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SUPPLEMENTARY MATERIAL

corresponding to:

Identification and expression analysis of two novel members of the Mesp family in zebrafish

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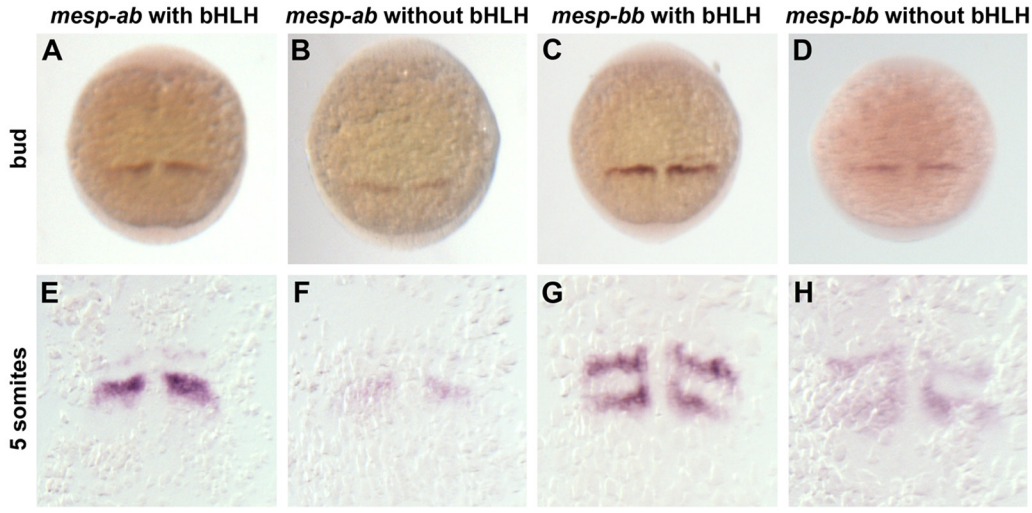
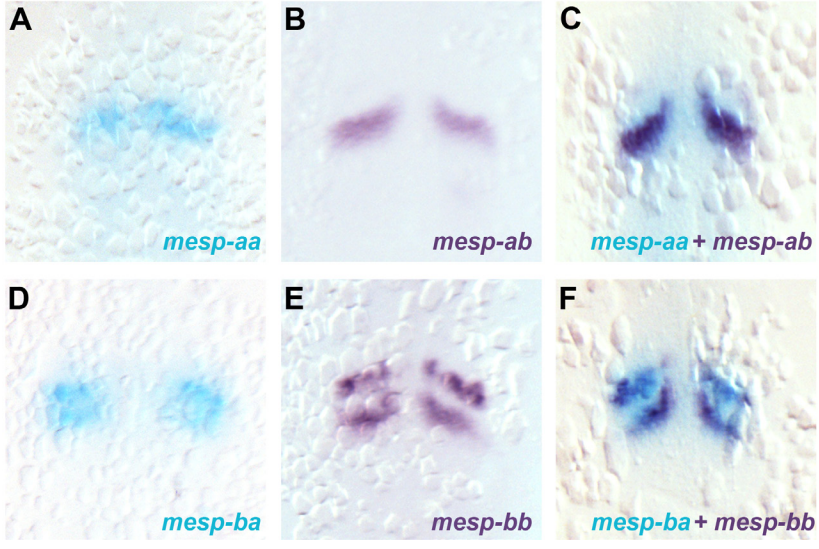
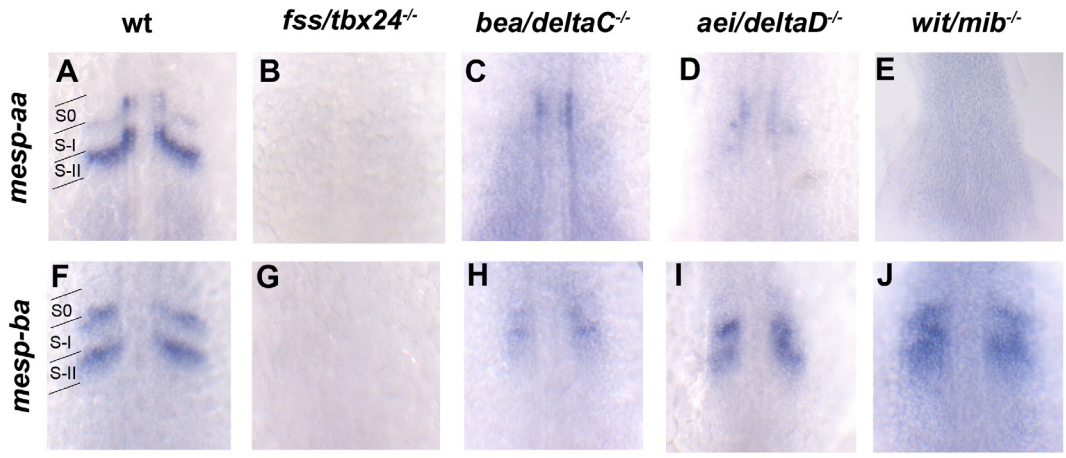


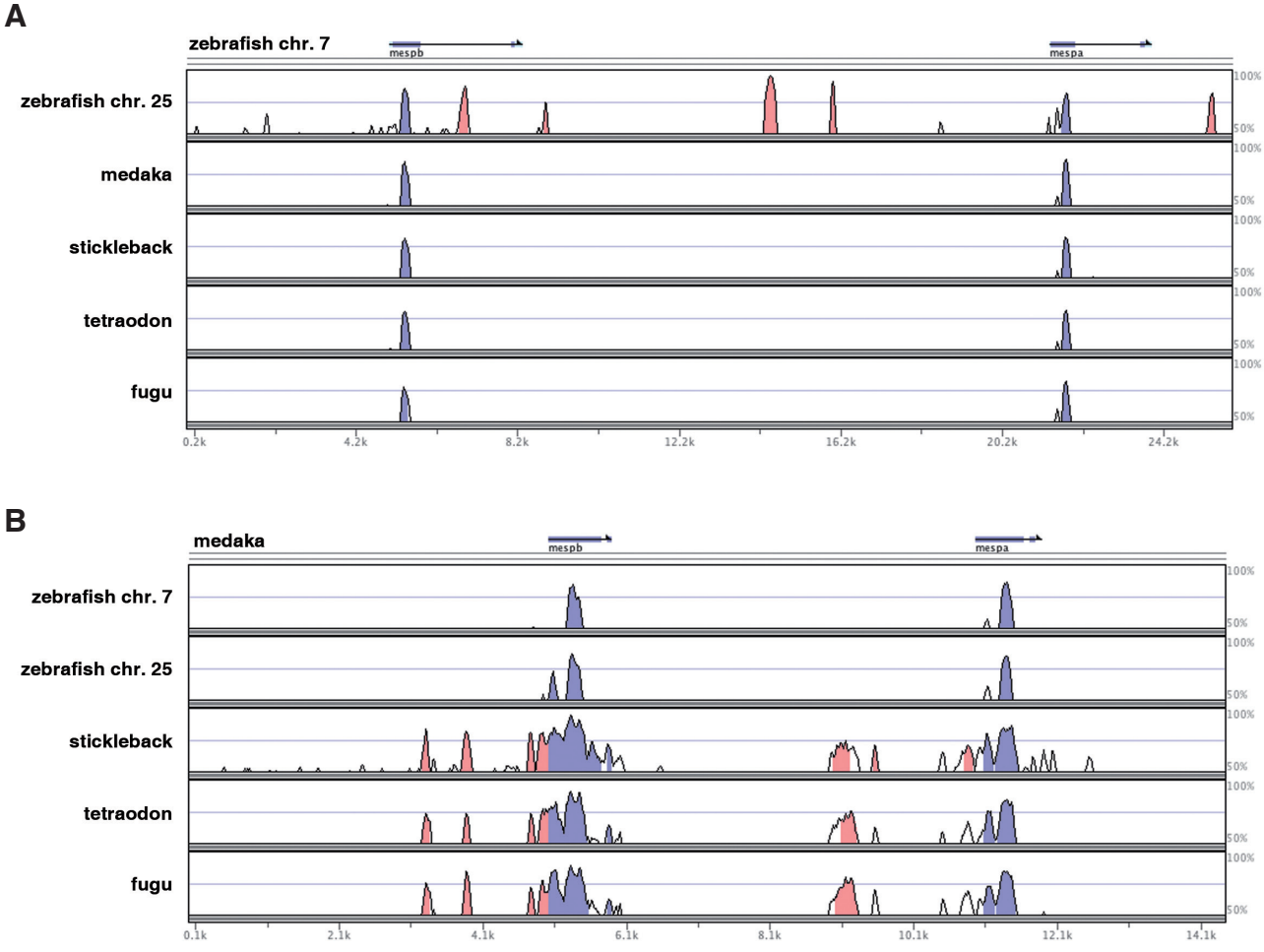
Supplementary Fig. S1. Comparison of *mesp-ab* and *mesp-bb* expression using *in situ* probes for full-length RNA (containing bHLH sequence) or for the 3′ end of RNA (lacking bHLH sequence). *Expression of* mesp-ab *and* mesp-bb *at bud stage* **(A-D)** *or 5-somite stage* **(E-H)** *shows spatial and temporal expression is the same for all probes. However expression of the probes lacking the bHLH sequence is weaker (compare A,C,E,G with B,D,F,H).*



Supplementary Fig. S2. Overlap of *mesp-aa/ ab* and *mesp-ba/ bb* expression. (A-C) In situ *of* mesp-aa *(pale blue) and* mesp-ab *(purple) at 12 somite stage shows that the expression of these genes overlap.* **(D-F)** In situ *of* mesp-ba *(pale blue) and* mesp-bb *(purple) at 12-somite stage shows that the expression of these genes overlap.*



Supplementary Fig. S3. **Expression of *mesp-aa* and *mesp-ba* in segmentation mutants. (A,F)** *Wild-type,* **(B,G)** fss/tbx24$^{-/-}$, **(C,H)** bea/deltaC$^{-/-}$, **(D,I)** aei/deltaD$^{-/-}$, **(E,J)** wit/mib$^{-/-}$ *embryos at the 8-somite stage hybridized with* mesp-aa **(A-E)** *and* mesp-ba **(F-J)** in situ *probes. S0, S-I and S-II mark the position of presumptive somites. All embryos were flat-mounted and are shown in dorsal views, anterior to the top.*



Supplementary Fig. S4. MVISTA analysis comparing the regions 5kb upstream of *mesp-b* to 2kb downstream of *mesp-a* of (A) zebrafish chr. 7 *mesp* locus to zebrafish chr. 25, medaka, stickleback, tetraodon and fugu mesp loci or (B) medaka *mesp* locus to zebrafish chr. 7, zebrafish chr. 25, stickleback, tetraodon and fugu *mesp* loci. *Exons are shown in blue, while conserved non-coding sequence is show in pink. The bHLH in the first exon shows high conservation between all species. In intronic and intergenic sequence small regions of conservation can be seen between the two zebrafish loci, but not the other fish* **(A)**. *Regions of conservation between medaka, stickleback, tetraodon and fugu, but not zebrafish, can be found upstream of* mesp-b *and* mesp-a **(B)**.

SUPPLEMENTARY TABLE S1

SEQUENCES USED IN THIS STUDY, INCLUDING FULL-LENGTH *MESP-AB* AND *MESP-BB* SEQUENCES

Organism	Name used	Notes (including identifiers)	Sequence
cDNA sequences			
Zebrafish	*Drmespaa*	ENSDART00000006018; Sawada et al, 2000; called mesp1 in Wang et al, 2009	CAGCCATGGACGCCTCCACGTTTTCTCTTCAGCTTCAAAACTGCAGCTTTTTTTCTTCCGGACTCTCAAAACCAGAGCTTTGCTGT ATCAGATGCTGGTTATTACAGCGCCACTGGTAGCCTTTCTCCAACCTCCTCCATCGATTCCTGCAGTTTTTCTCCACCAGCTTAC TCTTTGCTGCCTCAGATCTTCCCAAAAAGCATCCAGAAGACAGATGTCCAGCCGCCGAAGAGAACCGGACGTCCCAAATCGAA GTTTCCTGGAGTTAAACGGCAGACTGCAAGCGAGCGGGAGAAGTTGAGGATGAGGGATCTCACCAAAGCTCTTCATCACCTCA GGACCTTCCTGCCTGCGTCTGTGGCTCCCGTGGGAAAAACGCTGACCAAGATTGAGACGCTGCGGCTCGCCATAAAGTACATC TCCTGTTTATCTGATCAGCTCGGATGCGGTGAAGATGTGGAGATTTGTGAAGCGCAGGACGAGGTTATCAGCACATCAGCAAG CGTGTTTGACAACTTCAGTTCAGCTTCTTCGGCTTCTCAAAGTTTACCAGCTCAGCAGTTCATGTCTATGAGCTGTTATCAGACT CAGAATCCAGTTCAAGGTGATTTCCATTCATTCCCAGCTCAAGACGTCTGGTTTTCCCAGCAGCACAATTTTTTCCATGGACAGT GCTGACCAAAACTGACCTTATTGAAAATATGGATGCAGTAATTAATTTGTGCAATGCTTGCATGCTAATGGAAATGAAAGACTTTA TATATTTTTTGTAAATATATTTGTACAGCTATTTATAATTTTATATGTTTAAAATGATATCAGTATTTATAATTGCTACATCTTTCCGG CAAATAAAGACATGAAGACATC
Zebrafish	*Drmespab*	ENSDART00000099572; annotated as mesp2; also called mesp2 in Wang et al, 2009	AGCATTCACTCAAGCTCCAGAGAACCAGAAACATCTCCAAGAACTCGACCATGGAGTTTAACCTTCCTCCTTACTTGCTCCAAG CAGCCAGATGCAAACTCGAACCCATCTCGAGTGCTGATTGTGGTTACTTCAGCGCATGTGGGAGCCTTTCTCCAAGCTCCTCCA TCGATTCCGGATGCTTTTCTCCCCCTTGGGGAGCTGGAAGACAACTGGAAGGTCCTGAAAATGCCAATGTTGACTGTTTGCAAG CTAAAAAGCTAAAGCTAGCTCTTCCTGTTGATTCAAAGAGACGTTCCAGATCTAAAAACCCAGGAATGAAGCGACAATCAGCAA GCGAACGAGAGAAACTCCGAATGAGGGATTTGACCAAAGCTCTTCATCATCTCAGATCCTTCTTACCTCCATCTGTGGCTCCTG CTGGACAAACCTTGACTAAGATTGAGACCCTCCGTCTTGCCATTAGCTACATTTCACATCTTTCTGATCAACTCAGACAGGCTGA GGTGCCAAATTATGAGATGTGCTGCTCTGCTGAAGCTTCAGATAGGTTTCAGTCTGGTCTGGTTTTTGAAAACGTGTGTATGGAT GGACAACAGGGACTCATGCAAGATAATGTTCAGTATTGTCCAACACTCACAAGCTTTGGAGATTCCAGAGAACAGATGGAGAAC AGCTTTCCTGCTACTTCACATTTCAGAGATGCACAGTCTTATATGTTTCCCTGCACAACAATGGATGATGCTTCATATAGCCATCA GTTTTACCAATGAAGGATGATGAGAGGACGATGAGAGCTCAAGTTGTTACAGAATCAAACAGACTTTGTTTGTGTATATTATTTG TAATTATTTATCAGAAAACATATTTTTGTATTGGAGACATTTGTATATACTGCTTATTTATTGTCTTTTTTTAATTAAACCCCTTTAAA GATGAAAAAAAAAAAAAAAA
Stickleback	*Gamespa*	ENSGACT00000019530; *Mesp2*	ATGGACGTTTCCTACTGCTCTCCTCTCCAGCTGCAGGACAACTCTTTCCTGTTTGAGTCCCTGCTGGACAAGCCTTACGATCCT CTGGCCTACGATCCATCCTTGGACCCTGGTTACTTCAGCGCATGCAGCAGCAGCCTGTCGCCCACCTCCTCTGTGGACTCCTA CTGCTTCTCCCCCACCTCCCTCCAAGTGGCCGGAAGCGAGCCGAACTCCACGGATCGTTTCGTCTTCAAAAGCCCCGCAGTGC CTGGCCTCCCGCAGGGGACGCAGCGTCCGCCTTGCTCCGGATCATCCGCCGCCACGTCCTCCACCGCGAGGAAATCCAGATC CAGGTACCCGGGGAAGAAGCGGCAGACGGCCAGCGAGAGAGAGAAGCTGAGGATGAGGGACCTGACCAAGGCCCTGCAGCA CCTCAGGACATACCTGCCTCCCTCGGCGGCCCCCGCAGGACAGAACCTGACCAAGATCGAGACGCTGCGCCTCACCATCCGC TACATCTCCTACCTGTCGGCTCAGCTCGGCCTCAGCGAGGAGGCCCTGGAGCAGAGAGCCTGCGGGTTTTCGGAGAAGCCCC AAAACCTCATTGAGTTCTTGGGTCAGCCAGGAGCCGGCTACGGCCCCGTGAGCTCAGCACATCTGCAGCCCTCACACCAGAAT TTGTCTTGGCAGGTTTCAAATGGAGTTTGCTTCACCAGCGAGCAGTTCTGGATGCCACAACAGCAGCAACTCCAAAACGCCGTC TTCTCTGGACAGAGCTGA
Medaka	*Olmespa*	ENSORLT00000018374; Terasaki et al, 2006	ATGGAGATGTCCTTCTGCTTCCCCCTTCAGTTCCAGGAGAACCCTTTGCAGTTTGATTGGGAGTCTCTGCAGGAAAAACCTCTG GGTCCGGATCCGTCCTCCGATGCTGGTTACCACAGTGCCGCCAGCAGCCTGTCTCCCACCTCCTCTGTCGACTCCTGCTGCTT CTCCCCTGCCTCCCTGCAGACTGTGGGGACTGAACAAGATGTGCTGGAGAGTTTTCTCTTCTGCAGCCCAGCAGAGCTTCATC TCACCTGCCAGACTGGGCCACCTTCCAGCTTATCCTCTGCCAGCAGCCCCACCGCAAAGAAATCTAGGTCCAGGTATCTGGGA AAGAAGCGCCAGACTGCCAGCGAGCGGGAGAAACTGCGGATGAGGGATCTGACCAAAGCTCTTCATCACCTCAGAACGTACC TGCCTCCATCCGTCGCTCCTGCGGGTCAAACCCTGACCAAGATCGAGACGCTGCGTCTCACCATTCGATATATCTCCTACCTGT CAGCCAAGCTGGGCCTCAGCGAGGAAGTGCTGGAGCAGAGGAGATCCCTGGAGCCAACCCAAGCCCTCGGACACCTCCAAG GTCAGCAGAGAGCGAGCTACGGCGCCCAGGAAACGAGCTGCAGCACCGTGAACGAGCAGCGCTCCTCGCCACAGCAATCCA GCCAGGCTTCAGACGGAGTTCAGTTCTGGATTCAGCAGCAGCAACATCCAGCTGTGATCTTCTCAGGACAGTGTTGAAGTCTGT CCTCCCACATCTGCTCTGAACAAAAAATCTAAACTTTCTTGAATGAATTCACTTGTATTTGTACATAGATCTGTGTATTTATTAAGC TTTTTTTT
Tetraodon	*Tnmespa*	ENSTNIT00000003794 not full length; sequence found through scanning genomic sequence and homology with other fish mespa squences	ATGGAGCAGGCTCCCTGCTCCTCCTCATTCTCCCTGCCTCAGCCCAAGCAGACAGCAGCGATGGACCTCCAGCTCCAGGACA GCCCTCTGCTCTTTGATTGCGAGTCCCTGCTGGACGAGTCCTACCAGCACGTGGTCTTTGATCCAGCCGTGGACCCTGGATAC TTCAGCGCCGGCAGCTGCTCATCTCCCACTTCCTCTGTGGACTCCTTCAGCTTCTCCCCAACGTCCCTCCAGGCTGCTGGAGC TGAGCAAACTCCTCTGGACCGCCTCCTCTTCAGCAGCCCTGGTGCATCCGGTCGCAGCCGTGAGCCACACAGCCTGCAGTCC TGCACGTCCTCCAGCTCCAGCAGCAGGAGGTCCAGGTCCAAGTACCCAGGCAAGAAGCGGCAGACAGCCAGTGAGAGAGAGA AGCTTCGGATGAGGGATCTGACCAAAGCCCTGCACCACCTCAGGACCCACCTGCCGCCCTCGGTGGCTCCACCCGGTCAGAC TCTGACCAAGATCGAGACCCTGCGCCTCACCATCCGCTACGTGGCCCACCTGTGGGCTCAGCTGGGCCTCACCGAGGAGGTT CTGGAGCAGAGACGTTCCTGCGGGTGGCCCCAGAGCCTGAGCCAGGTCCAGCCGACAGAGCGTGGCGCCATGAGCAGCGCC CGCCTGCGCCACCTGCAGCCCCCACCTCAG
Fugu	*Trmespa*	ENSTRUT00000039278 not full length; sequence found through scanning genomic sequence and homology with other fish mespa squences	ATGGAGGTTTCCCACTGCTCTCCGTTCCAGCTCCAGGACACTTCATTGCTCTTCGATTGTGAGTCCCTGCTGGACAAGTCGTAT GACCACATGGTTTCTGATCCAGCTATGGACCCAGGATACTTCAGTGCCAGTAGTAGCCTGTCTCCCACATCTTCTGTGGACTCC TTCAGCTTCTCTCCCACATCCCTCCAAGCTGCTGAACCTGAGCAATGTCCTCTGGACGGGTTCCTCTTCAGCAGCCCAGCTGCA CCTCTGACCTCTGAGCCTCAGACCCTGCAGTCAAGCAGACCCTCCAGCTCTGACACCAAGAAGTCCAGGTCAAGGTATCCAGG CAAGAAGCGCCAGACAGCCAGTGAGAGGGAAAAGTTGAGGATGAGGGATCTGACCAAGGCCCTGCATCACCTTAGGACGTAC CTGCCACCATCAGTGGCACCAGCCGGTCAGACTCTGACCAAGATTGAGACCCTACGCCTCACCATCCGCTACATAGCCTACCT GTCGAGCCAGCTGGGCCTTACCGAGGAGGCTCTGGAGCAGAAATGTTCCTTGGGACTTACTGAGCAGCCCAAAACCCTGAGC CACATTCAGCCATCCAGCCAGGACTGTAGCCTCATGACCAGCACTCACCTGCAACCCTCATATCAG
Zebrafish	*Drmespba*	ENSDART00000045385; Sawada et al, 2000; called meso1c in Wang et al, 2009	GAGACAGCAATGGCTACCGTGAGCCTGCAGAGGTGTCACCTCGCACCTCCGAAATCCAACATATAAACCTCCATCCTCCTTTCA CCAGCACAGACACGACATGCAAACCTCAAGCAAGAACCAATGGAGCAGTTCCAGCTCCGAGTCCGAGTTTTCCAGCATTTCCT CTCCAGAGACAACTTCACCGGATCAGAGCTTCTCGCCGCCCCATCAAACCAAACCTCCGTGCTCCAAATTAGTCAAATCTTCTA ATATCATGAAGAAAAAGCGGAGATTGAGGCTGAAGAACCCGAGCGAGCAGCGGCAGAACGCTAGTGAGAAGGAAAAGCTGAG GATGAGGGATCTGACCAAAGCTCTTCATCATCTCAGGAGCTTCTTACCTGCTTCAGTAGCTCCGGTAGGACAAACCCTGACCAA AATCGAGACTCTGAGGCTGACCATACAATATATCTCCTTCTTGTCTTCTCAGCTTGGGCTCAGTGAAGAAGAGCTGAGCTACAG GAGACAAGAAAACTCCAGCGGATGCTCTTTGTCGAGTTTTGAGTGTTCGTCTGTGAGTGGAGGTTTTGTTGGGACGGAGCAGG GTTATGCTCTCTGTGATGGACAGTATGAGGACTGCTCTGGTTATGGAGGACAATACAGGGAGCGGTATGGAGGTTTGACACAG CAGCATTCAACGGAGCAAAACGGCTTGGTCAGTATTGACGGCTTCATCCAGAGTCAACAGTGTGGGCAGATGACACAGACACC GTACCAGGTTTACGGAAAAAACTTTGGCTATCATCTCGTTCCTCAGACTTACTGGAGATGACGGAAAGATCTCCATCACACCAAA AACTGAGGGCGGATAC
Zebrafish	*Drmespbb*	not annotated, but EST evidence maps to region within 25:11392500-11403500 (Zv9); called meso1b in Wang et al, 2009	ACAACCAATCTCCAACCACACAGAATGGACGCATCATCTCCTTTCTTCAACTACATCCAGCAAAACTCCTGGAGCTCAGACTCC GAACTCTACAACATCTCATCTCCAGAAACCGTTTCTCCTTCCTCCTACATGGACTTCTCTCCATCAGCGCAGGCTCAGAGCGTTT CTCCAAAACCAGAGATTTCGGGTTCCTCGTTTCAAGATGGTGGACGGTCCCGTGTTGGAGTTAGAAGAACGAGATGCAAGAAT CCTAGTAAACAAAGACAAAGCGCCAGTGAGAAGGAGAAGCTGAGAATGAGGGATCTGACCAAAGCTCTGCATCACCTCAGGAC GTACCTACCACCTTCTGTAGCTCCCGTTGGCCAAACGTTGACCAAAATCGAGACTCTTCGCCTTACCATCCGATATATTTCCTAT TTGTCTGCTCAACTAGGCCTCAGCGAAGAGTCTTTGTGCAAGATGAGAGACTTAAGGGTTTCCGGATATCAAGAGATGCCTCAA AACCACTGCTATTCCACTGCTGAGTTTTGGGGGTCATGTCAAAACAGCTGCGGAACTTCAGAATCTGTGTTGAGGAGGACGGAT ATGGATTGTCGGCAGGTTTTTATGGGAATGGAAAAACCGGCTTATGACGATTCCTTTAATTCCAGCTCAGAATCTCTTCTAGAGA GTCCGTTGTATGCTGATTCAGCATTGACATATCAGGGCTACAACAAAGGCGTCCACTGTTCGATCGCTCCAGAGTTCTGGGGAT GAATTCTCATCTAAATATTTAAAATTTTTCAAATGTTGAATATAAAGTTCAAATTTTTATGGACTTTTTTTGTACAGTATTTAATAAAT AACTTTTTATCTTAAAAAAAAAAAAAAA

SUPPLEMENTARY TABLE S1 (CONTINUED)

Stickleback	*Gamespb*	not annotated; sequence found by scanning genomic sequence and homology with other fish mespb squences	ATGGATACTTGCTCGGCCGCTCTGCTCAACCACAGCCTGCAGTACCAGTGGTTCTCCGACTCGGACCTCTCTAGCATCTCCTC CTCGGAGACCCTCTCGCCTGTCCTCTCCATGGACTCCAGCCTCTCTCCCTCCTCTTACCAGCAGCTGCATCAGTCCACTCCTAA GGGGGCCCAGACCGGATACTCCCAGACCCTCAGGTGCTCGCCCTGCTCGCGGTCCGGACGCGGCAGGAAGTCGGGCAGAG GCAGCCGGATGCGCAGCAAGCAGAGGGAGAGCGCCAGCGAGAAGGAGAAGCTGAGGATGCGAGATCTGACCAAGGCTCTGC ATCACCTCCGGTCCTACCTCCCGCCATCAGTGGCCCCCGCAGGACAGACCCTGACCAAGATAGACACCCTCCGGCTCACCATA AGCTACATCTCCTACCTGTCGGCCCAGCTGGGCCTCAGCGAGGAGGCGCTTTTCCAGAGGAGGGAACAAGGCGACACCTCGA CCAGCGACGCATCCTCGCCAGACATCCTCGGCTACTTCCAGCACGGCGCCGTGGGGGGACAGGAGGCCCAGCTGCAGGACC AGAGCCTGGACCAGAGCCTGAACCAGAGCCTGTACCAGGCCCAGTGCCACAGCCAGGGCACCGTGCTGCATTCTGGGAGCTG TGGTTTTGGGGCAGATCGGTACGACATGCAGTACTTTGAGGGTCCAATGGGAGACACGAGCTTGGAGGGAATCCTGCAGTCCT CTCCGGCAACACAGCCCTGCTGTCAGATGGGTGGCAAAGACTTCTGCATGCCGTTGGTTCCCAGAGAGTATTGGGGT
Medaka	*Olmespb*	ENSORLT00000018371; Terasaki et al, 2006	ATGGATACCTCCTCGGTCCCTTTTCTTGACTACAGCCTGCAGTACCAGTGGTGTTCCGACACGGACCTCTCCAGCACGTCTTCT CCAGAAACCCTGTCTCCTGTCTACTCCATGGACTCCAGCCTCTCCCCCTCCTACCAGCAGCCGTCACAGTCCACTCCCAGGGC AGCGAAGAACCCGTACTCCCAGAACCTCAAGTCCTCGCCCCGCTCCCCGTCTGGACGTGGCCGGAAGCTGGGCCAAGCCTCC CGGATCCGCAGCAAGCAGAGGGAGAGCGCCAGCGAGAAGGAGAAGCTGAGGATGAGGGATCTGACCAAGGCTCTTCATCAC CTCAGGTCCTACCTGCCGCCATCCGTCGCTCCTGCAGGCCAAACCCTGACCAAGATAGAAACGTTGCGCCTCACCATCCGCTA CATCTCCTACCTGTCCGCCCAGCTGGGCCTCAGCGAGGAGGTGCTGTTCCAGAGGAGGGAGCAGGCGGATACATCCGCCAGC TCCTCTCCTGACATCATCCGCTACTTCCAGAACGCCTCAGCAGCTGGACGGGCGGAGAGCCAGAGCCTGAACCAGAGCCTATA CCAGCTCCATCATTTCAGCCAGCATGCAGTGATGCATTCTGGGGAATGTAGTTTTGGAGCACCTCAGTTCAGCAGGCAGAACTC TGAGGGCGTTCAGGGAAACGTGAGGACCAGCGCAGAGCTACAGACACCTCCTGCCTCCCAGGCCTCCTGCCAGATGTGCGGC AAAGACTTCTGCACTCCTCTGGTTCCAAGAGAGTACTGGGGT
Tetraodon	*Tnmespb*	ENSTNIT00000015077 not full length; sequence found by scanning genomic sequence and homology with other fish mespb sequences	ATGGATACCTCCTCGGTGCCGCTGCACAGCTACGGCCTGCAGTGCCGGTGGTGCTGCACCGACTCGGACATGTCCAGCATCT CTTCCACGGAGACCCTGTCCCCTGTTCCTTCTCTGGACTCCAGCCTGTCCCCGTCCTACCAGCAGCCGTCCCAGTCCACTCCT CCGCTCAGGACGCCCAAGTCCTCACCCTGCTCCCTGTCCAGGCAAGGCCGGAGGGCCGGAAAAGCCGCTCGGATCCGAAGC AAACAGCGAGAGAGCGCCAGCGAGAAGGAGAAGCTGCGAATGAGGGATCTGACCAAGGCTCTGCATCACCTCCGGTCCTTCC TGCCTCCATCTGTGGTCCCGGCCGGACAGAACCTGACCAAGATCGAGACCCTGCGTCTCACCATCCGCTACATCTCCCACCTT TCAGCCCAGCTGGGCCTCAACGAGGAGGTGCTGTTTCAGCGGAGGGAGCAGAGGCACCGCTCAGCCGCCCACGGCTCCTCG ACAGGCATCCTCAGCTACCTCCAGCACCGCTCTGTGATTGGCCAGGAGGCCCAGCTGCCCAAGCAGAGCCCCAACCCGGGCC TGGAGCAGAGTCCCAGCCAGAACCCTGCCCTCCATGCTGAGAGCTGTAGTTTTGGAGCGCACCAGTTCGCGGCCGCTCCTGC GGAGGACCTGAGCCTGGACGCCATCCTGCACGCGCCGCCAGACACTCAAGCGTCCTGCCAGATGTGCGGCCCAGGGTTCTG CAGGCCGCTGGTTCCCAGAGAGTACTGGGCT
Fugu	*Trmespb*	ENSTRUT00000039275 not full length; sequence found by scanning genomic sequence and homology with other fish mespb sequences	ATGGATACCTCCTCGGTCCCACTGCACAACTGCGGCCTGCAGTTCCAGTGGTGTTCTGATTCGGACATCTCCAGCATGTCTTCA CCAGAGACCCTGTCCCCTGTTCCCTCTATGGACTCCAGCCTGTCTCCTTCCTACCAGCAGCTGCCAGAGTCCACTCCTCCGAA GGCGACCAGGACATTCAAGTCCTCACCCTGCTCTTTGTCAAGACGAGGCCGGAGGGCAGGCAAACCCACTCGGATCAGAAGC AAACAGCGAGAGAGCGCCAGTGAAAAGGAGAAGCTGAGAATGAGAGATCTGACCAAGGCTCTGCATCACCTGAGGTCCTACCT GCCACCATCTGTGGTCCCAGCTGGACAGAATCTGACTAAAATAGAGACACTGCGTCTCACCATCCGCTACATCTCCCACCTTTC AGCCCAACTAGGCCTCAACGAGGAGGTGCTGTTTCAGAGGAGGGAGCAGAGACACGCGTCAGCCACTGACAGCTCCTCACCA GACATTCTCAGCTACTTCCAGCACAGTTCTGCAATTGGCCAGGAGGTCCAGTTGCAGAACCAGAACCAGGGCCTGGATCAGCC CCTGTTCTCCTCCCACTGTCCCAGCCAGAACACTGCATTCCATTCTGGGACCTATAGTTTTGGAGTGAATCAGTACACTGTCGC TCCTCTAGAAGACATGAGTGTGGACGCCATCCCGCACACACCAACAGCCACACAACCATCCTGCCAGGTGTGCAGCACAGACT TCTGCATGCCGTTAGTTCCCAGAGAGTACTGGG
Amphioxus	Bfmesp	DQ395132	TCCAAACTTCCACAGTCGCGACCTTCAACAGGGTACAGTTTCTCCTCTCGTGACGACTTACAACGTTAGAAAGAAGCGTTGTGG GATCGTAAGACTTGGAAAAAGTGACAATTTCTGTGAGGAGCCCTCGGAAACTTTACAAACGTTATTCGCTTGTCACTGCGGTGT CCAGTTGACCGGGTGCGTTCTTGACGTTCAAAGTTTCTGACGACAGAGACTGAGACCTATGTATAGTAAGAATTGTATCAGAAA TGTCCATTCTCAGGGCTTGATATTTTGTGCGTACTCTGCTGGAGGCTTAGTTGAAGAGACGAGAGACGGCAAGCGGTGTTATG GCGTACGCAACCACTGACTTCTTCGAAAATGACGACGGATTGTCATCGCTTCTTCGGGCGGACACCCCGGTGACATCTGCCGA CCGAGACGGCTCGGACAGCTCCCCTTCTTTCGAAGACTCGGGCCTCAGTAGCGGGGGCAGCCCGGAGAGCTCAGCGCTGCT GCTAAACGGGGGAAGTCGCCGCCGTCGCCGAAGGAGGAAACCCCGTCTCACCGGGTTGAGCAAGCAGCGTCAGGCGGCTAA CGAACGCGAGAGGGTCCGCATGCAGAATCTCACCGCGGCGCTGGGAGTTCTACGGGAACACATCCCTCCACCGGTCGCTCCT AAAGACAAAAGACTATCAAAAATCGAGACTTTGAAGTTGGCCATCGGCTATATCGACTACTTGAGAAGAGTGCTCCAGGAATCG ACAGAGAATGCTGCGTCTCTTCTGCCACCTTCACTGGAAAGTCTGGCCAAGGAAGACGCAGAGTTCGACATCGACGGAAGTTT TGAGATTAAAGGACAGGACAAAGAGCAGAGGCGTCGAAGAAAGGACAGAACAGCAAGACATCGTCTCACTACTCCTCACTTTA ACGCTAAGAAGAGTCAGCAAACAAAGCCAGCACCAAGACCAACAGCCGCCAAGGTACGACCCAGACCATCAACTGTGTCATCC TGTAGCCCCAAGTCAGGCGGGAGTAACGACGGGATGTCAGTCAAACTGGAAACATGACGACGCTAAACATGTTGCTGCCACCT TATAGTTACTTTATGTAGTTCTTCTCGAAGTAGTTGTAGGGTACTCTCCAAGCAGAGGTTAGGCTCCGGCTGTTTTTTTTTTTGCG TTTTCTTTTTAGGCGTTTTTTATCGGGCTTTCTATTTTGTACCGTTTTCTTTATGTCTCGCGCAGAGGTTAGGCCGCAAGACATCA AGAAAACAGTACAAAATGGAAGGCCCGAAAAACGCCTAAAAAAAGTTGAAGTCTGCTTGGAGAGTAGATGTATGGTCCAGCTCA GAGTTTTACGCGTTTTTGAGGATTTTTTTCTGTGTCTTTCTCATTATTCGCAATTGAAACTNTTCGCTTCAAAAAGACACATTGAGT CGGATCCTACAGCTGCTTTGAGATTATAAACAGATGCGCTGCATTTATGATGTTGCTTGGGTTCCCTCAAATGGGCATCAAAATC TGGAAAAAAAAAGAAACTGTAGCCTGTATGCATGAAGAAATCCTGATTACTTGAAAGTGCCGTGGATGTGCTGTTATCCAACCG ACATAAAGGAAAAGAAGCCATATCATAACGAAAGTGTCCCGCCCCTGAATCGTCGCCAAAAAGATACCGTTACTCCTAAAAGAA AATATGTGTGTATGGATGGACGTTTTGCAAAGTGCTGATTGACCTGTCCTTAAGTCTTGCTCGTGATGTTAAAATGTTGATCATT GAAGTGTTCTCAGATGAGAAATTATTGCGGTACTGAAGAATACGTCTGGTTATCATATCATTGCGCCATGACATTGGTTTGTTAC TATTACTGTTCAGGTTTTGCTTGTTTGTGATATTATATAACAGGAAAACATTAAAGATTCTTATGT
Human	*HuMesp1*	ENST00000300057	CTGGAAGGGGCCACTTCACACCTCGGGCTCGGCATAAAGCGGCCGCCGGCCGCCGGCCCCCAGACGCGCCGCCGCTGCCAT GGCCCAGCCCCTGTGCCCGCCGCTCTCCGAGTCCTGGATGCTCTCTGCGGCCTGGGGCCCAACTCGGCGGCCGCCGCCCTC CGACAAGGACTGCGGCCGCTCCCTCGTCTCGTCCCCAGACTCATGGGGCAGCACCCCAGCCGACAGCCCCGTGGCGAGCCC CGCGCGGCCAGGCACCCTCCGGGACCCCCGCGCCCCCTCCGTAGGTAGGCGCGGCGCGCAGCAGCCGCCTGGGCAGCG GGCAGAGGCAGAGCGCCAGTGAGCGGGAGAAACTGCGCATGCGCACGCTGGCCCGCGCCCTGCACGAGCTGCGCCGCTTTC TACCGCCGTCCGTGGCGCCCGCGGGCCAGAGCCTGACCAAGATCGAGACGCTGCGCCTGGCTATCCGCTATATCGGCCACCT GTCGGCCGTGCTAGGCCTCAGCGAGGAGAGTCTCCAGCGCCGGTGCCGGCAGCGCGGTGACGCGGGGTCCCCTCGGGGCT GCCCGCTGTGCCCCGACGACTGCCCCGCGCAGATGCAGACACGGACGCAGGCTGAGGGGCAGGGGCAGGGGCGCGGGCTG GGCCTGGTATCCGCCGTCCGCGCCGGGGCGTCCTGGGGATCCCCGCCTGCCTGCCCCGGAGCCCGAGCTGCACCCGAGCC GCGCGACCCGCCTGCGCTGTTCGCCGAGGCGGCGTGCCCTGAAGGGCAGGCGATGGAGCCAAGCCCACCGTCCCCGCTCCT TCCGGGCGACGTGCTGGCTCTGTTGGAGACCTGGATGCCCCTCTCGCCTCTGGAGTGGCTGCCTGAGGAGCCCAAGTGACAA GGGACAACTGACGCCGTCTCTGTGAGCACCGAGGCTTTTTGGCCTCAGCACCTTCGAAGTGGTTCCTTGGCAGACTGCCTTTC CTGGAAGAGGGCACGGGCGATCCCGACGGGGGCATTCCTGCGGGTGAGAGCCGTCCCCACCGCGGCGGCCCTTCTCAGCCC CTCCCTCCATGGAGGGACCCATAGGGCTAGACACTTTGAGGCAAGCAGGAGGCTCTGCCTAATGTGAATTTATTTATTTGTGAA TAAACTGTACTGGTGTCAGTTGGCAATTTCTTCTTCCTACCCGTGGACACAGAGCTCCCTCTCTCCCTCCAAAGAAGAGCATGG GAGAGGTGGGAGGGGTTCTTGCAATCTTTAGCCCCCCGACCCCCACAGGCCCAGACCCCTTTGGCCTTACCCCCAGCCCTGG CTCAGCATCTAGTCCAGATGGGTCAGCCTGGAATGGGTGGGGAGGGACGTCCTGTGAGAAGGCAGCGGCAAGTAGAATCTGC TCATCTTTTCTTTGAACCTGGTGGGGAACTGGTTAAAACCAAAATATCTGTGTAGAAATACAACTCCATTATTGAGTATTTATTGT ATGTACATCAGGTACCTATTATACTCAAGTAACCATTTTACAGAAGGATGAGGATCAGCGCTCAAGCCCAGGTAGGCCTCCAGA GTCCCAGCGCTCAGCTCTTGTGGGATTTTGCCAGCTCCATACATGTTGGGGCCTGAGGGATAACAGCTCCAAGGGGTTATTTT CTTGCATCCTGTGGTCTTATTCTCCATGCACGGGAGCATCCTGGCCTTGGAACTCCCCCACCCTCCGCCGGCATTTTCCCATCT GCCTTTTCTCTGGTTTCCCCACCTTGTGGCTTAGAGACATAAATAATGGTGTGGCGGTCCTGAGTTTATATACCATGACCTCCTA CAGGCCTAGATGGGGTGAGATGAGGGGCCCATGGGGTTGCATCGGAATCCACACAGGCAGTTGCGTGCCTGTCTGCATTGGC TGGATTCACATCAGGGAGCAAGAAACGGGAGGCTTGAGCCCAGAAAGTGTGTCCTCATCCAGCCAGGGTGTCTGGGCAACAG TCATGATTAGAGGGTGCGGTGGGGAGAAGGGATGTGTAGCCTCTCTGCCAAGCGTCCTTTACCCTCTATGGATAGATACCCAG TTCTCCCCTCCTCTCCTTCAAGTGTCTGAAACACAGGCTTCAGTGTCTGTTTTTATAAGAGCTTTATTAGGATACAATTCACATAC CATAAAATTCACTCTTTTAACAACTGAATGGCTTTAGTACATCCACAGAGTTGTGCAAGCATTGCCACTAATTTTAGAACGTTTTC ACCCCCAAAAGAAACCGTATACCTGTTAACATCACTCCTCACTATTCCCTACTCCCAGTCCCTGGCACTCACTCTTCTAGTCTC TGTCTCTATAGGTTTGCTTTTTCAGGACATTTCATATAAAAGGAATCGCAAAATACG

SUPPLEMENTARY TABLE S1 (CONTINUED)

Human	*HuMESP2*	ENST00000341735	ATGGCCCAGTCGCCTCCTCCGCAGAGCCTCCTCGGCCACGACCACTGGATCTTCGCCCAGGGCTGGGGCTGGGCCGGCCAC TGGGACTCCACGTCCCCGGCCTCCTCCTCCGATTCGTCGGGTTCGTGCCCCTGCGACGGCGCCCGCGGACTCCCGCAGCCA CAGCCTCCGAGCTGCAGCTCCCGAGCCGCAGAGGCAGCCGCGACGACGCCCAGACGAGCGCGCACCGGACCAGCGGGCGG ACAGCGGCAGAGCGCCAGCGAGCGGGAGAAACTGCGCATGCGCACGCTGGCCCGCGCCCTGCACGAGTTGCGCCGCTTTCT GCCTCCCTCCTTGGCGCCGGCCGGCCAGAGCCTGACCAAGATCGAGACGCTGCGCCTGGCCATCCGCTACATCGGCCACCTA TCGGCCGTGCTGGGTCTCAGCGAGGAGAGTCTGCAGTGCCGGCGCAGGCAGCGCGGGGACGCGGGGTCCCCTTGGGGCTG CCCGCTGTGCCCCGACCGTGGCCCCGCAGAGGCGCAGACGCAGGCGGAGGGGCAGGGGCAAGGGCAGGGGCAGGGGCAG GGGCAAGGGCAGGGGCAAGGACAGGGGCAAGGACAGGGGCAAGGGCAGGGGCGCAGGCCGGGCCTGGTCTCCGCCGTCC TCGCCGAGGCGTCCTGGGGATCCCCGTCCGCCTGCCCCGGAGCCCAAGCCGCACCCGAGCGCCTGGGGAGGGGGGTCCAC GACACGGATCCCTGGGCAACACCCCCTTACTGCCCCAAGATACAGTCGCCCCCGTATTCGTCCCAAGGGACAACCTCCGACG CGTCTCTTTGGACGCCACCCCAAGGCTGTCCCTGGACGCAGTCGTCCCCAGAGCCCCGGAACCCACCAGTGCCCTGGACGGC GGCCCCAGCAACTTTGGAGCTGGCCGCAGTGTACCAGGGTCTCTCTGTGTCTCCAGAGCCCTGTCTGTCGCTGGGAGCTCCA TCTCTCCTGCCCCACCCATCATGCCAGAGACTGCAGCCTCAGACCCCCGGGAGGTGCTGGAGCCACAGTGCAGAGGTGGTGC CCAACTCAGAGGACCAGGGACCGGGCGCCGCCTTCCAGCTCAGTGAAGCAAGCCCTCCCCAGAGCTCAGGCCTGCGGTTCA GTGGCTGCCCTGAACTTTGGCAAGAAGATCTGGAGGGGGCCCGCCTGGGCATCTTCTACTAAATGGCCTCGGCTTCCCTCTTT CCATCCAGGAATCAGTCCTGTAGCTTGGGTGCCTCCTTATTTGTTAATTAGTGGCTTTTCATGTTCTCCTTTAGCCAAGGCTCCC TTTTTCCAAGTGATGTCTTTCAGGGAAGCAGTGTTTGAAATAGATAGCGGGTACCTTCCCTGGATGGAGTCAGGGCGGGGGCA CTGTCCTCCACTGCTAGACACCCCCAGAATGCCTGGCGCTCTGCAGAGCACAGTCTGAGCTGCTCTAAGAAGGGGTCTCCTTT ACCCTAAAGGCAGCTGGGCAGGGACAGGTGGGAGAATGGGTGTAGGAGGCAGGCCCCAGGCTCTGCTTCTTGGTGACAGTTG GCCAGAGCCCTGTATGCTTTGATTTTTTTGTACTTAAAAAGAAAAAACACACACAC
EST sequences			
Salmon	Ssmespaa	Salmon WGS trace read (ti|2271345710)	GGGAATCTTTTACCGGGATTTAAGGTCATGTCCTGATAGGAGACCGCTGATGTCAGGTAGTCTGGTTGTGGCTCTGTGTTGTT GGTACATGATGTGACCAGTGGCAGACAGTATTGATCATTGCTCTGGATGTTCCCCTGTAGTCTCTCCTGATACCATTTTCCAGA CATAGAGCTTCCCTGAGGGCATTGTGGCATATACTGGCATGGTGTGGTTTCCATCTCTCTTTTCAGGCATGGCTCCTTCTCGC TGAGCTCCAGCTGCGCCGACAGGTGGGAGATGTAGCCGATGGTGAGGCGCAGGGTCTCGATCTTGGTCAGAGTCTGTCTAG CCGGAACCACAGAAGGGGGCAGGTAGGTCCTGAGGTGGTTGAGGGCTTTGGTCAGGTCTCTCATCCTCAGCTTCTCCCTCTC GCTGGCGCTCTCCCGCTTCTTCCCAGGGAACTTGGACCTAGACCTCTTCTCCTGAGCTGGGAGTTTTTCTATCCTCTTTCTTTT GGCAACATGGCTGATGCAGCCTGAAGCGTTGGAATCTTCCTTCTCCTGACCACCTCCCCACTGTAAACAAGGGGGAGAGAGG CAGAAGGAGTCAATGGAGGAGGCAGGTGACAGGCTACTACAGGCACTGTAATAACCAGGGTCGGAGCTGGGACAGCTCGGC TTCAGAAAGCCATCACTGTCCAGCAGATGCTCTCCAGCCTGAAGAAACAAGAGTTTAGAGGAATCAACGGAATCCATTACTGC AGTGTTTTCTGAGCTATGAATATCTTCAGTCTGTCTGTCCTTTGGAGAGGTTGTGAGGAAT
Salmon	Ssmespab	Salmon WGS trace read (ti|2265529949)	CGACTGGCTCCTTCTCGCTGAGCTCCAGCTGCGCCGACAGGTGGGAGATGTAGCCGATGGTGAGGCGCAGGGTCTCGATCT TGGTCAGAGTCTGTCTAGCCGGAACCACAGAAGGGGGCAGGTAGGTCCTGAGGTGGTTGAGGGCTTTGGTCAGGTCTCTCA TCCTCAGCTTCTCCCTCTCGCTGGCGCTCTCCCGCTTCTTCCCAGGGAACTTGGACCTAGACCTCTTCTCCTGAGCTGGGAGT TTTTCTATCCTCTTTCTTTTGGCAACATGGCTGATGCAGCCTGAAGCGTTGGAATCTTCCTTCTCCTGACCACCTCCCCACTGT AAACAAGGGGGAGAGAGGCAGAAGGAGTCAATGGAGGAGGCAGGTGACAGGCTACTACAGGCACTGTAATAACCAGGGTCG GAGCTGGGACAGCTCGGCTTCAGAAAGCCATCACTGTCCAGCAGATGCTCTCCAGCCTGAAGAAACAAGAGTTTAGAGAAAT CAACGGAATCCATTACTGCAGTGTTTTCTGAGCTATGAATATCTTCAGTCTGTCTGTCCTTGGAGAGGTTGTGAGGAGTACTGG AGGACCCCAGAGCTGCTCCCCAATTTATCCTACAGGCAGGTGTGATATGGCACCTTCAGGGTGCCTGGACTTCAAAGTGACC AAGTACAGATCACACTAGACTTACGGGGTCCCTGGGAAACATCCTCCTAGAGCCAGGTGTTAGGTGGCAGGCAGATTAGAAT GAAATCTGCATCAAGTTCAAGAATTCATGGTGGGAGAGATTATTGTTTTGAACAATTCTCTAAATTGGGCAGTATCGGATAGGA ATGTATTTGATTAT
Salmon	Ssmespba	Salmon WGS trace read (ti|2272889492)	GTTTGAAGGTGATACCTGGGTGTCCCGACACGTTGACGTTCAGCTCCTTCCTCTGACACACAGCCTCCTCGCTGAGCTCCAG CTGCGCTGACAGGTGGGAGATGTAGCTGATGGTGAGGCGCAGCGTCTCGATCTTGGTCAGAGTCTGTCCAGCCGGAACCAC AGAAGGGGGCAGGTAGGTCCTGAGGTGGTTGAGGGCTTTGGTCAGGTCTCTCATCCTCAGCTTCTCCTTCTCGCTGGCACTC TGTCTCTGCTTGCTGGGGTTCTTGGAGCGGTTCTTTCTAATCCTCCCTCCGGAGAGTCCTCCCTCATCGCTGGAGGATGGGG AAGCGGATGCCTTGGCTCCTCCAGAGTGTGTGGATCTGTGAGGTTCTGTGGCGGTCCCCCGAGGCAGGCAGGAGGATGAGA AGTCCATGTAGGCAGAAGGGGAGAGGATACAGGTCTCTGGAGAGGAGACGTTATAGAACTCAGAGTCCGAACTGGGATAACT CCAGTGGTACTGAACACCAACACTATATTTGCTGAGAAGAGGGGCAGAGATATCCATGCTGTCTGTCTGTGTCCTGTCCTGCG TGTTGAGCGGTACGACTGAACTGAAGAGCTTGGCCTGTGGGCTGGTGAAGAGGAGAGCCCTGGTTTTATGCAGGAGTTGGA GGTGTGAAGTGACACCTCTGCAGGCCCTCTCAGGCCATCAACATGGCTTCCCAGAGCTTCTCAGAGCTTCCCAGAGCTCAGC CCTACTGGACAGAGAGAGGCGCCACCATGCAGTCCTCTGCTGGGAAATAATACAACTACTGCTGCTCAGAGAAGAGACGTGG TCAAATTTGACCCCCTGACCCAAAACAATAAAACATTTTTTTGCCTCCTCATAAAGGTTTTTTTGCCCCTTTTGTGGGCCTTCCA AAGTTTCTTC
Salmon	Ss mespbb	Salmon WGS trace read (ti|2278022697)	GAATTCGTCCTTCTCTGAGCAGCAGTAGTTGTATTTTTTCCCAGCAGAGGACTGCTTGGTGGCTACTCTCTCTGTCCAGGAGC TCTGGGAGGCCATGATGATGGTCTGAGAGGGTCTGTAGAGGTGTCACTTCACACCTCAGACTTCTGCATAAAACCAAGGCTCT CCGAATGACCAGCCCACAGGCCAAGCTCTTCAGTTCAGTCCTACTGCTCAACATACAGGACACAGCATGGATATCTCTGCTCC TCTACTCAGCAACTATAGTGTTGGTGTGCAGTACCACTGGAGTTATCCCAGTTCAGACTCTGAGTTCTATAACCTCTCTTCTCC AGAGACTTGTATCATCTCCCCGACCTCCTGCATGGACTTCTCTCTCTCCTGGCTACCTCGGGGGACCGCCACAGGACCTCAC AGGTCAACATACTCTGGGGGAGCCAAGGCATCCGCTTCCCCATCCTCCAGTGACGAAGGAAGACTCTCTGGAGGGAGGATTA GAAAGAACTGCTCCAAGAACCCCAGCAAGCAGAGACAGAGTGCCAGCGAGAAAGAGAAGCTGAGGATGCGAGACCTGACCA AAGCCCTCCACCACCTCAGGACCTACCTGCCCCCCTCTGTGGCCCCGCCTGAACAGACTCTGACCAAGATCGAGACGCTGC GCCTCACCATCAGCTACATCTCCCACCTGTCTGCCCAGCTGGGACTCAGCGAGGAGGCTCTGTGCCAGAGGAAGGAGCTAAA CCTCAACGCATCAGGAAACCCCATATCACCTCAACAAGAAGTGTGCCAGTTTCACCCCCTCCCTCCTCAGGGAACTGGTGGG GGAGAGGGAGGCCAAAAAATTGGGGAAGAATGGGTGCAGGGGGCAATCCACCCCGAAACCCCTTCCCCACCCAACCAA
Fathead minnow (*Pimephales promelas*)	*Ppmespbb*	EST (GenBank Acc: DT342990)	GACATTTAGATACTTTTTATTATTATAAATAGCAATAAATTAGTACTTCTGTACAAAAAAACGATAACATACAAAATATATAATATT AAAATAGACATCTTAAAATAAGATAAAACAATATATTAAAAATACATTAAATACTATACAGCACAGTCCATAAAAGTTTGAAATAT GTGAAAAAAGTCCAATGAGAGTTTCATCCCCAGAATTGCGGAGCAACCGGATAGTGCACGGCTTTGTTGTAGCCCTGGTATGC TGTGGCTGTATCTGCATACAAAGGGCTGGCCAGAAGAGATTCTGAGCTGGAGTTGAAGGAATCATCATAAGCAGGTGTTTCCA TGACCATCTCTGTCTGCCTCAAGGCATGCTCTGAAGGTTTGAAGGTGCTTTGACACAGTTCTTGATGTGATGTGCTGATTCCC CAATACTCTGGGGTTGAATTGCCCTGACATTGAGACGGTTCTTGGTATCTAGAAGCTCCAAGGTCCCTCATCTGGCAGAGAGA CTCTTCGCTGAAGCCTAGTTGAGCAGACAGATAAGAGATGTAGCGGATGGTGAGGCGAAGGGTCTCGATCTTCGTCAAGGTT TGACCGACAGGAGCCACTGAAGGAGGTAAGTAAGTCCTGAGGTGATTGAGAGCTTTGGTCAAGTCCCTCATTCTGAGCTTCTC TTTCTCGCTGGCACTCTGCCTTTGCTTGCTCGGGTTCTTGGAGCGCGTTCTTCTTGTTCCGACACGGGAACATGCGCCGTCCT GATGTAATGA
Turner's minnow (*Poeciliopsis turneri*)	*Ptmespb*	EST (GenBank Acc: HO912189)	CCTGAAGTCCTCACCTTGCTCCCTGCCTGGACGTGGCCGGAAGACGGGTCGGAACACCCGGATCCGCAGCAAGCAGAGGGA GAGCGCCAGTGAGAAGGAGAAGCTGAGGATGAGGGATCTGACCAAAGCTCTGCACCAACCTCAGGTCCTCACCTCCCACCTTCA GTCGCACCTGTTGGGCAGACTCTGACGAAGATAGAGACACTCCGTCTCACCATCCGCTACATCTCCTACCTGTCAGCTCAGCT GGGCCTGAGTGAGGAGGTGCTATTTCAGAGGAGGGAACAAGTGGACACCTCAGCCAGTGACACGTCTTCTCCTGATCTCATT AGCTACTTTCAAAACTCATCCGCTGGAAAACACAGGCAGAACCAGAACCCGTACTCCAGCCTGTGTTACAGCCAGAACAGACC GCTGCATTCTGGGCATTGTAGCTTTGGGGTGAATCAGTTGAGAACGCAGTACGGTGAAGGCCCTCAGGGAGACATGAGCGTG GATGCTGCTCTGCAGTCACCTCCAGCATCCCAGCCCTCTTGTCAGGTTTGTAAACATTTACTCATTCACATCTCCGATTTGTTT AATGCAACAGCATATTTTGTTCATTCTAACACATTCACTCTTTGTCTGTTTACAAACAGATGTGTGGCAAAGACTTCTGCATCCC ACTTGTGCCAAGAGACTACTGGGGCTGACCTCTCAGTGACCACAGAGCCAAACCCCTTC

SUPPLEMENTARY TABLE S1 (CONTINUED)

Protein sequences			
Zebrafish	Drmespaa	ENSDARP00000005591; Sawada et al, 2000; called mesp1 in Wang et al, 2009	MDASTFSLQLQNCSFFLPDSQNQSFAVSDAGYYSATGSLSPTSSIDSCSFSPPAYSLLPQIFPKSIQKTDVQPPKRTGRPKSKFPGV KRQTASEREKLRMRDLTKALHHLRTFLPASVAPVGKTLTKIETLRLAIKYISCLSDQLGCGEDVEICEAQDEVISTSASVFDNFSSASS ASQSLPAQQFMSMSCYQTQNPVQGDFHSFPAQDVWFSQQHNFFHGQC
Zebrafish	Drmespab	ENSDARP00000090346 is not full length; called mesp2 in Wang et al, 2009	MEFNLPPYLLQAARCKLEPISSADCGYFSACGSLSPSSSIDSGCFSPPWGAGRQLEGPENANVDCLQAKKLKLALPVDSKRRSRSK NPGMKRQSASEREKLRMRDLTKALHHLRSFLPPSVAPAGQTLTKIETLRLAISYISHLSDQLRQAEVPNYEMCCSAEASDRFQSGLV FENVCMDGQQGLMQDNVQYCPTLTSFGDSREQMENSFPATSHFRDAQSYMFPCTTMDDASYSHQFYQ
Stickleback	Gamespa	ENSGACP00000019492; *Mesp2*	MDVSYCSPLQLQDNSFLFESLLDKPYDPLAYDPSLDPGYFSACSSSLSPTSSVDSYCFSPTSLQVAGSEPNSTDRFVFKSPAVPGL PQGTQRPPCSGSSAATSSTARKSRSRYPGKKRQTASEREKLRMRDLTKALQHLRTYLPPSAAPAGQNLTKIETLRLTIRYISYLSAQ LGLSEEALEQRACGFSEKPQNLIEFLGQPGAGYGPVSSAHLQPSHQNLSWQVSNGVCFTSEQFWMPQQQQLQNAVFSGQS
Medaka	Olmespa	ENSORLP00000018373; Terasaki et al, 2006	MEMSFCFPLQFQENPLQFDWESLQEKPLGPDPSSDAGYHSAASSLSPTSSVDSCCFSPASLQTVGTEQDVLESFLFCSPAELHLT CQTGPPSSLSSASSPTAKKSRSRYLGKKRQTASEREKLRMRDLTKALHHLRTYLPPSVAPAGQTLTKIETLRLTIRYISYLSAKLGLS EEVLEQRRSLEPTQALGHLQGQQRASYGAQETSCSTVNEQRSSPQQSSQASDGVQFWIQQQQHPAVIFSGQC
Tetraodon	Tnmespa	ENSTNIP00000014876 not full length; sequence found through scanning genomic sequence and homology with other fish mespa squences	MDLQLQDSPLLFDCESLLDESYQHVVFDPAVDPGYFSAGSCSSPTSSVDSFSFSPTSLQAAGAEQTPLDRLLFSSPGASGRSREPH SLQSCTSSSSSSRRSRSKYPGKKRQTASEREKLRMRDLTKALHHLRTHLPPSVAPPGQTLTKIETLRLTIRYVAHLWAQLGLTEEVL EQRRSCGWPQSLSQVQPTERGAMSSARLRHLQPPPQVCSSFPSGQYWFPQQQQEEVEVEAWAFSHL
Fugu	Trmespa	ENSTRUP00000039137 not full length; sequence found through scanning genomic sequence and homology with other fish mespa squences	MEVSHCSPFQLQDTSLLFDCESLLDKSYDHMVSDPAMDPGYFSASSSLSPTSSVDSFSFSPTSLQAAEPEQCPLDGFLFSSPAAPL TSEPQTLQSSRPSSSDTKKSRSRYPGKKRQTASEREKLRMRDLTKALHHLRTYLPPSVAPAGQTLTKIETLRLTIRYIAYLSSQLGLT EEALEQKCSLGLTEQPKTLSHIQPSSQDCSLMTSTHLQPSYQTVYNRQSTSFVIACKPENNCLSGKTETIFFSGS
Zebrafish	Drmespba	ENSDARP00000045384; Sawada et al, 2000; called meso1c in Wang et al, 2009	MQTSSKNQWSSSSSESEFSSISSPETTSPDQSFSPPHQTKPPCSKLVKSSNIMKKKRRLRLKNPSEQRQNASEKEKLRMRDLTKAL HHLRSFLPASVAPVGQTLTKIETLRLTIQYISFLSSQLGLSEEELSYRRQENSSGCSLSSFECSSVSGGFVGTEQGYALCDGQYEDC SGYGGQYRERYGGLTQQHSTEQNGLVSIDGFIQSQQCGQMTQTPYQVYGKNFGYHLVPQTYWR
Zebrafish	Drmespbb	not annotated in Ensembl, but EST evidence maps to region within 25:11392500-11403500 (Zv9); called meso1b in Wang et al, 2009	MDASSPFFNYIQQNSWSSDSELYNISSPETVSPSSYMDFSPSAQAQSVSPKPEISGSSFQDGGRSRVGVRRTRCKNPSKQRQSAS EKEKLRMRDLTKALHHLRTYLPPSVAPVGQTLTKIETLRLTIRYISYLSAQLGLSEESLCKMRDLRVSGYQEMPQNHCYSTAEFWGS CQNSCGTSESVLRRTDMDCRQVFMGMEKPAYDDSFNSSSESLLESPLYADSALTYQGYNKGVHCSIAPEFWG
Stickleback	Gamespb	not annotated; sequence found by scanning genomic sequence and homology with other fish mespb squences	MDTCSAALLNHSLQYQWFSDSDLSSISSSETLSPVLSMDSSLSPSSYQQLHQSTPKGAQTGYSQTLRCSPCSRSGRGRKSGRGS RMRSKQRESASEKEKLRMRDLTKALHHLRSYLPPSVAPAGQTLTKIDTLRLTISYISYLSAQLGLSEEALFQRREQGDTSTSDASSPD ILGYFQHGAVGGQEAQLQDQSLDQSLNQSLYQAQCHSQGTVLHSGSCGFGADRYDMQYFEGPMGDTSLEGILQSSPATQPCCQ MGGKDFCMPLVPREYWG
Medaka	Olmespb	ENSORLP00000018370; Terasaki et al, 2006	MDTSSVPFLDYSLQYQWCSDTDLSSTSSPETLSPVYSMDSSLSPSYQQPSQSTPRAAKNPYSQNLKSSPRSPSGRGRKLGQASRI RSKQRESASEKEKLRMRDLTKALHHLRSYLPPSVAPAGQTLTKIETLRLTIRYISYLSAQLGLSEEVLFQRREQADTSASSSPDIIRYF QNASAAGRAESQSLNQSLYQLHHFSQHAVMHSGECSFGAPQFSRQNSEGVQGNVRTSAELQTPPASQASCQMCGKDFCTPLVP REYWG
Tetraodon	Tnmespb	ENSTNIP00000001974 not full length; sequence found by scanning genomic sequence and homology with other fish mespb sequences	MDTSSVPLHSYGLQCRWCCTDSDMSSISSTETLSPVPSLDSSLSPSYQQPSQSTPPLRTPKSSPCSLSRQGRRAGKAARIRSKQR ESASEKEKLRMRDLTKALHHLRSFLPPSVVPAGQNLTKIETLRLTIRYISHLSAQLGLNEEVLFQRREQRHRSAAHGSSTGILSYLQH RSVIGQEAQLPKQSPNPGLEQSPSQNPALHAESCSFGAHQFAAAPAEDLSLDAILHAPPDTQASCQMCGPGFCRPLVPREYWA
Fugu	Trmespb	ENSTRUP00000039134 not full length; sequence found by scanning genomic sequence and homology with other fish mespb sequences	MDTSSVPLHNCGLQFQWCSDSDISSMSSPETLSPVPSMDSSLSPSYQQLPESTPPKATRTFKSSPCSLSRRGRRAGKPTRIRSKQ RESASEKEKLRMRDLTKALHHLRSYLPPSVVPAGQNLTKIETLRLTIRYISHLSAQLGLNEEVLFQRREQRHASATDSSSPDILSYFQ HSSAIGQEVQLQNQNQGLDQPLFSSHCPSQNTAFHSGTYSFGVNQYTVAPLEDMSVDAIPHTPTATQPSCQVCSTDFCMPLVPRE YWG
Amphioxus	BfMesp	ABD57444.1	MAYATTDFFENDDGLSSLLRADTPVTSADRDGSDSSPSFEDSGLSSGGSPESSALLLNGGSRRRRRRRKPRLTGLSKQRQAANER ERVRMQNLTAALGVLREHIPPPVAPKDKRLSKIETLKLAIGYIDYLRRVLQESTENAASLLPPSLESLAKEDAEFDIDGSFEIKGQDKE QRRRRKDRTARHRLTTPHFNAKKSQQTKPAPRPTAAKVRPRPSTVSSCSPKSGGSNDGMSVKLET
Human	HuMESP1	ENSP00000300057	MAQPLCPPLSESWMLSAAWGPTRRPPPSDKDCGRSLVSSPDSWGSTPADSPVASPARPGTLRDPRAPSVGRRGARSSRLGSGQ RQSASEREKLRMRTLARALHELRRFLPPSVAPAGQSLTKIETLRLAIRYIGHLSAVLGLSEESLQRRCRQRGDAGSPRGCPLCPDDC PAQMQTRTQAEGQGQQGRGLGLVSAVRAGASWGSPPACPGARAAPEPRDPPALFAEAACPEGQAMEPSPPSPLLPGDVLALLET WMPLSPLEWLPEEPK
Human	HuMESP2	ENSP00000342392	MAQSPPPQSLLGHDHWIFAQGWGWAGHWDSTSPASSSDSSGSCPCDGARGLPQPQPPSCSSRAAEAAATTPRRARTGPAGGQ RQSASEREKLRMRTLARALHELRRFLPPSLAPAGQSLTKIETLRLAIRYIGHLSAVLGLSEESLQCRRRQRGDAGSPWGCPLCPDR GPAEAQTQAEGQGQGQGQGQGQGQGQGQGQGQGQGQGQGQGRRPGLVSAVLAEASWGSPSACPGAQAAPERLGRGVHDTDPWAT PPYCPKIQSPPYSSQGTTSDASLWTPPQGCPWTQSSPEPRNPPVPWTAAPATLELAAVYQGLSVSPEPCLSLGAPSLLPHPSCQR LQPQTPGRCWSHSAEVVPNSEDQGPGAAFQLSEASPPQSSGLRFSGCPELWQEDLEGARLGIFY
translated EST sequences			
Salmon	Ssmespaa	translation of Salmon WGS trace read (ti|2271345710)	MDSVDSSKLLFLQAGEHLLDSDGFLKPSCPSSDPGYYSACSSLSPASSIDSFCLSPPCLQWGGGQEKEDSNASGCISHVAKRKRIE KLPAQEKRSRSKFPGKKRESASEREKLRMRDLTKALNHLRTYLPPSVVPARQTLTKIETLRLTIGYISHLSAQLELSEKEPCLKREME TTPCQYMPQCPQGSSMSGKWYQERLQGNIQSNDQYCLPLVTSCTNNTEPQPDYLTSAVSYQDMTLNPGKRFC
Salmon	Ssmespab	translation of Salmon WGS trace read (ti|2265529949)	MDSVDFSKLLFLQAGEHLLDSDGFLKPSCPSSDPGYYSACSSLSPASSIDSFCLSPPCLQWGGGQEKEDSNASGCISHVAKRKRIE KLPAQEKRSRSKFPGKKRESASEREKLRMRDLTKALNHLRTYLPPSVVPARQTLTKIETLRLTIGYISHLSAQLELSEKEPV
Salmon	Ssmespba	translation of Salmon WGS trace read (ti|2272889492)	MDISAPLLSKYSVGVQYHWSYPSSDSEFYNVSSPETCILSPSAYMDFSSSCLPRGTATEPHRSTHSGGAKASASPSSSDEGGLSG GRIRKNRSKNPSKQRQSASEKEKLRMRDLTKALNHLRTYLPPSVVPAGQTLTKIETLRLTISYISHLSAQLELSEEAVCQRKELNVNV SGHPGITFK
Salmon	Ss mespbb	translation of Salmon WGS trace read (ti|2278022697)	MDISAPLLSNYSVGVQYHWSYPSSDSEFYNLSSPETCIISPTSCMDFSLSWLPRGTATGPHRSTYSGGAKASASPSSSDEGRLSGG RIRKNCSKNPSKQRQSASEKEKLRMRDLTKALHHLRTYLPPSVAPPEQTLTKIETLRLTISYISHLSAQLGLSEEALCQRKELNLNASG NPISPQQEVCQFHPLPPQGTGGGEGGQKIGEEWVQGAIHPETPSPPNQ
Fathead minnow (*Pimephales promelas*)	*Ppmespbb*	translation of EST (GenBank Acc: DT342990). Lacking N-term and second exon.	SLHQDGACSRVGTRRTRSKNPSKQRQSASEKEKLRMRDLTKALNHLRTYLPPSVAPVGQTLTKIETLRLTIRYISYLSAQLGFSEESL CQMRDLGASRYQEPSQCQGNSTPEYWGISTSHQELCQSTFKPSEHALRQTEMVMETPAYDDSFNSSSESLLASPLYADTATAYQ GYNKAVHYPVAPQFWG
Turner's minnow (*Poeciliopsis turneri*)	*Ptmespb*	translation of EST (GenBank Acc: HO912189). Lacking N-term and second exon.	LKSSPCSLPGRGRKTGRNTRIRSKQRESASEKEKLRMRDLTKALHHLRSYLPPSVAPVGQTLTKIETLRLTIRYISYLSAQLGLSEEVL FQRREQVDTSASDTSSPDLISYFQNSSAGKHRQNQNPYSSLCYSQNRPLHSGHCSFGVNQLRTQYGEGPQGDMSVDAALQSPPA SQPSCQVCKHLLIHISDLFNATAYFVHSNTFTLCLFTNRCVAKTSASHLCQETTGADLSVTTEPNPF

SUPPLEMENTARY TABLE S2

COMPARISON OF ZEBRAFISH MESP-AA, MESP-AB, MESP-BA, MESP-BB WITH OTHER MESP-RELATED PROTEINS

	% identity			
	Full length protein		bHLH domain	
	huMESP1	huMESP2	huMESP1	huMESP2
Mesp-aa	25.4	18.9	74.1	72.2
Mesp-ab	26.5	27.4	83.3	81.5
Mesp-ba	29.6	24.9	75.5	73.5
Mesp-bb	31.1	23.9	79.6	77.6

	% identity over full-length protein							
	Medaka mesp-a	Medaka mesp-b	Fugu mesp-a	Fugu mesp-b	Tetraodon mesp-a	Tetraodon mesp-b	Stickleback mesp-a	Stickleback mesp-b
Mesp-aa	38.5	36.3	35.3	33.3	38.9	34.3	39.8	36.2
Mesp-ab	38.1	33.6	37.2	31.9	35.7	32.5	39	31.7
Mesp-ba	35.4	41	35	40.5	35.1	40.8	34.3	40.4
Mesp-bb	34.6	42	34.2	41	37.9	39.9	33.7	40.3

	% identity over full length protein		
	Mesp-aa	Mesp-ab	Mesp-ba
Mesp-aa			
Mesp-ab	41.2		
Mesp-ba	38.9	32.3	
Mesp-bb	32.7	32.2	42.2

	% identity over bHLH domain (protein sequence)		
	Mesp-aa	Mesp-ab	Mesp-ba
Mesp-aa			
Mesp-ab	87.0		
Mesp-ba	85.7	85.7	
Mesp-bb	83.7	85.7	88.9

	% identity over bHLH domain (cDNA sequence)		
	Mesp-aa	Mesp-ab	Mesp-ba
Mesp-aa			
Mesp-ab	75.3		
Mesp-ba	80.2	71.7	
Mesp-bb	76.4	73.9	82.0

The table shows a high level of sequence identity over the bHLH domain but little over the whole protein sequence. Table shows pairwise identity (from CLUSTALW2 alignment) of full-length proteins or bHLH domains (54 amino acids; PF00010).

SUPPLEMENTARY TABLE S3

PCR PRIMERS USED IN THIS STUDY

Primer name	Primer sequence 5'-3'
1. Primers used to isolate mespab and mespbb from cDNA	
mespabF2	AGCATTCACTCAAGCTCCAG
mespabR2	GGGGTTTAATTAAAAAAAGACAAT
mespbbF	ATGGACGCATCATCTCCTTTC
mespbbR	TCATCCCCAGAACTCTGGAG
2. Primers used in 5' and 3' RACE	
5' RACE Primer	GGCCACGCGTCGACTAGTACGGGIIGGGIIGGGIIG
mespab RACE GSP1	GCAGGGAAACATATAA
mespab RACE GSP2	GCTGATTGTCGCTTCATTCC
3' RACE adaptorprimer	GGCCACGCGTCGACTAGTACTTTTTTTTTTTTTTTT
5' and 3' RACE abridged primer	GGCCACAGCGTCGACTAGTAC
mespbb 5' RACEGSP1	GTTGTAGCCCTGATAT
mespbb 5' RACEGSP2	CGTTTGGCCAACGGGAGCTA
3. Primers used for bHLH minus in situ probes (in conjunction with T7 or SP6)	
mespaa-bHLH	GTGAAGATGTGGAGATTTGT
mespab-bHLH	CTGAGGTGCCAAATTATGAG
mespba-bHLH	GTGAAGAAGAGCTGAGCTAC
mespbb-bHLH	GCGAAGAGTCTTTGTGCAAG
4. Primers used in qPCR	
qPCR mespaaF2	GCAGGACGAGGTTATCAG
qPCR mespaaR2	GGGAATGAATGGAAATCAC
qPCR mespbbF2	TTATGAGATGTGCTGCTCTG
qPCR mespabR2	GCTGTTCTCCATCTGTTCTC
qPCR mespba2	TGTGATGGACAGTATGAGGA
qPCR mespbaR2	GAACGAGATGATAGCCAAAG
qPCR mespabF2	CTCAAAACCACTGCTATTCC
qPCR mespabF2	TCTGAGCTGGAATTAAAGGA