Supplemental Table 8. Significantly enriched/depleted InterPro domains in *P. trifoliata* specific genes

InterPro ID	InterPro Name	P. trifoliata specific genes		Other genes		Ratio in P. trifoliata specific genes	Ratio in other genes	P-value	FDR
		w/ InterPro	w/o InterPro	w/ InterPro	w/o InterPro				
Enriched (FDR < 0.05)									
IPR028919	Viral movement protein	44	8,333	63	25,893	0.0053	0.0024	1.61.E-04	1.17.E-02
Depleted (FDR < 0.05)									
IPR011990	Tetratricopeptide-like helical domain superfamily	18	8,359	488	25,468	0.0021	0.0188	2.74.E-38	1.76.E-34
IPR013083	Zinc finger, RING/FYVE/PHD-type	20	8,357	464	25,492	0.0024	0.0179	3.51.E-34	1.13.E-30
IPR017441	Protein kinase, ATP binding site	43	8,334	533	25,423	0.0051	0.0205	1.24.E-26	2.65.E-23
IPR000719	Protein kinase domain	112	8,265	858	25,098	0.0134	0.0331	3.01.E-24	3.86.E-21
IPR001841	Zinc finger, RING-type	10	8,367	293	25,663	0.0012	0.0113	4.44.E-24	4.74.E-21
IPR008271	Serine/threonine-protein kinase, active site	61	8,316	599	25,357	0.0073	0.0231	9.90.E-24	9.07.E-21
IPR011009	Protein kinase-like domain superfamily	138	8,239	963	24,993	0.0165	0.0371	2.98.E-23	2.39.E-20
IPR009057	Homeobox-like domain superfamily	13	8,364	306	25,650	0.0016	0.0118	4.56.E-23	3.25.E-20
IPR027417	P-loop containing nucleoside triphosphate hydrolase	175	8,202	1,074	24,882	0.0209	0.0414	3.96.E-20	2.54.E-17
IPR001005	SANT/Myb domain	7	8,370	200	25,756	0.0008	0.0077	1.48.E-16	8.64.E-14
IPR001810	F-box domain	20	8,357	283	25,673	0.0024	0.0109	4.74.E-16	2.53.E-13
IPR015943	WD40/YVTN repeat-like-containing domain superfamily	15	8,362	243	25,713	0.0018	0.0094	2.53.E-15	1.25.E-12
IPR013320	Concanavalin A-like lectin/glucanase domain superfamily	54	8,323	456	25,500	0.0064	0.0176	2.98.E-15	1.36.E-12
IPR017986	WD40-repeat-containing domain	13	8,364	229	25,727	0.0016	0.0088	3.39.E-15	1.45.E-12
IPR002885	Pentatricopeptide repeat	50	8,327	432	25,524	0.0060	0.0166	4.52.E-15	1.81.E-12
IPR003593	AAA+ ATPase domain	16	8,361	241	25,715	0.0019	0.0093	1.50.E-14	5.66.E-12
IPR001680	WD40 repeat	11	8,366	206	25,750	0.0013	0.0079	3.20.E-14	1.14.E-11
IPR017930	Myb domain	4	8,373	153	25,803	0.0005	0.0059	3.77.E-14	1.27.E-11
IPR016024	Armadillo-type fold	24	8,353	284	25,672	0.0029	0.0109	4.56.E-14	1.46.E-11
IPR012677	Nucleotide-binding alpha-beta plait domain superfamily	13	8,364	201	25,755	0.0016	0.0077	1.92.E-12	5.87.E-10
IPR011989	Armadillo-like helical	18	8,359	228	25,728	0.0021	0.0088	2.88.E-12	8.40.E-10
IPR000504	RNA recognition motif domain	11	8,366	177	25,779	0.0013	0.0068	1.90.E-11	5.29.E-09
IPR019775	WD40 repeat, conserved site	4	8,373	125	25,831	0.0005	0.0048	4.13.E-11	1.06.E-08
IPR011992	EF-hand domain pair	9	8,368	154	25,802	0.0011	0.0059	1.87.E-10	4.62.E-08
IPR011011	Zinc finger, FYVE/PHD-type	1	8,376	91	25,865	0.0001	0.0035	3.77.E-10	8.95.E-08
IPR001356	Homeobox domain	0	8,377	73	25,883	0.0000	0.0028	2.85.E-09	6.54.E-07
IPR018247	EF-Hand 1, calcium-binding site	8	8,369	135	25,821	0.0010	0.0052	3.54.E-09	7.83.E-07
IPR029044	Nucleotide-diphospho-sugar transferases	5	8,372	114	25,842	0.0006	0.0044	4.90.E-09	1.05.E-06
IPR019734	Tetratricopeptide repeat	4	8,373	103	25,853	0.0005	0.0040	1.12.E-08	2.25.E-06
IPR003591	Leucine-rich repeat, typical subtype	40	8,337	294	25,662	0.0048	0.0113	1.85.E-08	3.60.E-06
IPR001965	Zinc finger, PHD-type	1	8,376	76	25,880	0.0001	0.0029	2.47.E-08	4.65.E-06
IPR019786	Zinc finger, PHD-type, conserved site	0	8,377	64	25,892	0.0000	0.0025	2.84.E-08	5.21.E-06
IPR001245	Serine-threonine/tyrosine-protein kinase, catalytic domain	47	8,330	317	25,639	0.0056	0.0122	5.42.E-08	9.66.E-06
IPR023214	HAD superfamily	11	8,366	138	25,818	0.0013	0.0053	8.67.E-08	1.50.E-05
IPR012340	Nucleic acid-binding, OB-fold	3	8,374	87	25,869	0.0004	0.0034	9.11.E-08	1.50.E-05
IPR013026	Tetratricopeptide repeat-containing domain	5	8,372	102	25,854	0.0006	0.0039	9.14.E-08	1.50.E-05
IPR011333	SKP1/BTB/POZ domain superfamily	1	8,376	68	25,888	0.0001	0.0026	1.41.E-07	2.26.E-05
IPR017853	Glycoside hydrolase superfamily	22	8,355	193	25,763	0.0026	0.0074	1.65.E-07	2.58.E-05
IPR020846	Major facilitator superfamily domain	20	8,357	184	25,772	0.0024	0.0071	1.75.E-07	2.66.E-05
IPR016177	DNA-binding domain superfamily	8	8,369	117	25,839	0.0010	0.0045	1.78.E-07	2.66.E-05
IPR006447	Myb domain, plants	0	8,377	57	25,899	0.0000	0.0022	1.87.E-07	2.72.E-05
IPR017451	F-box associated interaction domain	4	8,373	91	25,865	0.0005	0.0035	2.18.E-07	3.11.E-05
IPR002048	EF-hand domain	12	8,365	137	25,819	0.0014	0.0053	4.15.E-07	5.78.E-05
IPR001087	GDSL lipase/esterase	1	8,376	64	25,892	0.0001	0.0025	6.00.E-07	8.19.E-05
IPR013210	Leucine-rich repeat-containing N-terminal, plant-type	42	8,335	278	25,678	0.0050	0.0107	7.69.E-07	1.03.E-04
IPR001650	Helicase, C-terminal	8	8,369	111	25,845	0.0010	0.0043	8.66.E-07	1.13.E-04
IPR014001	Helicase superfamily 1/2, ATP-binding domain	9	8,368	116	25,840	0.0011	0.0045	9.64.E-07	1.24.E-04
IPR013087	Zinc finger C2H2-type	0	8,377	50	25,906	0.0000	0.0019	1.24.E-06	1.56.E-04
IPR020568	Ribosomal protein S5 domain 2-type fold	0	8,377	51	25,905	0.0000	0.0020	1.35.E-06	1.67.E-04
IPR011598	Myc-type, basic helix-loop-helix (bHLH) domain	11	8,366	125	25,831	0.0013	0.0048	1.68.E-06	2.03.E-04
IPR020472	G-protein beta WD-40 repeat	2	8,375	67	25,889	0.0002	0.0026	1.71.E-06	2.03.E-04
IPR017907	Zinc finger, RING-type, conserved site	2	8,375	68	25,888	0.0002	0.0026	1.83.E-06	2.13.E-04
IPR029058	Alpha/Beta hydrolase fold	43	8,334	274	25,682	0.0051	0.0106	1.98.E-06	2.27.E-04
IPR000210	BTB/POZ domain	1	8,376	58	25,898	0.0001	0.0022	2.18.E-06	2.41.E-04
IPR019787	Zinc finger, PHD-finger	1	8,376	58	25,898	0.0001	0.0022	2.18.E-06	2.41.E-04
IPR016040	NAD(P)-binding domain	56	8,321	327	25,629	0.0067	0.0126	2.77.E-06	3.01.E-04
IPR000008	C2 domain	5	8,372	85	25,871	0.0006	0.0033	3.35.E-06	3.58.E-04
IPR029071	Ubiquitin-like domain superfamily	5	8,372	84	25,872	0.0006	0.0032	5.10.E-06	5.36.E-04
IPR014729	Rossmann-like alpha/beta/alpha sandwich fold	8	8,369	101	25,855	0.0010	0.0039	5.44.E-06	5.63.E-04
IPR013783	Immunoglobulin-like fold	0	8,377	44	25,912	0.0000	0.0017	8.77.E-06	8.78.E-04
IPR001471	AP2/ERF domain	9	8,368	101	25,855	0.0011	0.0039	1.77.E-05	1.74.E-03
IPR015421	Pyridoxal phosphate-dependent transferase, major domain	6	8,371	83	25,873	0.0007	0.0032	1.94.E-05	1.89.E-03
IPR013766	Thioredoxin domain	1	8,376	50	25,906	0.0001	0.0019	2.18.E-05	2.09.E-03
IPR000571	Zinc finger, CCCH-type	2	8,375	57	25,899	0.0002	0.0022	2.37.E-05	2.23.E-03
IPR018253	DnaJ domain, conserved site	1	8,376	48	25,908	0.0001	0.0018	3.35.E-05	3.11.E-03
IPR017871	ABC transporter, conserved site	3	8,374	62	25,894	0.0004	0.0024	3.40.E-05	3.11.E-03
IPR000270	PB1 domain	3	8,374	63	25,893	0.0004	0.0024	3.57.E-05	3.21.E-03

IPR004827	Basic-leucine zipper domain	2	8,375	55	25,901	0.0002	0.0021	3.61.E-05	3.21.E-03
IPR006553	Leucine-rich repeat, cysteine-containing subtype	0	8,377	39	25,917	0.0000	0.0015	3.70.E-05	3.25.E-03
IPR006671	Cyclin, N-terminal	0	8,377	37	25,919	0.0000	0.0014	5.75.E-05	4.90.E-03
IPR025322	Protein of unknown function DUF4228, plant	0	8,377	37	25,919	0.0000	0.0014	5.75.E-05	4.90.E-03
IPR009072	Histone-fold	2	8,375	54	25,902	0.0002	0.0021	5.81.E-05	4.90.E-03
IPR023393	START-like domain superfamily	3	8,374	59	25,897	0.0004	0.0023	7.89.E-05	6.57.E-03
IPR032867	DYW domain	1	8,376	44	25,912	0.0001	0.0017	8.08.E-05	6.64.E-03
IPR002035	von Willebrand factor, type A	0	8,377	35	25,921	0.0000	0.0013	9.06.E-05	7.35.E-03
IPR011991	ArsR-like helix-turn-helix domain	30	8,347	191	25,765	0.0036	0.0074	1.05.E-04	8.45.E-03
IPR029052	Metallo-dependent phosphatase-like	3	8,374	57	25,899	0.0004	0.0022	1.18.E-04	9.34.E-03
IPR017877	Myb-like domain	1	8,376	42	25,914	0.0001	0.0016	1.27.E-04	9.94.E-03
IPR000048	IQ motif, EF-hand binding site	2	8,375	50	25,906	0.0002	0.0019	1.32.E-04	1.01.E-02
IPR013763	Cyclin-like	2	8,375	50	25,906	0.0002	0.0019	1.32.E-04	1.01.E-02
IPR014721	Ribosomal protein S5 domain 2-type fold, subgroup	0	8,377	33	25,923	0.0000	0.0013	1.45.E-04	1.09.E-02
IPR009060	UBA-like superfamily	0	8,377	34	25,922	0.0000	0.0013	1.57.E-04	1.15.E-02
IPR017970	Homeobox, conserved site	0	8,377	34	25,922	0.0000	0.0013	1.57.E-04	1.15.E-02
IPR001623	DnaJ domain	8	8,369	84	25,872	0.0010	0.0032	2.11.E-04	1.49.E-02
IPR015424	Pyridoxal phosphate-dependent transferase	8	8,369	84	25,872	0.0010	0.0032	2.11.E-04	1.49.E-02
IPR001752	Kinesin motor domain	2	8,375	49	25,907	0.0002	0.0019	2.15.E-04	1.50.E-02
IPR015422	Pyridoxal phosphate-dependent transferase domain 1	4	8,373	61	25,895	0.0005	0.0024	2.21.E-04	1.52.E-02
IPR000425	Major intrinsic protein	0	8,377	31	25,925	0.0000	0.0012	2.35.E-04	1.55.E-02
IPR010920	LSM domain superfamily	0	8,377	31	25,925	0.0000	0.0012	2.35.E-04	1.55.E-02
IPR011013	Galactose mutarotase-like domain superfamily	0	8,377	31	25,925	0.0000	0.0012	2.35.E-04	1.55.E-02
IPR023271	Aquaporin-like	0	8,377	31	25,925	0.0000	0.0012	2.35.E-04	1.55.E-02
IPR025110	AMP-binding enzyme, C-terminal domain	0	8,377	32	25,924	0.0000	0.0012	2.43.E-04	1.59.E-02
IPR004843	Calcineurin-like phosphoesterase domain, ApaH type	3	8,374	53	25,903	0.0004	0.0020	2.67.E-04	1.73.E-02
IPR014756	Immunoglobulin E-set	2	8,375	46	25,910	0.0002	0.0018	3.06.E-04	1.96.E-02
IPR003441	NAC domain	19	8,358	135	25,821	0.0023	0.0052	3.12.E-04	1.98.E-02
IPR008979	Galactose-binding-like domain superfamily	2	8,375	47	25,909	0.0002	0.0018	3.20.E-04	1.99.E-02
IPR032675	Leucine-rich repeat domain superfamily	246	8,131	977	24,979	0.0294	0.0376	3.23.E-04	1.99.E-02
IPR019793	Peroxidases heam-ligand binding site	4	8,373	58	25,898	0.0005	0.0022	3.23.E-04	1.99.E-02
IPR006153	Cation/H+ exchanger	1	8,376	40	25,916	0.0001	0.0015	3.37.E-04	2.06.E-02
IPR001611	Leucine-rich repeat	105	8,272	473	25,483	0.0125	0.0182	3.53.E-04	2.14.E-02
IPR000225	Armadillo	5	8,372	65	25,891	0.0006	0.0025	3.81.E-04	2.24.E-02
IPR002347	Short-chain dehydrogenase/reductase SDR	5	8,372	65	25,891	0.0006	0.0025	3.81.E-04	2.24.E-02
IPR011701	Major facilitator superfamily	0	8,377	30	25,926	0.0000	0.0012	3.82.E-04	2.24.E-02
IPR012336	Thioredoxin-like fold	27	8,350	168	25,788	0.0032	0.0065	4.08.E-04	2.38.E-02
IPR005202	Transcription factor GRAS	1	8,376	37	25,919	0.0001	0.0014	4.85.E-04	2.80.E-02
IPR000626	Ubiquitin domain	3	8,374	50	25,906	0.0004	0.0019	6.02.E-04	3.39.E-02
IPR027640	Kinesin-like protein	3	8,374	50	25,906	0.0004	0.0019	6.02.E-04	3.39.E-02
IPR001440	Tetratricopeptide repeat 1	0	8,377	28	25,928	0.0000	0.0011	6.09.E-04	3.39.E-02
IPR006073	GTP binding domain	0	8,377	28	25,928	0.0000	0.0011	6.09.E-04	3.39.E-02
IPR026992	Non-haem dioxygenase N-terminal domain	13	8,364	102	25,854	0.0016	0.0039	6.62.E-04	3.62.E-02
IPR006652	Kelch repeat type 1	0	8,377	29	25,927	0.0000	0.0011	6.67.E-04	3.62.E-02
IPR025659	Tubby-like, C-terminal	0	8,377	29	25,927	0.0000	0.0011	6.67.E-04	3.62.E-02
IPR006121	Heavy metal-associated domain, HMA	4	8,373	56	25,900	0.0005	0.0022	7.27.E-04	3.92.E-02
IPR004088	K Homology domain, type 1	1	8,376	35	25,921	0.0001	0.0013	7.61.E-04	4.03.E-02
IPR020845	AMP-binding, conserved site	1	8,376	35	25,921	0.0001	0.0013	7.61.E-04	4.03.E-02
IPR004839	Aminotransferase, class I/classII	1	8,376	36	25,920	0.0001	0.0014	7.76.E-04	4.08.E-02
IPR001932	PPM-type phosphatase domain	6	8,371	66	25,890	0.0007	0.0025	8.15.E-04	4.25.E-02
IPR013785	Aldolase-type TIM barrel	9	8,368	82	25,874	0.0011	0.0032	8.27.E-04	4.27.E-02
IPR003959	ATPase, AAA-type, core	13	8,364	99	25,857	0.0016	0.0038	8.93.E-04	4.58.E-02
IPR003439	ABC transporter-like	12	8,365	94	25,862	0.0014	0.0036	9.54.E-04	4.86.E-02
IPR001357	BRCT domain	0	8,377	26	25,930	0.0000	0.0010	9.84.E-04	4.97.E-02