

Genomic <sup>1</sup>	Allele	Functionality	Exons <sup>2</sup>	Exon sizes	Molecule type <sup>3</sup>	Accession numbers
<b>BAC_63n5-43b24 contig</b>	VCBP5S1*02	F	EX1-7	M58, 161, 238, 153, 117, 159, 185*	cDNA	BK006758
	VCBP2S1*02	F	EX1-7	M46, 167, 235, 165, 120, 165, 185*	cDNA	BK006760
	VCBP5S2*01	F	EX1-7	M58, 161, 232, 153, 114, 153, 185*	cDNA	BK006759
	VCBP5S3*01	P	EX7	M185*	gDNA	pending <sup>8</sup>
<b>BAC_62d19</b>	VCBP5S1*03	F	EX1-7	M58, 161, 238, 153, 117, 159, 185*	cDNA	BK006763
	VCBP2S1*03	F	EX1-7	M46, 161, 241, 165, 120, 165, 185*	cDNA	BK006762
	VCBP5S2*02	F	EX1-7	M53, 155, 229, 153, 114, 156, 185*	cDNA	BK006761
<b>PAC_37d15</b>	VCBP5S1*04	F	EX1-7	M58, 161, 238, 153, 117, 159, 185*	cDNA	BK006769
	VCBP2S1*04	F	EX1-7	M46, 167, 235, 207, 120, 165, 185*	cDNA	BK006768
	VCBP5S2*03	F	EX1-7	M58, 161, 226, 150, 114, 180, 185*	cDNA	BK006755
	VCBP2S2*01	ORF <sup>4</sup>	EX4-7	M167, 120, 153, 179*	gDNA	
<b>BAC_90f15 Scaffold_1</b>	VCBP3S1*02	F	EX1-8	M40, 170, 141, 91, 152, 211, 185, 15*	cDNA	BK006764
<b>BAC_54h3</b>	VCBP3S1*03	F <sup>5</sup>	EX1, EX3-8	M40, 141, 50, 175, 211, 185, 15*	cDNA	BK006765
<b>PAC_30b18</b>	VCBP3S1*04	F	EX1-8	M40, 170, 141, 91, 152, 211, 185, 15*	cDNA	BK006766
<b>BAC_100J9</b>	VCBP4S1*02	F	EX1-7	M55, 140, 244, 152, 176, 77, 179*	cDNA	BK006757
	VCBP1S1*02	F	EX1-9	M40, 137, 156, 111, 113, 180, 65, 188, 12*	cDNA	BK006756
<b>Scaffold_295 BAC-5h9</b>	VCBP4S1*03	F <sup>6</sup>	EX1-4, EX6-7	M55, 140, 244, 152, 67, 179*	cDNA	pending <sup>8</sup>
	VCBP1S1*03	F	EX1-9	M40, 137, 156, 97, 127, 180, 65, 188, 12*	cDNA	pending <sup>8</sup>
<b>PAC_34i7</b>	VCBP4S1*04	F	EX1-7	M55, 140, 244, 152, 176, 72, 179*	cDNA	BK006767
	VCBP1S1*04	ORF <sup>7</sup>	EX1-5	M40, 137, 156, 97, 125	gDNA	
<b>Scaffold_82</b>	VCBP1S2*01	F	EX1-10	M40, 59, 24, 156, 121, 125, 182, 89, 188, 102*	cDNA	pending <sup>8</sup>
	VCBP1S3*01	F	EX1-9	M46, 137, 156, 97, 125, 182, 65, 188, 204*	cDNA	pending <sup>8</sup>
<b>Scaffold_295</b>	VCBP1S4*01	P	EX2,4,5,8	EX5 is fragmented; EX1,3,6,7,9 missing	gDNA	

**Additional file 1: Table S1.** Characterization of new VCBP alleles. Genomic DNA from both the genome resource animal (JGI\_Brafl1), Scaffold\_295 and Scaffold\_82, along with supporting BAC clones, as well as PAC clones representing additional haplotypes, were used to model and predict new allelic variants of previously characterized full length VCBP cDNAs. All predicted transcripts were modeled with fgenesh+ using full-length VCBP cDNAs (AF520472, AF520473, AF520474, AF532182, and AF532183) as training queries. Splice sites, splicing frames, and exon types were visualized and confirmed with Splign (see Methods). F: functional; P: pseudogene; ORF: open reading frame.

<sup>1</sup> Accession numbers to BAC and PAC clones are listed in Additional file 1: Table S2.

<sup>2</sup> All exons of the VCBPs are of the M-type, using splicing frame 0 (Sf0).

<sup>3</sup> All transcripts are predicted only. Representative cDNAs from genomic resource animal are lacking.

<sup>4</sup> This VCBP2 allele appears to be disrupted by cloning.

<sup>5</sup> This VCBP3 allele has a disrupted (with stop codon) second exon, but a putative alternative transcript is predicted by fgenesh(+).

<sup>6</sup> This allele has a missing exon 5 (confirmed with BAC 5h9) but a putative alternative transcript is predicted by fgenesh(+).

<sup>7</sup> This VCBP1 allele appears to be disrupted by cloning.

<sup>8</sup> Accession numbers pending; Third Party Annotation (TPA) database (NCBI). BAC/PAC support lacking; sequences are attached for download.

BAC/PAC clone	Accession Number	Positive for VCBPs	Size (kb)	Sequenced	Notes
<b>BAC-63n5</b>	EU875590	2 and 5	153	Phase 3 finished	63n5 and 43b24 are same allele, overlap by 6kb, form 315kb contig; corresponds to the allele represented by scaffold_82.
<b>BAC-43b24</b>	EU875590	2 and 5	168	Phase 3 finished	
<b>BAC-62d19</b>	EU875589	2 and 5	113	Phase 3 finished	Allelic counterpart to 63n5-43b24 contig; represents scaffold_295 allele
<b>PAC-37d15</b>	AC135603.5	2 and 5	39	Phase 3 finished	Represents a third allele to the VCBP 2/5 gene cluster; misc. animal.
<b>PAC-30b18</b>	AC135602.14	3	57	2 ordered contigs	Represents a third allele to the VCBP 3 gene; represented by one allele in Braf1 in scaffold_1.
<b>BAC-90f15</b>	EU875591	3	196	partial; 10.7kb	90f15 represents allele from scaffold_1; 90f15 and 54h3 are alleles; only partial sequence as one assembled contig over VCBP3 gene region; used PCR and primer directed approach. Accession number reflects the 10.7kb sequenced and assembled contig.
<b>BAC-54h3</b>	EU875588	3	108	partial; 8.8kb	Accession number reflects the 8.8kb sequenced and assembled contig.
<b>PAC-34i17</b>	AC141443.12	1 and 4	33	Phase 3 finished	Represents a third allele to the VCBP1/4 cluster
<b>BAC-100j9</b>	EU875592	1 and 4	176	2 ordered contigs	Allelic counterpart to scaffold_295; represented by scaffold_869 (VCBP genes are misassembled onto scaffold_295 as a paralogous set, see text for details and Supplement Figure S4-S5).

**Additional File 1: Table S2.** BAC and PAC clones used to aid in the genomic description, annotation, and validation of the VCBP genomic region of Braf1. All BAC clones from this manuscript represent the same reference animal as the JGI genome, Braf1. PAC clones are from alternate animals and represent additional haplotypes. BAC 5h9 (not shown; only partially sequenced across gene region) is equivalent to scaffold\_295 over the VCBP1/4 region and allelic to BAC 100j9. NOTE: PAC 34i17 is incorrectly labeled as 34i7 in AC141443.12.

A.

VCBP 2/5		62d19 -5a	63n5-43b24 -5a	37d15 -5a	62d19 -2b	63n5-43b24 -2b	37d15 -2b	62d19 -5b	63n5-43b24 -5b	37d15 -5b
VCBP 5a	62d19	100								
	63n5-43b24	79   83	100							
	37d15	68   77	69   76	100						
VCBP 2b	62d19	49   59	51   60	52   61	100					
	63n5-43b24	48   58	51   60	51   61	80   84	100				
	37d15	46   56	49   58	49   58	78   81	93   95	100			
VCBP 5b	62d19	63   73	66   74	71   77	56   65	56   65	55   63	100		
	63n5-43b24	63   74	66   75	71   78	57   66	57   66	55   63	93   95	100	
	37d15	64   73	66   74	71   78	57   66	56   65	56   64	95   96	93   95	100

B.

VCBP 4	Scaff_295	BAC 100j9	PAC 34i17
Scaff_295	100		
BAC 100j9	99   99	100	
PAC 34i17	95   96	95   96	100
VCBP 1			
BAC 100j9	96   98	100	N/A

C.

VCBP 3	Scaffold_1	BAC 54h3	PAC 30b18
Scaffold_1	100		
BAC 54h3	89   91	100	
PAC 30b18	94   95	88   91	100

**Additional file 1: Table S3.** Pairwise comparison (identity | similarity percentages) of deduced amino acid sequences for the VCBPs that are supported by BAC and PAC evidence. Full length sequences were predicted from the BAC and PAC sequences using a combination of Blast comparisons and gene modeling with *fgenesh* and *genomescan*. A. comparison of the VCBP 2 and 5 alleles (as 5a, 2b, and 5b) from the 2/5 cluster. Only BAC and PAC (as the third allele) are compared; genomic scaffolds in this region possess misassembly artifacts. Interparalogous comparisons are done because of the close relationship between these two genes. B. comparison of VCBP4 alleles. BAC 100j9 (mostly represented by scaffold\_869) is allelic to scaffold\_295 across the VCBP1/4 region. PAC 34i17 is the third allele, which is disrupted across the VCBP 1 gene and therefore could not be used in the VCBP1 pairwise comparison. C. comparison of VCBP 3 alleles; BAC 54h3 is allelic to scaffold\_1 VCBP 3 gene and PAC 30b18 is a third allele.

A.

VCBP2/5	VCBP5S1*02	VCBP2S1*02	VCBP5S2*01	VCBP5S1*03	VCBP2S1*03	VCBP5S2*02	VCBP5S1*04	VCBP2S1*04	VCBP5S2*03
VCBP5S1*02	100								
VCBP2S1*02	73	100							
VCBP5S2*01	80	73	100						
VCBP5S1*03	94	72	80	100					
VCBP2S1*03	73	92	72	73	100				
VCBP5S2*02	79	72	88	80	71	100			
VCBP5S1*04	94	74	80	94	74	81	100		
VCBP2S1*04	72	97	72	73	92	72	74	100	
VCBP5S2*03	82	71	83	82	71	82	81	70	100

B.

VCBP1	VCBP1S1*02	VCBP1S1*03	VCBP1S2*01	VCBP1S3*01
VCBP1S1*02	100			
VCBP1S1*03	96	100		
VCBP1S2*01	86	87	100	
VCBP1S3*01	91	90	89	100

C.

VCBP4	VCBP4S1*02	VCBP4S1*03	VCBP4S1*04
VCBP4S1*02	100		
VCBP4S1*03	92	100	
VCBP4S1*04	96	93	100

D.

VCBP3	VCBP3S1*02	VCBP3S1*03	VCBP3S1*04
VCBP3S1*02	100		
VCBP3S1*03	88	100	
VCBP3S1*04	94	89	100

**Additional file 1: Table S4.** Pairwise DNA comparison of the VCBP alleles described in the manuscript. All alleles are predicted from the genomic DNA. Transcripts were predicted as described in the Methods (see Table 1 and Additional file 1: Table S1).

**Additional file 1: Table S5.** Annotation of coding regions and predicted genes from the VCBP containing BAC and PAC clones described. Numbers represent gene location & span; orientation of gene is implied by number direction. VCBPs are listed first; other genes follow. <sup>1</sup> VCBP5a and 2 are interrupted by 3 copies of a large interspersed element and alleles of 5a may incorporate element-derived ORFs. <sup>2</sup> Non-coding interspersed element; three copies are nearly identical (see text). Identity/similarity and e values are approximations; varies with sequence availability.

BAC/PAC clone/contigs	Gene-spanning region	Similar to known/predicted gene products	% identity   similarity	e value	comments
PAC 37d15	245...3278	VCBP 2 (VCBP2S2*01)			(1/2 gene -from cloning)
(39kb)	5262...19006	VCBP 5 (VCBP5S2*03) <sup>1</sup>	75   82	5E-145	2 copies of 4.3kb repeat (-/+)
Other animal	21821...30983	VCBP 2 (VCBP2S1*04)	72   79	2E-142	1 copy of 4.3kb repeat (+)
Haplotype C	32956...37990	VCBP 5 (VCBP5S1*04)	74   77	4E-167	
	10763...6366	4.3kb NCE;repeat <sup>2</sup>			
	12281...16894	4.3kb same repeat			
	24482...28880	4.3kb same repeat			
BAC 63n5-43b24	135804...145469	VCBP 5 (VCBP5S2*01)	71   79	6E-126	interspersed pseudogene
(315kb)	148776...154132	VCBP 2 (VCBP2S1*02)	75   83	2E-143	
JGI Haplotype	156065...161233	VCBP 5 (VCBP5S1*02)	95   97	0.0	
Haplotype A					
	43402...16590	TRAIL-like	30   45	1E-07	
	53501...54493	Hypothetical LRR protein	31   44	7E-09	
	75515...71245	Mitochondrial translocase-like partial	59   71	3E-17	
	84558...79306	RVT; endonuclease-like	39   55	6E-96	

	87776...97580	ADP-ribosylation factor interacting protein 1-like	50   65	7E-73	
	105293...102432	Ret tyrosine kinase receptor-like; FGF receptor 3-like	47   66	1E-44	
	107306...117139	Short chain dehydrogenase-like; male sterility protein-like	42   64	4E-53	
	117698...118954	RVT-like (different than above)	31   51	4E-46	
	139485...139069	Ribonucleotide reductase -partial	80   87	3E-59	
	140979...141395	Ribonucleotide reductase -partial	80   87	3E-59	
	172911...166980	Plasminogen-like; transmembrane protease	50   65	7E-70	
	229647...192975	Htra3 protein; serine protease	25   50	1E-16	
	231498...230254	Transposase-like fragment	36   55	6E-11	
	244637...238600	Alpha-galactosidase B-like	52   66	1E-127	
	245507...271539	Oral-facial-digital syndrome 1; Ofd1-like protein (partial)	36   56	9E-26	
	277960...274394	Tyrosine Recombinase RVT	44   63	6E-81	
	301091...300633	RVT fragment	38   59	4E-19	
	313995...311637	L-type amino acid transporter 1-like	45   66	1E-11	
BAC 62d19	63018...70481	VCBP 5 (VCBP5S2*02)	66   76	1E-123	
(113kb)	73607...86490	VCBP 2 (VCBP2S1*03)	76   83	2E-148	contains interspersed element
JGI Haplotype	88525...94237	VCBP 5 (VCBP5S1*03)	95   97	1E-179	
Haplotype B					
	10505...7674	Mitochondrial membrane protein-like	59   71	3E-17	
	19079...28604	ADP-ribosylation factor interacting protein 1	49   62	7E-106	
	35224...32369	Ret tyrosine-kinase receptor	47   66	1E-44	

	36958...59793	Short chain dehydrogenase; male sterility domain 2 protein	52   76	4E-33	
	111865...101864	Star fish protease-like; Plasminogen-like; transmembrane protease	49   67	4E-52	
PAC 30b18 (57.4kb)	36352...47466	VCBP 3 (VCBP3S1*04)	95   97	0.0	
Other animal	20293...2170	Similar to tudor domain proteins	29   44	5E-28	
	23510...27344	Unknown; contains Mid-1-related chloride channel 1-like domain	35   52 Mid-1 domain	4E-14	
	31939...29549	similar to Urchin RVT	51   65	4E-77	
	56877...51842	Similar to zebrafish and human upstream binding transcription factor, RNA Pol I	37   57	5E-41	
BAC 100j9 (176kb)	133287...121773	VCBP 4 (VCBP4S1*02)	83   88	3E-167	
	137590...142796	VCBP 1 (VCBP1S1*02)	97   98	0.0	
JGI Haplotype					
Haplotype A	63159...40792	Similar to Tetraodon protein; contains SLAIN motifs	77   92 motifs only	variable	
	71152...72681	Similar to homeobox transcription factor	31   48	8E-07	
	92750...78019	Similar to TBC1 protein (GRAM domain)	55   72	0.0	
	94810...111515	Similar to activating signal cointegrator 1 complex	36   51	3E-74	
	151400...153826	Unknown; contains LRR repeats; Drosophila GF20961	36   52	2E-13	
	170231...167852	Similar to x globin [Strongylocentrotus purpuratus]	26   50	4E-11	

PAC 34i17 (33.4kb)	19871...25710 29669...33400+	VCBP 4 (VCBP4S1*04) VCBP 1 (VCBP1S1*04)	84   89 95   97	2E-170 0.0	
Other animal					

>VCBP1S1\*03 [organism=Branchiostoma floridae] [molecule=DNA] [moltype=genomic]  
[location=genomic] [note=allele 03 of VCBP1; predicted transcript, BAC5h9, Scaffold\_295; Brafl01 genome resource animal] Amphioxus variable region-containing chitin-binding protein 1 (VCBP1), VCBP1S1\*03, mRNA; VCBP1 allele (predicted)

ATGAAGTTTGTACTTGGCTTGGTCCTTCTTGTGTTGGCGCGCACGCCATGACCATCGTG  
ACCGTCAGTACCCTGAACCGAAGGTTGAGGCTAGTGTGGGGGTTCCGCGGAACCAAG  
TGGGAGTTTACATCAACCAACTCTACACAGCCTCTACTATCGCCTGGTTCAAGGGC  
AATGACGACTTCCGCGGTGCCGAGCGGATCTACACGGGACACAAGGTGTGGGGGAACGAG  
ACGCAACGACGGGAGGACAGCTTCCGGGACTACATCGGGCGGTGGAGGTGGCGGATCTG  
GACAAACCCCGCATCAAGATCAGCGGCATCAAGAGTACCGACTTCGCGCGCTACTGGTGT  
ACTGTAGCGGAGTGGGTGTGCGGACGGAGTTCGGAGTGGACGCCAAGTCAGTTCTGCTG  
ACTGAAACTGGTGAGCTTAAATCGTCCATTGACATTTCCGTTTCCGGTGAGAAGGACGTG  
GATGAAGGTGGTGACGTAGAGATGACGTGTGTTGCCATGGCTGCACTTCTGCCGCGATA  
TTCGACTGGTTCAAGGTGGCGTTTCCGGAAGTGAGTGGGTGACAACCGGAACTACACT  
CATATCGCAGCAAGGTCGACGTTGGCGTTTTGGGATTTCAAACCCGATAGAGATTGAC  
GATGGATTTGGCCAGTTCAGCGTGACACCATCAATTCCCTCCGCTGACCGGGGCGAG  
GTAGCCGACGAGGAAGTACTGGTGTAAAGTGACAAGCGGTGGGAGCGTGGACATCAAG  
GCAACCGTGCTGAAGGTCAAAGTGCCGGAGTTCACCTGTGCCGGTAAGGCTGACGGGCAC  
TACCCTGACCCGGAGGACTGCGCCATGTACTACCAGTGTCTGTACGGCTTCCCTCAGCCC  
TTCCACCGCCCGTGTGGGTACCGCGCATGGTCTTCAAACCCGAGCACCTGTACTGCGAC  
TGGGCCTTCAACGTGGGACCGCCATGCGGGAGCAAGGCTTAG

>VCBP1S1\*02 [organism=Branchiostoma floridae] [molecule=DNA] [moltype=genomic]  
[location=genomic] [note=allele 02 of VCBP1; predicted transcript, BAC100J9 (EU875592), Scaffold\_295; Brafl01 genome resource animal] Amphioxus variable region-containing chitin-binding protein 1 (VCBP1), VCBP1S1\*02, mRNA; VCBP1 allele (predicted)

ATGAAGTTGATACTTGGCTTGGTCGTTTTTGTGTTGGCGCGCACGCCATGACCATCGTG  
ACCGTCAGTACCCTGAACCGAAGGTCGAGGCTAGTGTGGGGGTTCCGCGGAACCAAG  
TGGGAGTTTACATCAACCAACTCTACACAGCCTCTACTGTGCGCTGGTTCAAGGGC  
AATGACGACTTCCGCGGTGCCGAGCGGATCTACACGGGACACAAGGTGTGGGGGAACGAG  
ACGCAACGACGGGAGGACAGCTTCCGGGACTACATCGGGCGGTGGAGGTGGCGGACCTG  
GACAAACCCCGCATCAAGATCAGCGGCATCAAGAGTACCGACTTCGCGCGTACTGGTGT  
ACCGTAGCGGAGTGGGTGTGCGTACGGAGTTCGGAGTGGACGCCAAGTCAGTCCTGCTG  
ACTGAAACTGgGCATTTCCGAAGCCTCCATTGACATTTCCGTTTCCGGTGAGAAGGACGTG  
GAGGAGGGTGGTGACGTAGAGATGACGTGTGTTGCCATGGCTGCACTTCCGCCGCGATA  
TTCGACTGGTTCAAGGTGgCGTTTCCGGAAGTGAGTGGGTGACAACCGGAACTACACT  
CATATCGCAGCAAGGTCGACGTTGGCGTTTTGGGATTTCAAACCCGATAGAGATTGAC  
GATGGATTCGACCAGTTCAGCGTGACACCATCAATTCCCTCCGCTGACCGGGGCGAG  
GTAGCCGACGAGGAAGTACTGGTGTAAAGTGACGAGCGATGGGAGCGTGGACATCAAG  
GCAACCGTGTGAAGGTCAAAGTGCCGGAGTTCACCTGTGCCGGTAAGGCTGACGGGTAC  
TACCCAGACCCGGAGGACTGCGCCATGTACTACCAGTGTCTGTACGGCTTCCCTCAGCCC  
TTCCACCGCCCGTGTGGGTACCGCGTATGGTCTTCAAACCCGAGCACCTGTACTGTGAC  
TGGGCCTTCAACGTGGGACCGCCCTGTGGGAGCAAGGCTTAG

>VCBP1S2\*01 [organism=Branchiostoma floridae] [molecule=DNA] [moltype=genomic]  
[location=genomic] [note=allele 01 of VCBP1 paralog 2; predicted transcript, Scaffold\_82; Brafl1 genome resource animal] Amphioxus variable region-containing chitin-binding protein 1 (VCBP1), VCBP1S2\*01, mRNA; VCBP1 allele (predicted)

ATGAAGTTGGTGCTTAGCTTGGTCGTTCTTGTGTTGGCGCGCACGCCATGACCATCGTG  
ACCGTCAGCACTCCTGAACCGAAGGTCGAGGCTAGTGTGAGCCTCTACTATCGCCTGGTTC  
AAGGGTAATGCCGATTTCCGCGGTGCCGAGCGGATCTACACGGGACACAAGGTGTGGGGG  
AACGAGACGGAAACGGCGGGAGGACAGCTTCCGGGACTACATCGGGCGGGTGGAGGTGGCG  
GATCTGGACAAACCCGCATCAAGATCAGCGGCATCAAGAATAATTGCAAAAACTTTTCC  
CCTGCAGAGTACTTTCCGCGTACTGGTGTACCGTAGCGGAGTGGGTGTGCGTACGGAG  
TTCGGAGTGGACGCCAAGTCAGTTCTGTGACTGAAACTGGCCATTCATGGTACATCCC  
ATTTACATTTCCGTTTCCGGTGAGAAGGAAGTGGAGGAAGTGGTACGTAGAGATGACG  
TGTCAGTGTCAAAGTTGCTTACCCAACATTCGAATGGTTCAAAGGGCCCGCGTTTGGC  
GGAAGTGAGTGGGCGACGACCGGAAATTACACCCATATCGCATCAAGGAATATTTTGGC  
ATCATGGGATTTGTAGACTAGAGATTGAGGATGGATTTGGCCAGTTCAGCGTGACGCCA

TCCAATTCCTCCGCTGACCGGGGCACAGGTGACCGACGCCGGAAGGTACTGGTGAAG  
GTGACGAGCGGTGGAATTGCCGGACATCAAGGCCACCGTGTGAAGGTCAAAGGCATGTAC  
CCAAGGTCACACATTGCCGGAGTTCACCTGTGCCGGTAAGGCTGACGGTACTACCCA  
GACCCGGAGGACTGCGCCATGTACTACCAGTGTCTGTACGGCTTCCCCAGCCCTCCAC  
CGCCCGTGTGGGTACGCCGTATGGTCTTCAACCCGGAGCACCTGTACTGCGACTGGGC  
TTCAACGTGGACCGCCATGTGGGAAGTGTGCCGGGCAAAAAGTGAAGCGTGACAGCAAG  
GACAACTTAGAAAACGCTACCTGATTCGGCGACGCGTGGGGAGGGCGAGCTCAAGCTTG  
AAGTAA

>VCBP1S3\*01 [organism=Branchiostoma floridae] [molecule=DNA] [moltype=genomic]  
[location=genomic] [note=allele 03 of VCBP1 paralog 3; predicted transcript, Scaffold\_82; Brafl1  
genome resource animal] Amphioxus variable region-containing chitin-binding protein 1 (VCBP1),  
VCBP1S3\*01, mRNA; VCBP1 allele (predicted)

ATGAAGTTGGTACTTGGCTTGGCTTCTTAATCTTGCTGTTGGCGCGCACGCCATGACC  
ATCGTGACCGTCAGTACCCCTGAACCGAAGGTCGAGGCTAGTGTGGGGTTCCGCGGAA  
CTCAAGTGGGAGTTTGACATCAACCAACTCTACACAGCCTCTACTATCGCCTGGTTC  
AAGGGTAACGACGATTTCCGCGGTGCCGAGCGGATCTACACGGGACACAAGGTGTGGGG  
AACGAGACGGAACGGCGGGAGGACAGCTTCGGGGACTACATCGGGCGGGTGGAGGTGGCG  
GATCTGGACAAAACCCGCTATCAAGATCAGCGGCATCAGGAGTACTGACTTCGCGCGCTAC  
TGGTGTACGGTAGCGGAGTGGGGTGTGCGTACGGAGTTTGGAGTGGACGCGCAAGTCAGTT  
CTTCTGACTGAAACTGGCAATTCCTGGTACACCCATTGACATTTCCGTTTCCGGTGAG  
AAGGAAGTGGATGAAGGTGCTGATGTGCAGATGACGTGTCAAGTTGCTTCTAC  
CCTACATTCGACTGGTTCAAGGGCCCGCCTTTCGGGAAGTGAAGTGGGTGACGACCGGA  
AATTACCCCATATGCATCAAGGAATATCTCGGCATCATGGGATTTGAGACCTAGAG  
ATGGAGGACGATTTGACAGTTTACGCGTGACGCTTCAACTCCCTCCGTCGACCGGG  
GCGCAGGTAGCCGACGCAAGGTAAGTACTGGTGAAGGTGACGAACGGTGGGATTGCTGAC  
ATCAAGGCAACCGTGTGAAGGTCAAAGTTCCGGAGTTCACCTGTGCCGGTAAGGCTGAC  
GGGTACTACCCAGACCCGGAGGACTGCGCCATGTACTACCAGTGTCTGTACGGCTTCCCT  
CAGCCCTTCCACCGCCGTTGGGTACGCCGATGGTCTTCAACCCGGAGCACCTGTAC  
TGCGACTGGGCTTCAACGTGGGACCGCCATGTGGCGCTTCAAGATGGCGGTGCGCGTT  
AAGTGCAGTTACGGGACTATTCCTTACTACGAATGACATTGGGACAAAACCTGTTTTA  
GCCAAGGAGCTGTTGGCTCACAGCGAAGGGCTACATGCTCGGCGAAGGAGCTGTGTGCTC  
ACAGCAAAGGGGCTCGCTGCTGCCGACGGGAGCTGTGTGCTCACAGCGAACTAGGCTGA

>VCBP4S1\*03 [organism=Branchiostoma floridae] [molecule=DNA] [moltype=genomic]  
[location=genomic] [note=allele 03 of VCBP4; predicted transcript, BAC5h9, Scaffold\_295; note:  
lacks second exon of V2 domain; Brafl1 genome resource animal] Amphioxus variable region-  
containing chitin-binding protein 4 (VCBP4), VCBP4S1\*03, mRNA; VCBP4 allele (predicted)

ATGGCGCCGTTACACCGTTTGTCTGTGTATCATCCTGGCAGGTGCTATGGCACAATCG  
CCATTCGGAATCATGACAGTACAGTGCAGGAGCCGGAAGTACGCGCAAACACCGGAAGT  
GACATCAAAGTGCCTTCTTCTACGACATTCGGCTGCCGGTCCGGACTGAATCCGACC  
ATCAATTTGGTACAAGGGGATGAAGGGATCGCCAGCGCTACCAAGATCTTCTCCCTCTCC  
TACCACGGCTCGACACAAATAGCGGAGGCTTACGAGGGTACGAGCTGCGGGTGAAGT  
GAGAGTCTACCGACCCACCTGAAACTCAGCGCGTACGGCTTCCGATCACGGTCCG  
TACTGGTGGCGGTGTTGACTCCGACGAGCACAACCAATTCGGCATGGACTCCAAGTCG  
GTTCTCTCACAGTGATAGACCTAGCGTGCAGCAGGACAGGGTACGGGCGCCCGGGC  
CGTGTGAGGTGCACGTGCCTGCTGTGCGGCAGGTGTACCAGGGGAGGACGTGGAGCTC  
CCCTGCGAGTGCATGGGTGCCACTGGACCAGCATCAAGACTTGGTTCACGGTAGAAGAC  
GGTACCTTCAACACTCGCGCTCCGGAGTGGACGCTCAGTCCGTGGCTCTGGTCTCGAG  
TCACGTTGTGCGGGGAAGCCGGCCGGCGCTACCAGCACCTGACGACTGCTCCAAGTAC  
TACACCTGCGGGGAGGGCGGCTGCAGTACGACGGCATCAGTGCCTGTCCACCCGGCCTA  
ATGTACGACAGGCCAACGGCTACTGCAACTGGGCCACGCTCGTACCTGTCTGTAA

>VCBP4S1\*02 [organism=Branchiostoma floridae] [molecule=DNA] [moltype=genomic]  
[location=genomic] [note=allele 02 of VCBP4; predicted transcript, BAC100j9 (EU875592),  
Scaffold\_295; Brafl1 genome resource animal] Amphioxus variable region-containing chitin-binding  
protein 4 (VCBP4), VCBP4S1\*02, mRNA; VCBP4 allele (predicted)

ATGGCGCCGTTTACCCGTTTGTCTGTGTACCATCCTGGCAAGTGCACCTGCACAATCG  
CCATTCGGAATCATGACGGTACCGTGCAGGAGCCGGAAGTACGCGCAAATGTGGGAAGT  
GACGTCAAAGTGCCTGTTCTTACAGCATCCCGGCTCGCTCGTCCGGACTGAATCCGACC

ATCAACTGGTACAAGGGAGATGAAGGGATCGCCAGCGCTACCAAGATCTTCTCCCTCTCC  
TACCACGGCTCGACACAAATAGCGGAAGCTTACGAGGGGTACGAGTTGCGGGTTCGAACTG  
GAGAGTCTCACTGATCCCACCTGAAACTCAGCGCGTCAAGGGCTCCGACCACGGCCGG  
TACTGGTGCGCCGTGTTGACTCCGACGAGCACAACCAATTCGGCATGGACTCCAAGTCG  
GTTCTCTCACAGTGATAGACCCTAGCATAACAGCAGGACCAGGAACTGGCCGCCGGGC  
CGTGTGAGTGCATGTGCCGGCTGTACGGCAGGTGTACCAGGGGGAGGACGTGGAGCTC  
ACCTGCGAGTGGCATGATTGCCACTGGACTAGCACCAGTCTTGGTTCACGGTGTCAATTT  
GATGACACTTGGCGGCCACCGAGGAGCTGGTCGTACCGTAGGTCCGTGCGTGGCCAT  
CAGTGCCATGGAGGGACCACCGCTCGCCCCGCATTCCGAGACCACTTCTCGCAACT  
CGGAAGCCTTGAGGATTTTCGGCAGCCAAGCGCCTGGACAACGCAGGTAAGTGGTTCAG  
GTGGAAGATATGACCTTCAGTCGTGGCTCGGGAGTGGACGCTCAGTCCGTGGCTCTGGCT  
GTCGAGTACGTTGTGCGGGGAAGCCGGCCGGGGCTACCAACACCCTGACGACTGCTCC  
AAGTTCTACACTGCGCGGAGGGGGCTGCAGCAGCAGCGCATCGGTGCCTGTCCGGAC  
GGCCTGATGTACGATCAGGCACTCGGCTACTGCAACTGGGCCACGCTCGTACCTGTCTG  
TAA

>VCBP5S1\*02 [organism=Branchiostoma floridae] [molecule=DNA] [moltype=genomic]  
[location=genomic] [note=allele 02 of VCBP5; predicted transcript, BAC contig 63n5-43b24  
(EU875590), Scaffold\_82; Brafl1 genome resource animal] Amphioxus variable region-containing  
chitin-binding protein 5 (VCBP5), VCBP5S1\*02, mRNA; VCBP5 allele (predicted)

ATGTTGGGTCTACTGGTCAGCGTCTTCTACTGCTTTATGTAGGACCGGAAAGGGTTGAT  
GCGGTGTCCATCACAAACCGTGACGGTGCCGGATCGAGGCGGTTGGGTGGTGTGTGGCC  
CGCCAGGTGACCCTACCTGGGTGAACCGGATAGAGTTACAGTGTGAATATATCATCTCA  
CCTGCCTCGGCCACTCTCTACAATCACCTGGCTAAAGGGAGTGTGGCCGACGCAGAC  
CGACAGTGGTCTACAAGTGGAGTTCATCAGGAGAAGTCTACGTCATCCCGAGTTCGCA  
GGCCGGTCAAGCGTGGAGTCCCGAACCCGCCGACTCTCGTGTGACCGACGCGAAGTTT  
GACGACTGGGGCCGATACTGGTGTGCGGTTACGAACGAGGACCAGTCGGACGAGTTCGGC  
ACGAACGAGGAGTCTCTGCTTCTGGTACAAGTTGGGCTACGACCACCGAACCGTCTG  
TCGAGGTTAGCCTTGACAAAACCCAGTCCGCGTGGCTGCTGGCGAGACGGCTCGGCTC  
GACTGTACGGGAACAGCGCCGTGAAGCCTCATTCTCTGGTCAAAGGGCCGACGGGT  
TGTACCAAGGTGGAAGCTGTGACACTTACGAGACTGTCAATCACAAGTCCGCCGTGTGG  
GGCGTGGTAATCCAGAACCGGAAACATCACCATCTCCCCAGCTTCAACGGAAGGGTT  
TCCCTGGATCGCGACGGGTCTGGCTCCTTCACTCCGACCCTGACCATCACCGACATCCGC  
CCTAGCGACTCCGGCCGGTACTGGTGTGCTCCTGACATCTCCGAGGATTACTCTAACCTG  
GGTCTCTGAACCGGGACGCGCAGTCTGTGGTTCATCATCGTCAACGACCCAGGTACCGAG  
CCGACCTGTGCCGTAAGCCGGACGGGATGTACCAGACCCCGCCGACTGTGCCAGTTC  
TACACGTGCTCGGGCGTCTGTCTTACGGCACCAACACTGCCAGCTGGACTGGTCTTC  
AACCAGAACTACAGCTGTGCGACTGGGCAACAACGTCATCTGTGTGTA

>VCBP5S2\*01 [organism=Branchiostoma floridae] [molecule=DNA] [moltype=genomic]  
[location=genomic] [note=allele 01 of VCBP5 paralog 2; predicted transcript, BAC contig  
63n5-43b24 (EU875590), Scaffold\_82; Brafl1 genome resource animal] Amphioxus variable region-  
containing chitin-binding protein 5 (VCBP5), VCBP5S2\*01, mRNA; VCBP5 allele (predicted)

ATGCTGGGTCTGTTGGTCGCTATCTCCGCTGTAGCGTCTTGAATCAAGCTACGCAGAT  
GCAGTGTCCATCAGACCGTGACGGTACCGTATCACAATTATTACGTGTTGGCGCGGAC  
CGCCCGTGGGACCCTACCTGGGTGAACAGGGTAGAGATTAGGTGTGAATATACCATCTCA  
CCTGCACCAGCCACTCTCTACTATCACCTGGCTCAGGGGAACCTTTCAGACCCGAGAG  
GTGGTGTACAAGTGGAGCTCTCAGGAGAAGTGTACGTGCATCCCGAGTTCGAGGCCGC  
GTCAGTGTGGAGTCCAGGACCCGGCTACGCTGGTATTGTTCAACGAAAGGACCTGGGTT  
GACCGATACTGGTGCAGGGTACGAACGAGGAGCAACCGGACGAGTTCGGCACGGACGAG  
GAGTCTTGCGGCTTCTGGTACGTTGGGATTGGCTATAACTTGCCTAAACTTCTGGCGACA  
GTTCACTGGACAAAACCCCGTCCATGTGGATGTGCGGGGACAGTCCAACCTCAACTGT  
ACGGGAGTCCCAGACGGCCGTATGGCTACCATTTTCTGGTCAAAGGGCCGAGCTGCACT  
CAAGTGGAAGTTGTGACAGTATGAGACTGTGATCACAAGTCTCCGGTGGGGCGAA  
ACGAAACCAATTACCTCTCCCCAACTTCGCTGGAAGGGTTTCTCTGGCTACCGGGGT  
GTGTCTATCACCCCGACTTACCATCACCGACATTCGCCCTAGAGACCCGGTCCGGTAC  
TGGTGTCTATAAACTACCCCGATGATCGCTACTTCTAGTTTTGGCCGTTGGAACCGG  
GGCGCTCAGTCTGTGGTTCATCTCGTCAACGACCCAGTTACCGAGCCGACCTGTGCCGAT  
AAGGCGGACGGGAAATACCAGACCCCGCCGACTGTGCCAGTTCATACGCTGCTCGGGC

GGTCTGTCTTACGGCACCAACACTGCCCGGCTGGACTGGTCTTCAACCAGGACCTACAG  
CTGTGCGACTGGGCAAACAACGTCATCTGCCTGTAG

>VCBP2S1\*02 [organism=Branchiostoma floridae] [molecule=DNA] [moltype=genomic]  
[location=genomic] [note=allele 02 of VCBP2; predicted transcript, BAC contig 63n5-43b24  
(EU875590), Scaffold\_82; Brafl1 genome resource animal] Amphioxus variable region-containing  
chitin-binding protein 2 (VCBP2), VCBP2S1\*02, mRNA; VCBP2 allele (predicted)

ATGTTGGGTCTGTTGGTTCGCTGTCTCCGCGTAGCGTGCTACGCAGGTGCGGTGCCATC  
ACGAACGTGACGGTACCGGATCGAAGCGCCGCGCGGTTGGTCTATCTTCGATACAGC  
CCGGACCCTACCTGGTGAACAGGATAGAGTTCAGGTGTGAATATACCATCTCACCTGCC  
TCAGCCAATCCGCTACTATCACCTGGCTCAAGGGACCCTTCACAGACCGACAAGTGATC  
TACAAGTGGAGTTCATCAGGAGAAGTCTACGTCCATCCCGAGTTCGACGGCCGGTCCAGC  
GTGGAGTCCCGAACC CGCCGACTCTCGTGTGACCGACGCGAAGTATGACGACTGGGGC  
CGATACTGGTGTGCGGTACGAACGAGGACCAATCGGACGAGTTCGGCACTGACGAGGAG  
TCTCTGCTATTCTATTACAAGTCGACTGTCTACGATTACGACGTCCCTGCTCGTGGCGGC  
CAATATTCTTTGTGGAGGTGGACAAAACACCAGTCCGTGTGAAGCGGGTGGGACGGCC  
CGGCTCAACTGTGAGGGATCGGGCGCCCTCTGGCGTCCATTGTCTGGTCAAAGGGCCA  
AGTTGTACCCAAGACGGAAAGTGCAACGTATATGAGATGGTCATCAACAAAACAGCTGTA  
CCTCAGCCCCATCCGATTCTAGGTCCGGGAACCGTTAACGTGTGCGCCGAAGTACGCAGGA  
AGGGCTTCACTGGACTTCAACGACGGTGGCTACTACAATTACTATCCGGATCTAACC  
ATCACTGACATTCGCCCTACCAGCTCGGTCCGTTACTGGTGCACCGATGATGCGCCCTTA  
TGGTACCAGAATGATCTGCGCAGCCGCGATTCCAGTCTGTGGTGGTGTCTCTTACGAT  
GAAGCACCAACACCGTCATGTGATGGGAAGGCTGACGGGATGTACCAGGACCCTGGCGAC  
TGTTCCCGGTACTACAGCTGCTCGGTGGTGGCTGTACGGCCAGCGCCCTGTCTGACC  
GGGTGTTCTTAAACGAGGCCTTGAAGTGTGACTGGCCTAATAACGTTGCCTGTGCG  
TAA

>VCBP5S2\*02 [organism=Branchiostoma floridae] [molecule=DNA] [moltype=genomic]  
[location=genomic] [note=allele 02 of VCBP5 paralog 2; predicted transcript, BAC62d19  
(EU875589), Scaffold\_295; Brafl1 genome resource animal] Amphioxus variable region-containing  
chitin-binding protein 5 (VCBP5), VCBP5S2\*02, mRNA; VCBP5 allele (predicted)

ATGCTGGGTCTGTTGTTGCTATCTCAGCTGTAGCTTGTCTTGAATCAAGCTACGCAGAT  
GCGGTGTCAATCAGACTGTGACGGCACAGAACGGTGTGCTTTCGCGTATAACCGCTGG  
TGGGACCCTACTGGGTAAACAGGGTAGAGTTCAGGTGTGAATATACCATCTCACCTGCA  
CCAGCCACTCCTCTACAATCACCTGGCTCAGGGGAGTGTTCGACACCAAGAAGTGATC  
TACAAGTGGAGTTCATCAGGAGAAGTCTACGTGCATCCCGAGTACACAGGCCGCGTCAGT  
GTAGAGTCCAGGACCCGGCTACGCTGGTATTGTTCAACGAAACGGTGTGGGCCAACCGA  
TTCTGGTGCCGGGTACCAACGAGGAACAACCGGGCGAGTTCGGCATGGACGAGGAATCT  
AGCATCTTCTGGTTTCAAACGGCAGCGACTGGCCTAAAAGTCTGTGCGATGTTAGCCTG  
GACAAAACCCCGTTCATCGGATGCTGGAGGGACAGTCCAACCTCAACTGTACGGGAGGC  
CCAACCGCCGTTTGGCTACCAATTTTCTGGGTCAAAGGGCCGAGCTGCACTCAAGTGGA  
AGTTGTGACAGTTATGAGACTGTGATTCAAGTCTCCGGGTATGGCGAAAACGAAACC  
GTCACCGTCTCCCCAACTTTGCTGGAAGGGTTCCCTGGCTACCAGGCATCCCTTCTCC  
GACATACCCCGACCCTGACCATCACCAACATCCGCCCTAGCGACCGCGCGGACTG  
TGCTCAACTAAGTACCGGATATCTACTCTTAGTTTGGGCCCTTGAACCGGGCGCC  
CAGTCTGTGGTCATCCTCGTCAACGACCCAGGTACCGAGCCGACCTGTGCCGTAAGCCA  
GACGGGATGTACCAGACCCCGCCGACTGTGCCAGTTCTACACGTGCTCGGGCGGTCTG  
TCTTACGGCACCAACAACCTGCCGGTGGACTGGTCTTCAACCAGGAACTGCAGCTGTGT  
GACTGGCAAACAACGTCATCTGTCTGTAG

>VCBP2S1\*03 [organism=Branchiostoma floridae] [molecule=DNA] [moltype=genomic]  
[location=genomic] [note=allele 03 of VCBP2; predicted transcript, BAC62d19 (EU875589),  
Scaffold\_295; Brafl1 genome resource animal] Amphioxus variable region-containing chitin-binding  
protein 2 (VCBP2), VCBP2S1\*03, mRNA; VCBP2 allele (predicted)

ATGTTGGGTCTGTTGGTTCGCATCTCCGCTGTAGCGTGCTACGCAGGTGCTTTGCCATC  
ACCAACGTGACGCTACCGGATCGAAGCGCCGTTGGTCTATCTTCGGTACAGCCCGGAC  
CCTACCTGGGTGAACAGGATAGAGTTCAGATGTGAATATTCCATCTCACCTGCACCGCC  
ACTCCTCTACTATCACCTGGCTCAAGGGACCCTTCACAGACGACAGCCGACTGGTGGTC  
TACAAGTGGAGTTCATCAGGAGAAGTCTACGTCCATCCCGAGTTTGCAGGACGGTCCAGC  
GTACCGTCCCGAACC CGCCGACTCTCGTGTGACCGACGCGAAGTTTACGACTGGGGC

CGATACTGGTGTCCGGTACAAAACGAGGAACAATCGGACGAGTTCGGCACGGACGAGGAG  
TCTCTGCTCTTCTGGTACAAGTCCACTGTCTACGATTACGACGCCCTCCCCGTGGCGGC  
TATTCTTCTTTTGTGGAGGTGGACAAAACACCAAGTCCGTGTGAAGACCGGTGGGACAGCC  
CGGCTAAACTGTCAGGGAGCCGGCGCCCTCTGGCGTCCATTGTTTGGTTCAAAGGGCCA  
AGCTGTTCCCAAGACGGAAATTGCAACGTATATGAGATCGTCATCAAAAACTGCTGTA  
CCTCAGCCTCATGCGATTCTAGGTCGGGAACCGTTAACGTGTCGCCGAAGTACGCAGGA  
AGAGCTTCACTGGACTTCAACGACGGACCCTACTACAATGTTTACTATCCGGATTAACC  
ATCACTGACATTCGCCCTTCCGACGTCGGCCGGTACTGGTGCACCAATGATGCACCCTTA  
TGGTACCAGAATGATCTGCGCAGCCGCGATTCCAGTCTGTGGTGGTGTCTCTTGACGAT  
GAAGCACCGACCCGTACTGTGATGGGAAAGCGGACGGGATGTACCAGGACCCTGGCGAC  
TGTTCCCGTACTACACCTGCTCGGGTAGCTGGCTGTACGGCCAGTGCCCTGTCTGACA  
GGGCTGTTCTTAAAGCAAGCCCTGCAAGTGTGTGACTGGCCTAATAACGTTGCCTGTGCG  
TAA

>VCBP5S1\*03 [organism=Branchiostoma floridae] [molecule=DNA] [moltype=genomic]  
[location=genomic] [note=allele 03 of VCBP5; predicted transcript, BAC62d19 (EU875589),  
Scaffold\_295; Brafl1 genome resource animal] Amphioxus variable region-containing chitin-binding  
protein 5 (VCBP5), VCBP5S1\*03, mRNA; VCBP5 allele (predicted)

ATGTCGATTCTACTGTTATCATTATTCTACTGCTTACGTAGGACCGGAAAGTGC GGAT  
GCGGTGTCTATCAGACCGTGACGGTACCGGATCGAGCGGTTGGGTGGTGTATGTGGCC  
CGCCTGGGTGACCCTACCTGGGTGAACCGGATAGAGTTTCAAGTGTGAATATTCATCTCA  
CCTGCCTCAGCCACTCCGCCTACTATCACCTGGCTAAAGGGGGTGTGGCCGACGAAGAC  
CGACAGGTGATCTACAAGTGGAGTTCATCAGGAGAAGTCTACGTCCATCTGAGTTGCA  
GGACGGGTACGCGTACCATCCAGAACCACCCGACTCTCGTGTGACCGACGCGAAGTTT  
GACGACTGGGGCCGATCTACTGTCGGGTACGAACGAGGACCAATCGGACGAGTTCGGC  
ACGGACGAAGAGTCTCTGCTTCTGTTACAAGTTGGGCTACGACCCACCGACCCGCTCTG  
TCGCAGGTAACTGGACAAAACGCCAGTCCGCGTGGCTGTGGAGGGACAGCTCGGCTC  
GACTGTACGGGAACAGCGCCGTGAAGCCTTATTCTCTGGGTCAAGGGCCGCGCGAC  
TGACTCAAGGTGGAAGCTGTGACAGTTATGAGACTGTCATTACAAGTCCGCCGTGTGG  
GGCGTGGTAATCCAGAACCAGAAACATCACCATCTCCCCAGCTTCGACGGAAGGGTT  
TCCCTGGATGCCGACGGGTCTGGCTCTTACCCCGACCCGACTGACCATCACCGACATCCGC  
CCTAGCGACTCCGGCCGGTACTGGTGCGCCCTGACATTTCCGAGGATTACTCTAACCTG  
GGTCCTCTGAACCGGACGCGCAGTCTGTGGTTCATCATCGTCAACGGCCCAAGTACCGAG  
CCGACCTGTGCCGGTAAAGCCGACGGGATGTACCAGCACCCCGCCGACTGTGCCAGTTC  
TACACGTGCTCGGGCGGTCTGTCTTACGGCACCAACACCTGCCAGCTGGACTGGTCTTC  
AACCAGGAATACAGCTGTGCGACTGGGCAAAACACGTCATCTGTGTGTAA

>VCBP3S1\*02 [organism=Branchiostoma floridae] [molecule=DNA] [moltype=genomic]  
[location=genomic] [note=allele 02 of VCBP3; predicted transcript, Scaffold\_1, BAC90f15  
(EU875591); Brafl1 genome resource animal] Amphioxus variable region-containing chitin-binding  
protein 3 (VCBP3), VCBP3S1\*02, mRNA; VCBP3 allele (predicted)

ATGACGGTGTCTACTCGTCTCCATATGCCTCGGCATGGCCTATGGGACGTCATCATG  
ACCGTCCGACACCACACAGAAGTAGAGGTCCATGCCGCGGTACCGTGGAGTCCCC  
TGTGCGTACCAGCTGGCGAACGACACCCAGCCTCCCGTCACTCATGGCTCAAGGGGGCA  
TCACCGGACAGGACCAAGTCTTCAAGGGAACTACAACGAGGAGAGAGGGGCTG  
GGGTTCTGAGAGGACAGCTACAAGGAGAGTTTGGGGACTTCTCGGTGGGCTCG  
GTGGCAAACCTGGCCGCGCCACTCTGCGGTTACTCACGTTACCCACAGGACGGTGGG  
CGGACTGGTGTGAGTGGCGCAGTGGAGTATCCGGACAGAGTTCGGGCTGGACGCAAG  
TCCGTGGTGTGAAGGTGACAGGCCACCCCATCAATAATGTCCACGTCTCCACGGCG  
GAAGTTGTCCAGGTTGACGAGGGCAATGACATTACCATGACGTGCCCTGCACCGACTGC  
GCAAACGCCAACGTACGTTGACACCGGGCAACCTTCTCGAGAACTACGAGACCGGC  
ACCTACCAACCACTGGTAACAAGAACCAGTTCGGCATCACCTGGTTCTCGTCTGAGATC  
GCGGGCCGGGCGAGCTTACGCGGCGCGCAACCTGGTTCCTCGGGCCCAAGATCACA  
GACCGCGCCGCGTCTGGTGCAGCTCGGACTGGACAGGAGAGCTAGACGCGGACAGG  
TCCTCAACCATCTCAAGTCCAACGAAACGTTACCTGTGACGGTAAGCCGACTGGC  
CTGTACGCGGACCCACCGCTGTGACTACTACTACCAGTGCATCCCTGGCTATCTCC  
CTACACCGCCCTGCGGGTATGCCGCGATGGTATTCAACGAGGAGATGCAGTACTGCGAC  
TGGGACATCAACGTGCCCCACCTTGGGAAAGCAAGCCGGTGTGA

>VCBP3S1\*03 [organism=Branchiostoma floridae] [molecule=DNA] [moltype=genomic]

[location=genomic] [note=allele 03 of VCBP3; predicted transcript, BAC54h3 (EU875588), allele of Scaffold\_1; second exon excluded; Brafl1 genome resource animal] Amphioxus variable region-containing chitin-binding protein 3 (VCBP3), VCBP3S1\*03, mRNA; VCBP3 allele (predicted)

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ATGACCGTCCGCACGACCTATACAAAAGTGGAGGTGCACGCAGGCGGTACCGGAACTAC
AACTGGCAGGGTGAAGGGTTGGGGTTCGTGGAGAGCGACGCTACAAGGAGAGTTTCGGG
GACTCCCGCGGACGGGCTCTGTGGCAAACCTGGCCGCGCCCACTCTGCGGCTCACTCAC
GTCCATCCACAGGACGGTGGCCGCTACTGGTGCCCGGTGGCGCAGTGGAGCATCCGGACC
GATATTACCCCTTCAAACCCACCAGGTCATACGCCATCCAACAACGTTACAGTCTCCACG
GCGGAAGTTGTCCAGTTGACGAGGGCAATGACATTACCATGACGTGCCCTGCACTGAC
TGCGCAAACGCCAACGTACAGTGGTACACCGGGCCAACCTTCTTCGAGAAGTACGAGACC
GGCACCTACCAGCCTTAGCCAACAAGAACCAGTTCGGCATCACCTGGTTCTCGTCTGAG
ATCGCGGGCGGTGCGAGCTTCAAGGTCGCGCAACCTGGTCTTCGGGCGCCAAGATC
ACAGACGCGCGCGCTGTGGTGGAGCTCGCGACCGCCAAGGCGAGCTGGATGCAGAC
AGGTCCTCAACATTCTCAAGGTCCAACCTGGAGCCGTTACCTGTGATGGGAAGCCGACG
GGCCTGTACGCCGACCCACCGCTGTGACTACTACTACCAGTGTATCCCTGGCTATCCT
CCCCTCACCCGCCCTGCGGCTACGCCGGCATGGTGTCAACGAGGAGATGCAGTACTGC
GACTGGGACTTCAACGTGCAATCACCTTGGGAAGCAAGCCGGTGTGA
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>VCBP3S1\*04 [organism=Branchiostoma floridae] [molecule=DNA] [moltype=genomic]

[location=genomic] [note=allele 04 of VCBP3; predicted transcript, PAC30b18 (AC135602.14), independent to genomic resource, Brafl1] Amphioxus variable region-containing chitin-binding protein 3 (VCBP3), VCBP3S1\*04, mRNA; VCBP3 allele (predicted)

```
ATGCAGCCGTTTCTGCTTGTCTCCCTGTGCATTGGCATGGCCTATGGCAGTCCATCATG
ACAGTCCGCACGACCCATACAGAAGTAGAAGTGCACGCCGCGGTACCGTGGAGTCCCC
TGCCCTACCAGCTTGTCTAACGACACCCAGCCTCCCGTCACTCATGGCTCAAGGGGGCC
TCACCGGACAGGAGCAACCAAGGTCTTCAAGGGAACTACAACCTGGCAGGGAGAAGGGCTG
GGGTTCTGAGAGGACAGCTACAAGGAGAGTTTCGGGACTTCCGCGGACGGGCTCG
GTGGCAAACCTGGCCGCGCAACTCTGCGGCTTACTCACGTCCACCACAGGACGGTGGC
CGGACTGGTGCAGGTGGCGCAGTGGAGCATCCGGACAGAGTTTGGGCTGGATGCCAAG
TCCGTGGTGTCAAGGTGACAGGCCACCCCATCAATAATGTCCACGTCTCCACGGCG
GAAGTTGTCCAGGTTGACGAGGCAATGACATTACCATGACGTGCCCTGCACTGACTGC
GCAAACGCCAACGTACAGTGGTACACCGGGCAACCTTCTTCGAGAAGTACGAGACCGGC
AGTACCAGCCTCTGGCCAACAAGAACCAGTTCGGCATCACCTGGTCTCGTCTGAGGTC
GCGGGCCGGCGAGCTTCAAGGTCGCGCAACCTGGTCTCCGGGCGCCAAGATCACT
GACGCCGGCCGCTGTGGTGGAGCTCGCGACCGCCAGGGCGAGCTGGATGCAGACAGG
TCCTCAACATTCTGAAGGTCCAACCTGGAGCCGTTACCTGTGACGGGAAGCCGACAGGC
CTGTATGCCGACCCACCGCTGTGACTACTACTACCAGTGTATCCCGGTTACCCCTCCC
CTCCACCGCCCTGCGGATGCGCGCATGGTCTTCAACGAGGAGATGCAGTACTGCGAC
TGGGACATCAACGTGCCGCCACCTTGGGAAGCAAGCCGGTGTGA
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>VCBP4S1\*04 [organism=Branchiostoma floridae] [molecule=DNA] [moltype=genomic]

[location=genomic] [note=allele 04 of VCBP4; predicted transcript, PAC34i17 (AC141434.12), independent to genomic resource, Brafl1] Amphioxus variable region-containing chitin-binding protein 4 (VCBP4), VCBP4S1\*04, mRNA; VCBP4 allele (predicted)

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ATGGCTCCGTTACACCGTTTGTCTGTATCATCCTGGCAGGTGCTATGGCACAATCG
CCATTCCGAATCATGACGGTACCCTGCCGAGGCCGAAGTACGGCAAATGTCGGAAGT
GACGTCAAATGCCCTGTTTCTACAGCATCCCGGCTGCTCGTCCGGACTGAATCCGACC
ATCAACTGGTACAAGGAGATGAAGGGATCGCCAGCGCTACCAAGATCTTTCCCTCTCC
TACCACGGCTCCACACAATAGCGGAGGCTTACGAGGGGTACGAGTTGCGGGTCAACTG
GAGAGTCTCACTGATCCACCTGAAACTCAGCGCGTCAAGGCGTCCGACCACGGCCGG
TACTGGTGGCCGCTGTTGACTCCGACGAGCACAACCAATTCGGCATGGACTCCAAGTGC
GTTCTCTCACAGTATAGACCCTAGCATAACGACGAGGACAGGGTATGGGCGCCCGGGC
CGTGTGAGCTGCGTGTGCCGCTGTACGGCAGGTGTACCAGGGGAGGACGTGGAGCTC
ACATGCGAGTGCATGATTGCCACTGGACTAGCACCAAGTCTTGGTTCACGGTGTCAATTT
GATGACACCTGGGCGGCCACCGAGGTGCTCGTACCGTAGGTCCGTCGCTGAGCCAT
CAGTGCCATGGAGGGACCAACCGCTGCCCGCATTCGAGACCACTTCTCGGCAACT
CGGAAGCCTTGAGGATTTGCGGAGCAAGCGCTGGACAACGCAGGACTGGTGTGAG
GTGGAAGATATGACCTTCAAGTGTGGCTCGGGAGTGGACGCTCAGTCCGTGGCTGTGGCT
GTCGAGTACGTTGTGAGGGGAAGCCGGGGGCGCTATCAACACCTGACGACTGCTCC
```

AAGTACTACACCTGCGCGGAAGGGGGCTGCAGTACGACGGCATCAGTGCCTGTCCACCC  
GGCCTAATGTACGACCAGGCCAACGGCTACTGCAACTGGGCCACGAGGTACCTGTCTG  
TAA

>VCBP2S1\*04 [organism=Branchiostoma floridae] [molecule=DNA] [moltype=genomic]  
[location=genomic] [note=allele 04 of VCBP2; predicted transcript, PAC37d15 (AC135603.5),  
independent to genomic resource, Brafl1] Amphioxus variable region-containing chitin-binding

protein 2 (VCBP2), VCBP2S1\*04, mRNA; VCBP2 allele (predicted)  
ATGTTGGGTCTGTTGGTCGCTATCTCCGCCGTAGCGTGCTACACTGGTGCGGTGCCATC  
ACGAACGTGACGGTACCGGATCGAAGCGCCGCGCGGTTGGGTCTATCTTCGATACAGC  
CCGGACCCTACCTGGTGAACAGGATAGAGTTCAGGTGTGAATATACCATCTCACCTGCC  
TCAGCCAATCCGCCTACTATCACCTGGCTCAAGGGACCCTTCACAGACCGACAAGTGATC  
TACAAGTGGAGTTCATCAGGAGAAGTCTACGTCCATCCCGAGTTCGACGGCCGAGTCAGT  
GTACCATCCCGAACCCGCCGACTCTCGTGTGACCGACGCGAAGTTTGACGACTGGGGC  
CGATACTGGTGTGCGGTACGAACGAGGACCAATCGGACGAGTTCGGCACTGACGAGGAG  
TCTCTGCTATTCTATTACAAGTCGACTGTATTGACCAAGAATGCCCACTCACACTT  
GTTTGTGCGACTACGATTACGACGTCCCTGCTCGTGGCGGCCAATATTCTTTGTGGAG  
GTGGACAAAACGCCAGTCCCGTGTGGAGACAGGTGGGACGGCCCGCTCCACTGTGAGGGA  
TGGGGCGGCCCTCTGGCGTCCATTGTCTGGTTCAAAGGGCCAAGTTGTACCCAAGACGGA  
AATTGCAACGTATATGAGATGGTCATCAACAAAACAGCTGTACCTCAGCCCCATCCGATT  
CTAGGTCCGGGAACCGTTAACGTGTGCGCGAAGTACGAGGAAGGGCTTCACTGGACTTC  
AACGACGGTGGTACTACAATTACTATCCGGATTAACCATCACTGACATTCGCCCT  
ACTGACGTGCGTCCGTAAGTGGTGCACCGATGATGCGCCCTTATGGTACCAGAATGATCTG  
CGCAGCCGCGATTCCAGTTTGTGGTGGTCTCCTTGACGATGAAGCACCAACACCGTCA  
TGTGATGGGAAGGCTGACGGGATGTACCAGGACCCTGGCGACTGTTCCCGGTACTACACC  
TGCTCGGGTGGCTGGCTGTACGGCCAGTCTCCTGTCTGACAGGGCTGTTCTTCAACGAG  
GCCTTGAAGTGTGACTGGCCTGATAACGTTGCCTGTGCTTAA

>VCBP5S1\*04 [organism=Branchiostoma floridae] [molecule=DNA] [moltype=genomic]  
[location=genomic] [note=allele 04 of VCBP5; predicted transcript, PAC37d15 (AC135603.5),  
independent to genomic resource, Brafl1] Amphioxus variable region-containing chitin-binding

protein 5 (VCBP5), VCBP5S1\*04, mRNA; VCBP5 allele (predicted)  
ATGTCGGTCTACTGGTACGATTATTCTACTGCTTTACGTAGGACCGGAAAGTGCAGAT  
GCGGTGTCTATCACGACCGTGACAGTACCAGATCGAGGCGGTTGGGTGGTGTGGCCC  
CGCCAGGTGACCCTACCTGGTGAACAGGATAGAGTTCAGGTGTGAATATTCATCTCA  
CCTGCTTACGCCACTCTCCTACTATCACCTGGCTCAAGGGAGTGTGGCCGACGACAGC  
CGACAGGTGATCTACAAGTGGAGTTCATCAGGAGAAGTCTACGTCCATCCCGAGTACGCA  
GGCCGGTACGTGTACCGTCCCGAACCCACCCGACTCTCGTGTGACGGACGCGAAGTTT  
GACGACTGGGGCCGATACTGGTGTGCGGTACGAACGAGGACCAATCGGACGAGTTCGGC  
ACGGACGAGGAGTCTCTTCTTCTTCTGGTACAAGTTGGGCTACGACCCACCGACCCGCTG  
TCGACAGTTAGCTTACAAAACGCCAGTCCGCGTGGCTACTGGTGGGACGGCTCGGCTG  
GACTGTACGGGAACAGCGCCGTGAGGCATCCATTCTCTGGGTCAAAGGGCCGACAAGC  
TGTACTCAAGGTGAAAGCTGTGACAGTTACGAGACTGTCATTCAAGTCCGCCGTGTGG  
GGCGTGGTAACCCAGAACCGGAAAACATCACCATCTCCCCAGCTTCGACGGAAGGGTT  
TCCCTGGATGCTGACGGTCTGGCTCCTTCACTCCGACCCCTACCATCACCGACATCCGC  
CCTAGCGACTCCGGCCGTAAGTGGTGCCTCTGACATCTCCGAGGTTTACTCTAACCTG  
GGTCTGCTGAACCGGACGCTCAGTCTGTGGTTCATCATCGTCAACGACCCAGGTACAGAG  
CCGACCTGTGCCGTAAGCCGGACGGGATGTACCAGACCCCGCCGACTGTGCCAGTTC  
TACACCTGCTCGGGCGTCTGTCTTACGGCAACAACAACCTGCCCGCTGGACTGGTCTTC  
AACCAGGAACCTCAGCTGTGCGACTGGGCAACAACGTCATCTGTCTGTAG

>VCBP5S2\*03 [organism=Branchiostoma floridae] [molecule=DNA] [moltype=genomic]  
[location=genomic] [note=allele 03 of VCBP5 paralog 2; predicted transcript, PAC37d15  
(AC135603.5), independent to genomic resource, Brafl1] Amphioxus variable region-containing  
chitin-binding protein 5 (VCBP5), VCBP5S2\*03, mRNA; VCBP5 allele (predicted)

ATGTTGGGTCTGTTGGTCCCATCTCCGCTGTAGCGTGTGTTGAATCAAGTTACGCAGAC  
GCGGTGTCCATCACGACCGTGACGGTACCGAATCGAGGCGGTTGGGTGTTGGTGTGGCCC  
CGCCAGGTGACCCTAACTGGTGAACCGGGCAGAGATCGGGTGTGAATATACCATCTCA  
TCTGCACCAGCCACTCTCCTACTATCACCTGGCTCAGGGGAACATTGCGCGACAAAACAG  
GTGATCTACAAGTGGAGCTCTCAGGAGAAGTCTACGTGCATCCCGACTTCGACGGCCGG

GTCAGTGTGGAGTCCAGGACACATCCTACACTGATACTGGTCAACCAAGGAGGCTGGGGC  
CGATACTGGTGTCTGGGTCACCAACGAGGAGCAACCCGGCGAGTTCGGTACAGACGAGGAG  
TCTCGCCTCTTTTGGTACGGTTCAGGATACGACTTGCCTGGCCGTCTGTCTGGCTTAAC  
CTGGACAAGACCCCGTCCATGTGGAGGTTGGCGGGACAGTCCGACTCAACTGTAACGGA  
ACCAGTGGCTCTACCGCTTCCATTCTCTGGGTCAAAGGGCCGAGCTGCATTCAAGGTGGA  
GGCTGTGACAGTTACGAGACTGTAATTCACAAGTCTGCCAGTACGGCACTTCCAACACA  
GAACCGAAAATCACCATCTCCCCAACTACACTGGAAGGGTTTCTTGGATACACAATAT  
TACACCGTAAATGACTACACCTACTTGAATTCACCCCCACCCTGACCATCACTGACATC  
CGCCCTAGCGACGCCGGTTCGGTACTGGTGCTCTCCTGCCACACGGAATTGTACTTTAT  
CTGGGCACTCTGAACCGGGACGCTCAGTCTGTGGTCGTCATCGTCAACGACCCAGGTACC  
GAGCCGACCTGTGCGGGTAAGCCGGACGGGATGTACCAGCACCCGCGACTGTGCCAG  
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