

## Additional file 5

### Mapping results of ChIP-seq reads generated through different purification reagents <sup>[7]</sup>

Library Name	Algorithm	Total # of Pairs	Total # Uniquely Mapped Pairs	Unique Pairs (%)	Complexity	Total Peaks	Duplicates (%)
Input		51,040,698	39,982,163	78.50%	0.9349		6.51%
St K4me3	macs	42,913,066	33,584,141	78.50%	0.9251	37,679	7.49%
Qm K4me3	macs	28,610,640	22,443,663	78.70%	0.9158	34,228	8.42%
Ne K4me3	macs	24,329,553	19,232,263	79.30%	0.8745	34,498	12.55%
Zy K4me3	macs	28,444,136	22,232,194	78.40%	0.9330	34,923	6.70%
Ba K4me3	macs	29,818,138	23,595,325	79.40%	0.9238	35,282	7.62%
St K27me3	sicer	41,332,165	33,133,641	80.30%	0.9369	30,323	6.31%
Qm K27me3	sicer	30,060,890	23,524,187	78.40%	0.9248	33,513	7.52%
Ne K27me3	sicer	33,067,413	26,534,649	80.40%	0.9340	26,714	6.60%
Zy K27me3	sicer	31,501,790	25,243,738	80.30%	0.9407	29,099	5.93%
Ba K27me3	sicer	25,693,025	20,581,001	80.30%	0.9370	40,895	6.30%