Proposals requesting access to ALTTO Samples

Prospective evaluation of HLA-DRB1*07:01 with lapatinib-induced liver injury in adjuvant breast cancer using ALTTO

PIK3CA mutations and PTEN as predictor for response /resistance in HER2+ breast cancer

Immunological parameters and Tumor-infiltrating lymphocytes (TILs) are predictors for response to anit-HER2 therapy

Pharmacogenetic predictors of anti-HER2 directed therapies, validation of comprehensive GWAS analyses

Newly-diagnosed patients with HER2-overexpressing breast cancers and high tumor infiltrating. lymphocytes (TILs) at baseline define a good prognostic group that do not require dual anti-HER2 therapy.

Inter-observer variability study in TILs quantification

Primary tumor immune response in the ALTTO trial

Phosphorylated (tyrosine 705) STAT3 status as a predictor of benefit from anti-HER2 therapy in breast cancer

Predicting response to trastuzumab and/or lapatinib in the adjuvant setting based on an immune function gene expression score.

Quantitative, domain-specific HER2 protein analyses in NeoALLTO: The ECD/ICD project

Integrative multi-omic analysis: towards treatment de-escalation for early stage HER2-positive breast cancer

Proposals requesting access to NeoALTTO Samples

Identifying early biomarkers associated with pathological response of HER2-overexpressing breast cancer treated with trastuzumab, lapatinib or the combination using whole genome gene expression profiling

Genotype-drug response relationships uncovered through high throughput kinome re-sequencing.
Immunological biomarkers of therapeutic response to HER2 targeted therapies
Cardiac Troponin T and NT-proBNP as potential biomarkers for early detection and prediction of trastuzumab and/or lapatinib- induced cardiotoxicity in HER2 positive early breast cancer patients
Host genetics and study drug response (liver safety, efficacy/drug resistance and other safety) in NeoALTTO using GWAS and HLA genotyping
Plasma microRNA levels for predicting and monitoring therapeutic response to neoadjuvant treatment in HER2-positive breast cancer
Plasma Genomic Rearrangements in the NeoALTTO trial
Whole exome sequencing of pre-treatment, Day-14 and residual cancer samples from the NeoALTTO clinical trial
Quantitative, domain-specific HER2 protein analyses in NeoALLTO: The ECD/ICD project
Correlation of outcomes in NeoALTTO with changes in quantitative HER2 and p95HER2 in baseline biopsies, 2 week biopsies and residual tumors
Analysis of circulating tumour DNA in women with HER2/ErbB2 overexpressing primary breast cancer treated with neoadjuvant lapatinib, trastuzumab and the combination with paclitaxel chemotherapy
Gene expression profile to identify patients who benefit from HER2-targeted therapy
Pharmacogenetic predictors of anti-HER2 directed therapies, validation of comprehensive GWAS analyses
miR-205 as potential predictive biomarker of response to HER2-targeted therapy
Understanding the genomic causes of sensitivity and resistance to TRASTUZUMAB and LAPATINIB in early stang HER2-overexpressing breast cancer
Enabling Clinical Epigenetic Diagnostics: The Next Generation of Personalized Breast Cancer Care

Evaluating copy number aberrations (CNA) in HER2+ breast cancer: defining the repertoire of genomic alterations, intra-tumor heterogeneity and potential key genomic drivers associated with pCR and clinical outcome in patients enrolled in the NeoALTTO trial.

Quantitative proteomics analysis as a tool to better understand the mechanisms of resistance or sensitivity to trastuzumab and lapatinib in HER2-positive early breast cancer.