





# Correction: A consensus molecular subtypes classification strategy for clinical colorectal cancer tissues

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## Results Section

- Table 1: Column “Public ID” of the last row “FFPE-RNA application cohort” reads **NA**.  
OShould read: [GSE267010](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE267010).
- Title of Figure 3: **Mutations** characteristics of the CMSs in the FFPE application cohort.  
OShould read: **Molecular** characteristics of the CMSs in the FFPE application cohort.
- Paragraph “Molecular characteristics of the CMSs in the FFPE-RNA application cohort,” third sentence, reads: Next, we assessed gene set enrichment across the CMSs and could recover all previously reported **iCMS** features (Fig 3B).  
OShould read: Next, we assessed gene set enrichment across the CMSs and could recover all previously reported **CMS** features (Fig 3B).

## Discussion Section

- Fourth paragraph, last sentence, reads: “Hence, the observed OS patterns appear as intrinsic **feature** of the selected patient group and further strengthen the robustness of the CMSFFPE classifier.”  
OShould read: “Hence, the observed OS patterns appear as intrinsic **features** of the selected patient group and further strengthen the robustness of the CMSFFPE classifier.”

## Materials and Methods Section

- Paragraph “RNA-sequencing and targeted exome sequencing,” third paragraph, first sentence, reads: “The TSO500 High-Throughput assay was performed on genomic DNA of the FFPE-RNA application cohort as instructed by **IlluminaPaired-end** ...”  
OShould read: “The TSO500 High-Throughput assay was performed on genomic DNA of the FFPE-RNA application cohort as instructed by **Illumina. Paired-end** ...”



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