

Genome-wide transcriptome profiling of *Gossypium* spp. roots during early growth after infection with *Rotylenchulus reniformis*

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Supplementary Table 1. All annotated sequences from *Gossypium* libraries (GH1218, GHCoker, GA, and GB) containing known and/or unknown protein/enzymes.

nr	SeqName	Description	Length	# Hits	e-Value	sim mean	#GO	GO Names list	Enzyme Codes list
1	GH1218FHOD78O04 JSS07	hypothetical protein SINU_11800	201	1	1.50E -05	77%			-
2	GH1218FHOD78O04I DIBK	predicted protein	281	2	9.30E -13	52%			-
3	GH1218FHOD78O04 JQ8L5	predicted protein	228	1	2.60E -06	57%			-
4	GH1218FHOD78O04I E61N	PREDICTED: uncharacterized protein LOC105765937	223	2	2.10E -13	94%			-
5	GH1218FHOD78O04I NPAX	protein tar1-like	195	16	5.40E -14	90.44 %			-
6	GH1218FHOD78O04I 30QC	predicted protein	326	1	4.20E -07	58%			-
7	GH1218FHOD78O04 JBFPR	protein tar1-like	263	20	3.00E -25	92.25 %			-
8	GH1218FHOD78O04I 9Z3T	senescence-associated protein	238	20	1.00E -30	95.30 %			-
9	GH1218FHOD78O04I H2CD	predicted protein	212	1	2.40E -04	50%			-
10	GH1218FHOD78O04I FZE2	protein tar1-like	194	16	5.40E -14	90.44 %			-
11	GH1218FHOD78O04 JPMKL	protein tar1-like	194	16	5.40E -14	90.44 %			-
12	GH1218FHOD78O04I HQ7R	protein tar1-like	196	20	1.10E -22	93.05 %			-
13	GH1218FHOD78O04 J0DN4	protein tar1-like	209	20	4.70E -25	89.90 %			-
14	GH1218FHOD78O04 H4NVQ	PREDICTED:uncharacteri zed protein LOC104007098	269	1	1.20E -24	48%			-
15	GH1218FHOD78O04I ZDFK	protein tar1-like	195	20	1.10E -22	93.05 %			-
16	GH1218FHOD78O04I XU4X	protein tar1-like	264	20	1.10E -24	92.55 %			-
17	GH1218FHOD78O04 JM596	protein tar1-like	195	16	5.4E- 14	90.44 %			-
18	GH1218FHOD78O04I 48T1	protein tar1-like	194	16	5.4E- 14	90.44 %			-
19	GH1218FHOD78O04I ZVZS	protein tar1-like	196	16	5.4E- 14	90.44 %			-
20	GH1218FHOD78O04I	protein tar1-like	164	20	1.20E	87.90			-

	K0EE				-15	%			
21	GH1218FHOD78004I1Z7R	hypothetical protein	165	16	1.60E-07	72.38%			-
22	GH1218FHOD78004ISVGH	m030_arath ame: full=uncharacterized mitochondrial protein	0	1	0.00E+00	100.00%	1	C:mitochondrion	-
23	GH1218FHOD78004IB130	hypothetical protein	0	1	0.00E+00	100.00%	1	C:integral component of membrane	-
24	GH1218FHOD78004IOXBE	hypothetical protein	0	1	0.00E+00	100.00%	1	C:integral component of membrane	-
25	GH1218FHOD78004H4912	hypothetical protein	0	1	0.00E+00	100.00%	1	C:integral component of membrane	-
26	GH1218FHOD78004IVOSY	small related domain-containing family protein	0	1	0.00E+00	100.00%	2	F:hydrolase activity; P: metabolic process	-
27	GHCokerFHOD78004IWJJK	predicted protein	324	1	5.70E-09	58%			-
28	GHCokerFHOD78004IXTBF	predicted protein	256	2	8.30E-13	55.50%			-
29	GHCokerFHOD78004IW6CP	protein tar1-partial	126	11	2.60E-10	81.73%			-
30	GHCokerFHOD78004I3UKV	hypothetical protein	187	1	2.00E-08	80%			-
31	GHCokerFHOD78004JYXYO	senescence-associated protein	173	20	3.00E-17	88.80%			-
32	GHCokerFHOD78004I5JS4	hypothetical protein	189	1	9.20E-09	80%			-
33	GHCokerFHOD78004IMQNW	predicted protein	261	1	1.00E-05	57%			-
34	GHCokerFHOD78004IFWIT	protein tar1-like	275	8	2.60E-12	75.50%			-
35	GHCokerFHOD78004JGKD8	predicted protein	267	20	2.60E-25	91.65%			-
36	GHCokerFHOD78004NOM	protein tar1-like	254	1	2.30E-07	57%			-
37	GHCokerFHOD78004I01P4	predicted protein	262	20	1.10E-21	88%			-
38	GHCokerFHOD78004ITIBK	mediator of rna polymerase ii transcription subunit 1	264	1	1.10E-05	57%			-
39	GHCokerFHOD78004IG22J	retrotransposon-like protein 1	284	2	5.00E-15	51%			-
nr	SeqName	Description	Length	# Hits	e-Value	sim mean	#GO	GO Names list	Enzyme Codes list
40	GHCokerFHOD78004IFR3O	hypothetical protein B456_007G025700	301	1	2.90E-04	97%			-
41	GHCokerFHOD78004IYIS4	predicted protein	299	1	9.70E-19	90%			-
42	GHCokerFHOD78004I8OWM	predicted protein	322	1	8.80E-08	58%			-
43	GHCokerFHOD78004ILYQR	hypothetical protein	0	1	0.00E+00	100.00%	1	C:integral component of membrane	-
44	GHCokerFHOD78004IB7NV	m030_arath ame: full=uncharacterized mitochondrial protein	0	1	0.00E+00	100.00%	1	C:mitochondrion	-
45	GHCokerFHOD78004INGCJ	BnaA09g04420D	0	1	0.00E+00	100.00%	1	C:integral component of membrane	-
46	GHCokerFHOD78004IWKTZ	probable uridine nucleosidase 2	0	1	0.00E+00	100.00%	4	C:cytosol; F:UDP-glucosyltransferase activity; F:inosine	EC:3.2.2.2

								nucleosidase activity; P:inosine catbolic process	
47	GHCokerFHOD78O04ILF5P	receptor-like serine thronine-protein kinase at4g25390	0	1	0.00E +00	100.0 0%	3	F:protein serine/threonine kinase activity: F: ATP binding P: protein phosphorylation	EC:2.7.11
48	GHCokerFHOD78O04H4LZY	phosphoprotein ecpp44	0	1	0.00E +00	100.0 0%	2	P: response to stress; P: response to water	-
49	GAFHOD78O04JU294	hypothetical protein BVRB_8g200780	268	3	2.30E -21	84.67 %			-
50	GAFHOD78O04JXYJ5	hypothetical protein AMTR_s00115p00112450	267	3	7.10E -19	86.33 %			-
51	GAFHOD78O04JCTRY	protein tar1-like	219	19	3.70E -14	93.37 %			-
52	GAFHOD78O04IT415	hypothetical protein	220	6	7.90E -08	73.33 %			-
53	GAFHOD78O04JMJ01	protein tar1-like	228	20	2.30E -15	90.20 %			-
54	GAFHOD78O04JCTIU	PREDICTED: fibropellin- 1-like	306	1	1.40E -04	54%			-
55	GAFHOD78O04JZ8PO	hypothetical protein AMTR_s00115p00112450	312	3	8.20E -19	82.33 %			-
56	GAFHOD78O04H8RPT	hypothetical protein AMTR_s00115p00112450	311	3	2.00E -21	83.67 %			-
57	GAFHOD78O04IUL6B	hypothetical protein	212	3	1.90E -13	92%			-
58	GAFHOD78O04ILRLO	PREDICTED:uncharacteri zed protein LOC104007098	265	1	4.30E -09	48%			-
59	GAFHOD78O04ILOHY	predicted protein	328	1	2.70E -07	57%			-
60	GAFHOD78O04JO3BY	protein tar1-like	225	20	1.90E -15	89.30 %			-
61	GAFHOD78O04I2T23	protein tar1-like	226	20	1.90E -15	88.85 %			-
62	GAFHOD78O04JW38P	predicted protein	312	1	1.40E -08	51%			-
63	GAFHOD78O04I5PQL	senescence-associated protein	251	20	8.90E -22	93.20 %			-
64	GAFHOD78O04INSX3	PREDICTED: uncharacterized protein LOC105852854_partial	177	5	6.90E -07	72.20 %			-
65	GAFHOD78O04IQVKI	predicted protein	283	1	1.80E -11	53%			-
66	GAFHOD78O04JAYTP	hypothetical protein AMTR_s00115p00112450	267	3	1.50E -20	84.67 %			-
67	GAFHOD78O04I756D	senescence-associated protein	203	20	4.90E -22	93.20 %			-
68	GAFHOD78O04JIL85	hypothetical protein BVRB_8g200780	308	3	5.60E -17	83%			-
69	GAFHOD78O04JX1S8	heavy metal transport detoxification domain- containing protein	0	1	0.00E +00	100.0 0%	2	F: metal ion binding; P: metal ion transport	-
70	GAFHOD78O04I3MSR	heavy metal transport detoxification superfamily	0	1	0.00E +00	100.0 0%	2	F: metal ion binding; P: metal ion transport	-
71	GAFHOD78O04I82Q	senescence-associated	0	1	0.00E	100.0	1	C: integral	-

	C	protein			+00	0%		component of membrane	
72	GAFHOD78O04I256Z	hypothetical protein	0	1	0.00E+00	100.00%	1	C: integral component of membrane	-
73	GAFHOD78O04JDHXK	heavy metal transport detoxification superfamily	0	1	0.00E+00	100.00%	2	F: metal ion binding; P: metal ion transport	-
74	GAFHOD78O04I1FW6	heavy metal transport detoxification superfamily	0	1	0.00E+00	100.00%	2	F: metal ion binding; P: metal ion transport	-
75	GAFHOD78O04IY4R4	hypothetical protein	0	1	0.00E+00	100.00%	1	C: integral component of membrane	-
76	GAFHOD78O04I6O5U	heavy metal transport detoxification superfamily	0	1	0.00E+00	100.00%	3	C: endoplasmic reticulum; C: integral component of membrane; P: intracellular protein transport	-
77	GAFHOD78O04I0W2A	heavy metal transport detoxification superfamily	0	1	0.00E+00	100.00%	2	P: response to stress; P: response to water	-
78	GBFHOD78O04JQHVG	hypothetical protein	311	3	7.40E-20	83.00%			-
nr	SeqName	Description	Length	# Hits	e-Value	sim mean	#GO	GO Names list	Enzyme Codes list
79	GBFHOD78O04JC8G9	protein tar1-like	224	20	1.50E-15	87.40%			-
80	GBFHOD78O04ILJIK	hypothetical protein AMTR_s00115p00112450	311	3	7.40E-20	83%			-
81	GBFHOD78O04IDCVX	hypothetical protein	205	4	6.40E-11	90%			0
82	GBFHOD78O04JSU6F	hypothetical protein BVRB_8g200780	313	3	3.50E-22	85.67%			-
83	GBFHOD78O04IM7PY	hypothetical protein AMTR_s00115p00112450	268	3	5.60E-21	84%			-
84	GBFHOD78O04JOWCJ	hypothetical protein AMTR_s00115p00112450	312	3	1.60E-16	80.67%			-
85	GBFHOD78O04I8UXD	hypothetical protein	310	1	4.00E-04	71.00%			-
86	GBFHOD78O04JD45R	PREDICTED: fibropellin-1-like	271	1	8.30E-10	58%			-
87	GBFHOD78O04JD8IT	hypothetical protein LOTGIDREFT_126730, partial	275	4	4.60E-12	57.75%			-
88	GBFHOD78O04ICCCS	hypothetical protein B456_013G197500	240	3	2.60E-22	100%			-
89	GBFHOD78O04I8SCN	hypothetical protein AMTR_s00115p00112450	268	3	3.90E-21	84.00%			-
90	GBFHOD78O04JBRD9	PREDICTED: fibropellin-1-like	311	1	1.00E-05	56%			-
91	GBFHOD78O04IWH A2	senescence-associated protein	322	20	5.20E-15	92.15%			-
92	GBFHOD78O04JQ559	hypothetical protein B456_013G197500	186	3	2.10E-21	96%			-
93	GBFHOD78O04H9IQ6	ubiquitin-nedc8-like proein rub2	127	20	1.70E-12	86%			-
94	GBFHOD78O04H557	sieve element occlusion m	335	20	1.20E	84.10			-

	M				-25	%			
95	GBFHOD78O04I0AZ Z	predicted protein	283	1	3.20E -13	57%			-
96	GBFHOD78O04JUPP O	ubiquitin-nedd8-like protein rub2	0	1	0.00E +00	100.0 0%	3	C: nucleus; C: cytoplasm; P: ubiquitin-dependent protein catabolic process	-
97	GBFHOD78O04IDV4 J	hypothetical proteinB456_001G162300	0	1	0.00E +00	100.0 0%	1	F: nucleic acid binding	-
98	GBFHOD78O04JH59 A	hypothetical proteinB456_001G162300	0	1	0.00E +00	100.0 0%	1	F: nucleic acid binding	-
99	GBFHOD78O04JH7V D	coagulation factor v	0	1	0.00E +00	100.0 0%	1	P: hemostasis	-
10 0	GBFHOD78O04IFBL D	senescence-associated gene 18 isoform 1	0	1	0.00E +00	100.0 0%	3	C: integral component of membrane; F: hydrolase activity, acting on carbon- nitrogen (nut not peptide) bonds, in linear amides; P: ceramide metabolic process	-
10 1	GBFHOD78O04JAIA 3	ubiquitin-60s ribosomal protein I40	0	1	0.00E +00	100.0 0%	3	C: ribosome; F: structural constituent of ribosome; P: translation	-
10 2	GBFHOD78O04IWN W6	hypothetical proteinB456_001G162300	0	1	0.00E +00	100.0 0%	1	F: nucleic acid binding	-
10 3	GBFHOD78O04IH72 V	coagulation factor v	0	1	0.00E +00	100.0 0%	1	P: hemostasis	-
10 4	GBFHOD78O04I2PJ H	phosphoprotein ecpp44	0	1	0.00E +00	100.0 0%	2	P: response to stress; P: response to water	-
10 5	GBFHOD78O04JJI1J	coagulation factor v	0	1	0.00E +00	100.0 0%	1	P: single- multicellular organism process	-
10 6	GBFHOD78O04JID6 Z	coagulation factor v	0	1	0.00E +00	100.0 0%	1	P: hemostasis	-