Communication

The Arabidopsis MADS-domain transcription factor SEED-STICK controls seed size via direct activation of *E2Fa*.

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Supplementary Figures
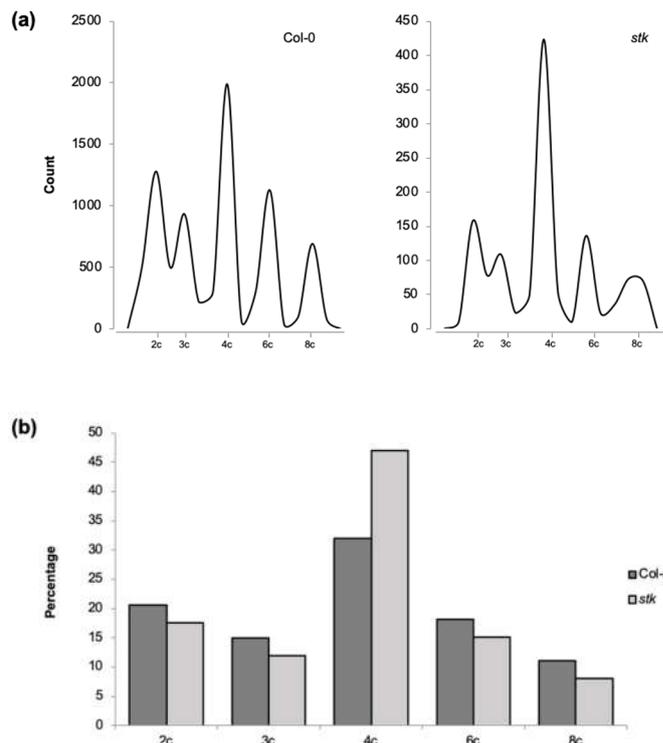
Supplementary Figure S1. DNA-content profile obtained from flow cytometry analysis of seeds. (**a**) DNA-content profile of wild-type (Col-0) and of *stk* mutant seeds showing the different peaks related to diploid nuclei (2C, 4C), highly endo-reduplicated nuclei (8C) and triploid/endospermal nuclei (3C, 6C). (**b**) quantitative representation of each peak relative to total measured samples.
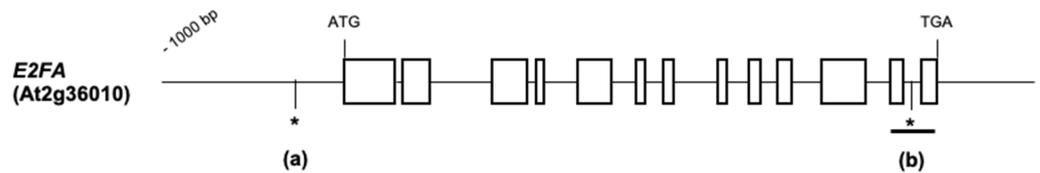
Supplementary Figure S2. Schematic representation of *E2Fa* gene with intron/exon structure, with asterisks indicating the positions of CArG boxes at the putative "a" and "b" binding sites of STK.

Supplementary Table 1. Primers used in this work

Primers for genotyping

stk-2	5'-GCTTGTTCTGATAGCACCAACACTAGCA-3'
	5'-CCACTAACCATTTGATGATGGTGTTGT-3'

Primers for expression analysis

STK	5'-ACGCGCAGAAAAGGGAGATTGAGC -3'
At4g09960	5'- TGTCGGGATCAGAGTAAGAACCTCC -3'
CYCD3;1	5'- CCAAACTAATCTCCTCGGTGTCC -3'
At4g34160	5'- TGATGATGAATCGTGACTCTTGCG -3'
CDKA;1	5'- CTGACAGGGATACCGAATGCTC -3'
At3g48750	5'- GGAGAAGGAACATACGGGAAAGTC -3'
CDKB1;1	5'- GGAGAAGGAACATACGGGAAAGTC -3'
At1g76540	5' ACGAAGAGCAGTTGGTGGAATAC -3'
CDKB2;2	5'- AGAGATTGATAGAGATGGACAACAAT -3'
At1g20930	5'- AGGATCACGAGCGAGCATAC -3'
E2Fa	5'- CTTTGGAAGGGAGTTGATGCGTGTC-3'
At2g36010	5'- TTGTGCCATGAGGAGCTTTGACG -3'
ACT	5'- CTCAGGTATTGCAGACCGTATGAG -3'
At3g18780	5'- CTGGACCTGCTTCATCATACTCTG -3'
UBQ	5'- CTGTTCACGGAACCCAATTC -3'
At4g05320	5'- GGAAAAAGGTCTGACCGACA -3'

Primers for ChIP experiment

E2Fa – region a	5'- AGCGGTACGAAAACTTTGCC -3'
	5'- GTTGTATCATGTATGGCAGTGG -3'
E2Fa – region b	5'- ACTGGCTTCTCTCAAATGCTGAG -3'
	5'- GGTGCTATTTCGCCCATTCCT -3'
VDD	5'- GGAAATATGACGCTTGTCTTTTTAG -3'
At5g18000	5'- CAGAAACAGCAATATGCTCGTG -3'
IAA8	5'- CAATGGCTTCTTCTACTTCG -3'
At2g22670	5'- CCAATCACCGTCTTTATCT -3'
ACT	5'- CGTTTCGCTTTCCTTAGTGTTAGCT -3'
At3g18780	5'- AGCGAACGGATCTAGAGACTCACCTTG -3'