

BLZ1

[illegible][illegible]

	230	240	250	260	270	280	290	300	310	320	330
BLZ1 gene	gtggcgtggcggggacggcgacgggcccggcggcgtggacccggcggagtagcaacgccatgctcaagcagaagctcgagaaggacctcgccgcccgtcgccatgtggagggtat										
BLZ1 cds	gtggcgtggcggggacggcgacgggcccggcggcgtggacccggcggagtagcaacgccatgctcaagcagaagctcgagaaggacctcgccgcccgtcgccatgtggagg--										
hpt01	-----										
hpt02	-----										
hpt03	-----										
hpt04	-----										
hpt05	-----										
hpt06	-----										
hpt07	-----										
hpt08	-----										

[illegible]

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      450      460      470      480      490      500      510      520      530      540      550
BLZ1 gene  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
BLZ1 cds   cttctcacggcgtctgtgatctgcagagccctgcattgcctgctcgggttctagcaatctgtagatgatgtacaatacggctgggttcagtccccgccttgccctatgatatt
hpt01     -----
hpt02     -----
hpt03     -----
hpt04     -----
hpt05     -----
hpt06     -----
hpt07     -----
hpt08     -----

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      560      570      580      590      600      610      620      630      640      650      660
BLZ1 gene  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
BLZ1 cds   ctagcatctgccgccttggctatgatattctagcatctgcgatctggatgggtttcgggcaaaatctgtcttcatagtgcatcatttgtccccaaaaaaaaaacaacaa
hpt01     -----
hpt02     -----
hpt03     -----
hpt04     -----
hpt05     -----
hpt06     -----
hpt07     -----
hpt08     -----

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      670      680      690      700      710      720      730      740      750      760      770
BLZ1 gene  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
BLZ1 cds   aaaaacaaaatgggtttatccttatgtgtggacattggctagaatagagatcagagtgtgctgcgagtttgatgattctgtgattttctgagtatttgggtgtcaatagcgat
hpt01     -----
hpt02     -----
hpt03     -----
hpt04     -----
hpt05     -----
hpt06     -----
hpt07     -----
hpt08     -----

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      780      790      800      810      820      830      840      850      860      870      880
BLZ1 gene  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
BLZ1 cds   acattttacactttgggtgagcgttgggcctcatctgatcctgtcataaagcgggtgtgcttgctgtagctggctgatgatgtcacctttattgtcttctgtctgtttccagtc
hpt01     -----
hpt02     -----
hpt03     -----
hpt04     -----
hpt05     -----
hpt06     -----
hpt07     -----
hpt08     -----

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      890      900      910      920      930      940      950      960      970      980      990
BLZ1 gene  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
BLZ1 cds   ttttagaccaatgaaattagcttgtcttgtaactccctccatcccataatatagatcttcttacatccaatatgtgagttaaactggatgtaatagatcttatattatggga
hpt01     -----
hpt02     -----
hpt03     -----
hpt04     -----
hpt05     -----
hpt06     -----
hpt07     -----
hpt08     -----

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     1000     1010     1020     1030     1040     1050     1060     1070     1080     1090     1100
BLZ1 gene  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
BLZ1 cds   cggaggaggagtataattctagaaatcatatgagccttttgatttttgactccagcacatcaataatttgttttgtttcgttaatcagaacttctctccttgagtttccccact
hpt01     -----
hpt02     -----
hpt03     -----
hpt04     -----
hpt05     -----
hpt06     -----
hpt07     -----
hpt08     -----

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     1110     1120     1130     1140     1150     1160     1170     1180     1190     1200     1210
BLZ1 gene  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
BLZ1 cds   aaagatgtgttggttaagtgtttgtcttttccctcttactgttatgatattgcaactgtagccttttcaaagaactaaccctaaacactcaatcgggggggaggggggagac
hpt01     -----
hpt02     -----
hpt03     -----
hpt04     -----
hpt05     -----
hpt06     -----
hpt07     -----
hpt08     -----

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     1220     1230     1240     1250     1260     1270     1280     1290     1300     1310     1320
BLZ1 gene  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
BLZ1 cds   agcccctggggggaaatttagaaggtaagggaactgcatcaaacacgcctcatgtggggagtcgcactacaggtgccagtgaggggcctttgtatgtgagaccaggcattg
hpt01     -----
hpt02     -----
hpt03     -----
hpt04     -----
hpt05     -----
hpt06     -----
hpt07     -----
hpt08     -----

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      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
BLZ1 gene  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
BLZ1 cds   aacccgggttggccgaccctctataggaggcgttacctggagctggatagtggtgttcgcttctaagaactaacctatatttaaaaggacaaattcatgtgcatttttat
hpt01     -----
hpt02     -----
hpt03     -----
hpt04     -----
hpt05     -----
hpt06     -----
hpt07     -----
hpt08     -----

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      1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540
BLZ1 gene  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
BLZ1 cds   tttaatttttaatgcattttctgttattctgctcatttgtcatactagctcgtgtcattttccgcccgcattttcattttataaatgcattttctgttattctgctcatttgttaa
hpt01     -----
hpt02     -----
hpt03     -----
hpt04     -----
hpt05     -----
hpt06     -----
hpt07     -----
hpt08     -----

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      1550      1560      1570      1580      1590      1600      1610      1620      1630      1640      1650
BLZ1 gene  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
BLZ1 cds   tactagctcatgtcattttctgcccgcaggcctctggtgccatgcctccagaacgtttttgagcctagtcctgcatgcccaaatgcagatggtcagcatataggcactatta
hpt01     -----gcctctggtgccatgcctccagaacgtttttgagcctagtcctgcatgcccaaatgcagatggtcagcatataggcactattaCTATTA
hpt02     -----CTATTA
hpt03     -----CTATTA
hpt04     -----CTATTA
hpt05     -----CTATTA
hpt06     -----CTATTA
hpt07     -----CTATTA
hpt08     -----CTATTA

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      1660      1670      1680      1690      1700      1710      1720      1730      1740      1750      1760
BLZ1 gene  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
BLZ1 cds   atcccataggaggtaacttatcttctggtaacatctttgaactagtttagga-ctgcggtaggggaatgaactaccgtgcatacaatatatttgcttaataattccttaaatcctt
hpt01     ATCCCATAGGAGGTACTTATCTTCTGGTAACATCTTTGAACTAGTTAGGAACCTGCGGTAGGGAATGAACTACCGTGCATACCATATTTTCTTAATAAATTCCTTAAATCTTT
hpt02     ATCCCATAGGAGGTACTTATCTTCTGGTAACATCTTTGAACTAGTTAGGAACCTGCGGTAGGGAATGAACTACCGTGCATACAATATTTGCTTAATAGTTCTTAAATCTTT
hpt03     ATCCCATAGGAGGTACTTATCTTCTGGTAACATCTTTGAACTAGTTAGGAACCTGCGGTAGGGAATGAACTACCGTGCATACAATATTTGCTTAATAAATTCCTTAAATCTTT
hpt04     ATCCCATAGGAGGTACTTATCTTCTGGTAACATCTTTGAACTAGTTAGGAACCTGCGGTAGGGAATGAACTACCGTGCATACAATATTTGCTTAATAAATTCCTTAAATCTTT
hpt05     ATCCCATAGGAGGTACTTATCTTCTGGTAACATCTTTGAACTAGTTAGGAACCTGCGGTAGGGAATGAACTACCGTGCATACAATATTTGCTTAATAAATTCCTTAAATCTTT
hpt06     ATCCCATAGGAGGTACTTATCTTCTGGTAACATCTTTGAACTAGTTAGGAACCTGCGGTAGGGAATGAACTACCGTGCACACAATATTTGCTTAATAAATTCCTTAAATCTTT
hpt07     ATCCCATAGGAGGTACTTATCTTCTGGTAACATCTTTGAACTAGTTAGGAACCTGCGGTAGGGAATGAACTACCGTGCATACAATATTTGCTTAATAAATTCCTTAAATCTTT
hpt08     ATCCCATAGGAGGTACTTATCTTCTGGTAACATCTTTGAACTAGTTAGGAACCTGCGGTAGGGAATGAACTACCGTGCACACAATATTTGCTTAATAAATTCCTTAAATCTTT

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		1770	1780	1790	1800	1810	1820	1830	1840	1850	1860	1870	
												
BLZ1 gene		tgaatttgttacatcctttccctgattctcatataaactctggcaatattctttttgaagtgaacgggtgttaaattacatttcttggaatcttgtaaacaatttcgt-gtttg											
BLZ1 cds		-----											
hpt01		TGATTTGTTACATCTTTTCCCTGATTCTCATAAATCTGGCAATATTCTTTTGAAGTGAACGGGTATTAATTTACATTTCTTGAATCTTGTTAAAACATTTCTTTGCTTG											
hpt02		TGATTTGTTACATCTTTTCCCTGATTCTCATAAATCTGGCAATATTCTTTTGAAGTGAACGGGTGTTAAATTTACATTTCTTGAATCTTGTTAAAACATTTCTTTGCTTG											
hpt03		TGATTTGTTACATCTTTTCCCTGATTCTCATAAATCTGGCAATATTCTTTTGAAGTGAACGGGTGTTAAATTTACATTTCTTGAATCTTGTTAAAACATTTCTTTGCTTG											
hpt04		TGATTTGTTACATCTTTTCCCTGATTCTCATAAATCTGGCAATATTCTTTTGAAGTGAACGGGTGTTAAATTTACATTTCTTGAATCTTGTTAAAACATTTCTTTGCTTG											
hpt05		TGATTTGTTACATCTTTTCCCTGATTCTCATAAATCTGGCAATATTCTTTTGAAGTGAACGGGTGTTAAATTTACATTTCTTGAATCTTGTTAAAACATTTCTTTGCTTG											
hpt06		TGATTTGTTACATCTTTTCCCTGATTCTCATAAATCTGGCAATATTCTTTTGAAGTGAACGGGTGTTAAATTTACATTTCTTGAATCTTGTTAAAACATTTCTTTGCTTG											
hpt07		TGATTTGTTACATCTTTTCCCTGATTCTCATAAATCTGGCAATATTCTTTTGAAGTGAACGGGTGTTAAATTTACATTTCTTGAATCTTGTTAAAACATTTCTTTGCTTG											
hpt08		TGATTTGTTACATCTTTTCCCTGATTCTCATAAATCTGGCAATATTCTTTTGAAGTGAACGGGTGTTAAATTTACATTTCTTGAATCTTGTTAAAACATTTATTGCTTG											

		1880	1890	1900	1910	1920	1930	1940	1950	1960	1970	1980	
												
BLZ1 gene		c-tgctggcaaccgtgtctgtggcatccttttttcgcagcctaggggggacactcagtatcctgttttgagttctcagaagaaatcatcctgttttttcccttgagcag											
BLZ1 cds		-----											
hpt01		CCTGCTGGCAAGCGTGTATTATGGCTATCCTTTTTTTCGCAGCCTAGGGGGGCACACTCAGTATCCTGTTTTGAGTTCTCAGAAGAAATCATCCTGTTTTTCCCTTGAGCAG											
hpt02		CCTGCTGGCAAGCGTGTCTGTGGCTATCCTTTTTTTCGCAGCCTAGGGGGGCACACTCAGTATCCTGTTTTGAGTTCTCAGAAGAAATCATCCTGTTTTTCCCTTGAGCAG											
hpt03		CCTGCTGGCAAGCGTGTCTATGGCTATCCTTTTTTTCGCAGCCTAGGGGGGCACACTCAGTATCCTGTTTTGAGTTCTCAGAAGAAATCATCCTGTTTTTCCCTTGAGCAG											
hpt04		CCTGCTGGCAAGCGTGTCTGTGGCTATCCTTTTTTTCGCAGCCTAGGGGGGCACACTCAGTATCCTGTTTTGAGTTCTCAGAAGAAATCATCCTGTTTTTCCCTTGAGCAG											
hpt05		CCTGCTGGCAAGCGTGTCTATGGCTATCCTTTTTTTCGCAGCCTAGGGGGGCACACTCAGTATCCTGTTTTGAGTTCTCAGAAGAAATCATCCTGTTTTTCCCTTGAGCAG											
hpt06		CCTGCTGGCAAGCGTGTCTATGGCTATCCTTTTTTTCGCAGCCTAGGGGGGCACACTCAGTATCCTGTTTTGAGTTCTCAGAAGAAATCATCCTGTTTTTCCCTTGAGCAG											
hpt07		CCTGCTGGCAAGCGTGTCTATGGCTATCCTTTTTTTCGCAGCCTAGGGGGGCACACTCAGTATCCTGTTTTGAGTTCTCAGAAGAAATCATCCTGTTTTTCCCTTGAGCAG											
hpt08		CCTGCTGGCAAGCGTGTCTATGGCTATCCTTTTTTTCGCAGCCTAGGGGGGCACACTCAGTATCCTGTTTTGAGTTCTCAGAAGAAATCATCCTGTTTTTCCCTTGAGCAG											

		1990	2000	2010	2020	2030	2040	2050	2060	2070	2080	2090	
												
BLZ1 gene		atagacttcacagtttaactgagtagtgtaaaccatagttccctggaaatcgtgttat-gccatgttgtgaaacataaacagaaaagcatattctgtgatgctgacatga											
BLZ1 cds		-----											
hpt01		ATAGACTTCACAGTTTAACTGAGTAGTGTAACCATAGTTCCTTGGAATCGTGTTATATGCCATGTTGTGAAACATAAACAGAAAAGCATATTCTGTGATGCTGACATGA											
hpt02		ATAGACTTCACAGTTTAACTGAGTAGTGTAACCATAGTTCCTTGGAATCGTGTTAT-gccatgttgtgaaacataaacagaaaagcatattctgtgatgctgacatga											
hpt03		ATAGACTTCACAGTTTAACTGAGTAGTGTAACCATAGTTCCTTGAAATCGTGTTAT-gccatgttgtgaaacataaacagaaaagcatattctgtgatgctgacatga											
hpt04		ATAGACTTCACAGTTTAACTGAGTAGTGTAACCATAGTTCCTTGGAATCGTGTTAT-gccatgttgtgaaacataaacagaaaagcatattctgtgatgctgacatga											
hpt05		ATAGACTTCACAGTTTAACTGAGTAGTGTAACCATAGTTCCTTGGAATCGTGTTAT-gccatgttgtgaaacataaacagaaaagcatattctgtgatgctgacatga											
hpt06		ATAGACTTCACAGTTTAACTGAGTAGTGTAACCATAGTTCCTTGGAATCGTGTTATGCCATGTTGTGAAACATAAACAGAAAAGCATATTCTGTGATGCTGACATGA											
hpt07		ATAGACTTCACAGTTTAACTGAGTAGTGTAACCATAGTTCCTTGGAATCGTGTTAT-gccatgttgtgaaacataaacagaaaagcatattctgtgatgctgacatga											
hpt08		ATAGACTTCACAGTTTAACTGAGTAGTGTAACCATAGTTCCTTGGAATCGTGTTATATGCCATGTTGTGAAACATAAACAGAAAAGCATATTCTGTGATGCTGACATGA											

		2100	2110	2120	2130	2140	2150	2160	2170	2180	2190	2200	
												
BLZ1 gene		catgcctggccttttggacacatatcaggtaatgtggttccacttcaaaaacaagctagctgggtggcgcaagcgggggtgtcgggtccacatctgggtacaaaatgctgatgcc											
BLZ1 cds		-----aattgtgggttccacttcaaaaacaagctagctgggtggcgcaagcgggggtgtcgggtccacatctgggtacaaaatgctgatgcc											
hpt01		CATGCCTGGCTTTTGGACACATATCAGGTAATGTGGTTCCACTTCAAAAACAAGCTAGCTGGTGGCGCAAGCGGGGTGTCGGGTCCACATCTGGTACAAAATGCTGATGCC											
hpt02		CATGCCTGGCTTTTGGACACATATCAGGTAATGTGGTTCCACTTCAAAAACAAGCTAGCTGGTGGCGCAAGCGGGGTGTCGGGTCCACATCTGGTACAAAATGCTGATGCC											
hpt03		CATGCCTGGCTTTTGGACACATATCAGGTAATGTGGTTCCACTTCAAAAACAAGCTAGCTGGTGGCGCAAGCGGGGTGTCGGGTCCACATCTGGTACAAAATGCTGATGCC											
hpt04		CATGCCTGGCTTTTGGACACATATCAGGTAATGTGGTTCCACTTCAAAAACAAGCTAGCTGGTGGCGCAAGCGGGGTGTCGGGTCCACATCTGGTACAAAATGCTGATGCC											
hpt05		CATGCCTGGCTTTTGGACACATATCAGGTAATGTGGTTCCACTTCAAAAACAAGCTAGCTGGTGGCGCAAGCGGGGTGTCGGGTCCACATCTGGTACAAAATGCTGATGCC											
hpt06		CATGCCTGGCTTTTGGACACATATCAGGTAATGTGGTTCCACTTCAAAAACAAGCTAGCTGGTGGCGCAAGCGGGGTGTCGGGTCCACATCTGGTACAAAATGCTGATGCC											
hpt07		CATGCCTGGCTTTTGGACACATATCAGGTAATGTGGTTCCACTTCAAAAACAAGCTAGCTGGTGGCGCAAGCGGGGTGTCGGGTCCACATCTGGTACAAAATGCTGATGCC											
hpt08		CATGCCTGGCTTTTGGACACATATCAGGTAATGTGGTTCCACTTCAAAAACAAGCTAGCTGGTGGCGCAAGCGGGGTGTCGGGTCCACATCTGGTACAAAATGCTGATGCC											

		2210	2220	2230	2240	2250	2260	2270	2280	2290	2300	2310	
												
BLZ1 gene		cttgtaaagcaagccgctagctctcttcctcgccggagcagtcagaagatgatgatatggaaggagaagatgagatcactgggaatggggtcacctactgatcaaaaggctg											
BLZ1 cds		cttgtaaagcaagccgctagctctcttcctcgccggagcagtcagaagatgatgatatggaaggagaagatgagatcactgggaatggggtcacctactgatcaaaaggctg											
hpt01		CTGTAAAGCAAGCCGCTAG-----											
hpt02		CTGTAAAGCAAGCCGCTAG-----											
hpt03		CTGTAAAGCAAGCCGCTAG-----											
hpt04		CTGTAAAGCAAGCCGCTAG-----											
hpt05		CTGTAAAGCAAGCCGCTAG-----											
hpt06		CTGTAAAGCAAGCCGCTAG-----											
hpt07		CTGTAAAGCAAGCCGCTAG-----											
hpt08		CTGTAAAGCAAGCCGCTAG-----											

		2320	2330	2340	2350	2360	2370	2380	2390	2400	2410	2420	
												
BLZ1 gene		gaggaggtaatcatttgtaacctcttctgtgattatatgaccatcatgttgtctcatcatgcataatgcccttttctctcaagttagcccttctcttagaatccccctca											
BLZ1 cds		gaggag-----											
hpt01		-----CA											
hpt02		-----CA											
hpt03		-----CA											
hpt04		-----CA											
hpt05		-----CA											
hpt06		-----CA											
hpt07		-----CA											
hpt08		-----CA											

		2430	2440	2450	2460	2470	2480	2490	2500	2510	2520	2530	
												
BLZ1 gene		ttcatccctttgccatgttacacag-ag-taattcgtatgggtgttcttatcttggctataggcatagctcggttgcttatatgatttatgattgttcagtggacaagtt											
BLZ1 cds		-----											
hpt01		TTCATCCCTTTGCCATGTTACACAG-AG-TAATTCGATGGGTGTTCTTATCTTGGCTATAGGCATAGCTCGTTGCTTATATGATTTATGATTGTTCAATGGACAAGTT											
hpt02		TTCATCCCTTTGCCATGTTACACAG-AG-TAATTCGATGGGTGTTCTTATCTTGGCTATAGGCATAGCTCGTTGCTTATATGATTTATGATTGTTCAAGTGGACAAGTT											
hpt03		TTCATCCCTTTGCCATGTTACACAG-AG-TAATTCGATGGGTGTTCTTATCTTGGCTATAGGCATAGCTCGTTGCTTATATGATTTATGATTGTTCAATGGACAAGTT											
hpt04		TTCATCCCTTTGCCATGTTACACAG-AGAGTAATTCGATGGGTGTTCTTATCTTGGCTATAGGCATAGCTCGTTGCTTATATGATTTATGATTGTTCAAGTGGACAAGTT											
hpt05		TTCATCCCTTTGCCATGTTACACAG-AG-TAATTCGATGGGTGTTCTTATCTTGGCTATAGGCATAGCTCGTTGCTTATATGATTTATGATTGTTCAATGGACAAGTT											
hpt06		TTCATCCCTTTGCCATGTTACACAGTAGAGTAATTCGATGGGTGTTCTTATCTTGGCTATAGGCATAGCTCGTTGCTTATATGATTTATGATTGTTCAATGGACAAGTT											
hpt07		TTCATCCCTTTGCCATGTTACACAG-AG-TAATTCGATGGGTGTTCTTATCTTGGCTATAGGCATAGCTCGTTGCTTATATGATTTATGATTGTTCAATGGACAAGTT											
hpt08		TTCATCCCTTTGCCATGTTACACAGTAGAGTAATTCGATGGGTGTTCTTATCTTGGCTATAGGCATAGCTCGTTGCTTATATGATTTATGATTGTTCAATGGACAAGTT											

		2540	2550	2560	2570	2580	2590	2600	2610	2620	2630	2640	
												
BLZ1 gene		aatggttaaaaaaagtatccatatcatattcgttagatgacctgtctgatactgacggagtgatgggtatcaagtagaataaaaaagatcagaatggcctgcttagtaca											
BLZ1 cds		-----											
hpt01		AATGGTTAAAAAAA-GTATCCATATCATATTTGTTAGATGACTTGTCTGATACTGACGGAGTGATGGTATCAAGTAGAATAAAAAAGATCAGAATGGCCTGCTTAGTACA											
hpt02		AATGGTTAAAAAAA-GTATCCATATCATATTCGTTAGATGACTTGTCTGATACTGACGGAGTGATGGTATCAAGTAGAATAAAAAAGATCAGAATGGCCTGCTTAGTACA											
hpt03		AATGGTTAAAAAAA-GTATCCATATCATATTCGTTAGATGACTTGTCTGATACTGACGGAGTGATGGTATCAAGTAGAATAAAAAAGATCAGAATGGCCTGCTTAGTACA											
hpt04		AATGGTTAAAAAAA-GTATCCATATCATATTCGTTAGATGACTTGTCTGATACTGACGGAGTGATGGTATCAAGTAGAATAAAAAAGATCAGAATGGCCTGCTTAGTACA											
hpt05		AATGGTTAAAAAAA-GTATCCATATCATATTCGTTAGATGACTTGTCTGATACTGACGGAGTGATGGTATCAAGTAGAATAAAAAAGATCAGAATGGCCTGCTTAGTACA											
hpt06		AATGGTTAAAAAAA-GTATCCATATCATATTCGTTAGATGACTTGTCTGATACTGACGGAGTGATGGTATCAAGTAGAATAAAAAAGATCAGAATGGCCTGCTTAGTACA											
hpt07		AATGGTTAAAAAAA-GTATCCATATCATATTCGTTAGATGACTTGTCTGATACTGACGGAGTGATGGTATCAAGTAGAATAAAAAAGATCAGAATGGCCTGCTTAGTACA											
hpt08		AATGGTTAAAAAAA-GTATCCATATCATATTCGTTAGATGACTTGTCTGATACTGACGGAGTGATGGTATCAAGTAGAATAAAAAAGATCAGAATGGCCTGCTTAGTACA											

		2650	2660	2670	2680	2690	2700	2710	2720	2730	2740	2750	
												
BLZ1 gene		tgactgaaaatgataccacggttagatacaagtaacaagtatgcacagcgacaaaggtatatggttgacaaatcccatctttagtaatgtcaaatattgaagt											
BLZ1 cds		-----											
hpt01		TGACTGAAAATGATACCACGGTTAGATACAAGTA-----TGACACAGCGCACAAAGGCATATAGGTTGCACAATGGCATTTGGGTCTTTAGTAATGTCAAATTATTGAAGT											
hpt02		TGACTGAAAATGATACCACGGTTAGATACAAGTA-----TGACACAGCGCACAAAGGCATATAGGTTGCACAATGGCATTTGGGTCTTTAGTAATGTCAAATTATTGAAGT											
hpt03		TGACTGAAAATGATACCACGGTTAGATACAAGTA-----TGACACAGCGCACAAAGGCATATAGGTTGCACAATGGCATTTGGGTCTTTAGTAATGTCAAATTATTGAAGT											
hpt04		TGACTGAAAATGATACCACGGTTAGATACAAGTA-----TGACACAGCGCACAAAGGCATATAGGTTGCACAATGGCATTTGGGTCTTTAGTAATGTCAAATTATTGAAGT											
hpt05		TGACTGAAAATGATACCACGGTTAGATACAAGTA-----TGACACAGCGCACAAAGGCATATAGGTTGCACAATGGCATTTGGGTCTTTAGTAATGTCAAATTATTGAAGT											
hpt06		TGACTGAAAATGATACCACGGTTAGATACAAGTA-----TGACACAGCGCACAAAGGCATATAGGTTGCACAATGGCATTTGGGTCTTTAGTAATGTCAAATTATTGAAGT											
hpt07		TGACTGAAAATGATACCACGGTTAGATACAAGTA-----TGACACAGCGCACAAAGGCATATAGGTTGCACAATGGCATTTGGGTCTTTAGTAATGTCAAATTATTGAAGT											
hpt08		TGACTGAAAATGATACCACGGTTAGATACAAGTA-----TGACACAGCGCACAAAGGCATATAGGTTGCACAATGGCATTTGGGTCTTTAGTAATGTCAAATTATTGAAGT											

		2760	2770	2780	2790	2800	2810	2820	2830	2840	2850	2860	
												
BLZ1 gene		gtacatcatggatagctgggtttgtgctttggtaactccctccgtcccaaaaagccttgtttagatttagtgtagtctgttagatacatccggtatctagataaaatctaagg											
BLZ1 cds		-----											
hpt01		GTACATCATGGTATGCTGGTTTGCGCTTTGGTACTCCCTCCGTCCCAAAAAGCTTGTTTATAGTTAGTGTTAGTCTGTTAGATACATCCGTATCTAGATAAAATCTAAGG											
hpt02		GTACATCATGGTATGCTGGTTTGCTGCTTTGGTACTCCCTCCGTCCCAAAAAGCTTGTTTATAGTTAGTGTTAGTCTGTTAGATACATCCGTATCTAGATAAAATCTAAGG											
hpt03		GTACATCATGGTATGCTGGTTTGCGCTTTGGTACTCCCTCCGTCCCAAAAAGCTTGTTTATAGTTAGTGTTAGTCTGTTAGATACATCCGTATCTAGATAAAATCTAAGG											
hpt04		GTACATCATGGTATGCTGGTTTGCTGCTTTGGTACTCCCTCCGTCCCAAAAAGCTTGTTTATAGTTAGTGTTAGTCTGTTAGATACATCCGTATCTAGATAAAATCTAAGG											
hpt05		GTACATCATGGTATGCTGGTTTGCGCTTTGGTACTCCCTCCGTCCCAAAAAGCTTGTTTATAGTTAGTGTTAGTCTGTTAGATACATCTGTATCTAGATAAAATCTAAGG											
hpt06		GTACATCATGGTATGCTGGTTTGCGCTTTGGTACTCCCTCCGTCCCAAAAAGCTTGTTTATAGTTAGTGTTAGTCTGTTAGATACATCCGTATCTAGATAAAATCTAAGG											
hpt07		GTACATCATGGTATGCTGGTTTGCGCTTTGGTACTCCCTCCGTCCCAAAAAGCTTGTTTATAGTTAGTGTTAGTCTGTTAGATACATCTGTATCTAGATAAAATCTAAGG											
hpt08		GTACATCATGGTATGCTGGTTTGCGCTTTGGTACTCCCTCCGTCCCAAAAAGCTTGTTTATAGTTAGTGTTAGTCTGTTAGATACATCCGTATCTAGATAAAATCTAAGG											

		2870	2880	2890	2900	2910	2920	2930	2940	2950	2960	2970	
												
BLZ1 gene		caagctt---gggatggaggtaatatatcttctcctgaatagtgtaactcctgatgttggtgccggggctctctcttatgacgctattgaggtccacttcttggatatt											
BLZ1 cds		-----											
hpt01		CAAGCTTTTTTGGGATGGAGGTAATATATTTTTATCCTGAATAGTGTAACCTCTGATGTTGTGCCGGGGTCTCTCTCTATGACGCTATTGA-----											
hpt02		CAAGCTTTTTTGGGATGGAGGTAATATATTTTTATCCTGAATAGTGTAACCTCTGATGTTGTGCCGGGGTCTCTCTCTATGACGCTATTGA-----											
hpt03		CAAGCTTTTTTGGGATGGAGGTAATATATTTTTATCCTGAATAGTGTAACCTCTGATGTTGTGCCGGGGTCTCTCTCTATGACGCTATTGA-----											
hpt04		CAAGCTTTTTTGGGATGGAGGTAATATATTTTTATCCTGAATAGTGTAACCTCTGATGTTGTGCCGGGGTCTCTCTCTATGACGCTATTGA-----											
hpt05		CAAGCTTTTTTGGGATGGAGGTAATATATTTTTATCCTGAATAGTGTAACCTCTGATGTTGTGCCGGGGTCTCTCTCTATGACGCTATTGA-----											
hpt06		CAAGCTTTTTTGGGATGGAGGTAATATATTTTTATCCTGAATAGTGTAACCTCTGATGTTGTGCCGGGGTCTCTCTCTATGACGCTATTGA-----											
hpt07		CAAGCTTTTTTGGGATGGAGGTAATATATTTTTATCCTGAATAGTGTAACCTCTGATGTTGTGCCGGGGTCTCTCTCTATGACGCTATTGA-----											
hpt08		CAAGCTTTTTTGGGATGGAGGTAATATATTTTTATCCTGAATAGTGTAACCTCTGATGTTGTGCCGGGGTCTCTCTCTATGACGCTATTGA-----											

		2980	2990	3000	3010	3020	3030	3040	3050	3060	3070	3080	
												
BLZ1 gene		atgctagcttcttgactgggttccaggaagcaatccaatcgggaatcggccaggcgttcaagaagcagaaaggcagctcacctgaatgaactcgaagcacaggtttgacaa											
BLZ1 cds		-----gaagcaatccaatcgggaatcggccaggcgttcaagaagcagaaaggcagctcacctgaatgaactcgaagcacag-----											
hpt01		-----											
hpt02		-----											
hpt03		-----											
hpt04		-----											
hpt05		-----											
hpt06		-----											
hpt07		-----											
hpt08		-----											

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          3090      3100      3110      3120      3130      3140      3150      3160      3170      3180      3190
BLZ1 gene  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
BLZ1 cds   ttta cattgttg tttcttg actgggc agtggattct gaaaaaggc gcta atg agt tttttgt tgtggatggg ctcg ttac aggtat cacag ttaag agttg aaaa ctcc tcgc
hpt01     -----
hpt02     -----
hpt03     -----
hpt04     -----
hpt05     -----
hpt06     -----
hpt07     -----
hpt08     -----

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          3200      3210      3220      3230      3240      3250      3260      3270      3280      3290      3300
BLZ1 gene  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
BLZ1 cds   tg ttaaggc ggc ttgct gatgt ttaatc agaaat acaatgg tgc tgc tgc ttgaca ataggg tgt taaaggc ggc atgttg aaac ctta agagc aaagg tacc gctcc tttatt
hpt01     -----
hpt02     -----
hpt03     -----
hpt04     -----
hpt05     -----
hpt06     -----
hpt07     -----
hpt08     -----

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          3310      3320      3330      3340      3350      3360      3370      3380      3390      3400      3410
BLZ1 gene  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
BLZ1 cds   at atgc cttat ctgct atgcat ctgc gctgtt ggattgg cca ctagt cttgtt cc aaatgg catg cccac ct cagacc gcaca ata cct agt tttt agagaa gaatac
hpt01     -----
hpt02     -----
hpt03     -----
hpt04     -----
hpt05     -----
hpt06     -----
hpt07     -----
hpt08     -----

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          3420      3430      3440      3450      3460      3470      3480      3490      3500      3510      3520
BLZ1 gene  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
BLZ1 cds   gctgc ctagt atcc tatag tctct atgtt ggcc attc attgt cctg ctct gaac ata cttcc acagg aaatttt gagg tga agatgg ccg agga ct cgg tga agc ggggtg
hpt01     -----
hpt02     -----
hpt03     -----
hpt04     -----
hpt05     -----
hpt06     -----
hpt07     -----
hpt08     -----

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		3530	3540	3550	3560	3570	3580	3590	3600	3610	3620	3630
											
BLZ1 gene		a	c	a	g	g	c	a	t	g	a	g
BLZ1 cds		a	c	a	g	g	c	a	t	g	a	g
hpt01		g	a	g	c	t	c	t	g	t	t	c
hpt02		c	c	c	t	g	c	a	g	g	t	c
hpt03		c	c	a	c	a	t	g	t	c	a	t
hpt04		g	t	c	a	t	g	t	c	a	t	g
hpt05		c	c	c	t	t	c	a	c	t	t	c
hpt06		a	c	a	a	g	c	c	a	a	g	c
hpt07		c	c	a	c	c	t	c	c	a	c	c
hpt08		a	c	a	c	c	t	c	c	a	c	c

		3640	3650	3660	3670	3680	3690	3700	3710	3720	3730	3740
											
BLZ1 gene		g	a	g	c	g	t	t	a	c	c	a
BLZ1 cds		g	a	g	c	g	t	t	a	c	c	a
hpt01		a	a	g	c	a	g	a	g	a	g	a
hpt02		c	t	g	a	g	a	g	a	g	a	g
hpt03		c	t	g	a	g	a	g	a	g	a	g
hpt04		c	t	g	a	g	a	g	a	g	a	g
hpt05		c	t	g	a	g	a	g	a	g	a	g
hpt06		c	t	g	a	g	a	g	a	g	a	g
hpt07		c	t	g	a	g	a	g	a	g	a	g
hpt08		c	t	g	a	g	a	g	a	g	a	g

		3750	3760	3770	3780	3790	3800	3810	3820	3830	3840
										
BLZ1 gene		g	c	a	a	g	a	t	g	g	g
BLZ1 cds		g	c	a	a	g	a	t	g	g	g
hpt01		c	a	a	g	a	t	g	g	g	c
hpt02		c	a	a	g	a	t	g	g	g	c
hpt03		c	a	a	g	a	t	g	g	g	c
hpt04		c	a	a	g	a	t	g	g	g	c
hpt05		c	a	a	g	a	t	g	g	g	c
hpt06		c	a	a	g	a	t	g	g	g	c
hpt07		c	a	a	g	a	t	g	g	g	c
hpt08		c	a	a	g	a	t	g	g	g	c

BLZ2

[illegible]

	-80	-70	-60	-50	-40	-30	-20	-10	-1	10	20
BLZ2 gene
BLZ2 CDS	CACGGGG	TAAACCA	TACGATT	TCTCGCT	CAATTTT	GTTCTAAT	CAATCACCT	TGCCCAA	ATTCCATT	CCGGAAAC	GTGCAAT
hpt01	-----atggagcccgtgttctcactgctggaggag										
hpt02	-----										
hpt03	-----										
hpt04	-----										
hpt05	-----										
hpt06	-----										
hpt07	-----										
hpt08	-----										
hpt09	-----										
hpt10	-----										
hpt11	-----										
hpt12	-----										
hpt13	-----										
hpt14	-----										
hpt15	-----										
hpt16	-----										
hpt17	-----										
hpt18	-----										

	40	50	60	70	80	90	100	110	120	130	140	
BLZ2 gene	GCGATGCCCGAGCCCCGACTCTAACCCCGGTCGGACCTCGCCGCCGCAGCTGCAGGCACACGTGCTCGCCGGAGGAGTCAGAGGAGCAGGAGGAGTGGGCGTCGGTGAGAT											
BLZ2 CDS	gcgatgcccgagccccgactctaaccccggtcggacctcgccgccgcagctgcaggcacacgtgctcgcggaggagtcagaggagcaggaggagtgggctcggtagat											
hpt01												
hpt02												
hpt03												
hpt04												
hpt05												
hpt06												
hpt07												
hpt08												
hpt09												
hpt10												
hpt11												
hpt12												
hpt13												
hpt14												
hpt15												
hpt16												
hpt17												
hpt18												

[illegible]

	260	270	280	290	300	310	320	330	340	350	360	
BLZ2 gene	<p>CTAATCCCCACGGCGGAGGTGAGCCGCAAGAGGCGGTACGACGTTTCATGAGGAGGAGGAGGTGGTGGGGGTTCATCCCCACGCCGCCCTGCGGCGGGCGCGGTGCTGGACCCC</p>											
BLZ2 CDS	<p>ctaatacccacggcggaaggtgagccgcaagaggcggtacgacgttcatgaggaggaggaggtggtgggggtcatccccacgccgcctgcggcgggcgcggtgctggacccc</p>											
hpt01	-----											
hpt02	-----											
hpt03	-----											
hpt04	-----											
hpt05	-----											
hpt06	-----											
hpt07	-----											
hpt08	-----											
hpt09	-----											
hpt10	-----											
hpt11	-----											
hpt12	-----											
hpt13	-----											
hpt14	-----											
hpt15	-----											
hpt16	-----											
hpt17	-----											
hpt18	-----											

	370	380	390	400	410	420	430	440	450	460	470	
BLZ2 gene	<div> <div>...</div> <div>...</div> <div>...</div> <div>...</div> <div>...</div> <div>...</div> <div>...</div> <div>...</div> <div>...</div> <div>...</div> <div>...</div> <div>...</div> </div>											
BLZ2 CDS	<div> <div>GTGGGCTACAACGCGATGCTGAGACGGAAGTTGGACGCGCATCTCGCCGTCGCCATGTGGAGGGTACGCTACTGCCCTACCCCCACCCACCCCTCCTCTACTCGAC</div> <div>gtgggctacaacgcgatgtgagacggaagttggacgcgcattctcgcgcgtcgccatgtggagg</div> </div>											
hpt01	-----											
hpt02	-----											
hpt03	-----											
hpt04	-----											
hpt05	-----											
hpt06	-----											
hpt07	-----											
hpt08	-----											
hpt09	-----											
hpt10	-----											
hpt11	-----											
hpt12	-----											
hpt13	-----											
hpt14	-----											
hpt15	-----											
hpt16	-----											
hpt17	-----											
hpt18	-----											

[illegible][illegible]

	700	710	720	730	740	750	760	770	780	790	800	
BLZ2 gene	<div> <div>...</div> <div>...</div> <div>...</div> <div>...</div> <div>...</div> <div>...</div> <div>...</div> <div>...</div> <div>...</div> <div>...</div> <div>...</div> <div>...</div> </div>											
BLZ2 CDS	<div> <div>CCAGCCTATCCATGTTGTG</div> <div>TCCATTGGTGGTCTGG</div> <div>CGTCATCTCTAACGAGAAC</div> <div>GATGCACGTTGCACAAGAGATT</div> <div>CATACCTTGGTTAAAGTTTCAA</div> <div>ATTGGGTATCT</div> </div>											
hpt01												
hpt02												
hpt03												
hpt04												
hpt05												
hpt06												
hpt07												
hpt08												
hpt09												
hpt10												
hpt11												
hpt12												
hpt13												
hpt14												
hpt15												
hpt16												
hpt17												
hpt18												

		810	820	830	840	850	860	870	880	890	900	910
BLZ2 gene											
BLZ2 CDS		T T T T A C T A A G T T T T T W A A A G A G G A T C A G T T A T C A C G A G C T G G A A A G T C A T C G A T T A G G A G G G T T G T G G C G A C A A C A G G G A G A G A G A C A A T G G A G T T A G C G T T A A G A T G T										
hpt01		- - - - -										
hpt02		- - - - -										
hpt03		- - - - -										
hpt04		- - - - -										
hpt05		- - - - -										
hpt06		- - - - -										
hpt07		- - - - -										
hpt08		- - - - -										
hpt09		- - - - -										
hpt10		- - - - -										
hpt11		- - - - -										
hpt12		- - - - -										
hpt13		- - - - -										
hpt14		- - - - -										
hpt15		- - - - -										
hpt16		- - - - -										
hpt17		- - - - -										
hpt18		- - - - -										

	920	930	940	950	960	970	980	990	1000	1010	1020	
BLZ2 gene	GTGGAATTTTACATACGGAGAGGACAGATAC	TTTTCAC	TTTATTTAAATATATATATTTCTCTCGAGAGATTCTTTGTTTCACATATGAATATGGTGCCCCATAAAATA								
BLZ2 CDS	-----											
hpt01	-----											
hpt02	-----											
hpt03	-----											
hpt04	-----											
hpt05	-----											
hpt06	-----											
hpt07	-----											
hpt08	-----											
hpt09	-----											
hpt10	-----											
hpt11	-----											
hpt12	-----											
hpt13	-----											
hpt14	-----											
hpt15	-----											
hpt16	-----											
hpt17	-----											
hpt18	-----											

	1030	1040	1050	1060	1070	1080	1090	1100	1110	1120	1130
BLZ2 gene	TTAACCGTGTATCTTGTTCCACTTTCAGTGGACAAGCAGCTTCTYATGTTACACTACTCGAGGAATTG	CCGACAAAGCTCCCATGACAATAGAGCATCACAAAAATCCAGA								
BLZ2 CDS	-----										
hpt01	-----										
hpt02	-----										
hpt03	-----										
hpt04	-----										
hpt05	-----										
hpt06	-----										
hpt07	-----										
hpt08	-----										
hpt09	-----										
hpt10	-----										
hpt11	-----										
hpt12	-----										
hpt13	-----										
hpt14	-----										
hpt15	-----										
hpt16	-----										
hpt17	-----										
hpt18	-----										

[illegible][illegible]

[illegible]

		2570	2580	2590	2600	2610	2620	2630	2640	2650	2660	2670
BLZ2 gene		AGTTCAC	TAGATGTAGGGGTGGATAGGTGACTAACGACG	TATATAAA	CGATATAC	CCCTTTTATGATATTGTTAAAA	YGAAAAGGTCGTTT	ARTGTAGTTCTATATT	AAACA			
BLZ2 CDS		AGTTCAC	TAGATGTAGGGGTGGATAGGTGACTAACGACG	TATATAAA	CGATA	--CCCTTTTATGATATTGTTAAAA	TGAAAAGGTCGTTT	AATGTAGTTCTATATT	AAACA			
hpt01		AGTTCAC	TAGATGTAGGGGTGGATAGGTGACTAACGACG	TATATAAA	CGATA	--CCCTTTTATGATATTGTTAAAA	TGAAAAGGTCGTTT	AATGTAGTTCTATATT	AAACA			
hpt02		AGTTCAC	TAGATGTAGGGGTGGATAGGTGACTAACGACG	TATATAAA	CGATATAC	CCCTTTTATGATATTGTTAAAA	CGAAAAGGTCGTTT	AGTGTAGTTCTATATT	AAACA			
hpt03		AGTTCAC	TAGATGTAGGGGTGGATAGGTGACTAACGACG	CATATAAA	CGATATAC	CCCTTTTATGATATTGTTAAAA	TGAAAAGGTCGTTT	AATGTAGTTCTATATT	AAACA			
hpt04		AGTTCAC	TAGATGTAGGGGTGGATAGGTGACTAACGACG	TATATAAA	CGATATAC	CCCTTTTATGATATTGTTAA	--TGAAAAGGTCGTTT	AGTGTAGTTCTATATT	AAACA			
hpt05		AGTTCAC	TAGATGTAGGGGTGGATAGGTGACTAACGACG	TATATAAA	CGATATAC	CCCTTTTATGATATTGTTAAAA	CGAAAAGGTCGTTT	AGTGTAGTTCTATATT	AAACA			
hpt06		AGTTCACT	AGATGTAGGGGTGGATAGGTGACTAACGACG	TATATAAA	CGATATAC	CCCTTTTATGATATTGTTAAAA	CGAAAAGGTCGTTT	AGTGTAGTTCTATATT	AAACA			
hpt07		AGTTGAC	TAGATGTAGGGGTGGATAGGTGACTAACGACG	TATATAAA	CAATATAC	CCCTTTTATGATATTGTTAAAA	TGAAAAGGTCGTTT	AGTGTAGTTCTATATT	AAACA			
hpt08		AGTTCAC	TAGATGTAGGGGTGGATAGGTGACTAACGACG	TATATAAA	CGATATAC	CCCTTTTATGATATTGTTAAAA	TGAAAAGGTCGTTT	AGTGTAGTTCTATATT	AAACA			
hpt09		AGTTCAC	TAGATGTAGGGGTGGATAGGTGACTAACGACG	TATATAAA	CGATATAC	CCCTTTTATGATATTGTTAAAA	TGAAAAGGTCGTTT	AGTGTAGTTCTATATT	AAACA			
hpt10		AGTTCACT	AGATGTAGGGGTGGATAGGTGACTAACGACG	CATATAAA	CGATATAC	CCCTTTTATGATATTGTTAAAA	TGAAAAGGTCGTTT	AATGTAGTTCTATATT	AAACA			
hpt11		AGTTCACT	AGATGTAGGGGTGGATAGGTGACTAACGACG	TATATAAA	CGATA	--CCCTTTTATGATATTGTTAAAA	TGAAAAGGTCGTTT	AATGTAGTTCTATATT	AAACA			
hpt12		AGTTCACT	AGATGTAGGGGTGGATAGGTGACTAACGACG	TATATAAA	CGATATAC	CCCTTTTATGATATTGTTAAAA	CGAAAAGGTCGTTT	AGTGTAGTTCTATATT	AAACA			
hpt13		AGTTCAC	TAGATGTAGGGGTGGATAGGTGACTAACGACG	TATATAAA	CGATATAC	CCCTTTTATGATATTGTTAAAA	CGAAAAGGTCGTTT	AGTGTAGTTCTATATT	AAACA			
hpt14		AGTTCAC	TAGATGTAGGGGTGGATAGGTGACTAACGACG	TATATAAA	CGATATAC	CCCTTTTATGATATTGTTAAAA	CGAAAAGGTCGTTT	AGTGTAGTTCTATATT	AAACA			
hpt15		AGTTCACT	AGATGTAGGGGTGGATAGGTGACTAACGACG	TATATAAA	CGATATAC	CCCTTTTATGATATTGTTAAAA	CGAAAAGGTCGTTT	AGTGTAGTTCTA	-ATTAA	CA		
hpt16		AGTTCAC	TAGATGTAGGGGTGGATAGGTGACTAACGACG	TATATAAA	CGATA	--CCCTTTTATGATATTGTTAAAA	TGAAAAGGTCGTTT	AATGTAGTTCTATATT	AAACA			
hpt17		AGTTCACT	AGATGTAGGGGTGGATAGGTGACTAACGACG	TATATAAA	CGATATAC	CCCTTTTATGATATTGTTAAAA	CGAAAAGGTCGTTT	AGTGTAGTTCTATATT	AAACA			
hpt18		AGTTCACT	AGATGTAGGGGTGGATAGGTGACTAACGACG	TATATAAA	CAATATAC	CCCTTTTATGATATTGTTAAAA	TGAAAAGGTCGTTT	AGTGTAGTTCTATATT	AAACA			

[illegible][illegible]

[illegible]

		3230	3240	3250	3260	3270	3280	3290	3300	3310	3320	3330
BLZ2 gene	GATGTGAGCAGCAACTACATCCCCGAGCTAGCTCCGGCATACCAGATCCATGATCAAATATCTTCGCTACATACGCAACCTATGCCATGCCTTGGATCATCACCCACGGAG											
BLZ2 CDS	gatgtgagcagcaactacatccccgagctagctccggcataccagatccatgatcaaatatcttcgctacatacgcaacctatgccatgcttggatcatcacccacggag											
hpt01	GATGTGAGCAGCAACTACATCCCCGAGCTAGCTCCGGCATACCAGATCCATGATCAAATATCTTCGCTACATACGCAACCTATGCCATGCTTGGATCATCA											
hpt02	GATGTGAGCAGCAACTACATCCCCGAGCTAGCTCCGGCATACCAGATCCATGATCAAATATCTTCGCTACATACGCAACCTATGCCATGCTTGGATCATCA											
hpt03	GATGTGAGCAGCAACTACATCCCCGAGCTAGCTCCGGCATACCAGATCCATGATCAAATATCTTCGCTACATACGCAACCTATGCCATGCTTGGATCATCA											
hpt04	GATGTGAGCAGCAACTACATCCCCGAGCTAGCTCCGGCATACCAGATCCATGATCAAATATCTTCGCTACATACGCAACCTATGCCATGATTGGATCATCA											
hpt05	GATGTGAGCAGCAACTACATCCCCGAGCTAGCTCCGGCATACCAGATCCATGATCAAATATCTTCGCTACATACGCAACCTATGCCATGCTTGGATCATCA											
hpt06	GATGTGAGCAGCAACTACATCCCCAAGCTAGCTCCGGCATACCAGATCCATGATCAAATATCTTCGCTACATACGCAACCTATGCCATGCTTGGATCATCA											
hpt07	GATGTGAGCAGCAACTACATCCCCGAGCTAGCTCCGGCATACCAGATCCATGATCAAATATCTTCGCTACATACGCAACCTATGCCATGCTTGGATCATCA											
hpt08	GATGTGAGCAGCAACTACATCCCCGAGCTAGCTCCGGCATACCAGATCCATGATCAAATATCTTCGCTACATACGCAACCTATGCCATGCTTGGATCGTCA											
hpt09	GATGTGAGCAGCAACTACATCCCCGAGCTAGCTCCGGCATACCAGATCCATGATCAAATATCTTCGCTACATACGCAACCTATGCCATGCTTGGATCGTCA											
hpt10	GATGTGAGCAGCAACTACATCCCCGAGCTAGCTCCGGCATACCAGATCCATGATCAAATATCTTCGCTACATACGCAACCTATGCCATGCTTGGATCATCA											
hpt11	GATGTGAGCAGCAACTACATCCCCGAGCTAGCTCCGGCATACCAGATCCATGATCAAATATCTTCGCTACATACGCAACCTATGCCATGCTTGGATCATCA											
hpt12	GATGTGAGCAGCAACTACATCCCCAAGCTAGCTCCGGCATACCAGATCCATGATCAAATATCTTCGCTACATACGCAACCTATGCCATGCTTGGATCATCA											
hpt13	GATGTGAGCAGCAACTACATCCCCGAGCTAGCTCCGGCATACCAGATCCATGATCAAATATCTTCGCTACATACGCAACCTATGCCATGCTTGGATCATCA											
hpt14	GATGTGAGCAGCAACTACATCCCCAAGCTAGCTCCGGCATACCAGATCCATGATCAAATATCTTCGCTACATACGCAACCTATGCCATGCTTGGATCATCA											
hpt15	GATGTGAGCAGCAACTACATCCCCGAGCTAGCTCCGGCATACCAGATCCATGATCAAATATCTTCGCTACATACGCAACCTATGCCATGCTTGGATCATCA											
hpt16	GATGTGAGCAGCAACTACATCCCCGAGCTAGCTCCGGCATACCAGATCCATGATCAAATATCTTCGCTACATACGCAACCTATGCCATGCTTGGATCATCA											
hpt17	GATGTGAGCAGCAACTACATCCCCGAGCTAGCTCCGGCATACCAGATCCATGATCAAATATCTTCGCTACATACGCAACCTATGCCATGCTTGGATCATCA											
hpt18	GATGTGAGCAGCAACTACATCCCCGAGCTAGCTCCGGCATACCAGATCCATGATCAAATATCTTCGCTACATACGCAACCTATGCCATGCTTGGATCATCA											

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          3340      3350      3360      3370      3380      3390      3400      3410      3420      3430      3440
BLZ2 gene  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
BLZ2 CDS   GATGCCCTTTGGTATTCCAAGTACATTGGTGCCTACCCCAACAACGGGAATCCACTACATTGGATTCAAATGAAATAGGCAAATGGTGATGCAGTAGGAATTATGTGAGA
hpt01      gatgccctttgggtattccaagtacattgggtgcctaccccacaacggggaatccactacattggattcaaataaggcaacatggtgatgcagtag
hpt02
hpt03
hpt04
hpt05
hpt06
hpt07
hpt08
hpt09
hpt10
hpt11
hpt12
hpt13
hpt14
hpt15
hpt16
hpt17
hpt18
```

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          3450      3460      3470      3480      3490      3500      3510      3520      3530      3540      3550
BLZ2 gene  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
BLZ2 CDS   GACCTGAGCCGGAATTATTATTTAAATAAATAATTGTCGTTGTTCTTGGTGGCCATTGGGGGTATTTGTAATGGTTTCTCACCTTGTTAAGCTCAGACTTGTTTAAGGA
hpt01
hpt02
hpt03
hpt04
hpt05
hpt06
hpt07
hpt08
hpt09
hpt10
hpt11
hpt12
hpt13
hpt14
hpt15
hpt16
hpt17
hpt18
```

BLZ2 gene
BLZ2 CDS

hpt01
hpt02
hpt03
hpt04
hpt05
hpt06
hpt07
hpt08
hpt09
hpt10
hpt11
hpt12
hpt13
hpt14
hpt15
hpt16
hpt17
hpt18

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....
ATATCTATCATTTGTTGTTTCAGAAAGAACCTATACATTGTTGGTATCCCAATAACTAATAAAATATATCAAAGGTATTATGGACAATAAAGTCATGTGGTTGAGTT

BPBF mRNA
BPBF_CDS

[illegible]

[illegible]

	450	460	470	480	490	500	510	520	530	540	550

BPBF mRNA	ca	ac	cc	cg	ac	gg	cg	tt	ga	tg	tcccc
BPBF_CDS	CA	AC	CC	GC	GC	GG	CG	TT	GA	TG	TCCCC
hpt01	-----										
hpt02	-----										
hpt03	-----										
hpt04	-----										
hpt05	-----										
hpt06	-----										
hpt07	-----										
hpt08	-----										
hpt09	-----										
hpt10	-----										
hpt11	-----										
hpt12	-----										
hpt13	-----										
hpt14	-----										
hpt15	-----										
hpt16	-----										
hpt17	-----										
hpt18	-----										
hpt19	-----										
hpt20	-----										
hpt21	-----										

	560	570	580	590	600	610	620	630	640	650	660

BPBF mRNA	ac	ta	tgg	tggg	cat	gcca	acgg	atca	agc	attggg	atg
BPBF_CDS	ACT	ATG	GTG	GGGCAT	GCCAA	CGGATCA	AGCATT	GGGATG	TTGATG	ACTCC	GCCAA
hpt01	--	TAT	GGT	GGGCAT	GCCAA	CGGATCA	AGCATT	GGGATG	TTGATG	ACTCC	GCCAA
hpt02	--	TAT	GGT	GGGCAT	GCCAA	TGGATC	AGGCATT	GGGATG	TTGATG	ACTCC	GCCAA
hpt03	--	TAT	GGT	GGGCAT	GCCAA	TGGATC	ANGCATT	GGGATG	TTGATG	ACTCC	GCCAA
hpt04	--	TAT	GGT	GGGCAT	GCCAA	CGGATCA	AGCATT	GGGATG	TTGATG	ACTCC	GCCAA
hpt05	--	TAT	GGT	GGGCAT	GCCAA	TGGATC	AGGCATT	GGGATG	TTGATG	ACTCC	GCCAA
hpt06	--	TAT	GGT	GGGCAT	GCCAA	NGGATCA	AGCATT	GGGATG	TTGATG	ACTCC	GCCAA
hpt07	--	TAT	GGT	GGGCAT	GCCAA	TGGATC	AGGCATT	GGGATG	TTGATG	ACTCC	GCCAA
hpt08	--	TAT	GGT	GGGCAT	GCCAA	NGGATCA	AGCATT	GGGATG	TTGATG	ACTCC	GCCAA
hpt09	--	TAT	GGT	GGGCAT	GCCAA	CGGATCA	AGCATT	GGGATG	TTGATG	ACTCC	GCCAA
hpt10	--	TAT	GGT	GGGCAT	GCCAA	CGGATCA	AGCATT	GGGATG	TTGATG	ACTCC	GCCAA
hpt11	--	TAT	GGT	GGGCAT	GCCAA	CGGATCA	AGCATT	GGGATG	TTGATG	ACTCC	GCCAA
hpt12	--	TAT	GGT	GGGCAT	GCCAA	CGGATCA	AGCATT	GGGATG	TTGATG	ACTCC	GCCAA
hpt13	--	TAT	GGT	GGGCAT	GCCAA	TGGATC	AGGCATT	GGGATG	TTGATG	ACTCC	GCCAA
hpt14	--	TAT	GGT	GGGCAT	GCCAA	TGGATC	AGGCATT	GGGATG	TTGATG	ACTCC	GCCAA
hpt15	--	TAT	GGT	GGGCAT	GCCAA	CGGATCA	ANGCATT	GGGATG	TTGATG	ACTCC	GCCAA
hpt16	--	TAT	GGT	GGGCAT	GCCAA	CGGATCA	ANGCATT	GGGATG	TTGATG	ACTCC	GCCAA
hpt17	--	TAT	GGT	GGGCAT	GCCAA	CGGATCA	AGGCATT	GGGATG	TTGATG	ACTCC	GCCAA
hpt18	--	TAT	GGT	GGGCAT	GCCAA	NGGATCA	ANGCATT	GGGATG	TTGATG	ACTCC	GCCAA
hpt19	--	TAT	GGT	GGGCAT	GCCAA	CGGATCA	AGGCATT	GGGATG	TTGATG	ACTCC	GCCAA
hpt20	--	TAT	GGT	GGGCAT	GCCAA	TGGATC	AGGCATT	GGGATG	TTGATG	ACTCC	GCCAA
hpt21	--	TAT	GGT	GGGCAT	GCCAA	TGGATC	AGGCATT	GGGATG	TTGATG	ACTCC	GCCAA

	670	680	690	700	710	720	730	740	750	760	770

BPBF mRNA	gg	aa	at	gg	aa	tag	gt	gg	ca	aa	ct
BPBF_CDS	GG	AA	AT	TG	GA	AT	AG	GT	TG	GC	CA
hpt01	GG	AA	AT	TG	GA	AT	AG	GT	TG	GC	CA
hpt02	GG	AA	AT	TG	GA	AT	AG	GT	TG	GC	CA
hpt03	GG	AA	AT	TG	GA	AT	AG	GT	TG	GC	CA
hpt04	GG	AA	AT	TG	GA	AT	AG	GT	TG	GC	CA
hpt05	GG	AA	AT	TG	GA	AT	AG	GT	TG	GC	CA
hpt06	GG	AA	AT	TG	GA	AT	AG	GT	TG	GC	CA
hpt07	GG	AA	AT	TG	GA	AT	AG	GT	TG	GC	CA
hpt08	GG	AA	AT	TG	GA	AT	AG	GT	TG	GC	CA
hpt09	GG	AA	AT	TG	GA	AT	AG	GT	TG	GC	CA
hpt10	GG	AA	AT	TG	GA	AT	AG	GT	TG	GC	CA
hpt11	GG	AA	AT	TG	GA	AT	AG	GT	TG	GC	CA
hpt12	GG	AA	AT	TG	GA	AT	AG	GT	TG	GC	CA
hpt13	GG	AA	AT	TG	GA	AT	AG	GT	TG	GC	CA
hpt14	GG	AA	AT	TG	GA	AT	AG	GT	TG	GC	CA
hpt15	GG	AA	AT	TG	GA	AT	AG	GT	TG	GC	CA
hpt16	GG	AA	AT	TG	GA	AT	AG	GT	TG	GC	CA
hpt17	GG	AA	AT	TG	GA	AT	AG	GT	TG	GC	CA
hpt18	GG	AA	AT	TG	GA	AT	AG	GT	TG	GC	CA
hpt19	GG	AA	AT	TG	GA	AT	AG	GT	TG	GC	CA
hpt20	GG	AA	AT	TG	GA	AT	AG	GT	TG	GC	CA
hpt21	GG	AA	AT	TG	GA	AT	AG	GT	TG	GC	CA

	780	790	800	810	820	830	840	850	860	870	880

BPBF mRNA	ta	at	gg	tg	cg	gt	gg	tg	tt	gt	ga
BPBF_CDS	TA	AT	TG	TG	CG	GT	TG	TT	GT	TG	GA
hpt01	TA	AT	TG	TG	CG	GT	TG	TT	GT	TG	GA
hpt02	TA	AT	TG	TG	CG	GT	TG	TT	GT	TG	GA
hpt03	TA	AT	TG	TG	CG	GT	TG	TT	GT	TG	GA
hpt04	TA	AT	TG	TG	CG	GT	TG	TT	GT	TG	GA
hpt05	TA	AT	TG	TG	CG	GT	TG	TT	GT	TG	GA
hpt06	TA	AT	TG	TG	CG	GT	TG	TT	GT	TG	GA
hpt07	TA	AT	TG	TG	CG	GT	TG	TT	GT	TG	GA
hpt08	TA	AT	TG	TG	CG	GT	TG	TT	GT	TG	GA
hpt09	TA	AT	TG	TG	CG	GT	TG	TT	GT	TG	GA
hpt10	TA	AT	TG	TG	CG	GT	TG	TT	GT	TG	GA
hpt11	TA	AT	TG	TG	CG	GT	TG	TT	GT	TG	GA
hpt12	TA	AT	TG	TG	CG	GT	TG	TT	GT	TG	GA
hpt13	TA	AT	TG	TG	CG	GT	TG	TT	GT	TG	GA
hpt14	TA	AT	TG	TG	CG	GT	TG	TT	GT	TG	GA
hpt15	TA	AT	TG	TG	CG	GT	TG	TT	GT	TG	GA
hpt16	TA	AT	TG	TG	CG	GT	TG	TT	GT	TG	GA
hpt17	TA	AT	TG	TG	CG	GT	TG	TT	GT	TG	GA
hpt18	TA	AT	TG	TG	CG	GT	TG	TT	GT	TG	GA
hpt19	TA	AT	TG	TG	CG	GT	TG	TT	GT	TG	GA
hpt20	TA	AT	TG	TG	CG	GT	TG	TT	GT	TG	GA
hpt21	TA	AT	TG	TG	CG	GT	TG	TT	GT	TG	GA

	890	900	910	920	930	940	950	960	970	980	990

BPBF mRNA	g	c	g	g	t	g	c	t	g	a	t
BPBF_CDS	g	c	g	g	t	g	c	t	g	a	t
hpt01	G	C	G	G	C	G	T	G	T	G	A
hpt02	G	C	G	G	C	G	T	G	T	G	A
hpt03	G	C	G	G	C	G	T	G	T	G	A
hpt04	G	C	G	G	C	G	T	G	T	G	A
hpt05	G	C	G	G	C	G	T	G	T	G	A
hpt06	G	C	G	G	C	G	T	G	T	G	A
hpt07	G	C	G	G	C	G	T	G	T	G	A
hpt08	G	C	G	G	C	G	T	G	T	G	A
hpt09	G	C	G	G	C	G	T	G	T	G	A
hpt10	G	C	G	G	C	G	T	G	T	G	A
hpt11	G	C	G	G	C	G	T	G	T	G	A
hpt12	G	C	G	G	C	G	T	G	T	G	A
hpt13	G	C	G	G	C	G	T	G	T	G	A
hpt14	G	C	G	G	C	G	T	G	T	G	A
hpt15	G	C	G	G	C	G	T	G	T	G	A
hpt16	G	C	G	G	C	G	T	G	T	G	A
hpt17	G	C	G	G	C	G	T	G	T	G	A
hpt18	G	C	G	G	C	G	T	G	T	G	A
hpt19	G	C	G	G	C	G	T	G	T	G	A
hpt20	G	C	G	G	C	G	T	G	T	G	A
hpt21	G	C	G	G	C	G	T	G	T	G	A

	1000	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100

BPBF mRNA	t	a	a	g	t	g	a	a	a	a	a
BPBF_CDS	T	A	A	g	t	g	a	a	a	a	a
hpt01	T	A	A	g	t	g	a	a	a	a	a
hpt02	T	A	A	g	t	g	a	a	a	a	a
hpt03	T	A	A	g	t	g	a	a	a	a	a
hpt04	T	A	A	g	t	g	a	a	a	a	a
hpt05	T	A	A	g	t	g	a	a	a	a	a
hpt06	T	A	A	g	t	g	a	a	a	a	a
hpt07	T	A	A	g	t	g	a	a	a	a	a
hpt08	T	A	A	g	t	g	a	a	a	a	a
hpt09	T	A	A	g	t	g	a	a	a	a	a
hpt10	T	A	A	g	t	g	a	a	a	a	a
hpt11	T	A	A	g	t	g	a	a	a	a	a
hpt12	T	A	A	g	t	g	a	a	a	a	a
hpt13	T	A	A	g	t	g	a	a	a	a	a
hpt14	T	A	A	g	t	g	a	a	a	a	a
hpt15	T	A	A	g	t	g	a	a	a	a	a
hpt16	T	A	A	g	t	g	a	a	a	a	a
hpt17	T	A	A	g	t	g	a	a	a	a	a
hpt18	T	A	A	g	t	g	a	a	a	a	a
hpt19	T	A	A	g	t	g	a	a	a	a	a
hpt20	T	A	A	g	t	g	a	a	a	a	a
hpt21	T	A	A	g	t	g	a	a	a	a	a

	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200	1210

BPBF mRNA	ctcgggtcatatttcatgtgtattttaagaagggattattttgtttatttgagtgaaactcgagagagtggtgcacattgggatgcttaatttaagtttatttgtttcttca										
BPBF_CDS	-----										
hpt01	CTCGGTCATTTTCATGTGTATTTTAAGAAGGGATTATTTTGTTTATTTGAGTGAA										
hpt02	CTCGGTCATTTTCATGTGTCTTTTAAGAAGGGATTATTTTGTTTATTTGAGTGAA										
hpt03	CTCGGTCATTTTCATGTGTCTTTTAAGAAGGGATTATTTTGTTTATTTGAGTGAA										
hpt04	CTCGGTCATTTTCATGTGTATTTTAAGAAGGGATTATTTTGTTTATTTGAGTGAA										
hpt05	CTCGGTCATTTTCATGTGTCTTTTAAGAAGGGATTATTTTGTTTATTTGAGTGAA										
hpt06	CTCGGTCATTTTCATGTGTCTTTTAAGAAGGGATTATTTTGTTTATTTGAGTGAA										
hpt07	CTCGGTCATTTTCATGTGTCTTTTAAGAAGGGATTATTTTGTTTATTTGAGTGAA										
hpt08	CTCGGTCATTTTCATGTGTNTTTTAAGAAGGGATTATTTTGTTTATTTGAGTGAA										
hpt09	CTCGGTCATTTTCATGTGTCTTTTAAGAAGGGATTATTTTGTTTATTTGAGTGAA										
hpt10	CTCGGTCATTTTCATGTGTATTTTAAGAAGGGATTATTTTGTTTATTTGAGTGAA										
hpt11	CTCGGTCATTTTCATGTGTATTTTAAGAAGGGATTATTTTGTTTATTTGAGTGAA										
hpt12	CTCGGTCATTTTCATGTGTATTTTAAGAAGGGATTATTTTGTTTATTTGAGTGAA										
hpt13	CTCGGTCATTTTCATGTGTCTTTTAAGAAGGGATTATTTTGTTTATTTGAGTGAA										
hpt14	CTCGGTCATTTTCATGTGTCTTTTAAGAAGGGATTATTTTGTTTATTTGAGTGAA										
hpt15	CTCGGTCATTTTCATGTGTCTTTTAAGAAGGGATTATTTTGTTTATTTGAGTGAA										
hpt16	CTCGGTCATTTTCATGTGTNTTTTAAGAAGGGATTATTTTGTTTATTTGAGTGAA										
hpt17	CTCGGTCATTTTCATGTGTATTTTAAGAAGGGATTATTTTGTTTATTTGAGTGAA										
hpt18	CTCGGTCATTTTCATGTGTNTTTTAAGAAGGGATTATTTTGTTTATTTGAGTGAA										
hpt19	CTCGGTCATTTTCATGTGTATTTTAAGAAGGGATTATTTTGTTTATTTGAGTGAA										
hpt20	CTCGGTCATTTTCATGTGTCTTTTAAGAAGGGATTATTTTGTTTATTTGAGTGAA										
hpt21	CTCGGTCATTTTCATGTGTCTTTTAAGAAGGGATTATTTTGTTTATTTGAGTGAA										
	1220	1230	1240	1250	1260	1270	1280				
				
BPBF mRNA	catthaattatttaaggatttatggtttaatctttataaaaagtatatgtgtgtcaaaaaaaaaaaaaaaaa										
BPBF_CDS	-----										
hpt01	-----										
hpt02	-----										
hpt03	-----										
hpt04	-----										
hpt05	-----										
hpt06	-----										
hpt07	-----										
hpt08	-----										
hpt09	-----										
hpt10	-----										
hpt11	-----										
hpt12	-----										
hpt13	-----										
hpt14	-----										
hpt15	-----										
hpt16	-----										
hpt17	-----										
hpt18	-----										
hpt19	-----										
hpt20	-----										
hpt21	-----										

HvGAMYB mRNA
HvGAMYB_CDS

HvGAMYB mRNA
HvGAMYB_CDS

Sequence logos for HvGAMYB binding sites. The top part shows a reference sequence with positions -580 to -480. Below are 18 HvGAMYB mRNA sequences (hpt01 to hpt18) with their corresponding HvGAMYB_CDS sequences. The sequences are color-coded to show conserved regions.

Reference sequence (top):

Positions: -580 -570 -560 -550 -540 -530 -520 -510 -500 -490 -480

Sequences (hpt01 to hpt18):

hpt01: CCCCAGAAATTCGGGTTCCTTTCGGGTGGGCGCGGGGATGCTGATCCGTGGCTGCTCGGGTGCTGGAATTGCGTGCTTGGCCTTTTTTT-CTTTCTTCGGCCCCGTGGGA

hpt02: CCCCAGAAATTCGGGTTCCTTTCGGGTGGGCGCGGGGATGCTGATCCGTGGCTGCTCGGGTGCTGGAATTGCGTGCTTGGCCTTTTTTTCTTTCTTCGGCCCCGTGGGA

hpt03: CCCCAGAAATTCGGGTTCCTTTCGGGTGGGCGCGGGGATGCTGATCCGTGGCTGCTCGGGTGCTGGAATTGCGTGCTTGGCCTTTTTTT-CTTTCTTCGGCCCCGTGGGA

hpt04: CCCCAGAAATTCGGGTTCCTTTCGGGTGGGCGCGGGGATGCTGATCCGTGGCTGCTCGGGTGCTGGAATTGCGTGCTTGGCCTTTTTTT-CTTTCTTCGGCCCCGTGGGA

hpt05: CCCCAGAAATTCGGGTTCCTTTCGGGTGGGCGCGGGGATGCTGATCCGTGGCTGCTCGGGTGCTGGAATTGCGTGCTTGGCCTTTTTTTCTTTCTTCGGCCCCGTGGGA

hpt06: CCCCAGAAATTCGGGTTCCTTTCGGGTGGGCGCGGGGATGCTGATCCGTGGCTGCTCGGGTGCTGGAATTGCGTGCTTGGCCTTTTTTTCTTTCTTCGGCCCCGTGGGA

hpt07: CCCCAGAAATTCGGGTTCCTTTCGGGTGGGCGCGGGGATGCTGATCCGTGGCTGCTCGGGTGCTGGAATTGCGTGCTTGGCCTTTTTTTCTTTCTTCGGCCCCGTGGGA

hpt08: CCCCAGAAATTCGGGTTCCTTTCGGGTGGGCGCGGGGATGCTGATCCGTGGCTGCTCGGGTGCTGGAATTGCGTGCTTGGCCTTTTTTT-CTTTCTTCGGCCCCGTGGGA

hpt09: CCCCAGAAATTCGGGTTCCTTTCGGGTGGGCGCGGGGATGCTGATCCGTGGCTGCTCGGGTGCTGGAATTGCGTGCTTGGCCTTTTTTTCTTTCTTCGGCCCCGTGGGA

hpt10: CCCCAGAAATTCGGGTTCCTTTCGGGTGGGCGCGGGGATGCTGATCCGTGGCTGCTCGGGTGCTGGAATTGCGTGCTTGGCCTTTTTTT-CTTTCTTCGGCCCCGTGGGA

hpt11: CCCCAGAAATTCGGGTTCCTTTCGGGTGGGCGCGGGGATGCTGATCCGTGGCTGCTCGGGTGCTGGAATTGCGTGCTTGGCCTTTTTTTCTTTCTTCGGCCCCGTGGGA

hpt12: CCCCAGAAATTCGGGTTCCTTTCGGGTGGGCGCGGGGATGCTGATCCGTGGCTGCTCGGGTGCTGGAATTGCGTGCTTGGCCTTTTTTT-CTTTCTTCGGCCCCGTGGGA

hpt13: CCCCAGAAATTCGGGTTCCTTTCGGGTGGGCGCGGGGATGCTGATCCGTGGCTGCTCGGGTGCTGGAATTGCGTGCTTGGCCTTTTTTT-CTTTCTTCGGCCCCGTGGGA

hpt15: CCCCAGAAATTCGGGTTCCTTTCGGGTGGGCGCGGGGATGCTGATCCGTGGCTGCTCGGGTGCTGGAATTGCGTGCTTGGCCTTTTTTTCTTTCTTCGGCCCCGTGGGA

hpt16: CCCCAGAAATTCGGGTTCCTTTCGGGTGGGCGCGGGGATGCTGATCCGTGGCTGCTCGGGTGCTGGAATTGCGTGCTTGGCCTTTTTTTCTTTCTTCGGCCCCGTGGGA

hpt17: CCCCAGAAATTCGGGTTCCTTTCGGGTGGGCGCGGGGATGCTGATCCGTGGCTGCTCGGGTGCTGGAATTGCGTGCTTGGCCTTTTTTTCTTTCTTCGGCCCCGTGGGA

hpt18: CCCCAGAAATTCGGGTTCCTTTCGGGTGGGCGCGGGGATGCTGATCCGTGGCTGCTCGGGTGCTGGAATTGCGTGCTTGGCCTTTTTTTCTTTCTTCGGCCCCGTGGGA

Figure 1 displays the multiple sequence alignment of HvGAMYB CDS. The alignment is shown in a color-coded format where identical nucleotides are the same color. The alignment is highly conserved, with most positions having the same nucleotide across all sequences. The alignment is shown in a color-coded format where identical nucleotides are the same color. The alignment is highly conserved, with most positions having the same nucleotide across all sequences.

Sequence logo for HvGAMYB binding sites. The y-axis represents the probability of each nucleotide (A, C, G, T) at each position from -360 to -260. The x-axis is labeled 'HvGAMYB mRNA' and 'HvGAMYB_CDS'. The logo shows a strong preference for T at positions -350 to -330, and a strong preference for A at positions -320 to -280. The sequence TCCCTTGGCTAAAACTGCTGTGCTTGAGCTCAAAACATGTTCAATTCAATTCCTTAACCGGGTATTAAATGCCCTGCCCTGCTGAATTTGGGAAGGAAGTGATTCCAGTCTG is highlighted in red.

Figure 1 displays a multiple sequence alignment of the HvGAMYB CDSs from 18 wheat accessions. The alignment is shown in a grid format with columns numbered from -250 to -150. The sequences are color-coded: G (green), T (red), C (blue), and A (black). The alignment shows high conservation across all accessions, with some variations in the 5' region (columns -250 to -200).

HvGAMYB mRNA
HvGAMYB_CDS

hpt01
hpt02
hpt03
hpt04
hpt05
hpt06
hpt07
hpt08
hpt09
hpt10
hpt14
hpt11
hpt12
hpt13
hpt15
hpt16
hpt17
hpt18

Sequence logo showing the conservation of nucleotides across 18 HvGAMYB mRNA sequences. The y-axis represents positions from -140 to -40. The x-axis represents positions from 1 to 20. The logo displays the conservation of nucleotides across 18 HvGAMYB mRNA sequences. The sequence logo shows a strong consensus for the sequence CAGTCTCTGTTGATTCGAGCAGTGGT, which is highlighted in red in the original image. The sequence is followed by a 20-nucleotide spacer (TCCACAAAAAGGTA) and a 20-nucleotide spacer (CTAGTTGTGGTCAA). The sequence ends with a 20-nucleotide spacer (TAACTAACAAAAAATTC).

Sequence logo for the HvGAMYB binding site. The x-axis represents positions from -30 to 80. The y-axis represents the probability of each nucleotide (A, C, G, T) at each position. The logo highlights the conserved regions: a G-rich region around position -10 and a C-rich region around position 10. The sequence is shown in a color-coded format: G (green), A (red), T (blue), C (yellow).

Sequence logo for the HvGAMYB binding site. The x-axis represents positions from -30 to 80. The y-axis represents the probability of each nucleotide (A, C, G, T) at each position. The logo highlights the conserved regions: a G-rich region around position -10 and a C-rich region around position 10. The sequence is shown in a color-coded format: G (green), A (red), T (blue), C (yellow).

[illegible]

Sequence logo for HvGAMYB binding sites. The x-axis represents positions 860 to 960. The y-axis lists HvGAMYB mRNA and HvGAMYB_CDS. The logo shows conserved regions for hpt01 through hpt18, with a color scale from 0.00 to 0.10.

	1300	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	
HvGAMYB mRNA											
HvGAMYB_CDS	-----ttgccagggcgta	ctgata	aatgaa	ataa	gaattact	ggaa	cactcg	aaataa	agagat	gtcagc	gagccg	gtttgcc
hpt01	TTCTCAGTTGCCAGGGCGTACTGATAACGAAATAAAGAAATTACTGGAACTCTCGAATAAAGAGATGTCAGCGAGCCGGTTTGCCAAATATATCCTGCTAGTGATGCAATC											
hpt02	TTCTCAGTTGCCAGGGCGTACTGATAATGAAATAAAGAAATTACTGGAACTCTCGAATAAAGAGATGTCAGCGAGCCGGTTTGCCAAATATATCCTGCTAGTGATGCAATC											
hpt03	TTCTCAGTTGCCAGGGCGTACTGATAACGAAATAAAGAAATTACTGGAACTCTCGAATAAAGAGATGTCAGCGAGCCGGTTTGCCAAATATATCCTGCTAGTGATGCAATC											
hpt04	TTCTCAGTTGCCAGGGCGTACTGATAATGAAATAAAGAAATTACTGGAACTCTCGAATAAAGAGATGTCAGCGAGCCGGTTTGCCAAATATATCCTGCTAGTGATGCAATC											
hpt05	TTCTCAGTTGCCAGGGCGTACTGATAACGAAATAAAGAAATTACTGGAACTCTCGAATAAAGAGATGTCAGCGAGCCGGTTTGCCAAATATATCCTGCTAGTGATGCAATC											
hpt06	TTCTCAGTTGCCAGGGCGTACTGATAACGAAATAAAGAAATTACTGGAACTCTCGAATAAAGAGATGTCAGCGAGCCGGTTTGCCAAATATATCCTGCTAGTGATGCAATC											
hpt07	TTCTCAGTTGCCAGGGCGTACTGATAATGAAATAAAGAAATTACTGGAACTCTCGAATAAAGAGATGTCAGCGAGCCGGTTTGCCAAATATATCCTGCTAGTGATGCAATC											
hpt08	TTCTCAGTTGCCAGGGCGTACTGATAATGAAATAAAGAAATTACTGGAACTCTCGAATAAAGAGATGTCAGCGAGCCGGTTTGCCAAATATATCCTGCTAGTGATGCAATC											
hpt09	TTCTCAGTTGCCAGGGCGTACTGATAATGAAATAAAGAAATTACTGGAACTCTCGAATAAAGAGATGTCAGCGAGCCGGTTTGCCAAATATATCCTGCTAGTGATGCAATC											
hpt10	TTCTCAGTTGCCAGGGCGTACTGATAATGAAATAAAGAAATTACTGGAACTCTCGAATAAAGAGATGTCAGCGAGCCGGTTTGCCAAATATATCCTGCTAGTGATGCAATC											
hpt14	TTCTCAGTTGCCAGGGCGTACTGATAACGAAATAAAGAAATTACTGGAACTCTCGAATAAAGAGATGTCAGCGAGCCGGTTTGCCAAATATATCCTGCTAGTGATGCAATC											
hpt11	TTCTCAGTTGCCAGGGCGTACTGATAATGAAATAAAGAAATTACTGGAACTCTCGAATAAAGAGATGTCAGCGAGCCGGTTTGCCAAATATATCCTGCTAGTGATGCAATC											
hpt12	TTCTCAGTTGCCAGGGCGTACTGATAATGAAATAAAGAAATTACTGGAACTCTCGAATAAAGAGATGTCAGCGAGCCGGTTTGCCAAATATATCCTGCTAGTGATGCAATC											
hpt13	TTCTCAGTTGCCAGGGCGTACTGATAACGAAATAAAGAAATTACTGGAACTCTCGAATAAAGAGATGTCAGCGAGCCGGTTTGCCAAATATATCCTGCTAGTGATGCAATC											
hpt15	TTCTCAGTTGCCAGGGCGTACTGATAATGAAATAAAGAAATTACTGGAACTCTCGAATAAAGAGATGTCAGCGAGCCGGTTTGCCAAATATATCCTGCTAGTGATGCAATC											
hpt16	TTCTCAGTTGCCAGGGCGTACTGATAACGAAATAAAGAAATTACTGGAACTCTCGAATAAAGAGATGTCAGCGAGCCGGTTTGCCAAATATATCCTGCTAGTGATGCAATC											
hpt17	TTCTCAGTTGCCAGGGCGTACTGATAACGAAATAAAGAAATTACTGGAACTCTCGAATAAAGAGATGTCAGCGAGCCGGTTTGCCAAATATATCCTGCTAGTGATGCAATC											
hpt18	TTCTCAGTTGCCAGGGCGTACTGATAATGAAATAAAGAAATTACTGGAACTCTCGAATAAAGAGATGTCAGCGAGCCGGTTTGCCAAATATATCCTGCTAGTGATGCAATC											

	1410	1420	1430	1440	1450	1460	1470	1480	1490	1500	1510	
HvGAMYB mRNA	aatcttcaaatgaagatcagcagggcgctccagcgattttcaactgcggcgagaatctttccagt	gac	cctcctgaat	ggaaatgg	tcctttat	ctcgcag	attttac	cctgtgac				
HvGAMYB_CDS	AAATCTTCAAATGAAGATCAGCAGGGCTCCAGCGATTTCAACTGCGGCAGAAATCTTTCCAGTGACCTCCTGAATGGAAATGGTCTTTATCTGCCAGATTTTACCTGTGAC											
hpt01	AAATCTTCAAATGAAGATCAGCAGGGCTCCAGCGATTTCAACTGCGGCAGAAATCTTTCCAGTGACCTCCTGAATGGAAATGGTCTTTATCTGCCAGATTTTACCTGTGAC											
hpt02	AAATCTTCAAATGAAGATCAGCAGGGCTCCAGCGATTTCAACTGCGGCAGAAATCTTTCCAGTGACCTCCTGAATGGAAATGGTCTTTATCTGCCAGATTTTACCTGTGAC											
hpt03	AAATCTTCAAATGAAGATCAGCAGGGCTCCAGCGATTTCAACTGCGGCAGAAATCTTTCCAGTGACCTCCTGAATGGAAATGGTCTTTATCTGCCAGATTTTACCTGTGAC											
hpt04	AAATCTTCAAATGAAGATCAGCAGGGCTCCAGCGATTTCAACTGCGGCAGAAATCTTTCCAGTGACCTCCTGAATGGAAATGGTCTTTATCTGCCAGATTTTACCTGTGAC											
hpt05	AAATCTTCAAATGAAGATCAGCAGGGCTCCAGCGATTTCAACTGCGGCAGAAATCTTTCCAGTGACCTCCTGAATGGAAATGGTCTTTATCTGCCAGATTTTACCTGTGAC											
hpt06	AAATCTTCAAATGAAGATCAGCAGGGCTCCAGCGATTTCAACTGCGGCAGAAATCTTTCCAGTGACCTCCTGAATGGAAATGGTCTTTATCTGCCAGATTTTACCTGTGAC											
hpt07	AAATCTTCAAATGAAGATCAGCAGGGCTCCAGCGATTTCAACTGCGGCAGAAATCTTTCCAGTGACCTCCTGAATGGAAATGGTCTTTATCTGCCAGATTTTACCTGTGAC											
hpt08	AAATCTTCAAATGAAGATCAGCAGGGCTCCAGCGATTTCAACTGCGGCAGAAATCTTTCCAGTGACCTCCTGAATGGAAATGGTCTTTATCTGCCAGATTTTACCTGTGAC											
hpt09	AAATCTTCAAATGAAGATCAGCAGGGCTCCAGCGATTTCAACTGCGGCAGAAATCTTTCCAGTGACCTCCTGAATGGAAATGGTCTTTATCTGCCAGATTTTACCTGTGAC											
hpt10	AAATCTTCAAATGAAGATCAGCAGGGCTCCAGCGATTTCAACTGCGGCAGAAATCTTTCCAGTGACCTCCTGAATGGAAATGGTCTTTATCTGCCAGATTTTACCTGTGAC											
hpt14	AAATCTTCAAATGAAGATCAGCAGGGCTCCAGCGATTTCAACTGCGGCAGAAATCTTTCCAGTGACCTCCTGAATGGAAATGGTCTTTATCTGCCAGATTTTACCTGTGAC											
hpt11	AAATCTTCAAATGAAGATCAGCAGGGCTCCAGCGATTTCAACTGCGGCAGAAATCTTTCCAGTGACCTCCTGAATGGAAATGGTCTTTATCTGCCAGATTTTACCTGTGAC											
hpt12	AAATCTTCAAATGAAGATCAGCAGGGCTCCAGCGATTTCAACTGCGGCAGAAATCTTTCCAGTGACCTCCTGAATGGAAATGGTCTTTATCTGCCAGATTTTACCTGTGAC											
hpt13	AAATCTTCAAATGAAGATCAGCAGGGCTCCAGCGATTTCAACTGCGGCAGAAATCTTTCCAGTGACCTCCTGAATGGAAATGGTCTTTATCTGCCAGATTTTACCTGTGAC											
hpt15	AAATCTTCAAATGAAGATCAGCAGGGCTCCAGCGATTTCAACTGCGGCAGAAATCTTTCCAGTGACCTCCTGAATGGAAATGGTCTTTATCTGCCAGATTTTACCTGTGAC											
hpt16	AAATCTTCAAATGAAGATCAGCAGGGCTCCAGCGATTTCAACTGCGGCAGAAATCTTTCCAGTGACCTCCTGAATGGAAATGGTCTTTATCTGCCAGATTTTACCTGTGAC											
hpt17	AAATCTTCAAATGAAGATCAGCAGGGCTCCAGCGATTTCAACTGCGGCAGAAATCTTTCCAGTGACCTCCTGAATGGAAATGGTCTTTATCTGCCAGATTTTACCTGTGAC											
hpt18	AAATCTTCAAATGAAGATCAGCAGGGCTCCAGCGATTTCAACTGCGGCAGAAATCTTTCCAGTGACCTCCTGAATGGAAATGGTCTTTATCTGCCAGATTTTACCTGTGAC											

[illegible]

[illegible][illegible]

Figure 1 displays the phylogenetic tree and sequence alignment of HvGAMYB mRNA and CDS. The top part shows a phylogenetic tree with 19 tips (HvGAMYB mRNA and 18 hpt lines) and a scale bar of 0.1. The bottom part shows a sequence alignment of the HvGAMYB_CDS region (100-200 bp) for the same 19 tips. The alignment is color-coded by nucleotide: A (green), C (blue), G (red), T (orange). The hpt lines show various mutations compared to the HvGAMYB mRNA sequence.

. . . . | | | | | | | | | | | | | | | | | | |
 HvGAMYB mRNA tgccttcataagcctcagggaactaaatctgggaagaatcagcagctctccgtgagaagtccaagtctcctctgtcagcacgccgtgtgataccacgggtggttagccccggag
 HvGAMYB_CDS TGCTTCATGAAGCTCAGGGACTAAGATCTGGGAAGAATCAGCAGCTCTCCGTGAGAAGTTCAAGTTCCTCTGT CAGCACGCCGTGTGATACCACGGTGGTTAGCCCCGGAG
 hpt01 TGCTTCATGAAGCTCAGGGACTAAGATCTGGGAAGAATCAGCAGCTCTCCGTGAGAAGTTCAAGTTCCTCTGT CAGCACGCCGTGTGATACCACGGTGGTTAGCCCCGGAG
 hpt02 TGCTTCATGAAGCTCAGGGACTAAGATCTGGGAAGAATCAGCAGCTCTCCGTGAGAAGTTCAAGTTCCTCTGT CAGCACGCCGTGTGATACCACGGTGGTTAGCCCCGGAG
 hpt03 TGCTTCATGAAGCTCAGGGACTAAGATCTGGGAAGAATCAGCAGCTCTCCGTGAGAAGTTCAAGTTCCTCTGT CAGCACGCCGTGTGATACCACGGTGGTTAGCCCCGGAG
 hpt04 TGCTTCATGAAGCTCAGGGACTAAGATCTGGGAAGAATCAGCAGCTCTCCGTGAGAAGTTCAAGTTCCTCTGT CAGCACGCCGTGTGATACCACGGTGGTTAGCCCCGGAG
 hpt05 TGCTTCATGAAGCTCAGGGACTAAGATCTGGGAAGAATCAGCAGCTCTCCGTGAGAAGTTCAAGTTCCTCTGT CAGCACGCCGTGTGATACCACGGTGGTTAGCCCCGGAG
 hpt06 TGCTTCATGAAGCTCAGGGACTAAGATCTGGGAAGAATCAGCAGCTCTCCGTGAGAAGTTCAAGTTCCTCTGT CAGCACGCCGTGTGATACCACGGTGGTTAGCCCCGGAG
 hpt07 TGCTTCATGAAGCTCAGGGACTAAGATCTGGGAAGAATCAGCAGCTCTCCGTGAGAAGTTCAAGTTCCTCTGT CAGCACGCCGTGTGATACCACGGTGGTTAGCCCCGGAG
 hpt08 TGCTTCATGAAGCTCAGGGACTAAGATCTGGGAAGAATCAGCAGCTCTCCGTGAGAAGTTCAAGTTCCTCTGT CAGCACGCCGTGTGATACCACGGTGGTTAGCCCCGGAG
 hpt09 TGCTTCATGAAGCTCAGGGACTAAGATCTGGGAAGAATCAGCAGCTCTCCGTGAGAAGTTCAAGTTCCTCTGT CAGCACGCCGTGTGATACCACGGTGGTTAGCCCCGGAG
 hpt10 TGCTTCATGAAGCTCAGGGACTAAGATCTGGGAAGAATCAGCAGCTCTCCGTGAGAAGTTCAAGTTCCTCTGT CAGCACGCCGTGTGATACCACGGTGGTTAGCCCCGGAG
 hpt11 TGCTTCATGAAGCTCAGGGACTAAGATCTGGGAAGAATCAGCAGCTCTCCGTGAGAAGTTCAAGTTCCTCTGT CAGCACGCCGTGTGATACCACGGTGGTTAGCCCCGGAG
 hpt12 TGCTTCATGAAGCTCAGGGACTAAGATCTGGGAAGAATCAGCAGCTCTCCGTGAGAAGTTCAAGTTCCTCTGT CAGCACGCCGTGTGATACCACGGTGGTTAGCCCCGGAG
 hpt13 TGCTTCATGAAGCTCAGGGACTAAGATCTGGGAAGAATCAGCAGCTCTCCGTGAGAAGTTCAAGTTCCTCTGT CAGCACGCCGTGTGATACCACGGTGGTTAGCCCCGGAG
 hpt15 TGCTTCATGAAGCTCAGGGACTAAGATCTGGGAAGAATCAGCAGCTCTCCGTGAGAAGTTCAAGTTCCTCTGT CAGCACGCCGTGTGATACCACGGTGGTTAGCCCCGGAG
 hpt16 TGCTTCATGAAGCTCAGGGACTAAGATCTGGGAAGAATCAGCAGCTCTCCGTGAGAAGTTCAAGTTCCTCTGT CAGCACGCCGTGTGATACCACGGTGGTTAGCCCCGGAG
 hpt17 TGCTTCATGAAGCTCAGGGACTAAGATCTGGGAAGAATCAGCAGCTCTCCGTGAGAAGTTCAAGTTCCTCTGT CAGCACGCCGTGTGATACCACGGTGGTTAGCCCCGGAG
 hpt18 TGCTTCATGAAGCTCAGGGACTAAGATCTGGGAAGAATCAGCAGCTCTCCGTGAGAAGTTCAAGTTCCTCTGT CAGCACGCCGTGTGATACCACGGTGGTTAGCCCCGGAG

	2180	2190	2200	2210	2220	2230	2240	2250	2260	2270	2280	
HvGAMYB mRNA	ttt	gat	ctc	tgt	cag	gaat	att	ggg	aag	aac	g
HvGAMYB_CDS	TTT	GAT	CTC	TGT	CAG	GAAT	ATT	GGG	AAG	AAC	G	
hpt01	TTT	GAT	CTC	TGT	CAG	GAAT	ATT	GGG	AAG	AAC	G	
hpt02	TTT	GAT	CTC	TGT	CAG	GAAT	ATT	GGG	AAG	AAC	G	
hpt03	TTT	GAT	CTC	TGT	CAG	GAAT	ATT	GGG	AAG	AAC	G	
hpt04	TTT	GAT	CTC	TGT	CAG	GAAT	ATT	GGG	AAG	AAC	G	
hpt05	TTT	GAT	CTC	TGT	CAG	GAAT	ATT	GGG	AAG	AAC	G	
hpt06	TTT	GAT	CTC	TGT	CAG	GAAT	ATT	GGG	AAG	AAC	G	
hpt07	TTT	GAT	CTC	TGT	CAG	GAAT	ATT	GGG	AAG	AAC	G	
hpt08	TTT	GAT	CTC	TGT	CAG	GAAT	ATT	GGG	AAG	AAC	G	
hpt09	TTT	GAT	CTC	TGT	CAG	GAAT	ATT	GGG	AAG	AAC	G	
hpt10	TTT	GAT	CTC	TGT	CAG	GAAT	ATT	GGG	AAG	AAC	G	
hpt14	TTT	GAT	CTC	TGT	CAG	GAAT	ATT	GGG	AAG	AAC	G	
hpt11	TTT	GAT	CTC	TGT	CAG	GAAT	ATT	GGG	AAG	AAC	G	
hpt12	TTT	GAT	CTC	TGT	CAG	GAAT	ATT	GGG	AAG	AAC	G	
hpt13	TTT	GAT	CTC	TGT	CAG	GAAT	ATT	GGG	AAG	AAC	G	
hpt15	TTT	GAT	CTC	TGT	CAG	GAAT	ATT	GGG	AAG	AAC	G	
hpt16	TTT	GAT	CTC	TGT	CAG	GAAT	ATT	GGG	AAG	AAC	G	
hpt17	TTT	GAT	CTC	TGT	CAG	GAAT	ATT	GGG	AAG	AAC	G	
hpt18	TTT	GAT	CTC	TGT	CAG	GAAT	ATT	GGG	AAG	AAC	G	

	2290	2300	2310	2320	2330	2340	2350	2360	2370	2380	2390
HvGAMYB mRNA	tttt	cag	ctc	tcc	aaa	att	tct	cct	g	
HvGAMYB_CDS	TTTT	CAG	CTC	TCC	AAA	ATT	TCT	CCT	CG		
hpt01	TTTT	CAG	CTC	TCC	AAA	ATT	TCT	CCT	CGG	TAG	TAT
hpt02	TTTT	CAG	CTC	TCC	AAA	ATT	TCT	CCT	GGT	GAG	TAT
hpt03	TTTT	CAG	CTC	TCC	AAA	ATT	TCT	CCT	GGT	GAG	TAT
hpt04	TTTT	CAG	CTC	TCC	AAA	ATT	TCT	CCT	GGT	GAG	TAT
hpt05	TTTT	CAG	CTC	TCC	AAA	ATT	TCT	CCT	GGT	GAG	TAT
hpt06	TTTT	CAG	CTC	TCC	AAA	ATT	TCT	CCT	GGT	GAG	TAT
hpt07	TTTT	CAG	CTC	TCC	AAA	ATT	TCT	CCT	GGT	GAG	TAT
hpt08	TTTT	CAG	CTC	TCC	AAA	ATT	TCT	CCT	GGT	GAG	TAT
hpt09	TTTT	CAG	CTC	TCC	AAA	ATT	TCT	CCT	GGT	GAG	TAT
hpt10	TTTT	CAG	CTC	TCC	AAA	ATT	TCT	CCT	GGT	GAG	TAT
hpt14	TTTT	CAG	CTC	TCC	AAA	ATT	TCT	CCT	GGT	GAG	TAT
hpt11	TTTT	CAG	CTC	TCC	AAA	ATT	TCT	CCT	GGT	GAG	TAT
hpt12	TTTT	CAG	CTC	TCC	AAA	ATT	TCT	CCT	GGT	GAG	TAT
hpt13	TTTT	CAG	CTC	TCC	AAA	ATT	TCT	CCT	GGT	GAG	TAT
hpt15	TTTT	CAG	CTC	TCC	AAA	ATT	TCT	CCT	GGT	GAG	TAT
hpt16	TTTT	CAG	CTC	TCC	AAA	ATT	TCT	CCT	GGT	GAG	TAT
hpt17	TTTT	CAG	CTC	TCC	AAA	ATT	TCT	CCT	GGT	GAG	TAT
hpt18	TTTT	CAG	CTC	TCC	AAA	ATT	TCT	CCT	GGT	GAG	TAT

. . . . | | | | | | | | | | | | | | | | | | | | |
 HvGAMYB mRNA agccctt cactggg atctgga gaggc aggcaat ggagc ctgcata tgaagccc ggggaggggac acttcgtct catcctgaaa acttgagg ccagacgcgtttcttctccgg
 HvGAMYB_CDS AGCCCTTCACTGGGATCTGGAGAGCAGGCCAATGGAGCCTGCATATGAGCCCCGGGGCAGGGGACACTTCGTCTCATCCTGAAAACTTGAGGCCAGACGCGTTCTTCTCCGG
 hpt01 AGCCCTTCACTGGGATCTGGAGAGCAGGCCAATGGAGCCTGCATATGAGCCCCGGGGCAGGGGACACTTCGTCTCATCCTGAAAACTTGAGGCCAGACGCGTTCTTCTCCGG
 hpt02 AGCCCTTCACTGGGATCTGGAGAGCAGGCCAATGGAGCCTGCATATGAGCCCCGGGGCAGGGGACACTTCGTCTCATCCTGAAAACTTGAGGCCAGACGCGTTCTTCTCCGG
 hpt03 AGCCCTTCACTGGGATCTGGAGAGCAGGCCAATGGAGCCTGCATATGAGCCCCGGGGCAGGGGACACTTCGTCTCATCCTGAAAACTTGAGGCCAGACGCGTTCTTCTCCGG
 hpt04 AGCCCTTCACTGGGATCTGGAGAGCAGGCCAATGGAGCCTGCATATGAGCCCCGGGGCAGGGGACACTTCGTCTCATCCTGAAAACTTGAGGCCAGACGCGTTCTTCTCCGG
 hpt05 AGCCCTTCACTGGGATCTGGAGAGCAGGCCAATGGAGCCTGCATATGAGCCCCGGGGCAGGGGACACTTCGTCTCATCCTGAAAACTTGAGGCCAGACGCGTTCTTCTCCGG
 hpt06 AGCCCTTCACTGGGATCTGGAGAGCAGGCCAATGGAGCCTGCATATGAGCCCCGGGGCAGGGGACACTTCGTCTCATCCTGAAAACTTGAGGCCAGACGCGTTCTTCTCCGG
 hpt07 AGCCCTTCACTGGGATCTGGAGAGCAGGCCAATGGAGCCTGCATATGAGCCCCGGGGCAGGGGACACTTCGTCTCATCCTGAAAACTTGAGGCCAGACGCGTTCTTCTCCGG
 hpt08 AGCCCTTCACTGGGATCTGGAGAGCAGGCCAATGGAGCCTGCATATGAGCCCCGGGGCAGGGGACACTTCGTCTCATCCTGAAAACTTGAGGCCAGACGCGTTCTTCTCCGG
 hpt09 AGCCCTTCACTGGGATCTGGAGAGCAGGCCAATGGAGCCTGCATATGAGCCCCGGGGCAGGGGACACTTCGTCTCATCCTGAAAACTTGAGGCCAGACGCGTTCTTCTCCGG
 hpt10 AGCCCTTCACTGGGATCTGGAGAGCAGGCCAATGGAGCCTGCATATGAGCCCCGGGGCAGGGGACACTTCGTCTCATCCTGAAAACTTGAGGCCAGACGCGTTCTTCTCCGG
 hpt14 AGCCCTTCACTGGGATCTGGAGAGCAGGCCAATGGAGCCTGCATATGAGCCCCGGGGCAGGGGACACTTCGTCTCATCCTGAAAACTTGAGGCCAGACGCGTTCTTCTCCGG
 hpt11 AGCCCTTCACTGGGATCTGGAGAGCAGGCCAATGGAGCCTGCATATGAGCCCCGGGGCAGGGGACACTTCGTCTCATCCTGAAAACTTGAGGCCAGACGCGTTCTTCTCCGG
 hpt12 AGCCCTTCACTGGGATCTGGAGAGCAGGCCAATGGAGCCTGCATATGAGCCCCGGGGCAGGGGACACTTCGTCTCATCCTGAAAACTTGAGGCCAGACGCGTTCTTCTCCGG
 hpt13 AGCCCTTCACTGGGATCTGGAGAGCAGGCCAATGGAGCCTGCATATGAGCCCCGGGGCAGGGGACACTTCGTCTCATCCTGAAAACTTGAGGCCAGACGCGTTCTTCTCCGG
 hpt15 AGCCCTTCACTGGGATCTGGAGAGCAGGCCAATGGAGCCTGCATATGAGCCCCGGGGCAGGGGACACTTCGTCTCATCCTGAAAACTTGAGGCCAGACGCGTTCTTCTCCGG
 hpt16 AGCCCTTCACTGGGATCTGGAGAGCAGGCCAATGGAGCCTGCATATGAGCCCCGGGGCAGGGGACACTTCGTCTCATCCTGAAAACTTGAGGCCAGACGCGTTCTTCTCCGG
 hpt17 AGCCCTTCACTGGGATCTGGAGAGCAGGCCAATGGAGCCTGCATATGAGCCCCGGGGCAGGGGACACTTCGTCTCATCCTGAAAACTTGAGGCCAGACGCGTTCTTCTCCGG
 hpt18 AGCCCTTCACTGGGATCTGGAGAGCAGGCCAATGGAGCCTGCATATGAGCCCCGGGGCAGGGGACACTTCGTCTCATCCTGAAAACTTGAGGCCAGACGCGTTCTTCTCCGG

	2620	2630	2640	2650	2660	2670	2680	2690	2700	2710	2720	
HvGAMYB mRNA	cgg	tgt	ggag	caact	tgc	cct	cat	gctt	gtc	aaat	gtc
HvGAMYB_CDS	CGG	TGT	GGAG	CAACT	TGC	CCT	CAT	GCTT	GTC	AAAT	GTC	CGG
hpt01	CGG	TGT	GGAG	CAACT	TGC	CCT	CAT	GCTT	GTC	AAAT	GTC	CGG
hpt02	CGG	TGT	GGAG	CAACT	TGC	CCT	CAT	GCTT	GTC	AAAT	GTC	CGG
hpt03	CGG	TGT	GGAG	CAACT	TGC	CCT	CAT	GCTT	GTC	AAAT	GTC	CGG
hpt04	CGG	TGT	GGAG	CAACT	TGC	CCT	CAT	GCTT	GTC	AAAT	GTC	CGG
hpt05	CGG	TGT	GGAG	CAACT	TGC	CCT	CAT	GCTT	GTC	AAAT	GTC	CGG
hpt06	CGG	TGT	GGAG	CAACT	TGC	CCT	CAT	GCTT	GTC	AAAT	GTC	CGG
hpt07	CGG	TGT	GGAG	CAACT	TGC	CCT	CAT	GCTT	GTC	AAAT	GTC	CGG
hpt08	CGG	TGT	GGAG	CAACT	TGC	CCT	CAT	GCTT	GTC	AAAT	GTC	CGG
hpt09	CGG	TGT	GGAG	CAACT	TGC	CCT	CAT	GCTT	GTC	AAAT	GTC	CGG
hpt10	CGG	TGT	GGAG	CAACT	TGC	CCT	CAT	GCTT	GTC	AAAT	GTC	CGG
hpt14	CGG	TGT	GGAG	CAACT	TGC	CCT	CAT	GCTT	GTC	AAAT	GTC	CGG
hpt11	CGG	TGT	GGAG	CAACT	TGC	CCT	CAT	GCTT	GTC	AAAT	GTC	CGG
hpt12	CGG	TGT	GGAG	CAACT	TGC	CCT	CAT	GCTT	GTC	AAAT	GTC	CGG
hpt13	CGG	TGT	GGAG	CAACT	TGC	CCT	CAT	GCTT	GTC	AAAT	GTC	CGG
hpt15	CGG	TGT	GGAG	CAACT	TGC	CCT	CAT	GCTT	GTC	AAAT	GTC	CGG
hpt16	CGG	TGT	GGAG	CAACT	TGC	CCT	CAT	GCTT	GTC	AAAT	GTC	CGG
hpt17	CGG	TGT	GGAG	CAACT	TGC	CCT	CAT	GCTT	GTC	AAAT	GTC	CGG
hpt18	CGG	TGT	GGAG	CAACT	TGC	CCT	CAT	GCTT	GTC	AAAT	GTC	CGG

	2730	2740	2750	2760	2770	2780	2790	2800	2810	2820	2830
HvGAMYB mRNA	t	gt	t	tt	g	agg	aaaa	att	c	ag
HvGAMYB_CDS	ttg	ttt	g	agg	aaaa	att	c	ag	aaa	g	c
hpt01	ttg	ttt	g	agg	aaaa	att	c	ag	aaa	g	c
hpt02	ttg	ttt	g	agg	aaaa	att	c	ag	aaa	g	c
hpt03	ttg	ttt	g	agg	aaaa	att	c	ag	aaa	g	c
hpt04	ttg	ttt	g	agg	aaaa	att	c	ag	aaa	g	c
hpt05	ttg	ttt	g	agg	aaaa	att	c	ag	aaa	g	c
hpt06	ttg	ttt	g	agg	aaaa	att	c	ag	aaa	g	c
hpt07	ttg	ttt	g	agg	aaaa	att	c	ag	aaa	g	c
hpt08	ttg	ttt	g	agg	aaaa	att	c	ag	aaa	g	c
hpt09	ttg	ttt	g	agg	aaaa	att	c	ag	aaa	g	c
hpt10	ttg	ttt	g	agg	aaaa	att	c	ag	aaa	g	c
hpt14	ttg	ttt	g	agg	aaaa	att	c	ag	aaa	g	c
hpt11	ttg	ttt	g	agg	aaaa	att	c	ag	aaa	g	c
hpt12	ttg	ttt	g	agg	aaaa	att	c	ag	aaa	g	c
hpt13	ttg	ttt	g	agg	aaaa	att	c	ag	aaa	g	c
hpt15	ttg	ttt	g	agg	aaaa	att	c	ag	aaa	g	c
hpt16	ttg	ttt	g	agg	aaaa	att	c	ag	aaa	g	c
hpt17	ttg	ttt	g	agg	aaaa	att	c	ag	aaa	g	c
hpt18	ttg	ttt	g	agg	aaaa	att	c	ag	aaa	g	c

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                2840      2850      2860      2870      2880      2890      2900      2910      2920      2930      2940
HvGAMYB mRNA    .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HvGAMYB_CDS     taaagttaggggagataagcgggttatctatTTTTTgtttgtttgtttcgaaactagagaaccctTTTTgtcatctctgtggcatttatttgaa
```

aatgtaagatcagtt

hpt01
hpt02
hpt03
hpt04
hpt05
hpt06
hpt07
hpt08
hpt09
hpt10
hpt14
hpt11
hpt12
hpt13
hpt15
hpt16
hpt17
hpt18

```
                2950      2960      2970      2980      2990
HvGAMYB mRNA    .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HvGAMYB_CDS     actgcttaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
```

hpt01
hpt02
hpt03
hpt04
hpt05
hpt06
hpt07
hpt08
hpt09
hpt10
hpt14
hpt11
hpt12
hpt13
hpt15
hpt16
hpt17
hpt18