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Errata

RUNX3 Attenuates β-Catenin/T Cell Factors in Intestinal Tumorigenesis

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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′-gatgttt gtttaggtcgtagcggtc-3′ and 5′-ccaaactcgaaattcgccgta-3′ (M2), and 5′-tgcgattggttgcgtttcgc-3′ and 5′-cgaaaatacgcataccgcg-3′ (M1). Primer sets used for detection of unmethylated DNA were 5′-ataaagagaaattaggtgt-3′ and 5′-ataaccctcaaaaaacaca-3′ (M3), 5′-tgtttg tttaggttgtagtggttgt-3′ and 5′-cccccaaactcaaaattcaccata-3′ (M2), and 5′-tgtgattggttgtgttttgt-3′ and 5′-caaaaatacacataccaca-3′ (M1).

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

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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.