**Mapping-by-sequencing**

To map causal *lazy* mutations, we generated three second-generation (F2) populations by crossing the three *lz* mutants with *S. pimpinellifolium*. From a total of XXX *lz5* F2 plants, we selected XX mutants and XX WT siblings for tissue collection and DNA extraction. The *lz8* mutant F2 population consisted of XXX individuals and XX and XX mutant and WT siblings, respectively, were selected for DNA extraction. From XXX *lz10* F2 individuals we chose XX mutant and XX wildtype siblings for extraction and sequencing. For each of the mutant and wildtype sibling pools, an equal amount of tissue from each plant (X g) was pooled for DNA extraction using standard protocols. Libraries were prepared with … from X µg genomic DNA sheared to XXX bp insert size. All DNA libraries were sequenced by Macrogen on the Illumina 2500 platform using paired-end 101-bp runs. In total we obtained 464.8 million read pairs (Supplemental Table XX) with an average of 77.5 million read pairs for each of the pools.

Genomic DNA reads were trimmed by quality using Trimmomatic v0.32 [Bolger2014] (HiSeq 2500 read parameters: ILLUMINACLIP:TruSeq3-PE-2.fa:2:40:15:1:FALSE LEADING:3 TRAILING:3 SLIDINGWINDOW:4:15 MINLEN:36 ; GAIIx read parameters: ILLUMINACLIP:TruSeq2-PE.fa:2:30:10:1:FALSE LEADING:3 TRAILING:3 SLIDINGWINDOW:4:15 MINLEN:36 TOPHRED33) and paired reads mapped to the reference tomato genome (SL2.50) using BWA-MEM 0.7.16a-r1181 (parameters: -M) (Li, 2013; Li and Durbin, 2009). Alignments were then sorted with samtools and duplicates marked with PicardTools v1.126 (parameters: VALIDATION\_STRINGENCY=LENIENT) (Li et al., 2009, <http://broadinstitute.github.io/picard>). SNPs were called with samtools/bcftools v1.3.1 (samtools mpileup parameters: --ignore-RG --max-depth 1000000 --output-tags DP,AN --min-BQ 0 --no-BAQ --uncompressed --BCF; bcftools call parameters: --multiallelic-caller --variants-only --output-type z) (Li, 2011; Li et al., 2009) using read alignments for the sequencing pools from this project in addition to reference M82 [Bolger2014] and *S. pimpinellifolium* [Consortium2012] reads. Called SNPs were then filtered for bi-allelic high quality SNPs at least 100 bp from a called indel using bcftools (Li, 2011). Following read alignment and SNP calling, all statistics and calculations were done in R (RTeam, 2015).

**\*\*Soon-ju, pick the one you want to use:**

**SNPindex method for mapping**

SNP index (mutant depth / total depth) was calculated for each SNP by sequencing pool. The difference in SNP index (deltaSNPindex) was then calculated between the mutant and wildtype pools for each *lz* mutant (mutant SNPidx – wildtype SNPidx). Finally, average deltaSNPindex (100 SNP windows, 0 SNP sliding windows) was plotted across the twelve tomato chromosomes and a significance threshold set at the 95th percentile of all individual deltaSNPindices.

**Ratio-of-ratio method for mapping**

Read depth for each allele at segregating bi-allelic SNPs in 1 Mb sliding windows (by 100 kb) was summed for the mutant pools and wild-type sequencing pools. Mutant:non-mutant SNP ratios were calculated then calculated for each *lz* mutant and the mutant SNP ratio was divided by wild-type SNP ratio (+ 0.5) and plotted across the 12 tomato chromosomes.