

ABCbot

Acta Biologica Cracoviensia
Series Botanica

SUPPLEMENTARY MATERIAL

Do et al., ABCbot 60(1) 2018

Supplementary TABLE 1

Pokkali				
Motif	Position	Sequence	AC	
-10PEHVPSBD	-856, +36	TATTCT	S000392	
2SSEEDPROTBANAPA	-1266	CAAACAC	S000143	
-300ELEMENT	-1400, -1335, -193, +99, +114, +178, +272	TGHAAARK	S000122	
AACACOREOSGLUB1	-430	AACAAAC	S000353	
AACACOREOSGLUB1	-152	AACAAAC	S000353	
ABRELATERD1	-1202	ACGTG	S000414	
ABRERATCAL	-1203, one more at 225 bp insertion fragment	MACGYGB	S000507	
ACGTATERD1	-1202, -1387	ACGT	S000415	
AMYBOX2	-1072	TATCCAT	S000021	
ANAERO1CONSENSUS	-431, -151, +419	AAACAAA	S000477	
ANAERO2CONSENSUS	+199, +203, +351, +450	AGCAGC	S000478	
ANAERO5CONSENSUS	-682	TTCCCTGTT	S000481	
ARR1AT	-1366, -1301, -1259, -1197, -868, -835, -797, -672, -612, -607, -569, -443, -249, -224, -40, -15, +183, +376, +486, +527	NGATT	S000454	

BIHD1OS	-1423, -1415, -145, +401	TGTCA	S000498
BOXLCOREDPCAL	+340	ACCWWCC	S000492
CAATBOX1	-1420, -1379, -1314, -1013, -961, -900, -715, -673, -468, -447, -372, -247, -162, +45, +172, +255, +365, +375	CAAT	S000028
CACTFTPPCA1	-1231, -1105, -1097, -1077, -1016, -1008, -929, -909, -851, --775, -770, -760, -753, -744, -727, -579, -562, -525, -487, -385, -360, -335, -314, -287, -180, -90, -71, -62, +93, +140, +215, +247, +259, +262, +265, +441, +494, +500, +506, +524	YACT	S000449
CANBNNAPA	-1266, -342	CNAACAC	S000148
CAREOSREP1	-409	CAACTC	S000421
CARGCW8GAT	-900, -495, +145	CWWWWWWWWWG	S000431
CCA1ATLHCB1	-249	AAMAATCT	S000149
CPBCSPOR	-997	TATTAG	S000491
CURECORECR	-1115, -1082, -934, -1082, -934, -908, -769, -761, -563, +232	GTAC	S000493
DOFCOREZM	-1458, -1435, -1399, -1358, -1334, -1293, -1245, -1135, -1124, -1087, -1053, -1040, -862, -755, -742, -737, -707, -669, -623, -617, -592, -587, -501, -474, -404, -383, -362, -349, -292, -283, -238, -204, -100, -92, -87, -19, +145, +158, +197, +296, +316	AAAG	S000265
DPBFCOREDCDC3	-123, two more at 225 bp insertion fragment	ACACNNG	S000292
EBOXBNNAPA	-880, -803, +54, +110, +186, +210, +439, +494, +500, -271, -43, +487	CANNTG	S000144
EECCRAH1	-271, -43, +487	GANTTNC	S000494
GATABOX	-1463, -1428, -1242, -1209, -1140, -1072, -1060, -1010, -927, -884, -722, -711, -704, -522, -423, -375, -280, +33, +288	GATA	S000039
GT1CONSENSUS	-1430, -1251, -1242, -1209, -1167, -1062, -822, -711, -644, -622, -605, -597, -586, -459, -282, -44, +100, +191, +273, +391, +488	GRWAAW	S000198
GT1GMSCAM4	-1167, -644, +100, +191, +273, +391	GAAAAA	S000453
GTGANTG10	-1391, -1326, -1211, -1198, -659, -461, -57, +141, +248, +141, +248, +400, +442	GTGA	S000378

HDZIP2ATATHB2	-1183	TAATMATTA	S000373
IBOXCORE	-1429,-1242, -1209, -1140, -1061, -722, -711-281	GATAA	S000199
INRNTPSADB	-1441, -1381, -1165, -675, -602, -276, -230, -224, -136, +177	YTCANTYY	S000395
INTRONLOWER	-949	TGCAGG	S000086
LTRE1HVBLT49	+155	CCGAAA	S000250
MYB2CONSENSUSAT	-24	YAACKG	S000409
MYBCORE	+68, -1389	CNGTTR	S000176
MYBST1	-1141	GGATA	S000180
MYBST1	-1072	GGATA	S000180
MYBST1	+287	GGATA	S000180
MYCATERD1	+110	CATGTG	S000413
MYCCONSENSUSAT	-880, -803, +110, +186, +201	CANNTG	S000407
NODCON1GM	-1245, -707, -671, -474, -373, --285, -234, -48	AAAGAT	S000461
NTBBF1ARROLB	-1459, -1359, -1294,-1136, -1125, -88	ACTTTA	S000273
POLASIG1	-1248, -480,-401, -1185, -988, -1181, -899, -838, -467, -299	AATAAA	S000080
OSE1ROOTNODULE	-1245, -707, -671, -474, -406, -285, -234, -48, +387	AAAGAT	S000467
POLLEN1LELAT52	-1043, -860, -821, -740, -645,-590, -584, +298, +383, +390	AGAAA	S000245
PREATPRODH	-133	ACTCAT	S000450
PRECONSCRHSP70A	+204	SCGAYNRNNNNNNNNNNNNNNNNNNHHD	S000506
PROXBBNNA	-1267	CAAACACC	S000263
PYRIMIDINEBOXOSRAMY1A	-863, -593, +393, +423	CCTTTT	S000259
QARBNEXTA	-1203	AACGTGT	S000244
RAV1AAT	-938,-370, -183, +68, +310, +409	CAACA	S000314
RBCSCONSENSUS	+376, +484	AATCCAA	S000127
ROOTMOTIFTAPOX1	-1150, -1131,-545, -513, -417, -374, +289	ATATT	S000098
RYREPEATBNNAPA	+41	CATGCA	S000264
S1FBOXSORPS1L21	-1081	ATGGTA	S000223
SEBFCONSSTPR10A	+400	YTGTCWC	S000391
SEF4MOTIFGM7S	-1240, -1085, -536, +12	RTTTTTTR	S000103
SITEIIATCYTC	-98	TGGGCY	S000474

SORLIP2AT	-1032	GGGCC	S000483
SORLIP3AT	+437	CTCAAGTGA	S000484
SORLREP3AT	-416	TGTATATAT	S000488
SP8BFIBSP8BIB	-490	TACTATT	S000184
SREATMSD	-1141	TTATCC	S000470
SURE1STPAT21	-861	AATAGAAAA	S000186
T/GBOXATPIN2	-1203	AACGTG	S000458
TATABOX2	+329	TATAAAT	S000109
TATABOX3	+329	TATTAAT	S000110
TATABOX4	-1129	TATATAA	S000111
TATABOX5	-1249, -839, -481, -400, +276	TTATTT	S000203
TATABOXOSPAL	-516, -399	TATTTAA	S000400
TATAPVTRNALEU	-1129	TTTATATA	S000340
TATCCAYMOTIFOSRAMY3D	-1072	TATCCAY	S000256
WBOXATNPR1	-1422, -499, -365, -146, +415	TTGAC	S000390
WBOXNTERF3	-1393, -1328, -1025, 663, 971, 1103, 1384, 1532, 1597, 1611, 1718, 1883	TGACY	S000457
WRKY71OS	-1422 -1414 -1392 -1327 -1024 -805 -498 -365 -145 -84 +63 +129 +142 +249 +407	TGAC	S000447

	Motif	Number	Sequence	AC
Cis- elements in 225 bp- insertion at position - 1035	ABRERATCAL	1	MACGYGB	S000507
	MYCCONSENSUSAT	2	CANNTG	S000407
	DPBFCOREDCDC3	2	ACACNNG	S000292
	MYB1AT	1	WAACCA	S000408

Figure S1

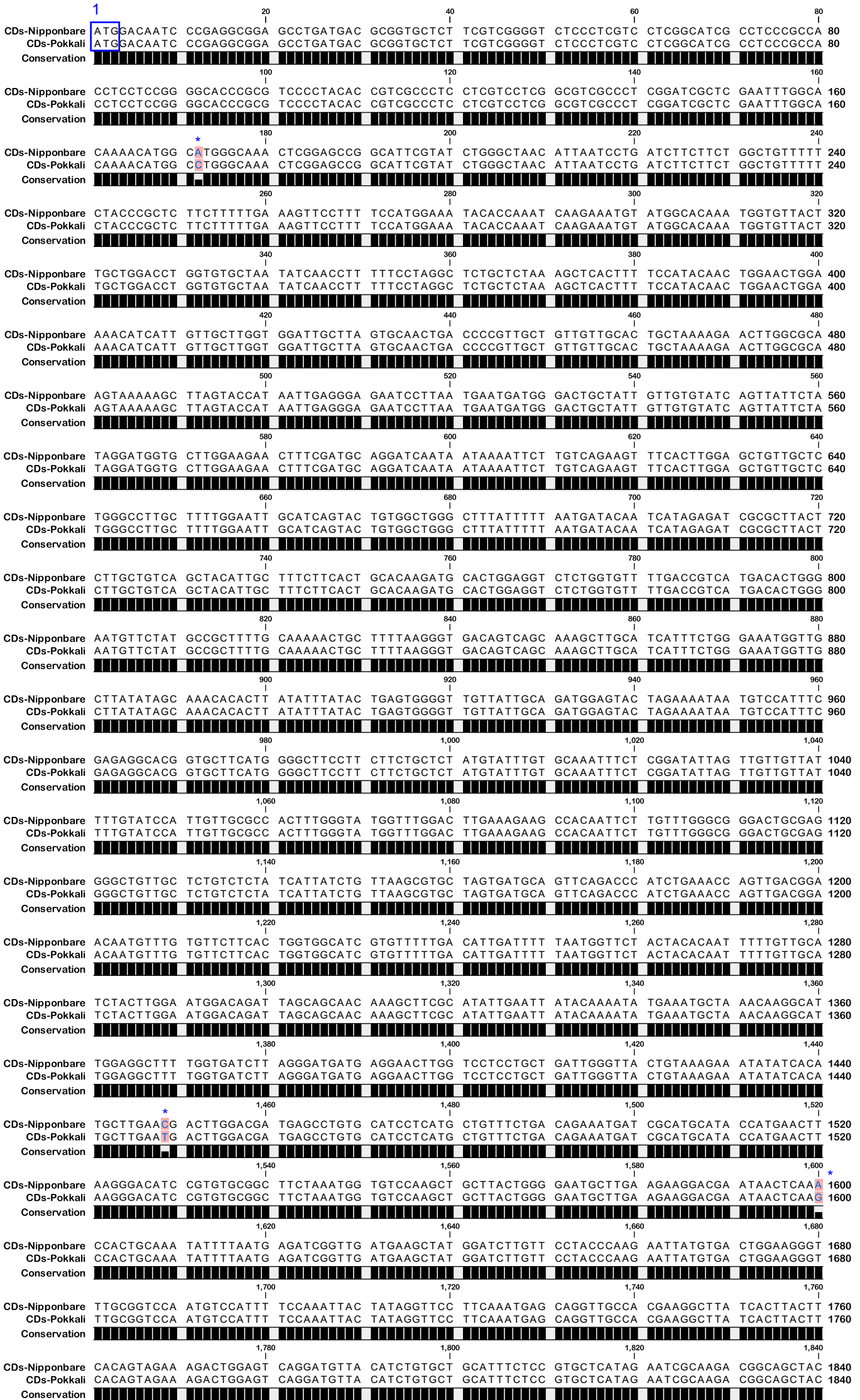


Figure S2

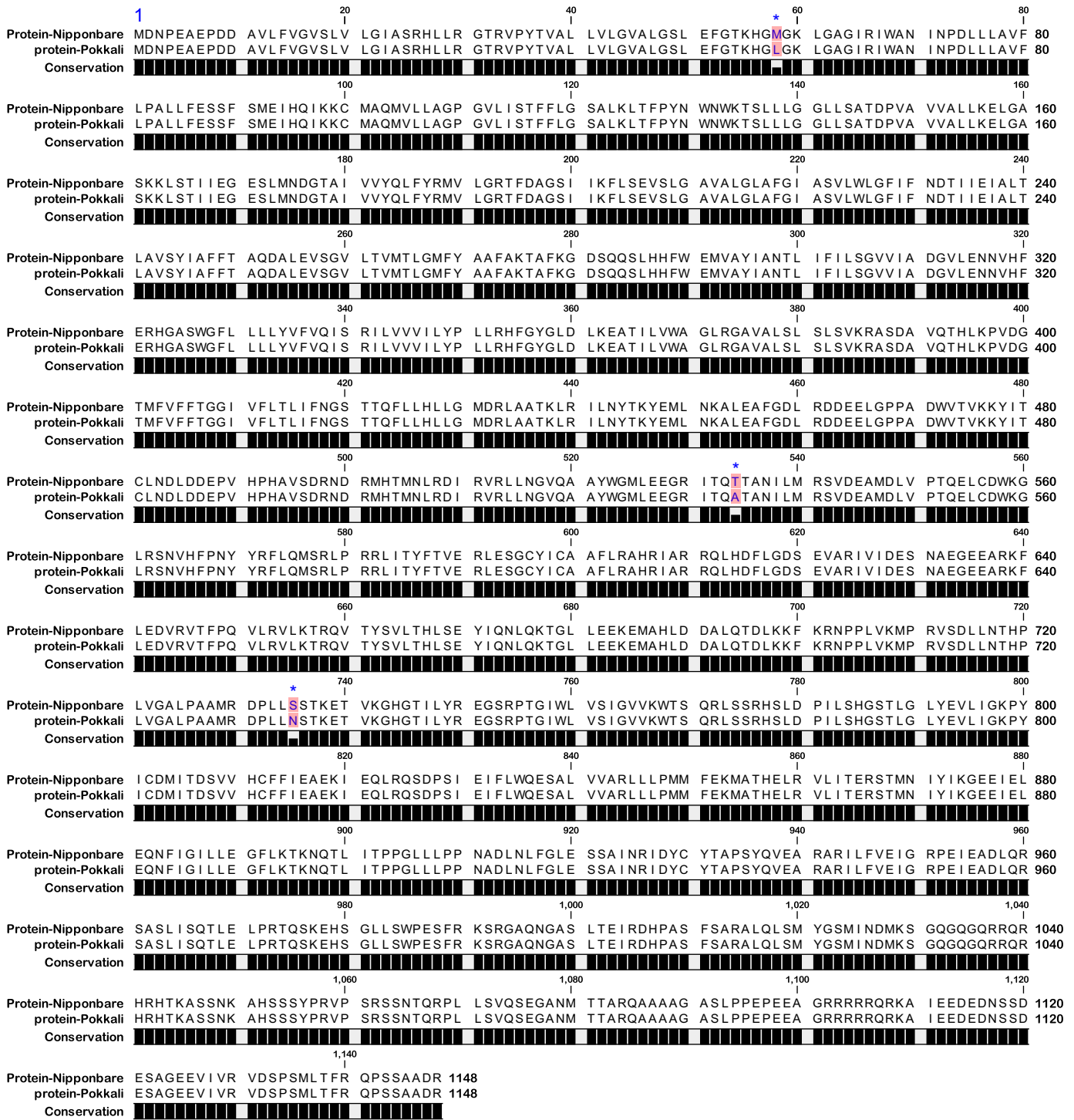
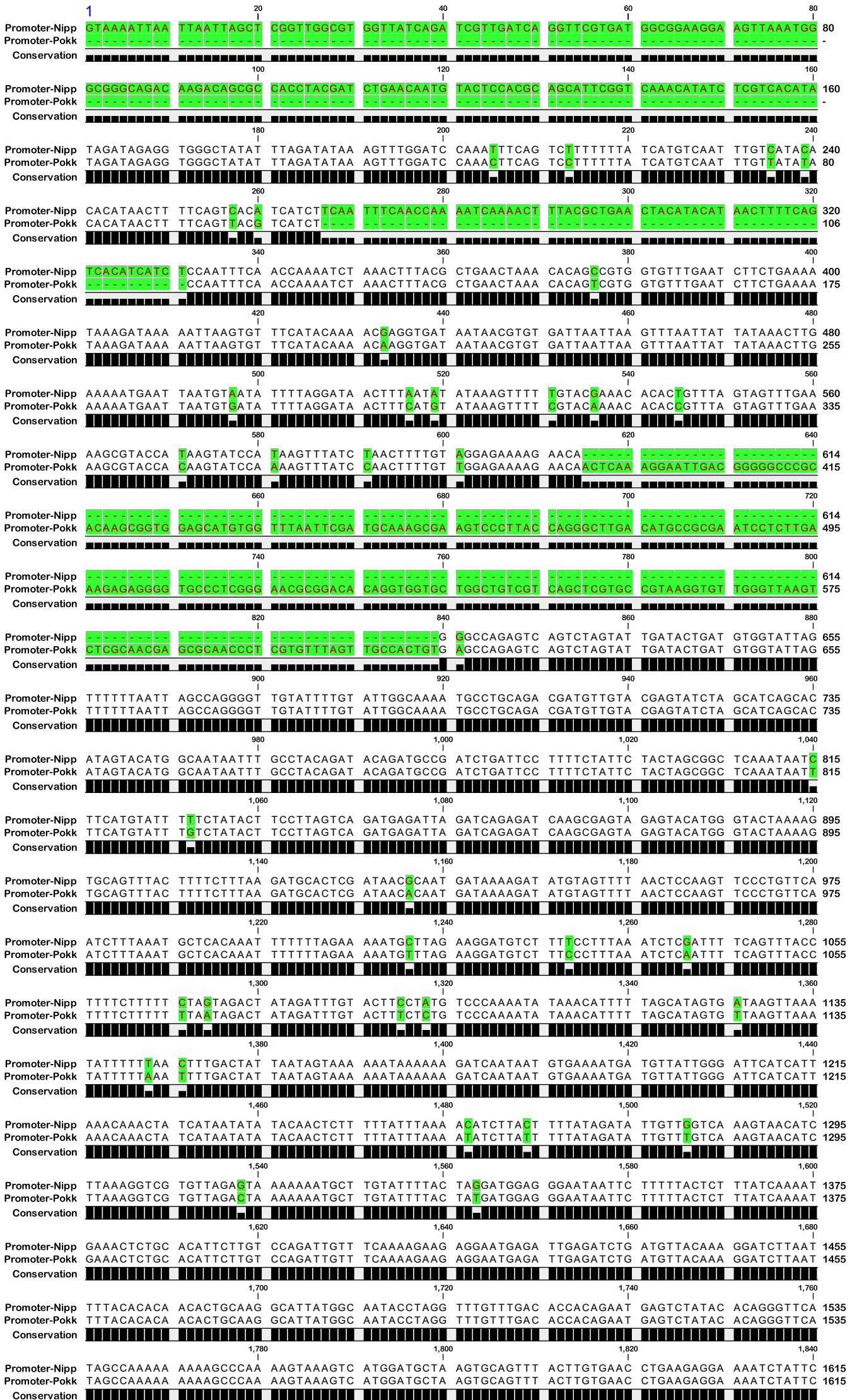


Figure S3



	1,860	1,880	1,900	1,920					
Promoter-Nipp	TCCGTTGTTA	CAAAAGAATC	TTAATTCTAC	GCACAGCACC	ATGTAAAAAC	ATGTAAATTC	AGGCTATCTG	GCCATGCAAT	1695
Promoter-Pokk	TCCGTTGTTA	CAAAAGAATC	TTAATTCTAC	GCACAGCACC	ATGTAAAAAC	ATGTAAATTC	AGGCTATCTG	GCCATGCAAT	1695
Conservation									
	1,940	1,960	1,980	2,000					
Promoter-Nipp	GAATTCATCT	TTCTGACCC	AACAGAAGGC	GTTTCTGCGT	TTGAACTGGA	ATTTTTCATG	GCACATGTAA	AATGAAACAA	1775
Promoter-Pokk	GAATTCATCT	TTCTGACCC	AACAGAAGGC	GTTTCTGCGT	TTGAACTGGA	ATTTTTCATG	GCACATGTAA	AATGAAACAA	1775
Conservation									
	2,020	2,040	2,060	2,080					
Promoter-Nipp	GTCATTAGCA	TAGTGACTTT	TTTTTGCCGA	AAGGTTCCGT	CGAATTGGGT	GTA AAAATCAA	ATGAAAAAAA	AGCAGCTGCT	1855
Promoter-Pokk	GTCATTAGCA	TAGTGACTTT	TTTTTGCCGA	AAGGTTCCGT	CGAATTGGGT	GTA AAAATCAA	ATGAAAAAAA	AGCAGCTGCT	1855
Conservation									
	2,100	2,120	2,140	2,160					
Promoter-Nipp	AACTACAGTG	TGCTGTGCGA	TCGGTACCGA	ACTAGCATAG	TGACTTATTG	AGTAGTAGTA	ATTTGAAAAA	TAAGTCTAGG	1935
Promoter-Pokk	AACTACAGTG	TGCTGTGCGA	TCGGTACCGA	ACTAGCATAG	TGACTTATTG	AGTAGTAGTA	ATTTGAAAAA	TAAGTCTAGG	1935
Conservation									
	2,180	2,200	2,220	2,240					
Promoter-Nipp	ATATTTTAAA	GAAATTTAGC	ATGTTGAAAA	GCATGCTCAT	TATAAATGAG	AGGATGGTTG	TAGCTGCTGT	GCACCCAT	2015
Promoter-Pokk	ATATTTTAAA	GAAATTTAGC	ATGTTGAAAA	GCATGCTCAT	TATAAATGAG	AGGATGGTTG	TAGCTGCTGT	GCACCCAT	2015
Conservation									
	2,260	2,280	2,300	2,320					
Promoter-Nipp	AGGATCCAAT	CAAAGAAAAA	GAGAAAAAGG	GGTGACAAAA	CAACAAGTCA	AAACAAAAGG	AAAGGGAGCT	CAAGTGAGGA	2095
Promoter-Pokk	AGGATCCAAT	CAAAGAAAAA	GAGAAAAAGG	GGTGACAAAA	CAACAAGTCA	AAACAAAAGG	AAAGGGAGCT	CAAGTGAGGA	2095
Conservation									
	2,340	2,360	2,380	2,400					
Promoter-Nipp	GGCTGCTGCA	TCTTCTTCTT	CTTCTCCCT	TTGCCTTGGG	TTTTCCACTT	GCATTGCAC	TTCCTCCTCC	TCATCAGTAA	2175
Promoter-Pokk	GGCTGCTGCA	TCTTCTTCTT	CTTCTCCCT	TTGCCTTGGG	TTTTCCACTT	GCATTGCAC	TTCCTCCTCC	TCATCAGTAA	2175
Conservation									
	Start codon								
Promoter-Nipp	TCCATG	2181							
Promoter-Pokk	TCCATG	2181							
Conservation									