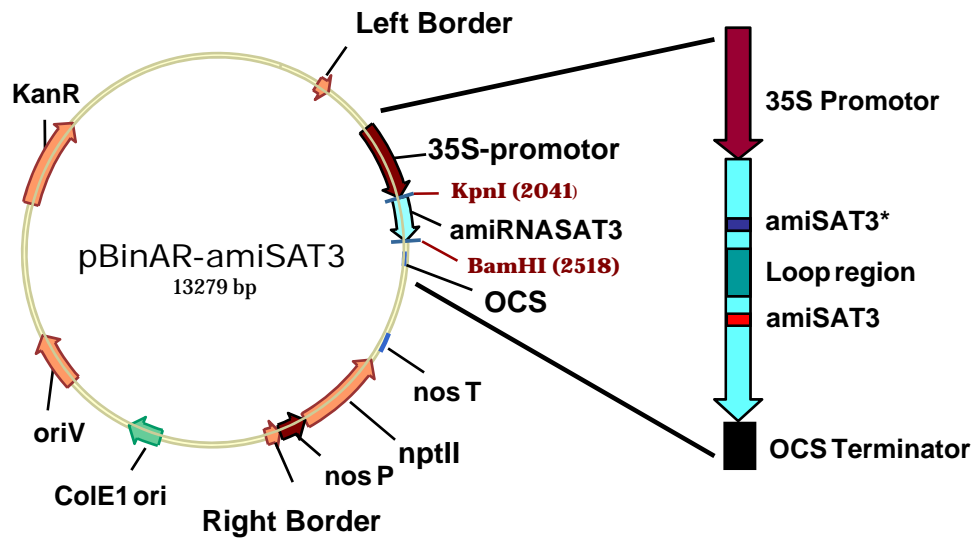


A



B

1144 1165 bp of SAT3 mRNA

```

At1g55920, AtSAT1 TGGTGTGTTGATTGGAGCTGGGAGTTGTATATTGGGGAATATAACAATCGG
At2g17640, AtSAT2 AGGTGCATTGCTTGGAGCTTGTGTGACTATACTTGGTAACATAAGCATAGG
AT3g13110, AT3SAT3 TGGGGTTTTGATTGGAGCTGGGACTTGTATTTTCGGGAATATCACGATTGG
amiRNA-SAT GGGGCTGGGACTTGTATTTTA
At4g35640, AtSAT4 CGGTGCTCTTCTTGGAGCATGTGTGACTATACTTGGTAACATAAGATAGG
At5g56760, AtSAT5 CGGTTGTTTGGATTGGAGCTGGAGCGACTATTCTTGGAAATGTGAAGATTGG
  
```

C

MIPS code	Hybridization energy	number of mismatches
At3G13110	-37.33 kcal mol⁻¹	2
At3G05290	-31.32 kcal mol ⁻¹	5
At2G28070	-30.15 kcal mol ⁻¹	5
At4G16530	-29.91 kcal mol ⁻¹	5
At1G63080	-29.68 kcal mol ⁻¹	5
At1G55920	-29.01 kcal mol ⁻¹	4
At1G65440	-27.64 kcal mol ⁻¹	4
At1G64890	-27.22 kcal mol ⁻¹	5
At3G10370	-27.10 kcal mol ⁻¹	5
At3G07420	-26.98 kcal mol ⁻¹	5

Supplemental data 1: Specificity of amiRNA-SAT3 approach

Panel A shows the Vector map of pBinAR-amiSAT3 that was used to express amiRNA for SAT3 under the control of the strong 35S-promotor. The amiRNASat3 construct consists of an anti-sense region (amiSAT3*) and a sense region (amiSAT3) for SAT3 mRNA, which are connected by a loop. The 21 nucleotide sequence of amiSAT* and amiSAT form a duplex with distinct mismatches for better recognition by DicerLike1 (DCL1) protein (A). The sequence alignment of all five SATs with the amiSAT3 sequence demonstrates the specificity of the approach while amiSAT3 has two favored mismatches to the SAT3 which are recognized by ARGONAUTE1, the other SAT genes show at least 4 mismatches (B). Additionally, SAT2, 4 and 5 show mismatches at the mismatch intolerant position 10 (Schwab et al 2005). These findings strongly suggest no degradation of other SAT transcripts than SAT3. An analysis of the hybridization energy of the entire transcriptome reveals that the hybridization energy of the amiSAT3 is significantly lower (-37.33 kcal mol⁻¹) than to any other mRNA, demonstrating a specific hybridization of amiRNA-SAT3 with SAT3 mRNA (C).