

**Supplementary Table 1 | PHE1 ChIP-seq read mapping and peak calling information.** Peak calling was done using the ChIP sample and its respective Input sample as control. The fraction of peaks present in both replicates was determined as the percentage of peaks where spatial overlap between Replicate 1 and Replicate 2 peaks is observed (see Methods).

Sample	Nr. of sequenced reads	% of mapped reads	Nr. of called ChIP-seq peaks	% of ChIP-seq peaks present in both replicates
Replicate 1 <i>PHE1::PHE1-GFP</i> ChIP	17 037 975	65.3	2818	88.5
Replicate 1 <i>PHE1::PHE1-GFP</i> Input	24 276 095	71.1		
Replicate 2 <i>PHE1::PHE1-GFP</i> ChIP	21 838 147	70.5	4521	55.2
Replicate 2 <i>PHE1::PHE1-GFP</i> Input	23 372 778	70.7		

**Supplementary Table 2 | Annotation of PHE1 ChIP-seq peaks within genomic features of interest.**

Annotation for each individual replicate, as well as for common peaks is presented. Common peaks are defined as the overlapping peak regions between Replicate 1 and Replicate 2 (see Methods). Promoter region was considered as the 1000 bp upstream, plus the 100 bp downstream of the transcription start site..

Sample	Total nr. of peaks	Average distance to nearest TSS (bp)	Associated genomic feature (% of peaks)			Nr.of targeted genes
			Promoter	Gene body	Intergenic	
Replicate 1 peaks	2818	837	68.5	16.1	15.3	2319
Replicate 2 peaks	4521	792	68.1	18.1	13.8	3430
Common peaks (PHE1 binding sites)	2494	761	71.5	15.3	13.3	1942

**Supplementary Table 3 | H3K27me3 ChIP-seq read mapping and purity information.**

<b>Sample</b>	<b>Nr. trimmed reads</b>	<b>% of mapped reads</b>	<b>Nr. of <i>Ler</i> reads</b>	<b>Nr. of Col reads</b>	<b>Purity (%)</b>
<i>Ler</i> x Col 4x Replicate 1 Input	30 337 933	68.3	1 844 412	1 563 394	95.7
<i>Ler</i> x Col 4x Replicate 1 H3 ChIP	22 644 505	73.3	1 439 255	1 211 446	
<i>Ler</i> x Col 4x Replicate 1 H3K27me3 ChIP	27 448 642	61.5	1 214 486	681 823	
<i>Ler</i> x Col 4x Replicate 2 Input	40 500 367	66.4	2 720 117	2 483 912	97.7
<i>Ler</i> x Col 4x Replicate 2 H3 ChIP	32 322 049	71.9	2 304 635	2 068 612	
<i>Ler</i> x Col 4x Replicate 2 H3K27me3 ChIP	34 978 215	63.0	2 681 981	1 636 717	