

# Human Negative Control Primer Set 1

**Catalog No:** 71001

**Format:** 96 rxns

**Background:** The Human Negative Control Primer Set 1 amplifies a 78 base pair fragment from a gene desert on human chromosome 12. It can be used as a negative control for almost all transcription factors and most histone modifications including:

LSD1, RNA pol II, 5-mC, and H3K9ac, H3K14ac, H3K4me2, H3K4me3, H3K27ac, H4K5ac, H4K8ac, H4K12ac, H4K16ac

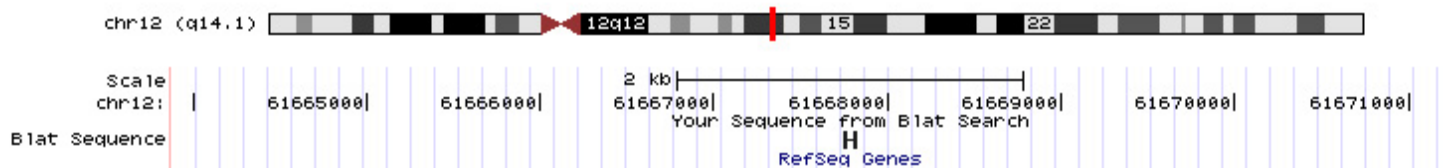
**Contents:** This control primer set contains both forward and reverse primers in 400 µl of nuclease-free distilled water. The final concentration for each primer is 2.5 µM.

**Application Notes:** Amplification should be carried out in a total volume of 20 µl, using the DNA template, 4 µl of the primer set, and 10 µl SYBR Green 2X qPCR Master mix with an annealing temperature of 58°C. For genomic DNA amplification, 12.5 ng of DNA was used as template.

**Quality Control:** This primer set was used to produce a single PCR product from PBMC genomic DNA using qPCR to generate an amplification curve with a Ct of fewer than 28 cycles. After amplification, melt curve analysis was performed to confirm the production of a single PCR amplicon.

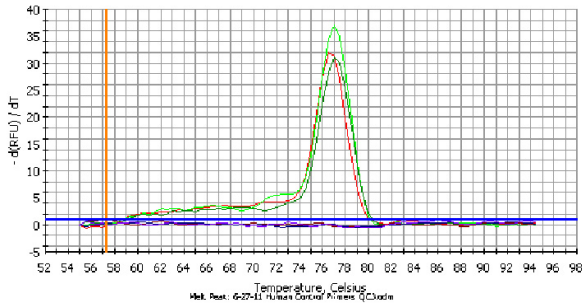
**Storage and Guarantee:** The primers are shipped at room temperature and should be stored at -20°C upon receipt to ensure stability. This product is guaranteed for 6 months from date of receipt.

This product is for research use only and is not for use in diagnostic procedures.



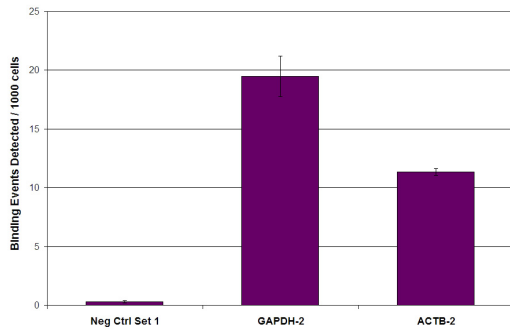
## Genomic Location

Image representing the relative location of the primer set amplicon within the genome, as generated by the UCSC Genome Browser.



### Melting Curve

PCR product melting curves were obtained for qPCR reactions. Data is shown for triplicate PCR reactions using 12.5 ng of total DNA or water as template. The single peak corresponds to a single amplicon.



### ChIP qPCR Data

ChIP was performed on chromatin from human PBMCs using an antibody to H3K4me2 and subjected to qPCR with the indicated primer set (X-axis). Data presented are normalized binding events per 1000 cells.