Text S1

Alignments

The identification of SUVR5 plant homologs, their sequences and their alignment was obtained from Phytozome.

SAM binding assay

The binding assay was performed as previously described with minor modification [41]. Specifically, proteins were incubated with 0.5 µCi of S-adenosyl-L-[methyl-3H] methionine in 30 µl reaction overnight at 4°C. They were exposed to UV in a crosslinker and the proteins were separated on SDS-PAGE and subjected to fluorography.

RT-qPCR

RNA was extracted from 0.2 g of tissue using Trizol (Invitrogen) and following the manufacturer's instructions. 1 µg of total RNA was used for RT-PCR using SuperScript III (Invitrogen). qPCR was performed using iQ SYBR Green Supermix (#170-8880, BioRad). Three biological replicas were sampled and standard deviations determined. The primers used were designed using QuantPrime qPCR primer design tool, for information on their sequence, see Supporting Information.

SELEX

For the SELEX experiments, 5 µg of a primer with 15 random nucleotides between two adaptor sequences (JP7666: GTT TTC CCA GTC ACT ACN NNN NNN NNN NNN NNG

TCA TAG CTG TTT CCT G) was annealed with 5 μg of the reverse adaptor primer JP7668 (CAGGAAACAGCTATGAC) by boiling and letting them cool down slowly. Then, 1 μg of the annealed primers was used to make dsDNA using Klenow fragment, followed by a standard phenol DNA extraction and resuspension in 200 μL of SELEX binding buffer (25mM HEPES pH7.5, 50mM KCl, 2.5mM $MgCl_2$, 0.1%NP40, 1μM $ZnSO_4$, 5% glycerol).

The purified and glutathione beads-bound GST-SUVR5 zinc finger domain was incubated with the dsDNA in SELEX buffer, 5μg of BSA and 5μg of salmon sperm DNA for 30 minutes at room temperature. The beads were washed 5 times with 1mL of SELEX binding buffer followed by a Phenol/Chloroform/IAA DNA extraction and precipitation. The recovered DNA was resuspended in 10 μL of TE buffer and used for PCR as follows: (95ºC for 3'), (95ºC for 30''; 60ºC for 1'; 72ºC for 30'')x10 cycles, (72ºC for 10'). The result of the PCR was used as a starting point for the next binding/eluting cycle.

For the standard SELEX experiment, 10 cycles of binding/eluting were done before TOPO ligating the recovered DNA to pCR2.1 vector (Invitrogen) and transforming E. coli TOP10 bacteria (Invitrogen). 20 colonies were sequenced, and the sequencing data were used to identify the consensus binding motif using the MEME Suite [43].

For the genomic SELEX experiment, Arabidopsis thaliana genomic DNA was extracted from wild type 3 week old plant leaves and fragmented to 100 bp using COVARIS. 2 μg of this DNA was processed for end repair and adaptor ligation following the manufacturer's

instructions (Illumina) and used as indicated above for incubation with purified GST-SUVR5 zinc finger domain protein. Two genomic SELEX experiments were performed, one using only one binding/eluting cycle (x1: control) and one with 9 cycles (x9). The recovered DNA was sequenced using an Illumina Genome Analyzer. gSELEX peaks were defined using MACS with the following parameters: band width = 100, model fold =32, p<1e-10, and for the definition of SELEX peaks we considered a peak positive when it showed over 50 fold increase.

A random thousand reads were used to identify a binding motif sequence using the analysis tool MEME Suite [43].

Primers used for ChIP-chip validation:

PRIMER NAME	**SEQUENCE**	**GENE**
JP2454	TCTCTCTCGCTGCTTCTCG	ACT7
JP2455	GCAAAATCAAGCGAACGG	ACT7
JP9836	GTGGCCGTGATCGGACTA	AT1G12160
JP9837	CAACGCTAACCGAGTCTGAA	AT1G12160
JP9842	GGTCGTGGCTTTGTTCAAGATA	AT1G31290
JP9843	GCCTTGACTCACTTGAGCTTG	AT1G31290
JP9838	CGGTGTTACAACTGGTGGAGT	AT3G22121
JP9839	CAAAACCTCCCATCGTAAAGC	AT3G22121
JP9787	TCGACTTGTTTGGACCTTGA	AT4G36510
JP9788	TCATGCGAATTATAGAAATTTAGACC	AT4G36510

Primers used for RT-qPCR:

PRIMER NAME	**SEQUENCE**	**GENE**
JP2452	TCGTGGTGGTGAGTTTGTTAC	ACT7
JP2453	CAGCATCATCACAAGCATCC	ACT7
JP9693	AGAAATCTTCGACGCGGTCGTG	AT1G12160
JP9694	TCCCAGGAATATGAGCAAGACGAG	AT1G12160
JP9721	TCTCACACCGCTAGTGGTTCTC	AT1G31290
JP9722	TCAGGACGCTTTACTGGTTCTTTC	AT1G31290
JP9709	CGGTTGGTGGTTTAGGATGGGTAG	AT3G22121

JP9710	TCTCCTATGCTTGCGACTGTACC	AT3G22121
JP9864	GCTGTTTGAGTTCGCCGCCC	AT4G36510
JP9865	CCGACCAAAACTCCACCCGCC	AT4G36510
JP9816	TTCCGATTCACAGCGACCTAGC	AT3G12830
JP9817	TTGCTTCTTTGAGCGGCGAGTC	AT3G12830
JP9949	GCAAAGGGTTCGAGCTTCTTATGG	AT5G54490
JP9950	CGTCGATGCGTTTCTTCGTAAGC	AT5G54490
JP9965	GTTGTCACAAATTTCGCTGGCTTG	AT5G13320
JP9966	GCGCGTTGTTGTAGAAACCAGTC	AT5G13320
JP2639	CAGGCGAGCACACTGAACTG	Primer A Figure S12
JP2640	TCGTGGTCCGAAGAAAGGAA	Primer A Figure S12
JP2695	GGCGTATAGACCGATATGAGC	Primer B Figure S12
JP2696	TACTGCGTGGCACATTTGTT	Primer B Figure S12

Primers used for EMSA assays:

PRIMER NAME	**SEQUENCE**	**PROBE**
JP8487	ACCAAGCAACACACCCCGT	UNSPECIFIC FWD
JP8493	ACGGGGTGTGTTGCTTGGT	UNSPECIFIC REV
JP8489	GTAGAATACTAGTTGATAAC	SPECIFIC FWD
JP8495	GTTATCAACTAGTATTCTAC	SPECIFIC REV

Primers used for BS-DNA amplification:

GENE	**PRIMER NAME**	**PRIMER SEQUENCE**
FWA	2004	GGTTTTATATTAATATTAAAGAGTTATGGGTYGAAGTTT
	2005	CAAAATACTTTACACATAAACRAAAAACAAACAAATCRAA
	4423	AACCAAAATCATTCTCTAAACAAAATATAAAAAAATC
Ta3	1269	GAGAATYAGGTTAATAAGAAAGTGAAGTGTT
	1274	CCACTRATTCCTRAAACACAACATTTCTRCTRATA
AtCOPIA4	3100	GGTTGTYTGTGTTTTTTATGGTTYAGATTTTATA
	3101	ATAACTRAACCACARATTCARACCCATTTTCATTT
AtSN1	1821	CAATATACRATCCAAAAAACARTTATTAAAATAATATCTTAA
	1822	GTTGTATAAGTTTAGTTTTAATTTTAYGGATYAGTATTAATTT