

SNPs in genes functional in starch-sugar interconversion associate with natural variation of tuber starch and sugar content of potato (*Solanum tuberosum* L).

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*           2620           *           2640           *           2660           *           2680           *           2700
Pho1a-HR : TTTTGAAGAGGTGAAGGAATTTGTTAGAAGCGGTGCTTTTGGCTCTTATAACTATGATGACCTAATTGGATCGTTGGAAGGAAATGAAGGTTTGGCCGT : 2700
Pho1a(2) : TTTTGAAGAGGTGAAGGAATTTGTTAGAAGCGGTGCTTTTGGCTCTTATAACTATGATGACCTAATTGGATCGTTGGAAGGAAATGAAGGTTTGGCCGT : 2700
Pho1a(3) : TTTTGAAGAGGTGAAGGAATTTGTTAGAAGCGGTGCTTTTGGCTCTTATAACTATGATGACCTAATTGGATCGTTGGAAGGAAATGAAGGTTTGGCCGT : 2700
Pho1a(4) : TTTTGAAGAGGTGAAGGAATTTGTTAGAAGCGGTGCTTTTGGCTCTTATAACTATGATGACCTAATTGGATCGTTGGAAGGAAATGAAGGTTTGGCCGT : 2700
Pho1a-HA : TTTTGAAGAGGTGAAGGAATTTGTTAGAAGCGGTGCTTTTGGCTCTTATAACTATGATGACCTAATTGGATCGTTGGAAGGAAATGAAGGTTTGGCCGT : 2700
Pho1a(6) : TTTTGAAGAGGTGAAGGAATTTGTTAGAAGCGGTGCTTTTGGCTCTTATAACTATGATGACCTAATTGGATCGTTGGAAGGAAATGAAGGTTTGGCCGT : 2700
Pho1a(7) : TTTTGAAGAGGTGAAGGAATTTGTTAGAAGCGGTGCTTTTGGCTCTTATAACTATGATGACCTAATTGGATCGTTGGAAGGAAATGAAGGTTTGGCCGT : 2700
Pho1a(8) : TTTTGAAGAGGTGAAGGAATTTGTTAGAAGCGGTGCTTTTGGCTCTTATAACTATGATGACCTAATTGGATCGTTGGAAGGAAATGAAGGTTTGGCCGT : 2700
Pho1a(9) : TTTTGAAGAGGTGAAGGAATTTGTTAGAAGCGGTGCTTTTGGCTCTTATAACTATGATGACCTAATTGGATCGTTGGAAGGAAATGAAGGTTTGGCCGT : 2700

*           2720           *           2740           *           2760           *           2780           *           2800
Pho1a-HR : GCTGACTATTTCCCTTGTGGGCAAGGACTTCCCCAGTTACATAGAATGCCAAGAGAAAAGTTGATGAGGCATATCGCGACCAGAAAAGGTGGACAAAGATGT : 2800
Pho1a(2) : GCTGACTATTTCCCTTGTGGGCAAGGACTTCCCCAGTTACATAGAATGCCAAGAGAAAAGTTGATGAGGCATATCGCGACCAGAAAAGGTGGACAAAGATGT : 2800
Pho1a(3) : GCTGACTATTTCCCTTGTGGGCAAGGACTTCCCCAGTTACATAGAATGCCAAGAGAAAAGTTGATGAGGCATATCGCGACCAGAAAAGGTGGACAAAGATGT : 2800
Pho1a(4) : GCTGACTATTTCCCTTGTGGGCAAGGACTTCCCCAGTTACATAGAATGCCAAGAGAAAAGTTGATGAGGCATATCGCGACCAGAAAAGGTGGACAAAGATGT : 2800
Pho1a-HA : GCTGACTATTTCCCTTGTGGGCAAGGACTTCCCCAGTTACATAGAATGCCAAGAGAAAAGTTGATGAGGCATATCGCGACCAGAAAAGGTGGACAAAGATGT : 2800
Pho1a(6) : GCTGACTATTTCCCTTGTGGGCAAGGACTTCCCCAGTTACATAGAATGCCAAGAGAAAAGTTGATGAGGCATATCGCGACCAGAAAAGGTGGACAAAGATGT : 2800
Pho1a(7) : GCTGACTATTTCCCTTGTGGGCAAGGACTTCCCCAGTTACATAGAATGCCAAGAGAAAAGTTGATGAGGCATATCGCGACCAGAAAAGGTGGACAAAGATGT : 2800
Pho1a(8) : GCTGACTATTTCCCTTGTGGGCAAGGACTTCCCCAGTTACATAGAATGCCAAGAGAAAAGTTGATGAGGCATATCGCGACCAGAAAAGGTGGACAAAGATGT : 2800
Pho1a(9) : GCTGACTATTTCCCTTGTGGGCAAGGACTTCCCCAGTTACATAGAATGCCAAGAGAAAAGTTGATGAGGCATATCGCGACCAGAAAAGGTGGACAAAGATGT : 2800

*           2820           *           2840           *           2860           *           2880           *           2900
Pho1a-HR : CAATCTTGAATACAGCGGGATCGTACAAGTTCAGCAGTGACAGAACAAATCCATGAATATGCCAAAGACATTTGGAACATTGAAAGCTGTGGAATAGCATA : 2900
Pho1a(2) : CAATCTTGAATACAGCGGGATCGTACAAGTTCAGCAGTGACAGAACAAATCCATGAATATGCCAAAGACATTTGGAACATTGAAAGCTGTGGAATAGCATA : 2900
Pho1a(3) : CAATCTTGAATACAGCGGGATCGTACAAGTTCAGCAGTGACAGAACAAATCCATGAATATGCCAAAGACATTTGGAACATTGAAAGCTGTGGAATAGCATA : 2900
Pho1a(4) : CAATCTTGAATACAGCGGGATCGTACAAGTTCAGCAGTGACAGAACAAATCCATGAATATGCCAAAGACATTTGGAACATTGAAAGCTGTGGAATAGCATA : 2900
Pho1a-HA : CAATCTTGAATACAGCGGGATCGTACAAGTTCAGCAGTGACAGAACAAATCCATGAATATGCCAAAGACATTTGGAACATTGAAAGCTGTGGAATAGCATA : 2900
Pho1a(6) : CAATCTTGAATACAGCGGGATCGTACAAGTTCAGCAGTGACAGAACAAATCCATGAATATGCCAAAGACATTTGGAACATTGAAAGCTGTGGAATAGCATA : 2900
Pho1a(7) : CAATCTTGAATACAGCGGGATCGTACAAGTTCAGCAGTGACAGAACAAATCCATGAATATGCCAAAGACATTTGGAACATTGAAAGCTGTGGAATAGCATA : 2900
Pho1a(8) : CAATCTTGAATACAGCGGGATCGTACAAGTTCAGCAGTGACAGAACAAATCCATGAATATGCCAAAGACATTTGGAACATTGAAAGCTGTGGAATAGCATA : 2900
Pho1a(9) : CAATCTTGAATACAGCGGGATCGTACAAGTTCAGCAGTGACAGAACAAATCCATGAATATGCCAAAGACATTTGGAACATTGAAAGCTGTGGAATAGCATA : 2900

Pho1a-HR : A : 2901
Pho1a(2) : A : 2901
Pho1a(3) : A : 2901
Pho1a(4) : A : 2901
Pho1a-HA : A : 2901
Pho1a(6) : A : 2901
Pho1a(7) : A : 2901
Pho1a(8) : A : 2901
Pho1a(9) : A : 2901

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Figure S1 Sequence alignment of nine Pho1a cDNA alleles.

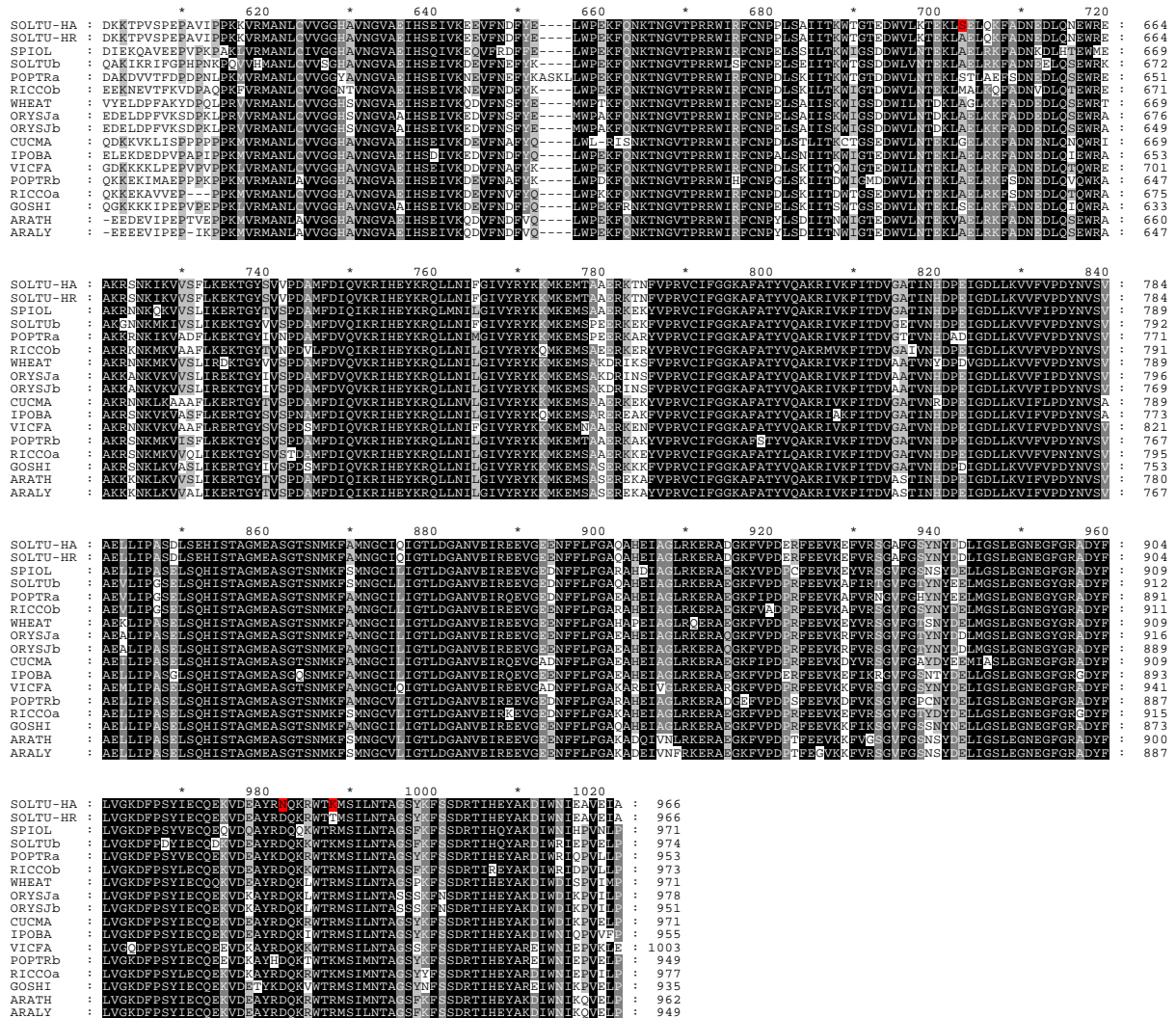


Figure S2 Alignment of plant Pho1a deduced protein sequences. *Solanum tuberosum*: SOLTU-HA (Pho1a-H_A, this paper), SOLTU-HR (P04045); *Spinacea oleracea*: SPIOL (O24363); *Populus trichocarpa*: POPTRa (B9HXLO), POPTRb (B9H0D3); *Ricinus communis*: RICOOb (B9SJB6); RICOCo (B9RCW0); *Triticum aestivum*: WHEAT (B2LXU4); *Oryza sativa ssp. japonica*: ORYSJa (B3IYE3), ORYSJb (Q9AUX8); *Cucurbita maxima*: CUCMA (B2DG13); *Ipomea batatas*: IPOBA (P27598); *Vicia faba*: VICFA (P53536); *Gossypium hirsutum*: GOSHI (D2D337); *Arabidopsis thaliana*: ARATH (Q9LIB2); *Arabidopsis lyrata*: ARALY (D7LNX4). The six amino acid changes in Pho1a-H_A versus Pho1a-H_R are highlighted red.

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]TTGTCGAACAGATAGAAACAGCTGAAAT
10629 10657
TGATGGCGGTGAACCTTGATAACA[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
AATTGACGACACAGTGCACACT[G/A]GCATT[C/T]GCCAACTTTAGTGAGGAGATG[
11140 11148 11151 11152
G/A]TTGTAGG[T/A]GG[C/T][A/C]ATCCCCCTGCTGACGGAGAAGTTATTCTCTTGACTGTGATTATAGCAAGAAACC
TTTACAATCGACCCATTTTCAGACGTCAGCTTGGTCAGAGGCTTGGCGCTGTTGGTTTCTACCTAGAACGCAAGTTTGGTT
CTCCTCAAGATGTCG

3. Beta amylase 1, *BMY1* (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) AGTGCAAACCTGTTCCACCAGAAGG (C/A) TTAGT
2657 2671 2686 2694
TC (A/G) ACAAGTTAAACT (G/A) CAGCTAGAAGCT (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
TGAGGCTGTAAAGGCAGAAACTACGAACGAAGAGGAGGAAACTGAGGTTAAGAAGGTTGAGGTGGAGGATAGTCAAGCAAAAA
TAAAACGTATATTTGGGCCACATCCAAATAAATCACAGGTGGTTCACATGGCAAATCTATGTGTAGTTAGCGGGCATGCAGTT
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
TATGTGAAAGAGATCTTTATAAACATCATAAGAACATGTGAAATGTAT (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) AGGCAGCTATTAAATA
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
TATGCGTGTTAGATGATTCCCTTATGAGTGCTTTCTGATATTCTTCTTTCCCTCTTACTCGAATTGTAATTTGGTAGGATATAT
GTTGATTGACGAGGCTTATGTACCAGCATTAGCTTCATTTCTAGTCAAGTCCTAACTTTTGTAAAACATGACCAGAGCCAAG
GCTAATTGTATTAATGACCTTCACCATGCATTTCTGTGTCTCTGAACCTTAGAAATTACTAGTTAATCTATCTCTACTTTTA
TGCAGGAATTACTAATGGAATAGATGTTAATGATTGGAACCCGTCGACAGATGAGCATATTGCTTCGCATTAATCCATCAATG
ACCTCTCCGGAAAGGTTATTAAACTTCTCAGTTTCACAATTTGCAAATTAAGTGATAAAGTGCAGCTAGAGAAAAGGACTAT
TAGCATATTTGGCCAATCTTCATAAAATTGCTTATTTTGGGAAGTGTTTTTTATTAGAAGTACTTTTGGAGAATAGTAGTTTG
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

GTCCAAAGGATATCATAGCATTACTTACTTTTCATGTTTATTCTACATGCA (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) CAAATACTCTTTTCGAACAATTTACCTGTTCCTTTCGTTGTGTCAGTGCATCCTCTGTTTCTCCATCATCTCC

TTCTACATCTGTTGCCAATCTCAGGATCTCAAGGTATCTA

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

TTACTACTGGTTTGTATTGTTGTTGGTTTATTAATTTTATTGCTTACTGTTTCAATTTGGATGACTTCTGCTTCTTTTGTCT

ATAGGTTAAAGTGTATTATGCAGGACAATTACCTTGCCAATTGGATAC

7. ADP-glucose pyrophosphorylase S, *AGPaseS* (PGSC0003DMG400000735)

Chr01: 86095512..86094580

GGAGATGGATTTGTTCGAGGTTTGAGACTATACTTTTGAATTCCTGAAGGAAACTGGATTAGTCTTGCTAGATATCACAGCTG
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
TATTGACAGGAATGCTGATATACTCTTTCATGTGCACCAGCTGAGGACAGGTTTGTTTAAATTCCAATAAGAAACAACCTAGT
AATGGTTAAGTGAATTGAGTGAGATCAGAAACAATATGGAGAAAGAGTGCTTCTCCTTTAATATTTCGTATGCATTACTTCGAA
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
TTACATGGTGTACCGGTACGGGTATGTGGGAATGTGT[G/A]GATTTTACCCGGTTTC[T
2134 2175 2182
/G]AAAATTGTTGAAAATGGGCTTGACACTTCAGAAAATGGGC[C/A]TGCAGT[G/A]AAA
2197
CATGTTTTGAA[G/A]TCCAGTCTTGACGATGATCGAAATGACTATTATGCCCTTGGAACCTT
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

File S2

Pair wise linkage disequilibrium (LD) between SNP markers scored in the CHIPS-ALL population.

Available for download as an Excel file at <http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.114.012377/-/DC1>

Table S1 Genes functional in plant starch-sugar interconversion as annotated in the potato genome and GeneBank accessions of corresponding cloned and characterized genes from potato and/or tomato. Loci highlighted green have been probed for association with tuber quality traits (this paper, BALDWIN *et al.* 2011, DRAFFEHN *et al.* 2010, KAWCHUK *et al.* 2008, LI *et al.* 2008, LI *et al.* 2005, LI *et al.* 2013, URBANY *et al.* 2011).

Enzyme/protein	Locus acronym ^a	Locus ID	GenBank accessions	Position (v4.03)
ADP-glucose pyrophosphorylase, large subunit	<i>AGPaseS-1/1</i>	PGSC0003DMG400009026	NM_001247048	chr01:62144770..62149140
ADP-glucose pyrophosphorylase, large subunit	<i>AGPaseS-1/2</i>	PGSC0003DMG400000735	X61187	chr01:86092270..86097270
ADP-glucose pyrophosphorylase, large subunit	<i>AGPaseS-7</i>	PGSC0003DMG400015952	NM_001247018	chr07:21365000..21370700
ADP-glucose pyrophosphorylase, small subunit	<i>AGPaseB-7</i>	PGSC0003DMG400031084	NM_001288195	chr07:51451500..51457400
ADP-glucose pyrophosphorylase, small subunit	<i>AGPaseB-12</i>	PGSC0003DMG400046891 ^c		chr12:1226600..1230220
1,4-alpha-glucan-maltohydrolase	<i>AMY-1</i>	PGSC0003DMG400010664	AJ849377	chr01:59361270..59364450
Alpha-amylase	<i>AMY-3</i>	PGSC0003DMG400020603	A21347	chr03:35999180..36002230
Alpha-amylase, AMY21	<i>AMY-4/1</i>	PGSC0003DMG400007974	M81682	chr04:68256940..68260200
Alpha-amylase, AmyZ	<i>AMY-4/2</i>	PGSC0003DMG400009891	M79328	chr04:71332570..71337470
Alpha-amylase	<i>AMY-5</i>	PGSC0003DMG401017626		chr05:5918690..5923240
Beta-amylase	<i>BMY-1</i>	PGSC0003DMG400000169		chr01:72104900..72114100
Beta-amylase	<i>BMY-7/1</i>	PGSC0003DMG400026199		chr07:47346060..47350380
Beta-amylase	<i>BMY-7/2</i>	PGSC0003DMG400026166		chr07:47402480..47403710
Beta-amylase	<i>BMY-7/3</i>	PGSC0003DMG400026198 ^d		chr07:47419377..47419678
Beta-amylase,PCT-BMYI	<i>BMY-8/1</i>	PGSC0003DMG402020509		chr08:1075900..1079370
Beta-amylase, plastidic, PCT-BMYI	<i>BMY-8/2</i>	PGSC0003DMG400001855	AF393847	chr08:50592100..50595690
Beta-amylase, BMYI	<i>BMY-8/3</i>	PGSC0003DMG400012129		chr08:56381800..56388400
Beta-amylase	<i>BMY-9</i>	PGSC0003DMG400001549	BD247483	chr09:57420530..57423450
Debranching enzyme, isoamylase isoform 3	<i>DBE-6/1</i>	PGSC0003DMG402007274	BD080224	chr06:368200..374700
Debranching enzyme, isoamylase isoform 3	<i>DBE-6/2</i>	PGSC0003DMG401007274	BD080224	chr06:375900..383000
Debranching enzyme, isoamylase isoform 1	<i>DBE-7</i>	PGSC0003DMG400020699	BD080223, A93395	chr07:7890210..7894280
Debranching enzyme, isoamylase isoform 2	<i>DBE-9</i>	PGSC0003DMG400000954	AY132997, BD080222	chr09:46684830..46688580

Debranching enzyme, isoamylase isoform 1	<i>DBE-10</i>	PGSC0003DMG400030253		chr10:38081140..38083210
Debranching enzyme	<i>DBE-11</i>	Not annotated	A52190	chr11:3945240..3949550
Disproportionating enzyme, 4-alpha-glucanotransferase	<i>DPE-2</i>	Not annotated	AY510449	chr02:5166700..5174600
Disproportionating enzyme, 4-alpha glucanotransferase, plastidic	<i>DPE-4</i>	PGSC0003DMG400016589	X68664	chr04:53993900..54001200
Fructokinase, StFrk3	<i>FRK-2</i>	PGSC0003DMG400030653	JX839755	chr02:41888630..41893510
Fructokinase, StFrk1	<i>FRK-3</i>	PGSC0003DMG400024246	U64817	chr03:41525810..41530530
Fructokinase	<i>FRK-5</i>	PGSC0003DMG400028311		chr05:687340..692010
Fructokinase	<i>FRK-6/1</i>	PGSC0003DMG400027017		chr06:53746100..53749420
Fructokinase, StFrk2	<i>FRK-6/2</i>	PGSC0003DMG400026916	JX576230, Z12823, U64818	chr06:53749700..53752940
Fructokinase	<i>FRK-9</i>	PGSC0003DMG400020361	NM_001288518	chr09:707190..710110
Alpha-glucan water dikinase	<i>GWD</i>	PGSC0003DMG400007677	Y09533	chr05:9823400..9839000
Glucose-6-phosphate/phosphate translocator, plastidic	<i>G6PPT-0</i>	PGSC0003DMG400005602		chr00:38861730..38863900 (DMB0000017769)
Glucose-6-phosphate/phosphate translocator, plastid	<i>G6PPT-1</i>	PGSC0003DMG400044320		chr01:67459560..67460820
Glucose-6-phosphate/phosphate translocator, plastid	<i>G6PPT-4</i>	PGSC0003DMG402012710		chr04:10972680..10976630
Glucose-6-phosphate/phosphate translocator, plastid	<i>G6PPT-5</i>	PGSC0003DMG400005269	AY163867, AF020816	chr05:42300210..42303690
Glucose-6-phosphate/phosphate translocator	<i>G6PPT-7/1</i>	PGSC0003DMG400025495		chr07:47074660..47077700
Glucose-6-phosphate/phosphate translocator, plastidic	<i>G6PPT-7/2</i>	PGSC0003DMG400001041		chr07:54548020..54553010
Hexokinase	<i>HXK-2</i>	PGSC0003DMG400030624		chr02:42162900..42168200
Hexokinase	<i>HXK-3</i>	PGSC0003DMG400002525	X94302	chr03:60521600..60527100
Hexokinase, plastidic	<i>HXK-4</i>	PGSC0003DMG400009861	NM_001288386, AF118134	chr04:70783660..70787820
Hexokinase	<i>HXK-6</i>	PGSC0003DMG400016521	NM_001287912	chr06:49126980..49131660
Hexokinase	<i>HXK-11</i>	PGSC0003DMG400013187		chr11:36684900..36690400
Hexokinase	<i>HXK-12</i>	PGSC0003DMG400000295	DQ056861	chr12:4039600..4049300
Hexose transporter	<i>HT-1</i>	PGSC0003DMG400045929		chr01:63002770..63005240
Hexose transporter	<i>HT-2/1</i>	PGSC0003DMG400022402	AJ132223, NM_001247920	chr02:34969850..34973440

Hexose transporter, plastidic	<i>HT-2/2</i>	PGSC0003DMG400026402	AF215853	chr02:41402000..41411600
Hexose transporter	<i>HT-4/1</i>	PGSC0003DMG400025054 ^c		chr04:61467750..61469290
Hexose transporter	<i>HT-4/2</i>	PGSC0003DMG402006401		chr04:63373150..63377240
Hexose transporter	<i>HT-4/3</i>	PGSC0003DMG400009994		chr04:71865900..71871700
Hexose transporter	<i>HT-7</i>	PGSC0003DMG402018758	AJ132225, NM_001247926	chr07:2681670..2686150
Hexose transporter	<i>HT-9</i>	PGSC0003DMG400031832	AJ132224, NM_001247856	chr09:53280800..53287100
Invertase, beta-fructofuranosidase, neutral	<i>INV-n-1/1</i>	PGSC0003DMG400013088		chr01:37067200..37072500
Invertase, beta-fructofuranosidase	<i>INV-1/2</i>	PGSC0003DMG400002756		chr01:78430100..78436100
Invertase, beta-fructofuranosidase	<i>INV-1/3</i>	PGSC0003DMG400001596		chr01:87160540..87164480
Invertase, beta-fructofuranosidase, soluble acid	<i>INV_Pain-1</i>	PGSC0003DMG400013856	X70368, NM_001288064	chr03:39255060..39259540
Invertase, beta-fructofuranosidase, cell wall	<i>INV-cw-3</i>	PGSC0003DMG400002583		chr03:61076900..61079820
Invertase, beta-fructofuranosidase	<i>INV-4</i>	PGSC0003DMG400009936	JX576233	chr04:70804760..70809220
Invertase, beta-fructofuranosidase, neutral /alkaline	<i>INV-na-6/1</i>	PGSC0003DMG400026107		chr06:46660300..46665800
Invertase, beta-fructofuranosidase, cell wall	<i>INV-6/2</i>	PGSC0003DMG400033142		chr06:47626000..47633600
Invertase, beta-fructofuranosidase, cell wall	<i>INV-cw-8/1</i>	PGSC0003DMG400027925		chr08:27921320..27925690
Invertase, beta-fructofuranosidase	<i>INV-8/2</i>	PGSC0003DMG400004790	NM_001247140	chr08:52701630..52705710
Invertase, beta-fructofuranosidase, cell wall	<i>InvGe</i>	PGSC0003DMG400008942	AJ133765, NM_001287894	chr09:2469540..2471550
Invertase, beta-fructofuranosidase, cell wall	<i>InvGf</i>	PGSC0003DMG400008943	AJ133765, NM_001288126	chr09:2474700..2477140
Invertase, beta-fructofuranosidase, cell wall	<i>INV-cw-10/1</i>	PGSC0003DMG400046915 ^c		chr10:15877770..15881930
Invertase, beta-fructofuranosidase	<i>INV-10/2</i>	PGSC0003DMG400008388		chr10:53235940..53238050
Invertase, beta-fructofuranosidase	<i>INV-10/3</i>	PGSC0003DMG400011037		chr10:53706680..53710620
Invertase, beta-fructofuranosidase, cell wall	<i>InvCD111</i>	PGSC0003DMG401028252	X95820, NM_001287886	chr10:55840810..55843010
Invertase, beta-fructofuranosidase, cell wall	<i>InvCD141</i>	PGSC0003DMG402028252	X95821, NM_001288398	chr10:55851950..55856800
Invertase, beta-fructofuranosidase	<i>INV-11/1</i>	PGSC0003DMG400019494		chr11:5046800..5053000
Invertase, beta-fructofuranosidase, neutral /alkaline	<i>INV-na-11/2</i>	PGSC0003DMG400009257		chr11:13676200..13683400
Invertase, beta-fructofuranosidase, neutral	<i>INV-n-11/3</i>	PGSC0003DMG400026530		chr11:39907600..39913800
Invertase/pectin methylesterase inhibitor family protein	<i>InvInh-3/1</i>	PGSC0003DMG400045232 ^c		chr03:39515876..39516269

Invertase inhibitor, Kunitz-type	KT-Invinh-3/2	PGSC0003DMG400010146	AF459077, AY594178, KC184127	chr03:49448370..49449150
Invertase inhibitor	<i>Invinh-5</i>	PGSC0003DMG400039425 ^c		chr05:42860389..42860866
Invertase inhibitor	<i>Invinh-8</i>	PGSC0003DMG400001844		chr08:50229740..50233130
Invertase/pectin methylesterase inhibitor family protein	<i>Invinh-10/1</i>	PGSC0003DMG400001276 ^c		chr10:22401030..22401750
Invertase inhibitor	<i>Invinh-10/2</i>	PGSC0003DMG400037656 ^c		chr10:50545200..50545720
Invertase inhibitor	<i>Invinh-10/3</i>	PGSC0003DMG400040471 ^c		chr10:51072890..51073410
Invertase inhibitor	<i>Invinh-10/4</i>	PGSC0003DMG400037039 ^c		chr10:59551460..59551980
Invertase inhibitor	<i>Invinh-11</i>	PGSC0003DMG400038811 ^c		chr11:7433850..7434380
Invertase inhibitor	Invinh-12/1	PGSC0003DMG400004616	KC007445, GU980595	chr12:59956850..59957600
Invertase inhibitor	Invinh-12/2	PGSC0003DMG400004617	NM_001247862, AY864820	chr12:59963540..59965500
Invertase inhibitor	<i>Invinh-12/3</i>	PGSC0003DMG400004618	GU980592	chr12:59967330..59968500
Maltose transporter	<i>MT</i>	PGSC0003DMG400024812		chr04:58261800..58269200
Glucose-6-phosphate isomerase	<i>PGI-0</i>	PGSC0003DMG400009848		chr00:32605770..32609090 (PGSC0003DMB000001156)
Glucose-6-phosphate isomerase	<i>PGI-1</i>	PGSC0003DMG400030128		chr01:20860570..20862590
Glucose-6-phosphate isomerase	<i>PGI-12</i>	PGSC0003DMG400015341 ^d	DQ451687	chr12:147900..160900
Phosphoglucomutase, plastidic	<i>PGM-0</i>	PGSC0003DMG400001912		chr00:12338800..12351200 (PGSC0003DMB000000431)
Phosphoglucomutase, plastidic, PGM1	PGM-3	Not annotated	AJ240053	chr03:41493531..41510113
Phosphoglucomutase, cytosolic	<i>PGM-4</i>	Not annotated	AJ240054	chr04:35685500..35706600
Phosphoglucomutase, plastidic	<i>PGM-8</i>	PGSC0003DMG400024224		chr08:50101900..50108200
Alpha-glucan phosphorylase, L-type, plastidic, Stp23	PHO1a	PGSC0003DMG400033858+ PGSC0003DMG400003495+ PGSC0003DMG400007782+ PGSC0003DMG400002479	D00520, X52385	chr03 (Chen et al. 2001), not on physical map
Alpha-glucan phosphorylase, L-type, plastidic, StpL	PHO1b	PGSC0003DMG400028382	X73684, BD056944	chr05:346700..352900

Alpha-glucan phosphorylase, H-type, cytosolic, StpH	PHO2	Not annotated	M69038, NM_001288189, L13771	chr09 (Chen et al. 2001), not on physical map (PGSC0003DMB000000644)
Phosphoglucan water dikinase	PWD	PGSC0003DMG400016613	AY747068	chr09:60560500..60572400
Starch branching enzyme I	<i>SBE I</i>	PGSC0003DMG400009981	X08786	chr04:71587800..71595800
Starch branching enzyme III	<i>SBE III</i>	PGSC0003DMG400022307		chr07:55034530..55039270
Starch branching enzyme II	<i>SBE II</i>	Not annotated	AJ000004	chr09:3737100..3755900
Phosphoglucan phosphatase (At3g52180)	<i>SEX4</i>	PGSC0003DMG400015246		chr03:50875700..50885600
Sucrose phosphate synthase	SPS-7	PGSC0003DMG400027936	X73477	chr07:3888900..3897800
Sucrose phosphate synthase	<i>SPS-8</i>	PGSC0003DMG400029892	JQ086765	chr08:20206590..20210220
Sucrose phosphate synthase isoform B	<i>SPS-9</i>	PGSC0003DMG400026428	JQ086766	chr09:59231200..59240200
Starch synthase IV	<i>SS IV</i>	PGSC0003DMG400008322	GQ221264	chr02:30142700..30152300
Starch synthase, soluble, plastidic	<i>Sss III</i>	PGSC0003DMG400016481	NM_001287873	chr02:36377150..36379320
Starch synthase V	<i>SS V</i>	PGSC0003DMG400030619	EU661369	chr02:42100900..42107600
Granule bound starch synthase II, plastidic, SSII	<i>GbssII</i>	PGSC0003DMG400001328	NM_001288048	chr02:46189600..46196700
Starch synthase, soluble	SssI	PGSC0003DMG402018552 ^b	NM_001288145	chr03:45887500..45896600
Starch synthase VI	<i>SS VI-7/1</i>	PGSC0003DMG401013540		chr07:40921600..40929800
Starch synthase VI	<i>SS VI-7/2</i>	PGSC0003DMG402013540		chr07:40932600..40939900
Granule bound starch synthase I, plastidic, waxy	GbssI	PGSC0003DMG400012111	X58453	chr08:56782190..56785790
Sucrose synthase	<i>SUS-2</i>	PGSC0003DMG400016730		chr02:36937430..36941850
Sucrose synthase	<i>SUS-3</i>	PGSC0003DMG400031046		chr03:48949000..48950010
Sucrose synthase	<i>SUS-7/1</i>	PGSC0003DMG400013547		chr07:40610340..40613980
Sucrose synthase, Sus3	<i>SUS-7/2</i>	PGSC0003DMG400013546	U24088, AY205084	chr07:40638500..40644900
Sucrose synthase	<i>SUS-9</i>	PGSC0003DMG400006672	AY205302	chr09:61464900..61472300
Sucrose synthase, Sus4	SUS-12	PGSC0003DMG400002895	U24087, DQ793135	chr12:3085100..3091500
Sucrose transporter	Sut2	PGSC0003DMG400025610	NM_001288509, AY291289	chr05:5692340..5694730
Sucrose transporter	Sut1	PGSC0003DMG400009213	X69165	chr11:9052430..9057350

Sucrose transporter	<i>Sut4</i>	Not annotated	NM_001288141, AF237780	chr04:65861800..65873100
UDP-glucose pyrophosphorylase	<i>UGPase-1</i>	PGSC0003DMG401031123		chr01:67210700..67220100
UDP-glucose pyrophosphorylase	<i>UGPase-11</i>	PGSC0003DMG401013333	D00667, NM_001288019	chr11:808300..814800
		Total 123	Total 66	

^a Loci without established names from the literature are distinguished based on chromosomal location, loci tested for association are highlighted green.

^b Not annotated in genome browser v4.03

^c Very low or no expression, pseudogene?

^d Only small gene fragment, incomplete annotation

Table S2 Correspondence between presence (1) or absence (0) of the Stp23-8b SSCP marker and PHO1a cDNA SNPs in 34 standard varieties of the CHIPS-ALL population (Li *et al.* 2008).

Variety	Stp23-8b	C ₂₂ T	G ₃₂₂ A	G ₈₂₄	A ₂₇₇₆
Leyla	0	CCCC	GGGG	0	0
Marabel	0	CCCC	GGGG	0	0
Solara	0	CCCC	GGGG	0	0
Vitara	0	CCCC	GGGG	0	0
Milva	0	CCCC	GGGG	0	0
Ponto	1	TCCC	AGGG	1	1
Tomensa	1	TCCC	AGGG	1	1
Marlen	1	TCCC	AGGG	1	1
Eldena	1	TCCC	AGGG	1	1
<u>Theresa</u>	1	TCCC	AGGG	1	1
Goldika	1	TCCC	AGGG	1	1
<u>Saturna</u>	1	TTCC	AAGG	1	1
Karlana	0	CCCC	GGGG	0	0
Kolibri	0	CCCC	GGGG	0	0
Fasan	0	CCCC	GGGG	0	0
Terra	0	TCCC	AGGG	1	1
Solist	0	CCCC	GGGG	0	0
Melina	1	TCCC	AGGG	1	1
Molli	0	CCCC	GGGG	0	0
Likaria	0	CCCC	GGGG	0	0
Valisa	0	CCCC	GGGG	0	0
Apart	0	CCCC	GGGG	0	0
Artis	0	CCCC	GGGG	0	0
Aula	0	CCCC	GGGG	0	0
Christa	0	CCCC	GGGG	0	0
<u>Diana</u>	1	TCCC	AGGG	1	1
Novara	0	CCCC	GGGG	0	0
Ilona	0	CCCC	GGGG	0	0
Orlando	0	CCCC	GGGG	0	0
Panda	1	TCCC	AGGG	1	1
<u>Satina</u>	0	CCCC	GGGG	0	0
Sempre	0	CCCC	GGGG	0	0
Sirius	1	TCCC	AGGG	1	1
Velox	0	CCCC	GGGG	0	0