## **Supplementary Material**

**SUPPLEMENTARY TABLE S1.** **Summary of field experiments conducted to fine map tipburn resistance in *qTB5.2*.**

| **Experiment** | **Replications** | **Agronomic practices** | **Traits scored** | **Harvest maturity** |
| --- | --- | --- | --- | --- |
| Yuma, AZ. Sown December 4, 2013, evaluated March 25, 2014 | 4 | Pre-irrigation fertilizer: 15-49-0 187 L / ha. Pre-plant fertilizer: 11-52-0 392 kg / ha. Side dress and fertigation: UN 32 561 L / ha. Pre-plant insecticide: Admire 877 mL / ha and Corogen 365 mL / ha. Side-dress insecticide: Movento 365 mL / ha and Sniper 438 mL /ha. Furrow irrigation. | Tipburn incidence. 10 plants evaluated/ replicate. | cv. El Dorado had hard, compact, and solid heads. cv. Emperor was over-mature; some heads bursting. |
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| Yuma, AZ Sown December 10, 2014, evaluated March 31, 2015 | 4 | Pre-irrigation fertilizer: 15-49-0 187 L / ha. Pre-plant fertilizer: 11-52-0 392 kg / ha. Side dress and fertigation: UN 32 561 L / ha. Pre-plant insecticide: Admire 877 mL / ha and Corogen 365 mL / ha. Side-dress insecticide: Movento 365 mL / ha and Sniper 438 mL / ha. Furrow irrigation. | Tipburn incidence. 20 plants evaluated/ replicate. | Both cultivars were hard and over-mature |
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| Yuma, AZ. Sown December 7, 2015, evaluated March 30 or April 17, 2016. | 5 | Pre-irrigation fertilizer: 15-49-0 187 L / ha. Pre-plant fertilizer: 11-52-0 392 kg / ha. Side dress and fertigation: side dress of 20 gal / acre two times and fertigation of 94 L / ha two times of UN 32. Pre-plant insecticide: Admire 877 mL / ha and Corogen 365 mL / ha. Side-dress insecticide: Movento 365 mL / ha and Sniper 438 mL / ha. Furrow irrigation. | Leaf crinkliness, Average plant weight, Head maturity, Tipburn incidence, Tipburn severity.10 plants evaluated/ replicate. | Both cultivars had hard, compact, and solid heads. |
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| Salinas, CA. Sown May 10, evaluated July 14 and 21, 2016 | 4 | Pre-plant fertilizer: 6-20-20 at 336 kg / ha. Side dress fertilizer: 21-0-0-24S at 336 kg / ha two times. Herbicide application: Kerb SC at 1.2 L / ha. | Leaf crinkliness, Average plant weight, Head maturity, Tipburn incidence, Tipburn severity. 6 plants evaluated/ replicate at each time point. | On July 14, both cultivars had firm, compact heads. On July 21, cv. Emperor had hard, solid heads; cv. El Dorado had slightly less hard heads. |
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### **SUPPLEMENTARY TABLE S2. Haplotypes of BC2S1 genotypes evaluated in Yuma 2014–2015.** The first column shows the number of genotypes with the respective haplotype. E symbolizes the homozygous Emperor allele, D indicates the homozygous El Dorado allele, and H denotes the heterozygotes.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Interval 1 | | Interval 2 | | Interval 3 | | Interval 4 | | Interval 5 | |
| **Number of genotypes** | **AVEP-OP4 CLSZ628** | **BGAP-OP4 CLS6395** | | **AXZQ-OP4 CLS1404** | | **AVJT-OP4 CLS10103** | | **AZRN-OP4 CLS2455** | | **BAMG-OP3 CLS2953** |
| 1 | D | **D** | | **D** | | **D** | | **D** | | D |
| 1 | E | **E** | | **E** | | **E** | | **E** | | E |
| 7 | D | **D** | | **D** | | **D** | | **D** | | H |
| 5 | E | **E** | | **E** | | **E** | | **E** | | H |
| 8 | D | **D** | | **D** | | **D** | | **H** | | H |
| 6 | E | **E** | | **E** | | **E** | | **H** | | H |
| 7 | D | **D** | | **D** | | **H** | | **H** | | H |
| 8 | E | **E** | | **E** | | **H** | | **H** | | H |
| 8 | H | **H** | | **H** | | **D** | | **D** | | D |
| 8 | H | **H** | | **H** | | **E** | | **E** | | E |
| 11 | H | **H** | | **H** | | **H** | | **D** | | D |
| 8 | H | **H** | | **H** | | **H** | | **E** | | E |
| 5 | H | **H** | | **H** | | **H** | | **H** | | D |
| 6 | H | **H** | | **H** | | **H** | | **H** | | E |
| 7 | H | **H** | | **H** | | **H** | | **H** | | H |

### **SUPPLEMENTARY FIGURE S3. Phenotype of leaf crinkliness at the margin of leaves of cultivars Emperor and El Dorado.** Cultivars Emperor (Left) and El Dorado (Right) grown in the Yuma, Arizona 2015–2016 field experiment. Cultivar Emperor had more leaf crinkliness than cultivar El Dorado.



### **SUPPLEMENTARY TABLE S4. Primers used for the dissection of *qTPB5.2*.** Sequences for forward and reverse primers are reported in the 5' to 3' direction. The PCR reactions were done with 35 cycles at their respective annealing temperature.

| **Marker name** | **Forward Primer Sequence (5' to 3')** | **Reverse Primer Sequence (5' to 3')** | **Fragment size (bp)** | **Annealing Temperature (°C)** |
| --- | --- | --- | --- | --- |
| AVEP-OP4 | TGG TCT TGC TGC TTC TGC TA | TTT GTG TCC CTA AAA ACC ACA | 174 | 60 |
| AXZQ-OP4 | AGG CTC AAT GGT TGT TGA GG | ATA TCG GAC GCC AAT CAA TC | 217 | 60 |
| AVJT-OP4 | TCA GAA ACA GTG GCA GCA TC | TCA CAA ATT GTC ACC GGA AA | 358 | 60 |
| AZRN-OP4 | GCA ATT CCA GAT CGA GGT GT | CGG TCA CAA ATT CTC GGT TT | 394 | 60 |
| BAMG-OP3 | TTT GGT TTC AGA GTT CTT AC | CAC GTT CAT AAA TCA ATT GC | 333 | 55 |
| 1234\_128860 | ATT GGC ATT GAC CAA CAA CA | TCG TAA TGG ATT GGC ATT TG | 265 | 55 |
| 1234\_129021 | CCA TCA TGG TCA ATC TTC GT | CGA GCC TTC GAT CCA AAA | 253 | 55 |
| 1234\_129180 | CGG AAG AGT GTG AAC AGA CG | AAG CAT AGC ATC GGG AAG TG | 209 | 55 |
| 1743\_126841 | TTT TGC GTT CAC AAC AGG AC | TTG AAA AGC TCA AAC CGA TG | 264 | 60 |

### **SUPPLEMENTARY TABLE S5. Haplotype of the genotypes used for RNA-seq.**

| **Genotype** | **AVJT-OP4 CLS10103** | **1234\_128860** | **1234\_129021** | **1234\_129180** | **1743\_126841** | **AZRN-OP4 CLS2455** |
| --- | --- | --- | --- | --- | --- | --- |
| El Dorado | D | D | D | D | D | D |
| Emperor | E | E | E | E | E | E |
| 15G174 | D | D | E | E | E | E |
| 15G267 | E | E | E | E | E | D |
| 15G368 | D | D | D | D | E | E |
| 15G209 | E | E | E | D | D | D |

### **SUPPLEMENTARY Table S6. Contrast results of tipburn severity for YAC 2015–2016, SAL 2016-65 days, and SAL 2016-71 days.** Orthogonal contrast results of tipburn severity for experiments conducted in Yuma, Arizona 2015–2016 and Salinas, California (65 and 71 days after imbibition). The "estimate" column is the estimated difference in the trait between the contrasting groups (i.e., haplotypes) and the standard error (Std. Error) of the difference. A P-value of 0.05 or less is considered significantly different.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **YAC 2015-2016** | | | **SAL 2016-65 days** | | | **SAL 2016-71 days** | | | |
| **Contrast** | **Estimate** | **Std. Error** | **P-value** | **Estimate** | **Std. Error** | **P-value** | **Estimate** | **Std. Error** | **P-value** |
| El Dorado vs. Emperor | -1.09 | 0.33 | 5.0E-03 | -1.17 | 0.65 | 0.09 | -0.58 | 0.68 | 0.40 |
| Haplotype 15, 16, and 14G1227 vs. Haplotype17 and 18 | -4.59 | 0.73 | <1.0E-04 | -8.04 | 1.45 | 1.0E-04 | -10.1 | 1.52 | <1.0E-04 |
| Haplotype 15 and 16 vs. 14G1227 | -1.66 | 0.50 | 5.4E-03 | -0.56 | 1.0 | 0.58 | -0.20 | 1.05 | 0.85 |
| Haplotype 15 vs. Haplotype 16 | 0.13 | 0.20 | 0.53 | 0.27 | 0.40 | 0.51 | 0.22 | 0.42 | 0.60 |
| Haplotype 17 vs. Haplotype 18 | 0.055 | 0.13 | 0.69 | 0.75 | 0.26 | 0.013 | 1.04 | 0.28 | 7.0E-04 |

### **SUPPLEMENTARY TABLE S7. Genes located in the dissected QTL region.** Genes found in the recombinant region from the Yuma 2015–2016 and Salinas 2016 experiments. A description of the gene’s primary transcript is provided from version 5 of the lettuce genome browser and the genes in the NCBI protein database that significantly match the gene protein sequence. The presence and location of mutations, if any, are provided along with a description of the type of mutation.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Scaffold** | **Gene** | **Start-end positions** | **Lettuce GBrowse descriptions** | **NCBI protein BLAST** | **Mutation on Gene** | **Type of mutation** | **SNP or indel 5 Kb upstream of gene** |
| Lsat\_1\_v5\_g\_5\_1234 | Lsat\_1\_v5\_gn\_5\_129040 | 267900 - 271868 | Ca2+ antiporter/cation exchanger | K07300 Ca2+:H+ | Sodium Calcium exchanger NCL-like | None | NA | 2 SNPs, 1 indel |
| Lsat\_1\_v5\_g\_5\_1234 | Lsat\_1\_v5\_gn\_5\_129100 | 294712 - 294942 | Unknown | Unknown | None | NA | no SNP |
| Lsat\_1\_v5\_g\_5\_1234 | Lsat\_1\_v5\_gn\_5\_129180 | 334294 - 338524 | VCX1, HUM1, MNR1 | Vacuolar H+/Ca2+ exchanger involved in control of cytosolic Ca2+ concentration | has similarity to sodium/calcium exchangers, including bovine Na+/Ca2+, K+ antiporter | K07300 Ca2+:H+ antiporter | Sodium Calcium exchanger NCL-like | 1 exon | A to T substitution | no SNP |
| Lsat\_1\_v5\_g\_5\_1234 | Lsat\_1\_v5\_gn\_5\_129201 | 339158 - 341005 | Unknown | Uncharacterized protein | None | NA | 1 SNP |
| Lsat\_1\_v5\_g\_5\_1234 | Lsat\_1\_v5\_gn\_5\_129241 | 409723 - 411211 | Unknown | Superoxide dismutase (Iron/Mn) | LLM class flavin-dependent oxidoreductase | None | NA | no SNP |
| Lsat\_1\_v5\_g\_5\_517 | Lsat\_1\_v5\_gn\_5\_126960 | 132978 - 133244 | Unknown | Hypothetical protein | None | NA | 2 SNPs |
| Lsat\_1\_v5\_g\_5\_517 | Lsat\_1\_v5\_gn\_5\_127001 | 204219 - 207007 | Unknown | Pmr5/Cas1p GDSL/SGNH-like acyl-esterase | SHUGOSHIN 1 and 2 isoform X1, 2, and 3 | serine/threonine-protein kinase | Protein kinase superfamily protein | 2 intron | T deletion and A to G substitution | no SNP |
| Lsat\_1\_v5\_g\_5\_517 | Lsat\_1\_v5\_gn\_5\_127021 | 246789 - 247966 | TCP4 Factor | TCP4 transcription factor | TEOSINTE BRANCHED 1, cycloidea and PCF transcription factor 3 | 3’UTR | Indel | 2 SNPs |
| Lsat\_1\_v5\_g\_5\_517 | Lsat\_1\_v5\_gn\_5\_127080 | 395944 - 396719 | TCP4 Factor | TCP10 | TCP domain protein 10 | TCP family transcription factor 4 | None | NA | 3 SNPs |
| Lsat\_1\_v5\_g\_5\_517 | Lsat\_1\_v5\_gn\_5\_127101 | 433712 - 433993 | Unknown | Oligoendopeptidase F | None | NA | no SNP |
| Lsat\_1\_v5\_g\_5\_517 | Lsat\_1\_v5\_gn\_5\_127121 | 434870 - 435019 | Unknown | Unknown | None | NA | no SNP |
| Lsat\_1\_v5\_g\_5\_517 | Lsat\_1\_v5\_gn\_5\_127161 | 470878 - 475594 | Protein SEC61 Subunit alpha | SECY and SEC61 subunit protein transport | 1 intron | AG deletion | 3 SNPs |

**SUPPLEMENTARY TABLE S8. List of differentially expressed genes in a minor effect region.** List of differentially expressed genes between susceptible and resistant pools. The pool with the cultivar El Dorado allele (susceptible pool) was used as the reference; therefore, the log2 fold change reports the change in expression of the pool with the cultivar Emperor allele (resistant pool) to the susceptible pool. A description of the gene's primary transcript is provided from version 8 of the lettuce genome browser obtained from the available KEGG, SWISS-PROT, or GO annotation.

| **Gene** | **Log2 Fold Change** | **Description** |
| --- | --- | --- |
| Lsat\_1\_v5\_gn\_5\_133461 | 6.5 | hypothetical protein LSAT\_5X133461 [*Lactuca sativa*] |
| Lsat\_1\_v5\_gn\_5\_133441 | 6.2 | KEGG-Description=Os08g0559600 | K01687 dihydroxy-acid dehydratase [EC:4.2.1.9] SWISS-PROT-Description=ILVD\_FLAPJ Dihydroxy-acid dehydratase OS=*Flavobacterium psychrophilum* (strain JIP02/86 / ATCC 49511) GN=ilvD PE=3 SV=1 GO\_annotations=GO:0003824: catalytic activity: Molecular Function |
| Lsat\_1\_v5\_gn\_5\_128960 | 1.9 | KEGG-Description=GA10197 gene product from transcript GA10197-RA | K01768 adenylate cyclase [EC:4.6.1.1] SWISS-PROT-Description=TMVRN\_NICGU TMV resistance protein N OS=*Nicotiana glutinosa* GN=N PE=1 SV=1 GO\_annotations=GO:0004888: transmembrane receptor activity: Molecular Function | GO:0005515: protein binding: Molecular Function | GO:0005524: ATP binding: Molecular Function | GO:0006915: apoptosis: Biological Process | GO:0006952: defense response: Biological Process | GO:0007165: signal transduction: Biological Process | GO:0031224: intrinsic to membrane: Cellular Component |
| Lsat\_1\_v5\_gn\_5\_128860 | 5.1 | KEGG-Description=Os09g0429400 | K05387 glutamate receptor, ionotropic, other eukaryote SWISS-PROT-Description=GLR32\_ARATH Glutamate receptor 3.2 OS=*Arabidopsis thaliana* GN=GLR3.2 PE=1 SV=2 GO\_annotations=GO:0004970: ionotropic glutamate receptor activity: Molecular Function | GO:0005215: transporter activity: Molecular Function | GO:0005234: extracellular-glutamate-gated ion channel activity: Molecular Function | GO:0006810: transport: Biological Process | GO:0016020: membrane: Cellular Component |
| Lsat\_1\_v5\_gn\_5\_140040 | Zero coverage in cv. Emperor | KEGG-Description=cellulose synthase (EC:2.4.1.12) | K10999 cellulose synthase A [EC:2.4.1.12] SWISS-PROT-Description=CESA1\_ORYSJ Probable cellulose synthase A catalytic subunit 1 [UDP-forming] OS=*Oryza sativa* subsp. japonica GN=CESA1 PE=2 SV=1 GO\_annotations=GO:0016020: membrane: Cellular Component | GO:0016760: cellulose synthase (UDP-forming) activity: Molecular Function |
| Lsat\_1\_v5\_gn\_5\_129380 | 5.7 | KEGG-Description=hypothetical protein | K12124 GIGANTEA SWISS-PROT-Description=GIGAN\_ARATH Protein GIGANTEA OS=*Arabidopsis thaliana* GN=GI PE=1 SV=2 |
| Lsat\_1\_v5\_gn\_5\_140080 | 0.44 | KEGG-Description=hypothetical protein | K08963 methylthioribose-1-phosphate isomerase [EC:5.3.1.23] SWISS-PROT-Description=MTNA\_POPTR Methylthioribose-1-phosphate isomerase OS=*Populus trichocarpa* GN=POPTRDRAFT\_832064 PE=3 SV=1 |
| Lsat\_1\_v5\_gn\_5\_142061 | 2.9 | hypothetical protein LSAT\_5X142061 [*Lactuca sativa*] |
| Lsat\_1\_v5\_gn\_5\_142101 | -1.3 | hypothetical protein LSAT\_5X142101 [*Lactuca sativa*] |
| Lsat\_1\_v5\_gn\_5\_139960 | -3.4 | SWISS-PROT-Description=FIP37\_ARATH FKBP12-interacting protein of 37 kDa OS=*Arabidopsis thaliana* GN=FIP37 PE=1 SV=1 |
| Lsat\_1\_v5\_gn\_5\_132900 | 0.68 | hypothetical protein LSAT\_5X132900 [*Lactuca sativa*] |
| Lsat\_1\_v5\_gn\_5\_136680 | 0.34 | KEGG-Description=RAP2.12 | DNA binding / transcription factor | K09286 EREBP-like factor SWISS-PROT-Description=ERF1\_ORYSJ Ethylene-responsive transcription factor 1 OS=*Oryza sativa* subsp. japonica GN=EREBP1 PE=1 SV=1 GO\_annotations=GO:0003677: DNA binding: Molecular Function | GO:0003700: sequence-specific DNA binding transcription factor activity: Molecular Function |
| Lsat\_1\_v5\_gn\_5\_132501 | -0.54 | KEGG-Description=hypothetical protein | K02160 acetyl-CoA carboxylase biotin carboxyl carrier protein SWISS-PROT-Description=BCCP\_NOSS1 Biotin carboxyl carrier protein of acetyl-CoA carboxylase OS=*Nostoc* sp. (strain PCC 7120 / UTEX 2576) GN=accB PE=1 SV=2 |
| Lsat\_1\_v5\_gn\_5\_135361 | 0.63 | KEGG-Description=BGAL2 | BGAL2 (beta-galactosidase 2) | beta-galactosidase/ catalytic/ cation binding | K01190 beta-galactosidase [EC:3.2.1.23] SWISS-PROT-Description=BGAL\_SOLLC Beta-galactosidase OS=Solanum lycopersicum PE=1 SV=1 GO\_annotations=GO:0004553: hydrolase activity, hydrolyzing O-glycosyl compounds: Molecular Function | GO:0005529: sugar binding: Molecular Function |
| Lsat\_1\_v5\_gn\_5\_128280 | -0.96 | KEGG-Description=ERF4 | ERF4 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 4) | DNA binding / protein binding / transcription factor/ transcription repressor | K09286 EREBP-like factor SWISS-PROT-Description=ERF78\_ARATH Ethylene-responsive transcription factor 4 OS=*Arabidopsis thaliana* GN=ERF4 PE=1 SV=1 GO\_annotations=GO:0003677: DNA binding: Molecular Function | GO:0003700: sequence-specific DNA binding transcription factor activity: Molecular Function |
| Lsat\_1\_v5\_gn\_5\_141920 | 0.57 | SWISS-PROT-Description=Y5208\_ARATH Uncharacterized protein At5g12080 OS=*Arabidopsis thaliana* GN=At5g12080 PE=1 SV=1 GO\_annotations=GO:0016020: membrane: Cellular Component |
| Lsat\_1\_v5\_gn\_5\_132000 | 0.43 | KEGG-Description=BGL2 | BGL2 (BETA-1,3-GLUCANASE 2) | cellulase/ glucan 1,3-beta-glucosidase/ hydrolase, hydrolyzing O-glycosyl compounds | K01199 glucan endo-1,3-beta-D-glucosidase [EC:3.2.1.39] SWISS-PROT-Description=E1314\_ARATH Glucan endo-1,3-beta-glucosidase 14 OS=*Arabidopsis thaliana* GN=At2g27500/F10A12.18 PE=1 SV=2 GO\_annotations=GO:0004553: hydrolase activity, hydrolyzing O-glycosyl compounds: Molecular Function |
| Lsat\_1\_v5\_gn\_5\_132400 | -0.73 | KEGG-Description=pco124429 | LOC100283372 | K10732 GINS complex subunit 1 SWISS-PROT-Description=PSF1\_MOUSE DNA replication complex GINS protein PSF1 OS=*Mus musculus* GN=Gins1 PE=2 SV=1 |
| Lsat\_1\_v5\_gn\_5\_143500 | 0.39 | uncharacterized protein LOC111892624 isoform X1 [*Lactuca sativa*] |
| Lsat\_1\_v5\_gn\_5\_127501 | -0.59 | SWISS-PROT-Description=NSE2\_ARATH E3 SUMO-protein ligase MMS21 OS=*Arabidopsis thaliana* GN=MMS21 PE=1 SV=1 |
| Lsat\_1\_v5\_gn\_5\_128320 | -0.61 | KEGG-Description=Cell division protein ftsH, putative (EC:3.6.4.3) | K03798 cell division protease FtsH [EC:3.4.24.-] SWISS-PROT-Description=PP354\_ARATH Pentatricopeptide repeat-containing protein At4g37380, chloroplastic OS=*Arabidopsis thaliana* GN=PCMP-H48 PE=2 SV=1 |
| Lsat\_1\_v5\_gn\_5\_132580 | 0.26 | uncharacterized protein LOC111910222 [*Lactuca sativa*] |
| Lsat\_1\_v5\_gn\_5\_140720 | 0.43 | uncharacterized protein LOC111892596 isoform X1 [*Lactuca sativa*] |
| Lsat\_1\_v5\_gn\_5\_141840 | 0.44 | KEGG-Description=hypothetical protein LOC100261060 | K13148 integrator complex subunit 11 [EC:3.1.27.-] SWISS-PROT-Description=ATL52\_ARATH RING-H2 finger protein ATL52 OS=*Arabidopsis thaliana* GN=ATL52 PE=2 SV=1 GO\_annotations=GO:0005515: protein binding: Molecular Function |
| Lsat\_1\_v5\_gn\_5\_127720 | -0.96 | KEGG-Description=DNA repair protein rhp16, putative | K01509 adenosinetriphosphatase [EC:3.6.1.3] SWISS-PROT-Description=SM3L2\_ARATH Putative SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 3-like 2 OS=*Arabidopsis thaliana* GN=At5g22750 PE=2 SV=1 |
| Lsat\_1\_v5\_gn\_5\_140700 | 0.46 | KEGG-Description=hypothetical protein LOC100244107 | K01366 cathepsin H [EC:3.4.22.16] SWISS-PROT-Description=CYSP3\_SOLLC Cysteine proteinase 3 OS=*Solanum lycopersicum* GN=CYP-3 PE=2 SV=1 GO\_annotations=GO:0006508: proteolysis: Biological Process |
| Lsat\_1\_v5\_gn\_5\_140541 | 0.82 | KEGG-Description=Os05g0110900 | K00924 [EC:2.7.1.-] SWISS-PROT-Description=Y5102\_ARATH Serine/threonine-protein kinase At5g01020 OS=*Arabidopsis thaliana* GN=At5g01020 PE=1 SV=1 GO\_annotations=GO:0004672: protein kinase activity: Molecular Function | GO:0004674: protein serine/threonine kinase activity: Molecular Function | GO:0005524: ATP binding: Molecular Function |
| Lsat\_1\_v5\_gn\_5\_135760 | -0.31 | SWISS-PROT-Description=BRXL3\_ARATH Protein Brevis radix-like 3 OS=*Arabidopsis thaliana* GN=BRXL3 PE=2 SV=1 |
| Lsat\_1\_v5\_gn\_5\_134540 | -0.49 | KEGG-Description=Os02g0102900 | K04077 chaperonin GroEL SWISS-PROT-Description=RUBB\_PEA RuBisCO large subunit-binding protein subunit beta, chloroplastic OS=*Pisum sativum* PE=1 SV=2 |
| Lsat\_1\_v5\_gn\_5\_133981 | 0.60 | KEGG-Description=hypothetical protein | K10640 E3 ubiquitin-protein ligase RNF25 [EC:6.3.2.19] SWISS-PROT-Description=RWDD1\_MOUSE RWD domain-containing protein 1 OS=*Mus musculus* GN=Rwdd1 PE=1 SV=1 |
| Lsat\_1\_v5\_gn\_5\_138341 | 0.96 | KEGG-Description=aminoadipic semialdehyde synthase, putative (EC:1.5.1.8 1.5.1.10) | K14157 alpha-aminoadipic semialdehyde synthase [EC:1.5.1.8 1.5.1.9] SWISS-PROT-Description=AASS\_ARATH Alpha-aminoadipic semialdehyde synthase OS=*Arabidopsis thaliana* GN=LKR/SDH PE=1 SV=1 GO\_annotations=GO:0016491: oxidoreductase activity: Molecular Function |
| Lsat\_1\_v5\_gn\_5\_129761 | 1.4 | KEGG-Description=oxidoreductase, 2OG-Fe(II) oxygenase family protein | K06892 SWISS-PROT-Description=G3OX3\_ARATH Gibberellin 3-beta-dioxygenase 3 OS=*Arabidopsis thaliana* GN=At4g21690 PE=2 SV=1 |
| Lsat\_1\_v5\_gn\_5\_132621 | -0.43 | uncharacterized protein LOC111910225 [Lactuca sativa] |
| Lsat\_1\_v5\_gn\_5\_135800 | -0.34 | protein BIG GRAIN 1-like B [*Lactuca sativa*] |
| Lsat\_1\_v5\_gn\_5\_137160 | -0.29 | uncharacterized protein LOC111910399 isoform X1 [*Lactuca sativa*] |
| Lsat\_1\_v5\_gn\_5\_132201 | -0.28 | KEGG-Description=polygalacturonase, putative / pectinase, putative | K01184 polygalacturonase [EC:3.2.1.15] SWISS-PROT-Description=PGLR5\_ARATH Probable polygalacturonase At1g80170 OS=*Arabidopsis thaliana* GN=At1g80170 PE=2 SV=1 GO\_annotations=GO:0004650: polygalacturonase activity: Molecular Function |
| Lsat\_1\_v5\_gn\_5\_128020 | -0.66 | KEGG-Description=Dynamin central region family protein | K01528 dynamin GTPase [EC:3.6.5.5] SWISS-PROT-Description=DLPC\_DICDI Dynamin-like protein C OS=*Dictyostelium discoideum* GN=dlpC PE=2 SV=2 GO\_annotations=GO:0003924: GTPase activity: Molecular Function |
| Lsat\_1\_v5\_gn\_5\_129460 | 0.29 | hypothetical protein LSAT\_5X129460 [*Lactuca sativa*] |
| Lsat\_1\_v5\_gn\_5\_129941 | -0.33 | SWISS-PROT-Description=NOC2L\_ARATH Nucleolar complex protein 2 homolog OS=*Arabidopsis thaliana* GN=At2g18220 PE=2 SV=1 |

### **SUPPLEMENTARY TABLE S9. Contrast results of leaf crinkliness, head firmness, and fresh plant weight.** Orthogonal contrast results of leaf crinkliness, firmness, and fresh plant weight for experiments conducted in Yuma, Arizona 2015–2016 and Salinas, California (65 and 71 days after imbibition). The "estimate" column is the estimated difference in the trait between the contrasting groups (i.e., haplotypes) and the standard error (Std. Error) of the difference. A P-value of 0.05 or less is considered significantly different. If the orthogonal contrast was not done and there are no results, then “NM” is assigned.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | **YAC 2015-2016** | | | **SAL 2016-65Days** | | | **SAL 2016-71Days** | | | |
| Trait | **Contrast** | **Estimate** | **Std. Error** | **P-value** | **Estimate** | **Std. Error** | **P-value** | **Estimate** | **Std. Error** | **P-value** |
| Leaf crinkliness | El Dorado vs. Emperor | -1.6 | 0.34 | <1.0E-04 | -2.0 | 0.32 | <1.0E-04 | NM | NM | NM |
| Leaf crinkliness | Haplotype 15, 16, and 14G1227 vs. Haplotype17 and 18 | -10.2 | 0.76 | <1.0E-04 | -10.9 | 0.72 | <1.0E-04 | NM | NM | NM |
| Leaf crinkliness | Haplotype 15 vs. Haplotype 16 | 0.30 | 0.21 | 0.15 | 0.0 | 0.20 | 1.0 | NM | NM | NM |
| Leaf crinkliness | Haplotype 17 vs. Haplotype 18 | 0.13 | 0.14 | 0.34 | -0.38 | 0.13 | 5.4E-03 | NM | NM | NM |
| Firmness | El Dorado vs. Emperor | 0.80 | 0.42 | 0.06 | -0.38 | 0.30 | 0.21 | -0.13 | 0.29 | 0.67 |
| Firmness | Haplotype 15, 16, and 14G1227 vs. Haplotype17 and 18 | -7.1 | 0.93 | <1.0E-04 | -6.4 | 0.66 | < 1.0E-04 | -3.25 | 0.66 | <1.0E-04 |
| Firmness | Haplotype 15 vs. Haplotype 16 | 0.30 | 0.26 | 0.24 | 0.50 | 0.18 | 6.8E-03 | 0.41 | 0.18 | 0.026 |
| Firmness | Haplotype 17 vs. Haplotype 18 | -0.32 | 0.17 | 0.07 | -0.21 | 0.12 | 0.096 | -0.021 | 0.12 | 0.86 |
| Fresh plant weight | El Dorado vs. Emperor | -41.9 | 85.0 | 0.63 | 9.6 | 102 | 0.93 | -82.9 | 99.8 | 0.41 |
| Fresh plant weight | Haplotype 15, 16, and 14G1227 vs. Haplotype17 and 18 | 2205 | 190 | <1.0E-04 | -669 | 228 | 4.2E-03 | -141 | 224 | 0.53 |
| Fresh plant weight | Haplotype 15 vs. Haplotype 16 | -46.3 | 52.0 | 0.38 | 53.3 | 62.4 | 0.40 | 24.6 | 61.1 | 0.69 |
| Fresh plant weight | Haplotype 17 vs. Haplotype 18 | 99.3 | 34.7 | 7.1E-03 | -24.3 | 41.6 | 0.56 | -46.1 | 41.2 | 0.27 |