Company Logo

Recipient: Patient/Doctor

Report ID:
Sample ID:
Report Date:

Patient Information:
Patient Name:
Gender:
Mailing Address:
Date of Birth:
Age:

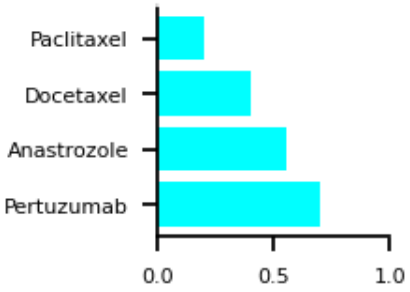
Doctor Information:
Doctor Name:
Hospital Id:
Hospital/Institute Name:

Sample Information:
Sample type:
tissue site:
Sample ID:
Date of Collection:
Handler Name:
Handler's affiliation:
Storage method:

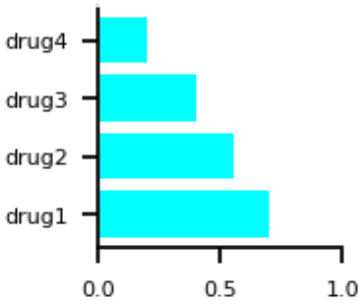
Sequencing Information:
Sequencing Center:
Sequencing Center ID:
Sequencer type:
Sequencer Name:
Handler Name:
Sequencing Date:

Cancer Type: Breast Cancer - <oncotree code BRCA/IDC/ILC etc.>
Severity: Benign/Malignant
Cancer subtype: Basal (Triple Negative)/HER2+/Luminal A/Luminal B/LuminalB-Like
Upregulated Gene Set: BRCA etc. (computationally computed)
Downregulated Gene Set: ... (computationally computed)
Activated Pathways: P53 etc. (computationally computed)
Oncogenes: ... (computationally computed)
Tumor suppresor genes: ... (computationally computed)

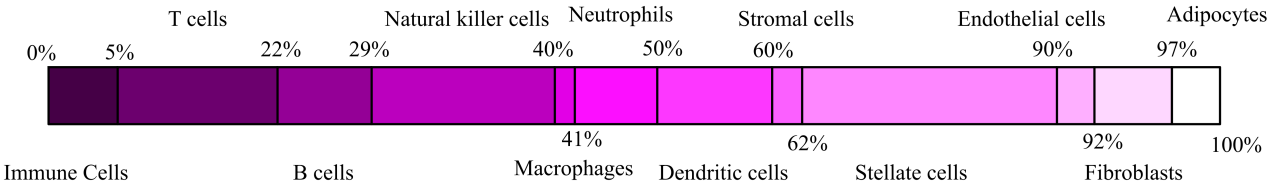
FDA approved Drugs:



In trial/Novel Drugs:



Percentage of Tumor Microenvironment:



Known Mutations seen: BRCA1-E23fs, BRCA1-C44Y

Unknonwn but potentially pathological mutations: (No information available yet – we will need to develop this method.) BRCA1-K45N, BRCA1-C39S

Observations & Findings: Possibly HER2+.

Proposed Drug: Pertuzumab, Drug1

Explanation of method:
Data Used: Public and in house data.
Method Used: In house methos for drug prediction using drug descriptors and gene expression profiles. Mutect2 and inhouse db for mutation calling.

Comments on Relapse: Less likely (in house software, analyszed based on mutations presents in the sequenced tissue)

References:
[1] Reference 1
[2] Reference 2

**Statement for Ethical responsibility
**Statement for Data confidentiality