

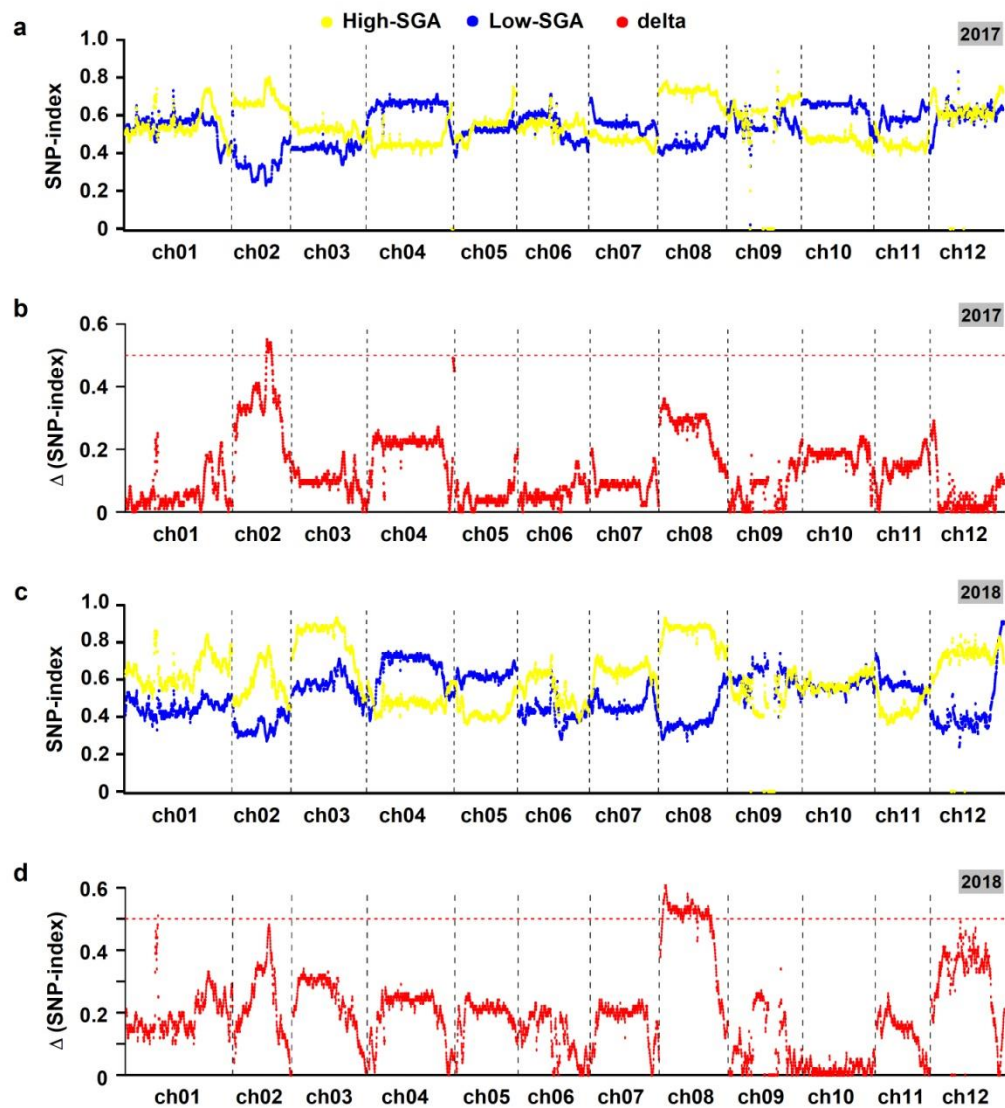
Appendix A. SNP markers used for KASP genotyping on *qSTF2* & *qSTF8*.

No.	Name	wild SNP	mutant SNP	seq
1	2_27011371	T	C	CATTGTCCTGTTTTGATTCCTCCATCATGGTTCCTGCATCAAATTCATAACTTT TGTCAGTGGAGATCTTGAAGGTGTCAAAGAATTGGACTGTA[T:C]ACGTACAG GTGATTCATATAGAAGTTTTCCGCCTTGTGTTGAAGTGGCTAATAACGTACAG GTGATTCATATAGAAGTTTTCCGCCTTGTGTTGAAGTGGCTAAT
2	2_27415361	A	T	CTGTCTATTAATAATTCTGCAGTCAATAACTTCTCCTTTTGTGTTTTCTATGCTCCC GCCAATTTCTTACTGGTAATCTTTGTTGGCAATCAAGTTGAT[A:T]AGGACT TTAATGCATAGATCCATGTAAAGATATGGCACCTAGGCCTAATTTAACCCCAA AAGCTTGCTCATGAGGGAGGATTGCCCAAGGCCACATAAGGAGACCACCAGT CCATTTTCCAACCAATTTGGGA
3	2_27921331	A	G	TCATATTGTGTATTTCATGAGACTATCAGTTTAAAGTTTGTTCATCCGAAAT TTTCAATTTTTGATATCCTTTGAAGCCTAGGGTTGAT[A:G]TCCTCTCTTCTCT TCATCCGCCATCTCTAAGGTAAGTTTCTCTAATGAAATTCTAAGTATTCAATC CTCATTATTAATGAAAATTCTACACCATAACCT
4	2_28043071	G	A	TCACCTGTCTCTTTTATATCTACCCAATCCCAGTAACGATTGTCTTCTCCCA AGTGATTGAGAGATCTTTTGCATATAACATAAAGCAGTTTGC[G:A]TTATTTCGT TCTGTCAATCCAGTACTTCTGCATATCATATCACTAATATTATCTGTAAGATTG CATAACACTGTAAACTTCAAATAAAT
5	2_28366211	A	T	GCATTTGTTAAGCATATGAACAAGGATTGCTCTATTGAAAGAAGAGATTTTCA ATGGATTGGCTGCAAGTGTGTGTCAGTGTCTGCTGTTATTAAGGAGCCCTCAAG AATC[A:T]TTTGACCAACTTGATGGGAAGGTCATCTTAGGCCAAGATTATCTTT TGTAATTTGGGTGTCAGATTACATCTATGTTTCGTGTGATCATCAATTAATGAT AAGCTTTTAGTG
6	2_28669261	C	G	CTCTCCATTTGCTTCAGATGATTTTGGACTAGACTGCACTGAAGACTCATCTAC ATCAGGCAGATCAACTTTCAAACCAGACCGAGGACTTCCCACAGGAGGGGAA TTCAATTTGGATGCTG[C:G]TAACCACCTTACAGATAATGACCGACCAAGAGG TTCATGTATTCTTTTGAAGCTGAATTAGGAGAATGTCTAT
7	2_29003341	T	C	CCGACAAGCTACGCATCACTCTCTGAAGCTATTCTCTTCGTCATAAATAATCC GTTTTGCCACAAAATGACCTGGACCAATAGGGAAATTCATTGGGTCTTTAGCT GGGTAGCCAAGTG[T:C]GGAACGGATGATTGCTGAAAACATCTAAGTAGTAAG CTCATCCTAAGATGAATGCTCTCCATTCTGACTTCCAATTACTAGTAC
8	2_29331791	T	A	AGCTATCTTGCATTTTCGTGGAGGAGTTCATCTACTCCTCCAACGAACATTGTA GTGAAAAGGCGTAGATAGTCCTTTG[T:A]CCACGCCTGATTGGAGATTCCT ACTCTTCAGGAAGAGCCTGAGGAGAAGATTGTCATCAACTTTGTCGCGATAT GTTGCCATTTGTAGACTAGTTGAGTTGCAT
9	2_29457101	A	T	CTCATGATAGATAGTGTGTGAACAAGGAGATTTTCTTGGTGCAGGATGTTTT ACAACATGTCTTTTCCACTCAGTTGTGTCCAAACAGAAATAATAAAAAGAA AAAGTTTACTGTCTTAAGAGTAA[A:T]GGGAGAAGCAAGTTGTTTCAGATGCA AATATTTAATGCTTCGACAGCAAGGTTCTCTGATCCTTACTATGATCTGAAGT GTAAAGGGAACATAAAATTTTACACCTTCCC

10	2_29504641	A	T	ATGCTTTGTTCAACAAGAAGTTCTCTTCATTTGCAATATTTGACGGAAAGAAT GATTCAAATTTCTCCCTTATCAATGTTCTTCTAAGTATCATGCTAGAGAGCAA GACAAGAAATTT[A:T]TACTGGGTTTGTATGAAGTGGTTGGTTGATCACAAAGATT GATACAGGTAAGTCTCGAAGTCGCATCACTAGTGCCAACTGCAGAGTGATGCTTA TAATAGAA
11	2_29865501	A	G	ATCAGGCCATGCTTGCTTTGATTGCTGTGACTTTTGGTGTGACAAAGGCAACT CATTCTGGTGAGGCTATCCAGGCTGCAATATGTGAACCTATCGTGGC[A:G]AT CTCCATAGAAAAGGGGAAAGAGAGAAAGGATAGAGCAACTTAAGTAATTG GTTTTTGTGTTGAAAGATGTATCCTTTTCTCAATATGTATAGCAAATATT
12	2_30075401	G	A	ACCCTCCTCAAGCTAGGAGCTATGAAGATATTCTTCATACCTAGCTTGGACA TAAGATGCACATGTGAAATTTCTCCAAGTGCTTTAGTGAGGATATCAGCTGGC T[G:A]TTCTGAAGATGATAGATATGTAGTGACAAGTAGTCCAGCTTGAATTTTC TCCCAATGAAATGACAATCTATGTCAATATGTTTCGTACGTTCA
13	2_30401011	C	T	AAGACTTCAATTGAGCAAACATGCTCTGCAAGCCCACTCACTCTTCAAGAAA CATGAACGTACAAAAATATGTGCAGGCTGACCTGCATGGTAGTGGTGCCAA[C:T]CCTGTGCTTAAGCAAAAAGCAGTTACTCCCTTTGTAAATTTTTACGCTTTT ACATTTCAAGTAGAATCTGGAAGGAGGTTATTTATCTTTTGGAGGAACCACTG
14	2_30950151	A	G	AATAGGACTAGCTACTCTCCGCGTTTGAACGGTTGAGTTTTGGATTGATG AATCACTTAATGGCTCCAACGTGCTTTCCATATTGAGCATCTCAACACT[A:G]G AATATTTGGATCTTGAAATGCTGGTTAACTGGTGATATCCCTTCTGATTTAT GTCATCACGTTCCAGATTGCAAGCTCTTGGAAGTACTCCAATGTGTTA
15	2_31145661	T	C	TCATCGAGGCCGATATGAGACTTCTTGCTTATAAGTTGGGGCGTCACATATA CCCCTCTATGGACTCAGCGTCCGCTGAGGTTTGGCCACCGTATGAGATA[T:C]GCCATCATGGGTTATTGCGCTGAGTTTCTTACCACAAATACTCAGCTTTGA TGTTTGCCTGTTGGGTGCTGACTGGAGTGGCTCTCATGACATTTGTAAC
16	2_31293431	G	A	ACCCAATCTAAGAGACAAATGCTAGTGTGGCTCGGCATGTAGTTATTGTTGTT CTTTCCACTGACAGTTTCCAAAAGTACAACCTCAAAGCTGTAAACATCTGCCT T[G:A]TCAGTCAAATAACCCAGAGTGCCTATTCTGGTGCCATGTATCCTCTGC AAGTGTTAAGATTAGAAGGTTTGTCAACGTAAAATAC
17	8_4017531	G	A	TGAGAACATTGTGTCATGGCTAAGCAAGATCTCCGGATAAAGAAATCTGCG ACGGAGGTGGTGTCAATGGTAATAACTATGTGCTAGATTCTTCCATATG[G: A]TGCTGTTGGACCTGAAGTCAGGTATGCAGCAACCTATTGCATGGATTGATG AAGCAGCAAGTGCTTTTTCCAGAAGTCTTTGCTTATTGCGATGAACTGC
18	8_4485471	C	T	TTGAAGTTTAGAGTATAATCTGTATGCATCATGGCTTCAATCACTTCATTTT CGACTACTAATTCAGCTTCTTGAATTTGTGTACGTGCATCATGCATGGCATT[C: T]GAGAAGCTGAAGTTTCAAGTTGTTGATATTGATGAAGAAATTAATAATTC TTAATGTTTGTATAGTAATTGTTGGATTTTCTCCATTTCTTTTTTGTGGATTT TTCTT
19	8_4739531	G	C	GTAAGTATAATGTTGCAATGGAATGAGCTCTAGGATCGGATATATGGAAGACT CATTTACCAATCCCAAAGTGGTTT[G:C]GCCTGAGGCATAGTTGCCTGATTTA TTGACTCCAGTCAGAGATTACAAATAGGAATTAATCAAAGAGATCTCTGCTA ACATTTGCTTTTAGTCTTAAAGTTCAAATTATGCACTTTGGTTTAACTCACTT TGTCATTG

20	8_5107061	T	G	GGTCTCAGCTCTCCAAGGTCTTCAGTTAGTAATTTGACATCCTGCAAACATGA TAAGAAATGCATAAGATAAGCTCTTACAACATTTTCATGAAAAGAGATGGACAT CT[T:G]ACCCCTCGCCAAAATCCTATTGAGGCGCCATGCCTAATGAAACATTCT TCAATCGCCCGATCAAAGATATGCGCCAAGGGAAGATATGAGAGATATACAT CATTTCAT
21	8_5354761	A	C	AGGAAAGTGCCCTGTGCTTGTCACAGCCAGGGTTGAGGCAGAAGAAAGAAG AAACAATATACGTTTGAGGGAGGAGCAAGATGCTGCTTATCGTGCTGC[A:C]C TAGAAGCTGATCAAGTAAGTGCTTTTAGGTTCCAAATATGCCTTTCCTCTCTTC AAGTTACTTTGTGAAGGGGAAAAAGCTTTACATTGATCAACTGTTTGCCCTTA ACTAGGCTAGAGAGCGCCAGAGGATAGAAGAGCAAGAGAGGC
22	8_5770191	C	G	TGAGGAGATCATGCAATGGCTTGACAAGAAACATAGAGGTTCAACTGTGTTTG TTTCATTTGGGAGTGAGTATTTTCTATCAAAGGAAGAAATTCATGAAGTAGCT[C:G]AAGGACTAGAGCTTAGCAAAGTGAACCTCGTTTGGGTCATCAGGTTTCCA CAAGGTGAAAGAATTAACATTTCGAGATGCATTACCGGAAGGGTTTCTTGAAC GGGTAGGAGAAAGAGGAATAATTATTGAAG
23	8_6022011	C	T	AGAAAGGGAATTCAGAAGTGAGTGAGAAGCTGTCAGTGCGTCAGCTCCCCT TCCCTTTCTTTCTTTATTTTTCTCTCAAAAATATACTGACAATGCCCAACCC[C:T]CCACCTCCACGCATGTTACACAAACATACCTTAAAATAATTAATTAACAT AATTTATCATCCTTTAATACTGATATACTCATATACAATGGCGATATT
24	8_6389791	C	T	GAAGATAAGTCCCGCAAGGAGAGATGACAGCTGCAAGAACATTTGGGACATC AAAGGACCTAATCTCTGTCAAGGTTTGCAATCAAAGATGCTAATTACAGAGT [C:T]TGATTTTCGTAACCATAAGTTTGGACCCATCATCACTGAACTTTGCACTGG TACAAGGAACCTATCCAGCTTGACACCAGGTTACCCGCTCGGGAAAGGAGG TCCA

Appendix B. QTL mapping of the SGAs content in tuber flesh in 2017 and 2018 with 260 and 350 F2 individuals, respectively. SNP-index of ‘High-SGA’ and ‘Low-SGA’ pools on 12 chromosomes in 2017 (a) and 2018 (c). The Δ (SNP-index) was calculated to identify the QTLs affecting the flesh SGAs content in 2017 (b) and 2018 (d).



Appendix C. Genes on *qSTF2* locus that co-expressed with *GAMEs* gene.

trans_ID	chr	start	end	annotation
PGSC0003DMT400024377	chr02	27010818	27015458	Tonoplast intrinsic protein, alpha (Alpha-TIP)
PGSC0003DMT400024386	chr02	27068991	27073923	Kinesin heavy chain
PGSC0003DMT400024361	chr02	27162898	27169334	Vacuolar ATP synthase subunit F
PGSC0003DMT400027090	chr02	27281186	27291149	Thioredoxin I
PGSC0003DMT400027083	chr02	27408577	27417302	Serine/threonine protein kinase
PGSC0003DMT400027070	chr02	27511074	27519810	Pyrroline-5-carboxylate reductase
PGSC0003DMT400027032	chr02	27522628	27524043	TRNA (Guanine-n(7)-)-methyltransferase
PGSC0003DMT400027065	chr02	27540399	27542051	CHP-rich zinc finger protein
PGSC0003DMT400027029	chr02	27546393	27550327	Conserved gene of unknown function
PGSC0003DMT400027015	chr02	27601590	27605630	2-oxo acid dehydrogenase, lipoyl-binding site
PGSC0003DMT400027091	chr02	27608039	27609565	Glycoprotein endopeptidase
PGSC0003DMT400027059	chr02	27614989	27619205	Structural constituent of ribosome
PGSC0003DMT400065915	chr02	27671769	27676948	Conserved gene of unknown function
PGSC0003DMT400026740	chr02	27848945	27854556	Pentatricopeptide repeat-containing protein
PGSC0003DMT400095779	chr02	28042333	28043103	Galactose-binding like
PGSC0003DMT400026836	chr02	28046119	28048422	Conserved gene of unknown function
PGSC0003DMT400026857	chr02	28134230	28143018	Zinc finger protein
PGSC0003DMT400054502	chr02	28375993	28378541	Alcohol dehydrogenase
PGSC0003DMT400054669	chr02	28396111	28402652	Argonaute protein group
PGSC0003DMT400054667	chr02	28408045	28411045	Argonaute protein group
PGSC0003DMT400054651	chr02	28554223	28557560	Conserved gene of unknown function
PGSC0003DMT400054483	chr02	28558010	28566627	CbbY protein
PGSC0003DMT400054479	chr02	28600289	28604907	Conserved gene of unknown function
PGSC0003DMT400054632	chr02	28653032	28657375	Conserved gene of unknown function
PGSC0003DMT400054458	chr02	28703077	28707245	Coatomer subunit epsilon-1
PGSC0003DMT400054452	chr02	28744720	28752505	Gamma-soluble nsf attachment protein
PGSC0003DMT400054613	chr02	28850164	28855771	Jumonji domain protein
PGSC0003DMT400054443	chr02	28863321	28865120	AAA ATPase
PGSC0003DMT400054413	chr02	29020388	29021396	Conserved gene of unknown function
PGSC0003DMT400054673	chr02	29384162	29385406	Nectarin 5
PGSC0003DMT400054364	chr02	29478893	29497078	Cation-chloride co-transporter
PGSC0003DMT400054357	chr02	29513928	29520655	Ubiquitin-protein ligase
PGSC0003DMT400054528	chr02	29661167	29662108	Conserved gene of unknown function
PGSC0003DMT400054524	chr02	29679195	29679905	Conserved gene of unknown function
PGSC0003DMT400054339	chr02	29708438	29712521	K+ channel inward rectifying
PGSC0003DMT400054518	chr02	29746814	29754357	Lupus la ribonucleoprotein
PGSC0003DMT400054515	chr02	29757239	29758829	Phospho-n-acetylmuramoyl-pentapeptide-transferase
PGSC0003DMT400021403	chr02	29910064	29912916	Nbs-1rr resistance protein
PGSC0003DMT400021418	chr02	29926747	29930176	3-beta hydroxysteroid dehydrogenase/isomerase
PGSC0003DMT400021423	chr02	29948673	29950997	DNA-directed RNA polymerase II 19 kD polypeptide rpb7

PGSC0003DMT400021424	chr02	29951178	29955600	50 kDa ketoavyl-ACP synthase
PGSC0003DMT400021384	chr02	30104844	30109296	LRR receptor-like serine/threonine-protein kinase FLS2
PGSC0003DMT400021444	chr02	30142740	30152314	Starch synthase IV
PGSC0003DMT400025123	chr02	30216580	30217993	Purine transporter
PGSC0003DMT400025118	chr02	30266152	30272423	Purine transporter
PGSC0003DMT400025128	chr02	30305444	30314962	O-acetyltransferase
PGSC0003DMT400018705	chr02	30901956	30905832	Conserved gene of unknown function
PGSC0003DMT400073020	chr02	31018528	31021542	Zinc finger protein
PGSC0003DMT400073149	chr02	31068828	31069804	Conserved gene of unknown function
PGSC0003DMT400073228	chr02	31294913	31301120	ATP binding protein
PGSC0003DMT400073239	chr02	31337110	31338154	Acetylglucosaminyltransferase
PGSC0003DMT400073052	chr02	31399657	31403144	Zinc ion binding protein
PGSC0003DMT400073250	chr02	31406150	31411543	BRASSINAZOLE-RESISTANT 2 protein
PGSC0003DMT400073071	chr02	31537372	31539647	UNE1
PGSC0003DMT400073300	chr02	31571145	31571758	Conserved gene of unknown function
PGSC0003DMT400073080	chr02	31654071	31655150	Conserved gene of unknown function
PGSC0003DMT400073268	chr02	31678780	31681494	Conserved gene of unknown function
PGSC0003DMT400073091	chr02	31707793	31714938	Glycogen synthase kinase-3 beta
PGSC0003DMT400073096	chr02	31761255	31762391	Ubiquitin-protein ligase
PGSC0003DMT400073110	chr02	31795876	31804506	Serine-threonine protein kinase, plant-type
PGSC0003DMT400073289	chr02	31863471	31866978	Receptor kinase
PGSC0003DMT400073131	chr02	31880731	31885458	Protein kinase SRK
PGSC0003DMT400073291	chr02	31899161	31901152	CBL-interacting protein kinase 16