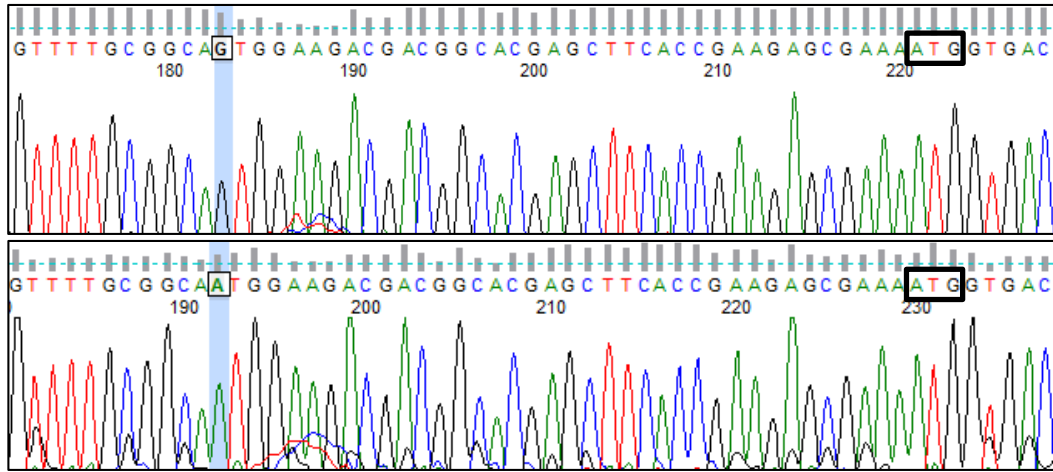


**Combined haploinsufficiency and purifying
selection drive retention of *RPL36a* paralogs in
*Arabidopsis***

Rubén Casanova-Sáez, Héctor Candela and José Luis Micol

Supplementary Information

Ler



api2

Supplementary Figure S1.- The *api2* mutation creates an out-of-frame ATG codon upstream of the wild-type translation start site of *API2* transcripts. Electropherograms showing the 5'-UTR of the *API2* gene from Ler and *api2/api2* plants. The G→A *api2* point mutation is highlighted in blue. The wild-type *API2* translation start codon is boxed in black.

	M V N I P K T K N T Y C K N K E C K K H
<i>API2</i>	ATGGTGAACATTCCGAAAACCTAAGAACACTTACTGCAAGAACAAGGAGTGCAAGAAAGCAT
<i>RPL36aA</i>	ATGGTGAACATTCCAAAGACAAAGAACACTTACTGTAAGAACAAGGAATGCAAAAAGCAT
	M V N I P K T K N T Y C K N K E C K K H
	T L H K V T Q Y K K G K D S L A A Q G K
<i>API2</i>	ACCTTGACACAAGGTGACGACGTATAAGAAAGGTAAAGATAGCCTTGCTGCCCAAGGAAAG
<i>RPL36aA</i>	ACTTTGCACAAGGTTACCCAATACAAGAAGGGTAAAGACAGTCTTGCTGCTCAAGGAAAG
	T L H K V T Q Y K K G K D S L A A Q G K
	R R Y D R K Q S G Y G G Q T K P V F H K
<i>API2</i>	CGTCGTTATGATCGTAAACAATCTGGTTATGGAGGTCAGACCAAGCCCGTCTTCCACAAG
<i>RPL36aA</i>	CGTCGTTATGACCGTAAACAATCTGGTTATGGTGGTCAGACTAAGCCTGTCTTCCACAAA
	R R Y D R K Q S G Y G G Q T K P V F H K
	K A K T T K K I V L R L Q C Q S C K H F
<i>API2</i>	AAGGCTAAGACAACCTAAGAAGATTGTCTGAGGCTTCAATGCCAAAGCTGCAAGCATTTT
<i>RPL36aA</i>	AAGGCTAAGACCACGAAGAAGATTGTTTGAGGCTTCAATGTTCAAAGCTGCAAGCACTTT
	K A K T T K K I V L R L Q C Q S C K H F
	S Q R P I K R C K H F E I G G D K K G K
<i>API2</i>	TCGCAACGCCCGATTAAAGAGGTGCAAGCACTTTGAGATCGGTGGAGACAAGAAGGGAAAG
<i>RPL36aA</i>	TCGCAACGTCCTATCAAGAGGTGCAAGCACTTTGAGATCGGTGGTGAACAAGAAGGGAAAG
	S Q R P I K R C K H F E I G G D K K G K
	G T S L F *
<i>API2</i>	GGAACATCTCTCTTTTAA
<i>RPL36aA</i>	GGAACATCTCTCTTTTAA
	G T S L F *

Supplementary Figure S2.- Synonymous substitutions along the *API2* and *RPL36aA* coding sequences. Alignment of the *API2* and *RPL36aA* coding sequences with indication of the amino acids encoded by each codon. An asterisk indicates the stop codon. The alignment was obtained with the PAL2NAL program. Synonymous substitutions affecting the first or third base of a codon are highlighted in pink and green, respectively.

Supplementary Table S1.- Primer sets used in this work

Purpose	Oligonucleotide names	Oligonucleotide sequences (5'→3')	
		Forward primer (F)	Reverse primer (R)
Linkage analysis	cer466314_F/R	CCGATTCTATTCCTCTAGGCT	GTAAAAAATCTGGACTTATCAAG
	cer459267_F/R	AGCAGCTGCCCTTTCAACAG	AGGTTACTGATGCCCGAGAG
	cer453616_F/R	GAGCATTGGCATGTTCAATTGTT	TTTGAGAGTTTTCGTGTGGCCT
API2 sequencing	API2_F1/R1	CTGATTTGCAGCACAAAACG	CCACGGGCCACTGATTATTA
	API2_R2	TGATTTAGGAGAAGCAGGAAAT	
Topo/Gateway cloning	API2cds_F/R	CACCATGGTGAACATTCCGAAAACATA	AAAGAGAGATGTTCCCTTTCC
	RPL36aAcds_F/R	CACCATGGTGAACATTCCAAGACAAA	AAACAGAGATGTTCCCTTTCCC
	API2pro_F/R	GGGGACCACTTTGTACAAGAAAGCTGGGT TTTCGCTCTTCGGTGAAGCTC	GGGGACAAGTTTGTACAAAAAAGCAGGCT TTGAGATTCAGAGAGCGTTAG
	RPL36aApro_F/R	GGGGACAAGTTTGTACAAAAAAGCAGGCT GATGAGGAACAAAGAAAGAGA	GGGGACCACTTTGTACAAGAAAGCTGGGT TTTCGCGTCTCTGATCTCCG
	M13_F/R	GTAAAACGACGGCCAG	CAGGAAACAGCTATGACCATGATT
qRT-PCR	18SrRNA_RTqPCR_F/R	AGGATCCATTGGAGGGCAAGT	CGACGTTTTTAACTGCAACAAC
	API2_RTqPCR_F/R	CCACAAGAAGGCTAAGACAAC	AAAGTGCTTGCACCTCTTAATC
	RPL36aA_RTqPCR_F/R	GACCACGAAGAAGATTGTTT	GAAATGCTTGCACCTCTTGATA
Genotyping of mutants, transgenic plants and constructs	LBb1.3_F ^a	ATTTTGCCGATTTTCGGAAC	
	rpl36aa_F/R	GATGTTCCCTTTCCCTTCTTG	TGGTTCAAACGAAACCAAAAC
	35S-F ^b	GACAGTGGTCCCAAAGATG	
	GUS-R ^c		CACAAACGGTGATACGTACACT

^{a-c}Each of these oligonucleotides was used together with: ^arpl36aa_R to genotype the *rpl36aa* mutant; ^bAPI2cds_R and RPL36aAcds_R to genotype transgenic plants putatively carrying the *35S_{pro}:RPL36aB* and *35S_{pro}:RPL36aA* transgenes; ^cAPI2pro_R and RPL36aApro_R to genotype transgenic plants putatively carrying the *API2_{pro}:GUS* and *RPL36aA_{pro}:GUS* transgenes.