

Additional file 6: Figure S5. Highly Expressed Interface Unigenes. The 20 most highly expressed (RPKM) unigenes (ID) in each indicated portion of the transcriptome Venn diagram for the interaction of *T. versicolor* with each host species. **NR BLASTx – description, species and %id.:** the description, species of origin, and percent pairwise identify, respectively, of the best unigene alignment ($<1e-10$) resulting from the NR database query, **17 genomes BLAST** and **%id.:** best hit species in a BLAST database of 17 annotated plant genomes with the percent pairwise identity in the nucleotide BLAST (**N**) or translated nucleotide BLAST (**P**). ^TXXX = IPS transmembrane prediction, ^SXXX = IPS secretion signal prediction.

Figure S5. A) Top expressed unigenes from shared orthogroups between parasite-host interface transcriptomes of *T. versicolor*.

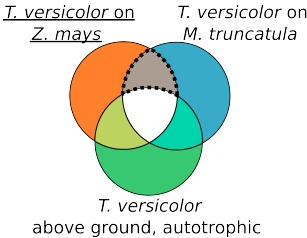
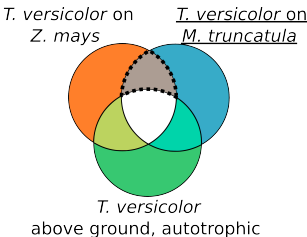
	RPKM	ID	NR BLASTx – description	NR BLASTx species	% id.	17 genomes BLAST	% id.
 <i>T. versicolor</i> on <i>Z. mays</i> <i>T. versicolor</i> on <i>M. truncatula</i> <i>T. versicolor</i> above ground, autotrophic	4351	772	^T beta-expansin precursor	<i>Vitis vinifera</i>	67	<i>Mimulus guttatus</i>	57 P
	2411	2150	disease resistance-responsive (dirigent-like)	<i>Populus trichocarpa</i>	78	<i>Populus trichocarpa</i>	63 P
	1464	1122	^S cysteine-rich repeat secretory protein 38	<i>Arabidopsis thaliana</i>	56	<i>Mimulus guttatus</i>	49 P
	1277	11517	^T PREDICTED: uncharacterized protein	<i>Glycine max</i>	90	<i>Solanum tuberosum</i>	72 P
	972	3187	pathogenesis-related protein sth-2	<i>Vitis vinifera</i>	69	<i>Vitis vinifera</i>	45 P
	836	571	PREDICTED: At5g39570-like	<i>Glycine max</i>	54	<i>Solanum lycopersicum</i>	52 P
	733	11012	^T nodule protein dg93-like protein	<i>Potamogeton distinctus</i>	90	<i>Mimulus guttatus</i>	71 P
	631	15459	pathogenesis-related protein	<i>Rehmannia glutinosa</i>	70	<i>Mimulus guttatus</i>	47 P
	616	494	acidic endochitinase	<i>Populus trichocarpa</i>	71	<i>Populus trichocarpa</i>	57 P
	560	5467	^T rsi-1 protein	<i>Solanum lycopersicum</i>	82	<i>Populus trichocarpa</i>	81 N
	493	3586	ap2 erf domain-containing transcription factor	<i>Populus trichocarpa</i>	62	<i>Mimulus guttatus</i>	89 N
	453	16555	^S PREDICTED: chemocyanin-like	<i>Brachypodium distachyon</i>	54	<i>Theobroma cacao</i>	43 P
	448	19049	PREDICTED: putative expansin-B2	<i>Vitis vinifera</i>	72	<i>Mimulus guttatus</i>	54 P
	412	7820	major allergen pru ar 1	<i>Vitis vinifera</i>	79	<i>Mimulus guttatus</i>	71P
	399	2405	Pectinesterase-1 precursor, putative	<i>Ricinus communis</i>	83	<i>Mimulus guttatus</i>	82 P
	397	6864	cysteine-rich repeat secretory protein 38-like	<i>Vitis vinifera</i>	60	<i>Glycine max</i>	47 P
	380	7395	pathogenesis-related protein 1a	<i>Vitis vinifera</i>	69	<i>Vitis vinifera</i>	52 P
	379	259	^T strictosidine synthase 1-like	<i>Vitis vinifera</i>	66	<i>Vitis vinifera</i>	49 P
	374	328	^S peroxidase protein	<i>Mikania micrantha</i>	86	<i>Solanum tuberosum</i>	74 N
	369	193	^S cytokinin dehydrogenase 3- partial	<i>Vitis vinifera</i>	66	<i>Mimulus guttatus</i>	59 P
 <i>T. versicolor</i> on <i>Z. mays</i> <i>T. versicolor</i> on <i>M. truncatula</i> <i>T. versicolor</i> above ground, autotrophic	19043	12004	pathogenesis-related protein	<i>Rehmannia glutinosa</i>	69	<i>Mimulus guttatus</i>	50 P
	7238	2255	pathogenesis-related protein	<i>Rehmannia glutinosa</i>	69	<i>Mimulus guttatus</i>	48 P
	6910	6809	pathogenesis-related protein sth-2	<i>Vitis vinifera</i>	68	<i>Vitis vinifera</i>	44 P
	4107	12313	pathogenesis-related protein	<i>Rehmannia glutinosa</i>	70	<i>Medicago truncatula</i>	48 P
	3525	331	pathogen-related protein sth-2	<i>Salvia miltiorrhiza</i>	80	<i>Mimulus guttatus</i>	71 P
	2151	11591	pathogenesis-related protein	<i>Rehmannia glutinosa</i>	71	<i>Mimulus guttatus</i>	50 P
	1396	416	^T cysteine-rich repeat secretory protein	<i>Vitis vinifera</i>	55	<i>Solanum tuberosum</i>	42 P
	1187	7825	^T chemocyanin precursor	<i>Populus trichocarpa</i>	65	<i>Populus trichocarpa</i>	57 P
	1138	20761	pathogenesis-related protein	<i>Rehmannia glutinosa</i>	68	<i>Mimulus guttatus</i>	50 P
	1132	11358	^T PREDICTED: uncharacterized protein	<i>Glycine max</i>	89	<i>Solanum tuberosum</i>	73 P
	1086	6	^S aspartic proteinase nepenthesin-1	<i>Ricinus communis</i>	54	<i>Mimulus guttatus</i>	83 P
	1045	5067	^T NA	NA	NA	<i>Sorghum bicolor</i>	40 P
	1029	4931	^T chemocyanin precursor	<i>Populus trichocarpa</i>	54	<i>Populus trichocarpa</i>	37 P
	906	837	^S cysteine-rich repeat secretory protein 38	<i>Arabidopsis thaliana</i>	51	<i>Arabidopsis thaliana</i>	36 P
	900	2050	^S disease resistance response protein 206-like	<i>Vitis vinifera</i>	69	<i>Vitis vinifera</i>	53 P
	707	1010	cysteine-rich repeat secretory protein 38	<i>Arabidopsis thaliana</i>	56	<i>Mimulus guttatus</i>	49 P
	652	13435	hypothetical protein ARALYDRAFT_473065	<i>Arabidopsis lyrata</i>	73	<i>Mimulus guttatus</i>	63 P
	620	7456	predicted protein	<i>Populus trichocarpa</i>	62	<i>Populus trichocarpa</i>	50 P
	574	5537	pathogenesis-related protein 1a	<i>Medicago truncatula</i>	97	<i>Medicago truncatula</i>	94 N
	566	5883	^T predicted protein	<i>Populus trichocarpa</i>	80	<i>Populus trichocarpa</i>	70 P

Figure S5. B) Top expressed unigenes from orthogroups unique to parasite-host interface transcriptomes *T. versicolor*.

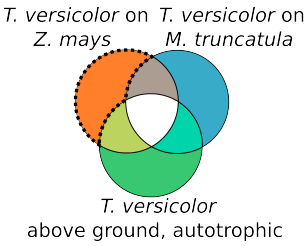
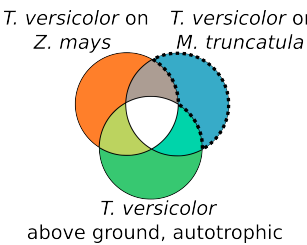
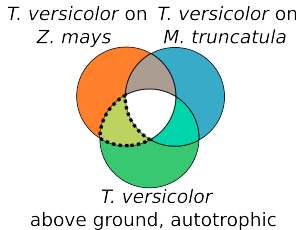
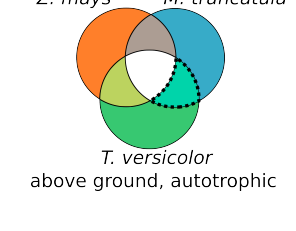
	RPKM	ID	NR BLASTx – description	NR BLAST species	% id.	17 genomes BLAST	% id.
 <i>T. versicolor</i> on <i>Z. mays</i> <i>T. versicolor</i> on <i>M. truncatula</i> <i>T. versicolor</i> above ground, autotrophic	1711	9854	^S NA	NA	NA	<i>Theobroma cacao</i>	40 P
	551	611	^T zinc transporter	<i>Nicotiana tabacum</i>	79	<i>Mimulus guttatus</i>	76 P
	416	3088	predicted protein	<i>Populus trichocarpa</i>	97	<i>Mimulus guttatus</i>	96 P
	409	11956	protein kti12 homolog	<i>Populus trichocarpa</i>	92	<i>Vitis vinifera</i>	88 N
	313	4049	hypothetical protein SORBIDRAFT_06g029810	<i>Sorghum bicolor</i>	92	<i>Sorghum bicolor</i>	89 N
	281	710	^T zinc transporter 5 isoform 1	<i>Vitis vinifera</i>	80	<i>Mimulus guttatus</i>	81 P
	279	9521	NA	NA	NA	<i>Solanum tuberosum</i>	57 P
	190	1258	^T zinc iron	<i>Ricinus communis</i>	86	<i>Mimulus guttatus</i>	81 N
	162	1590	polygalacturonase pectinase	<i>Arabidopsis lyrata</i>	77	<i>Mimulus guttatus</i>	76 P
	152	14303	gdsI esterase lipase at3g62280-like	<i>Vitis vinifera</i>	62	<i>Solanum lycopersicum</i>	45 P
	146	12610	conserved hypothetical protein	<i>Ricinus communis</i>	54	<i>Mimulus guttatus</i>	56 P
	136	4574	PREDICTED: uncharacterized protein LOC100254926	<i>Vitis vinifera</i>	86	<i>Mimulus guttatus</i>	88 P
	101	14713	^S uncharacterized wd repeat-containing protein alr3466-	<i>Vitis vinifera</i>	80	<i>Solanum tuberosum</i>	68 P
	101	13325	dna-binding protein escarola-like	<i>Vitis vinifera</i>	55	<i>Vitis vinifera</i>	46 P
	100	7730	af302808_1metallothionein-like protein	<i>Sesamum indicum</i>	84	<i>Mimulus guttatus</i>	70 P
	99	14437	proteinase inhibitor	<i>Jatropha curcas</i>	87	<i>Mimulus guttatus</i>	73 P
	97	9225	^T peptide nitrate transporter	<i>Populus trichocarpa</i>	80	<i>Populus trichocarpa</i>	66 P
	96	5684	NA	NA	NA	<i>Mimulus guttatus</i>	47 P
	95	5440	^T NA	NA	NA	<i>Populus trichocarpa</i>	36 P
	94	14819	NA	NA	NA	<i>Sorghum bicolor</i>	94 N
 <i>T. versicolor</i> on <i>Z. mays</i> <i>T. versicolor</i> on <i>M. truncatula</i> <i>T. versicolor</i> above ground, autotrophic	667	2072	^S brassinosteroid insensitive 1-associated receptor kinase	<i>Vitis vinifera</i>	60	<i>Vitis vinifera</i>	47 P
	419	4028	lob domain-containing protein 41-like	<i>Glycine max</i>	52	<i>Mimulus guttatus</i>	64 P
	344	337	PREDICTED: uncharacterized protein LOC100788950	<i>Glycine max</i>	68	<i>Carica papaya</i>	53 P
	148	15159	^T s proteinase inhibitor	<i>Oryza sativa Japonica</i>	69	<i>Fragaria vesca</i>	55 P
	146	2274	PREDICTED: uncharacterized protein LOC100793448	<i>Glycine max</i>	82	<i>Mimulus guttatus</i>	70 P
	145	6381	NA	NA	NA	<i>Glycine max</i>	43 P
	121	376	^S isoliquiritigenin 2 -o-methyltransferase-like	<i>Glycine max</i>	82	<i>Glycine max</i>	78 N
	111	1550	^T casp-like protein 9-like	<i>Glycine max</i>	93	<i>Glycine max</i>	86 N
	98	5544	zinc finger	<i>Populus trichocarpa</i>	84	<i>Mimulus guttatus</i>	81 P
	97	8801	PREDICTED: uncharacterized protein LOC100854976	<i>Vitis vinifera</i>	72	<i>Mimulus guttatus</i>	64 P
	95	4555	^T disease resistance protein	<i>Glycine max</i>	79	<i>Glycine max</i>	73 P
	95	646	PREDICTED: uncharacterized protein LOC100776135	<i>Glycine max</i>	67	<i>Mimulus guttatus</i>	79 N
	92	5876	PREDICTED: uncharacterized protein LOC100258555	<i>Vitis vinifera</i>	77	<i>Carica papaya</i>	80 N
	90	3020	ribosomal protein l16	<i>Nicotiana tabacum</i>	98	<i>Solanum lycopersicum</i>	96 N
	81	9746	predicted protein	<i>Populus trichocarpa</i>	81	<i>Mimulus guttatus</i>	75 P
	79	15676	predicted protein	<i>Populus trichocarpa</i>	95	<i>Mimulus guttatus</i>	82 N
	77	6390	germin-like protein	<i>Medicago truncatula</i>	100	<i>Medicago truncatula</i>	94 N
	72	1213	embryonic element binding factor 7	<i>Daucus carota</i>	73	<i>Solanum lycopersicum</i>	84 N
	72	11016	chaperone protein	<i>Ricinus communis</i>	72	<i>Mimulus guttatus</i>	77 N
	70	6242	dna binding	<i>Ricinus communis</i>	77	<i>Theobroma cacao</i>	60 P

Figure S5. C) Top expressed unigenes from host-specific yet above ground-shared orthogroups of *T. versicolor* transcriptomes.

	RPKM	ID	NR BLASTx – description	NR BLAST species	% id.	17 genomes BLAST	% id.
 <i>T. versicolor</i> on <i>Z. mays</i> <i>T. versicolor</i> on <i>M. truncatula</i> <i>T. versicolor</i> above ground, autotrophic	919	6408	protein auxin response 4	<i>Vitis vinifera</i>	66	<i>Fragaria vesca</i>	56 P
	834	463	conserved hypothetical protein	<i>Ricinus communis</i>	79	<i>Mimulus guttatus</i>	78 N
	766	2862	T ^s disease resistance response	<i>Vitis vinifera</i>	68	<i>Solanum tuberosum</i>	57 P
	523	277	atp-citrate synthase beta chain protein 2	<i>Populus trichocarpa</i>	95	<i>Mimulus guttatus</i>	88 N
	453	7624	UP-9A	<i>Nicotiana tabacum</i>	86	<i>Mimulus guttatus</i>	85 N
	329	59	PREDICTED: uncharacterized protein isoform 1	<i>Glycine max</i>	75	<i>Solanum tuberosum</i>	78 N
	274	4716	armadillo beta-catenin-like repeat-containing protein	<i>Glycine max</i>	91	<i>Solanum lycopersicum</i>	79 N
	266	10508	seed maturation protein pm35	<i>Phaseolus vulgaris</i>	77	<i>Solanum tuberosum</i>	69 P
	265	12720	T ^s hydrophobic protein	<i>Ricinus communis</i>	93	<i>Mimulus guttatus</i>	74 P
	240	14096	betanidin-5-O-glucosyltransferase	<i>Dorotheanthus bellidiformis</i>	72	<i>Solanum tuberosum</i>	64 P
	232	14660	conserved hypothetical protein	<i>Ricinus communis</i>	80	<i>Mimulus guttatus</i>	68 P
	231	3754	PREDICTED: uncharacterized protein LOC100263294	<i>Vitis vinifera</i>	53	<i>Mimulus guttatus</i>	43 P
	229	10547	NA	NA	NA	<i>Mimulus guttatus</i>	59 P
	218	512	PREDICTED: uncharacterized protein LOC100252003	<i>Vitis vinifera</i>	62	<i>Mimulus guttatus</i>	71 P
	206	1803	phosphate abc	<i>Ricinus communis</i>	91	<i>Solanum tuberosum</i>	82 P
	184	2144	fact complex subunit spt16	<i>Medicago truncatula</i>	90	<i>Phoenix dactylifera</i>	76 P
	177	12962	auxin-induced cp12 domain-containing protein	<i>Pisum sativum</i>	94	<i>Medicago truncatula</i>	82 P
	171	10358	NA	NA	NA	<i>Mimulus guttatus</i>	90 N
	171	10892	T ^h hypothetical protein	<i>Citrus unshiu</i>	80	<i>Mimulus guttatus</i>	72 P
	164	8348	kidney mitochondrial carrier protein 1-like	<i>Vitis vinifera</i>	96	<i>Mimulus guttatus</i>	98 P
 <i>T. versicolor</i> on <i>Z. mays</i> <i>T. versicolor</i> on <i>M. truncatula</i> <i>T. versicolor</i> above ground, autotrophic	2772	24566	PREDICTED: uncharacterized protein LOC100801029	<i>Glycine max</i>	78	<i>Carica papaya</i>	89 N
	263	147	T ^s aquaporin pip2-7	<i>Medicago truncatula</i>	98	<i>Medicago truncatula</i>	94 N
	249	9620	ubiquitin-fold modifier 1-like	<i>Glycine max</i>	100	<i>Mimulus guttatus</i>	89 N
	199	16638	small blue copper protein bcp1	<i>Paraboea crassifolia</i>	75	<i>Mimulus guttatus</i>	70 P
	181	1393	T ^p peroxisomal membrane protein	<i>Ricinus communis</i>	89	<i>Mimulus guttatus</i>	84 N
	169	22366	PREDICTED: uncharacterized protein At4g14450	<i>Glycine max</i>	59	<i>Mimulus guttatus</i>	70 P
	159	84	S ^f fructokinase 2	<i>Petunia integrifolia</i> subsp.	92	<i>Mimulus guttatus</i>	81 N
	125	10027	S ^p redicted protein	<i>Populus trichocarpa</i>	90	<i>Phoenix dactylifera</i>	77 N
	124	1041	inactive poly	<i>Ricinus communis</i>	65	<i>Mimulus guttatus</i>	61 P
	119	7997	small nuclear ribonucleoprotein e	<i>Glycine max</i>	98	<i>Carica papaya</i>	97 P
	104	10651	candidate beta-glucosidase, glycoside hydrolase family 1	<i>Postia placenta</i> Mad-698-R	82	<i>Mimulus guttatus</i>	82 P
	103	107	hypothetical protein	<i>Plantago major</i>	55	<i>Mimulus guttatus</i>	46 P
	97	1307	macro domain-containing protein vpa0103	<i>Vitis vinifera</i>	90	<i>Mimulus guttatus</i>	84 P
	91	8780	T ^s lysine histidine transporter	<i>Plantago major</i>	96	<i>Carica papaya</i>	91 P
	88	3129	PREDICTED: uncharacterized protein	<i>Vitis vinifera</i>	94	<i>Mimulus guttatus</i>	63 P
	87	9545	regulatory-associated protein of tor 1-like isoform 1	<i>Vitis vinifera</i>	88	<i>Mimulus guttatus</i>	90 P
	83	2665	cytochrome p450 81d1-like	<i>Glycine max</i>	85	<i>Fragaria vesca</i>	80 N
	80	12099	S ^p PREDICTED: uncharacterized protein	<i>Glycine max</i>	58	<i>Mimulus guttatus</i>	88 P
	75	7457	T ^u ncharacterized gpi-anchored protein at4g28100-like	<i>Vitis vinifera</i>	73	<i>Mimulus guttatus</i>	64 P
	74	5779	atp binding	<i>Ricinus communis</i>	70	<i>Solanum lycopersicum</i>	57 P