

# **Genetic characteristics of *Bursaphelenchus xylophilus* third-stage dispersal juveniles**

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Table S1 Statistical analysis of the RNA sequencing data.

Samples	Clean Reads	Clean Reads	Clean Reads	Gene Mapping
	Number	Rate (%)	Q20 (%)	Rate (%)
J2-1	22,133,728	99.62	97.50	71.27
J2-2	22,203,673	99.94	97.38	71.64
J2-3	24,112,070	99.90	97.94	71.58
J3-1	24,057,741	99.67	97.20	75.77
J3-2	24,145,341	99.56	97.64	74.66
J3-3	23,985,362	99.48	97.67	75.13
J4-1	24,037,515	99.59	96.90	76.96
J4-2	23,465,363	99.65	97.64	76.68
J4-3	24,013,521	99.56	97.68	76.84
Female-1	23,960,379	99.26	95.30	78.06
Female-2	24,013,135	99.46	97.34	78.99
Female-3	23,961,244	99.75	97.42	78.56
Male-1	21,359,122	99.41	94.80	76.86
Male-2	22,063,153	99.53	96.57	76.96
Male-3	21,624,233	99.75	97.31	76.66
J2-2-1	24,110,169	99.89	97.90	59.92
J2-2-2	23,951,367	99.39	97.86	64.57
J2-2-3	24,061,351	99.86	97.34	62.44
DJ3-lab-1	24,018,211	99.51	97.10	75.94
DJ3-lab-2	23,996,384	99.42	97.00	74.01
DJ3-lab-3	23,940,211	99.80	98.40	73.51
DJ3-field-1	23,821,746	99.21	98.60	73.39
DJ3-field-2	23,971,254	99.12	98.41	73.89
DJ3-field-3	23,814,547	99.39	98.76	74.06
DJ4-1	22,051,038	91.38	98.44	66.51
DJ4-2	23,023,245	95.89	98.76	67.88

DJ4-3

22,415,547

96.76

98.42

67.69

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Table S2 Number of genes in each module.

Module	Gene number
<hr/>	
colors	
<hr/>	
black	603
blue	2639
brown	2589
cyan	143
green	1010
greenyellow	234
grey	20
magenta	533
pink	583
purple	437
red	789
salmon	158
tan	202
turquoise	4775
yellow	1148
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Table S3 Genes with the top 30 highest IC values in the pink module.

No.	Gene annotation	IC	Homologous protein GenBank ID	Protein name	Blast nr p-value
1	<i>cath1-6</i>	159.5326073	AID50178.1	cysteine protease family cathepsin 1 [ <i>Bursaphelenchus mucronatus</i> ]	$3.4518 \times 10^{-108}$
2	<i>O-Gly-hydro30</i>	158.3084016	EPB74230.1	O-Glycosyl hydrolase family 30 [ <i>Ancylostoma ceylanicum</i> ]	$1.59787 \times 10^{-80}$
3	<i>asp</i>	157.6912185	KJH53579.1	eukaryotic aspartyl protease [ <i>Dictyocaulus viviparus</i> ]	$2.08533 \times 10^{-23}$
4	<i>gst-33</i>	155.5006374	ABN64198.1	glutathione S-transferase-1 [ <i>Meloidogyne incognita</i> ]	$3.11943 \times 10^{-22}$
5	<i>cath1-5</i>	154.8696696	AID50178.1	cysteine protease family cathepsin 1 [ <i>Bursaphelenchus mucronatus</i> ]	$1.31168 \times 10^{-107}$
6	<i>CBN-DHS-2</i>	154.3596573	EGT37950.1	CBN-DHS-2 protein [ <i>Caenorhabditis brenneri</i> ] Glycoside hydrolase domain	$4.56842 \times 10^{-68}$
7	<i>Gly-hydro</i>	153.8170115	CDJ96960.1	containing protein [ <i>Haemonchus contortus</i> ]	$4.85292 \times 10^{-21}$
8	<i>str-124</i>	153.2131533	CEF64053.1	7TM GPCR, serpentine receptor class r (Str) family-containing protein [ <i>Strongyloides ratti</i> ]	$2.54895 \times 10^{-06}$
9	<i>gst-36</i>	152.0856442	KKA74463.1	Glutathione S-transferase [ <i>Pristionchus pacificus</i> ]	$1.8039 \times 10^{-15}$
10	<i>irld-39</i>	151.0613212	-	-	-
11	<i>BUX.s01254.113</i>	150.5725348	-	-	-
12	<i>BUX.s01149.55</i>	150.4648858	-	-	-
13	<i>cath1-4</i>	149.3657473	AID50178.1	cysteine protease family cathepsin 1 [ <i>Bursaphelenchus mucronatus</i> ]	$1.10675 \times 10^{-90}$
14	<i>BUX.s00460.305</i>	149.1136527	-	-	-
15	<i>scl-13</i>	148.7282799	ADG86239.1	venom allergen-like protein VAP3 [ <i>Bursaphelenchus xylophilus</i> ]	$1.09812 \times 10^{-120}$
16	<i>BUX.s01149.58</i>	148.0852976	-	-	-
17	<i>cra-1</i>	147.8092805	XP_00314786 5.1	hypothetical protein LOAG_12304 [ <i>Loa loa</i> ]	$7.65088 \times 10^{-45}$
18	<i>cath1-1</i>	147.4758269	AID50178.1	cysteine protease family cathepsin 1	$6.95176 \times 10^{-76}$

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				[ <i>Bursaphelenchus mucronatus</i> ]	
19	<i>cath1-3</i>	147.2517936	AID50178.1	cysteine protease family cathepsin 1	1.05473×10 <sup>-41</sup>
				[ <i>Bursaphelenchus mucronatus</i> ]	
				hypothetical protein	
20	<i>BUX.s00609.55</i>	146.8648011	EYB86268.1	Y032_0282g1277	2.65302×10 <sup>-149</sup>
				[ <i>Ancylostoma ceylanicum</i> ]	
21	<i>BUX.s01281.196</i>	146.791013	-	-	-
22	<i>spp-20</i>	146.6361924	-	-	-
23	<i>BUX.s01149.57</i>	146.4990787	-	-	-
				CBN-SODH-2 protein	
24	<i>Cbn-sodh-2</i>	145.7646357	EGT60304.1	[ <i>Caenorhabditis brenneri</i> ]	4.08829×10 <sup>-91</sup>
				hypothetical protein CRE_26128	
25	<i>BUX.s01254.340</i>	145.7577156	XP_00311361 7.1	[ <i>Caenorhabditis remanei</i> ]	2.91415×10 <sup>-54</sup>
				cysteine protease family cathepsin 1	
26	<i>cath1-8</i>	145.1472441	AID50178.1	[ <i>Bursaphelenchus mucronatus</i> ]	3.33012×10 <sup>-103</sup>
27	<i>BUX.s00773.12</i>	145.1195146	-	-	-
				Src homology-3 and Tyrosine protein	
28	<i>Src-3</i>	144.8323753	CDJ86525.1	kinase domain containing protein	2.25183×10 <sup>-61</sup>
				[ <i>Haemonchus contortus</i> ]	
29	<i>BUX.s01066.169</i>	144.7103838	-	-	-
				Acyl-CoA synthetase family member	
30	<i>acs-14</i>	144.5409195	CEF60576.1	2,mitochondrial	3.21114×10 <sup>-76</sup>
				[ <i>Strongyloides ratti</i> ]	

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Table S4 Forty-two network genes for the pink module.

No.	Gene annotation	IC	GS	MM	log <sub>2</sub> fold	Homologous protein GenBank ID	Protein name	Blast nr p-value
1	<i>cath1-6</i>	159.532 6073	0.988 8461 64	0.974 1623 11	4.44657 8165	AID50178.1	cysteine protease family cathepsin 1 [ <i>Bursaphelenchus mucronatus</i> ]	3.4518×10 <sup>-108</sup>
2	<i>O-Gly-hydro30</i>	158.308 4016	0.950 9804 28	0.982 3716 7	2.39027 4998	EPB74230.1	O-Glycosyl hydrolase family 30 [ <i>Ancylostoma ceylanicum</i> ]	1.59787×10 <sup>-80</sup>
3	<i>asp</i>	157.691 2185	0.940 3891 2	0.987 0788 93	2.78486 744	KJH53579.1	eukaryotic aspartyl protease [ <i>Dictyocaulus viviparus</i> ]	2.08533×10 <sup>-23</sup>
4	<i>gst-33</i>	155.500 6374	0.946 2089 04	0.976 7892 13	3.84479 9544	ABN64198.1	glutathione S-transferase-1 [ <i>Meloidogyne incognita</i> ]	3.11943×10 <sup>-22</sup>
5	<i>cath1-5</i>	154.869 6696	0.986 5229 44	0.968 3950 33	4.44562 1127	AID50178.1	cysteine protease family cathepsin 1 [ <i>Bursaphelenchus mucronatus</i> ]	1.3117×10 <sup>-107</sup>
6	<i>CBN-DHS-2</i>	154.359 6573	0.987 0170 29	0.962 9187 69	4.49275 9739	EGT37950.1	CBN-DHS-2 protein [ <i>Caenorhabditis brenneri</i> ]	4.56842×10 <sup>-68</sup>
7	<i>Gly-hydro</i>	153.817 0115	0.951 2587 29	0.973 1865 85	2.69764 4098	CDJ96960.1	Glycoside hydrolase domain containing protein [ <i>Haemonchus contortus</i> ]	4.85292×10 <sup>-21</sup>
8	<i>str-124</i>	153.213 1533	0.973 0703 6	0.971 1502 09	3.94337 6809	CEF64053.1	7TM GPCR, serpentine receptor class r (Str) family-containing protein [ <i>Strongyloides ratti</i> ]	2.54895×10 <sup>-06</sup>
9	<i>gst-36</i>	152.085 6442	0.988 2188	0.958 1010	4.83776 1218	KKA74463.1	Glutathione S-transferase [ <i>Pristionchus pacificus</i> ]	1.8039×10 <sup>-15</sup>



			59	89				
			0.958	0.966				
10	<i>irld-39</i>	151.061	5539	8325	4.05568	-	-	-
		3212			5227			
			26	36				
			0.985	0.961				
11	<i>BUX.s01254.113</i>	150.572	3235	5258	4.23168	-	-	-
		5348			163			
			67	05				
			0.990	0.955				
12	<i>BUX.s01149.55</i>	150.464	3836	3638	6.91651	-	-	-
		8858			6288			
			67	66				
			0.987	0.953				
13	<i>cath1-4</i>	149.365	9976	1478	6.78676	AID50178.1	cysteine protease family cathepsin 1	1.10675×10 <sup>-90</sup>
		7473			5412		[ <i>Bursaphelenchus mucronatus</i> ]	
			92	69				
			0.996	0.950				
14	<i>scl-13</i>	148.728	7551	5994	7.98818	ADG86239.1	venom allergen-like protein VAP3	1.0981×10 <sup>-120</sup>
		2799			8299		[ <i>Bursaphelenchus xylophilus</i> ]	
			48	58				
			0.991	0.951				
15	<i>BUX.s01149.58</i>	148.085	3973	4531	6.71587	-	-	-
		2976			8015			
			61	04				
			0.980	0.951				
16	<i>cath1-1</i>	147.475	6078	0798	6.19801	AID50178.1	cysteine protease family cathepsin 1	6.95176×10 <sup>-76</sup>
		8269			2395		[ <i>Bursaphelenchus mucronatus</i> ]	
			84	09				
			0.983	0.950				
17	<i>cath1-3</i>	147.251	4606	3217	6.73070	AID50178.1	cysteine protease family cathepsin 1	1.05473×10 <sup>-41</sup>
		7936			1785		[ <i>Bursaphelenchus mucronatus</i> ]	
			7	45				
			0.972	0.959				
18	<i>BUX.s01281.196</i>	146.791	2815	7139	3.66956	-	-	-
		013			6309			
			84	11				
			0.991	0.948				
19	<i>BUX.s01149.57</i>	146.499	9.20532			-	-	-

		0787	6523	3568	3331			
			69	76				
			0.960	0.958				
20	<i>Cbn-sodh-2</i>	145.764	1241	6094	4.89620	EGT60304.1	CBN-SODH-2 protein [ <i>Caenorhabditis brenneri</i> ]	4.08829×10 <sup>-91</sup>
		6357	54	79	0997			
			0.998	0.945				
21	<i>BUX.s00773.12</i>	145.119	2008	0503	7.07993	-	-	-
		5146	34	3	3101			
			0.994	0.947			Src homology-3 and Tyrosine protein kinase	
22	<i>Src-3</i>	144.832	6294	7664	4.10500	CDJ86525.1	domain containing protein [ <i>Haemonchus contortus</i> ]	2.25183×10 <sup>-61</sup>
		3753	95	82	8558			
			0.992	0.944				
23	<i>BUX.s01066.169</i>	144.710	3626	0953	5.38064	-	-	-
		3838	62	88	778			
			0.998	0.943				
24	<i>BUX.s00713.823</i>	144.338	3589	1689	6.39806	-	-	-
		3328	89	68	5219			
			0.971	0.946				
25	<i>cath1-2</i>	144.119	2929	1234	5.44816	AID50178.1	cysteine protease family cathepsin 1 [ <i>Bursaphelenchus mucronatus</i> ]	5.50549×10 <sup>-82</sup>
		9535	13	93	7269			
			0.985	0.942				
26	<i>Pank-1</i>	143.634	9661	1577	3.71687	KHN77364.1	Pantothenate kinase 1 [ <i>Toxocara canis</i> ]	7.8244×10 <sup>-146</sup>
		1537	58	74	8439			
			0.991	0.945				
27	<i>asp-14</i>	142.773	2012	4153	4.67688	-	-	-
		9429	39	66	499			
			0.979	0.951				
28	<i>BUX.s01038.42</i>	142.562	7551	4480	4.54819	-	-	-
		0508	13	53	314			

			0.969	0.949	4.37019			
29	<i>oac-29</i>	142.343	7280	7735		-	-	-
		4777			5752			
			86	71				
				0.941				
30	<i>cath1-7</i>	140.082	0.974	3329	6.57930	AID50178.1	cysteine protease family cathepsin 1	5.13471×10 <sup>-15</sup>
		6661	976		3266		[ <i>Bursaphelenchus mucronatus</i> ]	
				97				
			0.968	0.934				
31	<i>acsf2</i>	140.013	4026	4594	3.04828	KHN84146.1	Acyl-CoA synthetase family member 2,	1.5861×10 <sup>-180</sup>
		4726			4161		mitochondrial [ <i>Toxocara canis</i> ]	
			14	28				
			0.976	0.940				
32	<i>BUX.s00110.118</i>	137.832	5632	9960	3.89475	-	-	-
		0848			684			
			87	49				
			0.985	0.932				
33	<i>sbp-1</i>	136.874	6165	6526	3.01863	KHN86442.1	Sterol regulatory element-binding protein 1	2.28728×10 <sup>-25</sup>
		8978			2387		[ <i>Toxocara canis</i> ]	
			22	06				
			0.967	0.939				
34	<i>epg-5</i>	135.361	2641	0191	4.76001	-	-	-
		8996			2785			
			58	32				
			0.979	0.918				
35	<i>BUX.s00773.15</i>	127.820	7985	7912	4.49593	-	-	-
		6086			605			
			01	47				
			0.953	0.916				
36	<i>acetyl-CoA</i>	124.517	4988	1128	2.67151	CEF71468.1	Carboxyl transferase domain and Biotin	0
		7749			04		[ <i>Strongyloides ratti</i> ]	
			58	18				
			0.969	0.901				
37	<i>Ddram-1</i>	122.893	9785	7335	3.54205	KHN72428.1	DNA damage-regulated autophagy modulator	7.98356×10 <sup>-22</sup>
		0373			3909		protein 1	
			49	66			[ <i>Toxocara canis</i> ]	
			0.969	0.900				
38	<i>acetyl-coenzyme</i>	120.900	0489	4126	3.11945	ERG80270.1	acetyl-coenzyme a cytoplasmic [ <i>Ascaris suum</i> ]	4.10816×10 <sup>-53</sup>
		9149			8652			

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			17	35				
39	<i>fae5</i>	113.140	0.951	0.884	2.58130	EJW88645.1	fatty acid elongation protein 5 [ <i>Wuchereria bancrofti</i> ]	1.41793×10 <sup>-84</sup>
		987	0620	9645	6214			
			62	75				
40	<i>elo-6</i>	112.933	0.950	0.883	2.58735	XP_0026338	<i>C. briggsae</i> CBR-ELO-6 protein [ <i>Caenorhabditis briggsae</i> ]	4.38478×10 <sup>-78</sup>
		2421	4359	6312	458	91.1		
			31	75				
41	<i>ALDH2</i>	108.130	0.943	0.876	2.32379	KHN86680.1	Aldehyde dehydrogenase, mitochondrial [ <i>Toxocara canis</i> ]	0
		3498	4452	5214	6869			
			8	63				
42	<i>tmem-135</i>	97.0444	0.936	0.861	2.89669	NP_508800.	TMEM (human TransMEMbrane protein) homolog	1.24721×10 <sup>-40</sup>
		7902	1454	9866	8411	2		
			96	89			[ <i>Caenorhabditis elegans</i> ]	

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Table S5 Top 30 genes with the highest weight value to each of the 7 genes.

No.	Number of genes	Number of genes	Weight value
1	21	1	0.492137315
2	14	1	0.48994234
3	19	1	0.489799172
4	1	24	0.488884436
5	15	1	0.487896545
6	13	1	0.486417876
7	13	1	0.486417876
8	12	1	0.486246042
9	1	38	0.486233078
10	1	22	0.485689578
11	30	1	0.485672596
12	30	1	0.485672596
13	17	1	0.485275634
14	17	1	0.485275634
15	16	1	0.482392852
16	16	1	0.482392852
17	1	35	0.48210381
18	9	1	0.481253274
19	1	27	0.480864513
20	13	6	0.480119286
21	1	26	0.480107618
22	1	11	0.479618217
23	17	6	0.479410971
24	30	6	0.479314339
25	32	1	0.479200002
26	23	1	0.478527701
27	6	1	0.478405224

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28	21	5	0.477791704
29	25	1	0.477422573
30	25	1	0.477422573
31	34	1	0.476765546
32	16	6	0.476657717
33	14	5	0.476154436
34	1	5	0.475697258
35	1	5	0.475697258
36	5	24	0.475196268
37	19	5	0.474910561
38	15	5	0.474557232
39	1	36	0.474272405
40	13	12	0.473994688
41	30	12	0.473905776
42	30	9	0.473658176
43	13	9	0.47357636
44	17	12	0.473520511
45	37	1	0.473350111
46	13	38	0.473160544
47	17	9	0.473133572
48	13	19	0.473009983
49	13	21	0.472701187
50	5	22	0.472496483
51	13	5	0.472444688
52	13	5	0.472444688
53	25	6	0.472428799
54	13	14	0.472399877
55	12	5	0.47222922
56	28	1	0.472021812

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57	13	15	0.471611443
58	13	24	0.471138116
59	30	13	0.47112965
60	30	13	0.47112965
61	16	9	0.470966846
62	16	12	0.470922726
63	5	38	0.470806323
64	17	13	0.470653266
65	17	13	0.470653266
66	17	5	0.470506191
67	17	5	0.470506191
68	30	14	0.470475606
69	1	33	0.470208337
70	17	14	0.470091778
71	30	5	0.469789444
72	30	5	0.469789444
73	1	42	0.469625388
74	29	1	0.469077662
75	5	35	0.468628749
76	13	16	0.468608779
77	13	16	0.468608779
78	16	5	0.468531731
79	16	5	0.468531731
80	5	27	0.467683275
81	16	14	0.467508077
82	25	9	0.467296145
83	9	5	0.467250861
84	25	12	0.467183058
85	5	26	0.467022205

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86	17	38	0.466919423
87	1	41	0.466721319
88	5	11	0.4665363
89	17	19	0.466387739
90	30	15	0.466211256
91	17	15	0.466056341
92	23	5	0.465923046
93	17	30	0.465491621
94	17	30	0.465491621
95	17	21	0.465326736
96	30	19	0.465324422
97	25	13	0.465300432
98	25	13	0.465300432
99	6	5	0.465054954
100	13	11	0.464746157
101	16	38	0.464583938
102	13	22	0.464408186
103	15	16	0.464076411
104	32	5	0.464003618
105	16	19	0.463967446
106	17	24	0.463675797
107	17	11	0.463336156
108	30	16	0.463303646
109	30	16	0.463303646
110	25	5	0.463233787
111	25	5	0.463233787
112	13	26	0.463064092
113	30	11	0.463038036
114	17	16	0.462781084

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115	17	16	0.462781084
116	25	14	0.462730003
117	13	35	0.462584436
118	21	16	0.462499118
119	37	5	0.462364065
120	34	5	0.461380517
121	16	11	0.46129075
122	16	24	0.461242755
123	5	36	0.460912942
124	13	36	0.460811926
125	13	37	0.46063131
126	30	21	0.460506513
127	25	15	0.459976306
128	17	25	0.459520409
129	17	25	0.459520409
130	13	2	0.459238335
131	25	16	0.458803845
132	25	16	0.458803845
133	30	24	0.458773489
134	13	34	0.458591772
135	13	23	0.458472272
136	17	2	0.458317814
137	13	27	0.458166764
138	30	2	0.458037937
139	5	33	0.457827981
140	28	5	0.457505494
141	25	19	0.457300119
142	5	42	0.457013271
143	13	8	0.456921826

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144	25	11	0.456916109
145	13	42	0.456592284
146	13	32	0.456564496
147	29	5	0.45623694
148	17	22	0.456161126
149	16	2	0.455921579
150	17	8	0.455750052
151	17	26	0.455598375
152	13	40	0.455461228
153	30	8	0.455365744
154	5	41	0.455096719
155	13	39	0.45476396
156	17	35	0.454539959
157	16	36	0.454405726
158	16	22	0.453921104
159	16	26	0.453742428
160	17	23	0.453574309
161	17	7	0.453353921
162	17	36	0.453341156
163	30	23	0.45332145
164	30	7	0.453297609
165	16	8	0.452917617
166	30	26	0.452673928
167	17	37	0.452647503
168	17	34	0.45262933
169	25	38	0.452097024
170	30	25	0.451991066
171	30	25	0.451991066
172	16	7	0.451978798

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173	16	35	0.451837711
174	25	2	0.45144753
175	25	21	0.451259305
176	16	37	0.451053463
177	30	22	0.45079755
178	23	16	0.450655766
179	25	7	0.450123176
180	25	24	0.450117136
181	17	27	0.450091837
182	17	32	0.449604669
183	16	34	0.449432102
184	16	42	0.449311923
185	17	42	0.448864586
186	25	8	0.447698177
187	17	40	0.447431316
188	16	40	0.447424374
189	16	27	0.447302278
190	30	38	0.446420502
191	16	39	0.446401037
192	25	26	0.445035837
193	25	23	0.444466987
194	30	27	0.444012965
195	25	36	0.443689919
196	30	4	0.442498894
197	25	22	0.442301326
198	30	31	0.441184503
199	30	18	0.439744592
200	25	42	0.438817696
201	30	3	0.437924211

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202	25	35	0.437828917
203	25	34	0.437688685
204	25	37	0.437076831
205	30	20	0.436962621
206	25	31	0.436040908
207	30	10	0.435822749
208	25	40	0.4353366
209	25	27	0.434892645
210	30	29	0.433026623

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Table S6 Primers used in this study.

Gene	Primer
<i>cath1-1</i>	F-`GGTCTTTTCGCACAATCGCTC`
	R-`TTCAAACCACTCATCGCCGT`
<i>cath1-2</i>	F-`GCTGTGTCATCCGCTCATCA`
	R-`TTGGAGGCAAACCTCAGCGA`
<i>cath1-3</i>	F-`CCAAAACCTCCGCGAATCCA`
	R-`AGTGGTTAGCAGGTTTGCT`
<i>cath1-4</i>	F-`GCTGTGTCATCCGCTCATCA`
	R-`TTGGAGGCAAACCTCAGCGA`
<i>cath1-5</i>	F-`ACATACCTTGATGCCGGACC`
	R-`ACCCAGTCTTCTCCCCATT`
<i>cath1-6</i>	F-`CTCACCAGGAGTGTTCGAT`
	R-`CATCGGGTGGGAGTTGTGTT`
<i>Gly-hydro</i>	F-`CAACGCTGAAAAACGGGCAA`
	R-`TCCGTAAAGGCTGCACCAAA`
<i>O-Gly-hydro30</i>	F-`TAACCCCGGATCTCATCGT`
	R-`AGCCAGCCGGATCTTTGATT`
<i>asp</i>	F-`CCTGCGATGTGGACTGCTTA`
	R-`GCGGCTGATGTAAGTGTTCG`
<i>elo-6</i>	F-`GCTGTTTTTCAGTATCGGCGG`
	R-`GCGGAGAACCAGGAAAATGG`
<i>ALDH2</i>	F-`AATATCGTGGCCCCTGAACC`
	R-`GCATCCTTTCAGCCTTGAC`
<i>Cbn-sodh-2</i>	F-`TGGTTTTGGTGTTCATTGCCG`
	R-`TCGTCCAGCGTCTCATTAG`
<i>acetyl-CoA</i>	F-`TCGCCAAAAGGTGGGCTAT`
	R-`ATGGCGGGGATGTTGATGTT`
<i>acsf2</i>	F-`GGAAAGTGGGAGTGTTCAGCA`

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	R-`GATGTTTGAGGTCGGGGAGG`
<i>fae5</i>	F-`AGTCGAGACCGAACCTTC`
	R-`TCTGATCCAAGTGGGGGTTG`
<i>mec-12</i>	F-`TTGAGCCCTACAACCTCCGTG`
	R-`AAGCGGTAATGGAGCTGACC`

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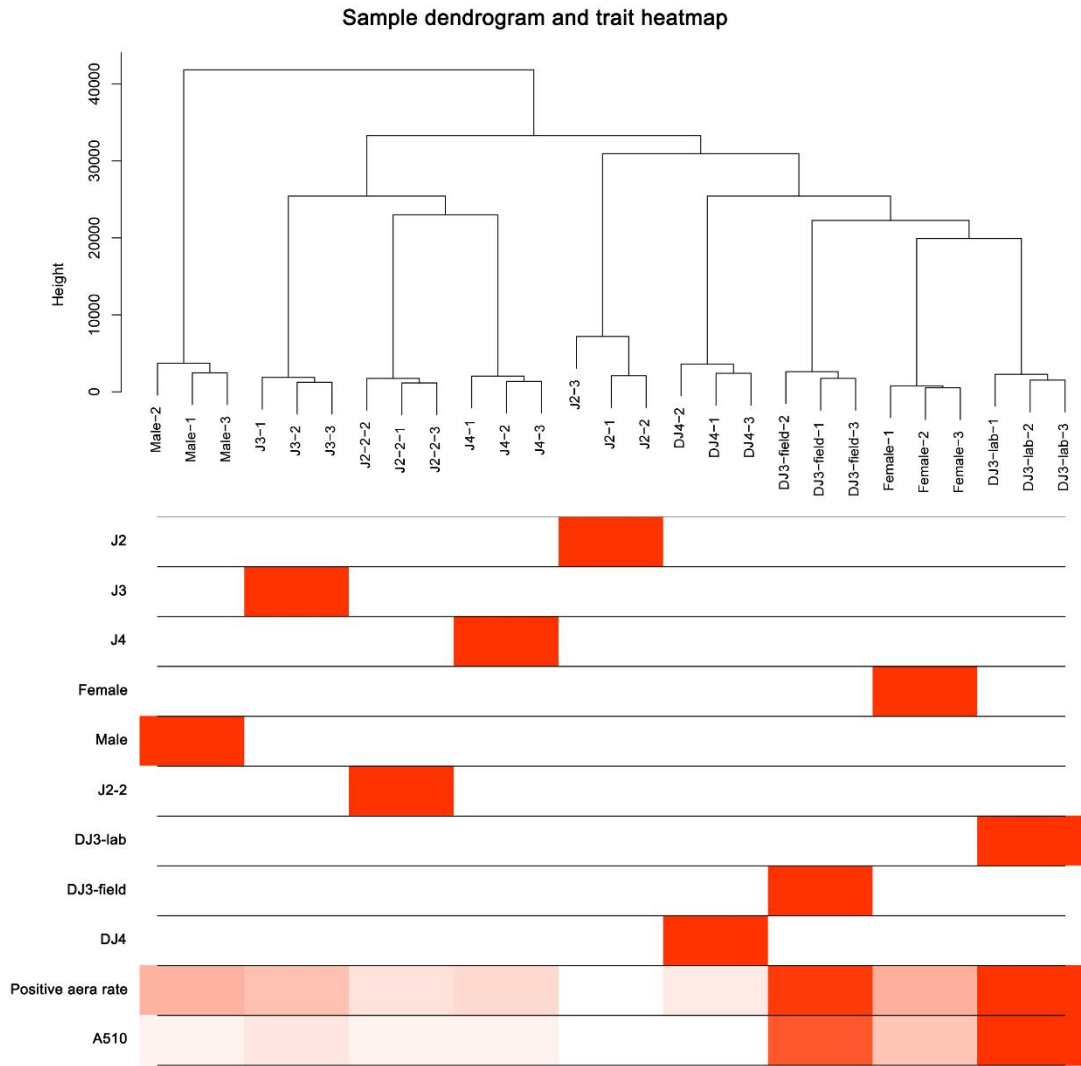


Figure S1. Clustering dendrogram of samples based on their Euclidean distance

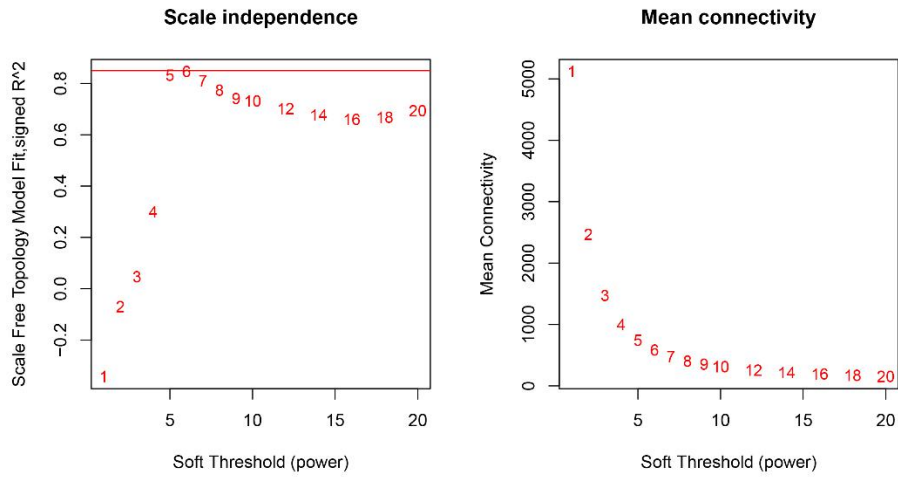


Figure S2. Analysis of network topology with various soft-thresholding powers. The left panel shows the scale-free fit index (y-axis) as a function of the soft-thresholding power (x-axis). The right panel displays the mean connectivity (degree, y-axis) as a function of the soft-thresholding power (x-axis). The red line indicates scale-free fit index is equal to 0.85.



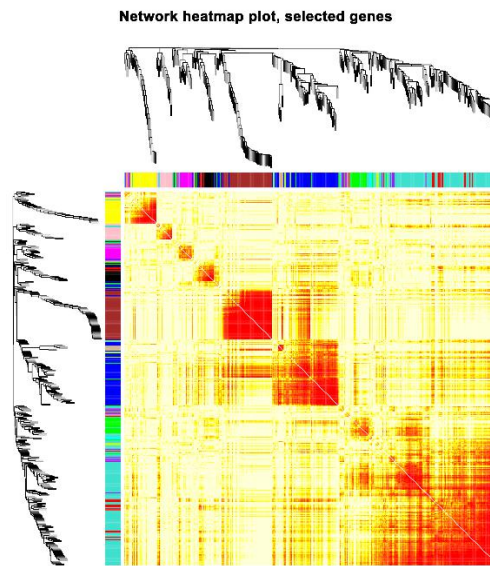


Figure S3. Visualization of the gene network using a heatmap plot. The heatmap depicts the Topological Overlap Matrix (TOM) among 400 genes in the analysis. Light color represents low overlap and progressively darker red color represents higher overlap. Blocks of darker colors along the diagonal are the modules. The gene dendrogram and module assignment are also shown along the left side and the top.

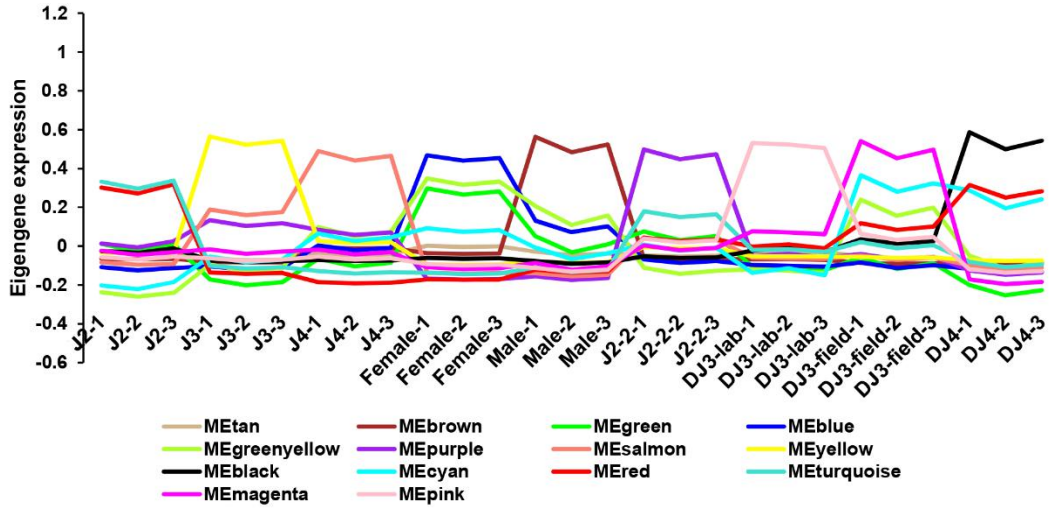


Figure S4 Module eigengene expression profile.

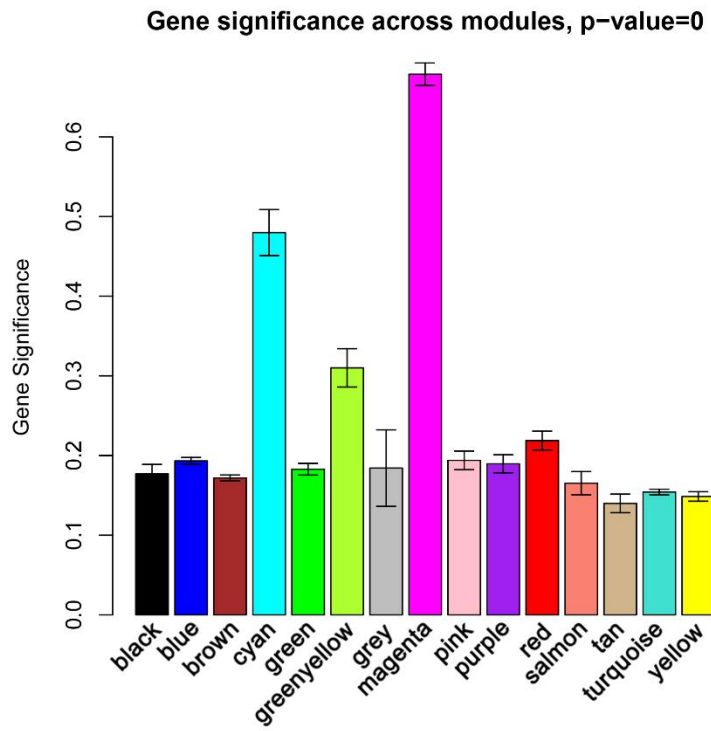


Figure S5. Bar plot of module significance defined as the mean gene significance across all genes in the module to the DJ3-lab trait. The magenta module is the most promising.

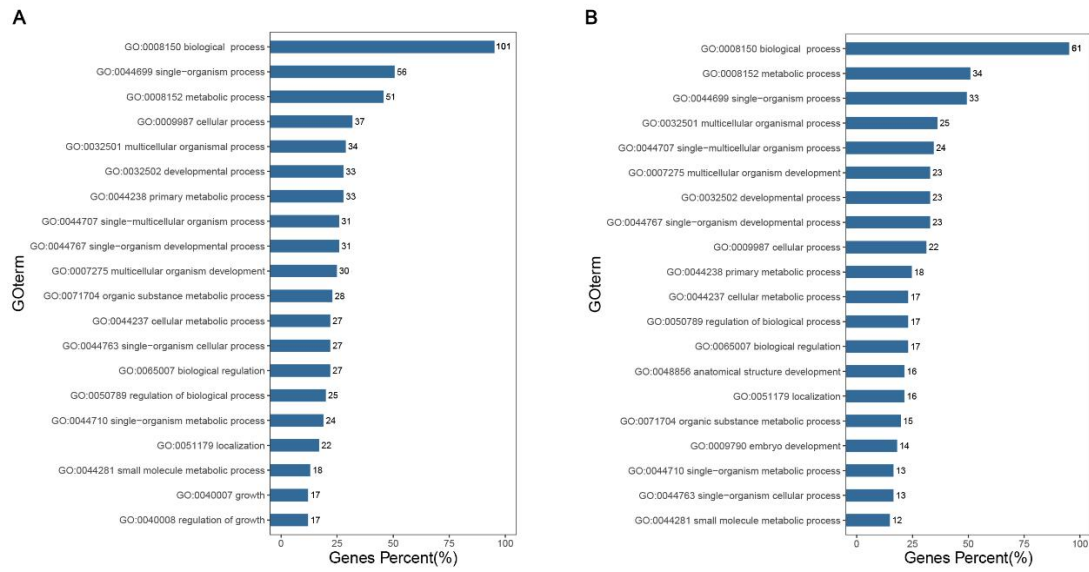


Figure S6. GO enrichment analysis (Biology Process) of the genes in the pink and magenta modules. **A:** Module pink. **B:** Module magenta.

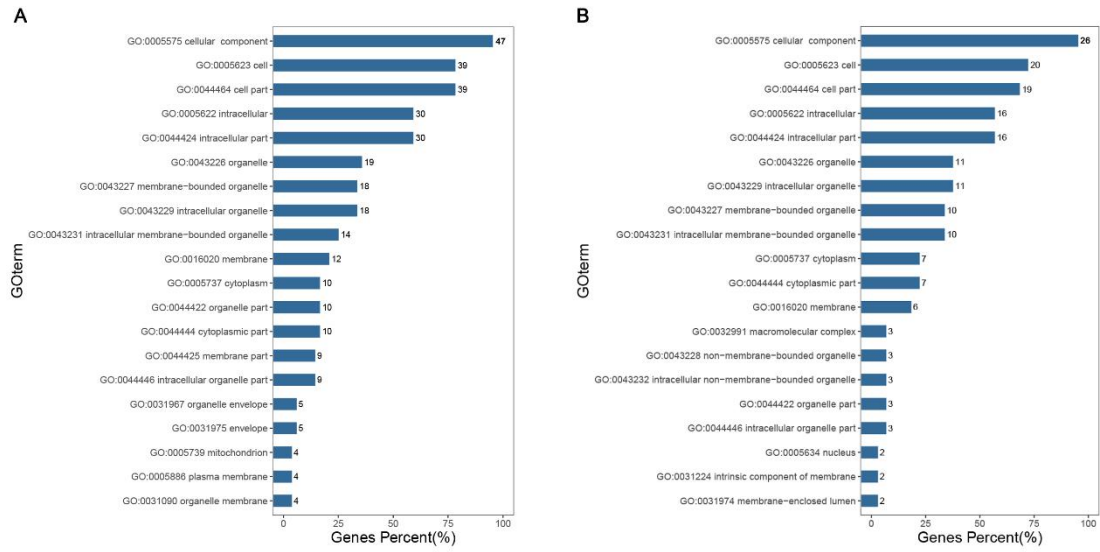


Figure S7. GO enrichment analysis (Cellular Component) of the genes in the pink and magenta modules. **A:** Module pink. **B:** Module magenta.

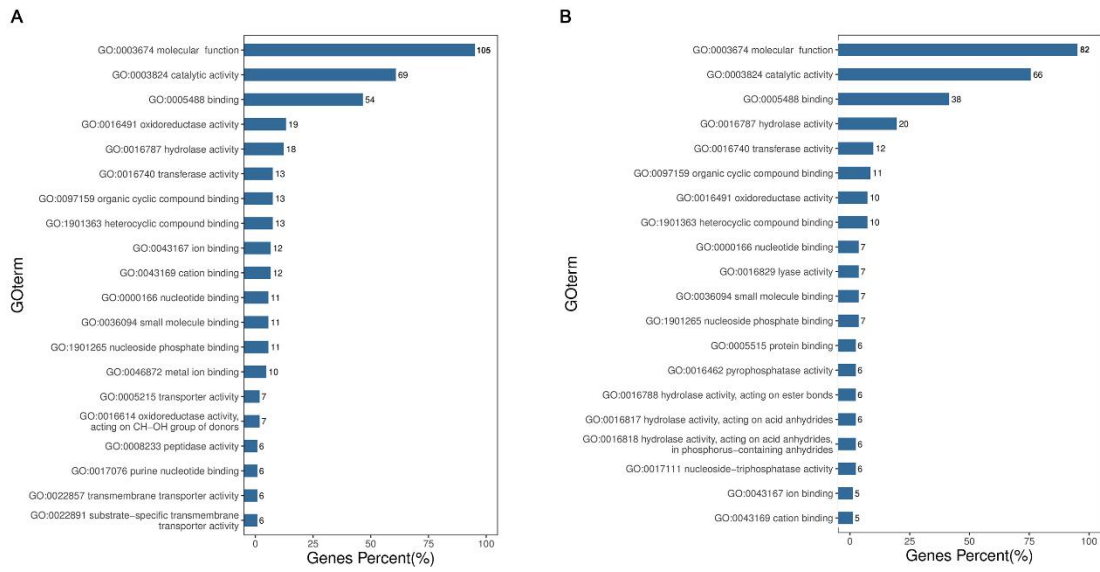


Figure S8. GO enrichment analysis (Molecular Function) of the genes in the pink and magenta modules. **A:** Module pink. **B:** Module magenta.

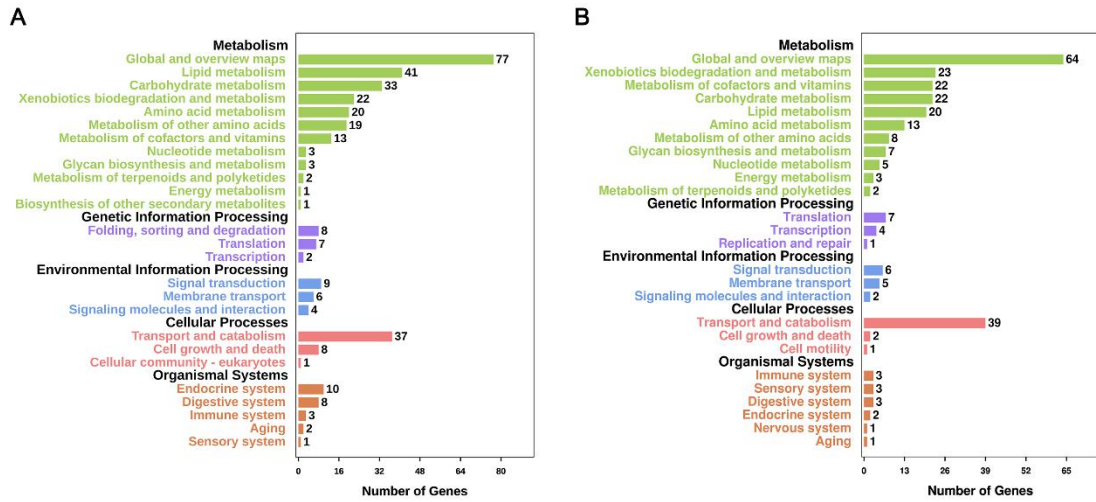


Figure S9. KEGG enrichment analysis of the genes in the pink and magenta modules. **A:** Module pink. **B:** Module magenta.

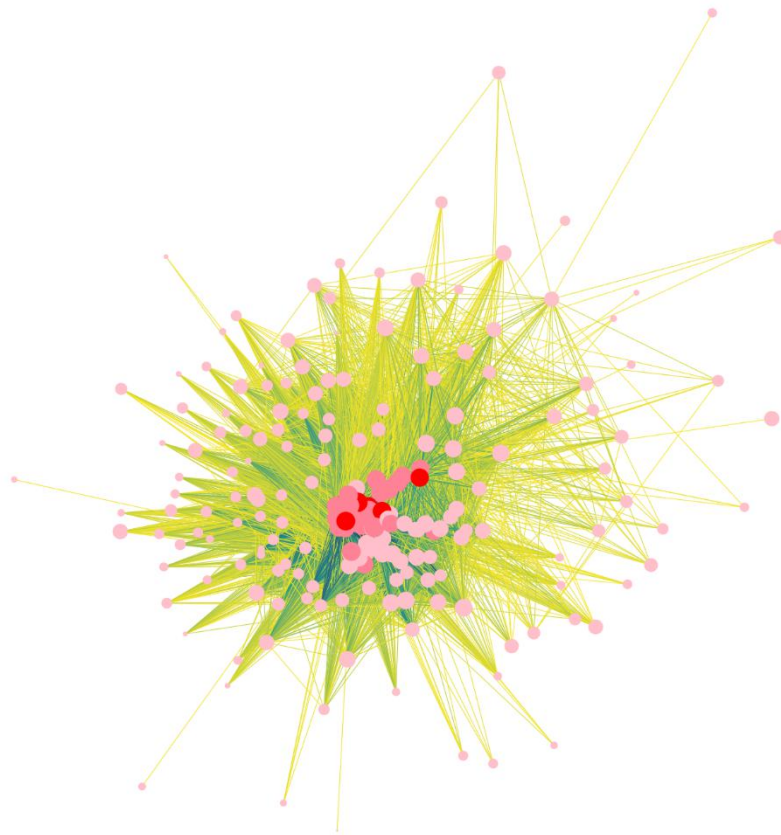


Figure S10. Visualization of pink module (weight value $>0.3$ ). Prefuse Force Directed Layout was applied based on weight value. Size of the dots represents IC (from 17.3445 to 159.5326). Deep pink highlights the top 30 hub genes. Red highlights 6 hub genes in the pink module with extremely high homology to cysteine protease family cathepsin 1.