Supplementary Online Content

Monosomy of Chromosome 10 Associated With Dysregulation of Epidermal Growth Factor Signaling in Glioblastomas

Ajay K. Yadav, PhD
Jaclyn J. Renfrow, MA
Denise M. Scholtens, PhD
Hehuang Xie, PhD
George E. Duran, BS
Claudia Bredel, PhD
Hannes Vogel, MD, PhD
James P. Chandler, MD
Arnab Chakravarti, MD
Pierre A. Robe, MD, PhD
Sunit Das, MD, PhD
Adrienne C. Scheck, PhD
John A. Kessler, MD
Marcelo B. Soares, PhD
Branimir I. Sikic, MD
Griffith R. Harsh, MD
Markus Bredel, MD, PhD

Formatted: Default Paragraph Font

Formatted: Default Paragraph Font

Suppl eFigure. Methylation Analysis of the *ANXA7* Gene Promoter

Pyrosequencing was used to assess the methylation percentage of 9 CpG sites close to the transcriptional start site within the ANXA7 promoter in 59 human gliomas from Stanford University and various control cells. Bar graphs indicate the promoter methylation profile per sample for 9 CpG sites. Dark red lines indicate the average methylation percentage across the samples in each of the graphs. The lowest graph reports the overall promoter methylation profile per sample by averaging the methylation profiles of all 9 CpG sites.

Yadav AK, Renfrow JJ, Scholtens DM, et al. Monosomy of Chromosome 10 Associated With Dysregulation of Epidermal Growth Factor Signaling in Glioblastomas. JAMA. 2009;302(3):3joc90051.

JAMA08-7769, Suppl. Fig. 1