Perduns et al. (2015) - Supplement

Supplemental figure S1: Read mapping statistics of ChIP-Seq and RNA-Seq libraries and comparison of RNA-Seq data from this study with data from Li et al., 2010.

A

RNA-Seq	Processed reads	Uniquely mapped reads	% (Uniquely mapped)
Base A	59,346,263	46,246,282	78%
Base B	33,432,364	24,687,777	74%
Blade A	74,724,999	53,086,298	71%
Blade B	27,582,965	18,668,247	68%

H3K9ac-ChIP	Processed reads	Uniquely mapped reads	% (Uniquely mapped)
Base A	29,553,783	23,724,782	80%
Base B	18,884,476	15,417,201	82%
Blade A	30,611,609	23,999,153	78%
Blade B	24,498,527	19,320,849	79%

H3K4me3-ChIP	Processed reads	Uniquely mapped reads	% (Uniquely mapped)
Base A	13,877,095	7,718,604	56%
Base B	7,915,293	6,624,821	84%
Blade A	16,204,778	10,212,086	63%
Blade B	25,950,063	21,664,983	83%

B

Base	Base A	Base B	Li et al., Base A	Li et al., Base B
Base A		0.9	0.94	0.89
Base B	0.9		0.9	0.93
Li et al., Base A	0.94	0.9		0.95
Li et al., Base B	0.89	0.93	0.95	

Blade	Blade A	Blade B	Li et al., Blade A	Li et al., Blade B
Blade A		0.93	0.96	0.96
Blade B	0.93		0.92	0.93
Li et al., Blade A	0.96	0.92		1
Li et al., Blade B	0.96	0.93	1	

Figure S1: Read mapping statistics of ChIP- and RNA-Seq libraries and comparison of RNA-Seq data from this study with data from Li et al., 2010. **A** Summary of processed reads and mapping statistics of ChIP- and RNA-Seq libraries for all replicates and samples. **B** Pearson correlation coefficients between analogous fragments from Li et al. (2010) and this study.