Supplemental Tables and Figures

The basis for haplotype complexity in VCBP, an immune-type receptor in amphioxus

L. J. Dishaw et al. 2010

Supplement table 1. Nucleotide substitution patterns among the VCBP2/5 gene loci.

Ps

	Within a locus			Between loci		
	5a	**2b**	**5b**	**5a-2b**	**2b-5b**	**5b-5a**
Entire region	0.218(0.019)	0.110(0.015)	0.127(0.017)	0.454(0.027)	0.419(0.022)	0.298(0.022)
V1 (420)	0.269(0.036)	0.111(0.025)	0.162(0.028)	0.347(0.041)	0.209(0.030)	0.344(0.036)
V2 (492)	0.186(0.030)	0.089(0.023)	0.119(0.028)	0.530(0.042)	0.513(0.044)	0.285(0.035)
Exon1 (58)	0.308(0.098)	0.206(0.086)	0.172(0.093)	0.274(0.071)	0.738(0.093)	0.749(0.077)
Exon2 (170)	0.199(0.047)	0.102(0.040)	0.185(0.047)	0.217(0.041)	0.216(0.040)	0.229(0.047)
Exon3 (250)	0.322(0.051)	0.116(0.034)	0.146(0.039)	0.440(0.057)	0.195(0.042)	0.440(0.053)
Exon4 (171)	0.148(0.045)	0.142(0.046)	0.192(0.052)	0.467(0.072)	0.459(0.063)	0.419(0.075)
Exon5 (135)	0.228(0.065)	0.051(0.035)	0.029(0.029)	0.662(0.092)	0.640(0.102)	0.204(0.065)
Exon6 (186)	0.202(0.050)	0.059(0.031)	0.098(0.040)	0.483(0.071)	0.464(0.084)	0.200(0.044)
Exon7 (182)	0.135(0.045)	0.134(0.043)	0.060(0.028)	0.548(0.071)	0.565(0.076)	0.091(0.025)

Ds

	Within a locus			Between loci		
	5a	**2b**	**5b**	**5a-2b**	**2b-5b**	**5b-5a**
Entire region	0.260(0.030)	0.121(0.019)	0.139(0.020)	0.698(0.069)	0.615(0.065)	0.380(0.035)
V1	0.336(0.063)	0.122(0.033)	0.182(0.036)	0.466(0.078)	0.245(0.042)	0.463(0.073)
V2	0.217(0.041)	0.096(0.027)	0.130(0.031)	0.926(0.182)	0.865(0.171)	0.360(0.065)
Exon1	0.425(0.237)	0.253(0.136)	0.197(0.131)	0.360(0.141)	2.038(0.638)	1.950(0.499)
Exon2	0.234(0.067)	0.114(0.046)	0.214(0.065)	0.258(0.066)	0.276(0.072)	0.263(0.064)
Exon3	0.435(0.100)	0.127(0.039)	0.163(0.046)	0.671(0.155)	0.227(0.057)	0.672(0.147)
Exon4	0.168(0.060)	0.161(0.063)	0.221(0.073)	0.733(0.221)	0.716(0.190)	0.617(0.179)
Exon5	0.280(0.109)	0.054(0.040)	0.030(0.031)	1.693(0.559)	1.510(0.566)	0.239(0.100)
Exon6	0.237(0.078)	0.062(0.038)	0.106(0.051)	0.780(0.261)	0.726(0.298)	0.234(0.062)
Exon7	0.149(0.055)	0.149(0.057)	0.064(0.032)	0.991(0.316)	1.062(0.366)	0.098(0.031)

Pn

	Within a locus			Between loci		
	5a	**2b**	**5b**	**5a-2b**	**2b-5b**	**5b-5a**
Entire region	0.114(0.011)	0.032(0.005)	0.026(0.005)	0.227(0.015)	0.211(0.017)	0.141(0.013)
V1	0.132(0.020)	0.031(0.009)	0.022(0.009)	0.160(0.020)	0.085(0.018)	0.149(0.021)
V2	0.148(0.020)	0.036(0.009)	0.021(0.007)	0.297(0.031)	0.282(0.034)	0.156(0.020)
Exon1	0.021(0.020)	0.042(0.028)	0.170(0.050)	0.031(0.017)	0.476(0.103)	0.481(0.102)
Exon2	0.149(0.037)	0.030(0.013)	0.018(0.014)	0.179(0.036)	0.117(0.035)	0.154(0.033)
Exon3	0.121(0.025)	0.032(0.014)	0.024(0.011)	0.148(0.027)	0.063(0.022)	0.145(0.028)
Exon4	0.198(0.039)	0.063(0.020)	0.037(0.017)	0.272(0.048)	0.242(0.053)	0.203(0.035)
Exon5	0.099(0.030)	0.018(0.012)	0.026(0.014)	0.316(0.057)	0.335(0.061)	0.117(0.030)
Exon6	0.131(0.031)	0.021(0.012)	0.000(N/5a)	0.309(0.050)	0.283(0.051)	0.135(0.031)
Exon7	0.032(0.012)	0.025(0.011)	0.010(0.007)	0.263(0.036)	0.253(0.036)	0.022(0.008)

Dn

	Within a locus			Between loci		
	5a	**2b**	**5b**	**5a-2b**	**2b-5b**	**5b-5a**
Entire region	0.123(0.013)	0.033(0.006)	0.027(0.005)	0.271(0.023)	0.248(0.024)	0.157(0.015)
V1	0.145(0.025)	0.032(0.010)	0.022(0.009)	0.181(0.028)	0.090(0.022)	0.166(0.027)
V2	0.167(0.028)	0.037(0.010)	0.022(0.007)	0.379(0.048)	0.354(0.051)	0.174(0.025)
Exon1	0.021(0.021)	0.043(0.027)	0.200(0.069)	0.032(0.018)	0.758(0.369)	0.773(0.373)
Exon2	0.167(0.046)	0.031(0.013)	0.018(0.013)	0.205(0.048)	0.127(0.043)	0.174(0.043)
Exon3	0.132(0.030)	0.033(0.014)	0.024(0.011)	0.165(0.034)	0.066(0.023)	0.161(0.034)
Exon4	0.233(0.054)	0.066(0.023)	0.038(0.018)	0.339(0.078)	0.293(0.078)	0.236(0.050)
Exon5	0.108(0.035)	0.019(0.012)	0.027(0.016)	0.411(0.094)	0.443(0.111)	0.128(0.040)
Exon6	0.146(0.038)	0.021(0.012)	0.000(N/5a)	0.398(0.097)	0.355(0.092)	0.151(0.040)
Exon7	0.033(0.012)	0.025(0.011)	0.010(0.007)	0.324(0.066)	0.308(0.064)	0.022(0.008)

Reference

MSDC2	Ps 0.078(0.016), Pn 0.011(0.003), Ds 0.083(0.018), Dn 0.011(0.003)
Arfaptin2	Ps 0.116(0.021), Pn 0.000(N/A), Ds 0.126(0.025), Dn 0.000(N/A)

Abreviations: Arfaptin2, ADP-ribosylation factor interacting protein 2b ; MSDC2, male sterility domain containing-2 (Rossmann-fold NAD(P)(+)-binding proteins). Data compares reference BACs and PACs.

Supplement table 2a. Nucleotide substitution; genetic regions unlinked to VCBP2/5 cluster.

Genes	#alleles	Ps	Pn	Ds	Dn
VCBP3	7	0.193(0.015)	0.008(0.002)	0.224(0.021)	0.008(0.002)
	V1	0.219(0.025)	0.008(0.004)	0.261(0.038)	0.008(0.004)
	V2	0.162(0.024)	0.010(0.004)	0.185(0.033)	0.010(0.004)
Big Dfsn	8	0.082(0.021)	0.011(0.004)	0.088(0.024)	0.011(0.005)
GAPDH	6	0.061(0.018)	0.004(0.003)	0.064(0.019)	0.004(0.003)

Supplement table 2b. Additional alleles compared; estimates of average codon-based evolutionary divergence between sequences.

Genes	# alleles	Domain	Ps	s.e.	Pn	s.e.
5a | VCBP5	4	V1	0.22	0.03	0.11	0.02
		V2	0.18	0.03	0.14	0.02
2b | VCBP2	8	V1	0.15	0.02	0.07	0.01
		V2	0.14	0.02	0.08	0.01
5b | VCBP5	6	V1	0.13	0.02	0.02	0.01
		V2	0.11	0.02	0.03	0.01

Supplement table 1 and 2

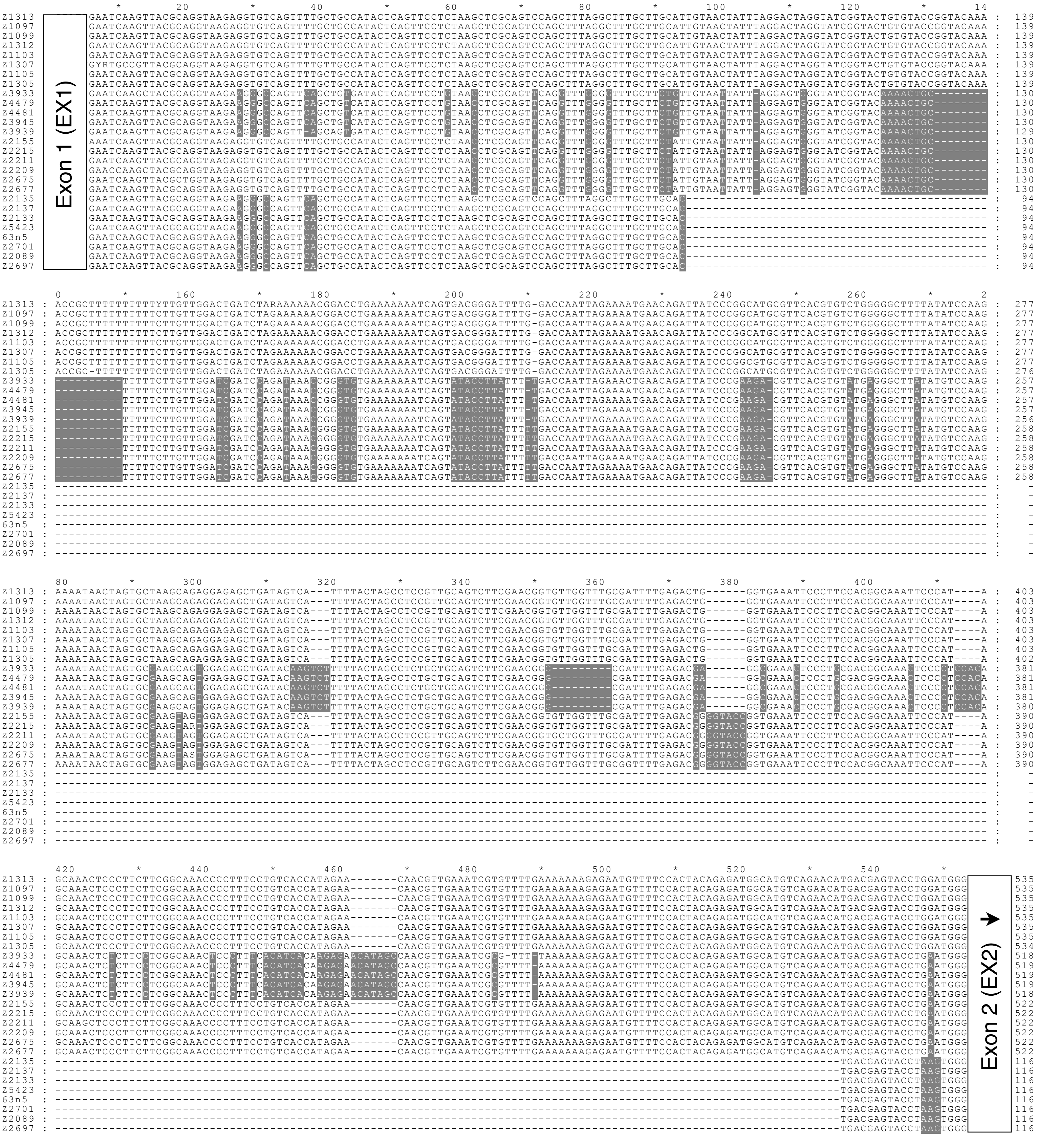
The proportion of synonymous (Ps) and non-synonymous substitutions (Pn) and the number of synonymous (Ds) and nonsynonymous (Dn) differences per site is shown with standard errors estimated by a bootstrap procedure (100 replicates; as implemented in MEGA4). For each gene, BAC/PAC reference alleles were included. Abbreviations: GAPDH, glyceraldehyde 3-phosphate dehydrogenase; Big Dfsn, Big Defensin.

Supplement table 3. Accession numbers of referenced sequences.

Gene (locus)	Allele	Genbank accession
VCBP5S1 (5b)	VCBP5S1*01-04	AF532183, BK006758, BK006763, BK006769
	VCBP5S1*05-07	HM048952-54
VCBP5b	VCBP5b-01	HM048966
VCBP5	VCBP5-01-04	HM048967-70
VCBP2/5-HV	VCBP2/5HV-NS04M	HM048971
VCBP5S2 (5a)	VCBP5S2*01-03	BK006759, BK006761, BK006755
	VCBP5S2*04	HM048946
VCBP5a	VCBP5a-01-04	HM048962-65
VCBP2S1 (2b)	VCBP2S1*01-09	AF520473, BK006760, BK006762, BK006768, HM048947-51
VCBP2-like	VCBP2*01-07	HM048955-61
VCBP2b	VCBP2b-01-05	HM048972-76
VCBP3S1	VCBP3S1*01-08	AF520474, BK006764-66, HM048936-38
Big Defensin	Bf-BD*01-08	HM048928-35
GAPDH	GAPDH*01-06	HM048940-45
Arfaptin2	JGI-ProteinID Brafl1_96986 Brafl1_79183	derived from EU875589-90
MSDC2	JGI-ProteinID Brafl1_79185 Brafl1_96985	

Reference Haplotype	Genbank accession
BAC contig 63n5-43b24	EU875590
BAC 62d19	EU875589
PAC 37d15	AC135603.5

Supplement figure 1. Point mutations that lead to single amino acid changes in EX2 can be consistent with distinct allelic lineges. (A.) Shown here are four distinct allelic lineges (i.e., subtype variants) of the -LAAD- type from gene 5a. Representative alleles have been recovered from multiple animals. Shown for illustration purposes is a portion of the intron between EX1 and EX2. Shading is only used to specify allelic groups or lineages; additional variation is not shaded. (B.) Single example from each group in (A) shown to illustrate EX2 peptide sequence subtype variation. Sequence numbers refer to internal identification system.

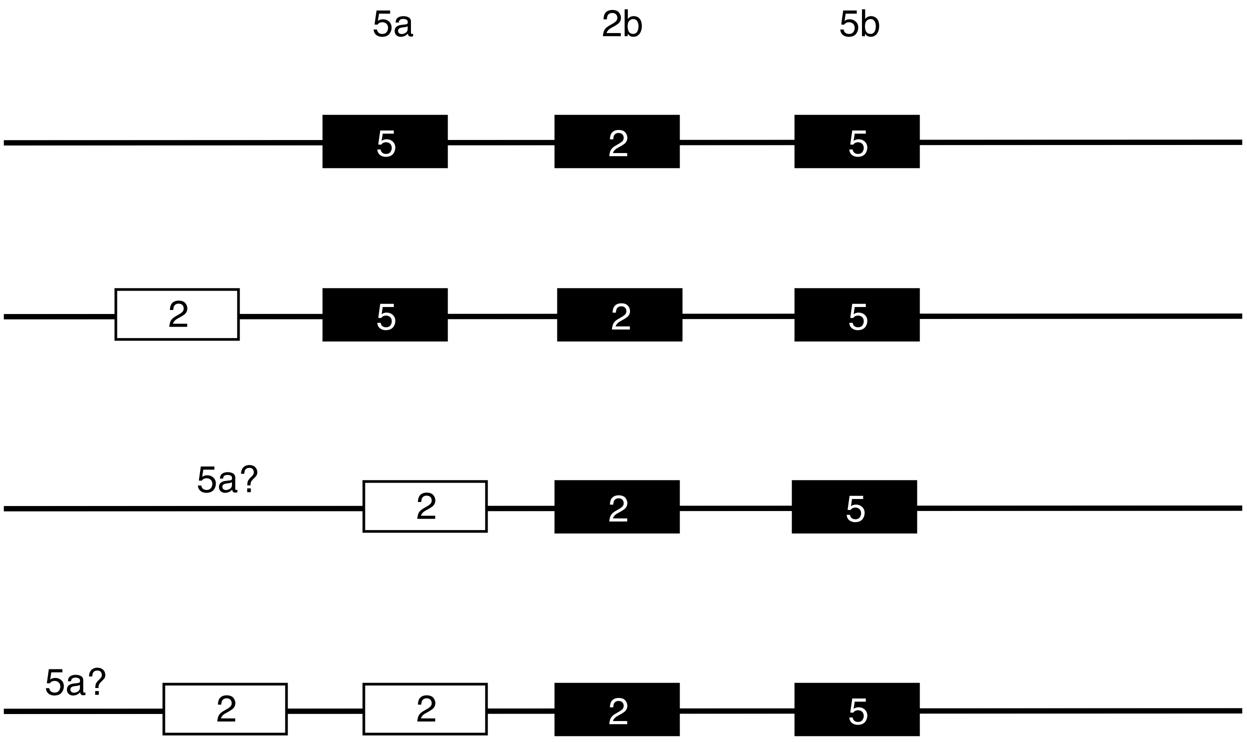


Supplement figure 1 continued:

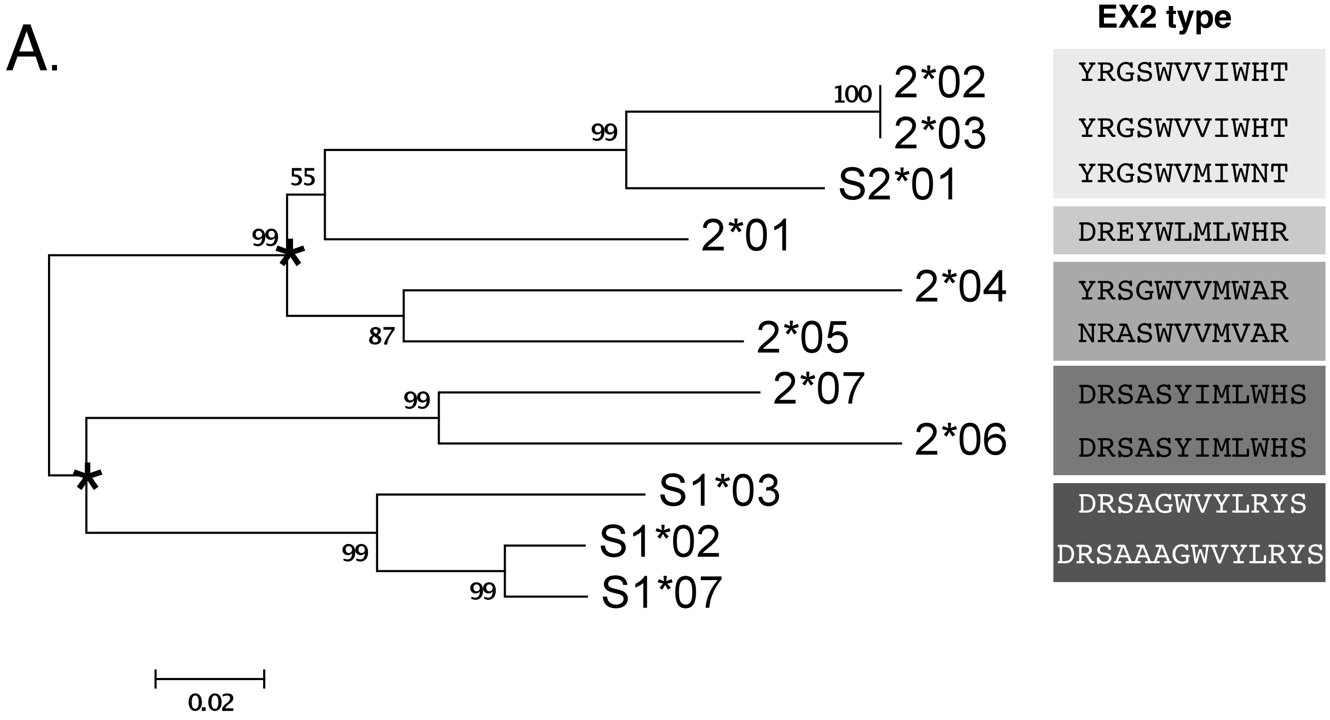
B.

```
>z1313_5a-01   DAVSITTVTVPYHNYYVLAADRPWDPTWVNRVEIGCEYTISPA
>z3933_5a-02   DAVSITTVTVPYHNYFVLAADRPWDPTWVNRVEIGCEYSISPA
>z2211_5a-03   DAVSITTVTVPYHNYYVLAADRPWDPTWVNRVETGCEYSISPA
>z2137_5a-04   DAVSITTVTVPYHNYYVLAADRPWDPTWVNRVEIRCEYTISPA
```

Supplement figure 2. Polymorphism of the VCBP2/5 cluster includes haplotype diversity with CNV. Predicted from genomic PCR haplotyping and sequencing performed on additional PAC library animals, as well as various independent animals.



Supplement figure 3. Genetic complexity in VCBP 2 genes; alleles or paralogous copies? VCBP2 genes (2b locus and others, i.e., CNVs) form as many as 6 major groups of sequences, each group possessing a specific hotspot type (encoded in EX2) with many subtype variants. Determining their relationships can be difficult due to varying degrees of polymorphism. VCBP2 alleles can be 99% identical to as low as 70%, which in some cases have been confirmed as paralogous genes. The presence of CNVs preclude the assignment of all 2-type alleles as 2b-type genes. Genomic comparison of introns and intergenic DNA is further required. **A**. Minimum evolution analysis of translated VCBP2 cDNA sequences form five major groups (clades) sharing specific, previously characterized, hotspot types. EX2 motifs are shown, as recognized between the first two proline residues. Genomic haplotyping further confirms that some of the clades represent CNV genes (i.e., paralogs); asterisks. Poisson corrected distances were implemented; gaps were eliminated via complete deletion; branching support was estimated with1000 bootstrap repetitions in Mega 4. **B.** Full length sequence alignment of the cDNA alleles from A.



Supplement figure 3 continued

B.

```
                 *        20         *        40         *        60         *        80
2*04  : DAVSITNVTVPYRS---GWVVMWARPGDPTWVNRIEFRCEYTISPASATPPTITWLRGSFADEDRQVVYKWSSSGEVYVH :  77
2*05  : DAVSITNVTVPNRA---SWVVMVARPDDPTWVNRIEFRCEYSISPASATPPTVTWLKGSFGHADRQVIYKWSSSGEVYVH :  77
2*02  : DAVAITNVTAPYRG---SWVVIWHTWGDPTFVNRVEIGCEYSISSAPATPPTITWLKGSFT--DRQVIYKLSSSGEVYVH :  75
2*03  : DAVAITNVTAPYRG---SWVVIWHTWGDPTFVNRVEIGCEYSISSAPATPPTITWLKGSFT--DRQVIYKLSSSGEVYVH :  75
S2*01 : DAVSITNVTAPYRG---SWVMIWNTWWDPTWVNRVEIGCEYTISPAPATPPTITWLKGSFT--DRQVIYKLTSSGEVYVH :  75
2*01  : DAVSITNVTVPDRE---YWLMLWHRPDDPTWVNRVEFGCEYSISPAPATPPTITWLKGSFT--DRQVIYKWSSSGEEYVH :  75
S1*02 : GAVSITNVTVPDRSAAAGWVYLRYSPD-PTWVNRIEFRCEYTISPASANPPTITWLKGPFT--DRQVIYKWSSSGEVYVH :  77
S1*07 : ----------------AGWVYLRYSPD-PTWVNRIEFRCEYTISPASANPPTITWLKGPFT--DRQVIYKWSSSGEVNVH :  61
S1*03 : GALSITNVTLPDRS--AGWVYLRYSPD-PTWVNRIEFRCEYSISPAPATPPTITWLKGPFTDADRLVVYKWSSSGEVYVH :  77
2*07  : DAVSITNVTVPDRS--ASYIMLWHRPDDPTWENRVEFRCEYNISPAPATPPTITWLMGSFTNAARHVIYKWSSSGEVYVH :  78
2*06  : DAVSITNVTVPDRS--ASYIMLWHRPEGPTWQNRVEFRCEYDISPAPATPPTITWLMGSFTNAARQVIYKWSSSGEVYVH :  78

                 *       100         *       120         *       140         *       160
2*04  : PEFAGRVSVESRTRPTLVLTDTKFADWGRYFCRITNENQSDDFGTDEGSVLFWYKY-GYD---PPRGSQFTSVEVDKTPV : 153
2*05  : PEYAGRVSVESRTRPTLVLTDAKLDDWGRYWCRVTNEEQSDDFGTDEGSLLFWYQW-GYS---PARGSHYTFVEVGKTPV : 153
2*02  : PEYAGRVSVPSRTRPTLVLTDSKFDGWGRYWCRVTNEEQSDEFGTDEESRLFWFRS-SYD---PARGDYYSFVKVDKTPV : 151
2*03  : PEYAGRVSVPSRTRPTLVLTDSKFDGWGRYWCRVTNEEQSDEFGTDEESRLFWFRS-SYD---PARGDYYSFVKVDKTPV : 151
S2*01 : PEYAGRVSVPSRTHPTLVLTDSKFDDWGRYWCRVTNEEQSDDFGTDEESRLFWFKS-GYD---PARGSHYSFVQVDKTPV : 151
2*01  : SEFAGRVSVPSRTHPTLVLTDAKFDDWGRYWCRVTNEDQSDDFGTDEESRLFWYRY-GYD---PARGSHYSFVEVDKTPV : 151
S1*02 : PEFAGRVSVESRTRPTLVLTDAKYDDWGRYWCRVTNEDQSDEFGTDEESLLFYYKSTVYDYDVPARGGQYSFVEVDKTPV : 157
S1*07 : PEFAGRVSVPSRTRPTLVLTDAKFDDWGRYWCRVTNEDQSDEFGTDEESLLFYYKSTVYDYDVPARGGQYSFVEVDKTPV : 141
S1*03 : PEFAGRVSVPSRTRPTLVLTDAKFDDWGRYWCRVTNEEQSDEFGTDEESLLFWYKSTVYDYDAPPRGGYSSFVEVDKTPV : 157
2*07  : PDYTGRVSVESRTHPTLILVNQ--GGWGRYWCRVTNEEQSDEFGTDEESLLFYYNTGAYN---PPRGSGYSFVEVDKTPV : 153
2*06  : PDFAGRVSVESRTHPTLILVNQ--GGWGRYWCRVTNEEQSDEFGTDEESLLFYYTTGAYN---PPRGSGFSFVEVDKTPI : 153

                 *       180         *       200         *       220         *       240
2*04  : RVETGGAARLNCDGLGGKEASIVWFKGPNCTQDGNCNVYEMVINKTAVEHFSP--DPGTVNVSPKYAGRASLGANNMGDT : 231
2*05  : RVKTGGTARLRCEGLGGKEASIVWFKGPSCTQDGNCNVYEMVINKTAVGHWSP--DPGTVNVSPKYAGRASLGANNMGDT : 231
2*02  : RVKTGGTAKLLCEGWGGKEASIVWFKGPSCTQDGNCNVYEMVINKTAEEHFSP--DPGTVNVSPKYAGRASLGANNMGYT : 229
2*03  : RVKTGGTAKLLCEGWGGKEASIVWFKGPSCTQDGNCNVYEMVINKTAEEHFSP--DPGTVNVSPKYAGRASLGANNMGYT : 229
S2*01 : RVKTGGTAKLHCEGWGGKSASIVWFKGPSCTQDGNCNVYEMVINKTAVEHFSP--DPGTVNVSPNYAGRASLGANNMGYT : 229
2*01  : RVKTGATARLHCEGLGGKEASIAWFKGPSCTQDGNCNVYEMVINKTAVGHRSP--DPGTVNVSPKYAGRASLGANNMGDT : 229
S1*02 : RVKAGGTARLNCEGSGGPLASIVWFKGPSCTQDGKCNVYEMVINKTAVPQPHPILGPGTVNVSPKYAGRASLDFNDGGYY : 237
S1*07 : RVETGGTARLHCEGWGGPLASIVWFKGPSCTQDGNCNVYEMVINKTAVPQPHPILGPGTVNVSPKYAGRASLDFNDGGYY : 221
S1*03 : RVKTGGTARLNCQGAGGPLASIVWFKGPSCSQDGNCNVYEIVINKTAVPQPHAILGPGTVNVSPKYAGRASLDFNDGPYY : 237
2*07  : RVKAGGTARLNCEGSGGPLASIVWFKGPSCTQDGKCNVYEMVINKTAVPQPHPILGPGTVNVSPKYAGRASLDFNDGGYY : 233
2*06  : HVKAGGTARLHCEGMGGKEASIAWFKGPSCTQDGNCNVYEMVINKTAVGHSSPDPGTAAVNVSPKYAGRASLGKLDS-YM : 232

                 *       260         *       280         *       300         *       320
2*04  : ---------LDLTITDIRPTDVGRYWCTNDWPLWF-MNEIHSRDSRSVVVLLDDEAP--SCDGKPDGMYQDPGDCSRYYT : 299
2*05  : ---------LDLTITDIRPADVGRYWCTNDWPFSM-WNE----------------------------------------- : 260
2*02  : ---------LDLTITDIRPADVGRYWCTNDWPLYF-RNEVQSRDSQSVVVLLDDEAP--SCDGKADGMYQDPGDCSRYYT : 297
2*03  : ---------LDLTITDIRPADVGRYWCTNDWPLYF-RNEVQSRDSQSVVVLLDDEAP--SCDGKADGMYQDPGDCSRYYT : 297
S2*01 : ---------LDLTITDIRPADVGRYWCTNDWPLYF-RNEVQSRDSQSVVVLLDDEAP--SCDGKADGMYQDPGDCSRYYT : 297
2*01  : ---------LDLTITDIRPTDVGRCWCTNDWPLAMPWNELRSRNAQSVVVLLDDEAP--SCDGKADGMYRDPGDCSRYYT : 298
S1*02 : NYYYP-----DLTITDIRPTDVGRYWCTDDAPLWYQ-NDLRSRDSQSVVVLLDDEAPTPSCDGKADGMYQDPGDCSRYYS : 311
S1*07 : NYYYP-----DLTITDIRPTDVGRYWCTDDAPLWYQ-NDLASRDSQSVVVLLDDEAPTPSCDGKADGMYQDPGDCSRYYT : 295
S1*03 : NVYYP-----DLTITDIRPSDVGRYWCTNDAPLWYQ-NDLRSRDSQSVVVLLDDEAPTPSCDGKADGMYQDPGDCSRYYT : 311
2*07  : NYYYP-----DLTITDIRPTDVGRYWCTDDAPLWYQ-NDLRSRDSQSVVVLLDDEAPTPSCDGKADGMYQDPGDCSRYYS : 307
2*06  : GLTFPDMRSLDLTITDIRPTDVGRYWCTNDWPLAEQFNDLHSRDSQSVVVLLDDEAT--SCDGKADGMYQDPGYCSRYYT : 310

                 *       340
2*04  : CSGGWLYGPVPCLTGLFFNEAL : 321
2*05  : ---------------------- :   -
2*02  : CSGGWLYGPAPCLTGLFFNEAL : 319
2*03  : CSGGWLYGPAPCLTGLFFNEAL : 319
S2*01 : CSGGWLYGPVPCISGLFFNEAL : 319
2*01  : CSGGWLYGPVPCLTGLFFNEAL : 320
S1*02 : CSGGWLYGPAPCLTGLFFNEAL : 333
S1*07 : CSGGWLYGPVSCLTGLFFNEAL : 317
S1*03 : CSGSWLYGPVPCLTGLFFNEAL : 333
2*07  : CSGGWLYGPAPCLTGLFFNEP- : 328
2*06  : CSGGWLYGPQPCLTGLFFNEAL : 332
```

Supplemental figure 4. Putative crossover example in an allele from animal SW01 in the intron just upstream to the hotspot exon, EX2. The first 510bp of allele 5a-01 from SW01 shows sequence identity to BAC clone 62d19 and the remainder of the sequence is most similar to BAC contig clone 63n5-43b24. Potential crossover region is boxed; small indel noted (arrow). Bold dashed lines in BAC alleles represent sequence removed for illustration purposes.

```
                 220       230       240       250       260       270       280
62d19-Ge... TGAACAGATTATCCCGAAGACGTTCACGTGTATGAGGGCTTATATGTCCAAGAAAATAACTAGTGCGAAGC
3927-392... TGAACAGATTATCCCGAAGACGTTCACGTGTATGAGGGCTTATATGTCCAAGAAAATAACTAGTGCGAAGC
63n5-43b... -----------------------------------------------------------------------
                290       300       310       320       330       340       350
62d19-Ge... AGTGGAGAGCTGATACAAGTCTTTTTACTAGCCTCTGCTGCAGTCTTCGAACGGGCGATTTTGAGACGAGG
3927-392... AGTGGAGAGCTGATACAAGTCTTTTTACTAGCCTCTGCTGCAGTCTTCGAACGGGCGATTTTGAGACGAGG
63n5-43b... -----------------------------------------------------------------------
               360       370       380       390       400       410       420
62d19-Ge... CGAAACTCCCTGCGACGGCAAACTCCCCTCCACAGCAAACTCTCTTCCTCGGCAAACTCCCTTTCACATCA
3927-392... CGAAACTCCCTGCGACGGCAAACTCCCCTCCACAGCAAACTCTCTTCCTCGGCAAACTCCCTTTCACATCA
63n5-43b... -----------------------------------------------------------------------
              430       440       450       460       470       480       490
62d19-Ge... CAAGAGAACATAGCCAACGTTGAAATCGCGTTTTGAAAAAAGAGAATGTTTTCCACTACAGATATGGTATG
3927-392... CAAGAGAACATAGCCAACGTTGAAATCGCGTTTTAAAAAAAGAGAATGTTTTCCACTACAGAGATGGCATG
63n5-43b... -----------------------------------------------------------------------
             500       510       520       530       540       550       560
62d19-Ge... TCAGAACATAACGAGAAAGTACCTGAATGGGGAAA------------------------------------
3927-392... TCAGAACATGACG----AGTACCTGAATGGGGAAATATGTCACAGTGGTCTGCAGACACCATGATTCACTC
63n5-43b... -----------------AGTACCTAAGTGGGGAAATATGTCACAGTGGTCTGCAGACACCATGATTCACTC
            570       580       590       600       610       620       630
62d19-Ge... -----------------------------------------------------------------------
3927-392... AAATACAGCCGCGTTCGAAGACTGCAACGGAGGTTACATTTTTACAAAGTTTCTACAGTCAAACTTAGTCT
63n5-43b... AAATACAGCCGCGTTCGAAGACTGCAATGGAGGTTACATTTTTACCAAGTTTCTACAGTCAAACTTAGTCT
           640       650       660       670       680       690       700       710
62d19-Ge... -----------------------------------------------------------------------
3927-392... AAACAGAGGCCGTTACTGTTTCACACGATCACGAAGATAGTATCTTAAAACGCCAGTGGACGTTGGACATT
63n5-43b... AAACAGAGGCCGTTAGTGTTTCACACGATCACGAAGATAGTATCTTAAAACGCCAGTGGACGTTGGACATT
                    720       730       740       750       760       770       780
62d19-Ge... -----------------------------------------------------------------------
3927-392... CAATCCTTTGTAGC---------GAAATTGACCATTGTTTGGAGTATCGCACATTTACAAGTTTTCACGGA
63n5-43b... CAATCCTTTGTAATTGAAAATTTGAAATTGACCATTGTTTGGAGTATCGCACATTTACAAGTTTTCACGGA
                   790       800       810       820       830       840       850
62d19-Ge... -----------------------------------------------------------------------
3927-392... CAATCAAGTCCAGGATCAGTTCCGGACCTGCATGGACTCTGAACCCGGACGGGACTCTGAACCTGGACCG-
63n5-43b... CAATCAAGTCCAGGATCAGATCCGGACCTGCATGGACTCTGAACCTGGACGGGACTCTGAACCTGGACCGG
```