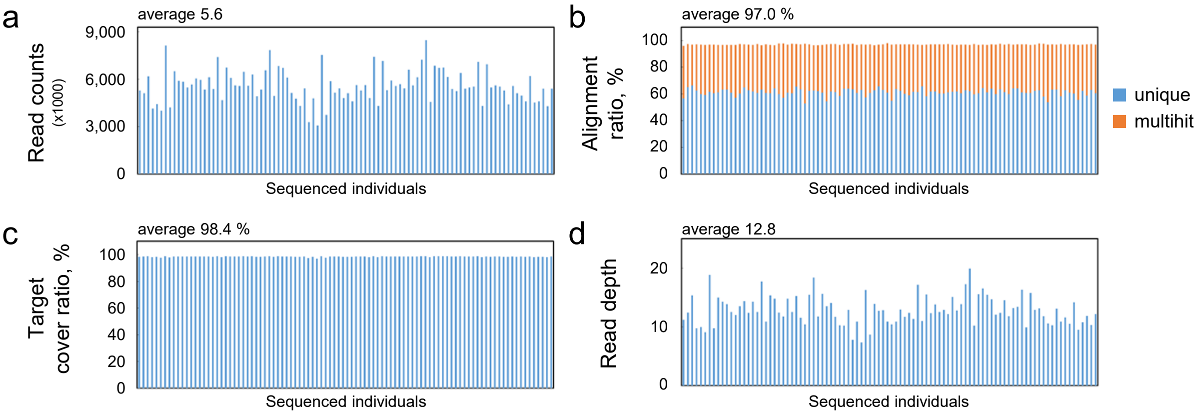
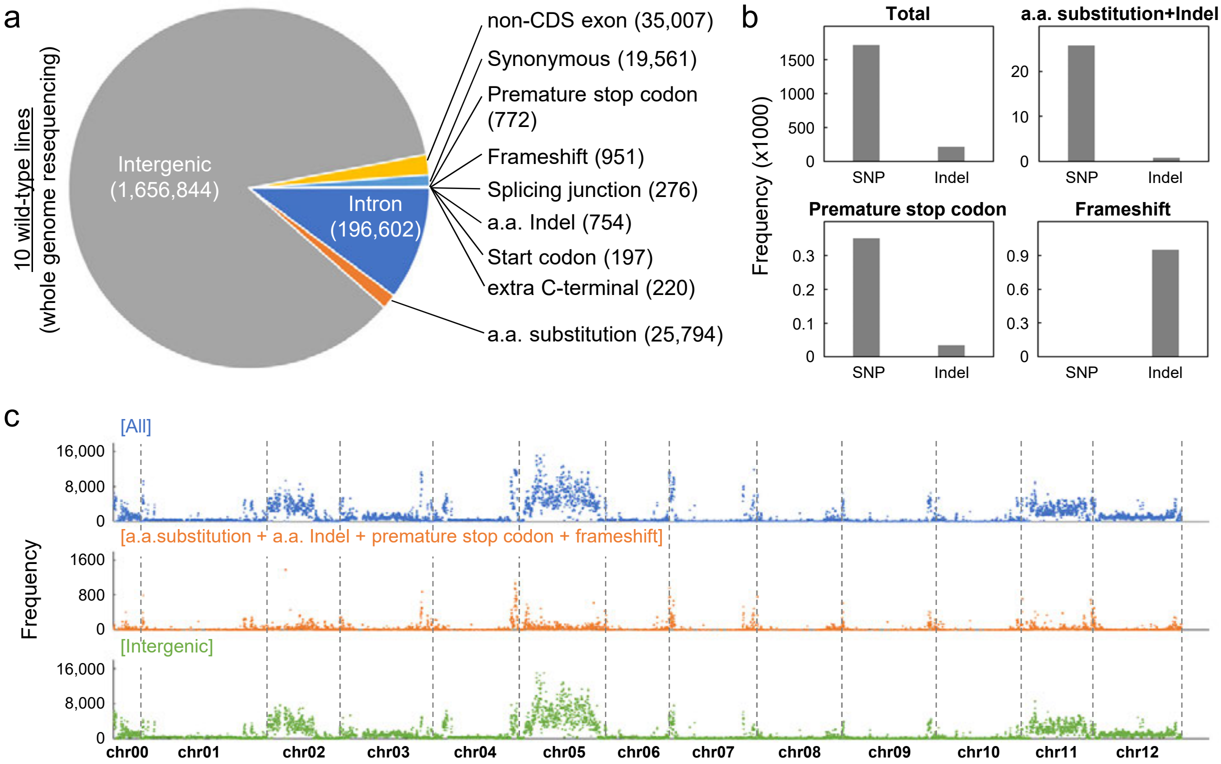


Supplementary Figure S1. Statistics of 96-plex exome sequencing. (a) Counts of short reads obtained in 96-plex exome sequencing. (b) Alignment ratio of short reads against the tomato genome reference SL3.0. (c) Coverage ratios against exome capture target regions. (d) Read depth of aligned genomic region.



Supplementary Figure S2. Statistic summary of DNA variants identified in 95 'Micro-Tom' mutants. (a) A diagram showing the frequency of mutation type in the DNA variant dataset of 10 wild types. (b) Frequencies of single nucleotide polymorphisms (SNPs) and Indels in each mutation type in the DNA variant dataset of 10 wild types. (c) Genome-wide distribution and frequency of DNA variants (natural polymorphisms) in 10 wild-type 'Micro-Tom' lines based on the tomato genome reference Heinz1706 SL3.0/ITAG3.10.

Supplementary Table S1. List of ‘Micro-Tom’ mutants subjected to exome sequencing. DRA accession Nos. are provided in the list.

TOMJP identifer	Generation	Num of bulked plants	DRA accession No.	TOMJP identifer	Generation	Num of bulked plants	DRA accession No.
TOMJPW304_1	M3M4	6	DRR184778	TOMJPW954_1	M3M4	7	DRR184826
TOMJPW306_1	M3M4	4	DRR184779	TOMJPW955_1	M3M3	9	DRR184827
TOMJPW324_1	M3M4	7	DRR184780	TOMJPW1065_1	M3M4	9	DRR184828
TOMJPW333_1	M3M3	2	DRR184781	TOMJPW1070_1	M3M4	6	DRR184829
TOMJPW334_1	M3M4	10	DRR184782	TOMJPW1107_1	M3M4	10	DRR184830
TOMJPW339_1	M3M4	6	DRR184783	TOMJPW1110_1	M3M4	5	DRR184831
TOMJPW378_1	M3M3	10	DRR184784	TOMJPW1112_2	M3M4	5	DRR184832
TOMJPW402_1	M3M4	4	DRR184785	TOMJPW1114_1	M3M4	8	DRR184833
TOMJPW424_1	M3M4	5	DRR184786	TOMJPW1145_1	M3M4	7	DRR184834
TOMJPW499_1	M3M4	3	DRR184787	TOMJPW1152_1	M3M4	7	DRR184835
TOMJPW518_1	M3M4	10	DRR184788	TOMJPW1157_1	M3M4	6	DRR184836
TOMJPW534_1	M3M3	10	DRR184789	TOMJPW1160_1	M3M4	7	DRR184837
TOMJPW545_1	M3M4	4	DRR184790	TOMJPW1163_1	M3M4	10	DRR184838
TOMJPW546_1	M3M4	9	DRR184791	TOMJPW1169_1	M3M4	10	DRR184839
TOMJPW550_1	M3M4	9	DRR184792	TOMJPW1173_1	M3M4	7	DRR184840
TOMJPW558_1	M3M3	7	DRR184793	TOMJPW1192_1	M3M4	3	DRR184841
TOMJPW563_1	M3M4	6	DRR184794	TOMJPW1197_1	M3M4	10	DRR184842
TOMJPW573_1	M3M4	6	DRR184795	TOMJPW1208_1	M3M4	6	DRR184843
TOMJPW581_1	M3M4	4	DRR184796	TOMJPW1209_1	M3M4	5	DRR184844
TOMJPW600_1	M3M4	10	DRR184797	TOMJPW1216_1	M3M4	7	DRR184845
TOMJPW601_1	M3M4	6	DRR184798	TOMJPE246_1	M6	5	DRR184846
TOMJPW602_1	M3M4	9	DRR184799	TOMJPE3093_1	M5	10	DRR184847
TOMJPW754_1	M3M3	6	DRR184800	TOMJPE5045_3	M5	7	DRR184848
TOMJPW773_1	M3M3	8	DRR184801	TOMJPE5066_1	M6	9	DRR184849
TOMJPW775_1	M3M4	3	DRR184802	TOMJPE5167_6	M5	9	DRR184850
TOMJPW791_1	M3M4	3	DRR184803	TOMJPE5212_3	M6	10	DRR184851
TOMJPW797_1	M3M4	7	DRR184804	TOMJPE5215_1	M5	4	DRR184852
TOMJPW815_1	M3M3	5	DRR184805	TOMJPE5262_1	M5	9	DRR184853
TOMJPW817_1	M3M4	4	DRR184806	TOMJPE5281_4	M5	8	DRR184854
TOMJPW819_1	M3M4	9	DRR184807	TOMJPE5401_1	M4	1	DRR184855
TOMJPW822_1	M3M4	8	DRR184808	TOMJPE5405_5	M5	8	DRR184856
TOMJPW823_1	M3M4	5	DRR184809	TOMJPE5508_2	M5	10	DRR184857
TOMJPW831_1	M3M4	10	DRR184810	TOMJPE5640_1	M5	2	DRR184858
TOMJPW836_1	M3M4	10	DRR184811	TOMJPE5813_2	M5	10	DRR184859
TOMJPW840_1	M3M4	8	DRR184812	TOMJPE6034_1	M6	8	DRR184860
TOMJPW865_2	M3M4	3	DRR184813	TOMJPE6270_1	M5	9	DRR184861
TOMJPW879_1	M3M4	6	DRR184814	TOMJPE6352_1	M5	7	DRR184862
TOMJPW884_1	M3M4	9	DRR184815	TOMJPE6483_1	M6	4	DRR184863
TOMJPW885_1	M3M4	8	DRR184816	TOMJPE7255_2	M5	9	DRR184864
TOMJPW889_2	M3M3	5	DRR184817	TOMJPE7310_1	M5	9	DRR184865
TOMJPW892_1	M3M3	6	DRR184818	TOMJPE7453_1	M5	7	DRR184866
TOMJPW914_1	M3M4	9	DRR184819	TOMJPE8937_1	M6	2	DRR184867
TOMJPW916_1	M3M4	6	DRR184820	TOMJPG400_1	M7	10	DRR184868
TOMJPW920_1	M3M4	8	DRR184821	TOMJPG1859_1	M5	8	DRR184869
TOMJPW927_1	M3M4	9	DRR184822	TOMJPG2543_1	M6	10	DRR184870
TOMJPW933_1	M3M4	10	DRR184823	TOMJPG2574_1	M6	5	DRR184871
TOMJPW934_1	M3M4	1	DRR184824	TOMJPG2614_2	M5	6	DRR184872
TOMJPW952_1	M3M4	7	DRR184825	controlMT-WT	-	10	DRR184873

Supplementary Table S2. List of hybridization enhancing (HE) oligos used for 96-plex exome capture. The ‘3SpC3’ indicates 3’-Spacer C3 modification. All HE oligos were synthesized by using outsourcing service of Integrated DNA Technologies, Inc.

name	Sequence
i501 HE oligo	AATGATACGGCGACCACCGAGATCTACACTATAGCCTACACTCTTTCCCTACACGACGCTCTTCCGATCT/3SpC3/
i502 HE oligo	AATGATACGGCGACCACCGAGATCTACACATAGAGGCACACTCTTTCCCTACACGACGCTCTTCCGATCT/3SpC3/
i503 HE oligo	AATGATACGGCGACCACCGAGATCTACACCTATCCTACACTCTTTCCCTACACGACGCTCTTCCGATCT/3SpC3/
i504 HE oligo	AATGATACGGCGACCACCGAGATCTACACGGCTCTGAACACTCTTTCCCTACACGACGCTCTTCCGATCT/3SpC3/
i505 HE oligo	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACGCTCTTCCGATCT/3SpC3/
i506 HE oligo	AATGATACGGCGACCACCGAGATCTACACTAATCTTAACACTCTTTCCCTACACGACGCTCTTCCGATCT/3SpC3/
i507 HE oligo	AATGATACGGCGACCACCGAGATCTACACCAGGACGTACACTCTTTCCCTACACGACGCTCTTCCGATCT/3SpC3/
i508 HE oligo	AATGATACGGCGACCACCGAGATCTACACGTACTGACACACTCTTTCCCTACACGACGCTCTTCCGATCT/3SpC3/
i701 HE oligo	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT/3SpC3/
i702 HE oligo	CAAGCAGAAGACGGCATACGAGATTCTCCGGAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT/3SpC3/
i703 HE oligo	CAAGCAGAAGACGGCATACGAGATAATGAGCGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT/3SpC3/
i704 HE oligo	CAAGCAGAAGACGGCATACGAGATGGAATCTCGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT/3SpC3/
i705 HE oligo	CAAGCAGAAGACGGCATACGAGATTTCTGAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT/3SpC3/
i706 HE oligo	CAAGCAGAAGACGGCATACGAGATACGAATTCGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT/3SpC3/
i707 HE oligo	CAAGCAGAAGACGGCATACGAGATAGCTTCAGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT/3SpC3/
i708 HE oligo	CAAGCAGAAGACGGCATACGAGATGCGCATTAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT/3SpC3/
i709 HE oligo	CAAGCAGAAGACGGCATACGAGATCATAGCCGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT/3SpC3/
i710 HE oligo	CAAGCAGAAGACGGCATACGAGATTTCGCGGAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT/3SpC3/
i711 HE oligo	CAAGCAGAAGACGGCATACGAGATGCGCGAGAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT/3SpC3/
i712 HE oligo	CAAGCAGAAGACGGCATACGAGATCTATCGCTGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT/3SpC3/

Supplementary Table S3. An example of *in silico* mutant screening based on the exome variant dataset of 95 ‘Micro-Tom’ mutants.

mutant ID	DP	GQ	Chr.	Position (bp)	REF	ALT	location	mutation type	aa change
Solyc02g077920 (CNR)									
TOMJPW306_1	5	34	SL3.0ch02	43309776	G	A	intergenic	1406 bp down of stop codon	-
TOMJPW754_1	5	69	SL3.0ch02	43309900	G	T	intergenic	1282 bp down of stop codon	-
TOMJPW754_1	5	74	SL3.0ch02	43309932	G	T	intergenic	1250 bp down of stop codon	-
TOMJPW1163_1	6	31	SL3.0ch02	43312256	G	T	intron.2	intron	-
TOMJPW306_1	8	57	SL3.0ch02	43312479	G	T	CDS.1	missense	L37I
Solyc10g006880 (NOR)									
TOMJPE5640_1	8	99	SL3.0ch10	1299270	CTTG	C	CDS.3	deletion	Q328-
TOMJPG400_1	8	67							Q328-
TOMJPE5813_2	12	50	SL3.0ch10	1301870	A	AT	-	exon (not CDS)	-
TOMJPW889_2	6	39							-
Solyc05g012020 (RIN)									
TOMJPW934_1	6	31	SL3.0ch05	5225109	T	TA	-	exon (not CDS)	-
TOMJPW1192_1	7	62	SL3.0ch05	5225500	G	T	-	exon (not CDS)	-
TOMJPW1197_1	6	71	SL3.0ch05	5225552	T	C	-	exon (not CDS)	-
TOMJPW879_1	6	31	SL3.0ch05	5225714	G	A	CDS.8	synonymous	no change
TOMJPW840_1	16	51	SL3.0ch05	5225970	G	T	intron.7	intron	-
TOMJPE5167_6	6	42	SL3.0ch05	5226302	TA	T	intron.6	intron	-
TOMJPW333_1	6	31	SL3.0ch05	5226583	A	G	CDS.6	synonymous	no change
TOMJPW1065_1	7	49	SL3.0ch05	5227256	T	A	CDS.3	missense	Q92H
TOMJPW822_1	6	72	SL3.0ch05	5227349	A	G	intron.2	intron	-
TOMJPE7255_2	6	72	SL3.0ch05	5227957	G	T	intron.1	intron	-
TOMJPW817_1	5	34	SL3.0ch05	5231101	T	A	-	exon (not CDS)	-
TOMJPW558_1	6	31	SL3.0ch05	5231112	T	C	-	exon (not CDS)	-