**Supplemental material**

Alt et al. (YEAR) Gene expression and allergenic potential of *Pseudoterranova bulbosa* L3 from different infection sites in North Atlantic cod (*Gadus morhua*)

Tables

Table S1: Samples of *Pseudoterranova* spp. taken at the 341. expedition of RV Walther Herwig III, October 2019.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Sample ID** | **Infection site** | **Host ID** | **Medium** | **Assembly** | **DEG** |
| **R10** | Viscera | Gm3 | RNAlater | x | x |
| **R11** | Viscera | Gm3 | RNAlater | x |  |
| **R12** | Viscera | Gm3 | RNAlater | x |  |
| **R13** | Liver | Gm3 | RNAlater | x |  |
| **R14** | Liver | Gm3 | RNAlater | x | x |
| **R16** | Liver | Gm3 | RNAlater | x |  |
| **R19** | Liver | Gm4 | RNAlater | x | x |
| **R22** | Viscera | Gm4 | RNAlater | x | x |
| **R28** | Liver | Gm9 | RNAlater | x |  |
| **R29** | Viscera | Gm9 | RNAlater |  |  |
| **R35** | Viscera | Gm11 | RNAlater | x | x |
| **R4** | Liver | Gm11 | TRI-Reagent | x | x |
| **R44** | Liver | Gm16 | RNAlater | x | x |
| **R46** | Viscera | Gm16 | RNAlater | x | x |

Table S2: Sampling locations of *Gadus morhua*.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Host ID** | **Date** | **Haul/No.** | **Depth min-max [m]** | **Latitude** | **Longitude** |
| **Gm3** | 12.10.2019 | 186/26 | 181-192 | 64°53'80"N | 036°02'50"W |
| **Gm4** | 16.10.2019 | 195/31 | 174-192 | 62°03'93"N | 041°00'35"W |
| **Gm9** | 21.10.2019 | 227/54 | 150-280 | 61°15'20"N | 041°40'52"W |
| **Gm11** | 21.10.2019 | 227/54 | 150-280 | 61°15'20"N | 041°40'52"W |
| **Gm16** | 24.10.2019 | 237/61 | 79-137 | 60°17'45"N | 046°34'98"W |

Table S3: Transcriptomes used as references for the taxonomic filtering of *Pseudoterranova bulbosa* raw reads.

|  |  |  |
| --- | --- | --- |
| **Species** | **Accession** | **Taxon-ID** |
| *Gadus morhua* | GCF\_902167405 | 8049 |
| *Acanthocheiloma vitae* | PRJEB1697 | 6277 |
| *Anisakis simplex (sensu stricto)* | PRJEB496 | 6269 |
| *Ascaris lumbricoides* | PRJEB4950 | 6252 |
| *Ascaris suum* | PRJNA62057 | 6253 |
| PRJNA80881 | 6253 |
| *Brugia malayi* | PRJNA10729 | 6279 |
| *Brugia pahangi* | PRJEB497 | 6280 |
| *Brugia timori* | PRJEB4663 | 42155 |
| *Caenorhabditis elegans* | PRJNA13758 | 6239 |
| *Dirofilaria immitis* | PRJEB1797 | 6287 |
| *Dracunculus medinensis* | PRJEB500 | 318479 |
| *Elaeophora elaphi* | PRJEB502 | 1147741 |
| *Enterobius vermicularis* | PRJEB503 | 51028 |
| *Gongylonema pulchrum* | PRJEB505 | 637853 |
| *Litomosoides sigmodontis* | PRJEB3075 | 42156 |
| *Loa loa* | PRJNA246086 | 7209 |
| PRJNA37757 | 7209 |
| *Onchocerca flexuosa* | PRJEB512 | 387005 |
| PRJNA230512 | 387005 |
| *Onchocerca ochengi* | PRJEB1204 | 42157 |
| PRJEB1465 | 42157 |
| *Onchocerca volvulus* | PRJEB513 | 6282 |
| *Parascaris equorum* | PRJEB514 | 6256 |
| *Parascaris univalens* | PRJNA386823 | 6257 |
| *Parastrongyloides trichosuri* | PRJEB515 | 131310 |
| *Strongyloides papillosus* | PRJEB525 | 174720 |
| *Strongyloides ratti* | PRJEB125 | 34506 |
| *Strongyloides stercoralis* | PRJEB528 | 6248 |
| *Strongyloides venezuelensis* | PRJEB530 | 75913 |
| *Syphacia muris* | PRJEB524 | 451379 |
| *Toxocara canis* | PRJEB533 | 6265 |
| PRJNA248777 | 6265 |
| *Wuchereria bancrofti* | PRJEB536 | 6293 |

Table S4: Taxonomic filtering of raw reads and identification of contamination (grey highlight) removed from the dataset.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample | No. raw reads | unclassified | Nematoda | *Anisakis simplex s.s.* | *Gadus morhua* | Bacteria | Archaea | Viruses | *Homo sapiens* |
| R10 | 25,854,660 | 12,650,383 | 12,501,070 | 9,082,744 | 18,381 | 157,640 | 2,521 | 10,072 | 319,124 |
| R11 | 27,879,575 | 15,811,305 | 11,158,222 | 9,223,652 | 51,821 | 176,660 | 3,763 | 19,498 | 467,311 |
| R12 | 26,252,473 | 12,617,215 | 10,670,235 | 8,314,394 | 2,156,643 | 167,542 | 2,685 | 6,666 | 480,708 |
| R13 | 31,713,214 | 16,914,283 | 13,605,661 | 11,346,661 | 258,282 | 204,859 | 4,072 | 12,476 | 522,160 |
| R14 | 30,032,888 | 16,230,327 | 12,908,542 | 10,842,379 | 31,525 | 189,047 | 3,828 | 12,219 | 500,111 |
| R16 | 30,218,368 | 16,326,589 | 13,088,093 | 11,094,156 | 21,407 | 200,367 | 3,496 | 18,773 | 406,313 |
| R19 | 27,941,091 | 13,477,696 | 13,713,780 | 9,967,572 | 28,625 | 164,666 | 2,768 | 14,409 | 347,508 |
| R22 | 32,437,480 | 17,986,831 | 13,487,797 | 11,210,363 | 34,147 | 204,216 | 3,998 | 12,566 | 489,391 |
| R28 | 28,867,356 | 14,154,867 | 13,923,123 | 10,230,490 | 21,407 | 187,162 | 3,967 | 15,120 | 374,664 |
| R35 | 29,352,044 | 15,334,522 | 12,179,977 | 9,975,217 | 28,625 | 222,179 | 2,366 | 16,511 | 487,258 |
| R4 | 31,034,481 | 18,551,609 | 11,605,485 | 9,772,428 | 36,238 | 259,572 | 3,112 | 9,753 | 392,419 |
| R44 | 28,254,524 | 15,781,266 | 11,519,017 | 9,328,752 | 175,889 | 216,968 | 3,303 | 9,149 | 406,188 |
| R46 | 29,341,134 | 17,551,822 | 10,896,651 | 9,395,059 | 57,721 | 194,458 | 3,193 | 10,023 | 453,123 |

Table S5: Assembly metrics of the Trinity assembly base metrics (total number of genes, total number of transcripts and GC content) and contig stats (based on "all" transcripts and based on the longest isoform per gene).

|  |  |
| --- | --- |
|  | **Filtered assembly** |
| **Total no. of genes** | 25405 |
| **Total no. of transcripts** | 65146 |
| **Percent GC** | 40.54 % |
| **Contig stats** | all | Long. isof. |
| **Contig N10** | 4649 | 4058 |
| **Contig N20** | 3229 | 2941 |
| **Contig N30** | 2530 | 2315 |
| **Contig N40** | 2049 | 1875 |
| **Contig N50** | 1740 | 1533 |
| **Median contig length** | 849 | 381 |
| **Average contig** | 1178.10 | 838.63 |
| **Total assembled bases** | 76748359 | 21305279 |

Table S6: Transcript coverage represented as BUSCOs of filtered nucleotide and peptide translation, based on the nematoda\_odb10 database from NCBI.

|  |  |  |
| --- | --- | --- |
| **BUSCOs** | **Nuc. filtered** | **Pep. filtered** |
|  | n | % | n | % |
| **Complete**  | 2542 | 81.1 | 2531 | 80.8 |
| **Single copy** | 1047 | 33.4 | 1199 | 38.3 |
| **Duplicated** | 1495 | 47.7 | 1332 | 42.5 |
| **Fragmented** | 112 | 3.6 | 128 | 4.1 |
| **Missing** | 477 | 15.3 | 472 | 15.1 |
| **Total** | 3131 |

Table S7: Count data of differentially expressed genes of the thirteen *P. bulbosa* samples. Mean counts, log2 foldchange and adjusted p-value, bold = sample from liver, italics = transcript upregulated in all liver specimen, underlined = transcript upregulated in all viscera specimen, box around samples from the same host individual.

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Transcript | R10 | **R14** | **R19** | R22 | R35 | **R4** | **R44** | R46 | mean | log2FC | padj | BLAST annotation |
| *DN4370\_c0\_g1\_i23* | 0 | **0** | **6593** | 2080 | 196 | **725** | **9553** | 1820 | 2583.42 | 2.09 | 0.0284 | hypothetical protein CRE\_19368 [*Caenorhabditis remanei*] |
| *DN3921\_c0\_g1\_i6* | 233 | **4123** | **3317** | 1613 | 766 | **2873** | **5283** | 1156 | 2319.51 | 2.32 | 0.0075 | Carboxylesterase, type B domain and von Willebrand factor, type A domain-containing protein[*Strongyloides ratti*] |
| *DN259\_c0\_g1\_i1* | 0 | **4223** | **6939** | 0 | 1961 | **0** | **1461** | 0 | 1719.07 | 15.48 | 0.0012 | NA |
| *DN7623\_c0\_g1\_i5* | 0 | **54** | **260** | 14 | 114 | **2754** | **687** | 49 | 515.17 | 4.69 | 4.55 E-08 | 40S ribosomal protein S23 [*Brugia malayi*] |
| *DN3280\_c0\_g1\_i2* | 82 | **1049** | **917** | 44 | 372 | **700** | **562** | 96 | 459.59 | 2.89 | 0.0190 | 26S proteasome regulatory complex subunit p97 [*Loa loa*] |
| *DN1306\_c0\_g1\_i6* | 77 | **524** | **384** | 157 | 93 | **1371** | **501** | 45 | 393.11 | 2.86 | 0.0035 | Uncharacterized protein CELE\_C26B9.5[*Caenorhabditis elegans*] |
| *DN1890\_c0\_g1\_i1* | 187 | **1009** | **161** | 46 | 294 | **940** | **538** | 41 | 391.02 | 2.38 | 0.0111 | actin 2 [Brugia malayi] |
| *DN3776\_c0\_g1\_i13* | 0 | **1449** | **699** | 228 | 0 | **41** | **81** | 0 | 274.27 | 8.17 | 0.0050 | proteasome A-type and B-type family protein [*Loa loa*] |
| *DN539\_c0\_g1\_i6* | 814 | **17** | **316** | 0 | 0 | **780** | **19** | 0 | 270.05 | 10.94 | 0.0044 | Enoyl-[acyl-carrier-protein] reductase, mitochondrial [Caenorhabditis elegans] |
| *DN3205\_c0\_g1\_i6* | 0 | **1226** | **47** | 0 | 0 | **122** | **411** | 624 | 269.39 | 8.52 | 0.0109 | AMP-binding enzyme family protein [*Brugia malayi*] |
| *DN225\_c0\_g1\_i64* | 305 | **994** | **537** | 43 | 0 | **120** | **160** | 2 | 255.17 | 4.93 | 0.0270 | hypothetical protein LOAG\_02255 [*Loa loa*] |
| *DN2996\_c0\_g1\_i1* | 0 | **1350** | **454** | 71 | 0 | **87** | **4** | 0 | 213.66 | 7.08 | 0.0211 | Aconitate hydratase, mitochondrial [*Strongyloides ratti*] |
| *DN539\_c0\_g1\_i12* | 8 | **371** | **507** | 30 | 56 | **596** | **0** | 0 | 191.71 | 4.04 | 4.76 E-05 | Enoyl-[acyl-carrier-protein] reductase, mitochondrial [*Caenorhabditis elegans*] |
| *DN1718\_c0\_g1\_i13* | 43 | **586** | **186** | 63 | 51 | **226** | **230** | 41 | 166.42 | 2.50 | 4.7 E-05 | Uncharacterized protein CELE\_F08G12.1[*Caenorhabditis elegans*] |
| *DN1478\_c0\_g1\_i6* | 0 | **37** | **432** | 3 | 0 | **362** | **50** | 463 | 164.12 | 6.99 | 0.0470 | hypothetical protein LOAG\_07919 [*Loa loa*] |
| *DN3474\_c0\_g1\_i12* | 0 | **142** | **402** | 0 | 52 | **408** | **252** | 0 | 157.63 | 9.02 | 0.0004 | acid phosphatase [*Brugia malayi*] |
| *DN928\_c0\_g1\_i30* | 24 | **78** | **270** | 1 | 0 | **261** | **379** | 0 | 128.68 | 8.67 | 0.0007 | Protein-tyrosine phosphatase [*Brugia malayi*] |
| *DN1603\_c0\_g1\_i2* | 0 | **796** | **85** | 0 | 0 | **96** | **183** | 0 | 128.06 | 10.00 | 2.84 E-09 | hypothetical protein [*Brugia malayi*] |
| *DN3570\_c0\_g1\_i5* | 0 | **473** | **70** | 12 | 3 | **502** | **6** | 0 | 126.50 | 6.45 | 0.0035 | Thioredoxin-like protein p19 precursor [*Brugia malayi*] |
| *DN2193\_c0\_g1\_i7* | 0 | **299** | **219** | 0 | 0 | **418** | **0** | 0 | 113.62 | 9.54 | 0.0363 | Esterase D [*Brugia malayi*] |
| *DN1239\_c2\_g1\_i17* | 0 | **334** | **348** | 0 | 0 | **147** | **0** | 114 | 109.64 | 11.37 | 0.0284 | hypothetical protein LOAG\_08654 [*Loa loa*] |
| *DN10628\_c0\_g1\_i1* | 103 | **464** | **145** | 25 | 5 | **129** | **49** | 10 | 108.69 | 2.84 | 0.0211 | Protein-tyrosine phosphatase-like, PTPLA family-containing protein [*Strongyloides ratti*] |
| *DN534\_c0\_g1\_i12* | 6 | **339** | **48** | 21 | 12 | **224** | **128** | 20 | 93.71 | 3.47 | 0.0099 | nuclear hormone receptor family member nhr-40 [*Loa loa*] |
| *DN2649\_c0\_g1\_i3* | 0 | **380** | **9** | 0 | 0 | **164** | **185** | 13 | 86.99 | 7.44 | 0.0018 | Putative 28S ribosomal protein S5, mitochondrial [*Caenorhabditis elegans*] |
| *DN2911\_c0\_g1\_i2* | 0 | **117** | **161** | 89 | 0 | **51** | **84** | 0 | 58.80 | 7.42 | 0.0222 | SAP domain containing protein [*Brugia malayi*] |
| *DN1579\_c0\_g1\_i22* | 62 | **107** | **151** | 0 | 0 | **69** | **60** | 0 | 55.90 | 7.85 | 0.0260 | hypothetical protein LOAG\_09918 [*Loa loa*] |
| *DN1640\_c0\_g1\_i10* | 0 | **56** | **59** | 0 | 0 | **116** | **139** | 72 | 54.39 | 7.35 | 0.0336 | GLutamate Receptor family (AMPA)[*Caenorhabditis elegans*] |
| *DN1350\_c0\_g1\_i11* | 0 | **277** | **34** | 0 | 0 | **48** | **12** | 0 | 40.44 | 8.10 | 0.0005 | SD24044p, partial [*Brugia malayi*] |
| *DN253\_c0\_g1\_i3* | 0 | **67** | **62** | 0 | 2 | **10** | **21** | 0 | 18.81 | 6.68 | 0.0417 | putative isoaspartyl peptidase/L-asparaginase[*Lucilia cuprina*] |
| *DN4513\_c0\_g1\_i4* | 0 | **27** | **71** | 0 | 0 | **30** | **12** | 0 | 17.12 | 7.34 | 0.0206 | *C. briggsae* CBR-PCP-1.1 protein, partial[*Caenorhabditis briggsae*] |
| *DN1249\_c0\_g1\_i33* | 0 | **52** | **41** | 0 | 0 | **8** | **34** | 0 | 15.82 | 7.28 | 0.0279 | hypothetical protein LOAG\_16710 [*Loa loa*] |
| *DN1635\_c0\_g1\_i17* | 0 | **46** | **21** | 0 | 0 | **32** | **15** | 0 | 13.50 | 7.16 | 0.0415 | hypothetical protein, variant [*Loa loa*] |
| DN1673\_c0\_g1\_i5 | 2325 | **0** | **0** | 14193 | 0 | **0** | **100** | 0 | 1843.15 | -15.32 | 0.0054 | malate dehydrogenase, NAD-dependent[*Necator americanus*] |
| DN2996\_c0\_g1\_i5 | 748 | **286** | **607** | 1426 | 2639 | **953** | **1149** | 3852 | 1391.73 | -1.45 | 0.0075 | Aconitate hydratase, mitochondrial [*Strongyloides ratti*] |
| DN1673\_c0\_g1\_i6 | 2316 | **0** | **0** | 9508 | 0 | **0** | **75** | 0 | 1349.71 | -15.05 | 0.0075 | malate dehydrogenase, NAD-dependent[*Necator americanus*] |
| DN8128\_c0\_g1\_i6 | 1577 | **26** | **2** | 2081 | 2 | **1213** | **0** | 3324 | 989.62 | -8.00 | 0.0361 | C. briggsae CBR-GST-7 protein [*Caenorhabditis* *briggsae*] |
| DN1804\_c0\_g1\_i6 | 1167 | **419** | **14** | 1137 | 2295 | **28** | **241** | 700 | 731.36 | -3.91 | 0.0345 | hypothetical protein LOAG\_16424 [*Loa loa*] |
| DN501\_c0\_g1\_i2 | 1534 | **0** | **0** | 2424 | 252 | **17** | **106** | 209 | 553.31 | -7.93 | 0.0222 | C6orf153 protein [*Brugia malayi*] |
| DN1469\_c0\_g1\_i11 | 861 | **43** | **4** | 823 | 1948 | **6** | **201** | 37 | 488.75 | -5.61 | 0.0245 | Hypothetical protein CBG21019 [*Caenorhabditis briggsae*] |
| DN225\_c0\_g1\_i3 | 631 | **5** | **122** | 643 | 1020 | **9** | **165** | 841 | 418.13 | -4.55 | 0.0141 | hypothetical protein LOAG\_02255 [*Loa loa*] |
| DN1011\_c0\_g1\_i4 | 172 | **62** | **92** | 319 | 918 | **343** | **398** | 1064 | 404.38 | -1.51 | 0.0050 | NA |
| DN2035\_c0\_g1\_i1 | 1006 | **0** | **0** | 1382 | 79 | **91** | **0** | 651 | 389.66 | -11.24 | 0.0002 | CBR-NSF-1 protein [*Loa loa*] |
| DN517\_c0\_g1\_i8 | 114 | **0** | **0** | 407 | 1503 | **0** | **603** | 510 | 377.25 | -9.88 | 0.0018 | CBR-PQN-73 protein, variant [*Loa loa*] |
| DN2447\_c0\_g1\_i4 | 0 | **0** | **0** | 2447 | 383 | **0** | **125** | 35 | 322.05 | -11.55 | 0.0053 | ankyrin repeat and BTB/POZ domain-containing protein 2 [*Cryptotermes secundus*] |
| DN1497\_c0\_g1\_i6 | 891 | **0** | **49** | 1186 | 49 | **0** | **0** | 29 | 272.91 | -7.64 | 0.0018 | fatty acid elongation protein 3 [*Brugia malayi*] |
| DN4692\_c0\_g2\_i4 | 562 | **0** | **0** | 29 | 0 | **78** | **0** | 1032 | 212.80 | -12.11 | 0.0155 | Cytosolic non-specific dipeptidase [*Strongyloides ratti*] |
| DN576\_c0\_g1\_i14 | 504 | **0** | **0** | 0 | 807 | **0** | **0** | 202 | 196.78 | -10.25 | 0.0270 | hypothetical protein LOAG\_00505 [*Loa loa*] |
| DN1528\_c0\_g1\_i7 | 24 | **252** | **0** | 559 | 521 | **0** | **0** | 20 | 153.52 | -8.56 | 0.0345 | aspartyl aminopeptidase [*Loa loa*] |
| DN1283\_c0\_g1\_i11 | 386 | **0** | **0** | 322 | 0 | **212** | **0** | 198 | 142.00 | -11.71 | 0.0260 | hypothetical protein [*Brugia malayi*] |
| DN4366\_c1\_g1\_i9 | 184 | **0** | **0** | 354 | 89 | **0** | **136** | 337 | 130.41 | -8.77 | 0.0036 | Cullin-5 [*Loa loa*] |
| DN2349\_c0\_g1\_i3 | 218 | **73** | **15** | 178 | 153 | **75** | **24** | 253 | 120.60 | -2.38 | 0.0431 | eIF4-gamma/eIF5/eIF2-epsilon family protein[*Brugia malayi*] |
| DN1718\_c0\_g1\_i6 | 194 | **0** | **0** | 169 | 289 | **41** | **7** | 232 | 114.30 | -6.53 | 0.0051 | Uncharacterized protein CELE\_F08G12.1[*Caenorhabditis elegans*] |
| DN8473\_c0\_g1\_i1 | 22 | **0** | **0** | 347 | 440 | **6** | **0** | 58 | 100.52 | -7.71 | 1.79 E-06 | S-phase kinase-associated protein 1 [*Loa loa*] |
| DN4252\_c0\_g1\_i2 | 119 | **0** | **0** | 126 | 0 | **74** | **0** | 532 | 100.16 | -11.16 | 0.0363 | succinyl-CoA ligase alpha-chain [*Loa loa*] |
| DN707\_c0\_g1\_i5 | 470 | **3** | **0** | 135 | 89 | **0** | **10** | 1 | 97.27 | -7.45 | 0.0361 | gamma-secretase subunit pen-2 [*Loa loa*] |
| DN2185\_c0\_g1\_i7 | 218 | **0** | **0** | 0 | 5 | **53** | **0** | 331 | 77.31 | -10.14 | 0.0368 | Xab2 protein [*Loa loa*] |
| DN4326\_c0\_g1\_i7 | 51 | **0** | **1** | 368 | 9 | **30** | **3** | 204 | 74.40 | -6.23 | 0.0335 | Nematode cuticle collagen N-terminal domain containing protein [*Brugia malayi*] |
| DN6423\_c0\_g1\_i13 | 187 | **0** | **0** | 121 | 159 | **0** | **0** | 121 | 73.61 | -9.62 | 4.55 E-08 | hypothetical protein LOAG\_04985 [*Loa loa*] |
| DN1052\_c0\_g1\_i8 | 242 | **20** | **3** | 222 | 78 | **10** | **0** | 7 | 73.58 | -4.34 | 0.0009 | hypothetical protein CRE\_11402 [*Caenorhabditis remanei*] |
| DN5289\_c0\_g1\_i5 | 101 | **0** | **92** | 76 | 150 | **0** | **0** | 29 | 56.08 | -7.62 | 0.0454 | Tim44-like domain protein [*Necator americanus*] |
| DN3573\_c0\_g1\_i6 | 139 | **0** | **0** | 46 | 70 | **9** | **10** | 124 | 50.53 | -5.44 | 0.0366 | Hypothetical protein CBG19223 [*Caenorhabditis briggsae*] |
| DN3412\_c0\_g1\_i3 | 83 | **35** | **14** | 81 | 97 | **24** | **11** | 64 | 49.83 | -2.06 | 0.0035 | hypothetical protein Bm1\_34270 [*Brugia malayi*] |
| DN7483\_c0\_g1\_i1 | 18 | **0** | **4** | 381 | 25 | **5** | **0** | 24 | 49.35 | -5.56 | 0.0183 | hypothetical protein LOAG\_09671 [*Loa loa*] |
| DN4101\_c0\_g1\_i6 | 70 | **0** | **86** | 107 | 68 | **0** | **0** | 72 | 48.68 | -7.42 | 0.0363 | hypothetical protein LOAG\_06297 [*Loa loa*] |
| DN3422\_c0\_g1\_i7 | 15 | **5** | **2** | 76 | 98 | **17** | **15** | 140 | 42.70 | -3.03 | 0.0162 | NA |
| DN3927\_c0\_g1\_i1 | 86 | **0** | **0** | 57 | 99 | **0** | **11** | 35 | 36.27 | -7.56 | 0.0211 | posterior sex combs protein [*Loa loa*] |
| DN542\_c0\_g1\_i40 | 13 | **2** | **14** | 97 | 10 | **0** | **20** | 165 | 36.17 | -3.09 | 0.0141 | uridine kinase [*Loa loa*] |
| DN2370\_c0\_g1\_i39 | 37 | **0** | **0** | 59 | 48 | **4** | **0** | 20 | 20.34 | -6.48 | 0.0211 | 6-phosphofructokinase [*Loa loa*] |
| DN5783\_c0\_g1\_i3 | 32 | **0** | **0** | 52 | 32 | **0** | **0** | 53 | 20.04 | -7.80 | 0.0050 | depsiphilin, partial [*Loa loa*] |
| DN4953\_c0\_g1\_i15 | 19 | **0** | **0** | 16 | 37 | **0** | **0** | 54 | 15.06 | -7.26 | 0.0284 | hypothetical protein LOAG\_04590 [*Loa loa*] |
|  |  |  |  |  |  |  |  |  |  |  |  |  |

Table S8: TopGO enrichment of gene ontology terms in samples of *P. bulbosa* collected from host liver (L, GO.ID in italics) and viscera (V, GO.ID underlined). Number of annotated GO terms, significant and expected, p-value (Fisher), ontology type (BP = biological process, CC = cellular component, MF = molecular function), topGO-algorithm = weight01.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| GO.ID | Term | Annotated | Significant | Expected | p-value | Site | Ontology | Algorithm |
| *GO:0046294* | formaldehyde catabolic process | 5 | 1 | 0.01 | 0.0054 | L | BP | weight01 |
| *GO:0042176* | regulation of protein catabolic process | 6 | 1 | 0.01 | 0.0065 | L | BP | weight01 |
| *GO:0007052* | mitotic spindle organization | 8 | 1 | 0.01 | 0.0086 | L | BP | weight01 |
| *GO:0032958* | inositol phosphate biosynthetic process | 25 | 1 | 0.03 | 0.0267 | L | BP | weight01 |
| *GO:0000502* | proteasome complex | 64 | 2 | 0.05 | 0.011 | L | CC | weight01 |
| *GO:0015935* | small ribosomal subunit | 34 | 1 | 0.03 | 0.022 | L | CC | weight01 |
| *GO:0005839* | proteasome core complex | 44 | 1 | 0.03 | 0.029 | L | CC | weight01 |
| *GO:0016592* | mediator complex | 68 | 1 | 0.05 | 0.044 | L | CC | weight01 |
| *GO:0003994* | aconitate hydratase activity | 4 | 1 | 0 | 0.0039 | L | MF | weight01 |
| *GO:0018738* | S-formylglutathione hydrolase activity | 5 | 1 | 0.01 | 0.0048 | L | MF | weight01 |
| *GO:0003993* | acid phosphatase activity | 12 | 1 | 0.01 | 0.0116 | L | MF | weight01 |
| *GO:0004298* | threonine-type endopeptidase activity | 16 | 1 | 0.02 | 0.0154 | L | MF | weight01 |
| *GO:0051539* | 4 iron, 4 sulfur cluster binding | 19 | 1 | 0.02 | 0.0182 | L | MF | weight01 |
| *GO:0003735* | structural constituent of ribosome | 246 | 2 | 0.25 | 0.0234 | L | MF | weight01 |
| *GO:0004970* | ionotropic glutamate receptor activity | 30 | 1 | 0.03 | 0.0287 | L | MF | weight01 |
| *GO:0008236* | serine-type peptidase activity | 289 | 2 | 0.29 | 0.0315 | L | MF | weight01 |
| *GO:0005548* | phospholipid transporter activity | 36 | 1 | 0.04 | 0.0343 | L | MF | weight01 |
| GO:0035494 | SNARE complex disassembly | 6 | 1 | 0.01 | 0.0065 | V | BP | weight01 |
| GO:0000469 | cleavage involved in rRNA processing | 7 | 1 | 0.01 | 0.0075 | V | BP | weight01 |
| GO:0006741 | NADP biosynthetic process | 8 | 1 | 0.01 | 0.0086 | V | BP | weight01 |
| GO:0019674 | NAD metabolic process | 11 | 1 | 0.01 | 0.0118 | V | BP | weight01 |
| GO:0045104 | intermediate filament cytoskeleton organisation | 13 | 1 | 0.02 | 0.014 | V | BP | weight01 |
| GO:0006002 | fructose 6-phosphate metabolic process | 19 | 1 | 0.02 | 0.0204 | V | BP | weight01 |
| GO:0006606 | protein import into nucleus | 21 | 1 | 0.03 | 0.0225 | V | BP | weight01 |
| GO:0006511 | ubiquitin-dependent protein catabolic process | 247 | 2 | 0.3 | 0.0287 | V | BP | weight01 |
| GO:0032039 | integrator complex | 28 | 1 | 0.02 | 0.018 | V | CC | weight01 |
| GO:0003994 | aconitate hydratase activity | 4 | 1 | 0 | 0.0039 | V | MF | weight01 |
| GO:0004854 | xanthine dehydrogenase activity | 6 | 1 | 0.01 | 0.0058 | V | MF | weight01 |
| GO:0004855 | xanthine oxidase activity | 6 | 1 | 0.01 | 0.0058 | V | MF | weight01 |
| GO:0051539 | 4 iron, 4 sulfur cluster binding | 19 | 1 | 0.02 | 0.0182 | V | MF | weight01 |
| GO:0051537 | 2 iron, 2 sulfur cluster binding | 21 | 1 | 0.02 | 0.0201 | V | MF | weight01 |
| GO:0003872 | 6-phosphofructokinase activity | 22 | 1 | 0.02 | 0.0211 | V | MF | weight01 |
| GO:0008536 | Ran GTPase binding | 28 | 1 | 0.03 | 0.0268 | V | MF | weight01 |
| GO:0004177 | aminopeptidase activity | 34 | 1 | 0.04 | 0.0324 | V | MF | weight01 |
| GO:0003951 | NAD+ kinase activity | 36 | 1 | 0.04 | 0.0343 | V | MF | weight01 |
| GO:0031625 | ubiquitin protein ligase binding | 42 | 1 | 0.04 | 0.0399 | V | MF | weight01 |

Table S9: Allergen BLAST additional output: query and sequence start (qstart, sstart) and end (qend, send), e-value (evalue), bit score (bitscore) and match subject.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Query | Reference | qstart | qend | sstart | send | evalue | bitscore | match subject |
| DN6446\_c0\_g1\_i26 | CAB93501.1 | 172 | 1023 | 1 | 284 | 7.42E-156 | 433 | tropomyosin [*Anisakis simplex*] |
| DN6446\_c0\_g1\_i33 | CAB93501.1 | 172 | 921 | 1 | 250 | 4.02E-129 | 365 | tropomyosin [*Anisakis simplex*] |
| DN7685\_c0\_g1\_i1 | AAF72796.1 | 3070 | 464 | 1 | 869 | 0 | 1406 | paramyosin [Anisakis simplex] |
| DN7685\_c0\_g1\_i2 | AAF72796.1 | 3069 | 463 | 1 | 869 | 0 | 1406 | paramyosin [*Anisakis simplex*] |
| DN7685\_c0\_g1\_i4 | AAF72796.1 | 3071 | 465 | 1 | 869 | 0 | 1406 | paramyosin [*Anisakis simplex*] |
| DN6446\_c0\_g1\_i16 | CAB93501.1 | 172 | 1023 | 1 | 284 | 7.31E-136 | 381 | tropomyosin [*Anisakis simplex*] |
| DN5493\_c0\_g1\_i3 | AAF72796.1 | 3378 | 763 | 1 | 865 | 0 | 1211 | paramyosin [*Anisakis simplex*] |
| DN5493\_c0\_g1\_i2 | AAF72796.1 | 3378 | 763 | 1 | 865 | 0 | 1211 | paramyosin [*Anisakis simplex*] |
| DN5493\_c0\_g1\_i4 | AAF72796.1 | 3378 | 763 | 1 | 865 | 0 | 1211 | paramyosin [*Anisakis simplex*] |
| DN15669\_c0\_g1\_i5 | AFY98826.1 | 1298 | 408 | 1 | 297 | 0 | 542 | Ani s 13 allergen hemoglobin, partial [*Anisakis pegreffii*] |
| DN15669\_c0\_g1\_i8 | AFY98826.1 | 1298 | 408 | 1 | 297 | 0 | 541 | Ani s 13 allergen hemoglobin, partial [*Anisakis pegreffii*] |
| DN15669\_c0\_g1\_i2 | AFY98826.1 | 1298 | 408 | 1 | 297 | 0 | 542 | Ani s 13 allergen hemoglobin, partial [*Anisakis pegreffii*] |
| DN15669\_c0\_g1\_i7 | AFY98826.1 | 1298 | 408 | 1 | 297 | 0 | 541 | Ani s 13 allergen hemoglobin, partial [Anisakis pegreffii] |
| DN409\_c0\_g1\_i4 | ABL77410.1 | 3483 | 1459 | 1 | 673 | 0 | 1202 | UA3-recognized allergen, partial [Anisakis simplex] |
| DN409\_c0\_g1\_i233 | ABL77410.1 | 3922 | 1898 | 1 | 673 | 0 | 1202 | UA3-recognized allergen, partial [Anisakis simplex] |
| DN409\_c0\_g1\_i79 | ABL77410.1 | 3922 | 1898 | 1 | 673 | 0 | 1202 | UA3-recognized allergen, partial [Anisakis simplex] |
| DN409\_c0\_g1\_i23 | ABL77410.1 | 2856 | 178 | 1 | 891 | 0 | 1584 | UA3-recognized allergen, partial [Anisakis simplex] |
| DN409\_c0\_g1\_i10 | ABL77410.1 | 2856 | 178 | 1 | 891 | 0 | 1585 | UA3-recognized allergen, partial [Anisakis simplex] |
| DN409\_c0\_g1\_i129 | ABL77410.1 | 3536 | 249 | 1 | 1094 | 0 | 1942 | UA3-recognized allergen, partial [Anisakis simplex] |
| DN409\_c0\_g1\_i56 | ABL77410.1 | 3536 | 249 | 1 | 1094 | 0 | 1942 | UA3-recognized allergen, partial [Anisakis simplex] |
| DN409\_c0\_g1\_i169 | ABL77410.1 | 3721 | 2396 | 1 | 442 | 0 | 788 | UA3-recognized allergen, partial [Anisakis simplex] |
| DN8128\_c0\_g1\_i4 | CAA53218.1 | 357 | 1 | 1 | 119 | 1.47E-73 | 209 | Asc s 13 glutathione transferase [Ascaris suum] |
| DN409\_c0\_g1\_i185 | ABL77410.1 | 3656 | 249 | 1 | 1094 | 0 | 1919 | UA3-recognized allergen, partial [Anisakis simplex] |
| DN409\_c0\_g1\_i75 | ABL77410.1 | 3656 | 249 | 1 | 1094 | 0 | 1919 | UA3-recognized allergen, partial [Anisakis simplex] |
| DN409\_c0\_g1\_i60 | ABL77410.1 | 3656 | 249 | 1 | 1094 | 0 | 1919 | UA3-recognized allergen, partial [Anisakis simplex] |

Figures



Figure S1: Flowchart of the data analysis process and samples used in each step. Genotyping was performed with all 54 nematode samples from 12 host individuals, with at least one corresponding pair of samples from liver and viscera per host. RNA-sequencing was performed with 14 samples from liver and viscera of five host individuals. The transcriptome was assembled using the thirteen samples, which had yielded sufficient sequencing results. A balanced dataset of eight specimens including corresponding samples from liver and viscera of four host individuals was used for differential gene expression analysis.



Figure S2: Principal components analysis of variance stabilised read counts with highlighted site of infection (red = liver, blue = viscera) and host individual (circle = Gm11, triangle = Gm16, square = Gm3, cross = Gm4).

Data

Data S1: Raw sequence data used for COI barcoding of *Pseudoterranova bulbosa*.

>KAPb24-R10\_COIf

AGTCTTTTTGTTTGACTGTTTTTGTTACTGTTTTTTTACTTGTTTTATCTTTGCCTGTGTTGGCGGGGGCTATTACTATGTTGTTAACTGATCGTAATTTGAATACTTCTTTTTTTGATCCTAGTACTGGGGGTAATCCTCTTATTTATCAGCATTTGTTTTGGTTTTTTGGTCATCCAGAAGTTTATATTCTTATTTTGCCTGCTTTTGGTATTATTAGTCAATCTAGTTTGTATTTAACTGGAAAAAAGGAGGTTTTTGGTTCTTTAGGGATGGTTTATGCTATTTTAAGGATTGGTCTTATTGGTTGTGTAGTTTGGGCTCACCATATGTATACTGTAGGTATGGATCTTGATTCCCGGGCTTATTTTACGGCTGCTACTATGGTTATTGCTGTGCCTACGGGTGTGAAAGTTTTTAGTTGGTTAGCTACTCTTTTTGGTATGAAAATGGTTTTTCAACCTTTATTGTTGTGGGTATTGGGCTTTATTTTCTTGTTTACTGTAGGTGGTTTGACTGGAGTTGTTCTTTCTAATTCTAGTTTAGATGTGATTTTGCATGATACTTATTATGTGGTTAGCCATTTTCATTATGTTTTGAGTCTAGGTGCTGTGTTTGGTATTTTTACTGGTGTTAGTTTGTGGTGAGGTTTTATGACTGGTTTTGTTTATGATAAGATGGTTATGAGAGTTGTTTTTATTTTGATGTTTATTGGTGTTRATATGACTTTTTTTCYTTTGY

>KAPb25-R11\_COIf

NRCTATAAGTCTTTTTGTTTGAACTGTTTTTGTTACTGTTTTTTTACTTGTTTTATCTTTGCCTGTGTTGGCTGGGGCTATTACTATGTTGTTAACTGATCGTAATTTGAATACTTCTTTTTTTGATCCCAGTACTGGGGGTAATCCTCTTATTTATCAGCATTTGTTTTGGTTTTTTGGCCATCCGGAAGTTTATATTCTTATTTTGCCTGCTTTTGGTATTATTAGTCAATCTAGTTTGTATTTAACTGGAAAAAAGGAGGTCTTTGGTTCTTTAGGGATGGTTTATGCTATTTTAAGGATTGGTCTTATTGGTTGTGTAGTTTGGGCTCACCATATGTATACTGTAGGTATGGATCTTGATTCTCGGGCTTATTTTACGGCTGCTACTATGGTTATTGCTGTGCCTACGGGTGTGAAAGTTTTTAGTTGGTTAGCTACTCTTTTTGGTATGAAAATGGTTTTTCAACCTTTATTGTTGTGGGTATTGGGCTTTATTTTCTTGTTTACTGTAGGTGGTTTGACTGGAGTTGTTCTTTCTAATTCTAGTTTAGATGTGATTTTGCATGATACTTATTATGTGGTTAGTCATTTTCATTATGTTTTGAGTCTAGGTGCTGTGTTTGGTATTTTTACTGGTGTTAGTTTGTGGTGAGGTTTTATGACTGGTTTTGTTTATGACAAGATGGTTATGAGAGTTGTTTTTATTTTGATGTTTATCGGTGTTAATATGACTTTTTTTCCTTTGCATTGTGCTGGTTTACATGGTTGTCCTCGTAARWAW

>KAPb26-R12\_COIf

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>KAPd33-R13\_COIf

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NNTATAAGTCTTTTTGTTTGAACTGTTTTTGTTACTGTTTTTTTACTCGTTTTATCTTTGCCTGTGTTGGCGGGGGCTATTACTATGTTGTTAACTGATCGTAATTTGAATACTTCTTTTTTTGATCCTAGTACCGGGGGTAATCCTCTTATTTATCAGCATTTGTTTTGGTTTTTTGGTCATCCAGAAGTTTATATTCTTATTTTGCCTGCTTTTGGTATTATTAGTCAATCTAGTTTGTATTTAACTGGAAAAAAGGAGGTTTTTGGTTCTTTAGGGATGGTTTATGCTATTTTAAGGATTGGTCTTATTGGTTGTGTAGTTTGGGCTCACCATATGTATACTGTAGGTATGGATCTTGATTCCCGGGCTTATTTTACGGCTGCTACTATGGTTATTGCTGTGCCTACGGGTGTGAAAGTTTTTAGTTGGTTAGCTACTCTTTTTGGTATGAAAATGGTTTTTCAACCTTTATTGTTGTGGGTATTGGGCTTTATTTTCTTGTTTACTGTAGGTGGTTTGACTGGAGTTGTTCTTTCTAATTCTAGTTTAGATGTGATTTTGCATGATACTTATTATGTGGTTAGCCATTTTCATTATGTTTTGAGTCTAGGTGCTGTGTTTGGTATTTTTACTGGTGTTAGTTTGTGGTGAGGTTTTATGACTGGTTTTGTTTATGATAAGATGGTTATGAGAGTTGTTTT

>KAPb36-R16\_COIf

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>KAPb42-R19\_COIf

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>KAPb46-R22\_COIf

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>KAPb52-R28\_COIf

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>KAPd59-R4\_COIf

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>KAPb90-R46\_COIf

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Data S2: ITS-Genotype of *Pseudoterranova bulbosa* samples.

>Geno\_ITS\_NC5

CGANAGTCTCCCAACGTGCATACCATCCATTTGCATGTTGTTGTGAGCCACATGGAAACTCATACACGTGTGGTGGCAGCCGTCTGCTGTGCTTTATCGTGCAGACAATGGCTTATGAGTGGCTGTGTGATTGTTGAACAACGGTGACCAATTTGGCGTCTACGCCGTATCTAGCTTCTGCCTGGACCGTCAGTAGCGATGAAAGATGCGGAGGAAGTTCCTCTGTTTTGGTACGCCAGCGCAGAGTTGAGCAGACTTAATGAGCCACGCTTGGTGGCCGCCAAAACCCAAAACACAACCAGTCTATTTTAACGTTTGTTGATATGTTAATGTACAAATCTTGGCGGTGGATCACTCGGTTCGTGGATCGATGAAGAACGCAGCCAGCTGCGATAAATAGTGCGAATTGCAGACACATTGAGCACTAAGAATTCGAACGCACATTGCGCTATCGGGTTCATTCCCGATGGCACGTCTGGCTGAGGGTCGAATTATAGTAAACTATCTTCGAGTACTTTTTATGGTCGTGAAGTATCCGGCAAGTAGTGCAGTTGGATTGTTTTTGTTGCTTGTCCGTTCGTTCGGTCGGTTAACAACAATATTCTGAGGCTCCTTGCTTAGTTGTGTTTTAGTAGACGTTAACACCTGAACAATATGTGGTGGTGATATTGGTGATGGCGAGAATCATGCCGCTTCAATGGGGCAGCAACCAGCATACGCTAATGACAGTTGGTTGATTGAAGCCAGGGCAACGGAGTGATGTACGTGTGGCGATCATTTAACGTTTGTATTTGACCTCAGCTCAGTCGTGATTACCCGCTGAATTTAAGCATATAATTAAGCAGAGAA