



Figure S1. Percent distribution of differentially expressed genes (DEGs) for cell compartment localization when copper resistant (RG) and nickel resistant (RG) were compared. DEGs from copper RG compared to nickel RG were annotated and allocated to terms within the cellular compartment category using Omicsbox/Blast2GO. Terms that had a total percentage of expressed genes lower than 2% were collectively categorized into the term “other.”

Table S1. Damage rating scale and plant classification based on reaction to nickel and copper treatments.

% of Leaf area with chlorosis/necrosis	Damage Rating	Genotype Classification
0-10	1	Resistant (RG)
10-20	2	
20-30	3	
30-40	4	Moderately Susceptible (MSG)
40-50	5	
50-60	6	
60-70	7	Susceptible (SG)
70-80	8	
> 80	9	

Table S2. Top 108 upregulated genes in copper RG in comparison to Nickel RG in *Pinus banksiana*

Rank	Gene ID	Cu Res1	Cu Res2	Cu Res3	Ni Res1	Ni Res2	Ni Res3	logFC	Adj. P. value	UniProt Description
0	TRINITY_DN2085_c0_g1	29.21	82.28	46.17	0.34	0.57	0.14	7.793	7.10E-05	Predicted Protein
1	TRINITY_DN1891_c0_g2	51.01	52.45	17.61	0.04	2.06	0.7	7.247	0.000114	Predicted Protein
2	TRINITY_DN8469_c0_g1	43.02	275.4	201.9	1.33	8.3	0.46	6.863	6.98E-05	Acid phosphatase 1, EC 3.1.3.2 (Acase-1(1))
3	TRINITY_DN1979_c0_g1	32.13	43.51	47.01	0.21	3.16	0.33	6.702	5.45E-06	Predicted Protein
4	TRINITY_DN4373_c0_g1	35.55	56.98	13.12	0.54	0.5	0.36	6.595	8.44E-05	Predicted Protein
5	TRINITY_DN5_c0_g1	18.7	16.84	12.27	0.1	0.8	0.23	6.538	0.000106	Pleiotropic drug resistance protein 1 (NtPDR1)
6	TRINITY_DN5_c0_g1	18.7	16.84	12.27	0.1	0.8	0.23	6.538	0.000106	ABC transporter G family member 32, ABC transporter ABCG32, AtABCG32 (Pleiotropic drug resistance protein 4) (Protein PERMEABLE CUTICLE 1)
7	TRINITY_DN5_c0_g1	18.7	16.84	12.27	0.1	0.8	0.23	6.538	0.000106	ABC transporter G family member 36, OsABCG36 (Pleiotropic drug resistance protein 9, OsPDR9)
8	TRINITY_DN5_c0_g1	18.7	16.84	12.27	0.1	0.8	0.23	6.538	0.000106	Pleiotropic drug resistance protein 1 (NpPDR1)
9	TRINITY_DN5_c0_g1	18.7	16.84	12.27	0.1	0.8	0.23	6.538	0.000106	ABC transporter G family member 44, OsABCG44 (Pleiotropic drug resistance protein 17, OsPDR17)
10	TRINITY_DN5_c0_g1	18.7	16.84	12.27	0.1	0.8	0.23	6.538	0.000106	ABC transporter G family member 31, OsABCG31 (Pleiotropic drug resistance protein 6, OsPDR6)
11	TRINITY_DN5_c0_g1	18.7	16.84	12.27	0.1	0.8	0.23	6.538	0.000106	ABC transporter G family member 34, OsABCG34 (Pleiotropic drug resistance protein 10, OsPDR10)
12	TRINITY_DN5742_c0_g1	25.47	76.4	14.17	0.6	1.07	0.41	6.162	5.17E-05	Predicted Protein
13	TRINITY_DN59895_c0_g1	107.34	136.22	54.47	0.8	4.56	2.36	6.155	1.45E-06	Predicted Protein
14	TRINITY_DN51306_c0_g1	32.05	61.43	35.69	0.53	0.7	1.91	6.153	1.48E-06	Predicted Protein
15	TRINITY_DN8170_c0_g1	50.21	123.33	300.25	1.81	1.13	8.48	6.150	5.72E-05	Predicted Protein
16	TRINITY_DN19606_c0_g1	31.77	21.11	20.22	0.5	1.66	0.29	5.866	4.22E-06	Granule-bound starch synthase 1, chloroplastic/amyloplastic, EC 2.4.1.242 (Granule-bound starch synthase I, GBSS-I)

17	TRINITY_DN6541_c0_g1	251.91	62.08	39.98	3.22	2.8	1.68	5.744	4.07E-05	Heavy metal-associated isoprenylated plant protein 20, AtHIP20, AtHIP20
18	TRINITY_DN6541_c0_g1	251.91	62.08	39.98	3.22	2.8	1.68	5.744	4.07E-05	Heavy metal-associated isoprenylated plant protein 26, AtHIP26, AtHIP26 (Farnesylated protein 6, AtFP6)
19	TRINITY_DN47729_c0_g2	7.89	24.87	20.63	0.46	0.23	0.87	5.668	0.000146	Predicted Protein
20	TRINITY_DN430_c0_g1	123.72	65.04	52.06	1.02	8.95	2.15	5.441	8.58E-06	Cytochrome P450 86A22, EC 1.14.14.129 (Long-chain acyl-CoA omega-monooxygenase)
21	TRINITY_DN1790_c0_g1	9.55	18.4	18.66	0.23	2.08	0.31	5.440	4.00E-05	Receptor-like protein kinase HSL1, EC 2.7.11.1 (Protein HAESA-LIKE1)
22	TRINITY_DN1072_c0_g1	97.21	115.92	41.8	4.4	9.29	0.62	5.334	6.56E-05	Predicted Protein
23	TRINITY_DN6055_c0_g1	18.79	22.98	21.77	0.56	1.18	0.81	5.330	5.78E-07	Predicted Protein
24	TRINITY_DN6813_c0_g1	235.35	117.07	35.45	1.7	10.19	3.65	5.309	6.74E-05	Predicted Protein
25	TRINITY_DN11710_c0_g2	150.88	92.2	20.39	1.17	7.66	2.13	5.304	0.000137	Predicted Protein
26	TRINITY_DN63319_c0_g1	28.39	21.29	22.62	0.58	1.05	1.41	5.255	8.92E-07	Predicted Protein
27	TRINITY_DN82353_c0_g1	13.94	23.06	17.36	0.87	0.98	0.45	5.156	2.89E-06	Predicted Protein
28	TRINITY_DN48473_c0_g1	56.5	107.55	80.8	1.68	5.59	4.91	5.085	9.27E-07	Predicted Protein
29	TRINITY_DN2130_c0_g1	22.32	44.82	44.69	2.2	1.09	1.68	5.050	4.23E-06	Predicted Protein
30	TRINITY_DN1441_c0_g2	340.37	453.06	121.8	13.03	19.89	9.5	4.943	5.01E-06	Predicted Protein
31	TRINITY_DN18305_c0_g1	12.58	17.34	7.24	0.21	1.24	0.93	4.934	4.54E-05	Predicted Protein
32	TRINITY_DN13702_c0_g1	199.68	359.26	315.24	12.82	34.72	6.66	4.907	2.16E-06	Predicted Protein
33	TRINITY_DN21077_c0_g1	104.2	111.9	29.03	1.46	13.71	2.65	4.883	8.29E-05	Predicted Protein
34	TRINITY_DN6218_c0_g2	633.56	1516.57	853.55	35.82	29.45	111.35	4.880	6.20E-06	Predicted Protein
35	TRINITY_DN234085_c0_g1	76.04	120.68	54.54	4.46	3.78	4.27	4.879	9.57E-07	Predicted Protein
36	TRINITY_DN590_c0_g1	200.71	160.06	49.6	4.56	6.07	9.65	4.833	1.59E-05	Predicted Protein
37	TRINITY_DN255785_c0_g2	10	9.31	5.83	0.27	0.7	0.49	4.799	4.24E-05	Predicted Protein
38	TRINITY_DN107212_c0_g1	73.86	56.2	27.06	2.12	3.39	2.87	4.777	3.19E-06	Predicted Protein
39	TRINITY_DN1091_c0_g1	107.98	82.18	33.01	3	8.72	2.4	4.706	1.41E-05	Predicted Protein
40	TRINITY_DN4262_c0_g2	6.71	7.64	4.96	0.32	0.6	0.28	4.652	0.000126	Predicted Protein
41	TRINITY_DN10240_c0_g1	9.94	8.21	10.71	0.46	0.21	1.82	4.629	8.89E-05	Blue copper protein
42	TRINITY_DN103915_c0_g1	7.46	29.74	24.59	0.55	2.53	0.98	4.595	0.000104	Predicted Protein
43	TRINITY_DN63319_c0_g2	57.41	39.86	23.94	2.04	2.44	2.92	4.591	3.30E-06	Predicted Protein

44	TRINITY_DN5693_c0_g1	315.06	441.27	270.61	9.95	42.87	23.88	4.584	8.61E-07	Predicted Protein
45	TRINITY_DN583_c0_g1	533.19	429.99	237.56	15.87	46.05	23.18	4.522	1.05E-06	Photosystem II 22 kDa protein, chloroplastic (CP22)
46	TRINITY_DN1967_c0_g1	16.28	29.89	19.85	1.39	0.84	2.46	4.504	1.16E-05	Shikimate O-hydroxycinnamoyltransferase, EC 2.3.1.133 (Hydroxycinnamoyl transferase) (Hydroxycinnamoyl-Coenzyme A shikimate/quinat hydroxycinnamoyltransferase)
47	TRINITY_DN13260_c0_g1	11	18.27	23.07	0.85	0.78	1.93	4.502	1.44E-05	Predicted Protein
48	TRINITY_DN5923_c0_g1	5.55	9.36	11.52	0.49	1.08	0.31	4.481	5.26E-05	Predicted Protein
49	TRINITY_DN1544_c0_g1	13.52	20.43	14.75	0.59	2.03	1.18	4.444	4.04E-06	Cellulose synthase-like protein E6, EC 2.4.1.- (OsCsIE6)
50	TRINITY_DN5006_c0_g1	8.07	9.8	7.28	0.24	1.58	0.58	4.404	3.12E-05	Cytochrome P450 750A1, EC 1.14.-.- (Cytochrome P450 CYPC)
51	TRINITY_DN2833_c0_g1	8.64	16.5	9.06	0.6	0.73	1.13	4.401	1.47E-05	Predicted Protein
52	TRINITY_DN139958_c0_g1	17.76	14.28	10.19	1.67	1.29	0.42	4.399	2.89E-05	Predicted Protein
53	TRINITY_DN5325_c0_g1	7.04	6.54	4.79	0.32	0.54	0.49	4.393	6.94E-05	Predicted Protein
54	TRINITY_DN2317_c0_g1	51.56	73.8	37.5	3.73	3.38	4.66	4.376	1.82E-06	Predicted Protein
55	TRINITY_DN4110_c0_g1	10.72	17.48	18.17	0.75	0.9	2	4.356	1.17E-05	Predicted Protein
56	TRINITY_DN792_c0_g2	397.04	322.71	190.6	14.08	73.46	10.46	4.349	2.23E-05	Granule-bound starch synthase 1, chloroplastic/amyloplastic, EC 2.4.1.242 (Granule-bound starch synthase I, GBSS-I)
57	TRINITY_DN3113_c0_g1	19.55	36.23	25.85	3.29	2.48	1.02	4.291	1.41E-05	Predicted Protein
58	TRINITY_DN62635_c0_g1	11.04	20.42	16.53	1.01	1.74	1.02	4.276	4.59E-06	Predicted Protein
59	TRINITY_DN20024_c0_g1	1387.36	3245.98	1849.75	109	181.45	219.45	4.259	8.19E-07	Predicted Protein
60	TRINITY_DN51306_c2_g1	456.91	1001.17	567.06	33.89	34.09	122.11	4.241	1.65E-05	Predicted Protein
61	TRINITY_DN452_c1_g1	7.49	12.56	6.92	0.27	1.63	0.82	4.237	4.90E-05	Receptor protein-tyrosine kinase CEPR1, EC 2.7.10.1 (Protein C-TERMINALLY ENCODED PEPTIDE RECEPTOR 1) (Protein XYLEM INTERMIXED WITH PHLOEM 1)
62	TRINITY_DN452_c1_g1	7.49	12.56	6.92	0.27	1.63	0.82	4.237	4.90E-05	Leucine-rich repeat receptor-like kinase protein SUNN, EC 2.7.11.1 (Protein SUPER NUMERIC NODULES)

63	TRINITY_DN13950_c0_g1	8.91	12.29	10.7	0.56	2.45	0.46	4.217	2.52E-05	Predicted Protein
64	TRINITY_DN8956_c0_g1	22.9	32.53	59.54	3.34	3.17	2.24	4.206	1.00E-05	Predicted Protein
65	TRINITY_DN5557_c0_g1	351.25	695.93	342.88	24.36	46.66	44.49	4.195	8.54E-07	Fructose-bisphosphate aldolase 2, chloroplastic, AtFBA2, EC 4.1.2.13
66	TRINITY_DN5557_c0_g1	351.25	695.93	342.88	24.36	46.66	44.49	4.195	8.54E-07	Fructose-bisphosphate aldolase, chloroplastic, EC 4.1.2.13
67	TRINITY_DN5557_c0_g1	351.25	695.93	342.88	24.36	46.66	44.49	4.195	8.54E-07	Fructose-bisphosphate aldolase 3, chloroplastic, AtFBA3, EC 4.1.2.13 (Protein PIGMENT DEFECTIVE 345)
68	TRINITY_DN5557_c0_g1	351.25	695.93	342.88	24.36	46.66	44.49	4.195	8.54E-07	Fructose-bisphosphate aldolase, chloroplastic, EC 4.1.2.13 (Chloroplastic aldolase, AldP)
69	TRINITY_DN13626_c0_g1	57.47	45.59	25.35	1.36	6.65	4.7	4.191	1.95E-05	Predicted Protein
70	TRINITY_DN5309_c0_g1	7.16	12.51	6.03	0.32	0.99	1.13	4.179	4.72E-05	Probable E3 ubiquitin-protein ligase RHY1A, EC 2.3.2.27 (RING-H2 finger Y1a) (RING-H2 zinc finger protein RHY1a) (RING-type E3 ubiquitin transferase RHY1A)
71	TRINITY_DN125498_c1_g1	121.27	373.21	247.23	9.74	17.65	44.82	4.123	4.22E-05	Predicted Protein
72	TRINITY_DN963_c0_g2	69.63	60.55	89.57	3.21	19.61	4.19	4.110	1.57E-05	Metal-nicotianamine transporter YSL3 (Protein YELLOW STRIPE LIKE 3, AtYSL3)
73	TRINITY_DN963_c0_g2	69.63	60.55	89.57	3.21	19.61	4.19	4.110	1.57E-05	Probable metal-nicotianamine transporter YSL7 (Protein YELLOW STRIPE LIKE 7, AtYSL7)
74	TRINITY_DN963_c0_g2	69.63	60.55	89.57	3.21	19.61	4.19	4.110	1.57E-05	Probable metal-nicotianamine transporter YSL12 (Protein YELLOW STRIPE LIKE 12, OsYSL12)
75	TRINITY_DN963_c0_g2	69.63	60.55	89.57	3.21	19.61	4.19	4.110	1.57E-05	Probable metal-nicotianamine transporter YSL14 (Protein YELLOW STRIPE LIKE 14, OsYSL14)
76	TRINITY_DN963_c0_g2	69.63	60.55	89.57	3.21	19.61	4.19	4.110	1.57E-05	Probable metal-nicotianamine transporter YSL11 (Protein YELLOW STRIPE LIKE 11, OsYSL11)
77	TRINITY_DN963_c0_g2	69.63	60.55	89.57	3.21	19.61	4.19	4.110	1.57E-05	Probable metal-nicotianamine transporter YSL9 (Protein YELLOW STRIPE LIKE 9, OsYSL9)

78	TRINITY_DN963_c0_g2	69.63	60.55	89.57	3.21	19.61	4.19	4.110	1.57E-05	Probable metal-nicotianamine transporter YSL16 (Protein YELLOW STRIPE LIKE 16, OsYSL16)
79	TRINITY_DN52249_c0_g3	7.28	5.78	4.03	0.21	1.21	0.51	4.088	0.000135	Predicted Protein
80	TRINITY_DN3604_c0_g1	5.48	6.5	4.61	0.29	1.04	0.41	4.075	6.63E-05	Predicted Protein
81	TRINITY_DN1217_c0_g1	48.16	71.15	146	2.86	8.85	14.44	4.074	5.54E-05	Putative anthocyanidin reductase, GbANR, EC 1.3.1.-
82	TRINITY_DN6386_c0_g1	11.97	34.03	18.9	1.71	0.92	3.86	4.059	0.000125	Predicted Protein
83	TRINITY_DN26976_c0_g1	82.95	53.31	76.71	1.91	16.63	8.7	4.054	4.59E-05	Aspartyl protease family protein At5g10770, EC 3.4.23.-
84	TRINITY_DN26976_c0_g1	82.95	53.31	76.71	1.91	16.63	8.7	4.054	4.59E-05	Protein ASPARTIC PROTEASE IN GUARD CELL 1, AtASPG1, EC 3.4.23.-
85	TRINITY_DN10188_c0_g1	7.31	6.61	3.43	0.4	0.82	0.4	4.048	0.000139	Cytochrome P450 750A1, EC 1.14.-.- (Cytochrome P450 CYPC)
86	TRINITY_DN5205_c0_g1	48.67	71.45	57.26	2.98	7.51	7.24	4.046	1.56E-06	Predicted Protein
87	TRINITY_DN224_c0_g1	15.09	15.45	6.33	0.48	1.72	1.63	4.031	6.75E-05	Subtilisin-like serine-protease S, SbtS, Subtilase S, EC 3.4.21.-
88	TRINITY_DN224_c0_g1	15.09	15.45	6.33	0.48	1.72	1.63	4.031	6.75E-05	Subtilisin-like protease SBT3.3, EC 3.4.21.- (Subtilase subfamily 3 member 3, AtSBT3.3)
89	TRINITY_DN224_c0_g1	15.09	15.45	6.33	0.48	1.72	1.63	4.031	6.75E-05	Subtilisin-like protease SBT3.5, EC 3.4.21.- (Subtilase subfamily 3 member 5, AtSBT3.5)
90	TRINITY_DN224_c0_g1	15.09	15.45	6.33	0.48	1.72	1.63	4.031	6.75E-05	Subtilisin-like protease SBT3.15, EC 3.4.21.- (Subtilase subfamily 3 member 15, AtSBT3.15)
91	TRINITY_DN1243_c0_g2	21.49	20.9	7.13	1.45	1.46	1.3	4.020	5.63E-05	Predicted Protein
92	TRINITY_DN3029_c0_g1	35.14	40.46	12.44	1.59	2.74	3.99	3.988	5.31E-05	Predicted Protein
93	TRINITY_DN54045_c0_g2	8.44	9.51	14.88	1.03	0.93	1.06	3.973	1.50E-05	Predicted Protein
94	TRINITY_DN5990_c0_g1	5.66	6.63	3.4	0.43	0.59	0.47	3.958	0.000133	Predicted Protein
95	TRINITY_DN2642_c0_g1	4.84	6.48	6.06	0.38	1.22	0.39	3.949	5.65E-05	Predicted Protein
96	TRINITY_DN3360_c0_g2	7.55	14.02	7.56	0.37	2.13	1.09	3.931	6.33E-05	Predicted Protein
97	TRINITY_DN28667_c0_g1	10.25	13.09	5.92	0.45	3.23	0.64	3.900	0.000142	Predicted Protein
98	TRINITY_DN1344_c0_g1	13.88	10.7	7.37	0.84	2.55	0.55	3.899	4.57E-05	Mannose-1-phosphate guanylyltransferase 1, EC 2.7.7.13 (GDP-mannose pyrophosphorylase 1)

										(Protein CYTOKINESIS DEFECTIVE 1) (Protein EMBRYO DEFECTIVE 101) (Protein HYPERSENSITIVE TO AMMONIUM ION 1) (Protein SENSITIVE TO OZONE 1) (Protein VITAMIN C DEFECTIVE 1)
99	TRINITY_DN7300_c0_g1	10.65	10.03	24.85	1.47	0.91	2.05	3.878	8.78E-05	Predicted Protein
100	TRINITY_DN4544_c0_g1	32.45	29.29	20.57	1.27	2.8	6.6	3.873	3.56E-05	Predicted Protein
101	TRINITY_DN3984_c0_g2	6.33	5.62	5.47	0.29	2.02	0.38	3.872	0.000121	Predicted Protein
102	TRINITY_DN3497_c0_g1	6.98	11.31	5.89	1.03	0.97	0.49	3.871	4.60E-05	Predicted Protein
103	TRINITY_DN35587_c0_g1	4.4	6.71	6.78	0.5	0.74	0.63	3.825	4.04E-05	Glyoxylase I 4, AtGLXI-like;4, AtGLYI4
104	TRINITY_DN26392_c0_g2	28.62	15.31	12.83	1.28	5.23	1.1	3.814	6.93E-05	Predicted Protein
105	TRINITY_DN57465_c0_g1	6.53	8.2	4.79	0.31	1.82	0.64	3.813	9.59E-05	Predicted Protein
106	TRINITY_DN262_c0_g2	8.8	20.03	10.55	1.16	1.57	1.39	3.788	2.18E-05	Polygalacturonase ADPG2, AtADPG2, PG ADPG2, EC 3.2.1.15 (Pectinase ADPG2) (Protein ARABIDOPSIS DEHISCENCE ZONE POLYGALACTURONASE 2)
107	TRINITY_DN262_c0_g2	8.8	20.03	10.55	1.16	1.57	1.39	3.788	2.18E-05	Probable polygalacturonase Atlg80170, PG, EC 3.2.1.15 (Pectinase Atlg80170)
108	TRINITY_DN262_c0_g2	8.8	20.03	10.55	1.16	1.57	1.39	3.788	2.18E-05	Polygalacturonase, PG, EC 3.2.1.15 (Pectinase)

Table S3. Top 112 downregulated genes in copper RG in comparison to Nickel RG in *Pinus banksiana*

Rank	Gene ID	Cu Res1	Cu Res2	Cu Res3	Ni Res1	Ni Res2	Ni Res3	logFC	Adj. P. value	UniProt Description
0	TRINITY_DN43547_c0_g1	0	0	0	24.15	39.01	23.93	-10.382	6.42E-05	Predicted Protein
1	TRINITY_DN1456_c0_g1	1.37	0	1.34	306.48	253.1	155.47	-9.527	0.00012871 ₉	Predicted Protein
2	TRINITY_DN2126_c0_g1	1.31	0.24	0.4	954.55	193.03	448.85	-9.030	4.26E-05	UDP-glycosyltransferase 75C1, Absciscic acid beta-glucosyltransferase, Indole-3-acetate beta-glucosyltransferase, SIUGT75C1, EC 2.4.1.121, EC 2.4.1.263
3	TRINITY_DN5965_c0_g1	0.28	0.12	1.02	159.21	70.92	203.21	-8.429	5.08E-05	Predicted Protein
4	TRINITY_DN5240_c1_g1	0.06	0.2	0.38	75.64	57.88	47.63	-7.894	0.00013167 ₅	Predicted Protein
5	TRINITY_DN2786_c0_g1	7.97	1.28	0.09	767.81	197.57	545.86	-7.817	0.00014700 ₂	Predicted Protein
6	TRINITY_DN7685_c0_g1	0.35	0.17	0.18	69.15	75.78	88.19	-7.718	1.68E-05	Predicted Protein
7	TRINITY_DN3685_c0_g2	7.54	1.2	0.09	524.13	169.45	298.36	-7.315	0.00014639 ₃	Copia protein (Gag-int-pol protein) [Cleaved into: Copia VLP protein; Copia protease, EC 3.4.23.-]
8	TRINITY_DN2463_c0_g1	5.21	0.97	0.68	301.76	196.16	568.86	-7.021	8.44E-06	Predicted Protein
9	TRINITY_DN2040_c0_g1	28.51	6	12.87	3943.91	1043.09	3644.25	-6.950	1.04E-05	Predicted Protein
10	TRINITY_DN5795_c0_g1	13.6	5.09	0.4	753.52	420.03	412.9	-6.580	5.36E-05	Predicted Protein
11	TRINITY_DN735_c0_g1	5.88	1.92	0.26	401.38	124.53	198.21	-6.422	9.90E-05	Predicted Protein
12	TRINITY_DN41085_c0_g1	1.46	0.55	8.2	230.93	100.32	461.71	-6.396	8.67E-05	Predicted Protein
13	TRINITY_DN5240_c0_g1	0.4	0.48	1.48	86.62	78.96	59.64	-6.375	1.11E-06	Protein TIFY 10b, OsTIFY10b (Jasmonate ZIM domain-containing protein 7, OsJAZ7) (OsJAZ6)
14	TRINITY_DN17_c0_g2	0.65	0.15	0.58	50.63	58.32	26.97	-6.307	1.89E-05	RING-H2 finger protein ATL60, EC 2.3.2.27 (RING-type E3 ubiquitin transferase ATL60)
15	TRINITY_DN800_c1_g1	2.53	0.34	0.33	127.84	44.55	121.22	-6.264	0.00010350 ₉	Predicted Protein
16	TRINITY_DN1755_c0_g1	0.73	0.19	0.22	37.36	42.04	37.53	-6.143	1.54E-05	Predicted Protein
17	TRINITY_DN1067_c0_g1	0.21	0.63	2.66	74.75	51.13	62.5	-6.138	1.50E-05	Predicted Protein

18	TRINITY_DN4963_c0_g1	1.2	1.08	0.26	107.91	63.25	101.25	-6.114	6.05E-06	Predicted Protein
19	TRINITY_DN3889_c0_g1	8.77	0.85	2.51	414.11	167.54	300.23	-6.071	3.22E-05	Predicted Protein
20	TRINITY_DN6289_c0_g1	0.34	0.08	0.38	23.79	21.01	21.41	-5.988	0.00013507 2	Predicted Protein
21	TRINITY_DN6111_c0_g1	0.47	0.11	0.98	29.31	29.12	29.02	-5.932	1.49E-05	Predicted Protein
22	TRINITY_DN4477_c0_g1	1.32	1.08	0.77	67.92	163.48	92.08	-5.924	1.74E-07	Predicted Protein
23	TRINITY_DN71807_c0_g1	0.75	0.09	1.03	29.61	23.8	49.04	-5.903	8.02E-05	Predicted Protein
24	TRINITY_DN971_c0_g1	0.32	0.18	3.12	40.71	30.9	35.98	-5.891	3.15E-05	1-aminocyclopropane-1-carboxylate synthase 7, ACC synthase 7, EC 4.4.1.14 (S-adenosyl-L-methionine methylthioadenosine-lyase 7)
25	TRINITY_DN971_c0_g1	0.32	0.18	3.12	40.71	30.9	35.98	-5.891	3.15E-05	1-aminocyclopropane-1-carboxylate synthase, ACC synthase, EC 1.4.-.-, EC 4.4.1.14 (S-adenosyl-L-methionine methylthioadenosine-lyase)
26	TRINITY_DN971_c0_g1	0.32	0.18	3.12	40.71	30.9	35.98	-5.891	3.15E-05	1-aminocyclopropane-1-carboxylate synthase 6, ACC synthase 6, EC 4.4.1.14 (S-adenosyl-L-methionine methylthioadenosine-lyase 6)
27	TRINITY_DN971_c0_g1	0.32	0.18	3.12	40.71	30.9	35.98	-5.891	3.15E-05	1-aminocyclopropane-1-carboxylate synthase 3, ACC synthase 3, EC 4.4.1.14 (Le-ACS3, ACS-3) (S-adenosyl-L-methionine methylthioadenosine-lyase 3)
28	TRINITY_DN971_c0_g1	0.32	0.18	3.12	40.71	30.9	35.98	-5.891	3.15E-05	1-aminocyclopropane-1-carboxylate synthase 1, ACC synthase 1, EC 4.4.1.14 (S-adenosyl-L-methionine methylthioadenosine-lyase)
29	TRINITY_DN756_c0_g1	7.06	0.88	8.25	578.57	195.91	235.86	-5.769	7.82E-05	Dirigent protein 21, AtDIR21
30	TRINITY_DN6061_c0_g1	3.75	2.9	7.44	355.22	178.84	637.66	-5.730	1.01E-05	Predicted Protein
31	TRINITY_DN1472_c0_g1	12.73	1.55	0.53	212.32	210.54	174.12	-5.729	5.80E-05	Triacylglycerol lipase OBL1, EC 3.1.1.- (Oil body lipase 1, NtOBL1)
32	TRINITY_DN6866_c0_g1	0.23	0.29	1.89	32.98	20.01	40.66	-5.649	4.37E-05	Predicted Protein
33	TRINITY_DN5723_c0_g1	5.47	0.91	0.48	147.25	109.75	89.9	-5.649	2.65E-05	Predicted Protein
34	TRINITY_DN7784_c0_g1	7.88	7.39	4.37	322.86	341.39	1073.69	-5.627	4.26E-06	Predicted Protein
35	TRINITY_DN5965_c1_g1	53.22	6.07	6.47	1173.34	760.7	1106.06	-5.627	2.34E-05	Predicted Protein

36	TRINITY_DN9734_c0_g1	0.08	0.49	1.59	23.73	24.47	17.56	-5.551	5.09E-05	Predicted Protein
37	TRINITY_DN565_c0_g1	2.22	1.22	1.18	93.13	68.83	155.62	-5.423	3.99E-06	Peroxidase 12, Atperox P12, EC 1.11.1.7 (ATP4a) (PRXR6)
38	TRINITY_DN565_c0_g1	2.22	1.22	1.18	93.13	68.83	155.62	-5.423	3.99E-06	Cationic peroxidase SPC4, EC 1.11.1.7
39	TRINITY_DN3459_c0_g1	2.36	0.56	3.89	101.88	77.2	153.38	-5.410	2.03E-05	Predicted Protein
40	TRINITY_DN2419_c0_g1	0.45	0.26	1.32	30.69	23.95	31.41	-5.361	1.25E-05	Predicted Protein
41	TRINITY_DN350_c0_g2	1.67	1.44	1.31	130.63	158.57	38.54	-5.351	1.57E-05	Benzyl alcohol O-benzoyltransferase, EC 2.3.1.196 (Benzoyl coenzyme A:benzyl alcohol benzoyl transferase)
42	TRINITY_DN1483_c0_g1	2.06	0.14	1.59	46.18	45.16	46.95	-5.347	8.11E-05	Predicted Protein
43	TRINITY_DN3428_c0_g2	11.13	4.13	5.23	540.1	213.89	516.93	-5.345	1.14E-05	Predicted Protein
44	TRINITY_DN38763_c0_g1	1.24	0.74	2.14	88.25	171.45	27.6	-5.333	5.55E-05	Glyoxylase I 4, AtGLXI-like;4, AtGLYI4
45	TRINITY_DN4971_c0_g2	11.63	2.63	2.86	386.29	249.26	229.67	-5.330	7.46E-06	Predicted Protein
46	TRINITY_DN1869_c0_g1	0.2	0.42	0.39	17.82	15.6	24.1	-5.277	6.23E-05	Predicted Protein
47	TRINITY_DN6746_c0_g1	0.98	1.33	0.37	50.95	34.06	77.5	-5.265	1.96E-05	Predicted Protein
48	TRINITY_DN3022_c0_g2	0.68	0.44	0.73	35.78	28.02	41.18	-5.261	5.46E-06	Predicted Protein
49	TRINITY_DN709_c0_g1	0.43	0.17	0.44	22.94	16.65	13.69	-5.231	0.000125	Predicted Protein
50	TRINITY_DN14557_c0_g1	13.84	7.83	6.14	671.5	289.97	665.67	-5.219	6.57E-06	Linoleate 9S-lipoxygenase A, EC 1.13.11.58 (Lipoxygenase A)
51	TRINITY_DN703_c0_g1	0.68	0.39	0.13	26.88	23.74	22.23	-5.206	6.39E-05	Auxin-responsive protein SAUR32 (Protein ABOLISHED APICAL HOOK MAINTENANCE 1) (Protein SMALL AUXIN UP RNA 32)
52	TRINITY_DN9217_c0_g2	0.28	0.3	0.4	16.06	31.56	10.18	-5.167	0.000108	Predicted Protein
53	TRINITY_DN3069_c0_g1	6.25	3.02	1.51	310.77	133.21	112.57	-5.095	2.97E-05	Predicted Protein
54	TRINITY_DN37281_c0_g1	0.4	0.73	0.64	46.45	19.21	27.73	-5.062	0.000061	Predicted Protein
55	TRINITY_DN2454_c0_g2	0.58	0.38	0.49	24.25	22.33	25.85	-5.023	7.54E-06	Predicted Protein
56	TRINITY_DN883_c0_g1	3.03	2.1	3.18	207.9	49.7	228.58	-5.004	0.000138	Class V chitinase, AtChiC, EC 3.2.1.14, EC 3.2.1.200
57	TRINITY_DN883_c0_g1	3.03	2.1	3.18	207.9	49.7	228.58	-5.004	0.000138	Class V chitinase CHIT5b, MtCHIT5b, EC 3.2.1.14
58	TRINITY_DN9201_c0_g1	6.29	2.46	13.2	471.59	149.72	307.61	-5.002	6.59E-05	Predicted Protein

59	TRINITY_DN3152_c0_g1	8.05	2.08	3.45	254.41	122.04	221.09	-4.989	1.71E-05	Predicted Protein
60	TRINITY_DN481_c0_g1	1.02	0.41	3.08	55.39	66.11	31.34	-4.983	2.66E-05	RING-H2 finger protein ATL2, EC 2.3.2.27 (Protein ARABIDOPSIS TOXICOS EN LEVADURA 2, Protein ATL2) (RING-type E3 ubiquitin transferase ATL2)
61	TRINITY_DN481_c0_g1	1.02	0.41	3.08	55.39	66.11	31.34	-4.983	2.66E-05	RING-H2 finger protein ATL60, EC 2.3.2.27 (RING-type E3 ubiquitin transferase ATL60)
62	TRINITY_DN12730_c0_g1	3.1	1.53	0.39	49.37	106.18	56.02	-4.966	1.36E-05	Predicted Protein
63	TRINITY_DN3537_c0_g1	0.97	0.36	0.32	29.67	31.28	18.67	-4.945	2.13E-05	Predicted Protein
64	TRINITY_DN36982_c0_g1	0.96	1.94	2.77	31.59	189.32	83.11	-4.937	2.58E-05	Predicted Protein
65	TRINITY_DN350_c0_g3	0.68	1.13	0.56	49.85	47.92	20.65	-4.911	1.63E-05	Benzyl alcohol O-benzoyltransferase, EC 2.3.1.196 (Benzoyl coenzyme A:benzyl alcohol benzoyl transferase)
66	TRINITY_DN7061_c1_g1	12.73	4.47	0.85	158.35	218.82	172.81	-4.899	5.55E-05	Predicted Protein
67	TRINITY_DN34079_c0_g1	2.25	1.33	1.66	139.04	63.67	49.4	-4.844	0.000024	Predicted Protein
68	TRINITY_DN2420_c0_g1	2.42	0.46	0.45	35.9	23.83	61.64	-4.820	0.000136	Predicted Protein
69	TRINITY_DN2309_c2_g1	3.77	4	3.12	266.25	96.82	148.11	-4.808	0.000015	Predicted Protein
70	TRINITY_DN104547_c0_g1	7.3	2.88	3.17	238.4	83.01	249.46	-4.753	5.79E-05	Predicted Protein
71	TRINITY_DN2423_c0_g1	4.25	0.64	2.98	104.81	46.82	107.91	-4.737	0.000133	Protein TIFY 9 (Jasmonate ZIM domain-containing protein 10) (Protein JASMONATE-ASSOCIATED 1) (Protein JAZ10)
72	TRINITY_DN2936_c0_g1	4.11	1.09	0.71	80.77	49.47	64.72	-4.714	3.89E-05	F-box protein Atlg67340
73	TRINITY_DN3428_c0_g1	8.15	5.52	8.95	405.93	189.91	322.41	-4.701	5.99E-06	Probable linoleate 9S-lipoxygenase 4, EC 1.13.11.58 (Root lipoxygenase)
74	TRINITY_DN3428_c0_g1	8.15	5.52	8.95	405.93	189.91	322.41	-4.701	5.99E-06	Linoleate 9S-lipoxygenase A, EC 1.13.11.58 (Lipoxygenase A)
75	TRINITY_DN2679_c0_g1	0.64	0.51	0.33	25.2	13.44	26.94	-4.690	0.000109	Predicted Protein
76	TRINITY_DN1630_c0_g1	1.33	0.31	0.8	30.88	27.11	23.21	-4.666	0.000025	Predicted Protein
77	TRINITY_DN662_c0_g1	18.61	3.39	4.79	297.28	215.67	292.16	-4.661	2.17E-05	Potassium transporter 5 (OsHAK5)
78	TRINITY_DN662_c0_g1	18.61	3.39	4.79	297.28	215.67	292.16	-4.661	2.17E-05	Potassium transporter 1 (OsHAK1)

79	TRINITY_DN11443_c0_g1	1.61	1.82	0.7	65.72	28.76	74.44	-4.651	5.76E-05	Predicted Protein
80	TRINITY_DN528_c0_g1	0.38	0.52	0.46	11.9	28.25	15.99	-4.628	1.17E-05	Phospholipase A1-Igamma1, chloroplastic, EC 3.1.1.- (DAD1-like lipase 4)
81	TRINITY_DN528_c0_g1	0.38	0.52	0.46	11.9	28.25	15.99	-4.628	1.17E-05	Phospholipase A1-Ialpha2, chloroplastic, EC 3.1.1.- (DAD1-like lipase 5)
82	TRINITY_DN528_c0_g1	0.38	0.52	0.46	11.9	28.25	15.99	-4.628	1.17E-05	Phospholipase A1-Igamma3, chloroplastic, EC 3.1.1.- (DAD1-like lipase 2)
83	TRINITY_DN9407_c0_g1	5.03	1.34	1.61	57.25	111.91	98.46	-4.605	5.9E-06	Predicted Protein
84	TRINITY_DN2515_c0_g1	8.97	2.8	1.1	140.76	123.23	98.31	-4.585	3.63E-05	Probable disease resistance protein At5g04720
85	TRINITY_DN5337_c0_g1	0.18	0.61	1.85	15.76	16.44	20.55	-4.551	8.04E-05	Predicted Protein
86	TRINITY_DN5340_c0_g1	3.12	0.37	0.34	27.6	47.12	22.31	-4.546	0.000131	Predicted Protein
87	TRINITY_DN16888_c0_g1	1.21	0.47	0.16	20.12	30.42	16.05	-4.523	5.85E-05	Predicted Protein
88	TRINITY_DN16040_c0_g1	2.49	0.68	0.76	39.04	44.31	36.54	-4.500	1.05E-05	Predicted Protein
89	TRINITY_DN345_c1_g1	22.4	4.62	15.75	490.53	255.64	488.01	-4.464	4.82E-05	Predicted Protein
90	TRINITY_DN7436_c0_g2	24.8	30.11	10.46	481.81	599.66	1125.65	-4.460	4.88E-06	Predicted Protein
91	TRINITY_DN22831_c0_g2	5.06	2.53	5.2	150.2	59.44	260.42	-4.428	0.000135	Predicted Protein
92	TRINITY_DN3878_c1_g1	1.79	0.87	1.35	39.5	57.78	30.4	-4.396	3.72E-06	Predicted Protein
93	TRINITY_DN9660_c0_g1	0.46	0.24	1.22	14.82	18.95	9.21	-4.364	6.54E-05	Predicted Protein
94	TRINITY_DN2724_c0_g1	3.12	1.88	2.84	84.24	77.44	75.63	-4.332	1.53E-06	Predicted Protein
95	TRINITY_DN750_c0_g1	15.85	2.67	2.14	135.54	192.95	114.14	-4.325	6.22E-05	Probable disease resistance protein At5g04720
96	TRINITY_DN2509_c0_g1	0.27	0.73	1.18	12.41	14.6	25.02	-4.270	0.000075	Predicted Protein
97	TRINITY_DN8616_c0_g1	1.97	1.48	1.13	56	34.08	47.26	-4.260	1.28E-05	Predicted Protein
98	TRINITY_DN7743_c0_g2	1.28	0.39	0.61	25.31	13.79	23.91	-4.258	0.000129	Probable phospholipid hydroperoxide glutathione peroxidase, PHGPx, EC 1.11.1.12
99	TRINITY_DN399_c0_g1	15.58	5.85	7.45	337.3	126.19	404.82	-4.250	9.96E-05	Predicted Protein
100	TRINITY_DN2157_c0_g1	5.52	6.21	4.61	301.86	102.86	127.49	-4.250	4.57E-05	Predicted Protein
101	TRINITY_DN9843_c0_g1	2.1	1.4	4.76	70.86	38.88	96.24	-4.181	7.29E-05	Predicted Protein
102	TRINITY_DN102451_c0_g1	0.86	0.49	0.5	10.88	15.85	28.2	-4.144	6.49E-05	Predicted Protein

103	TRINITY_DN1644_c0_g3	0.77	0.66	1.22	25.94	13.95	32.04	-4.139	8.63E-05	NAC transcription factor 56, AtNAC056 (NAC domain-containing protein 2, AtNAC2) (Protein NAC-REGULATED SEED MORPHOLOGY 1)
104	TRINITY_DN3401_c0_g1	2.04	0.88	1.07	37.44	30.11	31.61	-4.072	1.42E-05	Disease resistance protein L6 (NAD(+) hydrolase L6, EC 3.2.2.6) (NADP(+) hydrolase L6, EC 3.2.2.-)
105	TRINITY_DN3401_c0_g1	2.04	0.88	1.07	37.44	30.11	31.61	-4.072	1.42E-05	Disease resistance protein Roq1 (NAD(+) hydrolase RPV1, EC 3.2.2.6) (Recognition of XopQ 1 protein)
106	TRINITY_DN1002_c0_g1	1.9	2.6	5.47	69.19	51.5	114.83	-4.055	0.000034	Probable phospholipid hydroperoxide glutathione peroxidase, PHGPx, EC 1.11.1.12 (Salt-associated protein)
107	TRINITY_DN1002_c0_g1	1.9	2.6	5.47	69.19	51.5	114.83	-4.055	0.000034	Probable phospholipid hydroperoxide glutathione peroxidase, PHGPx, EC 1.11.1.12
108	TRINITY_DN34284_c1_g1	0.82	2.53	4.23	57.32	47.31	45.66	-4.044	4.39E-05	Probable phospholipid hydroperoxide glutathione peroxidase, PHGPx, EC 1.11.1.12
109	TRINITY_DN13745_c0_g1	14.93	3.08	2.83	115.9	156.73	125.21	-4.027	4.08E-05	Predicted Protein
110	TRINITY_DN36614_c0_g1	2.31	0.47	0.58	16.13	30.43	23.06	-4.002	6.45E-05	Predicted Protein
111	TRINITY_DN76829_c0_g1	0.6	0.75	2.06	16.59	19.19	35.57	-4.001	6.46E-05	Predicted Protein
112	TRINITY_DN162544_c0_g1	7.49	3.93	1.44	58.14	156.51	81.13	-3.986	3.16E-05	Probable phospholipid hydroperoxide glutathione peroxidase, PHGPx, EC 1.11.1.12

Table S4. Top 40 downregulated genes in copper SG in comparison to nickel SG in *Pinus banksiana*

Rank	Gene ID	Cu Sus1	Cu Sus2	Cu Sus3	Ni Sus1	Ni Sus2	Ni Sus3	logFC	Adj. P. value	UniProt Description
0	TRINITY_DN343_c0_g1	1.96	1.42	0.92	54.19	45.61	75.54	-5.26455	7.48E-06	Probable disease resistance protein At4g33300
1	TRINITY_DN1105_c0_g1	3.27	4.87	2.07	76.5	72.45	109.99	-4.74021	8.13E-07	Probable calcium-binding protein CML24 (Calmodulin-like protein 24)
2	TRINITY_DN1140_c1_g1	4.64	8.22	3.13	95.64	64.13	116.13	-4.21256	7.05E-06	Heavy metal-associated isoprenylated plant protein 39, AtHIP39
3	TRINITY_DN9069_c0_g1	3.08	3.94	1.43	39	35.11	55.72	-4.0072	7.49E-06	Predicted Protein
4	TRINITY_DN26455_c0_g1	5.55	5.56	3.67	47.82	81.22	105.73	-3.96197	1.86E-06	Predicted Protein
5	TRINITY_DN709_c0_g1	3.48	4.83	1.97	36.9	41.46	63.36	-3.84112	4.28E-06	Predicted Protein
6	TRINITY_DN24318_c0_g1	4.75	2.79	4.67	40.3	50.05	80.73	-3.79817	8.01E-06	Predicted Protein
7	TRINITY_DN2118_c0_g1	5.31	19.73	5.94	91.04	111.37	142.16	-3.79689	2.20E-06	Predicted Protein
8	TRINITY_DN66111_c1_g1	14.78	24.19	24.59	172.94	234.1	371.3	-3.66779	1.60E-06	Predicted Protein
9	TRINITY_DN9317_c0_g1	9.85	29.45	5.37	142.89	125.63	137.64	-3.56924	7.93E-06	Predicted Protein
10	TRINITY_DN25789_c0_g1	5.35	15.72	3.93	67.56	76.93	92.73	-3.54421	3.52E-06	Predicted Protein
11	TRINITY_DN2751_c0_g1	12.73	8.43	4.46	77.66	76.97	116.69	-3.4682	4.60E-06	Predicted Protein
12	TRINITY_DN1481_c0_g1	31.61	46.43	12.53	248.24	432.11	226.95	-3.44461	5.91E-06	Predicted Protein
13	TRINITY_DN37281_c0_g1	6.17	13.07	6.21	74.35	73.03	101.82	-3.42972	1.93E-06	Predicted Protein
14	TRINITY_DN11462_c0_g1	15.98	31.57	16.82	122.24	278.4	208.28	-3.29128	1.68E-06	Predicted Protein
15	TRINITY_DN3306_c0_g2	18.25	34.56	13.19	154.79	169.1	263.27	-3.27608	1.59E-06	Calcium-binding protein KIC (KCBP-interacting calcium-binding protein)
16	TRINITY_DN4522_c0_g1	12.58	21.21	9.5	81.86	98.59	152.54	-3.01301	3.71E-06	Predicted Protein
17	TRINITY_DN729_c0_g1	85.61	37.04	35.87	381.71	394.83	348.76	-2.92258	4.38E-06	Alcohol dehydrogenase 2, EC 1.1.1.1
18	TRINITY_DN729_c0_g1	85.61	37.04	35.87	381.71	394.83	348.76	-2.92258	4.38E-06	Alcohol dehydrogenase 1, EC 1.1.1.1 (ADH slow-allele)
19	TRINITY_DN41085_c0_g1	50.47	50.02	52.9	257.45	297.21	485.74	-2.76064	2.45E-06	Predicted Protein
20	TRINITY_DN3066_c1_g1	13.73	15.11	13.46	55.99	116.42	118.98	-2.74976	6.97E-06	Predicted Protein

21	TRINITY_DN2515_c0_g1	42.66	64	22.61	203.34	269.87	276.58	-2.66249	6.45E-07	Probable disease resistance protein At5g04720
22	TRINITY_DN1690_c0_g1	82.49	125.29	74.33	334.26	557.98	584.67	-2.43231	2.73E-07	Predicted Protein
23	TRINITY_DN1454_c0_g1	36.11	69.11	23.97	190.96	205.3	220.09	-2.42405	3.20E-06	Probable disease resistance protein At4g33300
24	TRINITY_DN1454_c0_g1	36.11	69.11	23.97	190.96	205.3	220.09	-2.42405	3.20E-06	Disease resistance protein ADR1 (Activated disease resistance protein 1)
25	TRINITY_DN187_c0_g2	34.07	59.55	27.12	157.12	214.46	204.87	-2.36432	8.35E-07	Probable disease resistance protein At4g33300
26	TRINITY_DN187_c0_g2	34.07	59.55	27.12	157.12	214.46	204.87	-2.36432	8.35E-07	Probable RNA-binding protein 19 (RNA-binding motif protein 19)
27	TRINITY_DN2581_c0_g1	73.03	104.45	74.62	307.26	360.65	549.82	-2.30639	2.39E-06	Ubiquitin-40S ribosomal protein S27a-1 [Cleaved into: Ubiquitin; 40S ribosomal protein S27a-1]
28	TRINITY_DN829_c0_g1	36.79	52.72	34.25	136.33	187.57	265.96	-2.27764	4.73E-06	Predicted Protein
29	TRINITY_DN871_c0_g1	77.17	92.43	46.57	254.71	317.44	342.34	-2.14567	5.09E-07	Lipase-like PAD4, EC 2.3.1.- (Protein ENHANCED DISEASE SUSCEPTIBILITY 9) (Protein PHYTOALEXIN DEFICIENT 4, AtPAD4)
30	TRINITY_DN2157_c0_g1	68.38	76.54	36.2	215.2	233.04	270.04	-2.06397	3.08E-06	Predicted Protein
31	TRINITY_DN13745_c0_g1	54.22	67.9	45.99	155.83	243.23	290.83	-2.04992	2.93E-06	Predicted Protein
32	TRINITY_DN750_c0_g1	52.81	76.65	41.32	153.78	225.7	259.13	-1.95617	3.05E-06	Probable disease resistance protein At5g04720
33	TRINITY_DN3793_c0_g1	366.62	499.73	371.86	1261.79	1399.25	1863.43	-1.92323	3.49E-07	Ubiquitin-40S ribosomal protein S27a-1 [Cleaved into: Ubiquitin; 40S ribosomal protein S27a-1]
34	TRINITY_DN3793_c0_g1	366.62	499.73	371.86	1261.79	1399.25	1863.43	-1.92323	3.49E-07	Polyubiquitin [Cleaved into: Ubiquitin]
35	TRINITY_DN1147_c0_g1	434.27	562.5	522.82	1377.47	1708.44	2534.14	-1.92099	3.94E-06	Polyubiquitin [Cleaved into: Ubiquitin]
36	TRINITY_DN1147_c0_g1	434.27	562.5	522.82	1377.47	1708.44	2534.14	-1.92099	3.94E-06	Ubiquitin-60S ribosomal protein L40 [Cleaved into: Ubiquitin; 60S ribosomal protein L40 (CEP52)]
37	TRINITY_DN1147_c0_g1	434.27	562.5	522.82	1377.47	1708.44	2534.14	-1.92099	3.94E-06	Ubiquitin-40S ribosomal protein S27a-1 [Cleaved into: Ubiquitin; 40S ribosomal protein S27a-1]

38	TRINITY_DN343_c0_g2	41.37	51.5	29.81	106.48	143.08	171.71	-1.81963	7.75E-06	Disease resistance protein ADR1 (Activated disease resistance protein 1)
39	TRINITY_DN3050_c0_g1	94.65	79.26	53.16	190.01	257.33	260.83	-1.67312	6.44E-06	Predicted Protein
40	TRINITY_DN5095_c0_g1	139.06	125.09	124.73	305.36	385.7	349.35	-1.44871	6.98E-06	Predicted Protein