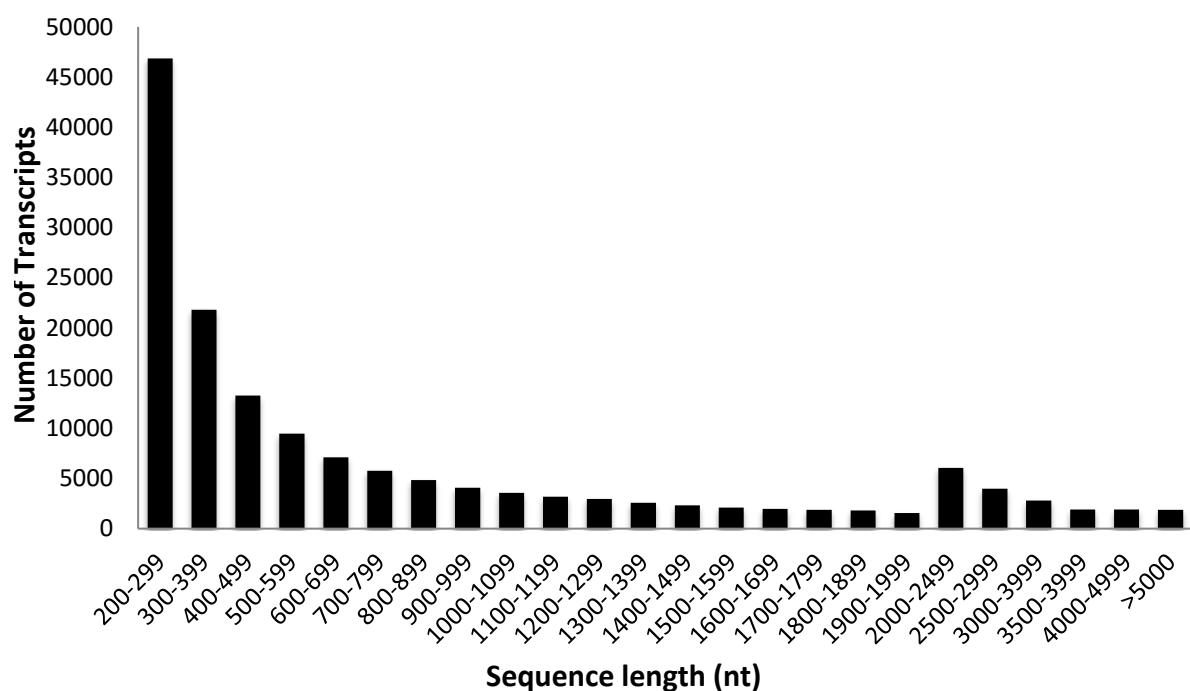
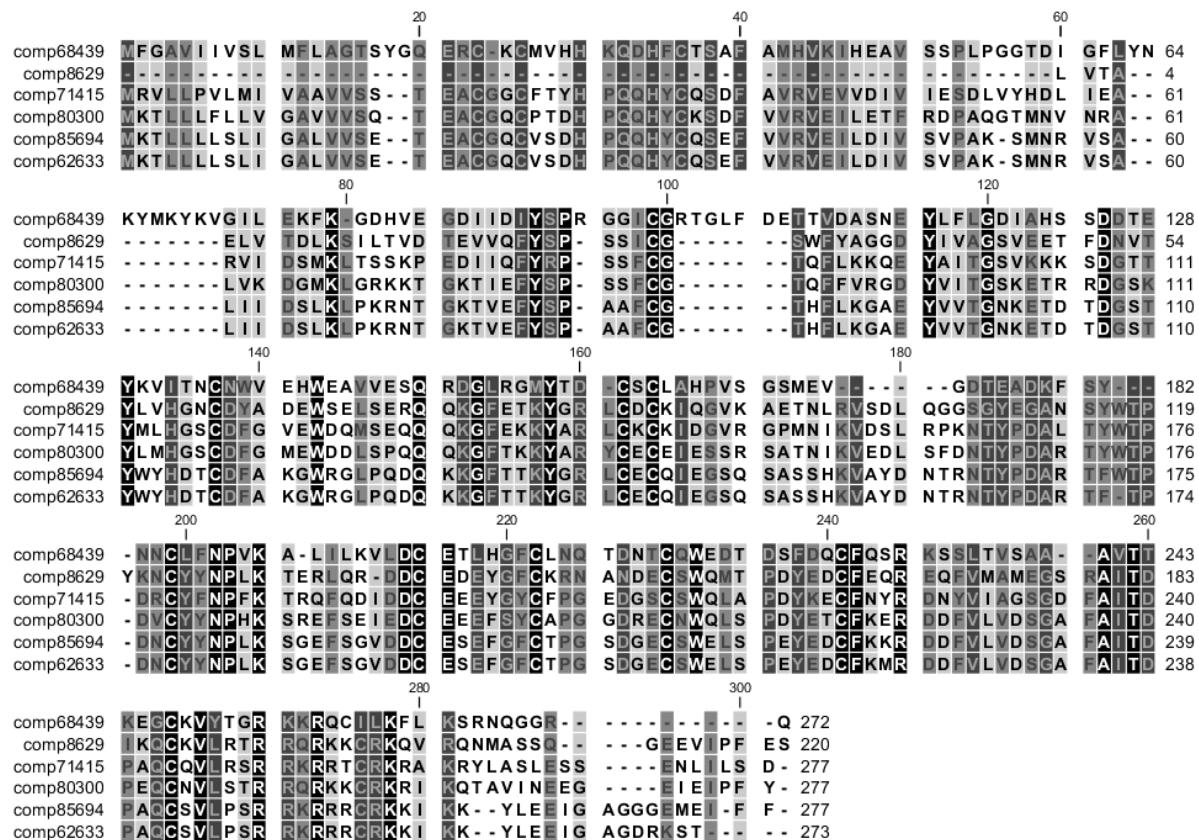


**Table S1.** Cuvierian tubule transcriptome. Statistical summary of sequencing output data and assembly results. N percentage is the proportion of unknown nucleotides in reads. N50 is the median length of contig or unigene.

OUTPUT DATA STATISTICS	
<i>Total raw reads</i>	179 601 824
<i>Average quality per reads</i>	38
<i>N percentage</i>	0
<i>GC percentage</i>	40
ASSEMBLY STATISTICS	
<i>Total length (bp)</i>	143 517 487
<i>Contig number</i>	156 918
<i>Contig mean length (bp)</i>	914
<i>Contig N50 (bp)</i>	466
<i>Contig smallest length (bp)</i>	201
<i>Contig largest length (bp)</i>	17 237
<i>Unigene number</i>	98 969
<i>Unigene mean length (bp)</i>	649
<i>Unigene N50 (bp)</i>	359



**Fig. S1.** Distribution of assembled transcripts in the Cuvierian tubule transcriptome of *Holothuria forskali*. Number of transcripts in function of their sequence length in nucleotides.



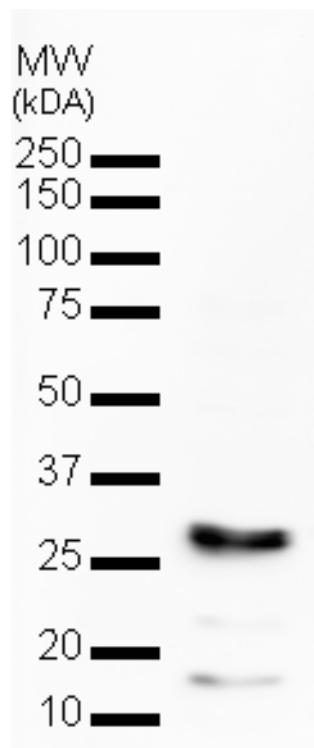
**Fig. S2.** Alignment of the translated protein sequences from the different transcript retrieved from the Cuvierian tubule transcriptome of *Holothuria forskali*. The sequences were aligned with Clustal Omega and the alignment was visualized using GenDoc. The grey scale represents the degree of similarity between sequences (from black: identical amino acid at the same position in all the sequences, to white: identical amino acid at the same position in only two of the six sequences).

**Table S2.** Top BLAST hits for the search for sequences similar to the tensilin of *Cucumariua frondosa* in the Cuvierian tubule transcriptome of *Holothuria forskali*.

Subject id	% identity	Alignment length	E-value	Bit score
comp80300_c1_seq2	45.3	256	1.03e-67	224
comp71415_c0_seq1	41.8	282	1.99e-58	202
comp62633_c0_seq1	42.9	275	2.13e-58	192
comp85694_c0_seq1	42.7	286	7.07e-57	200
comp85694_c0_seq3	42.7	286	7.32e-57	200
comp85694_c0_seq10	42.7	286	7.42e-57	200
comp85694_c0_seq11	42.7	286	7.67e-57	200
comp85694_c0_seq8	42.7	286	7.74e-57	200
comp85694_c0_seq12	42.7	286	8.08e-57	200
comp85694_c0_seq2	42.7	286	9.21e-57	200
comp85694_c0_seq9	42.7	286	9.43e-57	200
comp85694_c0_seq5	42.7	286	9.52e-57	200
comp85694_c0_seq7	42.7	286	9.74e-57	200
comp85694_c0_seq6	42.7	286	9.80e-57	200
comp85694_c0_seq4	42.7	286	1.01e-56	200
comp8629_c0_seq1	41.2	204	1.19e-48	165
comp68439_c0_seq1	24.7	287	5.50e-20	90.5

MKTLLLSLIGALVVSETEACGQCVDHPQQHYCQSEFVVRVEILDIVSVPAKSMNRVSALIIDSLKL  
 PKRNTGKTVEFYSPAFCGTHFLKGAEYVVTGNKETDTDGSTYWYHDTCDFAKGWRLPQDQKKGFTT  
 KYGRLCECQIEGSQSASSHKVAYDNTRNTYPDARTFWTPDNCYYNPLKSGEFSGVDDCESEFGFCTPG  
 SDGECSWELSPEYEDCFKKRDDFVLVDSGAFAITDPAQCSVLPSSRRCRKKIKKYLEEIGAGGGE  
 MEIFF

**Fig. S3.** Predicted amino acid sequence of tensilin from the Cuvierian tubules of *Holothuria forskali*. The signal peptide is underlined. Peptide sequences highlighted by green residues denote peptides retrieved by MS analyses in a former study (Demeuldre, 2015). The peptide sequence used for polyclonal antibody production is highlighted in red.



**Fig. S4.** Western blot analysis of tensilin from the Cuvierian tubules of *Holothuria forskali*. Proteins extracted from whole tubules were separated by reducing SDS-PAGE and immunolabeled with polyclonal antibodies directed against one peptide from the translated sequence of comp85694. Molecular weight markers (in kilodaltons) are indicated on the left.