

Table S3a. Summary of Arabidopsis mutant lines, genotyping and RT-PCR results.

NAME	AGI	accession	note		genotyping*	RT-PCR**	primer sequence 5'-3'	primer sequence 5'-3'		TAP (TEN-RID-Fw1C), ref.1
MCM2	At1g44900	SALK_026376	mcm2-1	NASC	HE	n.a.	ATGCCAGTCAAAAGGACCGT	CTTCAAGCTCCACTCCCTT		3(3)-0-0
		SALK_023429C	mcm2-3	NASC	HO	(+)	CTGGGTGAACCTAGATGCCAAG CTGGGTGAACCTAGATGCCAAG	CCTTGGCTGCAAAATGTAAGA AGAAAGCTGGGTC TTA CCA AGT GAT CAG CCT TTT TG		
MCM3	At5g46280	SAIL_1264_E07	mcm3-4	NASC	HE	n.a.	ATGCTATTGCTGAGGATGACC	AATCATGCTGTGCATACCAGC		0-1(1)-0
MCM5	At2g07690	SALK_000158 SALK_056939	mcm5-1 mcm5-2	NASC	HE	n.a.	AATTCGTAACGGAGACGAAGC AGACCCATCAACTGCAAAATCAC	ACAAGATGCCGATCAACTGAG GCAAGCAACGAAGCAAACTTTC		0
MCM6	At5g44635	SALK_025569	mcm6-4	NASC	HE	n.a.	TGTCCTCATATTGTGCGAGTTCA	TGTGCTCATGTTGTGTCACATTAGC		3(3)-1(1)-0
MCM7 (PROLIFERA)	At4g02060	SALK_095847	mcm7-2	NASC	HE	n.a.	CTGATCCCTATCAGCAGATTCC	ACAGACGTTGCTTCCAGATAGG		0
LIG1	At1g08130	EGU3	lig1-5	INRA	HE	n.a.	TTGCTTATGTTTAGTGTGGTGTGAA	AGAAGATGCTAGGCAACATCA		1(1)-0-0
RFC1	At5g22010	SALK_140231	rfc1-2	NASC	HO	(+)	TAGCCCACTTCAGACACTGC TAGCCCACTTCAGACACTGC	GGATCCCTGCAACCCGATTA GGAACCCGATGCGATTGGC		1(1)-0-0
ETG1	At2g40550	SALK_071046	etg1-1	NASC	HO	(+)	AGACCAAGATGGTCAGAGGATC AAAAAGCAGGCTAC ATGGGAGGACCAGCTTACGATTG	ACTGGAACACAGTAAAGCAAGC AGAAAGCTGGGT TTACTTGAGCCTCTCCTTTCTAAGTC		0
HON4	At3g18035	SALK_099887C	hon4	NASC	HO	(+)	ACAGAGGAAGCCCAAAATCCG	GAGCTTCAGTCTGTGGTGCTG		0-0-3(3)
HMGb4	At2g17560	GABI_455G12	hmgb4	NASC	HO	(+)	ATGAAAGCCGGCGAATCCA	CCAGTTTCAAGTTGATGTTGTGAC		0-1(1)-0
RLI2	At4g19210	GABI_509C06	rli2	NASC	HE	n.a.	GGAGAATGGTACAGGGAAGAC	CAATGGATGGTTGTCTTCTACATA		9(9)-2(2)-1(1)
SSB1	At3g18580	SALK_060713C	ssb1-1	NASC	HO	(+++)	GAGTTGACCACTTCTTGAGGG AAAAAGCAGGCTAC ATG GCG AAT TCA ATG GCT ACA	TGATCCACAGTTCTCTACAG AGAAAGCTGGGTC TCA GTA GTA GCC AAC GCC TC		1(1)-1(1)-2(2)
		SAIL_1263_A12	ssb1-2	NASC	HO	(+++)	GAGTTGACCACTTCTTGAGGG AAAAAGCAGGCTAC ATG GCG AAT TCA ATG GCT ACA	TGATCCACAGTTCTCTACAG AGAAAGCTGGGTC TCA GTA GTA GCC AAC GCC TC		
		GABI_034F02	ssb1-3	NASC	HE	n.a.	TCCTGTCACTGGTTTGGTTCGAC	AGAAAGCTGGGTC TCA GTA GTA GCC AAC GCC TC		
							TTGCGTTCTGCTGATGGTAAAG	TCAGTTTGTCTCTATCCGGTCAAC		
MtSSB	At4g11060	SALK_203889C	mtssb	NASC	HO	(+)	TTGCGTTCTGCTGATGGTAAAG	TCAGTTTGTCTCTATCCGGTCAAC		1(1)-1(1)-1(1)
NAT10	At1g10490	SAIL_406_G12	nat10	NASC	HO	(+)	ACTTTTGTGCGATGCTCCTG	CCACTTCCAGTTTCATCATCACC		4(6)-0-0
At3g57940	At3g57940	SALK_011936		NASC	HO	(+)	AGAGCTGTTGGTATTGATGAAGC	CAGGATTAGGCAGACAAGTAGC		1(3)-0-0
La1	At4g32720	SAIL_548_H11	la1	NASC	HE	n.a.	AAACAAGCCAGCAGATACTCC	ATTCTTCACGGCTAGTCCACC		0-1(1)-14(14)
THUMP	At5g12410	SALK_045222C		NASC	HO	(++)	AAAAAGCAGGCTACATGGCTTCCGGTGACCAGAG	CGGCATCGCAAGAGATGAA		2(2)-1(1)-0
At2g04520	At2g04520	SALK_093097C		NASC	HO	(+)	AAAAAGCAGGCTACATGCCGAAGAACAAGGAAAG AAAAAGCAGGCTACATGCCGAAGAACAAGGAAAG	CTTATGCAACAAGAACAACCAAGGA AGAAAGCTGGGTC TTA GAT CCT ATC GAT ATC TTC GTC C		1(1)-0-1(1)
At2g40660	At2g40660	SAIL_238_A04		NASC	HO	(+)	CTGCAGAAGGTGTAAGGCCTG	CATCTTCTGGCTTCTCTCAATCC		1(1)-1(1)-5(5)
RNA helicase 2	At3g19760	SALK_205343	rh2	NASC	HO	(+++)	CTATCCAACCTAAATGCATTGCAAC TCTCCGTTTGTCAAGTCGTTG	CTTCTCCAACACTATTCCACC CTTCTCCAACACTATTCCACC		1(4)-3(6)-2(3)
RNA helicase DEAH3	At2g47250	EAK73	deah3-1	INRA	HO	(+++)	CGCAGGTGGAAGAGTAGAATAC	CCGATAAGGGAAGGAAATGGT		1(1)-1(1)-0
RH42 (emb1507)	At1g20960	EGX301	rh42	INRA	HE	n.a.	GCTGGGTTATCAAGGGGTGA	TATTGCAGCTCGCTGTAGCC		2(2)-0-0
At2g42270	At2g42270	SALK_048780C		NASC	HO	(+++)	CGATTACGGAGAAGCGGAGAG ATGACGAATTTGGGTGGTGGTG	GCACCGCAACAATGTCCAA GCACCGCAACAATGTCCAA		0
CHR19	At2g02090	SALK_054130	chr19-1	NASC	HO	(++)	AGGATGAATTTGGAGGAGGAGG	ACTGGTACGGCTTGAGTATAGG		2(2)-0-0
TORMOZ	At5g16750	SAIL_905_G06	toz-2	NASC	HE	n.a.	GCTACCTCGTTTTTCTTCGCG	TTGCATTAAAGTCCCAGACAGC		2(2)-0-0
AT4G17950	At4g17950	SALK_014014		NASC	HO	(+)	GGATGTGTTGGTGTTCAGGG TGAGCTTTGGTGGTGTGTTG	ATCACCACTATGTTTCTGCG GGTGAAGCGGTTGAGGTGTA		1(1)-0-0
AT4G23540	At4g23540	SAIL_384_G08		NASC	HO	(+)	GCTTCTACTCTGGATTCTGTCAG GCTTCTACTCTGGATTCTGTCAG	GCACAAAACCAACCATGTTCTCT AGAAAGCTGGGTC TCA TGT TGC TTT CCT GAA TCT GTT CTT C		4(4)-0-0

* HO, homozygous progeny; HE, heterozygous progeny

** RT-PCR results of mutant plants using primers flanking the T-DNA insertion (exon and intron lines) or positioned downstream of the T-DNA insertion site (promoter lines *rh2*, *ssb1-1*, *ssb1-2*)

(+), transcript was amplified in wt control but not in mutant; (++), transcript was amplified in wt control and to a lesser amount in mutant; (+++), transcript was amplified comparable in wt control and mutant; n.a., not analysed

References:

1. Majerska et al. (2017) Tandem affinity purification of AtTERT reveals putative interaction partners of plant telomerase in vivo. *Protoplasma* (2017) 254:1547–1562. DOI 10.1007/s00709-016-1042-3

Table S3b. T-DNA primers and control RT-PCR primers

Collection	Name	primer sequence 5' - 3'
SALK	o5_Tinz	CAACACTCAACCTATCTCGG
SAIL	SAIL_LB3	TAGCATCTGAATTTATAACCAATCTCGATACAC
GABI	o8474	ATAATAACGCTGCGGACATCTACATTTT
INRA	INRA_LB4	CGTGTGCCAGGTGCCACGGAATAGT
Control gene		primer sequence 5' - 3'
ARM (At4g33945)	F-ex6	ATGGGTCTGGACAAGCTAATC
	R-ex7	GCAATGTTCCGTATCATGTTG
ACT2 (At3g18780)	ACT2-fw	ATTGAGATGCCCAAGTCTTGTC
	ACT2-rev	GCAAGTGCTGTGATTTCTTTGCTCA