Table 1 Comparison of ChIP–chip, ChIP–SAGE and ChIP–Seq

	ChIP-chip	ChIP-SAGE	Chip-seq
Quantification	Limited quantitative and depends on the hybridization efficiency	Quantitative	Quantitative
Resolution	Depends on size of the chromatin fragments for ChIP	Depends on restriction enzyme sites	Depends on the size of the chromatin fragments and sequencing depth
Cost	High for whole-genome tiling arrays	More expensive than ChIP–Seq	Low
Limitation	Only pre-selected genomic regions on a microarray	Recognition sites for the restriction enzyme	Only non-repetitive regions