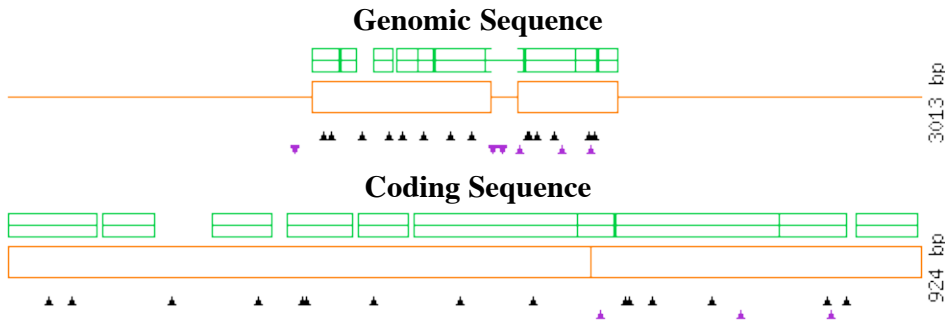


# hoxb1b

## IPB001827, IPB006711, IPB000047, and User BLOCKs



For help interpreting these results, view the [PARSENP Introduction](#) page.

#	View On Sequence	Nucleotide Change	Effect	Restriction Enzyme Differences from REBASE		PSSM Difference	SIFT Score	Description	Zygoty
				Gained in Variant	Lost from Reference				
1	<a href="#">G</a>	A945G	Non-coding	<a href="#">CviJI</a> , <a href="#">HaeIII</a>	<a href="#">AvaII</a> , <a href="#">FinI</a> , <a href="#">Hin4I</a>			8011	Homo
2	<a href="#">G C</a>	C1041A	S14Y	<a href="#">PsiI</a>		10.2	0.00	8001	Homo
3	<a href="#">G C</a>	G1065A	G22E		<a href="#">TaqII</a>	14.6	0.07	5034	Homo
4	<a href="#">G C</a>	G1166A	A56T	<a href="#">TaqI</a>	<a href="#">HgiCI</a> , <a href="#">NlaIV</a>		0.14	4905	Homo
5	<a href="#">G C</a>	G1254A	S85N		<a href="#">ApaBI</a> , <a href="#">MwoI</a>	6.2	0.27	2282	Homo
6	<a href="#">G C</a>	A1299G	H100R	<a href="#">AatII</a> , <a href="#">AcyI</a> , <a href="#">HindII</a> , <a href="#">MaeII</a> , <a href="#">MjaIV</a>		20.3	0.00	6656	Homo
7	<a href="#">G C</a>	A1302G	Q101R	<a href="#">Hin4I</a> , <a href="#">TaqI</a>		10.1	0.37	5848	Homo
8	<a href="#">G C</a>	G1371A	G124E		<a href="#">NlaIV</a>	16.0	0.02	7965	Homo
9	<a href="#">G C</a>	C1457A	P153T			7.7	0.34	8731	Homo
10	<a href="#">G C</a>	A1532T	I178F	<a href="#">AhaIII</a> , <a href="#">FaiI</a>		6.7	0.07	8106	Homo
11	<a href="#">G</a>	A1597G	Intron	<a href="#">MaeIII</a> , <a href="#">Tsp45I</a>				5565	Homo
12	<a href="#">G</a>	A1630C	Intron	<a href="#">DpnI</a> , <a href="#">MboI</a>				2798	Homo
13	<a href="#">G C</a>	C1689A	A200=					4279	Homo
14	<a href="#">G C</a>	A1714T	N209Y	<a href="#">RsaI</a> , <a href="#">TatI</a>		19.8	0.00	266	Homo
15	<a href="#">G C</a>	A1714T	N209Y	<a href="#">RsaI</a> , <a href="#">TatI</a>		19.8	0.00	439	Homo

16	<a href="#">G C</a>	A1717T	I210L	<a href="#">MseI</a>		5.9	0.09	464	Homo
17	<a href="#">G C</a>	A1742C	K218T			13.1	0.02	4848	Homo
18	<a href="#">G C</a>	A1801G	R238G	<a href="#">AciI</a> , <a href="#">BsaXI</a> , <a href="#">TstI</a>		19.3	0.00	7814	Homo
19	<a href="#">G C</a>	G1830A	L247=					7363	Homo
20	<a href="#">G C</a>	A1918G	R277G			5.0	0.19	7181	Homo
21	<a href="#">G C</a>	A1923G	V278=	<a href="#">Tsp45I</a>				6782	Homo
22	<a href="#">G C</a>	C1937T	S283F		<a href="#">Ksp632I</a> , <a href="#">MboII</a> , <a href="#">SapI</a>	5.1	0.06	4183	Homo

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[View Variants on 3D Structure](#)

No [protein homology model](#) was submitted. You may add one using any or all of the fields below.

**Blocks Families:**

**Blocks File:**  no file selected

**Sequence Alignment:**  no file selected

**-OR-**

## Genomic Sequence

```

gtttccacaaaactgcaaatccctagagcgtaaccataacaaagctacccttcaatgacaaaaagccaa      0
                                                                    72

tttcacgtattatttgcgaaattaatttcaatcatagaatattaggctttattaatgcacttactttattaa      0
                                                                    144

ataatgtaacctatthttgggtaataaatcagtcfaatcactgtgtaaaaaattaattgccattataatg      0
                                                                    216

aggthtttagtgctactttatattgcgthttatthtagaaagthttthtagctgcctaatagaatttagcgt      0
                                                                    288

ttactthtaggataaaattacacgctaaaccactatctgtcaaagataaagagagaaaaatttgaagattat      0
                                                                    360
    
```

taggaacaaaacttccctagctccataaatatcttactttaacgaaagattatagaccatagattatgttttc	0 432
tatgcttaaaatagatatgcccatatcttactttaaaagttaagacaaaactttatttgtgggggtctacta	0 504
agtctaagtaggacttcagatttcgaaacaatacaagaagatcaatattaggtaaaaatacaaaaggcaaac	0 576
taattcacgtcagatggtatttgcgcatcatgtatttcagcggcctattaaatttatagctcgcctaaacaaat	0 648
acagttgtcctcaccgtcacaggtacacaatagctataaattatctcttgctgtactcgccttaattcacat	0 720
tagacctacatagcgcactttatcagattgacgggtggattcgattgatgtgtttgtcatgtaaatacgaatc	0 792
gtttgatggacacctgcaacgccagagtgtaccgcaggcgcacactattggcgcaaaattagtcacatg	0 864
atctgtcacttaactgatatgagctcagatacaactttgcgtggtttgacatactgcttagaggtttaggg	0 936
	User BLOCK 1 (2.2e-29) IC 3.33
gcactgggaccacacatcagctcatattgaccctgcttaataatctttgcttggtcagtcaca	<u>M N</u> 2 1006
g[1]	
<u>S Y L D Y T I Y N R G S N T Y S S K</u>	20
tct tac tta gat tat acg att tat aac cgt ggt tct aac act tat agt tcg aaa	1060
	aS14Y[2]
	User BLOCK 2 (5.2e-15) IC 2.68
<u>V G C F P V E Q E Y</u> L P <u>S A C A S T</u>	38
gtt ggg tgt ttt cct gta gag caa gaa tac ttg cca agt gct tgt gca agt aca	1114
	aG22E[3]
<u>N S Y I P E G R P V G</u> G N T F T S A	56
aat agt tac att ccc gag gga cgg cca gtc gga gga aac act ttc aca tcg gca	1168
	aA56T[4]
	User BLOCK 3 (1.7e-15) IC 2.07
P H E T H G T S Y A Q I Q <u>S Q P F H</u>	74
ccg cac gaa act cat ggc aca tct tac gca caa att caa tcg cag ccc ttc cac	1222
<u>L N V D M G K T G H S N F C K</u> Q T R	92
ctc aac gtg gac atg ggt aaa aca gga cac agc aat ttc tgc aag caa acc aga	1276
	aS85N[5]
	User BLOCK 4 (2.8e-20) IC 2.75
P P <u>H S D Y G H Q H V L T Q A D D H</u>	110
cct cct cat tcg gac tat gga cat caa cac gtt ctc act caa gca gat gac cac	1330

gH100R[6]  
gQ101R[7]

User BLOCK 5 (2.0e-14) IC 2.82

M R L O S P G F S V V N M G A N I G 128  
atg cgc ctt cag tcc cct ggc ttt tcc gtc gtg aat atg gga gcc aat att gga 1384  
aG124E[8]

User BLOCK 6 (2.2e-48) IC 2.55

T Y S E S N C R P G S V S A S H Y O 146  
act tac agt gaa tca aac tgc agg cct ggc tcg gtc tct gca agc cac tat caa 1438

S Y A Y G E P E P H G Y G S F S K Y 164  
tca tat gca tat gga gaa ccc gaa cca cac ggc tat ggt tcg ttc agc aag tat 1492  
aP153T[9]

O V S P D S D S D S K T N I K O A P 182  
cag gtc tcc cct gac agt gac agc gac tcc aag acg aac att aaa caa gcg cca 1546  
tI178F[10]

User BLOCK 7 (3.9e-14) IC 3.51

T F D W M K V K R N P P K T V 197  
acc ttt gac tgg atg aaa gtc aag agg aat ccc cct aaa aca g gtagattatgacta 1603  
g[11]

gttacaatggctatagataatgtgatattaaatacagtttctaagtcgtgtttttattcaatgctaatttt 197  
c[12] 1675

User BLOCK 8 (1.6e-68) IC 4.32

K V A E Y G I H G O O N I I R T 213  
cag tt aaa gtc gcc gaa tac gga atc cat ggc cag cag aac ata ata cgc acc 1728  
aA200=[13] tN209Y[14]  
tN209Y[15]  
tI210L[16]

N F T T K O L T E L E K E F H F N K 231  
aat ttc acc acc aag cag ctc acg gaa ctt gag aag gag ttt cac ttc aac aaa 1782  
cK218T[17]

Y L T R A R R V E V A A T L E L N E 249  
tac ttg acc aga gcg cgc aga gtg gag gtg gcc gcc aca ctc gaa ctg aac gaa 1836  
gR238G[18] aL247=[19]

User BLOCK 9 (1.5e-21) IC 2.90

T O V K I W F O N R R M K Q K K R E 267  
acg cag gtt aaa atc tgg ttt cag aat cgc aga atg aag cag aag aag cgc gag 1890

K E G T A P V I K R V T L C S S G Q 285  
aag gaa ggc acg gcc ccg gtg att aaa aga gta acc ctt tgc tct tct ggt caa 1944  
gR277G[20] tS283F[22]  
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User BLOCK 10 (2.8e-24) IC 3.52

N A D H S T S S S P G A S P T S D S 303  
aac gca gac cac tca act agc tca tcg cct ggt gct tcg cct acc tcg gac tct 1998

S T A I \* 308  
 tcc act gca att tga tgagtgccagactttcgtttcgttgctggaggactatttaacttattctgtc 2065

308  
 gtgaaaaaaaaatattgtttacgtgctatattgtgtttttgtgctgcattagaactactaaatagatgcattaa 2137

308  
 cagggtatatgcttaacgttcaaagtctttttctgttggtgctgcgtccgggtcaattatatttgactacag 2209

308  
 attcattcctctgttgaaagagtaataaaatgtgaaaaagactgacatgtttatgtatttcgaatatattcg 2281

308  
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308  
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308  
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308  
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308  
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308  
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308  
 ttttaagttgagtaaaactcaaagtgcctgaggcttgttgcttaaaattttaagttgagtaaaactttttttt 2929

308  
 tacagtgaatgcaatccaatgcgcaattcaaaatcaacattttttagtttactcaacttataattgagtgtag 3001

308  
 taattaggttga 3013

**Coding Sequence**

User BLOCK 1 (2.2e-29) IC 3.33

M N S Y L D Y T I Y N R G S N T Y S 18  
 atg aat tct tac tta gat tat acg att tat aac cgt ggt tct aac act tat agt 54  
 aS14Y[2]

User BLOCK 2 (5.2e-15) IC 2.68

S K V G C F P V E O E Y L P S A C A 36  
 tcg aaa gtt ggg tgt ttt cct gta gag caa gaa tac ttg cca agt gct tgt gca 108  
 aG22E[3]

S T N S Y I P E G R P V G G N T F T 54  
 agt aca aat agt tac att ccc gag gga cgg cca gtc gga gga aac act ttc aca 162

User BLOCK 3 (1.7e-15) IC 2.07

S A P H E T H G T S Y A Q I Q S O P 72  
 tcg gca ccg cac gaa act cat ggc aca tct tac gca caa att caa tcg cag ccc 216  
 aA56T[4]

F H L N V D M G K T G H S N F C K Q 90  
 ttc cac ctc aac gtg gac atg ggt aaa aca gga cac agc aat ttc tgc aag caa 270  
 aS85N[5]

User BLOCK 4 (2.8e-20) IC 2.75

T R P P H S D Y G H O H V L T O A D 108  
 acc aga cct cct cat tcg gac tat gga cat caa cac gtt ctc act caa gca gat 324  
 gH100R[6]  
 gQ101R[7]

User BLOCK 5 (2.0e-14) IC 2.82

D H M R L O S P G F S V V N M G A N 126  
 gac cac atg cgc ctt cag tcc cct ggc ttt tcc gtc gtg aat atg gga gcc aat 378  
 aG124E[8]

User BLOCK 6 (2.2e-48) IC 2.55

I G T Y S E S N C R P G S V S A S H 144  
 att gga act tac agt gaa tca aac tgc agg cct ggc tcg gtc tct gca agc cac 432

Y O S Y A Y G E P E P H G Y G S F S 162  
 tat caa tca tat gca tat gga gaa ccc gaa cca cac ggc tat ggt tcg ttc agc 486  
 aP153T[9]

K Y O V S P D S D S D S K T N I K O 180  
 aag tat cag gtc tcc cct gac agt gac agc gac tcc aag acg aac att aaa caa 540  
 tI178F[10]

User BLOCK 7 (3.9e-14) IC 3.51

A P T F D W M K V K R N P P K T V |     197  
 gcg cca acc ttt gac tgg atg aaa gtc aag agg aat ccc cct aaa aca g | tt 591

User BLOCK 8 (1.6e-68) IC 4.32

K V A E Y G I H G O O N I I R T N F 215  
 aaa gtc gcc gaa tac gga atc cat ggc cag cag aac ata ata cgc acc aat ttc 645  
 aA200=[13]  
 tN209Y[14]  
 tN209Y[15]  
 tI210L[16]

T T K O L T E L E K E F H F N K Y L 233  
 acc acc aag cag ctc acg gaa ctt gag aag gag ttt cac ttc aac aaa tac ttg 699

