

# RUNX3 Attenuates $\beta$ -Catenin/T Cell Factors in Intestinal Tumorigenesis

Kosei Ito, Anthony Chee-Beng Lim, Manuel Salto-Tellez, Lena Motoda, Motomi Osato, Linda Shyue Huey Chuang, Cecilia Wei Lin Lee, Dominic Chih-Cheng Voon, Jason Kin Wai Koo, Huajing Wang, Hiroshi Fukamachi, and Yoshiaki Ito\*

\*Correspondence: [itoy@imcb.a-star.edu.sg](mailto:itoy@imcb.a-star.edu.sg)

DOI 10.1016/j.ccr.2009.02.002

(Cancer Cell 14, 226–237; September 9, 2008)

Due to a mistake made during manuscript preparation, the Supplemental Data for this article listed incorrect sequences for the primer sets for methylation-specific PCR (MSP). The correct sequences are given below. These corrections do not affect the findings or conclusions of the study.

Primer sets used for detection of methylated DNA were 5'-ataaagagaaattaggcgc-3' and 5'-ataaccctcgaaaaacgcg-3' (M3), 5'-gatgtttgtttaggtcgtagcggtc-3' and 5'-ccaaactcgaaattcgccgta-3' (M2), and 5'-tgcgattggttgcgttcgc-3' and 5'-cgaaaatacgcataccgcg-3' (M1). Primer sets used for detection of unmethylated DNA were 5'-ataaagagaaattagggt-3' and 5'-ataaccctcaaaaaacaca-3' (M3), 5'-tgtttgtttaggtgtagtggtgt-3' and 5'-cccccaactcaaaattcaccata-3' (M2), and 5'-tgtgattggtgtgtttgt-3' and 5'-caaaaatacacataccaca-3' (M1).

---

# Malignant Astrocytomas Originate from Neural Stem/Progenitor Cells in a Somatic Tumor Suppressor Mouse Model

Sheila Alcantara Llaguno, Jian Chen, Chang-Hyuk Kwon, Erica L. Jackson, Yanjiao Li, Dennis K. Burns, Arturo Alvarez-Buylla, and Luis F. Parada\*

\*Correspondence: [luis.parada@utsouthwestern.edu](mailto:luis.parada@utsouthwestern.edu)

DOI 10.1016/j.ccr.2009.02.008

(Cancer Cell 15, 45–56; January 6, 2009)

In this article, a recent publication by The Cancer Genome Atlas Research Network was incorrectly cited, and the reference was incorrectly listed. The sentence at the end of the first full paragraph on page 46 reading “In fact, these three genes are among the top five most mutated genes in human GBMs (McLendon et al., 2008)” should read as follows: “In fact, these three genes are among the top five most mutated genes in human GBMs (TCGA Research Network, 2008).”

## REFERENCE

Cancer Genome Atlas Research Network (2008). Comprehensive genomic characterization defines human glioblastoma genes and core pathways. *Nature* 455, 1061–1068.