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SUPPLEMENTARY MATERIAL

corresponding to:

The opsin repertoire of the European lancelet: a window into light detection in a basal chordate

CHRYSOULA N. PANTZARTZI, JIRI PERGNER, IRYNA KOZMIKOVA and ZBYNEK KOZMIK

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op1

op1		
B. lanceolatum		**ScanProsite[2]**
Genomic scaffold in Assembly BraLan2[1]	Comments	
Sc0000170 (505915..531566) 413aa e1= 373 e2= 188 e3= 147 e4= 243 e5= 291		GPCR + (58-311aa) OPSIN + (295-311aa)

>*Bl_op1*_1242bp
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CCTGCTACAACCCGGTTGTCTACTTCGCCATGAACAGCCAGTTCCGTCGGTACTTCCAAGACCTGCTGTG
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TCGCAAGATCTCCGCAAACCAGACTCGGACCGAAACAACGGCCTACCGACGCGAAGCTACATCGCCAGTG
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SSYLTYNKVGLAILFIYLYCLLWTTLPIVGWSSYELEGPEIGCSVAWEEH
SLSNTSYIVVLFIMCLVAPLLIIIYSYYRLWYKVKKGSRNLPAAIRKSSQ
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KTDEVDNGAANTS

op2

op2		
B. lanceolatum		**ScanProsite[2]**
Genomic scaffold in Assembly BraLan2[1]	Comments	
Sc0000009 (4027267..4043520) 420aa e1= 45 e2= 247 e3= 329 e4= 345 Repeats e5= 297		GPCR + (31-316aa) OPSIN - **K296** is at position 306

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AGCCTGCTGTGGACGGTACCACCGCTGATGGGGTGGAGCAGCTACGGACCGGAGGTACACGGCGTGTCCT
GCTCGGTCAACTGGGCGTCGCGGACCGCCAACGACACGTCCTACATCGTGGCCTATTTCGTGGGTTGCCT
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op3

op3		
B. lanceolatum		**ScanProsite[2]**
Genomic scaffold in Assembly BraLan2[1]	Comments	
Sc0000170 (545386..553817) 401aa e1= 190 e2= 219 e3= 185 e4= 138 e5= 240 e6= 234		GPCR + (70-318aa) OPSIN + (302-318aa)

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ACCCCATCATCTACGTGTTGATGAACAACCAGTTTCGCGAGTTTCTACTGGCACGTCTCGAGAGACTCTGCTGCCGTCAGCCGAGAG
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LVSVCGNTLSFASAVRHRWLWGRPGCVWYGFANSLFGIVSLVTLSALAFE
RYCVVVRSSDMLTYKSSLGVITFIWMYSLLWTSLPLLGWSSYQFEGHHIG
CSVNWVEHNLGNVSYIITLMVTCFFVPMVVVCWSYAGIWRTVRMSAEMKS
EFGNPKNTGRLVTTMVVVMIVCFLVCWTPYAVMALIVTFGADHLVTPTAS
VIPSLVAKSSTAYNPIIYVLMNNQFREFLLARLERLCCRQPRAPRVTPIG
IDDNTQVRLGGEGPSQAQPFLPSEENGDNVEMLTKAQENQLKGDGLSIIS
E

op4

op4		
B. lanceolatum		**ScanProsite[2]**
Genomic scaffold in Assembly BraLan2[1]	Comments	
Sc0000009 (4012428..4023488) 332aa e1= 355 e2= 329 e3= 243 e4= 72		GPCR + (52-303aa) OPSIN – **K296** is at position 293

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CTGCCCTACCGGGGCTTCATAGTGGTGGCGGCGGTGCTAGGTACCTTATGCGCCGGGGGGATCGTGTCCAACTTCGCGGTGCTGTTG
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WIWGRGGCVYYGFTNSFCGILSMITLTVIAYQRYKITVRPPGAANLKYHD
VTKAIVFIWIYSFVWTAPPLFGWSSYQLEGPRVGCSVDWSSHTGNDISYI
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VVVLITCFLLCWLPYGLVALVVTFGEPRLITPTAAIVCTLMAKSSVMWNP
VIYVVMNNQFRRHLVALLRCLRNAETTGPTPV

op5

op5		
B. lanceolatum		**ScanProsite**[2]
Genomic scaffold in Assembly BraLan2[1]	Comments	
Sc0000170 (495358..501839) 375aa e1= 364 e2= 182 e3= 150 e4= 234 e5= 198		GPCR + (55-304aa) OPSIN - **K296** is at position 294

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TCGCCGTGGCGTCCGCGGTGGGAGAGCGGTGGCTGTTCGGCCGCGCGGCGTGCGTTTGGTACGCCTTCGT
CAACTACTTCCTCAGTATCGTGTCCATCGTTACCATGGCAACCATGTCGTTCTCTCGGTACTGGCTCATC
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CATTCAGGTGGATCAGCCGGCGTACGAGAAGGCTGACGTGTACGTGGAGCGGCTGGTGACGGCGGAGCCC
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CGCTGTGA

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GERWLFGRAACVWYAFVNYFLSIVSIVTMATMSFSRYWLIIRPQSAPRLD
SLFGACVVNAFAWCYSFFWTIMPVLGWSRFTQVAAMTVCSLDWDHHTPLS
KSYIPVAFLTCLFLPLGVIIFSVVKTTMHLRRAAEVEDEVPNEVRVGRKT
MRITLVMAGCWLVAWLPYACMALVIAAGGQVSPTVEVLTTKFAKTSYIVN
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MVEMEPVDLRPRQQEPAREPFGTPL

op7

op7		
B. lanceolatum		**ScanProsite**[2]
Genomic scaffold in Assembly BraLan2[1]	Comments	
Sc0000005 + xfSc0029409 (5593502..>5607365) aa e1= 145 e2= 193 e3= 98 e4= 87 e5= 260 e6=185[#] e7= Ns	Last exon could not be predicted due to non-sequenced regions in the assembly	GPCR + (55-315aa) OPSIN + (299-315aa)

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GGACCCTACCCAACCCGCCCACAGACCTACGTCATCATCGCCATCGCGTGGCTCTACGGGCTCTTCTGGGCATGCGCACCACTGGCA
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AACCGCTTCAG

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LGRWSFGSAGCTWYGFTGFFFGTASIANMALMSIMRFMIVYKKYPGPYPT
RPQTYVIIAIAWLYGLFWACAPLAGWSRYHVEPFGLSCTVDWGGFSRGAA
GMSFILCLLVFCVALPVTAVVASFAGIFVIYRHAKKGVVTHLQNNPTMSK
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PLFAKSSSLWNPIIYLGTNNRF

op8

op8		
B. lanceolatum		**ScanProsite[2]**
Genomic scaffold in Assembly BraLan2[1]	Comments	
Sc0000019 (1226015..1261607) 366aa e1= 88 e2= 208 e3= 83 e4= 165 e5= 164 e6= 393		GPCR + (36-290aa) OPSIN + (274-290aa)

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LMPVCGWSRYTREPFDVACTLDYKTARESQEGAAFMMTLFAFCYFIPVAI
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PYSLVSIYATFRDLESIPVILSILPSMFAKSASIYNPIIYFFMNDSFRRD
VTALIKLSIPKAGTTSCSQTAWENTPTGRNCPQHMELCETHLSPAKTTTT
ALITHVDGREAPSTWV

op9

op9		
B. lanceolatum		**ScanProsite**[2]
Genomic scaffold in Assembly BraLan2[1]	Comments	
Sc0000182 (210518..>220518) 616aa e1= 97 e2= 197 e3= 100 e4= 97 e5= 150 e6= 79 e7= 171 e8= 960		GPCR + (39-292aa) OPSIN – **K296** is at position 282

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CAAGTGTAGTACAGATGCACATGATCTTGGGGGCTCGCACAGGTACATGGCTAGTATCAAGACATCTACA
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RPSVSGSERSLSLLLDVLPKRRSSSERAASSSVRGSHNTVSSSSLRQTTC
HHGSSQQPSGRKDTRTRQSHTDGKTRPTGGRVSKRSSSHFQQAFDAVAEA
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KRTVFGMSRKHAYIVD

op10

op10		
B. lanceolatum	**ScanProsite**[2]	
Genomic scaffold in Assembly BraLan2[1]	Comments	
Sc0000358 (60865..71904) 469aa e1= 145 e2= 114 e3= 180 e4= 117 e5= 236 e6= 173 e7= 145 e8=300		GPCR + (55-316aa) OPSIN – **K296** is at position 306

>*Bl_op10*_1410bp
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op11

op11		
B. lanceolatum		**ScanProsite[2]**
Genomic scaffold in Assembly BraLan2[1]	Comments	
Sc0000072 (1088219..1110938) 400aa e1= 217 e2= 294 e3= 117 e4= 212 e5= 363		GPCR + (79-332aa) OPSIN + (316-332aa)

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op12a

op12a		
B. lanceolatum		**ScanProsite[2]**
Genomic scaffold in Assembly BraLan2[1]	Comments	
Sc0000154 (194247..201469) 386aa e1= 172 e2= 153 e3= 141 e4= 117 e5= 212 e6= 366		GPCR + (64-318aa) OPSIN + (302-318aa)

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op13a + op13b

op13a		
B. lanceolatum		**ScanProsite[2]**
Genomic scaffold in Assembly BraLan2[1]	Comments	
Sc0000154 (175052..184700) 386aa e1= 172 e2= 153 e3= 141 e4= 117 e5= 212 e6= 366		GPCR + (64-318aa) OPSIN + (302-318aa)
op13b		
Sc0000040 (970123..981814) 387aa e1= 175 e2= 153 e3= 141 e4= 117 e5= 212 e6= 366		GPCR + (65-319aa) OPSIN + (303-319aa)

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op14

op14		
B. lanceolatum		**ScanProsite[2]**
Genomic scaffold in Assembly BraLan2[1]	Comments	
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op15

op15		
B. lanceolatum		**ScanProsite[2]**
Genomic scaffold in Assembly BraLan2[1]	Comments	
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op16

op16		
B. lanceolatum		**ScanProsite**[2]
Genomic scaffold in Assembly BraLan2[1]	Comments	
Sc0000242 (291516..293213) 295aa e1= 185 e2= 134 e3= 746		GPCR + (52-298aa) OPSIN – **K296** is at position 288

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op17a + op17b

op17a		
B. lanceolatum		**ScanProsite**[2]
Genomic scaffold in Assembly BraLan2[1]	Comments	
Sc0000011 (2130885..2133960) 335aa e1= 191 e2= 134 e3= 683		GPCR + (54-305aa) OPSIN – **K296** is at position 295
op17b		
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>*Bl_op17a*_1008bp
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CCTCCGCGGGGCTTGTCGACGAGCCGTCCGCCTGTGCTCAGACCGTGTTCGGGGTGGTTATTCTCCTGGC
AGGGTTGACGGGGATCCTCGGTAGCGGTCTGGCTCTTCAAGCTTTATATAGATGTAAAACCTTGCGGAAT
CCGAAGCACTACCTAACGGTAAACCTGTGCCTGACAGACGGCCTGCTGTGCGTGGTGTACTGCCCCGTCA
CAGTCTGGGCATGCTTCGCTCACACATGGACGTTTGGAGAAATCGGTCGCAACATGTTTGGCTTCAGTGT
CAGTGTGATGACCCTAGTGCTGATGACCACTCAACTCGCCATAGCCGTGCAGCGACTTACTGTCGCCTTC
GACCCGCTCACCGCTGTCTCAACCATCACACACGGGAAGATGCTGATGACTGCCGCCTTCACATGGCTCT
ACTCCATCCTCCTCATGCTGCCTCCTCTCTTAGGGTGGAACAGGTTCGTCATAGATGAAACTGGCGTTAG
TGTCATGTTTGACTACCTAGCTGATGATGACCTCTCCAGAGCATACGTCATTGCCATGTTGATTATCGCC
TTCGTGCTACCGTTAATTGGTGTAGTCTGTTGTTACTGCTACATTTTTGTCGCCGTAAGAAGGTCCAGGC
AGAATGCGAAAGTGCCGGCATCAGAGTTGACTTGTAAAAGGGACACAAAGACTGCGATTGTCGCACTGGG
CCTCTCAGCCTTGTTCTGTGTAAGCTGGACGCCATATGCCATGGTGATCCTCCTAAGTCTGTGTAACATA
GCGGTTCCTGTCACGCATGTCATGGTAGCTGCAGCCATAGCGAAGTGTTCTTCCACTATAGACCCAATGA
TGTTTGCGTTGTCACTACCTGCGGTCCGACAGTTTTACAAAGAAAGACTGGGAAAATATTTCTGTGACAA
ATCTGTGAAACTCGGGACTTCAGTGTAG

>Bl_Op17a_335aa
MDVRNNFRSNRLLLGDNHREDNVSSAGLVDEPSACAQTVFGVVILLAGLT
GILGSGLALQALYRCKTLRNPKHYLTVNLCLTDGLLCVVYCPVTVWACFA
HTWTFGEIGRNMFGFSVSVMTLVLMTTQLAIAVQRLTVAFDPLTAVSTIT
HGKMLMTAAFTWLYSILLMLPPLLGWNRFVIDETGVSVMFDYLADDDLSR
AYVIAMLIIAFVLPLIGVVCCYCYIFVAVRRSRQNAKVPASELTCKRDTK
TAIVALGLSALFCVSWTPYAMVILLSLCNIAVPVTHVMVAAAIAKCSSTI
DPMMFALSLPAVRQFYKERLGKYFCDKSVKLGTSV

>*Bl_op17b*_981bp
ATGGACGTCAGAAACATTTCCAACCGCTTATTTCTCGGAGACAAACACCGATAGGGCAATGTTTCCTCG
TCGGGGCTTGTCGACGCGCCGTCCGCCACTGCTCAGACGGTGTTCGGGGTGGTCATTCTCCTGGCTGGG
TTGACCGGGACCCTCGGAAACGGACTAGCTCTTCAAGCTTTATATGCGTGTAAAGCTTTGCGGAATCCT
GCGCACTACCTCACGGTGAACCTGTGCCTGACAAATGGCCTGCTGTGCGTGGTGTACTGCCCCGTCACA
GTCTGGGCAAGCTTCGCGCACACATGGACGTTTGGAGAATTCGGTCGCGACCTAGTCGGCTTCAGTGTC
AGTGTGATGACCATAGTGCTGATGATCACCCAACTCGCCATAGCCGTGCAGCGACTCATCGTGGCCTTC

AACCCGCTCGCCGCTGCAACAACCATCACACACGGGAAGATGCTGGTGTCTGTGGCTGCCACTTGGCTC
TACTCCACCCTGCTCATGCTGCCTCCTCTCGTAGGGTGGAACAGGTTCATAGTAGACCGTACCGGCGTT
AGTGTCATGTTTGACTACCTAGCTGTTGACGACCTCTCCAGATCGTACGTCATTGCTTTGTTGATGTGC
GCCTTTGCGTTACCGTTGATTAGTATAGTCTGTTGTTACTGCTACATTTTCGTGGCCGTTAGATGGTCT
AGACAGCATGCGAAAGTGCCGGCATCGGAGTTGACTTGTAAGAGAGATACAAAGACTGCGATTGTCGCA
CTAGGTCTTTCAGCCTTGTTCTGTGTAAGCTGGGCGCCATATGCTATGGTGGTCCTCCTGAGTCTGTGC
AACATCACGGTTCCTGTGACGTATGTCATGGTAGCTGCAGCCATTGCGAAGTGTGCGTCCAGTATCGAT
CCAATGATGTTTGCGTTGTCGCTACCTGTGGTCCGGAAGTATTACAAGGAAAGACTAGGAAATATCTCT
GTGGCAAATCTGTGA

op18

op18		
B. lanceolatum		**ScanProsite**[2]
Genomic scaffold in Assembly BraLan2[1]	Comments	
Sc0000212 (401872..406543) 349aa e1= 215 e2= 128 e3= 707		GPCR + (47-311aa) OPSIN – **K296** is at position 301

>*Bl_op18*_1050bp
ATGGACTCCTTTTATGATAATTCAAGCGACAACTCTCCCGTCCTCTGTAAGTTAACGTCGACCGGAAATG
AGAGCTTGTCGGACACAGAAAACCTGACAGACTGTGTTCACGCAGAACGCTTCCACATCGGTCAGACTGT
GAACGCGACTCTTATCCTGTTGTTTGGAGCGACTGGAACGGTGGGGAACACTTTGGCTGTCTACGCTTTC
TTCAGGGCTCTAAGAAAGCCTAAGAACTACCTGGTGGCAAATCTGTGCTTGGGTCAACTGCTCATGTGTC
TAGCATACAGTCCAGTGACTGCAGTATCTAACTATCTACACAGATGGGTTGGTGGCTATATAGGGTGCCA
GGTGGCAGGCTTTCTGACCGGCATGTCGTGCATGGTGTCCATCCTGTCAATCACTGCTATCGCTAGGCAA
CGGCTGGGCGTGGTCAGAGCTCCACTACACAGCCTAACAGCATTCACACACTCAGCAGAGTTGACACAAT
TAGCCTTGATTTGGTTTATATCTATAGTTTCCATGCTACCTCCTTTATTTGGGTGGAACCGGTTCGTCAT
AGACTCTATCCAGTTCAGCGTTACAATGGATTACTTGTCAACTGACATATCTTCAAAAGCGTATATAGTA
ACTCTTCTGGTCTGTGGGTTCTTTTTTCCCTTGGTAGATATTTGCTACTGCTATAGTTCTATATTCTATA
AAGTCGTTAAGCTAGGACGTAGCAAAGTTATCAGAAAAAGTGCAAAAAACGGCGTAAACGAAATCAGCAT
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CTGGGCATAGCAGAAGTGTATATACCACCGGAACTAGCTTTGGCTGCCTCTCCGCTTGCTAAACTGTCCA
CGACTGTCAACTCCATTTTGTTTGCGCTTTCGCTGCCTGCTTTTCGAAGGTATTTCTTTGGAAGTAAGAA
AGTGTATAGGGGGAGTGCAATAGCTATGAAAACATATAACAAGTCAGTCAAACATATGGGATATGTTTGA

>Bl_Op18_349aa
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LILLFGATGTVGNTLAVYAFFRALRKPKNYLVANLCLGQLLMCLAYSPVT
AVSNYLHRWVGGYIGCQVAGFLTGMSCMVSILSITAIARQRLGVVRAPLH
SLTAFTHSAELTQLALIWFISIVSMLPPLFGWNRFVIDSIQFSVTMDYLS
TDISSKAYIVTLLVCGFFFPLVDICYCYSSIFYKVVKLGRSKVIRKSAKN
GVNEISIALAGLLITSLFCICWLPYMVVVILGIAEVYIPPELALAASPLA
KLSTTVNSILFALSLPAFRRYFFGSKKVYRGSAIAMKTYNKSVKHMGYV

op19

op19		
B. lanceolatum		**ScanProsite**[2]
Genomic scaffold in Assembly BraLan2[1]	Comments	
Sc0000069 (1249266..1254369) 402 aa e1= 164 e2= 114 e3= 931		GPCR + (45-297aa) OPSIN – **K296** is at position 287

>*Bl_op19*_1209bp
ATGAGCCACAACCTCACCAACGTGTCTCTGCCGGCGAACCGGACGGACCAGCCCGAGCTGAGCCCGACCG
ACGTCACCATGCAGCTCATCTTCGGCTCGATGATGCTCGTCTTCGGGCTAATCGGAGTCATCGGGAACGT
CGTCGCCTTGTACGCGTTCTGCAGAAATCACAGTGTACGGAGACCGAAGAACTACCTGATAGCTAACCTG
TGTCTGACGGACCTGGCCGTGTGCCTGGTGTACTGTCCTATCATCGTCACCAGGAGTCTCAGCCACGGAT
TTCCGTCTGAAGAAAGCTGCATAGTGGAGGGTTTCGTGGTGGGAGTCGGCAGTGTCGCCAGTATCATCAG
TCTGGTGGCCATTGCTGTTGAGCGCTACCTCACCATCACCAAGCCCATGAAGTCCCTGACGATCTTGACC
CCACGGACACTTCTTGGCGCCGTCTCCGCAGTGTGGGCCTACTCGCTACTCCTTGCAGGTCCACCGCTTG
TCGGCTGGGGGCGCTACGTAAGGGAGAAGACTGACATCAGCTGCACGTTCGACTACCTGTCCACGGACGA
CGCTACTAGAGCACATGTCATCATGCTTGTGATTGGTGCGTTTGGATTCCCCCTCCTTATCATGACCTAT
TGCTACATCCGTGTCTTTACCACCGTCAGAAAGCGTGCAAAGGAAAGAAATATCATGTCCCCACTAAAAA
AGTCGGAGTCGAGGTCTGAAGTCAAATCAGCCGTGACAGGGTGCATCATAACTACGTCATTTTGCCTGTG
TTTTTGTCCCTACGCTGTCGTGGCCAGCTTGGGCCTCAGCGGTTTCCCTGCTCCAAGCCACGCCATATTC
GCAGCCGCTTTGTTGGCTAAGGTGACTGTACTCATCAACCCAGTCGTTTACGTGTTCTCCATACCAAGTT
TCCGGAAGGCTCTTTTCGCAAACGCACAGACGAAGAAACAGACCGCATATACAGGGGACGGTTTGATAGT
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GATATACAATCACCCATCGCTTATTCCGCGTCACGAGAGACCTGTTTGGTCAGTCTTGCTGCCACCGAGC
GGCTAGCGGAAAGAACCAACTCTATCTTAAGCCTCGGGAAGGAATTTGGACTTCAAGATACAGCGTCACA
TCAAGAAACCTGGGTATGA

>Bl_Op19_402aa
MSHNLTNVSLPANRTDQPELSPTDVTMQLIFGSMMLVFGLIGVIGNVVAL
YAFCRNHSVRRPKNYLIANLCLTDLAVCLVYCPIIVTRSLSHGFPSEESC
IVEGFVVGVGSVASIISLVAIAVERYLTITKPMKSLTILTPRTLLGAVSA
VWAYSLLLAGPPLVGWGRYVREKTDISCTFDYLSTDDATRAHVIMLVIGA
FGFPLLIMTYCYIRVFTTVRKRAKERNIMSPLKKSESRSEVKSAVTGCII
TTSFCLCFCPYAVVASLGLSGFPAPSHAIFAAALLAKVTVLINPVVYVFS
IPSFRKALFANAQTKKQTAYTGDGLIVPSPLVRERCTKSAEICRCSDMDN
DIQSPIAYSASRETCLVSLAATERLAERTNSILSLGKEFGLQDTASHQET
WV

op20

op20		
B. lanceolatum		**ScanProsite**[2]
Genomic scaffold in Assembly BraLan2)	Comments	
Sc0000069 (1239309..1246463) 389aa e1= 164 e2= 114 e3= 892		GPCR + (45-295aa) OPSIN – **K296** is at position 285

>*Bl_op20*_1170bp
ATGAGCCACAACCTCACCAACGTGTCTCTGCCGGCGAACCGGACGGACCAGCCCGAGCTGAGTTCGAAGGACGTCACCATGCAGCTC
ATCTTCGGCTCGATGATGCTCGTCTTCGGGCTGATCGGAGTCATCGGGAACGTCGTCGCCTTGTACGCATTCTGCAGTACACGCAAA
CTGCGCCGACCTAAAAACTACGTGGTGGCTAACCTGTGCCTGACGGACCTGGTAATGTGTCTGGTGTACTGTCCAGTCATCGTCTTC
AGCAGCTTCAGTAACAGCATCCCGACCGATGCAGCTTGCACGATGGAGGGGTTCGTGGTCGGCATGGCGAGCATCGCGAGTGTCGGC
AGTCTGGTCGCCATCGCGGTGGAACGGTTCTTCAGCATCACCCAGCCCATGAAATCCCTCGTCATCGTCACCAACCGGACCTTTCTC
GGCGCCGTCGCAGCCGTGTGGGTCTACGCGTTCTTCCTTGTCGTACCGCCACTTCTCGGCTGGGGGCGCTACGTACGAGAGGAGACA
AAACTGAGCTGTTCGTTCGACTACTCGTCCAAGGACACAGCCAACAGAGCCTACGTCATCACACTTTGTATTCTTGGGTTCGGATTT
CCCCTCATCATCATCGCTTATTGCTACATCCGTGTCTTCACGACAGTCAAGAAATGCTCGCAAAAGAGAAGACTCATGTCACCCCAC
AAGAAGTCGAAGTCAGAAGTAAAAACTGCCGTGAACGCTTTCATCATGACAACAGCGTTCTGCCTCTGCTGGTGCCCCTACACCGTC
GTAGCCATCATAGGCGCCAGCGGTTCTTCTGTCCAAGGGACCGTTGTCTTCGGCGCCGCCCTTCTCGCTAAGACGTCGGTGCTCATC
AACCCTGTTGCTTATGTCTTCTCCATCCCAAGTTTCCGGAAGGCCCTCTTCGGACGCAACAAACGGACCTGGAGCACATCCAACGGA
CCGGGAAACGATTCTTCGTCTGAGAAAAGACGAAAGCTGGACGCTAGCGCCAGCGAAAGCGGATACATTAAACTGACTGTTTACTCG
GCTTACAGTAGTACGCTTAGTCCTGCAGCGTCAAAGCGGCTTGCAGGGAGAACAGAATCAATGGTAGATCTCGCATCGGAGTTCGGG
CGCATGGGAACAAGGTCTCACAAAGAAAGCTGGGTTTGA

>Bl_Op20_389aa
MSHNLTNVSLPANRTDQPELSSKDVTMQLIFGSMMLVFGLIGVIGNVVAL
YAFCSTRKLRRPKNYVVANLCLTDLVMCLVYCPVIVFSSFSNSIPTDAAC
TMEGFVVGMASIASVGSLVAIAVERFFSITQPMKSLVIVTNRTFLGAVAA
VWVYAFFLVVPPLLGWGRYVREETKLSCSFDYSSKDTANRAYVITLCILG
FGFPLIIIAYCYIRVFTTVKKCSQKRRLMSPHKKSKSEVKTAVNAFIMTT
AFCLCWCPYTVVAIIGASGSSVQGTVVFGAALLAKTSVLINPVAYVFSIP
SFRKALFGRNKRTWSTSNGPGNDSSSEKRRKLDASASESGYIKLTVYSAY
SSTLSPAASKRLAGRTESMVDLASEFGRMGTRSHKESWV

op21

op21		
B. lanceolatum		**ScanProsite[2]**
Genomic scaffold in Assembly BraLan2[1]	Comments	
Sc0000322 (253878..258725) 295aa e1= 101 e2= 134 e3= 123 e4= 132 e5= 155 e6= 243		GPCR + (24-284aa) OPSIN – **K296** is at position 274

>*Bl_op21*_888bp
ATGTTGGACCCGATCATTTTCTACTCCTTGGGGGCGTTCGTCCTAGTGGTGGGCATCGTCGGTTGGATCG
GAAACCTGCTTATCATCTATGTCTTCTTCAGGTCGAAACATTTTCACCACACAAAGAACGTGCTGACGCT
GAACCTAGCCATCACGAACGTGCTCATGTGCCTAGCGACGGTGCCGACTTTCGTGACGTCAAGCTTCAGC
CGGAAGTGGATCTTCAGTGATACAGTTTGCCAGATGACCGGTTTCATGGCGGGGTGGTTCGGCACGCAGT
CTATCTGCACGCTGGCGGCGATCGCCCTCGACCGGTGCATCGCTATCACTATGCCGTTGACCGGTAAACT
TAATCGGGGCCGGAGGGTGACAATCAGTGTGGCGGTGGTGTGGCTGTGGTCCCTGATCTGGTGTTTACCC
CCGTTCTTCGGCTGGAACAAGTGGTCCATGCAGAAATACCAGACAGGCTGCACCTTCAACTACTTGTCAG
ATAATGCATTCCAAAGATGGTACATCATGGCCCTGACATTAGCAGTCTTCATCCTTCCGATGGTGGTGAT
GATAGTTTGCTACTACGCCATCTGGCGGGCCGCACGGCGCAGCACCCTTGCGCTCAAAGGCATGATGGAC
CGAAGGACGTTTCAGAAGATATCAAAAAAGCGGCGCCACGTCGACGTCCACACCGCCAAGGTCGGGGTCC
TGGTCACCCTGTTATTCATCCTGTCCTGGACACCCTTTGCAATCGTCGCTCTGATTGGTTGGGCTGGATA
TGGTCACTTGATAACACCACTTGCGGGAGCTATTCCGGCTGCAATTGCCAAAGCGGCTGTTATAGTGAAT
TACATCGTGTATGCGGCAATGATGCCGGACTTCAAGCGAGGTACGTAA

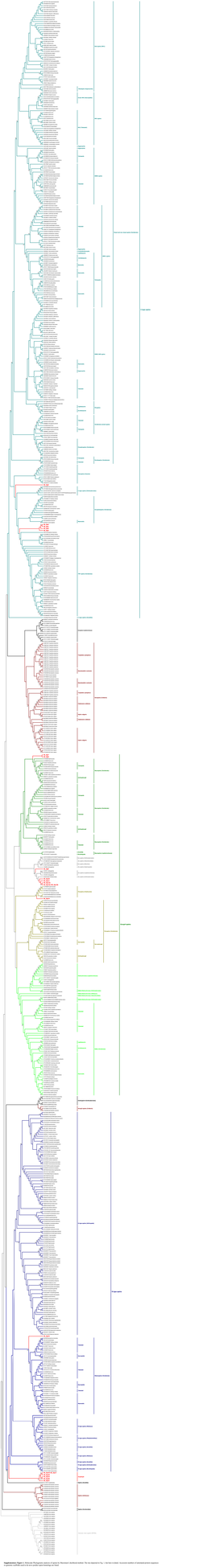
>Bl_Op21_295aa
MLDPIIFYSLGAFVLVVGIVGWIGNLLIIYVFFRSKHFHHTKNVLTLNLA
ITNVLMCLATVPTFVTSSFSRKWIFSDTVCQMTGFMAGWFGTQSICTLAA
IALDRCIAITMPLTGKLNRGRRVTISVAVVWLWSLIWCLPPFFGWNKWSM
QKYQTGCTFNYLSDNAFQRWYIMALTLAVFILPMVVMIVCYYAIWRAARR
STLALKGMMDRRTFQKISKKRRHVDVHTAKVGVLVTLLFILSWTPFAIVA
LIGWAGYGHLITPLAGAIPAAIAKAAVIVNYIVYAAMMPDFKRGT

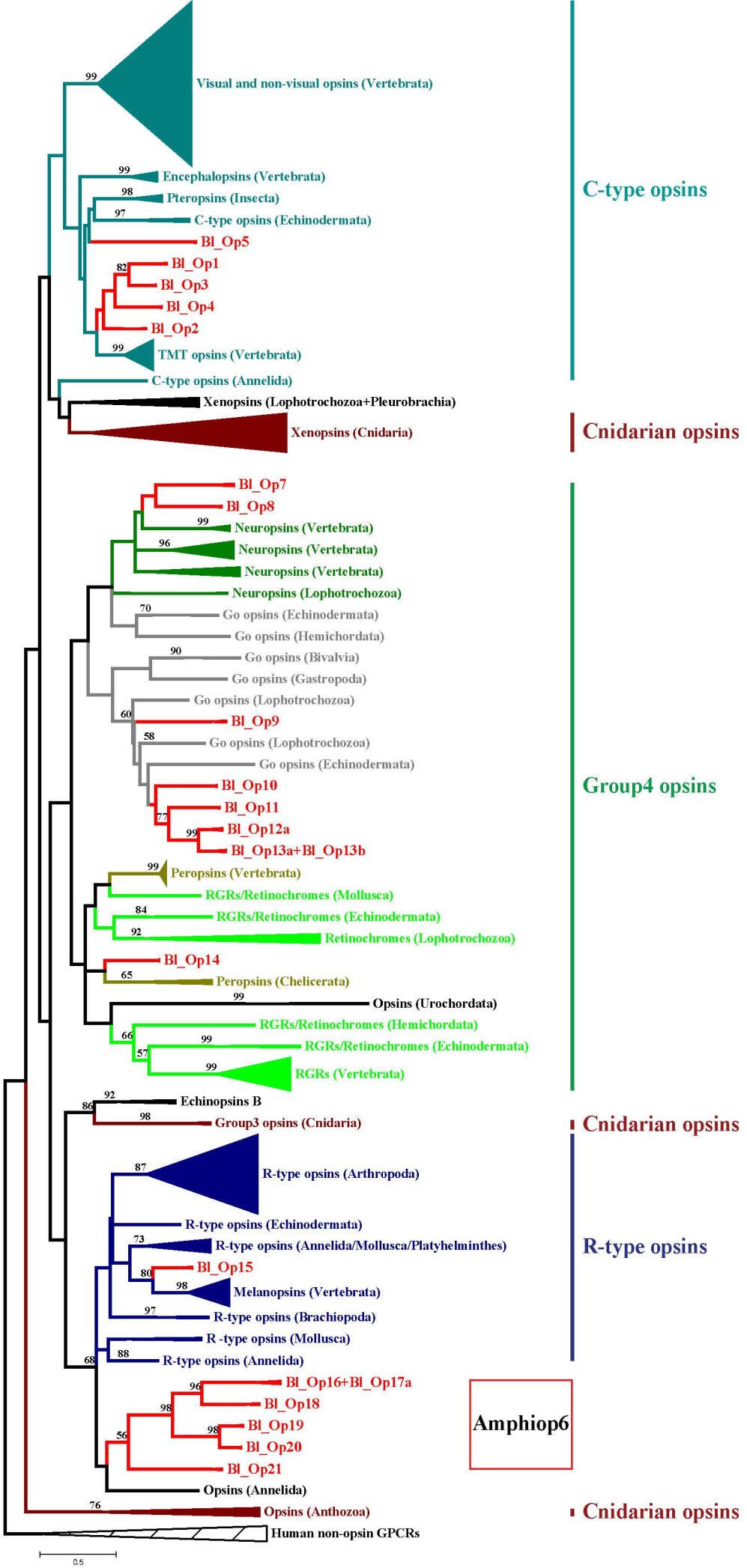
NOTES-

1. Numbers in brackets mark the gene location (from the translation initiation to the termination codon)

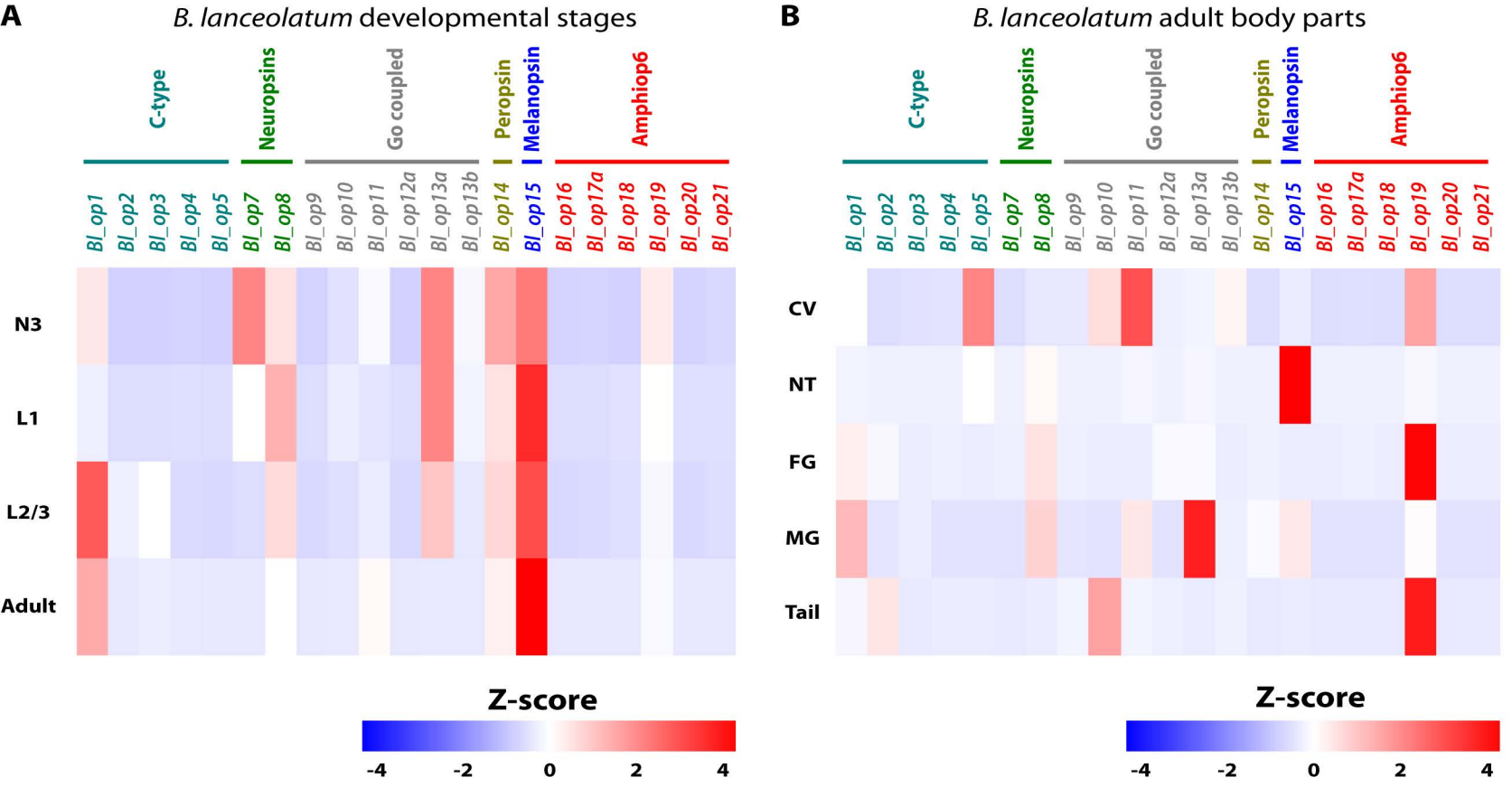
2. + / – denote presence or absence of respective motif in the protein according to ScanProsite analysis.

Supplementary file 1. Predicted transcripts and encoded opsin proteins from *Branchiostoma lanceolatum*, their genomic location and structure. Blue and black font in transcripts denote alternating exons. Green, blue and red letters in protein sequences mark the transmembrane domains, the extracellular and the cytoplasmic loops, respectively. The K296 lysine is colored pink.


Cryptococcus neoformans var. grubii
Cryptococcus neoformans var. neoformans
Cryptococcus neoformans var. gattii
Cryptococcus gattii species complex
Cryptococcus bacillisporus
Cryptococcus deuterogattii
Cryptococcus tetragattii
Cryptococcus gattii
Cryptococcus decagattii
Cryptococcus deneoformans
Cryptococcus deneoformans
Cryptococcus deneoformans



Supplementary Fig. S2. Molecular Phylogenetic analysis of opsins by Maximum Likelihood method. The evolutionary history of opsin proteins was inferred by using the Maximum Likelihood method based on the Le_Gascuel_2008 model. The tree with the highest log likelihood is shown. Bootstrap values are shown (only values>50) either at the nodes or above the branches in the case of non-expanded subgroups (e.g. neuropsin). A discrete Gamma distribution was used to model evolutionary rate differences among sites (2 categories). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 787 amino acid sequences. There were a total of 578 positions in the final dataset (third cytoplasmic loop is included).



Supplementary Fig. S3. Distribution of B. lanceolatum opsin genes expression in particular developmental stages and particular adult body tissues. (A) Heat map displaying proportion of opsin genes expression in each developmental stage (N3, L1, L2/3, Adult). Each row represents ratio of opsin genes expression for the particular developmental stage. Blue color represents expression bellow row average, white color represents average row expression, red color expression above row average. Staging was determined according to Hirakow and Kajita (1994) (see Materials and Methods). (B) Heat map displaying representation of opsin genes expression in particular parts of amphioxus adult body. Each row represents proportion of opsin genes expression in particular part of amphioxus adult body. CV: cerebral vesicle, NT: neural tube, FG: female gonads, MG: male gonads, Tail: most posterior part of adult tail.

Supplementary Table 1. Primers used for verifying *in silico* gene predictions, for expression pattern analysis through qRT-PCR and for generation of *in situ* hybridization probes

Primers for validation of *in silico* predicted models

Target	Name		5´ - 3´ sequence	Target	Name		5´ - 3´ sequence
Bl_op13a	JP536F	F	CTCTCTGGTCAGCATGTTC	*Bl_op13b*	JP536E	F	TTCTCTCTGGTCACCGAGGG
	JP536G	R	TTCTTGGCCTTCTCACTGG		JP536G	R	TTCTTGGCCTTCTCACTGG

Primers for RT-PCR

Target	Name		5´-3´sequence	Target	Name		5´-3´sequence
Bl_op1	JP571A	F	CTGATCTCCCTGGCTGTCAT	*Bl_op13a*	JP561A	F	ACGACGACCATTTTGGCTAC
	JP571B	R	CCACGATGTAGGACGTGTTG		JP561B	R	TGACGCCTAAGTCAGCAATG
Bl_op2	JP567E	F	CCCGTCGCCACTATAGTCAT	*Bl_op13b*	JP562A	F	GCGAGGATGTGTCTGGCTAT
	JP567D	R	ACCATCACCACCACCATCTT		JP562B	R	CAAGGGATTGACCTGCTTGT
Bl_op3	JP569C	F	TCTGTGAACTGGGTGGAACA	*Bl_op14*	JP565A	F	CCCTAGAGCCCTCAGGAACT
	JP569D	R	CAGACGATCATGACCACCAC		JP565B	R	CGTTAGAAGCGACAGGGAAG
Bl_op4	JP568C	F	ACGGCTTCACCAACAGTTTC	*Bl_op15*	JP566C	F	GAAAAAGGCGGTTGGTGATA
	JP568B	R	TCGTGTACGTGCTTCCAGAG		JP566D	R	CGTTCTCTGAGTCGGTGTCA
Bl_op5	JP570E	F	GCCGCTAGGTGTCATCATCT	*Bl_op16*	JP567E	F	CCCGTCGCCACTATAGTCAT
	JP570F	R	CTTGTCTTGGCGAACTTGGT		JP567D	R	ACCATCACCACCACCATCTT
Bl_op7	JP557A	F	CGGCATCTTCGTCATCTACA	*Bl_op17a*	JP576A	F	ACGGTAAACCTGTGCCTGAC
	JP557B	R	GATGATCGGGTTCCACAGAC		JP576B	R	CCGTGTGTGATGGTTGAGAC
Bl_op8	JP558C	F	GACTCTGTTCGCCTTCTGCT	*Bl_op18*	JP577E	F	GCTTCCACATCGGTCAGACT
	JP558D	R	GTTGTAGATGCTGGCGGACT		JP577D	R	TTGCCTAGCGATAGCAGTGA
Bl_op9	JP564A	F	ACGGGTTCAGTTGTTTCCTG	*Bl_op19*	JP574A	F	GTCGGAGTCGAGGTCTGAAG
	JP564B	R	TCACGTGGAAGTCGATGGTA		JP574B	R	TTTCTTCGTCTGTGCGTTTG
Bl_op10	JP563C	F	ACGTGGTGGGAAGCTGTATC	*Bl_op20*	JP575C	F	CACAACCTCACCAACGTGTC
	JP563D	R	CGAACATTGTCGGATACGTG		JP575D	R	GCTGCTGAAGACGATGACTG
Bl_op11	JP559A	F	TTCACCGTGCATGTTATCGT	*Bl_op21*	JP572A	F	TCGCTATCACTATGCCGTTG
	JP559B	R	ACCCGGATGTAGCAGAACAC		JP572B	R	TCGGAAGGATGAAGACTGCT
Bl_op12a	JP560A	F	GCTCTCTGGACTGGAAGGTG	*actin*	JP580A	F	CCTTCTACAACGAGCTGCGTATC
	JP560B	R	CGGCAGATCTTCATCAGACA		JP580B	R	TCGTGGACACCAGTGGACTC

Primers for generation of *in situ* hybridization probes

Target	Name		5´ - 3´ sequence	Target	Name		5´ - 3´ sequence
Bl_op11	JP559C	F	ATGGACAACTCTACATGTTGTTTG	*Bl_op12a*	JP560C	F	CGCCTGGCTGTCCAGCAG
	JP559B	R	ACCCGGATGTAGCAGAACAC		JP560B	R	CGGCAGATCTTCATCAGACA
Bl_op15		F	CGGACTCCTGCTAACTTCTT				
		R	CACGCTTGCCTGGGGATCATG				