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Supplemental Table 7. Significantly enriched/depleted GO terms in *P. trifoliata* specific genes

GO ID	GO Name	GO Category	P. trifoliata specific genes		Other genes		Ratio in P. trifoliata specific genes	Ratio in other genes	P-value	FDR
			w/ GO	w/o GO	w/ GO	w/o GO				
Enriched (FDR < 0.05)										
None										
Depleted (FDR < 0.05)										
GO:0005515	protein binding	molecular_function	286	8,091	2,823	23,133	0.0341	0.1088	1.25.E-113	2.38.E-110
GO:0003677	DNA binding	molecular_function	94	8,283	1,123	24,833	0.0112	0.0433	1.79.E-53	1.71.E-50
GO:0005524	ATP binding	molecular_function	176	8,201	1,536	24,420	0.0210	0.0592	4.51.E-52	2.87.E-49
GO:0005634	nucleus	cellular_component	22	8,355	470	25,486	0.0026	0.0181	2.85.E-33	1.36.E-30
GO:0003824	catalytic activity	molecular_function	72	8,305	744	25,212	0.0086	0.0287	5.53.E-31	2.12.E-28
GO:0008270	zinc ion binding	molecular_function	145	8,232	1,092	24,864	0.0173	0.0421	7.67.E-30	2.44.E-27
GO:0016020	membrane	cellular_component	87	8,290	808	25,148	0.0104	0.0311	9.79.E-30	2.67.E-27
GO:0006355	regulation of transcription, DNA-templated	biological_process	86	8,291	800	25,156	0.0103	0.0308	1.99.E-29	4.76.E-27
GO:0016021	integral component of membrane	cellular_component	73	8,304	719	25,237	0.0087	0.0277	2.03.E-28	4.32.E-26
GO:0004672	protein kinase activity	molecular_function	122	8,255	878	25,078	0.0146	0.0338	1.57.E-22	2.73.E-20
GO:0006468	protein phosphorylation	biological_process	122	8,255	878	25,078	0.0146	0.0338	1.57.E-22	2.73.E-20
GO:0003700	DNA-binding transcription factor activity	molecular_function	19	8,358	337	25,619	0.0023	0.0130	5.76.E-22	9.18.E-20
GO:0055085	transmembrane transport	biological_process	38	8,339	417	25,539	0.0045	0.0161	6.29.E-19	9.24.E-17
GO:0046872	metal ion binding	molecular_function	34	8,343	391	25,565	0.0041	0.0151	1.40.E-18	1.91.E-16
GO:0043565	sequence-specific DNA binding	molecular_function	7	8,370	200	25,756	0.0008	0.0077	1.48.E-16	1.89.E-14
GO:0008152	metabolic process	biological_process	99	8,278	664	25,292	0.0118	0.0256	2.70.E-15	3.22.E-13
GO:0000166	nucleotide binding	molecular_function	29	8,348	313	25,643	0.0035	0.0121	3.09.E-14	3.47.E-12
GO:0005488	binding	molecular_function	24	8,353	284	25,672	0.0029	0.0109	4.56.E-14	4.85.E-12
GO:0005737	cytoplasm	cellular_component	12	8,365	209	25,747	0.0014	0.0081	6.30.E-14	6.34.E-12
GO:0016491	oxidoreductase activity	molecular_function	97	8,280	632	25,324	0.0116	0.0243	8.27.E-14	7.90.E-12
GO:0003723	RNA binding	molecular_function	21	8,356	242	25,714	0.0025	0.0093	5.54.E-12	5.04.E-10
GO:0005975	carbohydrate metabolic process	biological_process	49	8,328	384	25,572	0.0058	0.0148	8.33.E-12	7.23.E-10
GO:0006886	intracellular protein transport	biological_process	6	8,371	145	25,811	0.0007	0.0056	1.32.E-11	1.09.E-09
GO:0005509	calcium ion binding	molecular_function	15	8,362	195	25,761	0.0018	0.0075	8.17.E-11	6.50.E-09
GO:0006810	transport	biological_process	26	8,351	241	25,715	0.0031	0.0093	1.15.E-09	8.82.E-08
GO:0005215	transporter activity	molecular_function	17	8,360	185	25,771	0.0020	0.0071	7.89.E-09	5.80.E-07
GO:0055114	oxidation-reduction process	biological_process	238	8,139	1,081	24,875	0.0284	0.0416	1.76.E-08	1.24.E-06
GO:0016788	hydrolase activity, acting on ester bonds	molecular_function	2	8,375	85	25,871	0.0002	0.0033	2.14.E-08	1.46.E-06
GO:0016787	hydrolase activity	molecular_function	25	8,352	218	25,738	0.0030	0.0084	3.05.E-08	2.01.E-06
GO:0006351	transcription, DNA-templated	biological_process	6	8,371	109	25,847	0.0007	0.0042	8.05.E-08	5.13.E-06
GO:0003676	nucleic acid binding	molecular_function	272	8,105	1,183	24,773	0.0325	0.0456	1.29.E-07	7.73.E-06
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	molecular_function	28	8,349	224	25,732	0.0033	0.0086	1.30.E-07	7.73.E-06
GO:0016192	vesicle-mediated transport	biological_process	2	8,375	74	25,882	0.0002	0.0029	2.95.E-07	1.71.E-05
GO:0006511	ubiquitin-dependent protein catabolic process	biological_process	2	8,375	71	25,885	0.0002	0.0027	7.26.E-07	4.08.E-05
GO:0009058	biosynthetic process	biological_process	7	8,370	104	25,852	0.0008	0.0040	1.10.E-06	5.98.E-05
GO:0046983	protein dimerization activity	molecular_function	58	8,319	338	25,618	0.0069	0.0130	2.21.E-06	1.17.E-04
GO:0045454	cell redox homeostasis	biological_process	5	8,372	88	25,868	0.0006	0.0034	2.38.E-06	1.23.E-04
GO:0008017	microtubule binding	molecular_function	2	8,375	65	25,891	0.0002	0.0025	2.66.E-06	1.34.E-04
GO:0030246	carbohydrate binding	molecular_function	7	8,370	96	25,860	0.0008	0.0037	4.84.E-06	2.37.E-04
GO:0005622	intracellular	cellular_component	50	8,327	292	25,664	0.0060	0.0112	1.13.E-05	5.41.E-04
GO:0030001	metal ion transport	biological_process	4	8,373	73	25,883	0.0005	0.0028	1.32.E-05	6.02.E-04
GO:0030170	pyridoxal phosphate binding	molecular_function	4	8,373	73	25,883	0.0005	0.0028	1.32.E-05	6.02.E-04
GO:0004842	ubiquitin-protein transferase activity	molecular_function	7	8,370	91	25,865	0.0008	0.0035	1.53.E-05	6.78.E-04
GO:0006281	DNA repair	biological_process	10	8,367	106	25,850	0.0012	0.0041	1.84.E-05	7.84.E-04
GO:0015031	protein transport	biological_process	9	8,368	102	25,854	0.0011	0.0039	1.85.E-05	7.84.E-04
GO:0046982	protein heterodimerization activity	molecular_function	2	8,375	54	25,902	0.0002	0.0021	5.81.E-05	2.41.E-03
GO:0016567	protein ubiquitination	biological_process	7	8,370	83	25,873	0.0008	0.0032	6.64.E-05	2.70.E-03
GO:0006457	protein folding	biological_process	13	8,364	114	25,842	0.0016	0.0044	7.13.E-05	2.84.E-03
GO:0006629	lipid metabolic process	biological_process	10	8,367	99	25,857	0.0012	0.0038	7.44.E-05	2.90.E-03
GO:0005525	GTP binding	molecular_function	28	8,349	181	25,775	0.0033	0.0070	9.77.E-05	3.74.E-03
GO:0015299	solute:proton antiporter activity	molecular_function	1	8,376	43	25,913	0.0001	0.0017	1.31.E-04	4.90.E-03
GO:0016887	ATPase activity	molecular_function	14	8,363	115	25,841	0.0017	0.0044	1.84.E-04	6.75.E-03
GO:0003924	GTPase activity	molecular_function	13	8,364	109	25,847	0.0016	0.0042	1.88.E-04	6.77.E-03
GO:0004252	serine-type endopeptidase activity	molecular_function	7	8,370	79	25,877	0.0008	0.0030	2.07.E-04	7.34.E-03
GO:0006396	RNA processing	biological_process	5	8,372	66	25,890	0.0006	0.0025	2.49.E-04	8.51.E-03
GO:0006812	cation transport	biological_process	5	8,372	66	25,890	0.0006	0.0025	2.49.E-04	8.51.E-03
GO:0050660	flavin adenine dinucleotide binding	molecular_function	8	8,369	82	25,874	0.0010	0.0032	2.97.E-04	9.94.E-03
GO:0016773	phosphotransferase activity, alcohol group as acceptor	molecular_function	2	8,375	46	25,910	0.0002	0.0018	3.06.E-04	1.01.E-02
GO:0000160	phosphorelay signal transduction system	biological_process	3	8,374	51	25,905	0.0004	0.0020	4.02.E-04	1.26.E-02
GO:0003777	microtubule motor activity	molecular_function	3	8,374	51	25,905	0.0004	0.0020	4.02.E-04	1.26.E-02
GO:0007018	microtubule-based movement	biological_process	3	8,374	51	25,905	0.0004	0.0020	4.02.E-04	1.26.E-02
GO:0006470	protein dephosphorylation	biological_process	8	8,369	79	25,877	0.0010	0.0030	4.12.E-04	1.27.E-02
GO:0043169	cation binding	molecular_function	2	8,375	45	25,911	0.0002	0.0017	4.79.E-04	1.45.E-02
GO:0016791	phosphatase activity	molecular_function	1	8,376	37	25,919	0.0001	0.0014	4.85.E-04	1.45.E-02
GO:0008565	obsolete protein transporter activity	molecular_function	0	8,377	26	25,930	0.0000	0.0010	9.84.E-04	2.89.E-02
GO:0016757	transferase activity, transferring glycosyl groups	molecular_function	4	8,373	53	25,903	0.0005	0.0020	1.03.E-03	2.94.E-02
GO:0016579	protein deubiquitination	biological_process	0	8,377	27	25,929	0.0000	0.0010	1.03.E-03	2.94.E-02
GO:0009055	electron transfer activity	molecular_function	15	8,362	109	25,847	0.0018	0.0042	1.05.E-03	2.95.E-02
GO:0006412	translation	biological_process	41	8,336	216	25,740	0.0049	0.0083	1.28.E-03	3.54.E-02
GO:0003899	DNA-directed 5'-3' RNA polymerase activity	molecular_function	3	8,374	46	25,910	0.0004	0.0018	1.33.E-03	3.54.E-02
GO:0004812	aminoacyl-tRNA ligase activity	molecular_function	3	8,374	46	25,910	0.0004	0.0018	1.33.E-03	3.54.E-02
GO:0006418	tRNA aminoacylation for protein translation	biological_process	3	8,374	46	25,910	0.0004	0.0018	1.33.E-03	3.54.E-02
GO:0007165	signal transduction	biological_process	29	8,348	166	25,790	0.0035	0.0064	1.42.E-03	3.72.E-02
GO:0008289	lipid binding	molecular_function	4	8,373	52	25,904	0.0005	0.0020	1.52.E-03	3.94.E-02
GO:0042546	cell wall biogenesis	biological_process	0	8,377	24	25,932	0.0000	0.0009	1.61.E-03	4.07.E-02
GO:0036459	thiol-dependent ubiquitinyl hydrolase activity	molecular_function	0	8,377	25	25,931	0.0000	0.0010	1.62.E-03	4.07.E-02
GO:0003735	structural constituent of ribosome	molecular_function	41	8,336	212	25,744	0.0049	0.0082	1.96.E-03	4.86.E-02