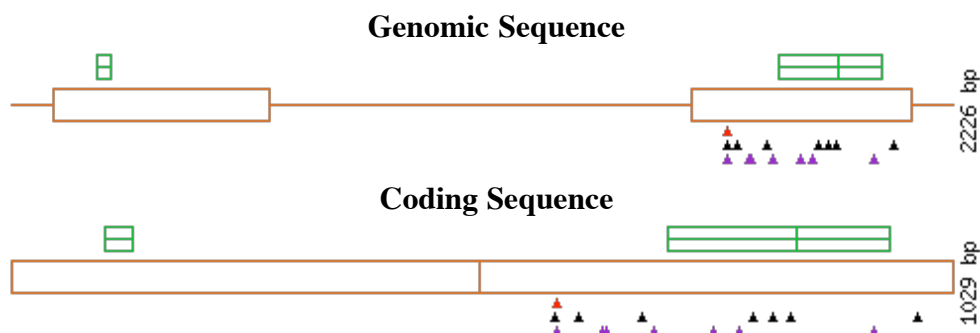


# gbx2\_2

IPB001827, IPB000747, IPB000327, IPB000047, IPB006820, IPB006711, IPB003106, and IPB003025



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 C</a>	A1690T	D198V	<a href="#">AccI</a> , <a href="#">MjaIV</a>	<a href="#">Hin4I</a>			8053	Homo
2	<a href="#">G C</a>	C1694T	Y199=	<a href="#">TspRI</a>				6112	Homo
3	<a href="#">G C</a>	C1694A	Y199*	<a href="#">MseI</a> , <a href="#">TspRI</a>				8125	Homo
4	<a href="#">G C</a>	G1716T	G207W	<a href="#">DraII</a> , <a href="#">EcoRII</a>	<a href="#">AvaI</a> , <a href="#">CauII</a> , <a href="#">HpaII</a> , <a href="#">SmaI</a>			8622	Homo
5	<a href="#">G C</a>	C1742T	D215=	<a href="#">BccI</a>	<a href="#">BbvII</a> , <a href="#">TspGWI</a>			5313	Homo
6	<a href="#">G C</a>	C1748T	D217=	<a href="#">BccI</a>	<a href="#">BceI</a> , <a href="#">BsmAI</a> , <a href="#">Esp3I</a>			2427	Homo
7	<a href="#">G C</a>	T1787A	N230K					3803	Homo
8	<a href="#">G C</a>	C1799T	N234=		<a href="#">AloI</a>			1887	Homo
9	<a href="#">G C</a>	G1865T	L256=	<a href="#">Bce83I</a> , <a href="#">SmlI</a>	<a href="#">BsaXI</a> , <a href="#">BsrI</a> , <a href="#">Eco57MI</a> , <a href="#">GsuI</a>			4321	Homo
10	<a href="#">G C</a>	C1893T	L266=	<a href="#">SspI</a> , <a href="#">TspRI</a>				741	Homo
11	<a href="#">G C</a>	C1908G	R271G	<a href="#">CviII</a>		27.3	0.00	6112	Homo
12	<a href="#">G C</a>	T1930C	L278S	<a href="#">MnlI</a>	<a href="#">MseI</a>	26.2	0.00	2781	Homo
13	<a href="#">G C</a>	G1949C	Q284H	<a href="#">ApaLI</a> , <a href="#">BseSI</a> , <a href="#">BtrI</a> , <a href="#">HgiAI</a> , <a href="#">MaeII</a> , <a href="#">MjaIV</a> , <a href="#">SduI</a>	<a href="#">BsgI</a> , <a href="#">BspMI</a>	21.1	0.00	1261	Homo
14	<a href="#">G C</a>	C2039T	N314=					2214	Homo
15	<a href="#">G C</a>	C2088A	R331S					1721	Homo

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

**Blocks Families:**

**Blocks File:** [Choose File](#) no file selected

**Sequence Alignment:** [Choose File](#) no file selected

[Redo analysis with homology model](#)

**-OR-**

[Reverse PSI-Blast/SIFT for Models](#)

### Genomic Sequence

```

tgtatgacgctgtccagcagtgagatcccaatctgagaagcgcagtgagaaaagctgctcccagacttcagg      0
                                                                                       72

                                                                 M  S  A  A  F  S  T  P  F  M  M      11
acttcagaaactgtccacattagatcat atg agt gca gct ttc agc aca ccg ttc atg atg      133

M  Q  R  P  V  G  S  T  T  A  F  S  I  D  S  L  I  G      29
atg cag cgt ccg gtg gga agc acc act gca ttc agc att gac tcg ctc atc ggc      187

                                                                 IPB006820B (3.2e-05) IC 2.82
G  P  P  Q  P  S  P  G  H  F  V  Y  T  G  Y  P  M  F      47
ggg ccg ccg cag ccc agt ccg gga cat ttc gtg tac aca ggt tat ccc atg ttc      241

M  P  Y  R  S  V  V  L  P  P  P  P  P  P  P  P  P  T      65
atg cca tac ccg tca gtg gtg ctt cct ccg ccg cct cct cca ccc cct cca aca      295

L  P  Q  S  A  L  P  T  T  H  P  H  H  P  I  P  G  L      83
ctc ccc caa agc gct ctc cct acg acc cat ccg cac cac ccg atc ccg ggc tta      349

P  S  S  F  C  S  S  L  A  Q  G  M  A  L  T  S  T  L      101
ccc agc agc ttc tgc tcc agc ctg gcg cag ggc atg gca ctc aca tcc acg cta      403

M  A  T  L  P  G  G  F  S  S  S  P  S  Q  Q  H  Q  D      119
atg gcc acg tta ccc ggc ggc ttc tcc tcc tcg ccg tcc caa cag cac caa gac      457

A  A  R  K  L  G  S  Q  S  I  H  A  M  F  D  K  S  Q      137
gcg gcg agg aag ctc ggc tct cag tct att cac gcc atg ttc gac aaa tct cag      511

D  I  R  L  D  G  E  D  G  K  T  F  A  T  K  D  S  T      155
gat att cgt ttg gat gga gag gat ggg aaa acg ttt gcg acg aaa gat tcg acg      565

```

S I P S F H D S Q S V H T S T V	171
agc att ccg tcc ttc cac gat tcg cag tcc gta cac acc tct aca g gtgagactaa	621
	171
actctgcacgcaattgttttcacagtgaatacttttatattaaactaacatagacaacggatttttaaagtc	693
	171
tttataaatgaaatttgatgtttaaaaacgccataagtgaaactggcagggttactgatttatgcggttctcc	765
	171
aattaaaaataaaatgtttttaaaagctaactcttaaaataatttaaaattttattattcaatattcgtaac	837
	171
gtctcgtgtttgaaataaatggttggtactcttaaacggctttctgtaagctagaatacattttccaactt	909
	171
aaaaaataatttagttgcaccgaggagggtcaaaaatgtaggacagaaataattatacaaatccgtacaata	981
	171
aggaattcagtggtcaaacacgtaaattaaaagcccctatgaagattttgagggaaatagtgccctgaggccgag	1053
	171
ctgccatcagtgactaaattagctcgctttaattgaggattggaaggccagcgggttcaaatgtccataa	1125
	171
aactgtaagcaaaattcactgtcgcctggatcatttatatgtatgcagagtgaaataaatgtagtcctggcc	1197
	171
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	171
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	171
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taaaagtggcagcaataaaccggaagagcgtggtgccagacaagacaagatttattctcacacaacttgttt	1485
	171
tttattgttcacaatatttaaaaacaaaatcatgtttaaaataatgtcttggtttcattctactttacatt	1557
	175
cttcttgggaaagaattataattctgcttgttttcctcactgtcatacag tg cga ggt cac agc	1622
	175
K D D S K E D D C H R K D E S F S M	193
aaa gac gac tcg aag gag gat gat tgt cac agg aaa gac gag agc ttc tcc atg	1676

D S D L D Y S S D D N G P G N A M C 211  
gac agt gat tta gat tac agc tcc gat gat aac ggg ccc ggg aac gcc atg tgt 1730  
tD198V[1] tG207W[4]  
tY199=[2]  
aY199\*[3]

Q K E D G D G S G G L D D G V H G G 229  
cag aag gaa gac gga gac ggc agc gga ggt ctg gac gac ggc gtt cac ggt ggg 1784  
tD215=[5]  
tD217=[6]

IPB000747C (3.5e-25) IC 3.09  
N G A G N T T S T G K N R R R R R T A 247  
aat ggg gcc ggg aac acc aca tcc act ggg aaa aat cgg aga agg agg acc gct 1838  
aN230K[7] tN234=[8]

F T S E O L L E L E K E F H C K K Y 265  
ttt acg agc gag caa ctg ttg gaa ctg gag aag gag ttt cac tgt aag aaa tat 1892  
tL256=[9]

L S L T E R S O I A H A L K L S E V 283  
ctg tcc ctc aca gaa cgc tcg caa atc gcg cac gcc tta aag ctc agc gag gtg 1946  
tL266=[10] gR271G[11] cL278S[12]

IPB000747D (1.8e-11) IC 2.99  
Q V K I W F O N R R A K W K R V K A 301  
cag gtc aag atc tgg ttt cag aac cgg aga gcc aag tgg aaa cgg gtc aaa gcg 2000  
cQ284H[13]

G N V N S K T G E P S R N P K I V V 319  
ggc aac gtc aac agc aaa acc gga gag cca tcc aga aac ccc aaa att gtg gtg 2054  
tN314=[14]

P I P V H V S R F A I R S Q H Q Q L 337  
ccc att ccg gtg cat gtt agt cgg ttt gcg ata cgc agc caa cac caa cag tta 2108  
aR331S[15]

E Q A R P \* 343  
gaa cag gcc cga cct tga tacacagggcttttagtttccacaggacaaattggagacttaaatcggc 2174

caataacttaatatgaccaaccttttcttgagaggaacaagtgcagtttg 343  
2226

## Coding Sequence

M S A A F S T P F M M M Q R P V G S 18  
atg agt gca gct ttc agc aca ccg ttc atg atg atg cag cgt ccg gtg gga agc 54

IPB006820B (3.2e-05) IC 2.82  
T T A F S I D S L I G G P P Q P S P 36  
acc act gca ttc agc att gac tcg ctc atc ggc ggt ccg ccg cag ccc agt ccg 108

G H F V Y T G Y P M F M P Y R S V V 54  
gga cat ttc gtg tac aca ggt tat ccc atg ttc atg cca tac cgg tca gtg gtg 162

L P P P P P P P P P T L P Q S A L P 72  
ctt cct ccg ccg cct cct cca ccc cct cca aca ctc ccc caa agc gct ctc cct 216

T T H P H H P I P G L P S S F C S S 90  
acg acc cat ccg cac cac ccg atc ccg ggc tta ccc agc agc ttc tgc tcc agc 270

L A Q G M A L T S T L M A T L P G G 108  
ctg gcg cag ggc atg gca ctc aca tcc acg cta atg gcc acg tta ccc ggc ggc 324

F S S S P S Q Q H Q D A A R K L G S 126  
ttc tcc tcc tcg ccg tcc caa cag cac caa gac gcg gcg agg aag ctc ggc tct 378

Q S I H A M F D K S Q D I R L D G E 144  
cag tct att cac gcc atg ttc gac aaa tct cag gat att cgt ttg gat gga gag 432

D G K T F A T K D S T S I P S F H D 162  
gat ggg aaa acg ttt gcg acg aaa gat tcg acg agc att ccg tcc ttc cac gat 486

S Q S V H T S T V | R G H S K D D S 179  
tcg cag tcc gta cac acc tct aca g | tg cga ggt cac agc aaa gac gac tcg 537

K E D D C H R K D E S F S M D S D L 197  
aag gag gat gat tgt cac agg aaa gac gag agc ttc tcc atg gac agt gat tta 591

D Y S S D D N G P G N A M C Q K E D 215  
gat tac agc tcc gat gat aac ggg ccc ggg aac gcc atg tgt cag aag gaa gac 645  
tD198V[1] tG207W[4] tD215=[5]  
tY199=[2]  
aY199\*[3]

G D G S G G L D D G V H G G N G A G 233  
gga gac ggc agc gga ggt ctg gac gac ggc gtt cac ggt ggg aat ggg gcc ggg 699  
tD217=[6] aN230K[7]

IPB000747C (3.5e-25) IC 3.09  
N T T S T G K N R R R R T A F T S E 251  
aac acc aca tcc act ggg aaa aat cgg aga agg agg acc gct ttt acg agc gag 753  
tN234=[8]

Q L L E L E K E F H C K K Y L S L T 269  
caa ctg ttg gaa ctg gag aag gag ttt cac tgt aag aaa tat ctg tcc ctc aca 807  
tL256=[9] tL266=[10]

IPB000747D (1.8e-11) IC 2.99  
E R S O I A H A L K L S E V O V K I 287  
gaa cgc tcg caa atc gcg cac gcc tta aag ctc agc gag gtg cag gtc aag atc 861  
gR271G[11] cL278S[12] cQ284H[13]

W F O N R R A K W K R V K A G N V N 305  
tgg ttt cag aac ccg aga gcc aag tgg aaa ccg gtc aaa gcg ggc aac gtc aac 915

S K T G E P S R N P K I V V P I P V 323

agc aaa acc gga gag cca tcc aga aac ccc aaa att gtg gtg ccc att ccg gtg 969  
tN314=[14]

H V S R F A I R S Q H Q Q L E Q A R 341  
cat gtt agt cgg ttt gcg ata cgc agc caa cac caa cag tta gaa cag gcc cga 1023  
aR331S[15]

P \* 343  
cct tga 1029