

*Title***Natural variation for sulfate content in *Arabidopsis* is highly controlled by adenosine 5'-phosphosulfate reductase***Authors*

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**Supplementary Table 1:** Predicted QTL parameters for sulfate content in 'N+' (SO10) and 'N-' (SO3) environments in the Bay-0 x Shahdara RIL population.

QTL <sup>a</sup>	Chromosome-Marker <sup>b</sup>	Position <sup>c</sup>	LOD score	R <sup>2</sup> <sup>d</sup>	2a <sup>e</sup>
SO10.1	Chrom 1 - F5I14	60.2	52.6	21	- 48
SO10.2	Chrom 3 - ATHCHIB2	8.5	37.8	23	+ 40
SO10.3	Chrom 3 - MSAT3.18	64.8	7.5	4	- 16
SO10.4	Chrom 4 - MSAT4.8	5.4	23.3	12	+ 32
SO10.5	Chrom 4 - MSAT4.18	47.4	2.9	2	+ 10
SO10.6	Chrom 5 - MSAT5.9	46.5	2.7	2	- 10
SO10.1 x SO10.2				2	
SO10.1 x SO10.3				2	
SO3.1	Chrom 1 - F5I14	60.9	95.4	48	- 62
SO3.2	Chrom 2 - MSAT2.38	10.0	2.8	2	+ 10
SO3.3	Chrom 2 - MSAT2.7	40.5	5.3	2	- 14
SO3.4	Chrom 3 - MSAT3.18	62.1	12.3	6	- 20
SO3.5	Chrom 4 - MSAT4.8	7.4	6.7	4	+ 16
SO3.6	Chrom 4 - MSAT4.18	49.3	20.0	7	+ 26
SO3.7	Chrom 5 - NGA249	3.1	6.4	2	+ 14
SO3.8	Chrom 5 - NGA139	19.3	5.1	2	- 14
SO3.9	Chrom 5 - MSAT5.9	54.7	3.3	2	+ 12
SO3.1 x SO3.4				2	

<sup>a</sup> The name given to a local LOD score peak contains the trait name suffixed with an order number.

<sup>b</sup> The corresponding marker is the one used in CIM Model 6, as well as in *anova* analysis.

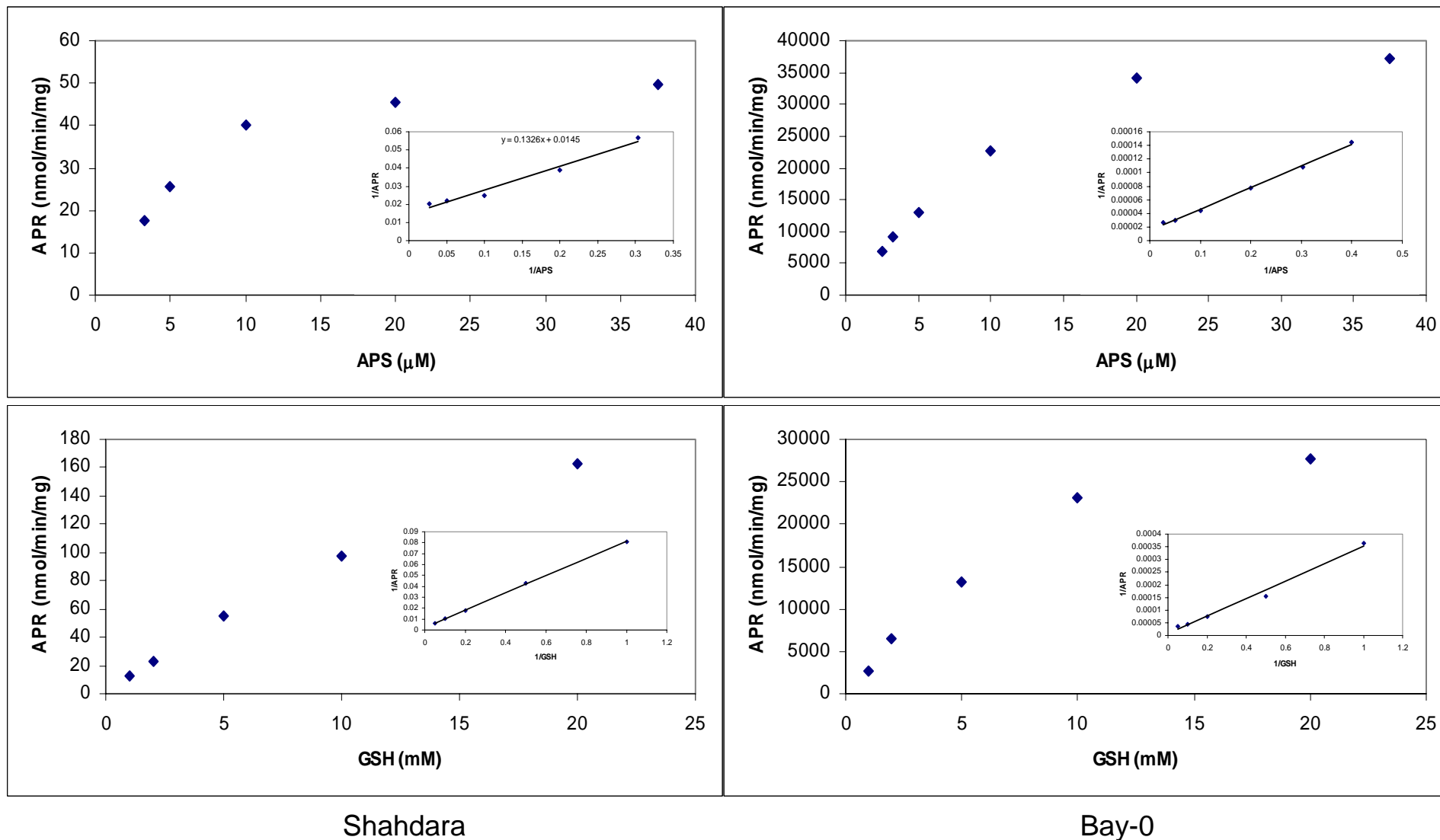
<sup>c</sup> The position of the QTL is expressed in cM from the first marker of the chromosome.

<sup>d</sup> Percentage of variance explained by the QTL or by QTL x QTL interaction, when significant.

<sup>e</sup> 2a represents the mean effect (in trait unit, nmol sulfate / mg DM) of the replacement of both Shahdara alleles by Bay-0 alleles at the QTL.

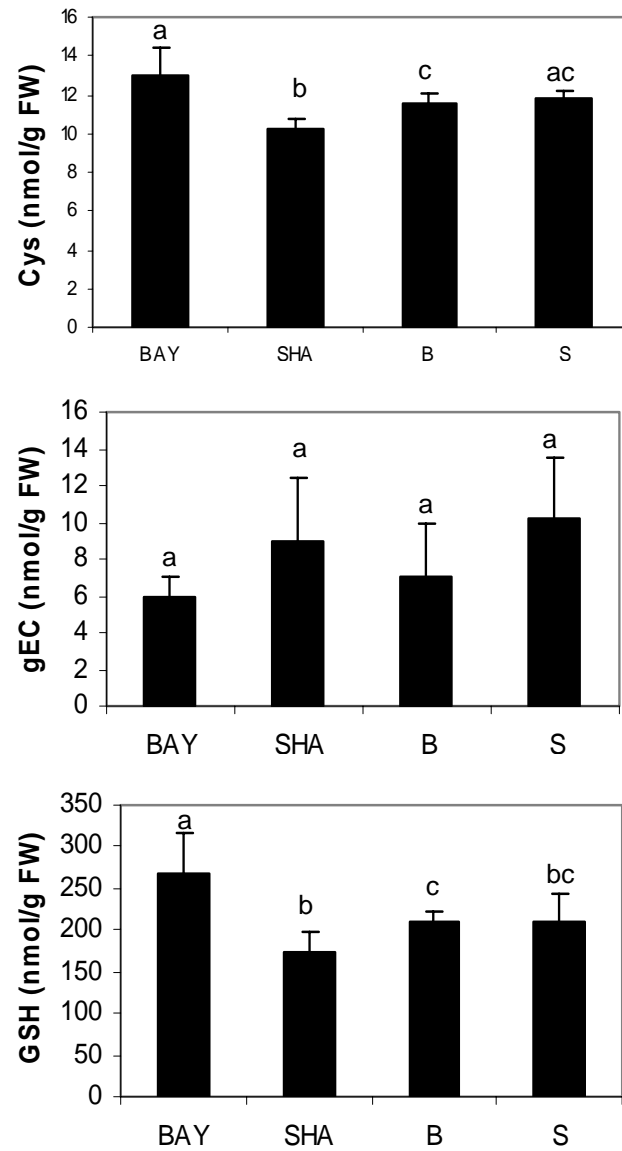
**Supplementary Table 2:** Primers used in the work and described in the Material and Methods section

MSAT22785-F	AGGGTTTTTGGGGTGTTAGC
MSAT22785-R	CATCTTTGACTAGGAAAACAACCA
MSAT23219-F	TCCCTTCATTCAAGAATTGGTC
MSAT23219-R	GGAAGGGGAAAAACAAGGAG
dCAPS-APR2-F	CTTGCGGGAAAAGGAGTTAAAGTGT
dCAPS-APR2-R	CAAACGACATGAGTGAATCAA
APR2Seq1-F	AATCTTTCTTCTAATGTGCCAACTA
APR2Seq1-R	TCAGCGTTTAAAGGTTTCATAGAGT
APR2Seq2-F	TTTGATTGTTTCATTGTTATACCCATT
APR2Seq2-R	CCTTGATGTTCCCTTTGTGTAGACCA
APR2Seq3-F	GGTATGTGTCAATCGGGTGT
APR2Seq3-R	GCTGTTACTTTTACTGCATTTTCGTT
APR2EN	GGTTCATATGGCTTCAACTCTAATTGC
APR123EC	TTTTGGATCCCATAACTCACCGAAGAAG



**Supplementary Figure 1:** Biochemical analysis of APR2 from Bay-0 and Shahdara.

Recombinant mature APR2 proteins from Bay-0 and Shahdara were purified from bacterial extracts by affinity chromatography on Ni-NTA. APR activity was determined at varying concentration of APS (2.5-37.5  $\mu\text{M}$ ) with 10 mM DTE as reductant (upper panels) and GSH (1-20 mM) with 37.5  $\mu\text{M}$  APS (lower panels). Insets show linearization of the data according to Lineweaver and Burk.



**Supplementary Figure 2:** Thiol content of Bay-0, Shahdara, and HIF068.

Thiols (cysteine -Cys-,  $\gamma$ -glutamylcysteine -gEC-, and glutathione -GSH-) were determined in leaves of Bay-0, Shahdara, HIF068-Bay (B) and HIF068-Sha (S) grown at low N input by HPLC analysis. Different indices represent values different at  $P \leq 0.05$ .