

Table S1 Population geography and habitat information

| Population | Elevation (m) | Latitude | Longitude | Description | Country |
|------------|---------------|------------|------------|---|---------|
| LA1963 | 200 | -18.066667 | -70.316667 | Very dry sandy situation | Peru |
| LA3111 | 3070 | -17.466667 | -70.033333 | On side of road | Peru |
| LA2931 | 2275 | -20.916667 | -69.066667 | Dry streambed with salt or algae deposits | Chile |
| LA4330 | 3126 | -22.350833 | -68.319722 | Rocky quebrada, plants growing among rocks | Chile |
| LA2932 | 300-400 | -22.468056 | -70.225 | dry quebrada in loma zone | Chile |
| LA4107 | 86 | -25.318889 | -70.446111 | In extremely fine alluvial soil below dry waterfall | Chile |

Population information was obtained from Tomato genetic Resource Center (TGRC) website.

Table S2 The mapping quality to reference genome *Solanum pennellii*

| Populations | LA1963 | LA3111 | LA2931 | LA4330 | LA2932 | LA4107 |
|---------------------------|------------|------------|------------|------------|------------|------------|
| SNPs | 27,181,900 | 25,041,882 | 26,482,733 | 24,341,829 | 23,517,649 | 21,757,938 |
| Unique SNPs ^a | 1,162,108 | 990,787 | 1,085,306 | 9,48,174 | 1,532,616 | 1,582,572 |
| Fixed SNPs ^b | 10,245,302 | 11,371,703 | 10,513,888 | 12,130,202 | 13,096,032 | 14,707,614 |
| Insertions | 2,462,707 | 2,312,682 | 2,417,195 | 2,190,179 | 2,082,451 | 1,933,860 |
| Deletions | 2,657,687 | 2,454,456 | 2,594,730 | 2,319,887 | 2,199,316 | 2,022,334 |
| Ts/Tv ^c | 1.11 | 1.11 | 1.11 | 1.11 | 1.12 | 1.12 |
| Variant rate ^d | 30 | 33 | 31 | 34 | 35 | 38 |

^aSNPs denote only detected in specific population.

^bSNPs denote the conserved in all individuals of the same population.

^cTs/Tv denotes of ratio of Transition with Transversion.

^dVariant rate refers to how many bases on average can detect one variant.

Table S3 The statistics in candidate regions and whole-genome

| Population | nucleotide diversity (π) | | Watterson's theta (θ_w) | | Tajima's D | | Fay and Wu's H | | LD (r^2) | |
|------------|-----------------------------------|-----------------------------------|----------------------------------|---------------------|---------------------------------|--------------------|----------------------------------|---------------------|---------------------------------|-----------------------------------|
| | genome ^a | candidate ^b | genome | candidate | genome | candidate | genome | candidate | genome | candidate |
| LA1963 | $0.00472 \pm 3.74 \times 10^{-5}$ | $0.00161 \pm 2.03 \times 10^{-4}$ | 1643.441 \pm 7.92 | 979.974 \pm 49.82 | $0.668 \pm 5.80 \times 10^{-3}$ | 0.138 \pm 0.091 | $0.081 \pm 2.21 \times 10^{-3}$ | 0.0348 \pm 0.017 | $0.197 \pm 3.61 \times 10^{-6}$ | 0.699 \pm 2.43 $\times 10^{-4}$ |
| LA2931 | $0.00452 \pm 3.60 \times 10^{-5}$ | $0.0015 \pm 1.57 \times 10^{-4}$ | 1561.081 \pm 7.88 | 882.284 \pm 37.53 | $0.719 \pm 5.85 \times 10^{-3}$ | -0.093 \pm 0.096 | $0.066 \pm 2.287 \times 10^{-3}$ | -0.127 \pm 0.018 | $0.197 \pm 3.85 \times 10^{-6}$ | 0.441 \pm 4.16 $\times 10^{-4}$ |
| LA2932 | $0.00268 \pm 2.40 \times 10^{-5}$ | $0.00178 \pm 2.28 \times 10^{-4}$ | 1073.650 \pm 6.72 | 724.949 \pm 48.47 | $0.782 \pm 7.59 \times 10^{-3}$ | -0.1189 \pm 0.14 | $-0.134 \pm 3.30 \times 10^{-3}$ | -0.355 \pm 0.062 | $0.312 \pm 9.19 \times 10^{-6}$ | 0.761 \pm 3.39 $\times 10^{-4}$ |
| LA3111 | $0.00393 \pm 3.30 \times 10^{-5}$ | $0.00191 \pm 2.17 \times 10^{-4}$ | 1380.304 \pm 7.20 | 912.403 \pm 48.47 | $0.705 \pm 6.15 \times 10^{-3}$ | -0.0544 \pm 0.11 | $0.012 \pm 2.59 \times 10^{-3}$ | -0.073 \pm 0.0219 | $0.218 \pm 4.60 \times 10^{-6}$ | 0.663 \pm 4.41 $\times 10^{-4}$ |
| LA4107 | $0.00174 \pm 1.88 \times 10^{-5}$ | $0.00138 \pm 2.18 \times 10^{-4}$ | 903.806 \pm 6.26 | 754.220 \pm 51.16 | $0.783 \pm 6.56 \times 10^{-3}$ | -0.0930 \pm 0.15 | $-0.144 \pm 2.70 \times 10^{-3}$ | -0.172 \pm 0.048 | $0.329 \pm 1.34 \times 10^{-5}$ | 0.552 \pm 9.33 $\times 10^{-4}$ |
| LA4330 | $0.00341 \pm 2.88 \times 10^{-5}$ | $0.00217 \pm 1.54 \times 10^{-4}$ | 1164.556 \pm 6.71 | 783.050 \pm 32.28 | $0.748 \pm 7.40 \times 10^{-3}$ | 0.105 \pm 0.08 | $-0.127 \pm 3.50 \times 10^{-3}$ | -0.519 \pm 0.042 | $0.316 \pm 7.25 \times 10^{-6}$ | 0.671 \pm 2.49 $\times 10^{-4}$ |

^aThe values were calculated in whole-genome level, the same blow.

^bThe values were calculated in candidate regions detected by SweeD and OmegaPlus, the same blow.

^cThe values give the average and standard error of mean, the same blow.

Table S4 Pairwise F_{ST} of different populations in whole genome and candidate regions

| Genome | Candidate |
|-----------------------------|-----------------------------|
| 0.058±9.48×10 ⁻⁴ | 0.064±9.53×10 ⁻³ |
| 0.086±9.88×10 ⁻⁴ | 0.092±1.11×10 ⁻² |
| 0.137±1.29×10 ⁻³ | 0.165±1.23×10 ⁻² |
| 0.139±1.25×10 ⁻³ | 0.196±1.21×10 ⁻² |
| 0.147±1.31×10 ⁻³ | 0.172±1.10×10 ⁻² |
| 0.210±1.43×10 ⁻³ | 0.267±1.27×10 ⁻² |
| 0.245±1.60×10 ⁻³ | 0.258±1.70×10 ⁻² |
| 0.252±1.65×10 ⁻³ | 0.288±1.61×10 ⁻² |
| 0.312±1.51×10 ⁻³ | 0.390±1.59×10 ⁻² |
| 0.315±1.86×10 ⁻³ | 0.367±1.91×10 ⁻² |
| 0.327±1.61×10 ⁻³ | 0.351±1.75×10 ⁻² |
| 0.346±1.92×10 ⁻³ | 0.460±1.36×10 ⁻² |
| 0.362±1.94×10 ⁻³ | 0.392±2.09×10 ⁻² |
| 0.384±1.79×10 ⁻³ | 0.439±1.72×10 ⁻² |
| 0.417±1.92×10 ⁻³ | 0.534±1.45×10 ⁻² |

Table S5 The summary of outlier SNPs from RDA models

| RDA model | Current | | | LGM | | | Overlaps |
|--|------------------|-------|-------|------|-------|-------|----------|
| | RDA1 | RDA2 | Total | RDA1 | RDA2 | Total | |
| All sweeps ^a | 280 ^b | 3,987 | 4,267 | 350 | 1,992 | 2,342 | 1,647 |
| Circadian rhythm and photoperiod/flowering | 25 | 79 | 104 | 14 | 66 | 80 | 61 |
| Vernalization response | 7 | 19 | 26 | 0 | 23 | 23 | 18 |
| Root hair cell differentiation | 7 | 39 | 46 | 0 | 129 | 129 | 39 |
| Protein lipidation | 25 | 31 | 56 | 31 | 34 | 65 | 42 |

^aAll sweeps denote candidate regions identified overlaps between SweeD and OmegaPlus.

^bThe values denote number of outlier SNPs detected from RDA1 and RDA2.

Table S6 The summary of correlation between outlier SNPs and climatic variables in RDA models

| climatic variables | All sweeps | | Circadian rhythm and photoperiodism flowering | | Vernalization | | Root hair development | | Protein lipidation | |
|---------------------|------------|-------|---|-----|---------------|-----|-----------------------|-----|--------------------|-----|
| | current | LGM | current | LGM | current | LGM | current | LGM | current | LGM |
| ann_AET | | | | | | | 5 | | | |
| ann_mTmin | | 249 | | 24 | 1 | 6 | | | | 18 |
| ann_PETmax | | | 13 | | | | | | | |
| ann_PETmin | | | | | | | 4 | | | |
| ann_Rmax | | | | | | | 6 | | | |
| ann_Rmean | 540 | | | | | | 4 | | | |
| ann_Rmin | | | 12 | | | | | | | |
| ann_Wmin | 510 | | | | | | | | | |
| annualPET | 1,184 | | 13 | 8 | | | | 18 | | |
| Bio15 | | | | 22 | | | | | | |
| Bio19 | 480 | 350 | | 16 | | 3 | | | | |
| Bio4 | | | 10 | | 4 | 2 | 21 | 12 | 10 | 21 |
| Bio7 | 372 | 473 | 21 | 9 | 10 | | 3 | 4 | 24 | 1 |
| Bio8 | | | | | 3 | | | | | |
| continentality | 294 | | 35 | | | | 3 | | 10 | |
| CV_AET | 386 | | | | 4 | | | | | |
| CV_R | 501 | | | | | | | | | |
| CV_VAPR | | | | | | | | | 10 | |
| MaxTempColdestMonth | | | | | | 12 | | | | |
| MinTempWarmestMonth | | | | | | | | | 2 | |
| PETColdestQuarter | | 1,090 | | | | | | 14 | | 25 |
| PETDriestQuarter | | 377 | | | | | | | | |
| PETWarmestQuarter | | | | 1 | | | | | | |
| PETWettestQuarter | | | | | 4 | | | 81 | | |

The number of outlier SNPs denote number of strongest correlated SNPs with specific climatic variable.

Table S7 Enrichment of biological process in two networks

| Terms of sub-blue | Number of genes | Terms of sub-turquoise | Number of gens |
|---|-----------------|---|----------------|
| DNA replication initiation | 8 | response to heat | 23 |
| double-strand break repair via break-induced replication | 7 | response to water deprivation | 23 |
| ribosomal large subunit assembly | 10 | SCF-dependent proteasomal ubiquitin-dependent protein catabolic process | 11 |
| cell cycle | 16 | protein complex oligomerization | 8 |
| ribosomal large subunit biogenesis | 7 | response to hydrogen peroxide | 11 |
| cell division | 21 | peptidyl-tyrosine dephosphorylation | 8 |
| microtubule-based movement | 11 | cellular amino acid catabolic process | 6 |
| DNA replication | 11 | lipid storage | 6 |
| mitotic cell cycle | 6 | killing of cells of other organism | 6 |
| DNA-dependent DNA replication | 4 | response to salt stress | 21 |
| protein folding | 14 | galactose metabolic process | 5 |
| anaphase-promoting complex-dependent catabolic process | 4 | cinnamic acid biosynthetic process | 5 |
| spliceosomal snRNP assembly | 4 | aromatic amino acid family catabolic process | 5 |
| | | erythrose 4-phosphate/phosphoenolpyruvate family amino acid catabolic process | 5 |
| hydrotropism | 4 | positive regulation of transcription, DNA-templated | 16 |
| RNA modification | 12 | cuticle development | 4 |
| DNA repair | 13 | L-phenylalanine metabolic process | 5 |
| maturation of LSU-rRNA | 3 | | |
| embryo development ending in seed dormancy | 14 | cellular response to heat | 6 |
| mitochondrion organization | 4 | lipid droplet organization | 4 |
| rRNA metabolic process | 4 | negative regulation of abscisic acid-activated signaling pathway | 6 |
| ncRNA processing | 3 | cellular response to unfolded protein | 4 |
| ribosomal small subunit biogenesis | 3 | abscisic acid-activated signaling pathway | 11 |
| regulation of cyclin-dependent protein serine/threonine kinase activity | 5 | response to abscisic acid | 17 |
| negative regulation of translation | 4 | signal transduction | 14 |
| response to cadmium ion | 10 | protein folding | 15 |
| polar nucleus fusion | 3 | seed maturation | 4 |
| DNA recombination | 7 | translational initiation | 12 |
| cytokinesis by cell plate formation | 3 | ubiquitin-dependent protein catabolic process | 15 |

| | | | |
|--|----|---|----|
| rRNA processing | 8 | negative regulation of transcription, DNA-templated | 9 |
| pseudouridine synthesis | 4 | DNA methylation | 4 |
| ribosome biogenesis | 6 | response to freezing | 3 |
| cellular response to cold | 3 | negative regulation of endopeptidase activity | 8 |
| ribosomal small subunit assembly | 3 | arginine biosynthetic process | 3 |
| RNA biosynthetic process | 7 | stomatal movement | 3 |
| lipid metabolic process | 9 | protein dephosphorylation | 11 |
| fatty acid biosynthetic process | 6 | negative regulation of nucleic acid-templated transcription | 5 |
| meiotic cell cycle | 3 | lipid metabolic process | 11 |
| chromatin organization | 5 | protein polyubiquitination | 5 |
| floral organ abscission | 2 | regulation of transcription by RNA polymerase II | 16 |
| histone deacetylation | 2 | intracellular signal transduction | 10 |
| phosphate ion transmembrane transport | 2 | chromatin silencing | 3 |
| histone modification | 3 | negative regulation of seed germination | 3 |
| microtubule-based process | 4 | chaperone-mediated protein folding | 3 |
| DNA duplex unwinding | 12 | negative regulation of cellular macromolecule biosynthetic process | 5 |
| regulation of anthocyanin biosynthetic process | 2 | nuclear-transcribed mRNA catabolic process, nonsense-mediated decay | 3 |
| DNA endoreduplication | 2 | transcription elongation from RNA polymerase II promoter | 3 |
| cell redox homeostasis | 2 | jasmonic acid mediated signaling pathway | 4 |
| positive regulation of translational fidelity | 2 | response to ethylene | 5 |
| regulation of meristem development | 2 | regulation of abscisic acid-activated signaling pathway | 3 |
| response to brassinosteroid | 3 | rhythmic process | 3 |
| protein peptidyl-prolyl isomerization | 5 | regulation of secondary shoot formation | 3 |
| glutamine metabolic process | 3 | cold acclimation | 4 |
| negative regulation of cell population proliferation | 2 | protein refolding | 4 |
| cytoskeleton organization | 4 | protein sumoylation | 3 |
| nucleosome assembly | 5 | cellular response to cold | 3 |
| cytoplasmic microtubule organization | 2 | positive regulation of response to water deprivation | 3 |
| | | vegetative to reproductive phase transition of meristem | 5 |
| | | defense response to bacterium | 11 |
| | | phosphorelay signal transduction system | 6 |
| | | mRNA cis splicing, via spliceosome | 3 |

| | | |
|--|--|---|
| | root development | 8 |
| | response to chitin | 7 |
| | cellular response to hypoxia | 5 |
| | cellular response to lipid | 3 |
| | embryo sac development | 4 |
| | gene silencing by RNA | 5 |
| | regulation of circadian rhythm | 2 |
| | positive regulation of translational elongation | 2 |
| | positive regulation of translational termination | 2 |
| | phosphate ion homeostasis | 2 |
| | positive regulation of proteasomal ubiquitin-dependent protein catabolic process | 3 |

Table S8 Enrichment of cellular component in two networks

| Terms of sub-blue | Number of genes | Terms of sub-turquoise | Number of gens |
|--|-----------------|---|----------------|
| cytosolic ribosome | 24 | SCF ubiquitin ligase complex | 11 |
| ribonucleoprotein complex | 38 | monolayer-surrounded lipid storage body | 6 |
| large ribosomal subunit | 15 | CCAAT-binding factor complex | 5 |
| nucleolus | 34 | protein-containing complex | 9 |
| microtubule | 18 | autophagosome | 3 |
| polysomal ribosome | 8 | cytoplasmic stress granule | 3 |
| small ribosomal subunit | 9 | nuclear speck | 4 |
| chromocenter | 5 | chromatin | 14 |
| MCM complex | 5 | lipid droplet | 3 |
| nucleosome | 11 | secretory vesicle | 4 |
| intracellular organelle lumen | 22 | vacuole | 16 |
| organelle lumen | 22 | P-body | 4 |
| chloroplast thylakoid | 8 | endoplasmic reticulum lumen | 3 |
| small-subunit processome | 7 | mitochondrial respiratory chain complex I | 2 |
| mitochondrial matrix | 8 | intrinsic component of membrane | 2 |
| preribosome, large subunit precursor | 6 | vacuolar membrane | 11 |
| chromosome | 6 | plant-type cell wall | 5 |
| cytosolic small ribosomal subunit | 3 | ribonucleoprotein complex | 11 |
| kinesin complex | 4 | organelle envelope | 3 |
| phragmoplast | 6 | cell wall | 10 |
| plastid stroma | 8 | Golgi cisterna membrane | 1 |
| plastid | 15 | cytoskeleton | 3 |
| plastid envelope | 6 | large ribosomal subunit | 2 |
| cyclin-dependent protein kinase holoenzyme complex | 5 | spliceosomal complex | 4 |
| Cul4-RING E3 ubiquitin ligase complex | 4 | microbody | 4 |
| plastid thylakoid | 3 | peroxisome | 2 |
| chloroplast stroma | 15 | plastid | 9 |
| plant-type cell wall | 7 | chloroplast thylakoid | 2 |
| anaphase-promoting complex | 3 | plant-type vacuole | 2 |
| nuclear envelope | 3 | endoplasmic reticulum | 12 |
| cell plate | 3 | phragmoplast | 2 |
| U5 snRNP | 2 | chloroplast stroma | 10 |
| intracellular non-membrane-bounded organelle | 6 | Golgi trans cisterna | 1 |

| | | | |
|--|---|--|---|
| condensed chromosome, centromeric region | 2 | intracellular non-membrane-bounded organelle | 3 |
| 90S preribosome | 2 | plastid envelope | 2 |
| site of double-strand break | 2 | nucleosome | 4 |
| replication fork | 2 | | |
| spindle microtubule | 2 | | |