Supplemental Figure 1. Sublines of IL10-2-2. This figure shows the selected recombinants of IL10-2-2. The first red bar represents the cultivated genome marked as 10-2-2 (G=1). The second bar, colored in green, represents IL 10-2-2. The two markers that defined the break point between the cultivated and the wild genomes are shown at the break point. The name of the marker is indicated in bold and the genomic position on chromosome 10 is indicated under the marker name. On the right side of the figure, mean total yield (TY) and mean coefficient of variation (CV) for the different lines, and t test analysis of the CV values of each recombinant as compared to M82 (i.e., 10-2-2 (G=1)), are listed. Two recombinants showed a significant difference (rec 32, rec 22) in their CV values. The two shared a *S. pennellii* segment, which contains about 44 genes with none of the usual suspects.
Supplemental Figure 2

A

M-82 TTGAACCACCAGCGAAAGGACGAGGGTCCGC

B

M-82 TTGAACCACCAGCGAAAGGACGAGGGTCCGC

C

M-82 MLPLINSCIFTPLSSLLPPRSTVISCQAAADPSAAGGPSSFRWAAAAPGFG/ /DLDDKPP-

D

E

CR9 MLPLINSCIFTPLPFITSSS-

CR6.1 MLPLINSCIFTPLVLHYFLLVDPSSLVAKPLLTHQLPAdPRPFRWAAAAPGFG/ /DLDDKPP-

CR9 MLPLINSCIFTPLPFITSSS-
Supplemental Figure 2. CRISPR/Cas9 mutations generated in Solyc01g108200. Validation of the Solyc01g108200 as the gene causing the canal-1 mutation using the CRISPR/Cas9 system. (A) Scheme and sequence of the CRISP/Cas 9 mutation position CR9, i.e., a deletion of 6 nucleotides, in the first exon of the gene Solyc01g108200. Also shown is the sequence of the guided RNA and the protospacer adjacent motif (PAM) site. (B) Scheme and sequence of mutant CR6.1, which involved deletion and insertion of a nucleotide. (C) The amino acid sequence of M82 and the two mutations (CR6.1 – change of 29 amino acids, CR9 – stop codon after 22 amino acids). (D) Image of CR9 cotyledons; the severity of the mutation did not allow for true leaves to develop. (E) Image of CR6.1 about 30 days after germination. This plant did not produce seeds.
**Supplemental Table 1**

| Introgression Line | Genotype | Mean (CV (%)) | Tukey-Kramer's (α=0.05) | Mean (Total Yield (Kg)) | Tukey-Kramer's (α=0.05) |
|--------------------|----------|---------------|-------------------------|-------------------------|-------------------------|
| IL 1-1             | 1        | 29.1          | B                       | 8.8                     | A                       |
|                    | 2        | 48.9          | B                       | 5.8                     | A                       |
|                    | 3        | 89.2          | A                       | 0.5                     | B                       |
| IL 3-3             | 1        | 39.6          | B                       | 6.3                     | A                       |
|                    | 2        | 47.4          | AB                      | 3.9                     | B                       |
|                    | 3        | 64.3          | A                       | 0.7                     | C                       |
| IL 3-4             | 1        | 32.6          | AB                      | 8.1                     | A                       |
|                    | 2        | 30.4          | B                       | 6.7                     | A                       |
|                    | 3        | 51.0          | A                       | 1.6                     | B                       |
| IL 10-2-2          | 1        | 32.7          | A                       | 6.6                     | A                       |
|                    | 2        | 21.9          | B                       | 8.1                     | A                       |
|                    | 3        | 31.8          | A                       | 7.2                     | A                       |
| IL 12-1-1          | 1        | 27.7          | A                       | 7.5                     | A                       |
|                    | 2        | 30.1          | A                       | 8.0                     | A                       |
|                    | 3        | 37.1          | A                       | 8.0                     | A                       |

**Supplemental Table 1. Summary of field trial Akko 2013.** A validation of yield canalization prediction conducted in 3 unstable lines (IL1-1, IL3-3, IL3-4) and two stable lines (IL10-2-2, IL12-1-1). Each of these lines was tested in six canalization replications plots in the spring season of 2013. Mean total yield (TY) and mean coefficient of variation (CV) for each of the ILs tested are shown. Tukey-Kramer's range test was performed for the three genotypic groups of each of the ILs; values followed by the same letter are not significantly different from each other. IL12-1-1 was not as stable as predicted based on the historical data; other lines were stable or not as expected. For each of the ILs genotype 1 represents M82 genome, genotype 2 represent heterozygous, and genotype 3 represent the introgression line homozygous for the wild species segment.
**Supplemental Table 2**

| Trait                          | Genotype | Mean (CV%) | Tukey-Kramer's (α=0.05) | Mean | Tukey-Kramer's (α=0.05) |
|-------------------------------|----------|------------|--------------------------|------|--------------------------|
| **1000 Seeds Weight (g)**    | 1        | 7.4        | A                        | 3.1  | A                        |
|                               | 2        | 6.7        | A                        | 3.1  | A                        |
|                               | 3        | 7.1        | A                        | 3.1  | A                        |
| **Brix (%)**                  | 1        | 6.8        | A                        | 3.7  | A                        |
|                               | 2        | 6.8        | A                        | 3.9  | A                        |
|                               | 3        | 7.1        | A                        | 4.0  | A                        |
| **Plant Weight (Kg)**         | 1        | 30.1       | A                        | 2.1  | B                        |
|                               | 2        | 28.3       | A                        | 2.3  | AB                       |
|                               | 3        | 30.4       | A                        | 2.4  | A                        |
| **Single Fruit Weight (g)**  | 1        | 12.2       | A                        | 71.7 | B                        |
|                               | 2        | 11.6       | A                        | 74.2 | AB                       |
|                               | 3        | 11.6       | A                        | 76.4 | A                        |
| **Total Yield (Kg)**          | 1        | 33.8       | A                        | 9.6  | A                        |
|                               | 2        | 26.1       | B                        | 10.6 | A                        |
|                               | 3        | 27.4       | B                        | 9.4  | A                        |

**Supplemental Table 2. A comparison of different traits of IL10-2-2.** This table gathered the mean value of five traits (1000 seeds weight, brix, plant weight, single fruit weight, total yield) that were measured in the field trials of the three IL10-2-2 genotypes; values followed by the same letter are not significantly different from each other. It can be seen that the mean CV index was significant only for the total yield trait. Genotype 1 represents M82 genome, genotype 2 represents heterozygous, and genotype 3 represents the introgression line 10-2-2.
## Supplemental Table 3

| Line name                  | Mutant number | Description                                   | N  | Mean CV (Total Yield) |
|----------------------------|---------------|-----------------------------------------------|----|-----------------------|
| *canal-1*                  | e4058         | Tomato DNAJ                                   | 6  | 100.7                 |
| double feathered           | n4596         | double feathered                              | 3  | 98.0                  |
| M3                         | e4936         | Thick stem SD                                 | 6  | 93.0                  |
| M3                         | e0112         | high yield                                    | 5  | 80.6                  |
| M3                         | e4895         | late                                          | 6  | 80.5                  |
| M3                         | e2871         | large plant, late                             | 6  | 73.2                  |
| e0137                      |               |                                               |    | 64.3                  |
| Clausa                     | e3545         | Clausa                                        | 6  | 60.9                  |
| M3                         | e9003         | Black. Long a-symmetrical inflo.              | 5  | 58.1                  |
| dwarf                      | e0862         | dwarf                                         | 6  | 57.7                  |
| N15                        | n5296         | N15                                           | 5  | 56.1                  |
| 0.0163                     |               |                                               | 5  | 55.7                  |
| M3                         | e4944         | SD, nipple                                    | 6  | 53.0                  |
| M3                         | e1297         | high HI                                       | 6  | 52.8                  |
| 0.023                      |               |                                               | 6  | 49.9                  |
| N2                         | e4489         | N2                                            | 4  | 49.2                  |
| La-2/+                     |               |                                               |    | 49.0                  |
| M3                         | e4894         | high HI                                       | 6  | 44.3                  |
| 0.075                      |               |                                               | 6  | 44.0                  |
| ago7                       | e4714         | ago7                                          | 5  | 42.6                  |
| La-6                       |               |                                               |    | 42.3                  |
| N10                        | e0988         | N10                                           | 6  | 42.1                  |
| 0.093                      |               |                                               | 6  | 38.3                  |
| dwarf                      | e4052         | dwarf                                         | 6  | 37.7                  |
| M3                         | e4464         | S                                             | 6  | 35.8                  |
| 0.089                      |               |                                               | 6  | 35.5                  |
| M82                        |               |                                               |    | 34.6                  |
| strigo 1                   |               |                                               |    | 34.3                  |
| N5                         | n1258         | N5                                            | 5  | 32.5                  |
| N6                         | e3118         | N6                                            | 5  | 32.2                  |
| dwarf                      | e4064+        | dwarf                                         | 6  | 31.5                  |
| M3                         | e9181         | high yield                                    | 6  | 30.1                  |
| N8                         | e3321         | N8                                            | 6  | 30.1                  |
| N1                         | n5568         | N1                                            | 4  | 29.9                  |
| N7                         | n1669         | N7                                            | 6  | 29.5                  |
| N3                         | e4632         | N3                                            | 6  | 29.4                  |
| j1, sp- from 2010-111-2    |               |                                               | 6  | 28.5                  |
| M3                         | e0478         | late                                          | 4  | 28.1                  |
| M3                         | e4203         | high yield, late                              | 6  | 28.0                  |
| N9                         | n2537         | N9                                            | 6  | 27.9                  |
| e850                       |               |                                               | 6  | 27.2                  |
| entire                     | e3335         | entire                                        | 6  | 25.4                  |
|     |     | N4   |     |     |
|-----|-----|------|-----|-----|
|     |     | e4130| N4  | 7   |
| M3  |     | e1137| small plant, large fruit | 6   |
| M3  |     | e2674| high HI | 6   |
| M3  |     | e4724| potato leaf | 6   |
| P&P |     |      |      | 2   |
| M3  |     | e9381| small bushy | 6   |
| entire |     | e2978| entire | 5   |

**Supplemental table 3 – A mutant screen for the yield canalization effect.**

Forty-eight ethyl methanesulfate (EMS) mutants were screened in a canalization replications plots field trial design. The table is sorted by CV index, from high to low value. e4058 *canal-1* is at the first place, which means it has high environmental sensitivity. M82 is located at the middle of the list. N represents the number of CANAREPs included in the analysis.
Supplemental Table 4 – Markers used to validate introgressions in 2013. These markers are part of a set of markers designed to differentiate wild species from the cultivated species. These five markers were used to identify and validate the introgression in the populations tested in the spring season of 2013.

| Marker name     | Forward sequence | Reverse sequence | Enzyme | (S. pennellii / M82)bps |
|-----------------|------------------|------------------|--------|-------------------------|
| 10-2-2 M2       | ATATGAGCACATTTGCATGTGATGA | GTCTCTTTATATGGTGTTGGATAAT | 405 / 480 |
| 10-2-2 M3       | GCAGTTGTTCCAGCAATATTG | GGAAATCTACCTCCAAGGTTAG | 480 / 630 |
| 10-2-2 M5       | AAGCACAATГАCTАCACTАAAАCAGT | ATATTTATTAGGATGCTCAATTCCTTTT | 414 / 590 |
| 10-2-2 M6       | AAGCAAAATTATАСТААСТАГАСГАГГ | GACTAGAGGAGAATCТТАААТАCГТG | 475 / 412 |
| 10-2-2 M8       | ТТАТГССGАGАААGАGАCГТТ | ТТАAАGGGCTTТТGAGАГТТ | 475 / 672 |

Supplemental Table 5 – Markers developed to differentiate between the different recombinants of IL10-2-2. These markers are based on indels between the genomes of the wild species S. pennellii (LA0716) and the cultivated inbred variety S. lycopersicum cv.M82.
