

File S1

Amplified potato genomic fragments including SNP positions, nucleotide alleles and identifications.

Sequences were retrieved from pseudomolecules (v4.03) at <http://potato.plantbiology.msu.edu/cgi-bin/gbrowse/potato/>. Primer sequences are underlined. SNP numbering starts with A = 1 in the ATG initiation codon in the genomic locus PGSC0003DMG*****.

1. Glucan water dikinase, GWD (PGSC0003DMG400007677)

chr05:9827209..9827979

ATAAAAGTCAAAGCAAAGAAGAGCCTCTTCATGTAACAAAGAGTGAAATACCTGATGACCTTGCCCAAGCACAAAGCTTACATT
AGGTGGGAGAAAAGCAGGAAAGCCGAACTATCCTCCAGAAAA
3058 3072 3089
GCAAATTGTAAATGCTGAAC (T / C) TTTCTTACAGTTT (A / T) TGTAGTGTGTGTATAT (G /
3092 3104 3113
C) TC (T / C) AGGCGCATAAA (T / G) CTGGGTAT (T / G) CTGTCTTCTATAGATGTGAGACTT
3145
TGATCAA (G / A) CATTGTTTTATTAAACAGGAAGAAGCTCGAAGAAGCAAGAAGAGAATTGCAA
3246
CTTGAGCTTGAGAAAAGCATTACCCTTGATGAGTTGCGGAAAAAGATTAC (A / C) AAAGGGG
3259 3269 3280 3281 3291
AGATA (A / G) AAATAAGG (C / T) GGAAAAGCAC (G / C) (T / A / C) GAAAAGAAG (C / T) TC
3298 3339
TTTT (G / T) CCGTTGAAAGAATCCAAAGAAAGAAGAGACTTTGGGCA (G / T) CTTATTAA
3355 3372 3389
TAAGTAT (C / A) CTTCCAGTCTGCAGT (A / G) CAAGTACAAAAGGTCT (/ C) GGAAGAAC
3400 3419 3421
CA (C / G) CAGCCTTATCTAAAATTA (A / G) G (C / A) TGTATGCCAAGGAGAAGGAGGAGCAG
3452 3465 3469 3487
ATTG (A / G) TGATCCGATCCT (A / T) AAT (G / A) AAAAGATCTTTAAGGTC (G / A) ATGATG
3504 3550
GGGAGCTACT (G / T) GTGAGTGCTAACTTATTCTTGACTGTAACCTAATCTCAGAAGC (T
3558 3600
/ A) AGTTTGA (A / G) TGCATATTGAGAATCTTCCATTGTCTCCACATTTTAAGGTA (C / G) T
3606
GGTA (G / T) CAAAGTCCTCTGGGAAGACAAAAGTACATCTAGCTACAGATCTGAATCAGCCAATTACTCTTCACTGGGCATTA
TCC

2. Phosphoglucan water dikinase, PWD (PGSC0003DMG400016613)

chr09:60571111..60571981

GGTCTGATGATCTATCTGATTGCAGTTTATAGTGACCAAGGTGCACCAGCATCATTAAACGT
10503 10543 10547
TCCTGC[A/T]GGAGCAGTTATTCCATTTGGTTCCATGGAAACGGCATTG[G/A]AAA[T/C
10576
]GAACAAGTTAATGGAGACCTTCACATTC[C/T]TTGTGCGAACAGATAGAAACAGCTGAAAT
10629 10657
TGATGGCGGTGAACTTGATAACA[T/C]TGTGAGGATCTCCAGAAGTTAATATCT[T/A]C
10689 10700 10701
TCTATTGCCTGGACAAGATGTCATTGAAAAG[C/G]TTGGGAGAAG[T/C][A/G]TTTCCCG
10746 10758
GTAATGCACGTTTAAATAGTGCCTTCAAGTGCTAATGT[C/T]GAGGACTTGGC[G/A]GG[G
10761 10770 10773
/A]ATGTCAGC[T/A]GC[T/C]GGACTTTATGATTCAATTCCTAATGTTAGCCCTTCAGAT
10815
CC[G/A]ATAAGGTTTGGACATGCTGTAGCCCGTGTGGGCCTCGTTGTATACTAGAAGAG
10911 10916 10917
CAGTACTGAGCCGCAGAGCTGCTGGTGTGTCCCAGAAAAGA[C/T]GCTA[C/A][A/G]ATG
10923 10932 10962
GC[C/T]GTGCTAGT[G/T]CAAGAAATGCTTTCACCAGATTTATCTTT[C/T]GTCCTCCA
11022
CACACTGAGCCCAACGGACAACAATCATAACTTCATTGAGGCTGAAATTGC[A/T]CCTGGA
11064
CTCGGTGAAACACTCGCTTCAGGAACAAGGGGTAC[A/T]CCGTGGCGTCTATCTAGTGGTA
11112 11218
AATTTGACGACACAGTGCACACT[G/A]GCATT[C/T]GCCAACTTTAGTGAGGAGATG[
11140 11148 11151 11152
G/A]TTGTAGG[T/A]GG[C/T][A/C]ATCCCCCTGCTGACGGAGAAGTTATTCTCTTACTGTGCGATTATAGCAAGAAACC
TTTACAATCGACCCATTTTCAGACGTCAGCTTGGTCAGAGGCTTGGCGCTGTTGGTTTCTACCTAGAACGCAAGTTTGGTT
CTCCTCAAGATGTCG

3. Beta amylase 1, *AMY1* (PGSC0003DMG400001855)

Chr08:50594548..50595107

GCTACTGGAGCATGGTGACAGAATAGTAGCAGCAGGAGAAAGTATATACCAAGGAACTGGGGCTAAACTATCTGGAAAGGTAG
CTGGGATTCATTGGCATTACAATACTAGATCACATGCTGCA
2533
GAGTAACTTCAGGATATTATAATACAAGACACAGA (G/A) ATGGTTATCTACCTATAGCAC
2565 2576 2583
GTATGTTAGC (G/A) AAACATGGTG (C/T) TGTACT (T/G) AACTTTACATGTATGGAAATG
2613 2625 2649
AGGGATGG (T/G) GAACAGCCCCA (G/A) AGTGCAAAGTTCACCAGAAGG (C/A) TTAGT
2657 2671 2686 2694
TC (A/G) ACAAGTTAAACT (G/A) CAGCTAGAAGTCT (A/G) AAGTAGA (A/G) CTTGCT
2751
GGAGAAAATGCTCTAGAAAAGGTATGATGGAGGAGCATTTTCTCAAGTTTT (G/A) GCAACAA
2767 2811
GCATGTCA (A/G) ATTCTGGAAATGGATTGAGTGCATTTACATTCCTTGCGAATGAA (C/T) AAACGGTTGTTTGAGCCAGAAA
ATTGGCGGAATCTAGTGCAATTTGTGAAGAGCATGTCTGAAGGAGGTCGAAATGCTAGCCTTCCAGAGTGTGACTCAAGCAGG
ACAGACCTCTATGTAA

4. Starch phosphorylase, chloroplastic/amyloplastic, *PHO1b* (PGSC0003DMG400028382)

Chr05:350160..351337

TGTTGCAAGAAAAGCTAAACCAAATGAGGATTCGGATAATGTTGAAATACCAACTTCTGTTTTGGAGTTGCTTATAAAAGCC
GAAGAAAATGCTGCTGATGTCTGAAAAAGCAGCAGATGAAGAACAAGAAGAAGGTAAGGATGACAGTAAAGATGAGGAAAC
TGAGGCTGTAAGGCAGAAACTACGAACGAAGAGGAGGAAACTGAGGTTAAGAAGGTTGAGGTGGAGGATAGTCAAGCAAAAA
TAAACGTATATTTGGGCCACATCCAAATAAATCACAGGTGGTTCACATGGCAAATCTATGTGTAGTTAGCGGGCATGCAGTT
AACGGTGTGCTGAGATTCATAGTGAATAGTTAAAGATGAAGTTTTCAATGAATTTACAAGGTACGATGATTATCACACGG
CTAGAAGTGGCAGATATCA

3882
TTTTCAGTTCTCCTCTTTCAATGTTGTGTTTTGATTGATCCAAACTCTTTGTTTC (A/C) TC
3931 3934
GACAGTTATGGCCAGAGAAAATCCAAAAACAAGACAAATGGTGTGAC (A/G) CC (A/T) AGAA
3958 3982 3990
GATGGCTAAGTTTTCTGTAA (T/C) CCAGAGTTGAGTGAAATTATAAC (A/C) AAGTGG (C/
4018 4038
T) AGGATCTGATGATTGGTTAGTAAACAC (T/A) GAAAAATTGGCAGAGCTTC (G/A) AAAG
4049 4052 4076 4088
GTAAAC (G/A) AG (T/C/G) TGTATCTGACTGTGATCTTATT (G/A) ATTCCTAAACC (G/A
4106 4109 4112 4122
) TCGTCAACAGCTTTCAT (A/G) AA (C/G/A) GG (A/G) TTATTTCCCT (T/C) TAGTCCTTC
4181
TATGTGGAAGAGATCTTTATAAACATCATAAGAACATGTGAAATGTAT (G/A) TACTAA (C
4188 4198 4206 4207
) TTCATGCAT (T/G) TAACTGT (T/C/G) (G/T/A) AACAGTTTGCTGATAACGAAGAAC
4236 4248 4258
TCCA (G/A) TCTGAGTGGAG (G/A) AAGGCAAAA (G/A) GAAATAACAAAATGAAGATTGTC
4302 4319 4320
TCTCTCATTAAAGAAAAAAC (A/T) GGATACGTGGTCAGTC (C/G) (C/T) GATGCAATGTT
4350 4356 4365
TGATGTTGAGATCAAGCG (C/T) ATCCA (T/C) GAGTATAA (A/G) AGGCAGCTATTAATA
4383 4389 4404 4407 4413
T (A/T) TTTGG (A/T) ATCGTTTATCGCTA (T/C) AA (G/A) AAGAT (G/T) AAAGAAATGA
4431 4457 4437
GCCCTGA (A/T) GAACGAAAAGAAAAGTTTGTCCCTC (G/A) AGTTTGCATATTTGG (G/A) GGAAAAGCATTTGCTACATAT
GTTTCAGGCCAAGAGAATTGTAATAATTATCACTGATGTAGGGGCAACAGTCAACCATGATCCCGAGATTGGTGATC

5. Soluble starch synthase I, *SssI* (PGSC0003DMG402018552)

Chr03:45608638..45609659

GGATACTCATGGGAAATAACAACCTCCTGAAGGGGGATATGGGCTACATGAGCTGTTGAGCAGTAGACAGTCTGTTCTTAATGG
TATGCGTGTTAGATGATTCTTATGAGTGCTTTCTGATATTCTTCTTTCTCTTACTCGAATTGTAATTTGGTAGGATATAT
GTTGATTGACGAGGCTTATGTACCAGCATTAGCTTCATTTCTAGTCAAGTCTTAACCTTTGTTAAAACATGACCAGAGCCAAG
GCTAATTGTATTAATGACCTTACCATGCATTTCTGTGTCTCTGAACCTTTAGAAATTACTAGTTAATCTATCTCTACTTTTA
TGCAGGAATTACTAATGGAATAGATGTTAATGATTGGAACCCGTGACAGATGAGCATATTGCTTCGCATTAATCCATCAATG
ACCTCTCCGGAAAGGTTATTAACCTTCTCAGTTTCACAATTTGCAAATTAAGTGATAAAAGTGCAGCTAGAGAAAAGGACTAT
TAGCATATTTGGCCAATCTTCCATAAAATTGCTTATTTTGGGAAGTGTTTTTTATTAGAAGTACTTTTGGAGAATAGTAGTTTG
TATTTGGCTAATCAATTTGAAAAAAGCCTTTGTCAATATTAGAGCAGTAATTTGTGCTTGACAAAGGTTCCAATAGTGCTTC
GAGGGGAAAAGCTATTTT

5803

TTTCTTCCAACCTCAGCTACTACTCAAAGTCAAAGCAC (**indela**) GCTTGGCTGAACAG

5824 5839 5850 5858

ACAATA (C/T) GTCTACAAAAGCTT (C/A/T) TTAAGTGTG (C/T) GAAATTC (A/G) ATC

5871 5877 5880

CAAATGAGG (A/G) TTCCT (C/T) TA (G/A) AGGATTGTCCATAATCCATTAAGGGAACA

5964

GTCCAAAGGATATCATAGCATTACTTCTTTTCATGTTTATTCTACATGCA (G/A) TTGTG

6001 6010

CACAACTCTCTTTTCTCTGTTCTCTACAT (A/G) CCACTGCT (C/T) AAATTGTCTCTGCTAACTTTCCATTTAATTATAC

AGGTTCAAGTGAAGACTGATCTGCAAAAGGAAGTGGGCCTTCCAATTCGACCTGATTG

6. Phosphoglucomutase, *PGM-3* (not annotated)

Chr03:41510113..41509054

ATGGCTATGGAGAGTGCATTGACATCCACACGAGTTTCAATTCCATCGTTGTGTTCTGGGAT
93
CAGTTCATCTCATCATCACCATAGATCCTT [C / A / T] TCATTTCTCAATTTCCCAAATTGT
125
CTTCAT (T / G) CAAATACTCTTTTTCGAACAATTTACCTGTTCCTTTCGTTGTGTCAGTGCATCCTCTGTTTCTCCATCATCTCC
TTCTACATCTGTTGCCCAATCTCAGGATCTCAAGGTATCTA
241 242 254
AT (T / A / C) (G / A) CTTCCAAATAT (C / T) ACTATATAACGTGTATATTTTTATGTGATTTA
320 339
ATGGAAAATTTGATTTACTTGAATGCCAGATTA (A / T) ATCAGTTCCTACCAAGCC (T / A) ATTGAAGGTCAAAGACCGGTA
CCAGTGGTCTACGCAAAAAGGTGCCTTTTCTTTTGGTTTTA
408 409 410 411 413 440
TTAAA (A / T) (T / A) (T / A) (T / A) T (A / T) CACTTTGTTTGGATGATTGTTACCCG (C / T)
467 468
TGTATTGTATTGTTAGTTCAAATACG (A / G) (T / C) GTTTATTTTGATTGTTATATAAAATTTGTTGTTTAGTATCATTTAAAT
TCATTTTCATTGTTAGCTACAAAAAGTCCCATTTTGTGTAAGGACCAATTTGGTGTGATTGCCTTGGTTACTTTTAAATATTTT
CTTCTCATTTATCACATTTTAAATGTTTATCCTTTACCCTATTTTTTCGTTAGTAGCTACATCCCCTGCCTTACTTTTCTCGTA
GGCTTATCAGACATATCGCAATGACGAGAAATGATACAATCTATCCAAATGTTGTATTATTAAAAATAATATTGTACGATACA
ATACAACACAATATGATACATAATGAAATAATACATAACAGCCCTCCAAGCAGAGTGAACCTCCGCTGCGTGAAGGTGTGCCA
AAATAAATAGGAAAACCTCTCTACCCTTAAGGTAGGGTTAAGGCTGCGTATATTTTACCTTCCTCAGACCTCACTTGTGCGA
TTACTGTTTGTATTGTTGTTGGTTTATTAATTTTATTGCTTACTGTTTCAATTTGGATGACTTCTGCTTCTTTTGTCT
ATAGGTTAAAGTGTATTATGCAGGACAATTACCTTGCCAATTGGATAC

7. ADP-glucose pyrophosphorylase S, *AGPaseS* (PGSC0003DMG40000735)

Chr01: 86095512..86094580

GGAGATGGATTGTGTCGAGGTTTGAGACTATACTTTTGAATTCTTGAAGGAACTGGATTAGTCTTGCTAGATATCACAGCTG
AGCTAATTAATATGAGTAAATTTGTTGGTCCTCCAAGTGAT

1259 1265
TTGTTACACAAAATCTGTAACAATTCGGATGATTTTTTTCATTGTT (T/C) TTCTG (A/C
1268 1276 1284 1286
) TT (A/T) CTTGCTT (C/A) GTTTTAC (T/C) G (A/G) CTGAAAGGAATTCGTCATTAAAC
1336 1348
AGGTACTAGCTGCAACTCAGACACC (C/T) GGGGAAGCAGG (A/G) AAAAAATGGTTTCAAG
1392 1411
GAACAGCAGATGCTGTTAGAAAATTTA (T/C) ATGGGTTTTTGAGGTTTGT (C/T) TCTACA
1426 1456 1457 1459
ACTCTTTA (A/G) GACACACTAATCCACCACTGCTCTTCTGT (T/C) (G/) A (C/) CTGATA
1482 1501 1509
TAATTTCTGAAAAATG (A/T) TTCATTATTTTTTCCTGA (T/A) TCAGTTA (G/) TATGTAC
1520 1529 1546 1547
AGA (T/C) ATATAGTA (C/T) TTTTGTGTTTACAAGG (T/C) (G/A) ACCAATTCCTGCAGG
1564 1592 1612
A (C/T) GCTAAGAACAAGAATATTGAAAATATC (G/C) TTGTACTATCTGGGGATCA (T/C) CTTTATAGGATGGATTATATG
GAGTTGGTGCAGGTATGTCCACTTTAACTACCTATGCACTC
1689
CTCATCTTTGTTT (A/G) CTTTTTTTTTTTTTTTTTTTTTAAACAACAAGTTTCTGACTGCCTCCGATCTTCAAACAGAACCA
TATTGACAGGAATGCTGATTA TACTCTTTCATGTGCACCAGCTGAGGACAGGTTTGTTTAAATTC CAATAAGAAACA ACTAGT
AATGGTTAAGTGAATTGAGTGAGATCAGAAACAATATGGAGAAAGAGTGCTTCTCCTTTAATATT CGTATGCATTACTTCGAA
GTA AAAACATCACCACATTTCTTTATACCTTATTGTGATTATGTTAAGCTGAGATTTAAGCTTTACTTATCAGCCGAGCATCA
GATTTGGGCTGGTCA

8. Invertase, *INV-8/2* (PGSC0003DMG400004790)

Chr08:52703547..52704642

GTTCTCATCCCACCACCCGGAATTGGGCTCAAGGACTTCCGTGACCCCACCACCGCGTGGACCACACCGGAAGGCAAATGGCG
TATTACTATTGGTTCAAAGATTAATAAAAACCGGAATCTCAT

2065 2075 2076
TGGTCTATGACACAATTGATTTTAAAAAATTTGAATT[G/A]TTGAAGGT[G/A][C/T]G
2116
TTACATGGTGTACCGGGTACGGGTATGTGGGAATGTGT[G/A]GATTTTACCCGGTTTC[T
2134 2175 2182
/G]AAAATTGTTGAAAATGGGCTTGACACTTCAGAAAATGGGC[C/A]TGCAGT[G/A]AAA
2197
CATGTTTTGAA[G/A]TCCAGTCTTGACGATGATCGAAAATGACTATTATGCCCTTGGAACCTT
2255 2272
ATGATGCAGGG[G/A]CAGGAAAATGGGTACC[T/A]GATAATCCAATAATTGATGTTGGTA
2302 2320
TTGG[G/A]TTAAGATATGATTATGG[T/C]AATTTTATGCATCAAAAACATTTTATGATC
2369 2371
AAGAAAAAAGAGAAGA[G/A]T[T/A]CTTTGGGCTTGGATTAAAGAACTGATAGTGAAG
2425
CTGCTGATATTTGCAGGG[T/C]TTGGGCCTCACTTCAGGTATCTCTTTTTTAGCGTATCATTTAGATTTGTCCTTATTTTT
AAAAGTCGTGCAAGTAGATACATAATTTGAAGTGTGACAAGTAATCAAAAATCAGACAATGACAGAACGGCCTATGATTAAGA
ACTAAAACTAAAACCTTTATACAACCTTTTACAATTCATTGAACAAAATGGTAACGTGTGATTTTTTATTATTTTATTTTCGAAA
ACAGTCAATTTCCAAGAACTATAAAGTATGATAAGAAGACAGGAAGCAACATAATTACATGGCCAGTGGCTGAGGTAGAGAATT
TGAGATCAAACAACAATGAATTCACAAGGTTGTAGTTAAACAGGTTCAATTGTCCCACTAGAAAGTTGGTTCTGCCACTCAG
GTTAGTACATTTTGTGCGATTAAATTCAACTTATATACATTGACAATATATATACTTATATCGTTGAATTATTGTTACAGTTGG
ACATAATGGCTGAATTTGAAATAGACCAAAATGTGTTGAAGAAAGTAGATGGAAGTAATGCTACATATGATTGTATAAAGAGT
GGTGGATCTGGTGAACG