

Supplementary Materials

Identification of the *SUT* gene family in pomegranate (*Punica granatum* L.) and functional analysis of *PgL0145810.1*

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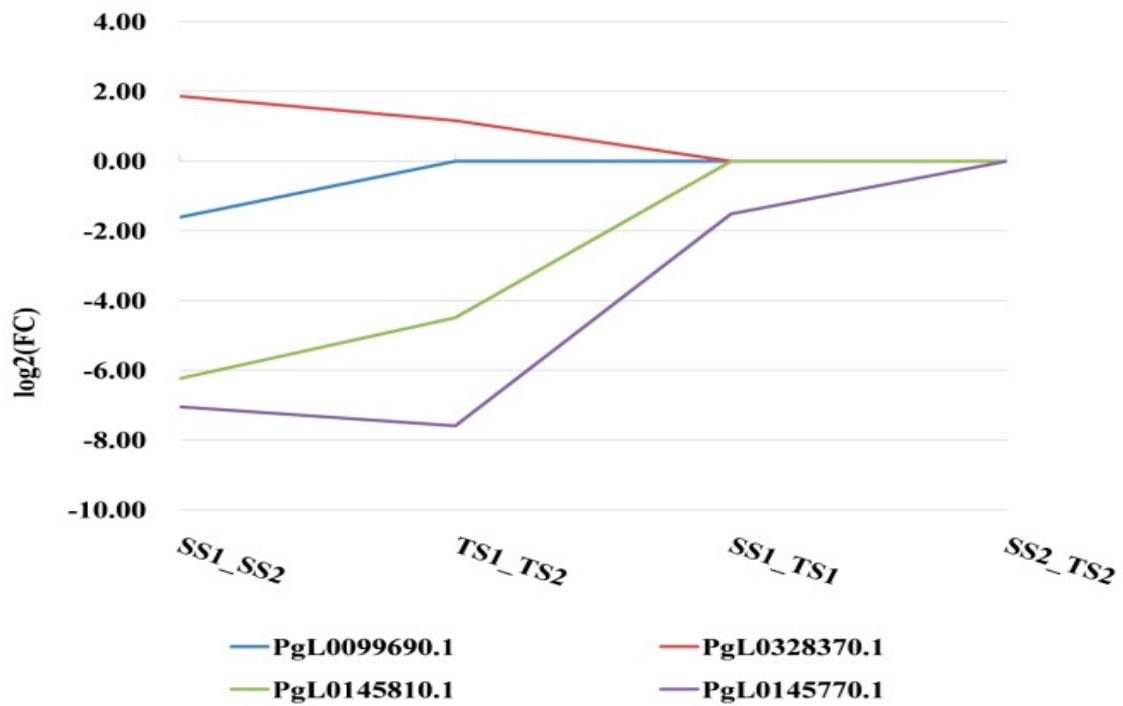


Figure S1. Expression of *SUT* genes during the development of seed in pomegranates
TS1: Seeds of ‘Tunisia’ at 60days after flowering (DAF); TS2: Seeds of ‘Tunisia’ at 120DAF; SS1:Seeds of ‘Sanbai’ at 60DAF; SS2: Seeds of ‘Sanbai’ at 120DAF; FC: fold change; SS1_SS2,TS1_TS2, SS1_TS1 and SS2_TS2: comparison group, text before ‘_’ represents reference group,text after ‘_’ represents treatment group.

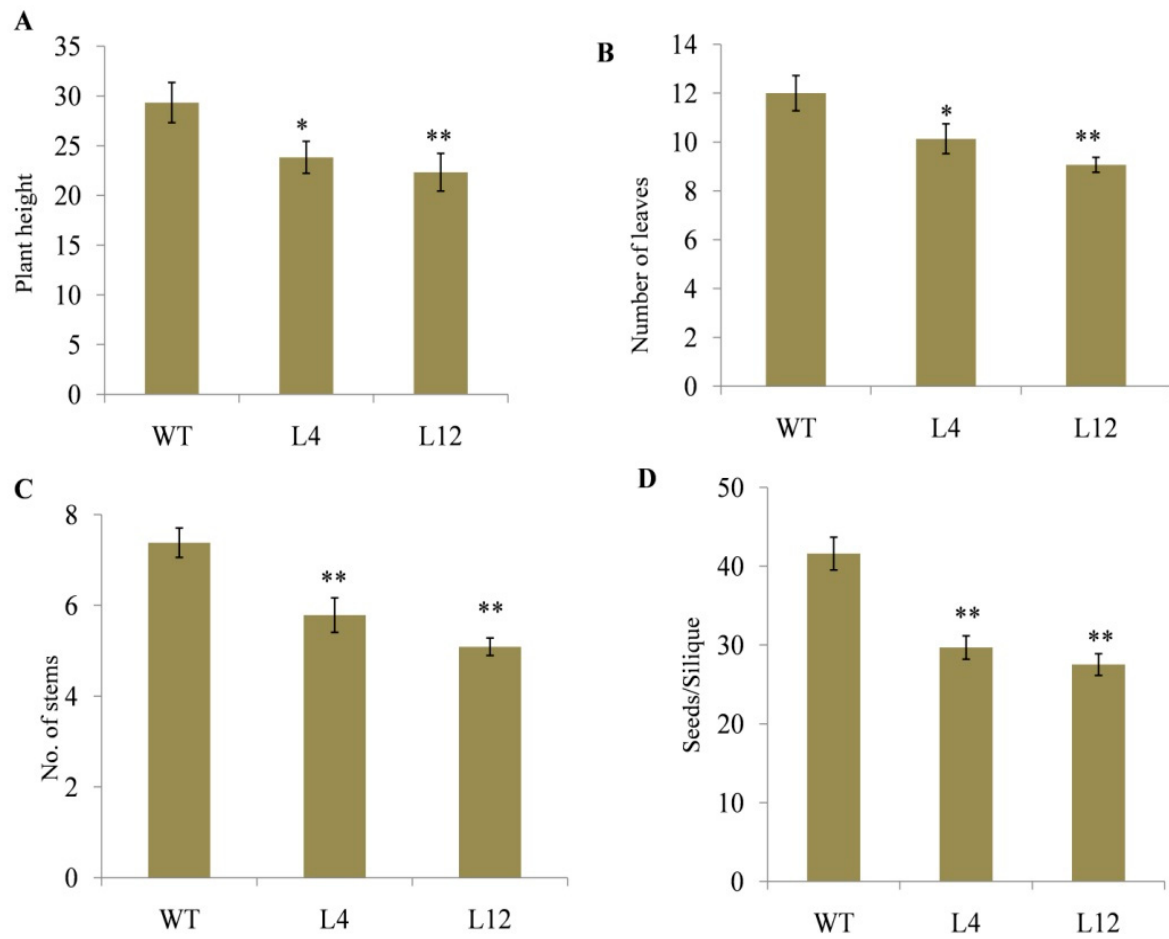


Figure S2. Growth parameters of wild-type (WT) *Arabidopsis* plants and transgenic *Arabidopsis* lines (L4 and L12). Data shown are plant height statistics of 42 days old seedlings (A), number of leaves of 35 days old seedlings (B), number of stems of 42 days old seedlings (C) and number of seeds per silique (D). Error bars indicates standard deviations from three repeats (n=3). Values are means $\pm$ SD ($n = 3$). * significant at $p < 0.05$ and ** significant at $p < 0.01$ probability levels.

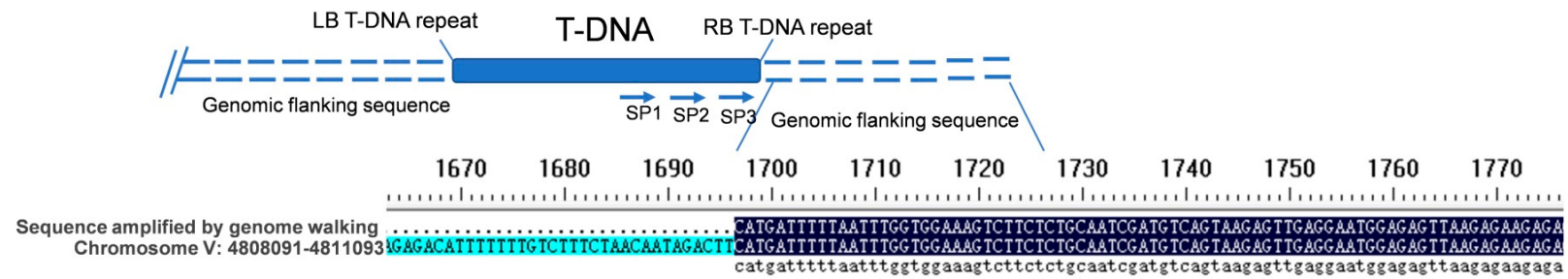


Figure S3. Schematic representation of the T-DNA insertion regions. Blue box: region of the T-DNA insertion; RB: right border; LB: left border; SP1, SP2 and SP3: specific primers; dotted lines: flanking plant DNA.

Table S1. The component of amino acid for *SUT* genes in pomegranate.

Protein_ name	<i>PgL0145</i> 770.1	<i>PgL00996</i> 90.1	<i>PgL0145</i> 810.1	<i>PgL0181</i> 920.1	<i>PgL02337</i> 80.1	<i>PgL02370</i> 30.1	<i>PgL02818</i> 20.1	<i>PgL03283</i> 70.1	<i>PgL0281</i> 810.1	<i>PgL02818</i> 00.1	Mean
Length	498	1236	581	515	1187	1251	92	507	155	289	631.1
M/W	53641.48	142986.14	60951.37	55655.52	133412.98	142472.24	10260.37	54848.93	18001.63	33693.48	70592.4
Ala	10.24	6.23	12.22	9.51	7.67	7.19	5.43	10.06	3.87	8.3	8.072
Cys	1.41	0.65	1.55	1.36	0.84	0.8	1.09	1.38	0	0.35	0.943
Asp	2.81	5.91	2.93	4.66	4.63	6	3.26	3.55	4.52	4.84	4.311
Glu	2.01	12.14	2.24	3.5	10.53	11.99	5.43	2.56	3.87	16.26	7.053
Phe	6.43	3.16	5.34	5.63	2.78	2.4	5.43	6.11	2.58	1.04	4.09
Gly	10.64	4.61	8.95	8.35	4.97	4.96	8.7	10.06	6.45	3.11	7.08
His	2.61	1.38	0.69	3.69	1.43	1.44	5.43	1.18	4.52	2.08	2.445
Ile	5.82	5.42	4.99	5.05	5.64	5.28	5.43	7.5	5.81	4.84	5.578
Lys	4.02	11.41	2.58	2.14	10.78	11.75	6.52	1.58	5.81	13.49	7.008
Leu	13.25	10.28	12.56	10.87	10.78	10.31	10.87	10.65	9.68	9.69	10.894
Met	3.01	1.78	2.07	2.52	2.11	2.72	2.17	2.76	3.23	2.08	2.445
Asn	3.01	4.13	3.79	5.05	4.8	3.68	5.43	2.96	3.87	3.46	4.018
Pro	5.42	2.18	7.23	5.05	1.94	2.4	3.26	5.92	5.81	1.38	4.059
Gln	3.01	5.34	2.07	4.08	6.32	4.4	2.17	2.96	2.58	4.84	3.777
Arg	3.21	6.72	3.96	4.08	4.38	5.52	6.52	5.72	7.74	7.96	5.581
Ser	5.62	6.31	9.12	9.51	7.33	6.95	7.61	6.71	9.68	6.57	7.541
Thr	3.61	4.37	5.85	3.3	3.71	3.84	3.26	5.33	6.45	2.42	4.214
Val	9.24	4.77	8.26	8.54	7.33	5.52	9.78	8.28	4.52	4.5	7.074
Trp	2.21	0.65	1.89	1.75	0.34	0.4	0	2.76	2.58	0	1.258
Try	2.41	2.59	1.72	1.36	1.68	2.48	2.17	1.97	6.45	2.77	2.56

Table S2. Raw quantitative real-time PCR (qRT-PCR) data for different pomegranate varieties.

<i>PgL0145810.1</i>		$2^{-\Delta\Delta CT}$			Avg.
Varieties	Type of variety	1	2	3	
ZSL8	Soft seeded	1.8921	1.6245	1.9318	1.8161
Jiu Zi Hong	Hard seeded	0.6029	0.5069	0.4383	0.5160
Yi3	Soft seeded	0.9054	0.9180	0.9771	0.9335
Yi 2000-1	Hard seeded	0.0834	0.0919	0.0645	0.0799
Sanbai	Hard seeded	0.0311	0.0397	0.0309	0.0339
Tunisia	Soft seeded	0.5573	0.5236	0.6402	0.5737

Table S3. Raw quantitative real-time PCR (qRT-PCR) data for different transgenic *Arabidopsis* lines.

<i>PgL0145810.1</i>		$2^{-\Delta\Delta CT}$			Avg.
Transgenic lines		1	2	3	
2		5.5148	1.0594	2.7574	3.1106
3		5.5918	3.6637	2.2868	3.8475
4		0.4362	0.2558	0.2918	0.3280
5		0.4233	0.4897	0.3035	0.4055
6		4.8680	4.9703	2.7194	4.1859
7		7.0779	6.6039	5.6699	6.4506
9		3.7407	3.8193	3.3948	3.6516
10		2.4116	1.8660	1.5691	1.9489
11		0.4919	0.3780	0.3430	0.4044
12		9.7360	8.4757	8.5346	8.9155
13		8.6139	6.5735	4.1315	6.4396

* Note; (2,3,4,5,6,7,9,10,11,12,13): Transgenic *Arabidopsis* Lines

Table S4. Raw quantitative real-time PCR (qRT-PCR) data for different tissues of both transgenic *Arabidopsis* lines.

<i>PgL0145810.1</i>		$2^{-\Delta\Delta CT}$			Avg.
Tissues		1	2	3	
Leaf	L4	1.3348	0.8991	0.8331	1.0223
	L12	1.0942	1.4539	2.0279	1.5253
Stem	L4	2.9759	1.5404	3.9540	2.8234
	L12	2.9553	4.6697	2.3839	3.3363
Flower	L4	1.2226	1.9318	2.5140	1.8895
	L12	2.4509	1.0594	0.9159	1.4754
Silique	L4	1.8108	1.2454	1.5122	1.5228
	L12	1.3534	1.3073	2.1987	1.6198

* Note; L4: Transgenic *Arabidopsis* Line L4
L12: Transgenic *Arabidopsis* Line L12

Table S5. The flanking sequence amplified by genome walking.

Flanking Sequence
tttttgcccataatgactacactttaacgtcttcttatctatagagaaatcaggctcatctggttg aatagttgaggcatcttcaaaactggtggaagatccatcttctaccagtactactactgaagcctttt gatttgctctctctcgtgttcgccgcaaatttagatgctaagatcgttgctcccagatttggtgtgc cattgatccgcttctcgtcacttccatagtaatactctctagtttctcgtcttctcattgtaacct gttcatccgggtaatagtatccgctactctcgtgaaggctgagctcttgcgaagcttctcgttgt atctctccatgcagattggacaaaacatgtcccatgctctccattgatgtgagtagtacctgaaagc gtgtgaagcttttgccttgaagacgttgaactgatgagcaaaaacttaagatcctctgcgcttaat gcaaaggcttctacttcagagagggcacggacgcttcgtgtgaagacggaagattgagtgtagagttg gcattaaggcccatgtaagaagttcttccccacagaaatcgccaggtcgtagtagtgagggtgaagaa accagatcttctccattgtgttgagctctctattgtcctcggatcacaaatagcatctcattcacc ggatcaccttcacggaatatgtatgtcccgccgtgcttaagatgagacaaggcatcccatatagcat caagaagttgatcatccatttgagagaagaacgggacctgcactaccacaacaatgtgactctgaatt gaaaaacaatcaaatccataacagttttgatgactgagttgatgtatgtacccggcgaacaaggagag acaaagatgacgttggaattcacggcgtaaatctgtaggaatgaatggaggattgattctcatcgaca cctctggttgcaagccatttgattggacaaatctcggacacgttctgaagctctggaggtagttgac gatgtctcatccattctcagtgctctctcttaactctcattctcaactcttactgacatcgattg cagagaagacttccacaaattaaaaatcatgaagtctattgttagaaagacaaaaaatgtctctgta ttgaaaagtttgagagtgatgcataagctctgaatcttacttgcatgttaccatcaggagtgtaag agaatacaacccaaaaatacaaatgttatagacaagaaggtctcgcaaggtatacactgtggttatat tctgtccataagaactgtgaacaaaacctttattaactaaaaactcgata

Table S6. Primers for cloning and for quantitative real-time PCR (qRT-PCR) assay of *PgL0145810.1*.

Primer name	Sequence (5'-3')	Function
<i>PgL0145810.1</i> -F	CTTTCTAGAATGGCGAAAGTTGAGGAGG	Gene cloning
<i>PgL0145810.1</i> -R	CTTGAGCTCTCAGTGCTGAGACTTCCAT	Gene cloning
Q <i>PgL0145810.1</i> -F	ATCACCAAGCTGGCTGACTC	qRT-PCR
Q <i>PgL0145810.1</i> -R	GCACCGGAGGAATTGGAGAA	qRT-PCR
Q <i>PgActin</i> -F	AGTCCTCTTCCAGCCATCTC	qRT-PCR
Q <i>PgActin</i> -R	CACTGAGCACAATGTTTCCA	qRT-PCR
Q <i>Actin</i> -F	GGTAACATTGTGCTCAGTGGTGG	qRT-PCR
Q <i>Actin</i> -R	AACGACCTTAATCTTCATGCTGC	qRT-PCR
RB-SP1	AGACTCTAATTGGATACCGAGG	Thermal asymmetric interlaced PCR
RB-SP2	TTAAACTCCAGAAACCCGCGGCTG	Thermal asymmetric interlaced PCR
RB-SP3	CTCCGCTCATGATCAGATTGTCGTT	Thermal asymmetric interlaced PCR