

Supplementary Information

Polycomb Repressive Complex 2 attenuates the very high expression of the *Arabidopsis* gene *NRT2.1*

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Supporting Information Legends

Figure S1: Position of primers used for ChIP experiments. Schematic representation of target and control genes used in this study, and position of primers used for ChIP experiments.

Figure S2: Genome Browser view of H3K27me3 enrichment at the *NRT2.1* locus. Snapshot of H3K27me3 enrichment at the *NRT2.1* locus, obtained from the Epigara GBrowser (<http://epigara.biologie.ens.fr/>).

Figure S3: Expression levels of *ProNRT2.1:LUC* reporter line under limiting nitrate (0.3 mM NO₃⁻) condition. Relative expression of *ProNRT2.1:LUC* by qRT-PCR in roots of 7-days old *WT* and *clf-29* plants grown under low nitrate (0.3 mM NO₃⁻) condition. Quantification by qRT-PCR is shown as the percentage of *ACT2* transcript levels. Error bars represent standard errors of the mean based on 3 biological replicates.

Figure S4: CLF is associated to the *NRT2.1* locus under limiting NO₃⁻ condition. ChIP experiments were performed with chromatin from roots of 7-days old *clf-29* plants carrying a *ProCLF:CFP:CLF* transgene, grown under low nitrate (0.3 mM NO₃⁻) condition. Signals were detected by qRT-PCR and normalized against the input for *NRT2.1*, *LEC2* (positive control) and *ACT7* (negative control).

Figure S5: Expression of *NRT2.1* transcriptional regulators is not affected in *clf-29*. Relative expression of the main transcriptional regulators of *NRT2.1*. qRT-PCR in roots of 7-days old *WT* or *clf-29* plants grown under low nitrate (0.3 mM NO₃⁻) condition. Error bars represent standard errors of the mean based on 3 biological replicates.

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42 **Supplementary file 1:** Primers used in this study

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44 **Table S1:** Expression values from transcriptomic experiments using *Arabidopsis* roots grown
45 under limiting nitrate.

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47 **Table S2:** List of highly or poorly expressed genes marked by H3K27me3 and regulated by
48 CLF in *Arabidopsis* roots.

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50 **Table S3:** Gene ontology analysis of highly or poorly expressed genes marked by H3K27me3
51 in *Arabidopsis* roots.

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Figure S1

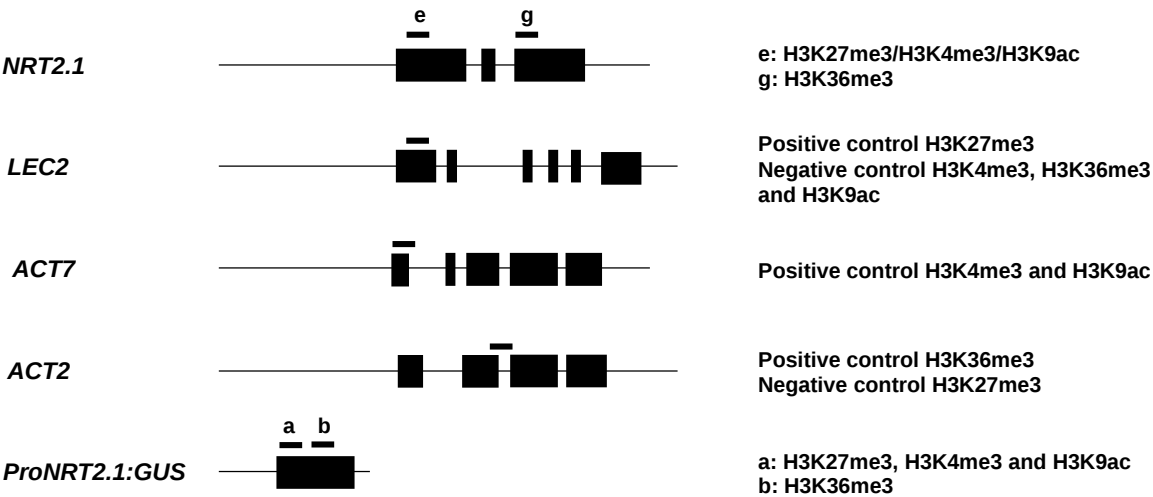


Figure S1

Figure S2

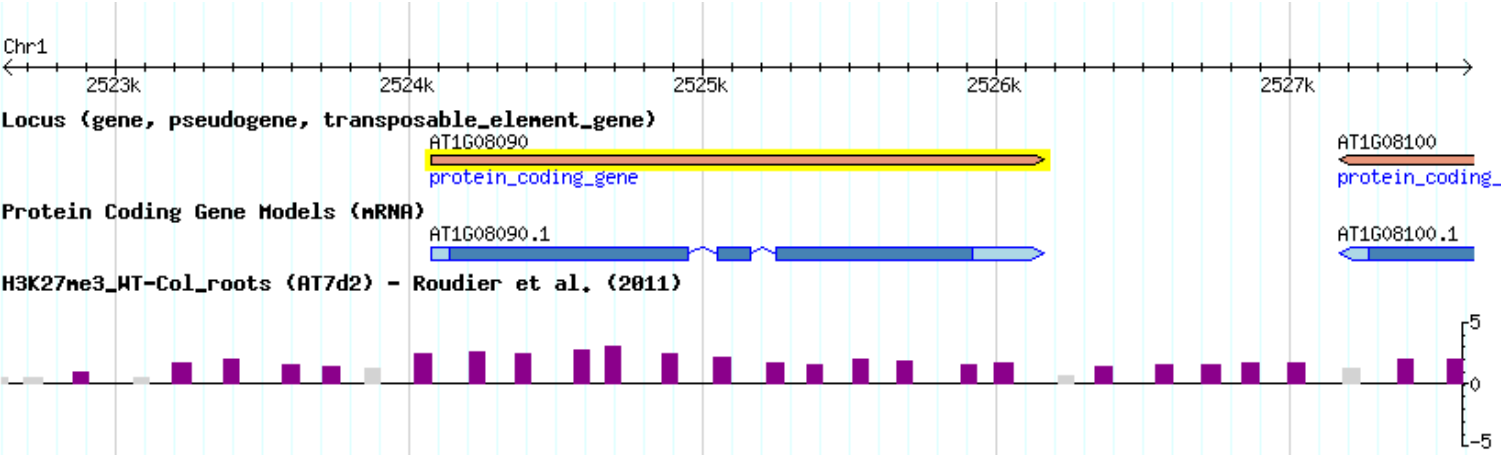


Figure S2

Figure S3

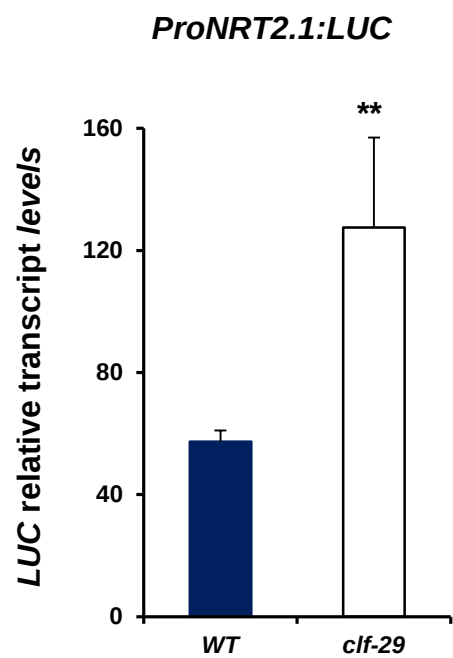


Figure S3

Figure S4

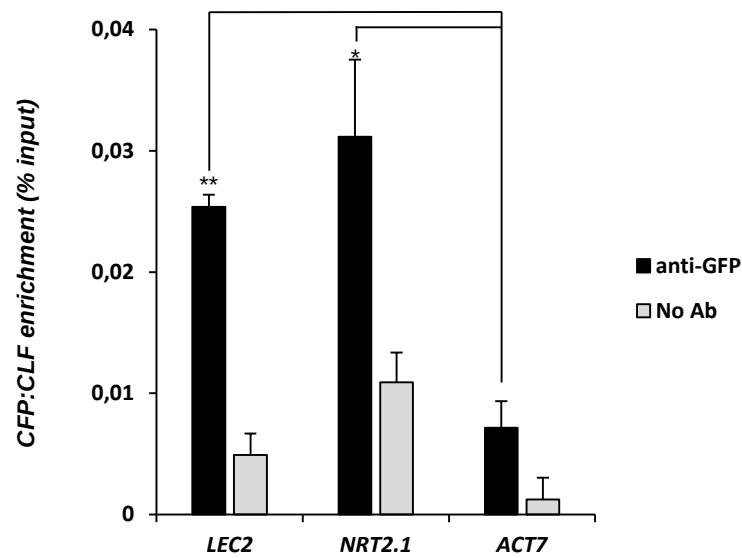


Figure S4

Figure S5

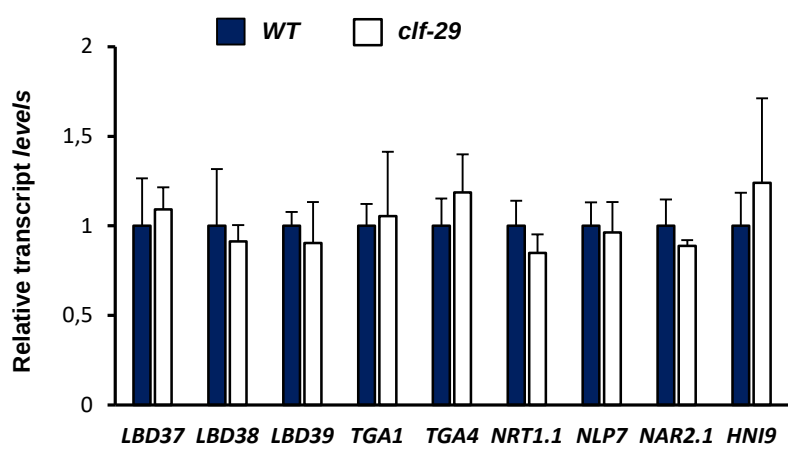


Figure S5

Supplementary file 1: Primers used in this study

Target gene	AGI	Forward/Reverse	Sequence	Application
<i>LUC</i>	-	R	GGTGTGGAGCAAGATGGAT	RT- & ChIP-qPCR
		F	TCAAAGAGGCGAACTGTGTG	
<i>GUS (a)</i>	-	R	ACAGTTTTCGCGATCCAGAC	RT- & ChIP-qPCR
		F	TGGTCCGTCCTGTAGAAACC	
<i>GUS (b)</i>	-	R	TCGGCTTCAAATGGCGTATAG	ChIP-qPCR
		F	TTTCATGCGGTCCTCATTAC	
<i>ProNRT2.1 (a)</i>	<i>AT1G08090</i>	R	AGGATCTTCGGAACAGTGATG	ChIP-qPCR
		F	ACAAAGTGGTTCCTTCACGA	
<i>ProNRT2.1 (b)</i>	<i>AT1G08090</i>	R	TCGTGTGTGTACATGTCTTCATCT	ChIP-qPCR
		F	AGTTTGCCGTTTTTCTTTGTCT	
<i>ProNRT2.1 (c)</i>	<i>AT1G08090</i>	R	CTACCCTTCCCTCATCTTGC	ChIP-qPCR
		F	TTTGGTTTTCCACGCAATTTGACG	
<i>ProNRT2.1 (d)</i>	<i>AT1G08090</i>	R	GGGTTCTTAGCCAGTGTTGA	ChIP-qPCR
		F	TTTGGAAGGATATCGGCAAC	
<i>NRT2.1 (e)</i>	<i>AT1G08090</i>	R	TCGAACCTGGCCGCTTGTC	ChIP-qPCR
		F	TGGGTGATTCTACTGGTGAGC	
<i>NRT2.1 (f)</i>	<i>AT1G08090</i>	R	GTTGAGATTCTCCCGGATGATAG	RT- & ChIP-qPCR
		F	CCATCTCTCGTGGATCTCTTTC	
<i>NRT2.1 (g)</i>	<i>AT1G08090</i>	R	ATGGAGTATCCGTAGAGAAGAACGA	ChIP-qPCR
		F	GTTGTAGATTCTGTGGTATGCCG	
<i>NRT2.1 (h)</i>	<i>AT1G08090</i>	R	CTGCTTCTCCTGCTCATTCC	ChIP-qPCR
		F	AACAAGGGCTAACGTGGATG	
<i>LEC2</i>	<i>AT1G28300</i>	R	TCATCACCGCCGCCATCTGC	RT- & ChIP-qPCR
		F	CGCTCGCACTTCACAACAGTCC	
<i>ACT7</i>	<i>AT5G09810</i>	R	AGCGAGAGATCGACAGAAGC	ChIP-qPCR
		F	GCATGCGTTGTGGTTTTATG	
<i>ACT2</i>	<i>AT3G18780</i>	R	CCCTCGTAGATTGGCACAGT	RT- & ChIP-qPCR
		F	GCCATCCAAGCTGTTCTCTC	
<i>LBD37</i>	<i>AT5G67420</i>	R	CAAAGCAGGACGTTGAGAATCC	RT-qPCR
		F	ATGGATTGAAACCGCCGATG	
<i>LBD38</i>	<i>AT3G49940</i>	R	ATGAGTTGCAATGGTTGTCG	RT-qPCR
		F	GGCCTTGAGCTTCAGGTGAT	
<i>LBD39</i>	<i>AT4G37540</i>	R	AGTTCCTGGTCCACAACATACC	RT-qPCR
		F	CTCCAACGTCCTGCTTTGTTTC	
<i>NLP7</i>	<i>AT4G24020</i>	R	CAGCTGCTGATGGAGAAGAGTAAG	RT-qPCR
		F	TTCTCCGACGGTGGAGGAAATG	
<i>NAR2.1</i>	<i>AT5G50200</i>	R	TGGAGCGTAGCATAGCTTAAC	RT-qPCR
		F	GGCAAGGATACGTTGAACATTAC	
<i>TGA 1</i>	<i>AT5G65210</i>	R	CTCTATTTATTCAGAGTAGTCCTCTGT	RT-qPCR
		F	GAACCAACGTAGGTTTGAGTTAT	
<i>TGA4</i>	<i>AT5G10030</i>	R	TATGTTGCAGTTTCTCCATACCT	RT-qPCR
		F	TCCTTTGACGGATCAACAACCTT	
<i>NRT1.1</i>	<i>AT1G12110</i>	R	GCACATTGGCATTAGGCTTT	RT-qPCR
		F	CTCAATCCCCACCTCAGCTA	
<i>HNI9</i>	<i>AT1G32130</i>	F	GTGGCGAAAGGAAGTCAGAA	RT-qPCR
		R	CTCACCCCTTCTGCTGAG	