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Supplementary Information for

A shared *cis*-regulatory module activates transcription in the suspensor of plant embryos

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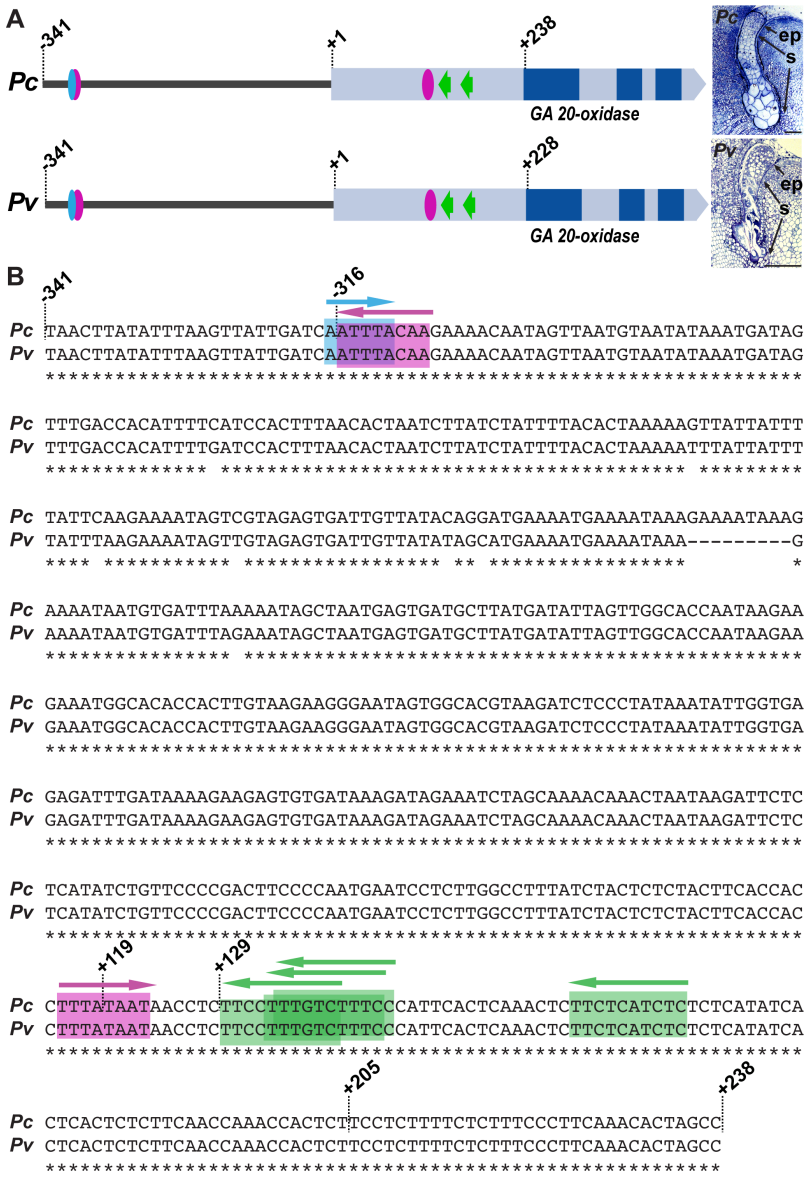

Fig. S1. Conservation of suspensor *cis*-regulatory elements in the upstream region of *GA 20-oxidase* in SRB and Common Bean. (*A*) Conceptual representation of SRB and Common Bean *GA 20-oxidase* genes and location of functional suspensor *cis*-regulatory motifs. Green arrows, purple ovals and blue ovals indicate the 10-bp motif, Region 2 motif and Fifth motif, respectively. Dark blue boxes represent exons. Light blue boxes represent UTRs and introns. Numbers indicate nucleotide positions relative to the SRB transcription start site (+1). Suspensor images were reproduced from Fig. 1*B* and *D*. (*B*) Nucleotide sequence alignment of the SRB and Common Bean *GA 20-oxidase* upstream regions. Nucleotides conserved in SRB and Common Bean are indicated by asterisks. Green, purple and blue boxes indicate the 10-bp motif, Region 2 motif and Fifth motif, respectively. Arrows indicate the orientation of the motifs. ep, embryo proper; *Pc*, *Phaseolus coccineus*; *Pv*, *Phaseolus vulgaris*; s, suspensor. (Scale bar: 50 μm.)

Table S1. GA biosynthesis enzyme mRNA prevalence in the globular-stage suspensor and embryo proper. mRNA prevalence for each GA biosynthesis gene in SRB and Common Bean suspensor and embryo proper regions. RNA-Seq data were taken from GEO accession GSE57537. Numbers indicate average reads per kilobase per million (RPKM) of two biological replicates.

		SRB RPKM		Common Bean RPKM	
Enzyme	***Phaseolus vulgaris* Gene ID**	**Suspensor**	**Embryo Proper**	**Suspensor**	**Embryo Proper**
ent-kaurene synthase A	**Phvul.001G152100**	**1,934**	**234**	**1,097**	**109**
ent-kaurene synthase B	**Phvul.005G048500**	**501**	**27**	**671**	**28**
ent-kaurene oxidase	**Phvul.005G183600**	**3,783**	**333**	**3,645**	**163**
ent-kaurenoic acid hydroxylase	**Phvul.006G123500**	**26,915**	**1,220**	**24,713**	**932**
GA 20-oxidase	**Phvul.010G087500**	**34,805**	**517**	**31,799**	**473**
GA 3-oxidase	**Phvul.009G097100**	**3,265**	**56**	**3,757**	**37**
GA 2-oxidase	**Phvul.005G061000**	**0**	**0**	**21**	**10**
GA 2-oxidase	**Phvul.005G061200**	**0**	**0**	**3**	**0**
GA 2-oxidase	**Phvul.006G165000**	**0**	**7**	**7**	**7**

Table S2. Probes used for SRB *in situ* hybridization. Probes were generated from cDNA clones made from micro-dissected suspensor and embryo proper regions of globular-stage SRB embryos 6 DAP (1). SRB EST sequences were compared to the *Phaseolus vulgaris* protein database (http://phytozome.jgi.doe.gov) using BLASTX, and the top *Phaseolus vulgaris* gene ID is displayed for each SRB EST (2).

Enzyme	GenBank Accession Number	SRB EST Length	*Phaseolus vulgaris* Gene ID
ent-kaurene synthase A	**CA914587**	**415**	**Phvul.001G152100**
ent-kaurene synthase B	**CA899647**	**526**	**Phvul.005G048500**
ent-kaurene oxidase	**CA914551**	**466**	**Phvul.005G183600**
ent-kaurenoic acid hydroxylase	**CA914608**	**257**	**Phvul.006G123500**
GA 20-oxidase	**CA914823**	**582**	**Phvul.010G087500**
GA 3-oxidase	**CA915026**	**733**	**Phvul.009G097100**

Table S3. Oligonucleotide sequences for generating constructs**.** Underlined nucleotides are incorporated restriction sites. Lower case nucleotides are mutated relative to the *GA 20-oxidase* upstream sequence.

Construct	Forward Oligonucleotides (5' to 3')	Reverse Oligonucleotides (5' to 3')
D-4509	GTGACGTCCCCGGGCTGCAGGAATTCG	GAGGGATCAACATGtCTAGTGTTTG
D-2000	TCATGAATTCTTATTCTTTATTCACAAGAAAGCA	CCAGTTGCAACCACCTGT
D-1500	ATTTGAATTCTGTAGCTCTAGGTTAGATCTTCC	CCAGTTGCAACCACCTGT
D-925	GTTGGAATTCTTATACTAATTAAATTAGATACTATTTTAA	CCAGTTGCAACCACCTGT
D-750	AATAGAATTCGATTAGAGCCTTTCATTGTATATAAG	CCAGTTGCAACCACCTGT
D-600	ATTTGAATTCTGTCTAGTGGTAGTGAAATAATGAG	CCAGTTGCAACCACCTGT
D-450	AAATGAATTCGAAAAAGAAACCTTAAAAAGAATT	CCAGTTGCAACCACCTGT
D-275	AAATGAATTCTTGACCACATTTTCATCCAC	CCAGTTGCAACCACCTGT
GUS-only	GTTGGAATTCATGGTCCGTCCTGTAGAAA	CCAGTTGCAACCACCTGT
GOF1	AAATGAATTCGAAAAAGAAACCTTAAAAAGAATT	GATCCCCGGGTACCGAGCTCGGGCTAGTGTTTGAAGGGAA
GOF2	GCTGGAATTCTATCGTCTATATATGCTAATAACTTATATT	GATCCCCGGGTACCGAGCTCGGGCTAGTGTTTGAAGGGAA
GOF3	GCTGGAATTCTAACTTATATTTAAGTTATTGATCAATTTAC	GATCCCCGGGTACCGAGCTCGGGCTAGTGTTTGAAGGGAA
GOF4	GCTGGAATTCATTTACAAGAAAACAATAGTTAATGTA	GATCCCCGGGTACCGAGCTCGGGCTAGTGTTTGAAGGGAA
GOF5	AAATGAATTCTTGACCACATTTTCATCCAC	GATCCCCGGGTACCGAGCTCGGGCTAGTGTTTGAAGGGAA
GOF6	AAATGAATTCGAAAAAGAAACCTTAAAAAGAATT	GATCCCCGGGTACCGAGCTCGTAAAGGTGGTGAAGTAGAGAGTAG
GOF7	AAATGAATTCGAAAAAGAAACCTTAAAAAGAATT	GATCCCCGGGTACCGAGCTCGTCTTTTATCAAATCTCTCACCA
GOF8	GCTGGAATTCTATCGTCTATATATGCTAATAACTTATATT	GATCCCCGGGTACCGAGCTCGGAGGTTATTATAAAGGTGGTGAA
GOF9	GCTGGAATTCTATCGTCTATATATGCTAATAACTTATATT	GATCCCCGGGTACCGAGCTCGAGAGTGGTTTGGTTGAAGAGA
M1	GCTGGAATTCTATCGTCTATATATGCTAATAACTTATATT	GGTTcggcgcccGGTGGTGAAGTAGAGAGTAGATAAA
M1	CACCgggcgccgAACCTCTTCCTTTGTCTTTCC	GATCCCCGGGTACCGAGCTCGGGCTAGTGTTTGAAGGGAA
M2	GCTGGAATTCTATCGTCTATATATGCTAATAACTTATATT	TGAGTGATATGAGAtctcgtctccGAGTTTGAGTGAATGttcctcacccttccGAGGTTATTATAAAGGTGGTGAA
M2	TCTCATATCACTCACTCTCTTCAACCAAACCACTCTaaaaaaaaaaaaaaaaCTTCAAACACTAGCCCGAG	GATCCCCGGGTACCGAGCTCGGGCTAGTGTTTGAAGttttttttttttttttAGAGTGGTTTGGTTGAAGAGA
M3	GCTGGAATTCTATCGTCTATATATGCTAATAACTTATATT	GATCCCCGGGTACCGAGCTCGGGCTAGTGTTTGAAGttttttttttttttttAGAGTGGTTTGGTTGAAGAGA
M5	GCTGGAATTCTATCGTCTATATATGCTAAgccaggATATTTcctggcTTGATCAATTTACAAGAAAACAA	GATCCCCGGGtaccgagctcgGGCTAGTGTTTGAAGGGAA
M6	GCTGGAATTCTATCGTCTATATATGCTAAaaaaaaATATTTaaaaaaTTGATCAATTTACAAGAAAACAA	GATCCCCGGGtaccgagctcgGGCTAGTGTTTGAAGGGAA
M7	GCTGGAATTCTATCGTCTATATATGCTAAgccaggATATTTcctggcTTGATCAattataaaGAAAACAATAGTTAATGTAATATAAATG	GATCCCCGGGtaccgagctcgGGCTAGTGTTTGAAGGGAA
M8	GCTGGAATTCTATCGTCTATATATGCTAATAACTTATATTTAAGTTATTGATCAATTTAtAAG	GATCCCCGGGtaccgagctcgGGCTAGTGTTTGAAGGGAA

References

1. Weterings K, *et al.* (2001) Regional localization of suspensor mRNAs during early embryo development. *The Plant cell* 13(11):2409-2425.
2. Altschul SF, *et al.* (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic acids research* 25(17):3389-3402.