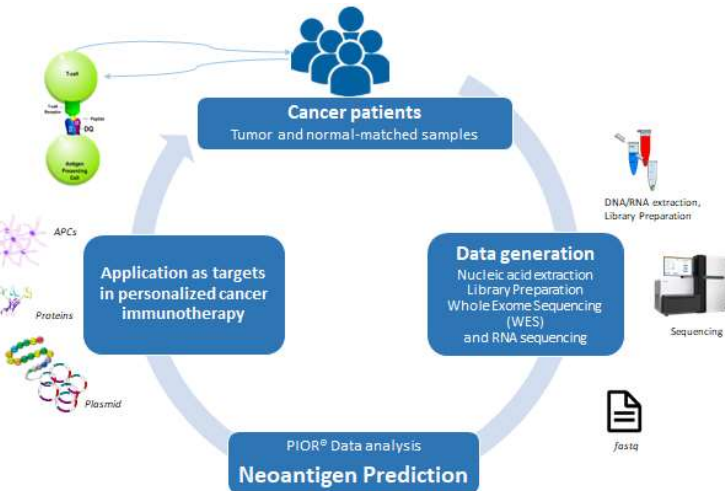


# PIOR® - Personalized Immuno-Oncology Ranking - User-friendly analysis of NGS data from patients

Ola Nilsson, Luigi Notari and Hans Grönlund

## Conclusions

- Analysis of WES and RNA-seq data from matched tumour-normal samples enables the identification of tumour-specific mutations that form neoantigens.
- PIOR® is a user-friendly solution for analysis of NGS-data through a web portal.
- Multiple tools are built-in to facilitate all steps throughout the process.
- PIOR® detects tumour-specific mutations and ranks peptide candidates to be used in targeted therapies for cancer.

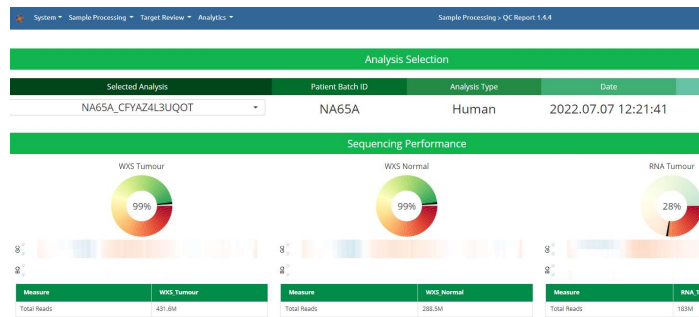


## Background

- Personalized medicine in cancer involves next-generation sequencing (NGS) of tumour samples, which allows for extensive evaluation of tumour characteristics, and opens for novel targeted therapies.
- Whole exome/genome sequencing (WES/WGS) and transcriptome sequencing (RNA-seq) offer substantial improvements over selective gene panels.
- WES, WGS and RNA-seq data adds to the complexity of data analysis, which in turn puts requirements on the bioinformatics software, which typically lacks a user-friendly interface.

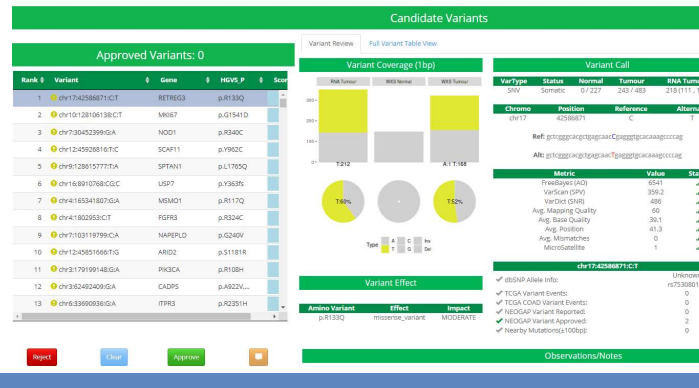
## PIOR®

- Developed by NEOGAP Therapeutics AB to facilitate unsupervised analysis of NGS data from cancer patients, operated through a user-friendly web portal.
- PIOR® comes with audit-trail, personal logins, file management, encryption, and GDPR compliance.



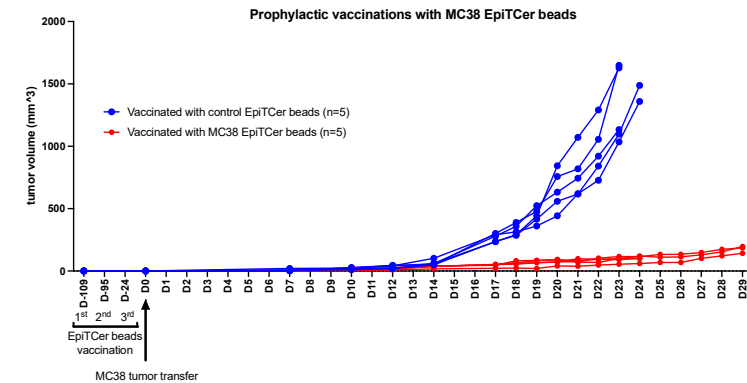
## Specialised built-in apps

To support each step in the process, from bioinformatics analysis, QC, variant approval and automated batch reporting, PIOR® offers built-in tools accessible through several sub-menus.



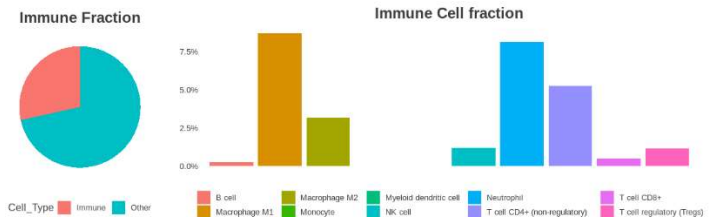
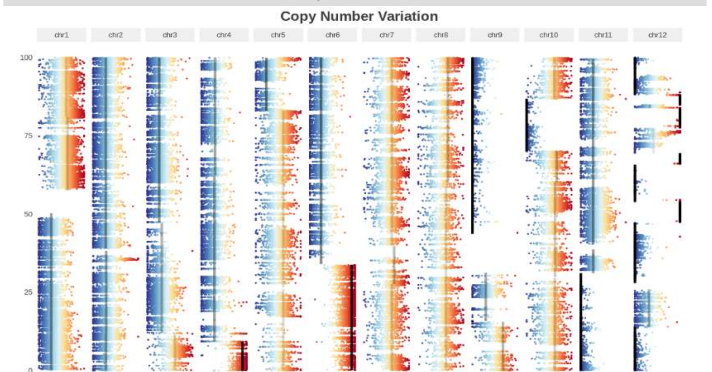
## Neoantigens identified by PIOR® inhibits tumour development in a Murine MC38 tumour model

Acknowledgements to Long Jiang for his work with the Murine MC38 tumour model.



## Not only neoantigens!

The analysed data from WES and RNA-seq can be used for a multitude of analyses, providing a molecular view of the analysed tumour, as depicted by copy number variation and immune cell infiltration analyses.



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