

# An online tool to validate predictive biomarkers of therapy response using transcriptomic data of 3,651 ovarian cancer samples

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### Background

- Systemic therapy of ovarian cancer can include chemotherapy and targeted therapy.
- Prognostic biomarkers are capable to predict survival and predictive biomarkers are capable to predict therapy response.
- To date, multiple online tools were established to identify prognostic biomarkers, but no platform is yet available for predictive biomarkers.

# Objectives

Here, we describe the first release of an online available tool capable to validate gene expression based predictive biomarkers using transcriptomic data of a large set of ovarian cancer patients.

## Methods

Published gene expression data of 35 publicly available datasets was integrated with treatment data into a unified database.

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The classification is based on either author-2. reported pathological complete response (n=1,022) or relapse-free survival status at 6 (n=1,347) or 12 (n=1,282) months:



#### **Treatment data includes (at 6 months):**

- Platin therapy (n=1,209)
- Taxol therapy (n=694)
- Docetaxel (n=97)
- Gemcitabine (n=126)
- Paclitaxel (n=208)
- Topotecan (n=118)
- The transcriptomic database includes 20,089 unique genes and 54,675 probe sets.
- Gene expression and therapy response are 5. compared using receiver operating characteristics and Mann-Whitney tests:





#### Summary

- The analysis pipeline enables to validate and rank predictive biomarker nominees. By analysing the candidate genes in a large set of independent patients, we can select the
  A select the selec most reliable candidate and abolish those which are most likely to fail in a clinical setting.
- The registration-free interface of the online analysis platform is accessible at

www.rocplot.org/ovar



