

Table S2. The top 5 single-gene knockouts and over-expressions that minimize the agronomic properties of the tomato fruit based on improve only one objective.

Gene	Gene Annotation	Efficiency (%) [†]	RIL
Vitamin C			
<i>LE33G09</i>	Not found	-1.91	28
<i>LE33H21</i>	Chloroplast inner membrane import protein Tic22, putative	-1.77	28
<i>LE9K02</i>	Not found	-1.27	28
<i>LE14J12</i>	40S Ribosomal protein S3a-like	-0.75	28
<i>LE17I11</i>	Potential GTPase activation protein	-0.73	28
<i>LE14J14</i>	SRFR1, protein complex scaffold	-19.31	28
<i>LE14B20</i>	Clathrin adaptor complexes medium subunit family protein	-18.28	28
<i>LE27C02</i>	Phytoene dehydrogenase, chloroplastic/chromoplastic	-14.78	28
<i>LE15D07</i>	Polynucleotide kinase- 3'-phosphatase, putative	-14.35	28
<i>LE3H15</i>	Non-cell-autonomous protein pathway1, plasmodesmal receptor	-13.84	28
Fructose and glucose			
<i>LE25A03</i>	Ribosomal protein S27-like protein	-7.66	24
<i>LE33H21</i>	Chloroplast inner membrane import protein Tic22, putative	-5.33	24
<i>LE20D08</i>	Cyclic nucleotide-gated calmodulin-binding ion channel	-5.19	24
<i>LE25M02</i>	Auxin response factor 8	-3.63	24
<i>LE9K02</i>	Histone H3.2	-2.98	24
<i>LE13M10</i>	Ribosomal protein L30e	-12.73	24
<i>LE1K08</i>	Not found	-10.46	24
<i>LE16L04</i>	Ureide permease, putative	-9.27	24
<i>LE23D07</i>	Transcription factor-related	-6.34	24
<i>LE1B05</i>	Integral membrane Yip1 family protein	-6.83	24

Malic and citric acids

<i>LE13F23</i>	Chloroplast phosphate transporter precursor	-34.10	159
<i>LE8C21</i>	Tubulin-specific chaperone C-related	-31.50	159
<i>LE18G02</i>	Heat shock protein, putative	-30.91	159
<i>LE2C24</i>	ATAB2; RNA binding	-27.77	159
<i>LE26N09</i>	6-Phosphogluconolactonase-like protein	-26.09	159
<i>LE15D07</i>	Polynucleotide kinase- 3'-phosphatase, putative	-42.18	159
<i>LE12J12</i>	Chloroplast methionine sulfoxide reductase B1 precursor	-40.03	159
<i>LE29L04</i>	ER33 protein	-40.45	159
<i>LE20K20</i>	Cation efflux protein/ zinc transporter, putative	-34.99	159
<i>LE27I24</i>	Katanin P80 subunit, putative	-31.69	159

Notice that the first five genes is the top 5 of single-gene knockouts (light rows) and the following five is the top 5 in over-expression (dark rows).

† Efficiencies were selected in the RIL where the perturbation maximizes the fitness.