

Corrigendum

MicroRNA-182 drives metastasis of primary sarcomas by targeting multiple genes

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In the process of transferring the miR-182-flox and LSL-miR-182 mice to the Jackson Laboratory, the authors realized that the description of how the LSL-miR-182 mice were generated in the manuscript contained an error. Although the miR-182-flox mice were generated by crossing the mice to a flpO deleter strain to delete the Neo cassette, as was stated in the Methods section, the R26-LSL-miR-182 mice were not crossed to a deleter strain. Instead, the R26-LSL-miR-182 mice that were utilized in this work retained the Neo cassette. Two corrected sentences for the Methods section are below.

Chimeric males were mated to WT C57BL/6 females to generate heterozygotes. These mice were subsequently crossed to a flpO deleter strain to excise the frt-Neo-frt cassette to generate miR-182-flox mice.

The R26-LSL-miR-182 mice that were utilized in this work retained the Neo cassette.

The authors regret the error.

Corrigendum

Genetic landscape of metastatic and recurrent head and neck squamous cell carcinoma

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An incorrect accession number for the sequencing data appeared twice in the manuscript, once in Results and once in Methods. The two corrected sentences appear below.

Results

All SSNVs identified by exome sequencing are enumerated in Supplemental Table 10, and sequencing files were deposited in the NCBI's database of Genotypes and Phenotypes (dbGaP phs001007.v1.p1).

Methods

Sequencing data were deposited in the NCBI's database of Genotypes and Phenotypes (dbGaP phs001007.v1.p1).

The authors regret the error.