Table S1. The top 5 single-gene knockouts and over-expressions that maximize the agronomic properties of the tomato fruit based on improve only one objective.

Gene	Gene Annotation	Efficiency (%)†	RIL	Probability‡
Vitamin C				
LE4I20	Serine/threonine protein kinase, putative	2.61	15	1
LE8C21	Tubulin-specific chaperone C-related	2.55	15	1
LE3E12	ABO1, transcription elongation regulator	2.37	15	1
LE29C10	Adenylate kinase 1, putative	2.19	15	1
LE28L05	Longevity assurance factor, putative	1.98	15	1
LE20K20	Cation efflux protein/zinc transporter, putative	6.74	15	1
LE16D22	Superoxide dismutase [Cu-Zn] 2	4.84	15	1
LE12J12	Chloroplast methionine sulfoxide reductase B1 precursor	3.27	15	1
LE12P18	Alcohol dehydrogenase, putative	2.77	15	1
LE4K23	Triosephosphate isomerase, chloroplastic	1.83	15	1
Fructose and glucose				
LE13F23	Chloroplast phosphate transporter precursor	23.66	86	0.01
LE8C21	Tubulin-specific chaperone C-related	19.88	86	0.05
LE26N09	6-Phosphogluconolactonase-like protein	17.45	86	1
LE2C24	ATAB2; RNA binding	17.41	86	0.99
LE32B05	YABBY2-like transcription factor YAB2	16.56	86	0.98
LE15D07	Polynucleotide kinase- 3'-phosphatase, putative	52.65	86	1
LE8A19	Putative glycerophosphoryl diester phosphodiesterase family protein	42.42	86	1
LE27C02	Phytoene dehydrogenase, chloroplastic/chromoplastic	40.59	86	1
LE14B20	Clathrin adaptor complexes medium subunit	40.56	86	0.92

	family protein			
LE12J12	Chloroplast methionine sulfoxide reductase B1 precursor	52.49	86	0.01

Malic and citric acids

LE33H21	Chloroplast inner membrane import protein Tic22, putative	16.88	13	0.79
LE20D08	Cyclic nucleotide-gated calmodulin-binding ion channel	13.99	13	1
LE25M02	Auxin response factor 8	12.05	13	1
LE25A03	Ribosomal protein S27-like protein	9.63	13	0.63
LE18N13	Not found	8.03	13	1
LE16L04	Ureide permease, putative	31.00	13	0.02
LE1K08	Not found	25.90	13	1
LE23D07	Transcription factor-related	23.38	13	0.79
LE13M10	Ribosomal protein L30e	21.37	13	0.02
LE14J14	SRFR1, protein complex scaffold	5.80	13	0.04

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.

‡ Probability of selecting the given perturbation across the set of RILs at the maximum level of efficiencies.