# Article information:

Cross-species genomic landscape comparison of human mucosal melanoma with canine oral and equine melanoma | Nature Communications
<https://www.nature.com/articles/s41467-018-08081-1>

# Article summary:

1. Mucosal melanoma, which develops in mucosal sites such as the oral and nasal cavities, represents around 1-2% of all cases of melanoma and has a low single nucleotide mutation burden with no evidence of a UV signature.

2. The genomes of tumors that develop at mucosal sites have not been well characterized, but a cross-species genomic landscape comparison of human mucosal melanoma with canine oral and equine melanoma reveals similarities in terms of mutant genes and pathways, suggesting evolutionarily conserved mechanisms of tumor development.

3. The study also identifies germline predisposing alleles implicated in disease development and highlights the differences between species that help inform on the biology of mucosal melanoma.

# Article rating:

May be slightly imbalanced: The article presents the information in a generally reliable way, but there are minor points of consideration that could be explored further or claims that are not fully backed by appropriate evidence. Some perspectives may also be omitted, and you are encouraged to use the research topics section to explore the topic further.

# Article analysis:

The article "Cross-species genomic landscape comparison of human mucosal melanoma with canine oral and equine melanoma" published in Nature Communications provides a comprehensive analysis of the genetic landscape of mucosal melanomas in humans, dogs, and horses. The study highlights similarities and differences between the three species, shedding light on potential mechanisms of tumor development and informing future research directions.

One potential bias in the study is the limited sample size for human mucosal melanomas. While hundreds of genomes of cutaneous melanoma have been sequenced, only ~20 human mucosal cases have been sequenced to date. This may limit the generalizability of the findings to a larger population. Additionally, while the study identifies similarities in terms of mutant genes and pathways across species, it does not explore potential differences in gene expression or epigenetic modifications that may contribute to tumor development.

The article also notes that immunotherapies have yielded impressive results in tumors with a high mutational load but appear less effective in mucosal melanomas due to their lower neo-antigen burden. However, it does not explore potential alternative treatment options for these types of tumors or discuss potential risks associated with immunotherapy.

Overall, while the study provides valuable insights into the genetic landscape of mucosal melanomas across species, further research is needed to fully understand the mechanisms underlying tumor development and identify effective treatment options for these types of tumors.

# Topics for further research:

* Gene expression differences in mucosal melanomas
* Epigenetic modifications in tumor development
* Alternative treatment options for mucosal melanomas
* Risks associated with immunotherapy for mucosal melanomas
* Neo-antigen burden in mucosal melanomas
* Larger sample sizes for human mucosal melanoma studies

# Report location:

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