

Table S4. BLASTP analysis of tunicate and lancelet genomes using lamprey LRRTM sequences as query and reciprocal BLASTP analysis against all vertebrate genomes

| Query sequence | Best BLASTP hit [<i>species</i>] | Accession number | E-value | Best reciprocal BLASTP hit* [<i>species</i>] |
|----------------|---|------------------|---------|--|
| LRRTM_A | slit homolog protein 2 [<i>Ciona intestinalis</i>] | XP_002124095 | 3e-29 | slit homolog 2 [<i>Melopsittacus undulatus</i>] |
| | hypothetical protein ID: 92046 [<i>Branchiostoma floridae</i>] | XP_002606179 | 3e-44 | slit homolog 3 [<i>Sarcophilus harrisii</i>] |
| LRRTM_B | vasorin-like [<i>Ciona intestinalis</i>] | XP_002128185 | 2e-29 | vasorin precursor [<i>Xenopus (Silurana) tropicalis</i>] |
| | hypothetical protein ID: 88462 [<i>Branchiostoma floridae</i>] | XP_002611139 | 4e-46 | leucine-rich repeat- containing protein 15-like [<i>Maylandia zebra</i>] |

*Reciprocal BLASTP was run against vertebrates (taxid:7742) with default parameters except that low complexity filter was on and compositional adjustments option was off.