Chromatin immuno precipitation quantitative PCR (ChIP-qPCR) is the method of choice to quantify direct binding of specific regulatory proteins to genomic DNA sequences.

Unfortunately, conflicting information in literature about the proper controls and normalization strategy make accurate quantification of ChIP-qPCR data a major challenge for many users. A simple workflow implemented in qbase+ addresses these challenges and produces reliable ChIP-qPCR results.

ChIP-qPCR data need to be normalized to correct for variability related to differences in amount of chromatin, precipitation efficiency and DNA recovery. Here we present the so-called ‘fold-enrichment method’ in which ChIP-qPCR data are analyzed relative to an input sample and normalized to one or multiple non-specific genomic regions (not enriched).

miRNAs belonging to the oncogenic miR-17-92 cluster are upregulated by the MYCN transcription factor. In Mestagh et al., (Genome Biology, 2009) we applied ChIP-qPCR to assess binding of the MYCN transcription factor to the miR-17-92 promoter region. qPCR was performed on a MYCN ChIP sample and input sample from a cell line using SYBR Green I detection chemistry. Data were normalized using 2 non-specific control regions in qbase+ version 2.4.

We could demonstrate strong MYCN binding to the miR-17-92 promoter region (10-fold enrichment in ChIP-sample compared to input sample). The non-specific genomic region did not show any evidence of MYCN binding.