yes	
591761	eugene3.00400106	POPTR_0014s04880.1	<u>97</u>	16.3/6.1	6	102	Nucleoside diphosphate kinase	100%	A9PAF2	<i>Populus trichocarpa</i>	no	yes
591761	eugene3.00400106	POPTR_0014s04880.1	<u>96</u>	16.3/6.1	7	75	Nucleoside diphosphate kinase	100%	A9PAF2	<i>Populus trichocarpa</i>	no	yes

Table S3. continued

256059	gw1.XVI.1998.1	POPTR_0016s06310.1	<u>107</u>	22.6/9.8	5	67	40S ribosomal protein S5	91%	O65731	<i>Cicer arietinum</i>	no	no
727272	estExt_Genewise1_v1.C_LG_XI0817	POPTR_0011s15170.1	<u>107</u>	21.9/9.5	5	64	60S ribosomal protein L9	86%	P30707	<i>Pisum sativum</i>	no	yes
Cell structure												
813612	estExt_fgenesH4_kg.C_LG_I0082	POPTR_0001s31700.1	<u>25</u>	41.7/5.3	18	527	Actin	99%	A4ZS24	<i>Populus trichocarpa</i>	no	no
707456	estExt_Genewise1_v1.C_LG_I4174	POPTR_0001s29670.1	<u>83</u>	49.6/4.9	8	67	Alpha-tubulin 3	99%	A5YRY0	<i>Populus tremuloides</i>	no	no
Unclassified												
828728	estExt_fgenesH4_pg.C_2100027	POPTR_0008s22310.1	<u>41</u>	19.1/4.5	7	278	Translationally controlled tumor-like protein	85%	Q06H31	<i>Arachis hypogaea</i>	no	yes
732264*	estExt_Genewise1_v1.C_LG_XIV3377	POPTR_0014s15330.1	<u>71</u>	26.2/5.2	10	164	Carboxymethylenebutenolidase	84%	O80889	<i>Arabidopsis thaliana</i>	no	no
732264*	estExt_Genewise1_v1.C_LG_XIV3377	POPTR_0014s15330.1	<u>4</u>	26.2/5.2	11	161	Carboxymethylenebutenolidase	84%	O80889	<i>Arabidopsis thaliana</i>	no	no
732264*	estExt_Genewise1_v1.C_LG_XIV3377	POPTR_0014s15330.1	<u>19</u>	26.2/5.2	10	167	Carboxymethylenebutenolidase	84%	O80889	<i>Arabidopsis thaliana</i>	no	no
718495	estExt_Genewise1_v1.C_LG_VII1106	POPTR_1698s00200.1	<u>83</u>	26.4/5.8	9	236	Cysteine-rich repeat secretory protein 38	58%	Q9LRJ9	<i>Arabidopsis thaliana</i>	yes	
814847*	estExt_fgenesH4_pg.C_LG_I0347	POPTR_0001s05560.1	<u>15</u>	95.2/5.5	9	262	no sequence similarity to a known protein				yes	

protein sequence in JGI database is incomplete

* protein was also identified via 2D-LC MSMS