VEGFR-3 expression profiling by histology and biomarkers strategy to classify patient population for the selective VEGFR-3 inhibitor EVT801

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**EV801: A differentiating anti-tumour approach**

**ETV801 activity on tumour microenvironment**

- Hypoxia
- Endothelial cell immunomodulation
- Tumour associated macrophages
- Cytokines
- Myeloid-derived suppressor cells
- Multiple cooperative modes of action

**Example of histology labelling on HGS-OC patient**

- **VEGFR3 H-score (%) of positive surface (Hscore)**
- **CD3 quantification (%) of tumour surface**
- **CAIX quantification (%) of tumour surface**

**Correlation analysis in ovarian cancer patients**

- Data analysis was performed on 6 patients with high grade serous ovarian cancer (HGS-OC) included into the clinical trial
- Hypotheses need to be confirmed with inclusion of new patients in different indications
- Bioinformatics team has designed signatures based on VEGFR3 associated genes and genes regulated differentially in resistant versus sensitive patients to PDs mAb therapy
- Stage 3 will be pivotal to consolidate our hypotheses

**Conclusion and next steps**

- In HGS-OC patients enrolled, VEGFR3 expression tends to be positively correlated with hypoxia and PDs resistance signature & negatively correlated with CD3+ T-cells infiltration.
- The correlations in HGS-OC patients are highly encouraging and informational while aligning with the EVT801 mechanism of action.
- Patients with hypoxic HGS-OC tumour pO2 infiltrated with CD3+ T-cells and with high VEGFR3 expression could benefit from EVT801 treatment