

Additional file 16. Comparison of PA peaks identified by PolyA-seq (Derti) and PA-seq (this study).

	Peaks \geq 50 tags*	Peaks that overlap RefSeq annotation**
Our Kidney Dataset	6,646	3,914 (58.9%)
Derti's Kidney Dataset (SRR299107)	7,606	3,510 (46.1%)

* The starting bed file for F-seq peak calling is based on bwa mapping allowing maximum 2 mismatches (see Additional Table 6 for details). We used paired-end mapping for our kidney dataset and single end mapping for Derti's kidney dataset.

** The percentage of peaks overlap RefSeq annotation (within \pm 5bp of known PA sites) was indicated in parentheses.