

Involvement of Metalloproteases in the Fertilization of the Ascidian *Halocynthia roretzi*

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Supplemental Data

Figure S1. Nucleotide and predicted amino acid sequences of the HrTast1, HrTast2b, HrTast2c and HrTast3c gene models (website: <https://www.aniseed.fr/>)

Figure S2. Determined nucleotide sequences (upper) of the RT-PCR products of the *HrTast1*, *HrTast2b*, *HrTast2c* and *HrTast3c* genes and the predicted nucleotide sequence (lower) from the respective gene model.

Figure S3. Preparation and Western blotting of HrTast2c peptide antibodies

Figure S4. SDS-PAGE of the VC incubated with sperm extract

Figure S5. Vitellogenin fragments were detected in the 120-kDa band via SDS-PAGE

Table S1. LC-MS analysis of the 120-kDa protein, which newly appeared after incubation with the isolated VC and sperm extracts *

Predicted amino acid sequence of HrEF1a

>Harore.CG.MTP2014.S31.g10104.01.p

MVKEK F H I N I V V I G H V D S G K S T T T G H M I Y K C G G I D K R T I D K F E K E A Q E T G K G S F K Y A W V L D K L K A E R E R G
I T I D I A L W K F E T T K Y Y I T I I D A P G H R D F I K N M I T G T S Q A D C A V L I I A A G T G E F E A G I S K S G Q T R E H A L L A
F T L G V K Q M I C A I N K M D N T E P P Y S E A R F K E I V T E V S S Y M K K V G Y N P K K I P F V P I S G W H G D N M M E K S D K T P W
Y K G F T K M S D K P V G A T L K E A F D L I E Q P T R P T D K P L R L P L Q D V Y K I G G K C I G T V P V G R V E T G I I K P G Q I V K F
S P V N L T T E V K S V E M H H E S L V E G C P G D N V G F N V K N V S V K D I R R G N V C G D A K N C P P Q K T S S F L A Q V I I L N H P
G N I S K G Y T P V L D C H T A H I A C K F A E I K E K I D R R S G K T M E E N P K S V K S G D A A M I E L I P S K P M C V E K F S E F P P
L G R F A V R D M R Q T V A V G V I K D V T V A V E T G G K V T K A A M K S K G K K

cDNA sequence of HrEF1a model

(PCR product using the primers in Table 1 (highlighted sequences): 364 nucleotides)

>Harore.CG.MTP2014.S31.g10104.01.t

T C C A C C T C A T C G T T C C T T T T A G C G T G C G G C A T C T T G G T C T T G A G T T C C A A T T C T T T G T C A A A A A T A A G A A
A A C A C C A T G G T T A A A G A A A A A T T T C A T A T T A A C A T C G T C G T A A T T G G T C A T G T C G A C T C C G G C A A G T C C A
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A G C T C A A G A G A C G G G T A A A G G T T C G T T C A A G T A T G C C T G G G T G T T G G A T A A G T T G A A G G C T G A G A G A G A A
C G T G G T A T T A C C A T C G A C A T T G C T C T A T G G A A G T T T G A A C C A C C A A A T A C T A T A T C A C C A T C A T T G A T G
C C C C T G G A C A T C G T G A T T T C A T T A A A A C A T G A T C A C A G G A A C A T C T C A A G C A G A C T G T G C T G T C C T C A T
T A T A G C G G C T G G T A C T G G G G A A T T C G A A G C T G G A A T T T C T A A G A G T G G C C A A C G A G A G A G C A T G C T C T T
T T G G C T T T C A C C C T T G G T G T G A A A C A G A T G A T T T G T G C T A T T A C A A A A T G G A C A A C A C G G A G C C T C C A T
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G A A A A A A A T T C C A T T C G T G C C C A T C T C T G G A T G G C A T G G T G A T A A C A T G A T G G A A A A G T C T G A C A A A A C C
C C T T G G T A T A A A G G A T T C A C G A A A A T G A G T G A C A A G C C A G T T G G T G C T A C T C T A A A A G A A G C C T T T G A T C
T T A T T G A G C A A C C A A C A C G T C C C A C T G A T A A A C C C T T G C G T T T G C C T C T A C A A G A T G T G T A C A A A A T A G G
A G G C A A G T G T A T T G G A A C A G T G C C A G T G G G A A G A G T G G A G A C T G G A A T T A T A A A A C C A G G C C A G A T T G T T
A A G T T T T C T C C T G T A A A T C T T A C G A C T G A A G T C A A A T C T G T C G A A A T G C A T C A T G A G A G T T T A G T G G A G G
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G T G T G G G G A T C G A A G A A T T G C C C T C C A C A G A A A C T A G T A G T T T C T T A G C T C A G G T T A T A A T C T T G A A C
C A T C C C G G A A C A A T T T C A A A G G G C T A C A C G C C A G T T T T G G A C T G C C A T A C T G C T C A C A T C G C T T G C A A G T
T C G C A G A T C A A G G A G A A A A T C G A T C G T C G C T C T G G T A A G A C T A T G G A G G A A A A C C C A A G A G T G T A A A
G T C T G G T G A T G C T G C C A T G A T T G A G C T A A T T C C C T C G A A A C C A A T G T G T G T T G A A A A G T T T T C C G A A T T C
C C T C C T C T G G G T C G T T T T G C T G T C C G T G A C A T G C G T C A G A C G G T T G C A G T C G G T G T T A T C A A G G A T G T T A
C G G T T G C T G T C G A A A C G G G A G G A A A A G T G A C A A A A G C C G C C A T G A A A A G T A A A G G C A A G A A G T G A C T C G A
A C C G G A G A A T G A T C G C T C T C G A A C T A A T T T A G G A T T A A A A A G C T C T T T T G T G T T A A T A T T G G T G T T A A T T
T T G T C A T G T C G C A T G T T T C A C T T G G T C A T A T T T T T G A A C T C T A C T C A C C G T A A A C A T T T C C G G C G G A A A A
A A C C T G T C T T T T A C T A G C T G A C T G G C G T G G T T G T C C C C T A A G A T T T C A T G T G A T A A A T G T A A T T G T A T G
A A T C A A T A A A T T T C

Predicted amino acid sequence of HrTast1

>Harore.CG.MTP2014.S147.g09103.01.p aa (Molecular mass: 99.43 kDa)

R L F H S T L Q Q Q L S R M P H P P K P R K P H H H R T K R T G V G I R R A Y Q P L T E C Q T L F K K I S A P Q K K K I S P S A N K V P W
M F A S V V V S F L A A I A V V I G V I V A K S Q K S L L E Q K C E E L L K R I N S N E T D T S I S P Y M I N T C I E V G S D C N F E Y T S
C Q S P C P F G Y A R D K E S G C Y T C A C A Q E G L H E M D I Q F H E E D V A G L L E D Y G Y K L L F N D E E E S F S L F I S S V K K S V
G L W T K W Q K N G R Y K V P Y E I D A K L T S G Y S D V I R E S I Q V I S K E S C I D L I P R D K E K D Y I V F I S L R G C W A K V G Y R
T W I Q D V S I G L G C D K V E I V I H E I L H A L G F Y H E H S R P D R D G F V D V L L E N V K E D M K N N F K K L I E G E T Q D L N S E
Y D I K S V M H Y D G L S F T K N F K P T M T Y K G T Q D Y V D I S G I L T L S S E D K D E L N L L Y K C K P E N I G Q T V T G S W S E W G
S W N D C Y M T C K D H E T P Y R R K F R K C V D K D G N G V V G C E G K T S I R E E C P V P Y C E K A G A E W E H W G A W S E C S K S C G
K G K R N R E R K C P Y S G E C S M F Y G G Y F D R D S C A T H K C G E K P E L K W T L W T V W L A C K G E C G E G V Q K R I R K C E H G D
E L V E D C S G G K Y E E D E T G I G Y E T Q S C V V E C T T P L V S L S S E P P T T P E T I A M T S A T T T T A G P N K T P T K T T T K T
P N T I A K T T T K A T G P T T T P V T T N R A T T E K I T E T A N P D W R A W G L W G S C S K S C D G G Q R E R E R V C K S Y T C E G D
K K M S E Y C N T R S C R A Q S R P H T I F S A T E A I I P I F C P Y G R I V P G D F N A D R R T D L L C L F S D G Y I R I Y L A N A R G V
F D E V G W E G Q T N F C Q F S E D S L A P P Q V F A K D L N A D K F I D I L C Y N K R S G K M Q I L L N Q K L Q F H T K V D W E G K K M N
C D V N M G A V I Q L Q D V N G D S R A D L V C G D E K T R V K E I F L N K T

cDNA sequence of HrTast1 model

(PCR product using the primers in Table 1 (highlighted sequences): 314 nucleotides)

>Harore.CG.MTP2014.S147.g09103.01.t nt

A G G T A T A T T C A T T C C A C G C T G C A G C A A C A A C T T A G C A G G A T G C C T C A T C C T C C A A A A C C T A G G A A A C C G C
A C C A T C A T C G T C G T A C C A A G A G G A C T G G A G T T G G A A T T A G A A G A C A T A T C A A C C T T T A A C T G A A T G C C A

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 CTCAAAAGAGTCTACTGGAACAGAAATGTGAAGAACTTTTGAAGAATAAATTCAAACGAAACAGACAC
 ATCTATTTCTCCTTACATGATCAACACGTGCATCGAAGTGGGCAGTGACTGTAACCTTTGAATACACCTCT
 TGTGAGTCTCCGTGTCCTTTTGGATATGCCAGAGATAAAGAATCGGGATGCTACACATGTGCTTGTGCAC
 AAGAAGGACTTCATGAAATGGACATTCAGTTCATGAAGAAGATGTGGCTGGATTACTGGAGGATTACGG
 TTACAAACTTCTTTTCAATGACGAAGAAGAATCTTTTCTTTGTTTATATCTTCAGTTAAGAAAAGTGTT
 GGGTTGTGGACAAAAATGGCAGAAAAATGGAAGATACAAAGTCCCTTATGAAATAGATGCAAAATTAACCT
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 ATGCTCTTGGCTTTTATCACGAGCACTCAAGACCAGACAGAGATGGATTTGTGGATGTGCTCCTTGAAAA
 TGTCAAAGAAGATATGAAAAACAACCTCAAGAACTGATTGAAGGGGAACTCAAGATTTAACTCGGAG
 TATGACATCAAAATCGGTGATGCATTACGACGGTTTGTGATTTACTAAAAATTTCAAGCCGACAATGACAT
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 GAACCTGCTGTACAAATGCAAGCCTGAGAATATTTGGGCAAACTGTCACAGGTTTCATGGTCTGAATGGGGC
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 GAACTAGTAGAAGATTGTTCTGGTGGAAAGTATGAGGAAGATGAACTGGTATTGGGTACGAGACGCAGT
 CATGCGTCGTTGAATGCACTACTCCTCTGTGTTCAATTGTCAAGTGAACCTCCAACAACCTCTGAAACAAT
 CGCAATGACCAGCGCTACCACGACAACCGCTGGACCAAACAAAACCTCCACAAAAACCACAACGAAGACA
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 GGGCAACTACTGAAAAAATAACAGAACTGCAAAATCCAGATTGGAGAGCATGGGGTTTGTGGGGATCTTG
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 AAGTCTTCGCTAAAGATCTTAATGCAGATAAAATTCATTGATATCTTGTGCTACAATAAGCGCTCGGGGAA
 AATGCAGATTTTGTGTAACCAGAAATTACAGTTCCATACAAAAGTTGATTGGGAGGGGAAAGAAAATGAAC
 TGTGATGTGAACATGGGCGCAGTTATACAGCTGCAGGATGTAAATGGTGACAGTAGAGCTGATCTTGT
 GTGGAGATGAAAAAACGAGAGTCAAGGAAATATTTCTGAATAAGACTTAGTACGGAACATAATAAGTTTA
 TCACGAAGCTATTTACTTGAGTTCAGCTTCAATCAAGTCTGTTTTGTTGTGATTTAAAAAATACTT
 GGTGAGCTCATTAGTACTGATTCGAACAGTTTTTTTCTTATTAATGGAAGTGGTCCATATTTCTAAATA
 AGACTTAATACGGAATATATTAAGTTTATCACAAAGCTAGTTACTTGAGTTCAGCTTCAATCAAGTCTGT
 TTTGTTGTGATTTAAAAAATACTTGGTCAGCCTCATTTAGTACTGATTCGAATAGTTT

Predicted amino acid sequence of HrTast2b

>Harore.CG.MTP2014.S41.g12587.01.p (Molecular mass: 70.24 kDa)

MESKDPPPGPSTVKGRSMTVRRKNVYIMFGVVVFTAIGIITVVSILLQGSTRMISELRYYSKMSCDAGKMN
 SPIQINECMKATCIFDPQACISPCPFGYRKNKRGCDVSCACASEGNFQGDVHFDEDSLPELSELYGHTER
 AGDFSVFASSVESSTKLWNNLVDGRHKIPYQMSLLGKAAKGAIKEALSTFTTKSCIDFIPWTDEKHSV
 LFKAEAGCWSEIGKNMKKSPQVLSVGDSCSEKTGIVQHEVLHMLGFQHEHVRPDRDAYVIVDYDNI IATNV
 IQFNKLEQTEVVDLGSSEYDFSSLLQFSSDMFSKNGKDTITNRVTGGEILGQQIEFSVGDIRELNSLYNCY
 EDKPGKWTEWQWSLDCQTCGQGRKRRYRSCLDGSDSVKGGNLEYLECESETPCPSKDGWGWKWEYDECS
 NSCGGGYQWRLRECSQDDCEGSESEGKKNLQSCFDRSLSEDSQTEGPKPKPGPDFFENTEVTIPLNLCD
 VKTYNEWYFGDFNGDKRTDTLCINPDGEAKLAYTNDRGILTEPQWEGKLEGCLNCIKYVGDFNGDGKDDV
 LCKNIYSRTIAIKFTTSDGIFDEGFTDAGNFCCGNDHFHVIVSDVNGDGKADIICGSRDTNIEIRINRFEK

cDNA sequence of HrTast2b model

(PCR product using the primers in Table 1 (highlighted sequences): 287 nucleotides)

>Harore.CG.MTP2014.S41.g12587.01.t

AGTCTGTTATCTAGCATATCACAAACGACGATCACCTTCTCTTTCCTGTGAAGAATAAGACTCCAATCCT
 TTGTTATTGGAAAGCCTCGCGTCATCATGGAATCCAAGGATCCTCCCGGTCCATCAACTGTTAAAGGAAG
 ATCCATGACCGTGAGAAGGAAAAATGTATACATTATGTTTGGTGTGTCGCTTTTACAGCAATTGGGATC
 ATTACTGTAGTTTCTATCTTGTGCAAGGTAGCACAAAGATGATCTCTGAACTACGATACTATTCAAAAA
 TGTCTTGTGATGCCGAAAAATGAATTCACCAATTCAAATTAATGAATGCATGAAGGCTACATGTATATT

CGATCCGCAAGCTTGCATTTCTCCGTGTCCTTTTGGGTACAGAAAAACAAGAGAGGATGCGATGTCAGT
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CTGAGTTGTATGGACACACAGAACGTGCTGGAGACTTTTCAGTGTTTGCTAGTTCTGTAGAATCGAGTAC
AAAGTTATGGAACAATAACCTTGTGATGGCCGCCACAAAATTCATATCAAATGGATTCTTTATTGGGG
AAAGCTGCGAAGGGTGCAATAAAAAGAGGCGCTTAGCACATTTACAACGAAATCCTGCATCGATTTTATAC
CGTGGACAGACGAGAAACATTTCGGTTTTATTCAAGGCTGAAGCCGGTTGCTGGTCTGAAATAGGAAAAAA
CATGAAAAAATCTCCCCAAGTCCTCTCAGTTGGAGATAGCTGTGAAAAAACAGGAATAGTTTCAGCATGAA
GTGCTTTCACATGTTGGGTTTTCCAACACGAACACGTCCGGCCCTGATCGAGACGCTTACGTGATTGTCGATT
ATGATAATATAATAGCAACCAACGTTCATCCAATTTAACAACTGGAACAAACCGAGGTTGTTGACTTGGG
TTCGGAATATGATTTTCAGTTCGTTGCTGCAGTTCTCCAGCGATATGTTTCAGTAAGAACGGTAAAGACACC
ATCACCACCGTGTGACAGGTGGAGAGATTCTAGGACAACAGATTGAATTTTCTGTGGGAGACATACGAG
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AAAGGAGGCAATCTGGAATACCTGGAGTGCTCAGAAACACCATGCCCTAGTAAAGACGGTGGCTGGGGGA
AGTGGGGTGAATACGACGAGTGTAGCAACTCATGTGGGGGAGGATATCAGTGGAGGTTGAGAGAGTGCTC
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CTTTCTGACGAACTTTCACAGACGGAGGGCAAACCAAACAGGCCCGATTTCTTCGAGAACACTGAGG
TCACCATCCCGCTAAATCTATGTGATGTCAAAACATATAACGAATGGTATTTTCGGAGATTTTAACGGTGA
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TA

Predicted amino acid sequence of HrTast2c

>Harore.CG.MTP2014.S41.g06549.01.p (Molecular mass: 72.84 kDa)

MNSNRKHRTRTQADSKKKLHLLALGFIIVLIAGILGVIITLVQGSAKKPIAEQRMYSARMSCDDETPNSLE
VNECQKATCMFVDVTTCAHDCPFGYQPDARGCDIGCDCATESNFQGDIIHFDEHTLPTYMKMFRAKSEDDFE
IFSGSAVHAYPLFNENPQNGRHRIPYELDNSRGQLAVTQIEEAIKIYSEKTCIDFVPKTSSDGQDFVKFS
KGPGCWAFIGKTKYPQDVSI GVECGTTAI IQHEMLHLLGFAHEQCRPDRDGYVQIKKENINPRNLHNFDK
KTEDEISDLGSEYDVKSSIMQYDSLWSTNGQSTMVEKKTGAFIFAKHEFAESDLYELNKLYDCLDHVEGE
KGSEEGGEEGGEEGDEEGGGGGGSKWTDWGEWSACPRTCGPANLRRYRFLDSSDQLVTGCEGYDQDASI
SCSGPTCPGIIAEWGSWGEYGDCTKTTCGMGLKFRFRNCSVEGECWTGWAGEGEFCNPEACNYPASGHAGV
GGKDDGGGQDSVSGVRYFKDDPLKIESSLCKGDASTDWLFGDVGDKKIEAICIDSQGKTEIGRPDENGMA
MHTNWKGNMDGCSGRYRYTGDVDGDGKDDIICKDETAGMLKVKFAGEKGEFDSSFTGVGNFCTDEKQGML
LFDVNGDGKIDILCQSIDLSMEIRLNNFESN

cDNA sequence of HrTast2c model

(PCR product using the primers in Table 1 (highlighted sequences): 200 nucleotides)

>Harore.CG.MTP2014.S41.g06549.01.t

AGGTTAACACCTTTATAGCTTGTATAAAAATTTGCTTAGGGTTGAATTCATCAGATGCAAGTGATTAT
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GCAAAGTCAGAAGATGACTTTGAAATATTTTCGGGGTCAGCTGTGCATGCATACCCTTTATTCAATGAAA
ATCCTCAGAATGGAAGACATAGAATCCCTTACGAACTAGACAACAGTAGAGGTCAATTAGCTGTAACCTCA
AATTGAAGAAGCAATCAAGATATATTCAGAAAAAAGCTTGCATCGATTTTGTTCCAAAGACTAGCAGTGAC
GGACAGGACTTTGTTAAATTTTCTAAAGGCCCTGGATGTTGGGCATTTCATTGGAAAGACAAAATATCCCC
AAGACGTCTCAATTGGAGTTGAATGTGGAACAACGGCAATCATACAACATGAAATGCTTCACCTTGCTAGG
ATTTGCACACGAGCAGTGTAGACCTGATAGAGATGGTTATGTTCAAATCAAGAAGGAAAAATATTAACCCA
AGAAATTTGCACAACCTTTGATAAAAAAGACGGAAGACGAAATTTTCGGACCTAGGTTTCAGAATACGATGTAA
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CGGGCCTGCGAATTTGAGGAGATATAGATTTTGTCTGGATTTCATCAGATCAGCTGGTCACCGGCTGCGAA
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TGACTCCTACTTTTTACAATGTTGTTCAATACTTACTGTTCCCTGTATTTATTTCTACAGA

Predicted amino acid sequence of HrTast3c

>Harore.CG.MTP2014.S261.g06577.01.p (Molecular mass: 91.18 kDa)

MESSKKQKRSESRADRPRSKNPKHVSAGKDRSSARDKKKPAQNSSNKVLLSIVVCVVLAAIGALMFAL
FGMSTSDCQKYLKSQLKGGKNKDIALSPIAISECLETMCTFDVLQCNAPCFPGFETSQESGCTKSCDAV
EGKFQGDVHFGADDVPEMLEKFHGHKEEDEYEVFFATTKMLWNNLEMEGRFKVPYKMPGLPKEDYQVWVD
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DTGEREIFSNILEHQLSEIQAVVDGIYGEWADWFEWEHCDVTCGTGERLRLRICKRKEKEIATNRCKADE
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EKQSGAVTGKISWHGPTSLCAFVVKINIKIYARDMDDDDIVCYNPLTREVEIGINNGGKFRAVKDW
RGQRQSCDSVIHIEDVNGDGKNDLVCNADNAVKQVYVLYNGYD

cDNA sequence of HrTast3c model

(PCR product using the primers in Table 1 (highlighted sequences): 334 nucleotides)

>Harore.CG.MTP2014.S261.g06577.01.t

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TTCTTCAATGCAACGCCCCATGCCCTTTCGGCTTTGAAACTTCCCAAGAAAGCGGATGTACAAAAAGTTG
CGACTGCGCTGTGCAAGGAAAAATTTCAAGGGGGATGTTTCATTTTGGTGCGGATGATGTCCCGGAAATGTTG
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 CAAAGCAGATGAAAAAATAGGGAAGGTTTATAGAGACGGACAGGCCCAAGTCGAGGAATGTAAAATTCGA
 GACTGTAAAGATGTGCCCCCTGGACTTACTGAAACCAAATCACCACCTGGACCAGCCCCCGTGAATACTCCATC
 CGACGAAAAATGATGCGAGCTCTGGAATAACACCTTCACCACCTGGACCAGCCCCCGTGAATACTCCATC
 CTCATCAGGACCCACTCCTGCTCCCATAAACACCCCATCCAAGCGACCTACCCCAAGTAAAGATAAACCC
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 CTGGGAAGTTCAACTCAGATAAGTATGAAGATTTGATGTGCCTATATCCAGATGGCTACATGTATGTGTA
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 TGTGAAGGACTGGAGAGGACAACGACAGTCATGCGATAGTGTATACACATTGAAGATGTGAATGGCGAT
 GGAAAAACGATTTGGTTTGTGGAAATGCTGACAATGCCGTTAAACAAGTCTATCTCAATGGCTATGGTG
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 AAAAAATATATTGCCATTATTCTACTTTCAAAAAAAGTTGCATTTGTTTATAAAACTTGATTTACATTCAT
 GT

Figure S1. Nucleotide and predicted amino acid sequences of the HrTast1, HrTast2b, HrTast2c and HrTast3c gene models (website: <https://www.aniseed.fr/>)

The yellow and green highlighting indicate the forward and reverse primer sites, respectively. The cDNA sequences highlighted in yellow, purple and green indicate the predicted PCT products. The nucleotide sequence underlined in HrTast1 was missing in RT-PCR, suggesting the presence of an intron sequence. The initiation methionine codon (ATG) is indicated by a bold letter.

HrTast1: Determined nucleotide sequence of RT-PCR product (275 nt)

CTAGGAAACCGCACCATCATCGTCGTACCAAGAGGACTGGAGTTGGAATTAGAAGAGCACCTCAGAAAAAATAT
CACCATCAGCTAATAAAGTGCCATGGATGTTGTCATCTGTTGTCAGCTTCTTGCAGCCATAGCAGTCGTCATCG
GGGTAATAGTAGCCAAATCTCAAAAGAGTCTACTGGAACAGAAATGTGAAGAACTTTGAAAAGAATAAATTCAAACG
AAACAGACACATCTATTTCTCCTTACATGATCAACACGTGC

HrTast1: Predicted nucleotide sequence from the gene model (Gray-highlighted sequence was lacking in the cloned cDNA, suggesting this region is intron.)

CTAGGAAACCGCACCATCATCGTCGTACCAAGAGGACTGGAGTTGGAATTAGAAGAGCATATCAACCTTTAACTGAAT
GCCAAACGCTTTTAAAAAATTTTCAGCACCTCAGAAAAAATATCACCATCAGCTAATAAAGTGCCATGGATGT
TTGCATCTGTTGTTGTCAGCTTCTTGCAGCCATAGCAGTCGTCATCGGGTAATAGTAGCCAAATCTCAAAAGAGTC
TACTGGAACAGAAATGTGAAGAACTTTGAAAAGAATAAATTCAAACGAAACAGACACATCTATTTCTCCTTACATGA
TCAACACGTGC

HrTast2b: Determined nucleotide sequence of RT-PCR product (287 nt)

CACAAACGACGATCACCTTCCTTTTCCTGTGAAGAATAAGACTCCAATCCTTTGTTATTGGAAGCCTCGCGTCATCA
TGGAATCCAAGGATCCTCCCGGTCCATCAACTGTTAAAGGAAGATCCATGACCGTGAGAAGGAAAAATGTATACATTA
TGTTTGGTGTGTCGTTTACAGCAATTGGGATCATTACTGTAGTTTCTATCTTGTGCAAGGTAGCACAGAATGA
TCTCTGAACACGATACATTTCAAAAATGTCTTGTGATGCCGGAATAATGAAT

HrTast2b: Predicted nucleotide sequence from the gene model (Identical sequence between the predicted sequence and determined sequence except one nucleotide)

CACAAACGACGATCACCTTCCTTTTCCTGTGAAGAATAAGACTCCAATCCTTTGTTATTGGAAGCCTCGCGTCATCA
TGGAATCCAAGGATCCTCCCGGTCCATCAACTGTTAAAGGAAGATCCATGACCGTGAGAAGGAAAAATGTATACATTA
TGTTTGGTGTGTCGTTTACAGCAATTGGGATCATTACTGTAGTTTCTATCTTGTGCAAGGTAGCACAGAATGA
TCTCTGAACACGATACATTTCAAAAATGTCTTGTGATGCCGGAATAATGAAT

HrTast2c: Determined nucleotide sequence of RT-PCR product (200 nt)

GGCTCTTGGATTTCATCATCGTTCTTATAGCTGGCATTCTTGGTGTAATCATAACTCTTGTACAAGGCAGCGCTAAAAA
ACCTATAGCAGAACAAGAAATGTATGCAAGAATGTCATGTGATGATGAAACGCCAAATTCATTGGAAGTCAATGAATG
CCAAAAGGCAACTTGCATGTTTGA CGTCACTACCTGTGCACACG

HrTast2c: Predicted nucleotide sequence from the gene model (Identical sequence between the predicted sequence and determined sequence)

GGCTCTTGGATTTCATCATCGTTCTTATAGCTGGCATTCTTGGTGTAATCATAACTCTTGTACAAGGCAGCGCTAAAAA
ACCTATAGCAGAACAAGAAATGTATGCAAGAATGTCATGTGATGATGAAACGCCAAATTCATTGGAAGTCAATGAATG
CCAAAAGGCAACTTGCATGTTTGA CGTCACTACCTGTGCACACG

HrTast3c: Determined nucleotide sequence of RT-PCR product (334 nt)

AAGAACCCAAAGCACGTGAGCGCGAAAGCCGGGGATCGCTCTTCAGCTCGAGATAAGAAGAAGCCCGCACAAAACCTCA
TCCAACAAAGTTTGTCTCAGCATTGTAGTTTGCGTTGTTCTTGCTGCGGCAATCGGAGCTTTGATGTTTGCTTTATTT
GGAATGTCAACATCGGATTGTCAAAAGTATCTGAAATCTCAAGCTAAAGGCGGCAAAAATAAAGATATTGCGTTAAGT
CCTATTGCGATCTCAGAATGTTTAGAAACCATGTGTACATTTGACGTTCTTCAATGCAACGCCCCATGCCCTTTCGGC
TTTGAAACTTCCCAAGAAAGCG

HrTast3c: Predicted nucleotide sequence from the gene model (Identical sequence between the predicted sequence and determined sequence)

AAGAACCCAAAGCACGTGAGCGCGAAAGCCGGGGATCGCTCTTCAGCTCGAGATAAGAAGAAGCCCGCACAAAACCTCA
TCCAACAAAGTTTGTCTCAGCATTGTAGTTTGCGTTGTTCTTGCTGCGGCAATCGGAGCTTTGATGTTTGCTTTATTT
GGAATGTCAACATCGGATTGTCAAAAGTATCTGAAATCTCAAGCTAAAGGCGGCAAAAATAAAGATATTGCGTTAAGT
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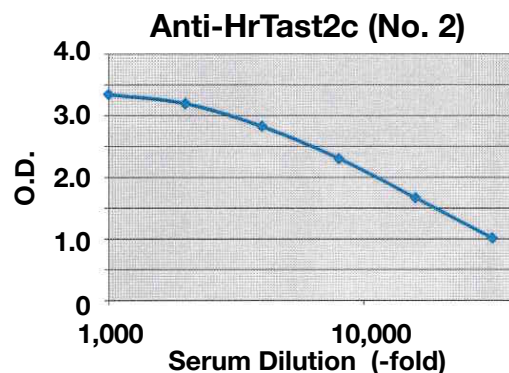
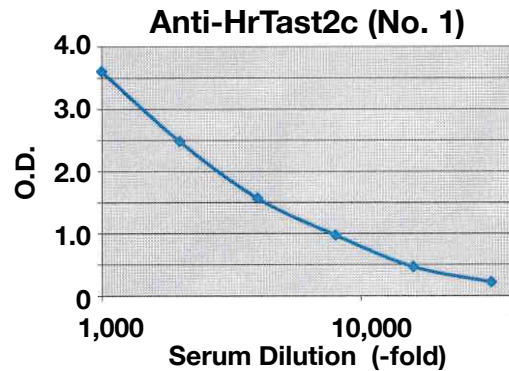
Figure S2. Determined nucleotide sequences (upper) of the RT-PCR products of the *HrTast1*, *HrTast2b*, *HrTast2c* and *HrTast3c* genes and the predicted nucleotide sequence (lower) from the respective gene model.

The yellow and green highlighting indicate the forward and reverse primers, respectively. The purple highlighting indicates the predicted sequence amplified by RT-PCR. The red highlighting indicates the determined nucleotide sequence. The gray highlighted sequence was not detected in the determined sequence, suggesting the presence of an intron region.

(a)

CiTast1	MEELYVSTGPAPEVGEKEPRHRRKQAEAGGVGSGKRPTKXKDTTKVIAWVGILVVG 60
HrTast2c	-----MNSNRKRHRTTGADS-----KKKLHLLALGFIIVLIAG 33
Aa-astacin	-----MDGAVLLALLG 11
CiTast1	VIALILAIVLGMSPS---EESYSCORAKNEGEKVSFDVNECEAAKKKQDFDITTCSDACP 117
HrTast2c	ILGVITLTVGSSAKKPIAEGRMYARMSDDETPNSLEVNECOKAT---CMFDVTTCAHDCP 91
Aa-astacin	VVAASPIIP----- 20
CiTast1	LGYNKEG-GCAVSLCATDGTYESDIFNEANIORALDRFIAPPDNGSDFVFTNTIKTT 176
HrTast2c	FGYQPDARGDIGDCATESNFQGDIFHDEHTLPTYMKMFRASED-DFEIFSASAHAY 150
Aa-astacin	-----EAARALYNDGMFEGDILKLRAGROP-----ARVRAAILGD 55
CiTast1	APLWELGVNRRVQIPYVDFPTITTDGYRAVYKASYWFSRHSICDLVPRKKE---KAHILFI 234
HrTast2c	PLFNEPNGRRHRIPELNSRGLAVTQIEEAIXIYSEKTCIDFVPKTSDDGDFVKFS 210
Aa-astacin	EYLWSGG---VIPYTFAGVSG-ADGSAILSGMDELEKTCIRFPVPTTES-DYVEIFT 108
CiTast1	RNGGCSFICKTKWRYVSLGIG-CSKASIVNHLIAAFYEQSRPDRDLYIKVYYEN 293
HrTast2c	KPGGWAFICKTKYQDVSI GVE-OGTTAIGMMLLFAFCQCRPDRDGYVQIKKEN 269
Aa-astacin	SGSGWYVYGRISGAQVSLQANGGVYHGTIIHLMLAIFYEHTRMDRDNYVTINYON 168
CiTast1	IQKEYHROYDKARPEAVDFGYEYDVKSLMHHYSRAFIQVG---KLTFFVLTKGYSIAS- 349
HrTast2c	INPRNLHNFDKTEDEISDLGSEYDVKSIMQYDSLWSTNG---OSTMVEKKTGAIFA- 325
Aa-astacin	VDPSMTSNFIDTYSRY---VGEDYQYYSIMHYGYSFSIQWGLVETIVPLQNGIDLTPY 226
CiTast1	SNEHPSSETDAEISLKYCKRKAANKGRWGEWAPWAGACRATCGTIGATVORYRROEYKD 409
HrTast2c	KHEF-AESDLYELNKLVDCLDHVEGEG---SEEGEE 359
Aa-astacin	DKAHMLDWDANILNLYTNEGSLRH----- 251
CiTast1	GQFADCKGKMEIKVCKLKACSPKYSEWSWASCSLTHFEHGIHALETERRRNCINKKE 469
HrTast2c	GGEGGDEEG---GGGSKWTDWGSACPRTCGPAN---LRRRYFLDSSD 405
Aa-astacin	
CiTast1	GLCPNSWIFGADIYQSYRCPPEPKTKEDIKEKALYKLRREIHRNPWTGSHWYPAC 529
HrTast2c	QLVTGCEGYDQASIS---CSGPTCP-----GIIAENGWGEYG-DC 443
Aa-astacin	
CiTast1	PFNCDGVTKKKRRTCAEYSAKYSKCEGNTPGSKIASQEIQRFCACAYMTPTTKGLSLT 589
HrTast2c	TKTCG-MGLKFRFRNCVGECHTGMAGEG-----EFCNPEACNYPASGHAGVG 491
Aa-astacin	
CiTast1	TVIIESDGLGSEIRRRSYEGGIMDVNSRLFCSSGKYVRKFNEDSDVVCVESNHSFY 649
HrTast2c	GKDGSGGDSVSGVRYFKDDPLKIESSLGKDASTDLWFGDVGDKTEAIGIDSGGK- 548
Aa-astacin	
CiTast1	PTINGETNYDSSFOOSYFCQSENGLLNESADFNTDNDLACIDRNSGOMIILSFFDN 709
HrTast2c	TEIGRPDENGMAMHTWKGMDGSGRYRYTGDDVDGDKDIIKDETAG-MLKVKFAGE 607
Aa-astacin	
CiTast1	RFEVHSDWAGLQDFCVGRKSHIFAGYGGDDGRADLILCLNKITNRESIIINWNF- 763
HrTast2c	KGEFDSSTFGVGNFCTDEKGMILLFDVNGDGKIDILCQS-IDLSMEIRLNNFESN 661
Aa-astacin	

(b)



(c)

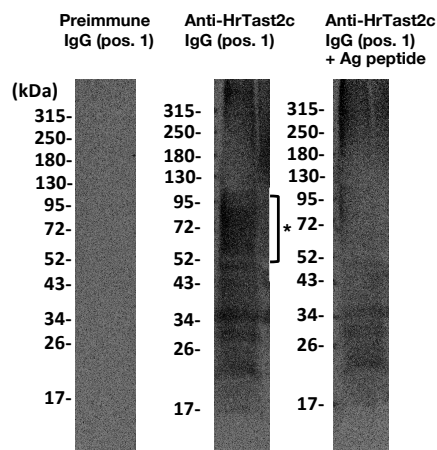


Figure S3. Preparation and Western blotting of HrTast2c peptide antibodies

(a) The amino acid sequence of HrTast2c was aligned with the sequences of *C. intestinalis* CiTast1 and *Astacus astacus* (crayfish) Aa-astacin. The amino acid residues indicated in red correspond to the antigenic peptides (position 1: antigenic peptide region No. 1 (238–254) and position 2 (antigenic peptide region No. 2 (371–384)). The residues highlighted in green are the Zn-binding consensus sites of the metalloprotease. (b) Titers of the antibodies were examined via ELISA. (c) Western blotting of the sperm extract using anti-HrTast2c (position 2) in the presence or absence of the antigenic peptide. The asterisk indicates the specific band of HrTast2c. No appreciable band was observed with anti-HrTast2c IgG (position 1).

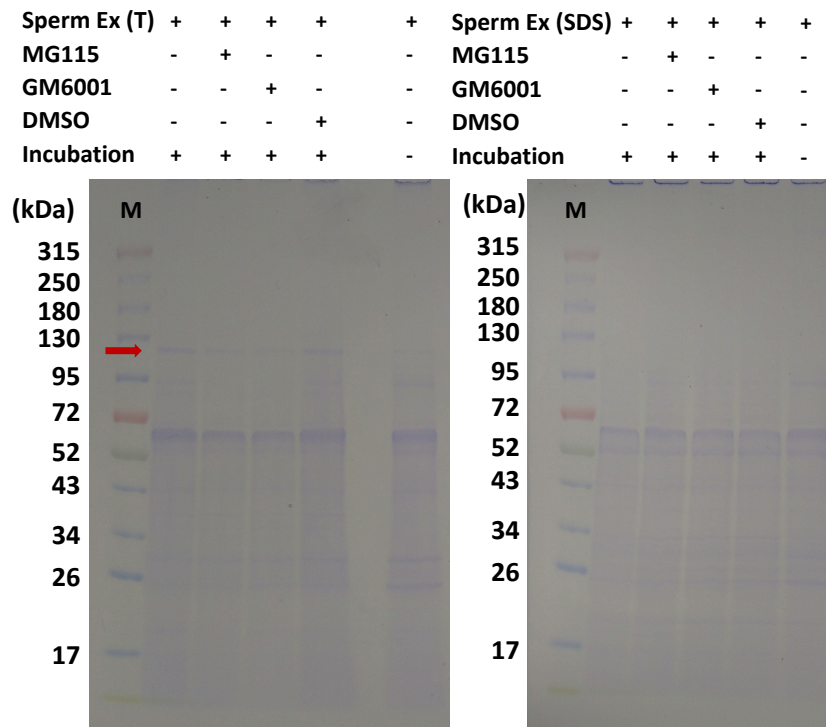


Figure S4. SDS-PAGE of the VC incubated with sperm extract.

A portion (0.2 g) of frozen sperm was thawed, suspended in 1.2 mL of 1% Triton X-100 (or 1% SDS) in 50 mM Tris/HCl (pH of 8.0) and homogenized, followed by centrifugation at 9,000xg for 20 min. The supernatant (sperm extract) was mixed with the isolated VC in the presence or absence of 100 μ M GM6001 or MG115, followed by incubation overnight at 13 $^{\circ}$ C, representing the ideal temperature for *H. roretzi* fertilization. After centrifugation, the precipitated VC was washed repeatedly, subjected to SDS-PAGE under reducing conditions and stained with Coomassie Brilliant Blue R-250. A 120-kDa band of the VC (red arrow) was newly detected after treatment with the sperm extract with 1% Triton X-100 (left panel) but not with 1% SDS (right panel). The appearance of this band was slightly inhibited by GM6001 or MG115 (a proteasome inhibitor). This band was cut from the gel and subjected to LC-MS analysis (Table S1 and Figure S5).

1 MRVAALSVCF LLLHAVTARR LHRIRERN SM PVPEDNCEIV QPFDQDYVYT YSYEALTEHE
61 DVS NVLKKAL KISCEVTITV PRRC SGKLRL NDCAIAEAVV SARDEVTYRK LPESEAFDRE
121 MRINELAFHF NGGEITH IFV DKAERTNVTN LKR GILTSLO VYNPRPKKEF EVGDVVEIPQ
181 VNVYGHGIVE QRILSKAEAGF PSSVEIIRDS ARLRLPWERR QWNFIRMRRN DADPFTMAMR
241 NYLAYESENT WSR AKQTECEC SLFRGRQVKV CKCMEYHPME MAHPLLSGLM KGEAVATTIR
300 QSIRVTNTRK MTKKDRSLWD VSRFEDENIM FEEWEETNK IYSEGFNAEE TLCYIITEPV
361 NNRFPALVTK LTRWLTAGQ EDIETAYNRC YGKLSGENKE LARISWVEML NTCINNEWCO
421 VPYCDSENV TCENALDSFI RSTTSKEEGV KSAIYRALEA INDPACTIVE ATLRLCREEA
481 ETTPCEVRTL GAVVNKYAS CEDCERKKPV ENAKKFLMKK LKNDCTASED DEVVSAVIDC
541 IRGLGEKGVF AAEIMLSCGT NPGARNEVAV RALLAYRELT GEVLEKQAE T KILATFKNVK
601 NSF EIRLTCF HLLMSKN IEM PVIAEILRPV FEGPEQSALK AHIVEDLRTQ LKLRGTEYCS
661 LHQAVADRVL ECIKNKWDI GVAYAKLDAK AIERKSEITR EIFIPYLNAR LNCTVKTSLV
721 YTKENAILPV IAKIAVIANI EGK DVTLVEA ALDIVGLKPF LDRLFGENFT YSEFLMKLMN
781 TPMSEINSFT RENSALRLLG EGRYNYLIN LFRHQTPLYI KLLGYELNLQ DLMNFESIR
841 MTLANIWKIV DTLEGGFEHE AFGAVRPLMI QHAVPTCLGA PIVSSIDISY VFANKMNLKL
901 NIKLLFVFN EEAVFDVTPS IYGTAITTRT ILPQFCCKSG TEMEVTVGHN SAIQCNMHT
961 PSGIRMVIEP KPGKSEILYI KVKRSLIGET GHEPKATTCH QIRWENLSSF QYCYQPVSKS
1021 GLAYELFVEN EEHTEYNVAI SMEGIAQKKA YTKELNINCT VRGRATSEME QAIESTKFTY
1081 IPAENEVRCS IISDVLKWKV AANYMIYRME GNARGCFVSL NATGLNDLQM MYKNKFMILP
1141 AKENDYIEG ASEWVSGSLN GGYMSGKCV EGTEGGNVTR TTDLRVYDKK EPRVSMIVSS
1201 LIVKKIAQTA QIMPGYESRL LVSGAWIPIY KKIEMMMVTM DDARFEKVM AIRGYFAAGE
1261 TMGPHFYMHR VTGTWKAEGS EEEYAASMYAT SNFFHIENSI AYKADGIVTY SKCSFPPEEI
1321 VCGKDMAVSP CVSPCTCEAR TGGSCRCESK CNNGAYVEME WNTVADEKN RNYSCKIGYN
1381 LWNPELREYS YKKAIASYVN YRECKYCHSF EVTHPKIEIR SITRRSPLEH EKWMKVHYSL
1441 LSYITLYPEV TYFIINHIKN EYFQVGFKNV PINTKTEVTG YKCEGAFFDN LGECNVNEN
1501 KYSRCKARCE FNLPSIDTSM NTTALFSSSS RPISLDFGIN MVYATLHYDL DGSFTLNERD
1561 RMDCTLKAKY EVYPGEYYEA TAVTRMMNYG SKYNGEGSYT TTRVGAEESQ TVKYSLLSNM
1621 EDSLRYFVVK EICPESETEE PCMSFSINRD GKWLKYDRKL EDNLHDMITV DSNSEGYKLE
1681 VKMAKEIGMK LKSFRVDLGL ENHYGLNIES EFCNISCWYN AEQGLIAKSN VNTNLINYTM
1741 DATVTSAAVK YNILYNTVEN RGMRMESTMD MKFAIFNAEN PLEIDYRVGI KPGSFGCNLN
1801 MPDLRCMLDI SVEDRLPVER GLKYVLEARV RPQKMIIVNL TLPLGEDSVE ITDITVGYES
1861 SVDNR LASAY VENINLWRH ACR AETTVF TGCCKINSEK ILVNIADGQR SICVADIDFG
1921 YKDPNKHVEL LLNTTMGKLD ILFNVKKEAK NWMMSKCEI SMVDYVTERM TPVFKIAIEQ
1981 MIAETQPSAN LPDYIFSIMI AHDMHMLTIP KNINVTSSRV AQGAR SIGET IAVVDGKIVT
2041 HATGNLIGCH ARFEAFAGYS FCMLPHTDVA MVMEIPLFNS YDHVTCIKTG DSWKFDWISN
2101 ATFFPGYALDM DDHFIITSEG DIWKFDYSYR DSIRNAPDRG SKMNCKFDLK YGHCLTQSIF
2161 GINVCLPSTI SIENADVTSI GISELLYAYL PMEFIEFKDI RLQNCMDYA CSIRGDVVDY
2221 TLKSILR GPS LASPVDVSMK AAFAPNNFEC ATTVMYEDSK FSGWNPETW GMITKTMDS
2281 AWYNSNLEIT SPAFMESML AFALKTKGAA HDIIPIDINV HYKANGIWI AKQFCR TASW
2341 EVELNKEAEA YYCKLGCKEY SLLNQTVYMT TTARGRATEC ALAWKSDYV CTKKFAVEGW
2401 MLEGKRLAVH FPKOECGLEA EYVLNGNSRS CNARIYSREH AEVRCETTEM TAERSFGMMK
2461 CNKQAEETGMV NIAIVPVKMS DFPFLRK DSV YDKL FVTRS ASYVYKTISY DEEALAKDCQ
2521 ETFNCTDQEA CKAMSRSLKT IVSACWKELN RIAGAKIYYL TKPELFAYTI DKWVPGLSNI
2581 PKLSSMMSLF TASERGEITI AHWSEFEPYVE AHVGVMTDKT NAFVLHVKAS SEKYSWMDGE
2641 IHLVSMEMEN HTAVNFTHTV YEAMSTIIFD VTESSFILRE VDVSLRGKGV TMKTSGLMQD
2701 GRQTIITMTLW EGKTVEYTCL LKTVPNTWKG SEMRCFEGTS EKEVSGSIKL KMSKITFEFS
2761 IDAVLERLFN IENENTRIHI RSTLLNLVKL ATDSHTIEPV NRVS DIAWRS VOYASAWSIH
2821 EAAKMISTTS EMYQIISKFT RNLYNLEPNI GETYERIVEY VGEINLYPEI EKIVINMLTP
2881 LMEFLDRILE GSVSMKFNVE GEELIVEMAL ISAR YPFLNC NQVIRLRQHG WNNLTAFAVH
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3001 DQYFCCKGGKI SAASPVLFHF CFKEFEGTEIP ANPPASSLIA YWDVAIEDVP SIYGSVTGLV
3061 RCVTRLMRVL NACYEDPSTI NELLKTYHV HDEKIRARLS KTITESTCRKW WNEVITSTEG
3121 VLNPEVNKYI KKEGLSVTTV TENLKSYSYD SLYNSLIAEV REPRGAVINI ADLSMTGDIA
3181 SVLFSYSAPI VHYGTGIIIM TEVSSSFNAR RLPARSDRAL MLVTRSERLP ILNMEMEKKV
3241 IPDGMINASI SNSLMYSYVL CDIEGALIMP SRAMIGLHHM TESTVEIVFW PEDGTRNPPI
3301 ISCIFGVENR HCCDARFESI VMSTVKCFPY EHGRGAEVV AKCEISPVEI GTSGAMIVYE
3361 IATGKVDQNR LVDRVLEETC NIKSPEIRKN VITTCERALT TIADYCRDEL INIAKFSNDI
3421 MNATYSHLLE GLVNMFDWSS IVRR AEGIN VNYLYDLVKD CMDAVVELCS QYSGGVYDVL
3481 EYLYLAGRSL NEICFNFTY MNESYSTYSL YEWMLQMVAN TATAR NCNFG VISTTEYEQA
3541 VTFNNNFYNL PKRVRECDYL LAGDIATNTF SVVLSKNNII INLPKGLSLV DPQMOMYEMR
3601 GSRGEKEYEIT LPHFDGHVRC IRTAEHLTCQ TPHVKVIAQA RNGRRFMYST HVAETVCNKA
3661 RGLMGIGGDT SIVPKWMMN GKVASTYKEF INSYSTNAC LIETIPVIPA IEPMPCKTF
3721 FNSKELNKGV PALHAVLLEA CESVATNTEE ACIYANMYVQ ESLNSGYRAE INPECAVCKN
3781 QOMRAEIERV DVTLMIALSG NTHATRL EEV VTAVERNANT ERKHYNIRYI TFGGRGEMHH
3841 PYFSVPSGRL VIPAEQPWTL PRFEFNGMKP TIPMIKHCEI FAYRNSKHAV EGVANMFLFV
3901 MPEEMEIDEL IKLPCVENLE KDLAMSYVYI PNACETKGAH ARSPYGVRL VTKEEICAR
3961 PEALATDIAN PYYGRSTTCT CTMEGPFPGM YSDNCKIVA

Figure S5. Vitellogenin fragments were detected in the 120-kDa band via SDS–PAGE.
A 120-kDa band in the SDS–PAGE gel was removed from the gel and subjected to reduced carboxymethylation, trypsin/Lys-C digestion, and LC–MS analysis. The green highlighted sequences were identified as *H. roretzi* vitellogenin fragments (S367.g04226). Sixty-two peptides were identified, which covered 22% of the total sequence of vitellogenin.

Table S1. LC–MS analysis of the 120-kDa protein, which newly appeared after incubation with the isolated VC and sperm extracts *

Checked	Accession	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	# Aas	MW [kDa]	calc. pI	Score Sequest HT: Sequest HT	# Peptides (by Search Engine): Sequest HT	# Protein Groups	Annotation
TRUE	Harore.CG.MTP2014.S563.g04764.01.p	62	57	1058	57	1050	119.2	7.72	3151.29	57	1	2-Oxoglutarate dehydrogenase-like
TRUE	Harore.CG.MTP2014.S367.g04226.01.p	22	62	498	62	3999	453.5	6.24	1503.98	62	1	Vitellogen, open beta-sheet, Lipid transporter
TRUE	Harore.CG.MTP2014.S135.g10885.02.p	49	37	283	37	1029	114.8	6.8	899.97	37	1	
TRUE	Harore.CG.MTP2014.S647.g10783.01.p	36	29	131	29	1096	119.1	5.8	457.04	29	1	Ankyrin repeat-containing domain superfamily, Ser/Thr-protein phosphatase-6
TRUE	Harore.CG.MTP2014.S2.g03075.01.p	39	31	119	31	1150	129.3	6.37	437.44	31	1	Creatine kinase M-type
TRUE	Harore.CG.MTP2014.S386.g03899.01.p	44	16	95	2	510	57.3	5.06	314.24	16	1	
TRUE	Harore.CG.MTP2014.S336.g01836.01.p	48	16	92	1	467	52.4	4.91	303.59	16	1	
TRUE	Harore.CG.MTP2014.S31.g07310.04.p	36	28	93	0	888	103.5	6.07	299.34	28	1	
TRUE	Harore.CG.MTP2014.S34.g13706.01.p	36	26	97	26	977	111	8.03	288.61	26	1	
TRUE	Harore.CG.MTP2014.S2.g00517.01.p	47	15	81	2	477	52.9	5.11	264.97	15	1	
TRUE	Harore.CG.MTP2014.S35.g03177.01.p	41	13	78	2	446	50.1	4.82	245.01	13	1	
TRUE	Harore.CG.MTP2014.S35.g10317.01.p	47	14	73	3	448	50.3	4.79	241.56	14	1	
TRUE	Harore.CG.MTP2014.S31.g15882.01.p	41	29	81	29	914	105.1	5.31	240.91	29	1	
TRUE	Harore.CG.MTP2014.S184.g10971.01.p	42	13	73	5	453	50.3	5.07	236.65	13	1	
TRUE	Harore.CG.MTP2014.S1.g00695.01.p	16	30	70	30	2619	291	5.08	217.94	30	1	Otoancorin, proteinaceous extracellular matrix
TRUE	Harore.CG.MTP2014.S60.g15555.01.p	30	19	63	19	968	110.4	5.55	214.94	19	1	
TRUE	Harore.CG.MTP2014.S35.g05771.01.p	40	12	63	1	448	50.2	4.79	211.34	12	1	
TRUE	Harore.CG.MTP2014.S31.g07310.01.p	41	19	60	1	596	70	6.28	199.16	19	1	
TRUE	Harore.CG.MTP2014.S13.g15972.01.p	21	20	54	20	1421	161.5	5.82	195.8	20	1	Clathrin heavy chain, N-terminal
TRUE	Harore.CG.MTP2014.S42.g14417.02.p	41	12	60	1	451	50.1	5.06	194.97	12	1	
TRUE	Harore.CG.MTP2014.S422.g05364.01.p	40	12	60	4	400	44.4	5.3	186.04	12	1	
TRUE	Harore.CG.MTP2014.S31.g07310.02.p	42	19	58	1	586	68.9	5.96	184.03	19	1	
TRUE	Harore.CG.MTP2014.S18.g10655.02.p	49	16	49	16	518	55.7	5.68	181.73	16	1	
TRUE	Harore.CG.MTP2014.S250.g09381.01.p	39	11	60	4	408	45.6	6.2	180.35	11	1	
TRUE	Harore.CG.MTP2014.S41.g05014.01.p	24	16	51	16	846	94.2	7.43	179.18	16	1	
TRUE	Harore.CG.MTP2014.S70.g04342.01.p	20	19	49	19	1265	148.2	5.25	167.9	19	1	Myosin head, motor domain
TRUE	Harore.CG.MTP2014.S669.g14984.01.p	31	8	42	8	442	48.3	5.67	153.96	8	1	
TRUE	Harore.CG.MTP2014.S31.g10104.02.p	24	10	45	10	467	51.5	9.28	141.57	10	1	
TRUE	Harore.CG.MTP2014.S41.g10119.01.p	18	11	39	11	1118	126.1	8.59	138.94	11	1	Haem peroxidase domain superfamily, animal type
TRUE	Harore.CG.MTP2014.S746.g04281.01.p	26	12	41	12	650	71.7	5.05	138.04	12	1	
TRUE	Harore.CG.MTP2014.S149.g09374.01.p	18	12	37	12	935	103.3	5.22	131.48	12	1	
TRUE	Harore.CG.MTP2014.S429.g10994.01.p	29	8	34	8	489	54	8.57	127.39	8	1	
TRUE	Harore.CG.MTP2014.S31.g07310.05.p	35	11	38	1	320	36.5	6.96	126.84	11	1	
TRUE	Harore.CG.MTP2014.S528.g00963.01.p	27	14	37	10	657	71.7	5.34	124.9	14	1	
TRUE	Harore.CG.MTP2014.S4.g08850.01.p	27	8	42	1	378	42.2	5.25	123.58	8	1	

TRUE	Harore.CG.MTP2014.S71.g01621.02.p	16	7	39	2	547	59.6	8.28	121.18	7	1	
TRUE	Harore.CG.MTP2014.S237.g03443.01.p	16	15	38	15	1503	169.7	6.43	118.27	15	1	Glycoside hydrolase superfamily
TRUE	Harore.CG.MTP2014.S49.g15467.01.p	17	7	46	1	453	50.6	4.83	118.24	7	1	
TRUE	Harore.CG.MTP2014.S71.g01621.01.p	26	7	35	2	367	39.8	7.59	114.43	7	1	
TRUE	Harore.CG.MTP2014.S156.g08353.02.p	20	14	38	14	996	113.9	5.57	105.48	14	1	
TRUE	Harore.CG.MTP2014.S764.g05199.01.p	12	10	29	10	1192	130.9	5.82	101.2	10	1	P-type ATPase, cytoplasmic domain N
TRUE	Harore.CG.MTP2014.S111.g12265.01.p	25	13	33	13	873	99	5.92	100.4	13	1	
TRUE	Harore.CG.MTP2014.S44.g11791.02.p	7	15	30	15	2668	293.1	7.02	98.18	15	1	HEAT type 2, Stalled ribosome sensor GCN1
TRUE	Harore.CG.MTP2014.S289.g03473.01.p	22	10	33	10	578	63.3	8.72	92.16	10	1	
TRUE	Harore.CG.MTP2014.S321.g06252.02.p	13	10	22	10	1278	146.3	6.74	88.42	10	1	Regulation of nuclear pre-mRNA domain-containing protein 2
TRUE	Harore.CG.MTP2014.S78.g07592.01.p	3	3	28	3	1173	127.9	7.17	86.72	3	1	EGF-like domain, Zona pellucida domain (UNKOWN)
TRUE	Harore.CG.MTP2014.S385.g09733.01.p	5	15	28	15	4558	520.4	6.37	86.54	15	1	Dynein heavy chain domain, Dynein axonemal heavy chain 8
TRUE	Harore.CG.MTP2014.S142.g09627.01.p	11	9	23	9	1262	143.7	7.39	81.53	9	1	Met/Val/Ile-tRNA synthetase, anticodon-binding, Valine-tRNA ligase
TRUE	Harore.CG.MTP2014.S3.g08671.02.p	20	13	27	13	978	110	4.98	81.41	13	1	
TRUE	Harore.CG.MTP2014.S216.g07471.01.p	6	10	21	10	2877	314.4	4.92	77.55	10	1	HrTTSP-1 (Sushi/SCR/CCP domain)
TRUE	Harore.CG.MTP2014.S98.g02137.01.p	9	13	23	13	2326	258.8	6.87	75.02	13	1	Asp/Orn carbamoyltransferase, Multifunctional protein CAD
TRUE	Harore.CG.MTP2014.S124.g10802.01.p	18	11	21	11	1026	115	6.25	73.72	11	1	
TRUE	Harore.CG.MTP2014.S10.g05616.02.p	22	8	26	8	558	61.2	7.88	71.55	8	1	
TRUE	Harore.CG.MTP2014.S614.g07251.02.p	25	9	22	9	479	52.3	8.07	69.83	9	1	
TRUE	Harore.CG.MTP2014.S430.g11250.01.p	5	14	22	14	4786	549.4	6.89	69.42	14	1	Dynein heavy chain, Cytoplasmic dynein 1 heavy chain 1
TRUE	Harore.CG.MTP2014.S113.g02269.02.p	16	10	21	10	895	102.8	4.74	67.69	10	1	
TRUE	Harore.CG.MTP2014.S591.g10684.01.p	21	8	20	8	570	63.3	5.33	67.48	8	1	
TRUE	Harore.CG.MTP2014.S151.g00081.02.p	28	7	18	7	377	41.2	7.96	66.16	7	1	
TRUE	Harore.CG.MTP2014.S458.g12264.01.p	16	5	18	5	519	58.1	7.36	65.74	5	1	
TRUE	Harore.CG.MTP2014.S142.g16064.01.p	17	9	18	9	858	96.7	6.62	62.98	9	1	
TRUE	Harore.CG.MTP2014.S105.g01421.02.p	12	7	21	7	880	97.4	5.05	62.13	7	1	
TRUE	Harore.CG.MTP2014.S110.g15936.02.p	15	7	24	7	765	85	5.52	59.82	7	1	
TRUE	Harore.CG.MTP2014.S354.g07111.01.p	3	9	18	9	4314	495.6	6.18	59.67	9	1	P-loop containing nucleoside triphosphate hydrolase, Dynein heavy chain,
TRUE	Harore.CG.MTP2014.S131.g04501.01.p	7	11	20	11	2506	283.2	7.8	57.22	11	1	Metalloendopeptidase of the mitochondrial matrix , Peptidase M16, C-terminal
TRUE	Harore.CG.MTP2014.S36.g13871.01.p	13	8	20	8	758	87.5	5.02	57.07	8	1	
TRUE	Harore.CG.MTP2014.S298.g08896.01.p	8	8	16	8	1969	220.3	5.81	55.56	8	1	P-loop containing nucleoside triphosphate hydrolase, ABC transporter-like
TRUE	Harore.CG.MTP2014.S261.g08345.01.p	12	6	14	6	696	77	5.9	54.99	6	1	
TRUE	Harore.CG.MTP2014.S12.g12746.01.p	10	7	19	7	902	99	7.08	53.98	7	1	
TRUE	Harore.CG.MTP2014.S44.g01906.01.p	6	5	16	5	1346	150.4	6.96	53.91	5	1	Splicing factor 3B subunit 1
TRUE	Harore.CG.MTP2014.S340.g05164.01.p	13	5	14	5	653	73.2	8.46	52.36	5	1	

TRUE	Harore.CG.MTP2014 .S95.g12701.01.p	7	5	14	5	1230	135.4	5.88	50.51	5	1	C-type lectin-like/link domain superfamily, Zona pellucida domain
TRUE	Harore.CG.MTP2014 .S429.g10468.02.p	16	6	16	6	453	50.2	7.85	48.42	6	1	
TRUE	Harore.CG.MTP2014 .S472.g12698.01.p	11	3	14	3	553	60.8	6.86	47.09	3	1	
TRUE	Harore.CG.MTP2014 .S27.g15762.01.p	11	5	12	5	722	81.1	4.91	46.36	5	1	
TRUE	Harore.CG.MTP2014 .S1.g03782.02.p	11	5	12	5	778	84.5	6.27	45.86	5	1	
TRUE	Harore.CG.MTP2014 .S79.g05222.01.p	18	6	16	6	366	43.2	5.4	44.15	6	1	
TRUE	Harore.CG.MTP2014 .S109.g10097.01.p	16	5	11	5	377	42.4	8.16	44.03	5	1	
TRUE	Harore.CG.MTP2014 .S147.g10281.01.p	19	8	14	8	734	80.3	6.43	43.2	8	1	
TRUE	Harore.CG.MTP2014 .S221.g10564.01.p	17	5	12	5	470	51.8	8.41	41.66	5	1	
TRUE	Harore.CG.MTP2014 .S708.g09756.01.p	18	7	13	7	634	68.7	7.83	41.3	7	1	
TRUE	Harore.CG.MTP2014 .S140.g03403.01.p	10	7	13	7	1050	115.8	5.99	40.86	7	1	
TRUE	Harore.CG.MTP2014 .S1580.g12691.01.p	12	6	11	3	626	68.9	5.27	38.64	6	1	
TRUE	Harore.CG.MTP2014 .S4.g10388.01.p	10	7	10	7	1264	135.6	6.24	37.19	7	1	13 EGF-like, conserved site, Zona pellucida domain
TRUE	Harore.CG.MTP2014 .S1108.g06775.01.p	10	5	12	4	681	75.1	6.07	36.31	5	1	
TRUE	Harore.CG.MTP2014 .S30.g12434.01.p	13	5	11	5	539	59.1	6.02	36.2	5	1	
TRUE	Harore.CG.MTP2014 .S107.g13256.01.p	9	4	11	0	636	70.1	5.53	35.89	4	1	
TRUE	Harore.CG.MTP2014 .S67.g03499.01.p	13	4	11	4	545	59.2	6.64	35.79	4	1	
TRUE	Harore.CG.MTP2014 .S13.g00843.01.p	16	5	11	5	539	58.7	6.76	35.74	5	1	
TRUE	Harore.CG.MTP2014 .S41.g15878.01.p	14	4	10	4	536	57.9	7.85	35.06	4	1	
TRUE	Harore.CG.MTP2014 .S561.g05685.01.p	22	3	20	3	176	20.1	9.67	34.73	3	1	
TRUE	Harore.CG.MTP2014 .S23.g05715.01.p	13	6	10	6	712	79.3	8.25	34.65	6	1	
TRUE	Harore.CG.MTP2014 .S60.g02316.01.p	8	5	9	5	1066	119.7	6.4	34.44	5	1	Ubiquitin/SUMO-activating enzyme E1
TRUE	Harore.CG.MTP2014 .S316.g06125.01.p	7	2	9	2	315	35.8	6.34	33.76	2	1	
TRUE	Harore.CG.MTP2014 .S267.g12320.01.p	22	3	10	3	234	26.9	8.72	33.1	3	1	
TRUE	Harore.CG.MTP2014 .S40.g01801.01.p	18	6	11	6	465	51.8	8.47	32.79	6	1	
TRUE	Harore.CG.MTP2014 .S67.g02593.01.p	6	4	11	4	937	105.9	8.6	32.76	4	1	
TRUE	Harore.CG.MTP2014 .S113.g07932.02.p	14	4	9	4	383	43.1	4.64	32.54	4	1	
TRUE	Harore.CG.MTP2014 .S99.g00520.01.p	8	6	9	6	1101	125.8	6.67	32.51	6	1	Importin-beta, N-terminal domain, Armadillo-like helical, Exportin-7
TRUE	Harore.CG.MTP2014 .S6.g03382.01.p	14	6	10	6	738	81.2	9.22	31.75	6	1	
TRUE	Harore.CG.MTP2014 .S15.g01108.01.p	6	5	10	5	1249	137.7	6.28	31.64	5	1	Aldolase-type TIM barrel, Carbamoyl- phosphate synthetase large subunit-like, Pyruvate carboxylase
TRUE	Harore.CG.MTP2014 .S196.g04933.01.p	1	3	9	3	4602	524.9	5.58	31.38	3	1	Dynein axonemal heavy chain, ATPase, dynein-related, AAA domain, LDL receptor class A repeat
TRUE	Harore.CG.MTP2014 .S790.g08811.02.p	10	6	9	6	936	106.5	7.01	30.15	6	1	
TRUE	Harore.CG.MTP2014 .S75.g01289.01.p	2	7	16	7	4899	553.1	5.8	29.91	7	1	von Willebrand factor, type D domain, Vitellinogen, open beta-sheet
TRUE	Harore.CG.MTP2014 .S148.g02958.01.p	19	6	8	6	604	67.2	5.3	28.83	6	1	
TRUE	Harore.CG.MTP2014 .S445.g03801.01.p	6	5	9	5	1185	133	6.62	28.71	5	1	

TRUE	Harore.CG.MTP2014 .S1.g13663.01.p	3	5	9	5	2144	244.1	5.99	28.16	5	1	AAA+ ATPase domain, Helicase superfamily
TRUE	Harore.CG.MTP2014 .S181.g12829.01.p	7	1	17	1	349	40.3	9.55	28.08	1	1	
TRUE	Harore.CG.MTP2014 .S28.g00713.01.p	7	5	9	5	1098	120.8	7.42	27.74	5	1	Citrate synthase-like, small alpha subdomain, ATP-citrate synthase
TRUE	Harore.CG.MTP2014 .S6.g04858.01.p	9	6	8	6	918	103.9	5.1	27.52	6	1	
TRUE	Harore.CG.MTP2014 .S354.g09366.03.p	12	4	7	4	566	62.1	8.32	26.99	4	1	
TRUE	Harore.CG.MTP2014 .S331.g12301.01.p	23	3	9	3	220	23.5	5.24	26.62	3	1	
TRUE	Harore.CG.MTP2014 .S147.g08883.01.p	8	5	8	5	926	103.6	5.55	26.48	5	1	
TRUE	Harore.CG.MTP2014 .S134.g12112.01.p	5	5	7	5	1706	189.9	6.43	26.24	5	1	von Willebrand factor, type A, Inter-alpha-trypsin inhibitor heavy chain H4
TRUE	Harore.CG.MTP2014 .S353.g10047.01.p	11	4	7	4	552	59.1	8.05	26.13	4	1	
TRUE	Harore.CG.MTP2014 .S308.g08259.01.p	10	3	7	3	526	58.7	5.35	25.64	3	1	
TRUE	Harore.CG.MTP2014 .S212.g13755.01.p	10	4	8	4	689	77.7	5.88	25.63	4	1	
TRUE	Harore.CG.MTP2014 .S355.g07067.01.p	14	3	8	3	207	23.4	7.11	25.41	3	1	
TRUE	Harore.CG.MTP2014 .S627.g10954.01.p	18	5	6	5	770	84.3	8.18	25.4	5	1	
TRUE	Harore.CG.MTP2014 .S194.g10300.02.p	8	4	7	4	666	73.1	6.93	25.39	4	1	
TRUE	Harore.CG.MTP2014 .S52.g00264.02.p	6	4	10	4	977	109.5	6.23	25.26	4	1	
TRUE	Harore.CG.MTP2014 .S14.g03118.02.p	9	3	6	3	631	67.9	6.83	25.18	3	1	
TRUE	Harore.CG.MTP2014 .S16.g03171.01.p	16	5	6	5	456	50.2	6.02	24.64	5	1	
TRUE	Harore.CG.MTP2014 .S27.g01868.01.p	5	5	8	5	1550	175.3	6.01	24.59	5	1	Nucleotide-diphospho-sugar transferases
TRUE	Harore.CG.MTP2014 .S69.g04620.01.p	4	6	7	6	2344	274	8.9	24.55	6	1	
TRUE	Harore.CG.MTP2014 .S157.g00824.02.p	16	4	6	4	442	49.8	7.06	24.43	4	1	
TRUE	Harore.CG.MTP2014 .S307.g06187.01.p	2	4	7	4	2612	298.1	6.35	24.29	4	1	Centrosomin, N-terminal motif 1
TRUE	Harore.CG.MTP2014 .S472.g10985.01.p	14	4	9	4	432	48.2	7.15	24.2	4	1	
TRUE	Harore.CG.MTP2014 .S145.g05258.01.p	14	4	7	4	386	43.2	8.16	24.07	4	1	
TRUE	Harore.CG.MTP2014 .S332.g13530.02.p	11	4	6	4	553	61.6	6.76	22.47	4	1	
TRUE	Harore.CG.MTP2014 .S4.g06929.01.p	7	4	7	4	812	91.2	4.97	22.17	4	1	
TRUE	Harore.CG.MTP2014 .S13.g05237.01.p	14	2	5	2	267	30.4	4.97	22.03	2	1	
TRUE	Harore.CG.MTP2014 .S486.g04514.01.p	12	4	6	4	535	58.2	6.16	21.22	4	1	
TRUE	Harore.CG.MTP2014 .S6.g03931.01.p	15	4	7	4	475	51.2	9.11	20.97	4	1	
TRUE	Harore.CG.MTP2014 .S494.g05051.01.p	11	5	6	5	962	109	6.84	20.87	5	1	
TRUE	Harore.CG.MTP2014 .S186.g06032.01.p	24	3	6	3	160	18.2	9.91	20.67	3	1	
TRUE	Harore.CG.MTP2014 .S123.g15970.01.p	11	4	7	4	541	59.4	6.74	20.29	4	1	
TRUE	Harore.CG.MTP2014 .S645.g07698.01.p	5	4	6	4	1139	125.6	4.44	20.18	4	1	SIT4 phosphatase-associated protein family
TRUE	Harore.CG.MTP2014 .S383.g06004.01.p	11	3	6	3	444	49.9	8.18	19.91	3	1	
TRUE	Harore.CG.MTP2014 .S153.g11623.01.p	7	3	4	3	469	53.4	8.22	19.45	3	1	
TRUE	Harore.CG.MTP2014 .S330.g00890.01.p	7	3	6	2	585	66	7.05	19.38	3	1	
TRUE	Harore.CG.MTP2014 .S136.g10424.01.p	3	3	5	3	1763	201.2	6.1	18.73	3	1	CH-like domain in sperm protein, Sperm flagellar protein 2
TRUE	Harore.CG.MTP2014 .S371.g01082.01.p	12	3	5	3	400	43.6	6.7	17.83	3	1	

TRUE	Harore.CG.MTP2014.S75.g08394.01.p	8	5	5	5	1029	111.6	7.12	17.18	5	1	
TRUE	Harore.CG.MTP2014.S80.g01333.01.p	5	4	7	4	1272	143.3	7.4	17.01	4	1	WD40 repeat, Coatomer subunit alpha
TRUE	Harore.CG.MTP2014.S157.g02180.01.p	8	4	7	4	811	90.2	8.47	16.86	4	1	
TRUE	Harore.CG.MTP2014.S450.g08886.01.p	14	3	5	3	265	30.3	4.88	16.79	3	1	
TRUE	Harore.CG.MTP2014.S16.g10824.01.p	4	5	5	5	1686	190	6.04	16.73	5	1	
TRUE	Harore.CG.MTP2014.S79.g09933.01.p	13	3	6	3	336	35.6	9.06	16.54	3	1	
TRUE	Harore.CG.MTP2014.S77.g11516.01.p	16	4	6	4	506	54.8	7.36	16.42	4	1	
TRUE	Harore.CG.MTP2014.S280.g07136.01.p	11	3	5	3	538	60.5	6.4	16.29	3	1	
TRUE	Harore.CG.MTP2014.S43.g08812.01.p	1	1	6	1	1780	201.5	5.39	16.2	1	1	IQ motif, EF-hand binding site, Leu-rich repeat domain superfamily
TRUE	Harore.CG.MTP2014.S214.g10227.01.p	6	2	5	2	539	59.3	7.84	16.09	2	1	
TRUE	Harore.CG.MTP2014.S465.g09135.01.p	2	4	6	4	2610	290.7	6.38	16.07	4	1	Ankyrin repeat-containing domain superfamily
TRUE	Harore.CG.MTP2014.S6.g10660.01.p	17	3	6	3	307	34.1	8.63	15.95	3	1	
TRUE	Harore.CG.MTP2014.S19.g14776.01.p	14	3	4	3	344	35.8	7.96	15.8	3	1	
TRUE	Harore.CG.MTP2014.S186.g08439.01.p	4	3	5	3	763	86	6.07	15.57	3	1	
TRUE	Harore.CG.MTP2014.S28.g12475.01.p	2	2	5	2	1178	130.9	5.33	15.46	2	1	WD40/YVTN repeat-like-containing domain superfamily
TRUE	Harore.CG.MTP2014.S147.g10997.01.p	3	1	6	1	517	54.7	7.88	15.23	1	1	
TRUE	Harore.CG.MTP2014.S583.g05089.01.p	7	4	4	4	875	98.6	5.45	15.14	4	1	
TRUE	Harore.CG.MTP2014.S46.g04753.02.p	6	2	4	2	544	59.6	6.67	15.12	2	1	
TRUE	Harore.CG.MTP2014.S571.g10074.01.p	5	3	4	3	916	102.6	6.74	14.8	3	1	
TRUE	Harore.CG.MTP2014.S391.g06117.01.p	9	3	5	3	558	60	6.89	14.77	3	1	
TRUE	Harore.CG.MTP2014.S67.g10005.01.p	3	3	5	3	1206	136.6	9.04	14.74	3	1	Myosin head, motor domain
TRUE	Harore.CG.MTP2014.S42.g05517.01.p	6	3	4	3	863	96	6.33	14.68	3	1	
TRUE	Harore.CG.MTP2014.S333.g10767.03.p	10	3	5	3	434	48.5	6.04	14.3	3	1	
TRUE	Harore.CG.MTP2014.S423.g09913.01.p	7	3	5	3	625	68.3	6.7	14.07	3	1	
TRUE	Harore.CG.MTP2014.S18.g02500.01.p	5	3	4	3	1056	121.1	4.88	14.03	3	1	Armadillo-like helical, Importin-beta, N-terminal domain
TRUE	Harore.CG.MTP2014.S261.g06577.01.p	4	2	7	2	813	91.1	6.28	13.82	2	1	HrTast3c
TRUE	Harore.CG.MTP2014.S1111.g02890.01.p	4	3	4	3	1037	110.9	4.48	13.69	3	1	EGF-like, conserved site, Zona pellucida domain
TRUE	Harore.CG.MTP2014.S195.g02243.01.p	8	3	4	3	587	67.3	6.68	13.51	3	1	
TRUE	Harore.CG.MTP2014.S847.g02600.01.p	10	2	4	2	274	30.2	9.64	13.47	2	1	
TRUE	Harore.CG.MTP2014.S103.g09461.02.p	4	1	3	1	508	56.1	5.48	13.24	1	1	
TRUE	Harore.CG.MTP2014.S156.g05923.01.p	5	2	4	2	533	59.1	8.16	13.13	2	1	
TRUE	Harore.CG.MTP2014.S30.g10399.01.p	6	2	4	2	552	59.1	7.39	13.12	2	1	
TRUE	Harore.CG.MTP2014.S224.g01430.01.p	7	3	4	3	612	69.6	6.21	12.63	3	1	
TRUE	Harore.CG.MTP2014.S67.g07046.01.p	7	3	4	3	508	55.3	6.92	12.51	3	1	
TRUE	Harore.CG.MTP2014.S831.g04134.01.p	3	2	4	2	826	94.7	6.2	12.49	2	1	
TRUE	Harore.CG.MTP2014.S767.g02331.01.p	6	1	4	1	225	25.4	10.67	12.24	1	1	
TRUE	Harore.CG.MTP2014.S525.g03800.01.p	2	3	3	3	2942	325.1	5.59	12.16	3	1	P-loop containing nucleoside triphosphate hydrolase, Immunoglobulin-like fold

TRUE	Harore.CG.MTP2014.S4.g01451.01.p	2	1	4	1	827	92.9	5.19	12.13	1	1	
TRUE	Harore.CG.MTP2014.S23.g12563.01.p	5	2	5	2	540	60.1	7.69	12.1	2	1	
TRUE	Harore.CG.MTP2014.S110.g10196.01.p	6	1	3	1	265	29.6	5.45	11.96	1	1	
TRUE	Harore.CG.MTP2014.S746.g13749.01.p	5	3	3	3	892	102.1	6.65	11.9	3	1	
TRUE	Harore.CG.MTP2014.S108.g02133.01.p	9	3	3	3	531	58.9	7.05	11.84	3	1	
TRUE	Harore.CG.MTP2014.S162.g10534.01.p	7	3	5	3	550	59.7	6.06	11.69	3	1	
TRUE	Harore.CG.MTP2014.S64.g10372.01.p	19	2	4	2	171	19.8	10.58	11.47	2	1	
TRUE	Harore.CG.MTP2014.S47.g10422.01.p	7	2	3	2	471	51.3	7.87	11.44	2	1	
TRUE	Harore.CG.MTP2014.S35.g01689.01.p	5	2	3	2	708	80.1	7.17	11.44	2	1	
TRUE	Harore.CG.MTP2014.S30.g03976.01.p	9	2	7	2	268	30.4	9.77	11.43	2	1	
TRUE	Harore.CG.MTP2014.S103.g12155.01.p	9	2	3	2	302	34.1	6.89	11.42	2	1	
TRUE	Harore.CG.MTP2014.S41.g06549.01.p	4	2	6	2	661	72.8	4.87	11.38	2	1	HrTast2c
TRUE	Harore.CG.MTP2014.S50.g04071.01.p	11	3	3	3	421	48.6	6.99	11.17	3	1	
TRUE	Harore.CG.MTP2014.S236.g11437.03.p	3	2	3	2	1310	146.2	5.86	11.13	2	1	Armadillo-like helical, TATA-binding protein interacting (TIP20)
TRUE	Harore.CG.MTP2014.S46.g14756.02.p	4	2	4	2	575	62.8	6.9	11.1	2	1	
TRUE	Harore.CG.MTP2014.S523.g09804.01.p	2	2	3	2	1466	167.6	8.09	11.09	2	1	Sushi/SCR/CCP superfamily, Zona pellucida domain
TRUE	Harore.CG.MTP2014.S5.g14725.01.p	12	2	3	2	244	28.7	10.35	10.87	2	1	
TRUE	Harore.CG.MTP2014.S205.g08933.01.p	7	2	4	2	345	38.3	7.8	10.72	2	1	
TRUE	Harore.CG.MTP2014.S100.g05627.01.p	6	2	3	2	556	62.8	6.01	10.64	2	1	
TRUE	Harore.CG.MTP2014.S23.g02817.02.p	5	1	2	1	348	40.5	5.05	10.19	1	1	
TRUE	Harore.CG.MTP2014.S6.g12905.01.p	4	2	3	2	695	76.1	6.05	10.13	2	1	
TRUE	Harore.CG.MTP2014.S7.g05985.02.p	7	2	3	2	449	47.9	8.15	10.01	2	1	
TRUE	Harore.CG.MTP2014.S92.g13373.01.p	7	3	6	3	742	82.4	7.24	10	3	1	
TRUE	Harore.CG.MTP2014.S621.g13981.01.p	10	2	3	2	327	35.8	8.02	9.97	2	1	
TRUE	Harore.CG.MTP2014.S36.g05846.01.p	7	2	5	2	388	42.8	8.62	9.9	2	1	
TRUE	Harore.CG.MTP2014.S298.g05232.01.p	4	2	3	2	1131	124.3	7.02	9.84	2	1	Zinc finger, Sec23/Sec24-type, von Willebrand factor A-like domain superfamily
TRUE	Harore.CG.MTP2014.S85.g11614.01.p	5	1	2	1	408	44.6	5.26	9.77	1	1	
TRUE	Harore.CG.MTP2014.S22.g06725.01.p	6	3	3	3	736	85.2	7.53	9.63	3	1	
TRUE	Harore.CG.MTP2014.S15.g13541.01.p	7	2	3	2	412	45.4	7.17	9.57	2	1	
TRUE	Harore.CG.MTP2014.S90.g01676.01.p	21	2	4	2	103	11.3	11.36	9.55	2	1	
TRUE	Harore.CG.MTP2014.S150.g09769.01.p	4	2	3	2	603	66.4	7.01	9.4	2	1	
TRUE	Harore.CG.MTP2014.S43.g09856.01.p	6	2	4	2	708	79.6	6.79	9.32	2	1	
TRUE	Harore.CG.MTP2014.S413.g15056.01.p	15	2	3	2	155	18.1	10.76	9.28	2	1	
TRUE	Harore.CG.MTP2014.S223.g11286.01.p	12	2	3	2	221	24.6	7.3	9.06	2	1	
TRUE	Harore.CG.MTP2014.S82.g02718.01.p	7	1	3	1	248	28.3	10.43	9.04	1	1	
TRUE	Harore.CG.MTP2014.S205.g08426.01.p	11	1	2	1	137	15.6	11.15	8.9	1	1	
TRUE	Harore.CG.MTP2014.S110.g06301.01.p	4	2	3	2	756	85.5	6.84	8.83	2	1	

TRUE	Harore.CG.MTP2014 .S502.g15320.01.p	6	2	3	2	482	54	8.53	8.69	2	1	
TRUE	Harore.CG.MTP2014 .S30.g01378.01.p	1	2	2	2	2792	320.8	5.24	8.65	2	1	CH domain superfamily, Calponin homology domain
TRUE	Harore.CG.MTP2014 .S106.g01066.01.p	9	1	3	1	136	16	10.92	8.58	1	1	
TRUE	Harore.CG.MTP2014 .S84.g13805.01.p	7	2	2	2	512	58.5	5.4	8.53	2	1	
TRUE	Harore.CG.MTP2014 .S149.g13454.01.p	1	2	2	2	2701	300.8	7.72	8.42	2	1	CCR4-Not complex component, Not1, C-terminal, MIF4G-like domain superfamily
TRUE	Harore.CG.MTP2014 .S24.g01199.01.p	1	2	3	2	3607	408.3	5.38	8.32	2	1	NACHT nucleoside triphosphatase, von Willebrand factor A-like domain superfamily
TRUE	Harore.CG.MTP2014 .S383.g09914.01.p	26	2	2	2	116	13	9.07	7.97	2	1	
TRUE	Harore.CG.MTP2014 .S445.g09290.01.p	3	1	2	1	467	53.2	5.68	7.93	1	1	
TRUE	Harore.CG.MTP2014 .S95.g08963.01.p	6	2	2	2	522	59.5	8.24	7.92	2	1	
TRUE	Harore.CG.MTP2014 .S46.g10726.01.p	20	2	2	2	140	15.7	7.4	7.89	2	1	
TRUE	Harore.CG.MTP2014 .S1007.g12818.01.p	2	1	3	1	779	86.4	5.92	7.87	1	1	
TRUE	Harore.CG.MTP2014 .S141.g08538.01.p	3	2	3	2	727	81	8.46	7.79	2	1	
TRUE	Harore.CG.MTP2014 .S305.g10083.01.p	3	2	2	2	1147	128.1	8.19	7.77	2	1	Zona pellucida domain
TRUE	Harore.CG.MTP2014 .S737.g07016.01.p	3	1	3	1	415	46.3	10.02	7.74	1	1	
TRUE	Harore.CG.MTP2014 .S172.g06608.02.p	5	2	2	2	619	68.8	5.91	7.71	2	1	
TRUE	Harore.CG.MTP2014 .S68.g01484.01.p	8	2	3	2	596	68.2	6.74	7.4	2	1	
TRUE	Harore.CG.MTP2014 .S34.g15643.01.p	13	1	2	1	115	13.3	11.03	7.37	1	1	
TRUE	Harore.CG.MTP2014 .S140.g11429.01.p	4	1	2	1	364	40.8	5.21	7.33	1	1	
TRUE	Harore.CG.MTP2014 .S140.g01661.01.p	3	2	2	2	1193	130.5	6.87	7.31	2	1	WD40 repeat
TRUE	Harore.CG.MTP2014 .S631.g12579.01.p	3	2	2	2	1154	129.3	6.79	7.02	2	1	von Willebrand factor A-like domain superfamily
TRUE	Harore.CG.MTP2014 .S30.g01044.02.p	2	1	2	1	725	82.4	8.25	6.97	1	1	
TRUE	Harore.CG.MTP2014 .S450.g01203.01.p	6	1	2	1	261	30.3	4.75	6.94	1	1	
TRUE	Harore.CG.MTP2014 .S146.g14145.01.p	6	2	2	2	403	45.9	6.6	6.91	2	1	
TRUE	Harore.CG.MTP2014 .S56.g01213.01.p	3	2	3	2	946	105.6	6.11	6.89	2	1	
TRUE	Harore.CG.MTP2014 .S575.g02915.01.p	14	2	2	2	187	22	5.07	6.85	2	1	
TRUE	Harore.CG.MTP2014 .S71.g06759.02.p	2	1	2	1	935	100.9	7.77	6.83	1	1	
TRUE	Harore.CG.MTP2014 .S157.g15980.01.p	1	1	2	1	1289	148.3	5.1	6.71	1	1	EF-hand domain
TRUE	Harore.CG.MTP2014 .S372.g10597.01.p	5	1	3	1	369	42.2	5.64	6.71	1	1	
TRUE	Harore.CG.MTP2014 .S3.g11362.01.p	6	1	2	1	420	47.7	7.05	6.62	1	1	
TRUE	Harore.CG.MTP2014 .S101.g04847.01.p	5	1	2	1	476	52.9	6.96	6.59	1	1	
TRUE	Harore.CG.MTP2014 .S15.g10121.01.p	3	2	2	2	948	105.2	7.2	6.54	2	1	
TRUE	Harore.CG.MTP2014 .S161.g12646.01.p	2	2	2	2	1192	134.4	6.06	6.53	2	1	Six-hairpin in glycosidase-like superfamily
TRUE	Harore.CG.MTP2014 .S14.g01603.01.p	2	1	2	1	777	89	4.97	6.52	1	1	
TRUE	Harore.CG.MTP2014 .S326.g00898.01.p	1	1	2	1	1253	138.8	6.24	6.4	1	1	P-type ATPase, A domain superfamily, Cation-transporting P-type ATPase, N-terminal
TRUE	Harore.CG.MTP2014 .S127.g14166.01.p	11	1	2	1	125	13.8	8.57	6.37	1	1	
TRUE	Harore.CG.MTP2014 .S168.g02673.01.p	2	1	3	1	482	53.3	5.01	6.36	1	1	

TRUE	Harore.CG.MTP2014 .S8.g14446.01.p	10	2	2	2	326	36.7	9.74	6.35	2	1	
TRUE	Harore.CG.MTP2014 .S419.g01234.01.p	1	2	2	2	2323	261.9	6.38	6.23	2	1	WD40-repeat-containing domain superfamily, RZZ complex, subunit KNTC1/ROD, C-terminal
TRUE	Harore.CG.MTP2014 .S48.g14248.01.p	2	1	2	1	679	75.5	4.65	6.19	1	1	
TRUE	Harore.CG.MTP2014 .S304.g11637.01.p	11	1	2	1	193	22.3	10.02	6.17	1	1	
TRUE	Harore.CG.MTP2014 .S3.g13829.01.p	1	1	2	1	1184	135.1	5.72	6.16	1	1	Cysteine-rich Golgi apparatus protein 1 repeat, eukaryote
TRUE	Harore.CG.MTP2014 .S267.g11175.01.p	7	1	2	1	200	22.8	6.21	6.16	1	1	
TRUE	Harore.CG.MTP2014 .S107.g06022.01.p	1	1	2	1	1105	123.8	6.54	6.07	1	1	Armadillo-like helical, MMS19, C-terminal
TRUE	Harore.CG.MTP2014 .S832.g14609.01.p	9	2	2	2	328	37.8	6.62	6.03	2	1	
TRUE	Harore.CG.MTP2014 .S2.g09887.01.p	8	1	2	1	161	17.7	6.62	5.93	1	1	
TRUE	Harore.CG.MTP2014 .S16.g09648.03.p	4	1	2	1	492	55.5	6.48	5.9	1	1	
TRUE	Harore.CG.MTP2014 .S891.g06367.01.p	3	1	2	1	627	71.6	5.17	5.87	1	1	
TRUE	Harore.CG.MTP2014 .S374.g05972.02.p	5	2	2	2	608	68.6	7.15	5.83	2	1	
TRUE	Harore.CG.MTP2014 .S208.g09216.01.p	6	1	2	1	177	20.7	11.08	5.82	1	1	
TRUE	Harore.CG.MTP2014 .S119.g00635.01.p	1	1	2	1	3362	373.1	9.48	5.68	1	1	BAT2, N-terminal, Protein PRRC2
TRUE	Harore.CG.MTP2014 .S33.g11458.01.p	5	1	1	1	368	43.1	9.25	5.64	1	1	
TRUE	Harore.CG.MTP2014 .S90.g05849.01.p	8	1	2	1	139	15.9	10.23	5.63	1	1	
TRUE	Harore.CG.MTP2014 .S87.g03995.01.p	3	1	2	1	440	48.6	7.81	5.43	1	1	
TRUE	Harore.CG.MTP2014 .S835.g15832.01.p	4	1	2	1	274	29.9	10.29	5.42	1	1	
TRUE	Harore.CG.MTP2014 .S449.g08835.02.p	2	1	2	1	646	70.4	6.62	5.4	1	1	
TRUE	Harore.CG.MTP2014 .S413.g09530.02.p	1	1	2	1	904	103.3	9.77	5.32	1	1	
TRUE	Harore.CG.MTP2014 .S63.g10260.01.p	3	1	3	1	451	51.2	7.78	5.32	1	1	
TRUE	Harore.CG.MTP2014 .S311.g02959.01.p	3	1	2	1	390	42.3	5.85	5.3	1	1	
TRUE	Harore.CG.MTP2014 .S1.g13128.01.p	11	1	2	1	168	19.4	10.04	5.23	1	1	
TRUE	Harore.CG.MTP2014 .S214.g09308.01.p	2	1	2	1	722	79	4.87	5.2	1	1	
TRUE	Harore.CG.MTP2014 .S429.g09491.02.p	2	1	2	1	663	76.2	6.33	5.07	1	1	
TRUE	Harore.CG.MTP2014 .S623.g08848.01.p	6	1	2	1	308	33.6	7.56	4.98	1	1	
TRUE	Harore.CG.MTP2014 .S4.g00773.01.p	4	1	5	1	290	33.4	10.86	4.94	1	1	
TRUE	Harore.CG.MTP2014 .S26.g12147.01.p	0	1	2	1	5894	682	8.78	4.84	1	1	
TRUE	Harore.CG.MTP2014 .S650.g08219.01.p	3	1	2	1	478	55.6	6.77	4.72	1	1	
TRUE	Harore.CG.MTP2014 .S125.g04129.01.p	2	1	3	1	892	102.1	8.47	4.69	1	1	
TRUE	Harore.CG.MTP2014 .S31.g02867.01.p	5	1	1	1	348	39.7	10.04	4.56	1	1	
TRUE	Harore.CG.MTP2014 .S340.g06256.01.p	18	1	1	1	120	13.6	5.29	4.52	1	1	
TRUE	Harore.CG.MTP2014 .S74.g15677.01.p	2	1	2	1	388	43.8	4.87	4.51	1	1	
TRUE	Harore.CG.MTP2014 .S372.g15251.01.p	2	1	2	1	818	92.1	8.12	4.41	1	1	
TRUE	Harore.CG.MTP2014 .S13.g10960.01.p	5	1	1	1	362	41.2	6.84	4.33	1	1	
TRUE	Harore.CG.MTP2014 .S130.g12323.01.p	6	1	1	1	713	77.6	7.56	4.31	1	1	
TRUE	Harore.CG.MTP2014 .S414.g10728.01.p	8	1	1	1	274	31.5	7.46	4.3	1	1	

TRUE	Harore.CG.MTP2014 .S385.g07417.01.p	5	1	2	1	746	82.4	8.12	4.23	1	1	
TRUE	Harore.CG.MTP2014 .S7.g02985.01.p	3	1	1	1	503	55.8	8.81	4.23	1	1	
TRUE	Harore.CG.MTP2014 .S50.g03819.02.p	4	1	1	1	547	62.1	8.18	4.2	1	1	
TRUE	Harore.CG.MTP2014 .S60.g16068.01.p	3	1	1	1	679	76.3	6.77	4.19	1	1	
TRUE	Harore.CG.MTP2014 .S118.g15652.01.p	2	1	1	1	850	93.3	7.8	4.17	1	1	
TRUE	Harore.CG.MTP2014 .S123.g02789.02.p	4	1	1	1	442	49.6	5.14	4.13	1	1	
TRUE	Harore.CG.MTP2014 .S149.g16046.01.p	4	1	1	1	515	57.8	9.5	4.09	1	1	
TRUE	Harore.CG.MTP2014 .S31.g14580.01.p	3	1	3	1	535	60.3	8.18	4.08	1	1	
TRUE	Harore.CG.MTP2014 .S117.g03302.01.p	1	1	1	1	1465	169.1	6.25	4.01	1	1	
TRUE	Harore.CG.MTP2014 .S126.g01852.01.p	0	1	1	1	21269	2354.9	5.82	4	1	1	Not accesible
TRUE	Harore.CG.MTP2014 .S1776.g14135.01.p	5	1	1	1	256	28	5.3	3.97	1	1	
TRUE	Harore.CG.MTP2014 .S15.g02198.01.p	1	1	1	1	2707	302.3	8.57	3.94	1	1	Zinc finger, FYVE/PHD-type, Rab-binding domain
TRUE	Harore.CG.MTP2014 .S4.g00229.01.p	3	1	1	1	522	57.6	5.72	3.93	1	1	
TRUE	Harore.CG.MTP2014 .S64.g12694.01.p	8	1	3	1	547	62.3	8.47	3.91	1	1	
TRUE	Harore.CG.MTP2014 .S299.g05035.01.p	2	1	1	1	888	97.3	7.02	3.89	1	1	
TRUE	Harore.CG.MTP2014 .S89.g00434.01.p	3	1	1	1	695	79.6	5.8	3.87	1	1	
TRUE	Harore.CG.MTP2014 .S288.g14328.01.p	3	1	1	1	577	68.8	7.18	3.82	1	1	
TRUE	Harore.CG.MTP2014 .S56.g05509.01.p	5	1	1	1	300	33.5	8.81	3.81	1	1	
TRUE	Harore.CG.MTP2014 .S247.g14709.01.p	2	1	2	1	870	94.2	8.76	3.81	1	1	
TRUE	Harore.CG.MTP2014 .S110.g15936.04.p	12	1	1	1	182	20.9	8.88	3.79	1	1	
TRUE	Harore.CG.MTP2014 .S243.g08637.01.p	3	1	1	1	1161	129.8	8.32	3.79	1	1	Tyr-protein kinase, active site, Ser-thr/tyr-protein kinase, ATP binding site
TRUE	Harore.CG.MTP2014 .S60.g06435.01.p	1	1	1	1	1691	187.1	5.02	3.77	1	1	Laminin EGF domain
TRUE	Harore.CG.MTP2014 .S226.g09901.01.p	4	1	1	1	622	69.7	4.92	3.76	1	1	
TRUE	Harore.CG.MTP2014 .S21.g13223.01.p	2	1	2	1	1327	147.5	6.96	3.76	1	1	
TRUE	Harore.CG.MTP2014 .S168.g12138.01.p	11	1	1	1	140	14.7	10.58	3.73	1	1	
TRUE	Harore.CG.MTP2014 .S371.g11506.01.p	1	1	1	1	1559	174	6.65	3.71	1	1	
TRUE	Harore.CG.MTP2014 .S509.g02694.01.p	1	1	1	1	1470	164.1	6.24	3.67	1	1	
TRUE	Harore.CG.MTP2014 .S168.g09155.02.p	5	1	1	1	313	34.8	6.2	3.66	1	1	
TRUE	Harore.CG.MTP2014 .S76.g13401.01.p	3	1	1	1	887	102	9.38	3.66	1	1	
TRUE	Harore.CG.MTP2014 .S10.g02106.01.p	4	1	2	1	512	55.4	8.03	3.66	1	1	
TRUE	Harore.CG.MTP2014 .S73.g01831.01.p	3	1	1	1	744	84.1	8.13	3.65	1	1	
TRUE	Harore.CG.MTP2014 .S47.g15565.01.p	2	1	1	1	700	79.9	4.86	3.64	1	1	
TRUE	Harore.CG.MTP2014 .S74.g07562.01.p	3	1	1	1	946	107.8	6.27	3.62	1	1	
TRUE	Harore.CG.MTP2014 .S534.g09325.01.p	4	1	2	1	739	82.9	8.75	3.61	1	1	
TRUE	Harore.CG.MTP2014 .S93.g14844.01.p	7	1	1	1	452	51.1	6.15	3.6	1	1	
TRUE	Harore.CG.MTP2014 .S75.g07902.01.p	4	1	1	1	582	65.4	8.63	3.6	1	1	
TRUE	Harore.CG.MTP2014 .S149.g09326.01.p	1	1	1	1	1017	113.7	4.96	3.56	1	1	

TRUE	Harore.CG.MTP2014 .S1046.g02016.01.p	2	1	1	1	726	83.4	5.71	3.55	1	1	
TRUE	Harore.CG.MTP2014 .S2.g15152.02.p	3	1	1	1	604	68.4	8.44	3.54	1	1	
TRUE	Harore.CG.MTP2014 .S244.g04568.01.p	5	1	1	1	338	37.3	6.71	3.5	1	1	
TRUE	Harore.CG.MTP2014 .S118.g14167.01.p	4	1	2	1	451	49.6	7.08	3.49	1	1	
TRUE	Harore.CG.MTP2014 .S175.g04271.01.p	0	1	1	1	4538	498.1	5.05	3.47	1	1	
TRUE	Harore.CG.MTP2014 .S628.g01969.01.p	2	1	1	1	736	81.5	7.15	3.47	1	1	
TRUE	Harore.CG.MTP2014 .S28.g10387.01.p	4	1	1	1	422	48.8	7.02	3.47	1	1	
TRUE	Harore.CG.MTP2014 .S122.g00894.01.p	5	1	1	1	283	32.7	7.75	3.45	1	1	
TRUE	Harore.CG.MTP2014 .S311.g06071.01.p	8	1	2	1	153	17.5	11.08	3.44	1	1	
TRUE	Harore.CG.MTP2014 .S461.g12874.01.p	2	1	1	1	690	75	5.44	3.43	1	1	
TRUE	Harore.CG.MTP2014 .S679.g05466.01.p	2	1	1	1	660	75	8.13	3.4	1	1	
TRUE	Harore.CG.MTP2014 .S183.g02724.02.p	3	1	1	1	490	55.2	7.84	3.36	1	1	
TRUE	Harore.CG.MTP2014 .S143.g04060.01.p	1	1	1	1	1148	127.6	5.16	3.35	1	1	
TRUE	Harore.CG.MTP2014 .S205.g15409.03.p	5	1	1	1	319	36.7	5.41	3.31	1	1	
TRUE	Harore.CG.MTP2014 .S2.g11886.03.p	1	1	1	1	1273	144	7.28	3.3	1	1	
TRUE	Harore.CG.MTP2014 .S6.g03763.01.p	1	1	2	1	2617	297.8	6.01	3.3	1	1	
TRUE	Harore.CG.MTP2014 .S387.g09369.02.p	2	1	1	1	1006	112	6.2	3.29	1	1	
TRUE	Harore.CG.MTP2014 .S306.g02139.01.p	4	1	1	1	319	35.5	4.83	3.29	1	1	
TRUE	Harore.CG.MTP2014 .S76.g11452.01.p	2	1	1	1	946	108.3	6.4	3.28	1	1	
TRUE	Harore.CG.MTP2014 .S192.g13237.01.p	5	1	1	1	274	30.6	9.28	3.26	1	1	
TRUE	Harore.CG.MTP2014 .S669.g10298.01.p	3	1	1	1	389	45.7	5.73	3.24	1	1	
TRUE	Harore.CG.MTP2014 .S17.g08304.01.p	5	1	1	1	295	32.4	8.47	3.24	1	1	
TRUE	Harore.CG.MTP2014 .S458.g05196.01.p	15	1	1	1	239	27.6	7.61	3.23	1	1	
TRUE	Harore.CG.MTP2014 .S7.g12019.01.p	6	1	1	1	287	31.1	5.87	3.21	1	1	
TRUE	Harore.CG.MTP2014 .S38.g00174.01.p	2	1	1	1	819	91	5.1	3.19	1	1	
TRUE	Harore.CG.MTP2014 .S15.g15019.01.p	6	1	1	1	305	34.8	8.57	3.17	1	1	
TRUE	Harore.CG.MTP2014 .S7.g09104.01.p	1	1	1	1	2524	288.9	5.3	3.13	1	1	
TRUE	Harore.CG.MTP2014 .S73.g08441.01.p	2	1	3	1	770	85	8.54	3.13	1	1	
TRUE	Harore.CG.MTP2014 .S607.g00966.02.p	3	1	1	1	484	56.1	6.49	3.12	1	1	
TRUE	Harore.CG.MTP2014 .S368.g05207.01.p	0	1	1	1	3268	364.3	5.94	3.09	1	1	
TRUE	Harore.CG.MTP2014 .S48.g11671.01.p	3	1	2	1	514	59.1	5.12	3.09	1	1	
TRUE	Harore.CG.MTP2014 .S121.g01710.02.p	3	1	1	1	558	60.4	8.27	3.07	1	1	
TRUE	Harore.CG.MTP2014 .S188.g00623.01.p	8	1	1	1	186	21.7	11.75	3.07	1	1	
TRUE	Harore.CG.MTP2014 .S390.g07331.01.p	2	1	1	1	969	105.9	6.81	3.06	1	1	
TRUE	Harore.CG.MTP2014 .S226.g13679.01.p	1	1	1	1	1357	153.8	6.89	3.05	1	1	
TRUE	Harore.CG.MTP2014 .S1.g04124.01.p	3	1	1	1	472	53.2	5.96	3.04	1	1	
TRUE	Harore.CG.MTP2014 .S62.g10547.01.p	1	1	1	1	746	84.1	5.71	3.03	1	1	
TRUE	Harore.CG.MTP2014 .S1082.g06650.01.p	3	1	1	1	450	50.6	8.43	3.02	1	1	

TRUE	Harore.CG.MTP2014 .S91.g12135.01.p	1	1	3	1	721	83.9	5.96	3.01	1	1	
TRUE	Harore.CG.MTP2014 .S38.g11303.01.p	3	1	1	1	444	48.1	8.37	3	1	1	
TRUE	Harore.CG.MTP2014 .S222.g13084.01.p	8	1	1	1	159	18.4	10.26	2.99	1	1	
TRUE	Harore.CG.MTP2014 .S447.g06021.01.p	1	1	1	1	1257	145.8	6.79	2.98	1	1	
TRUE	Harore.CG.MTP2014 .S140.g12641.01.p	3	1	1	1	357	40.5	8.34	2.97	1	1	
TRUE	Harore.CG.MTP2014 .S19.g03035.01.p	3	1	1	1	415	47.6	6.92	2.97	1	1	
TRUE	Harore.CG.MTP2014 .S446.g10162.01.p	4	1	1	1	366	41.6	8.35	2.96	1	1	
TRUE	Harore.CG.MTP2014 .S27.g08265.01.p	2	1	1	1	729	82.6	6.24	2.96	1	1	
TRUE	Harore.CG.MTP2014 .S28.g12910.01.p	1	1	1	1	1902	217.3	7.21	2.96	1	1	
TRUE	Harore.CG.MTP2014 .S226.g05546.01.p	2	1	1	1	819	90.8	5.68	2.94	1	1	
TRUE	Harore.CG.MTP2014 .S100.g02713.01.p	2	1	1	1	489	54.4	7.99	2.94	1	1	
TRUE	Harore.CG.MTP2014 .S79.g03111.01.p	2	1	1	1	553	60	6.87	2.94	1	1	
TRUE	Harore.CG.MTP2014 .S138.g03243.01.p	0	1	1	1	23333	2586.8	6.39	2.94	1	1	
TRUE	Harore.CG.MTP2014 .S258.g05422.01.p	8	1	2	1	216	24.9	6.55	2.93	1	1	
TRUE	Harore.CG.MTP2014 .S856.g11039.01.p	8	1	1	1	151	16.7	8.78	2.93	1	1	
TRUE	Harore.CG.MTP2014 .S140.g12867.01.p	4	1	1	1	388	44	8.32	2.92	1	1	
TRUE	Harore.CG.MTP2014 .S216.g11302.01.p	2	1	1	1	734	84.1	7.08	2.92	1	1	
TRUE	Harore.CG.MTP2014 .S62.g02057.02.p	2	1	1	1	752	85.1	5.27	2.92	1	1	
TRUE	Harore.CG.MTP2014 .S106.g15906.01.p	2	1	1	1	686	74.9	9.01	2.91	1	1	
TRUE	Harore.CG.MTP2014 .S74.g13908.01.p	5	1	2	1	255	27.1	4.6	2.9	1	1	
TRUE	Harore.CG.MTP2014 .S329.g06332.01.p	1	1	1	1	871	102.3	7.4	2.9	1	1	
TRUE	Harore.CG.MTP2014 .S3.g01965.01.p	3	1	1	1	472	50.9	6.79	2.89	1	1	
TRUE	Harore.CG.MTP2014 .S326.g07218.01.p	2	1	1	1	546	61.5	4.94	2.89	1	1	
TRUE	Harore.CG.MTP2014 .S346.g00379.01.p	1	1	1	1	1663	185.3	6.54	2.88	1	1	
TRUE	Harore.CG.MTP2014 .S270.g05292.02.p	1	1	1	1	1009	115.9	6.64	2.88	1	1	
TRUE	Harore.CG.MTP2014 .S431.g11829.01.p	2	1	1	1	840	93	8.65	2.86	1	1	
TRUE	Harore.CG.MTP2014 .S56.g00817.01.p	2	1	1	1	760	85.4	8.24	2.85	1	1	
TRUE	Harore.CG.MTP2014 .S217.g01139.01.p	2	1	1	1	822	93	5.63	2.84	1	1	
TRUE	Harore.CG.MTP2014 .S575.g14321.01.p	3	1	1	1	514	56.2	6.67	2.84	1	1	
TRUE	Harore.CG.MTP2014 .S108.g14969.01.p	4	1	1	1	376	42.4	7.08	2.83	1	1	
TRUE	Harore.CG.MTP2014 .S217.g03510.01.p	2	1	1	1	496	54.5	6.24	2.83	1	1	
TRUE	Harore.CG.MTP2014 .S288.g06079.01.p	5	1	1	1	208	23.9	10.36	2.83	1	1	
TRUE	Harore.CG.MTP2014 .S134.g09823.01.p	1	1	2	1	1104	122.2	7.36	2.83	1	1	
TRUE	Harore.CG.MTP2014 .S917.g14209.01.p	6	1	2	1	483	57	8.68	0	1	1	
TRUE	Harore.CG.MTP2014 .S74.g00446.01.p	5	1	3	1	537	59.8	8.41	0	1	1	
TRUE	Harore.CG.MTP2014 .S8.g05712.01.p	6	1	1	1	651	73.1	7.06	0	1	1	
TRUE	Harore.CG.MTP2014 .S190.g04310.01.p	2	1	3	1	1781	199.7	9.17	0	1	1	
TRUE	Harore.CG.MTP2014 .S16.g15062.01.p	7	1	3	1	390	44.2	9.23	0	1	1	

TRUE	Harore.CG.MTP2014.S18.g11724.01.p	5	1	2	1	642	72.9	5.52	0	1	1	
TRUE	Harore.CG.MTP2014.S68.g08098.01.p	4	1	6	1	697	77.3	4.68	0	1	1	

* A 120-kDa VC band on SDS–PAGE, which appeared after incubation of the VC with the sperm extract, was cut from the gel and subjected to reduced carboxymethylation, trypsin and Lys–C digestion and LC–MS analysis via an Orbitrap Fusion Lumos Tribrid mass spectrometer (Thermo Fisher Scientific, CA, USA) connected to an UltiMate 3000 RSLCnano System (Thermo Fisher Scientific). The analytical column was a reversed-phase column (PepMap RSLC C18, 0.075 × 150 mm; Thermo Fisher Scientific). The mobile phase was composed of 0.1% formic acid (FA) solution (buffer A) and acetonitrile containing 0.1% FA (buffer B). The flow rate was set to 300 µl/min, and the gradient program was as follows: an isocratic flow at 0% B for 5 min and a linear gradient from 0% B to 40% B for 145 min. Full mass spectra and MS/MS spectra were acquired using an Orbitrap and an ion trap, respectively. The spectral data obtained via MS/MS were used for database search analysis with the Sequest HT algorithm (Proteome Discoverer 2.4 SP1, Thermo Fisher Scientific) via protein data encoded from the *H. roretzi* genome (Harore.MTP2014.protein.fasta, ANISEED database [30]).

Proteins with a molecular mass greater than 110 kDa (red) and with more than a single unique peptide are annotated in the right column, where possible VC proteins and sperm proteins are indicated by purple and red letters, respectively. Notably, two fragments of HrTast2c and HrTast3c were also detected (yellow), suggesting the existence of the proteins in the mixture of the VC and sperm extract. HrTTSP-1 (314.4 kDa) indicated by yellow is a sperm membrane protein, which is capable of binding to HrVC70, a sperm receptor [20, 21].