

SM > bc comprehensive genomic breast cancer databases:		
Norwegian breast cancer study (NBCS)	The Norwegian breast cancer study possesses detailed molecular data (see Table) with unique patient follow up provided by the Cancer Registry of Norway.	Perou, Sørli et al, Nature 2000 Aure et al Genome Biology 2013 Fleisher et al Genome Biology 2014 Kristensen et al. Nature Rev Cancer 2014
OSLO2	A consecutive sample collection (n=1400) of samples collected in the Oslo area. All molecular levels (DNA meth, CNA, mRNA and miRNA) characterized for a core subset of 500 cases,	Aure et al. Genome Medicine 2014 (under review)
OSLO3 (NeoAva trial)	A randomized phase II study of breast cancer tumors treated with neoadjuvant chemotherapy with and without Avastin (bevacizumab). All molecular levels at 3 time points, blood sample	Engebråten et al Cancer Research: December 15, 2012; Volume 72, Issue 24, Supplement 3, P5-17-02
Subpopulations from one lung tumor	Copy number and transcriptomic sequencing data from one squamous cell lung carcinoma, sorted into CD133+ and CD133- cell populations	Barrett et al PLoS One, 2013; PMID: 23527012
Subpopulations from one breast tumor	Copy number data from several subpopulations sorted from ER+ breast cancer.	Data not published
NeoTax	Tumor biopsies obtained before and after neoadjuvant treatment with epirubicin or taxol. Genome-wide data on methylation, RNA and miRNA expression, from paired samples from xx patients	Chrisanthar et al. PloS One 2011 PMID: 21556366
SAFIR01&02	1 000 metastases from Breast Cancer ready end of 2015. 500 patients already included (SAFIR01 and recruitment of SAFIR02 as of sept 2014). Whole exome sequencing ongoing and 100 metastases have already been profiled and analysed.	Andre, Lancet Oncol, 2014 Andre, ESMO, 2014
METABRIC	1980 samples with copy number (SNP 6), expression (Illumina Ht12), miRNA (custom Agilent array) and long-term follow-up. More data types currently generated. 473 samples have also matched normal.	Curtis, Christina, et al. Nature 486(7403) (2012): 346-352.
RATHER - Rational Therapy for Breast Cancer	317 ILC and TN breast cancers. As in METABRIC, plus DNA kinome sequencing, RNA kinome sequencing and RPPA. 127 samples have also matched normal. Long follow-up.	Simon, I. M., et al., , Annals of Oncology 25.suppl 1 (2014): i8-i8.
NEOTANGO	Neo-adjuvant clinical trial to test if the ordering of two drugs alter the response. Copy number (SNP 6) and expression data (Illumina Ht12) 3 time points, blood sample available	Earl HM et al., 2014, Lancet Oncol 15(2):201-12
EUROCAN	EU driven project to produce a public access dataset (n=2000) as well as a research dataset with more restricted access used here, mRNA and miRNA	www.ncin.org.uk/view?rid=790
TRANSCAN	Sharing of relevant results, data sets and/or resources within ERA-NET on Translational Cancer Research (TRANSCAN), DNA methylation (n=2300)	Ongoing
BASIS	500 ER+, HER2- breast cancer cases, whole genome shotgun sequencing, genome-wide copy number analysis, mRNA expression analysis, miRNA expression analysis and genome-wide methylation analysis	http://www.basisproject.eu/ Nik-Zainal 2012, Cell 149, 994–1007
COMING DATA	There will be more data from oncoming clinical trials (Artemis I, for example) and from the primary/metastasis study (OsloVal).	Ongoing
Single-cell and bulk genome sequences	~200 single-cell low coverage genomes of different sectors of primary breast tumours. Current funding will deliver additional ~800 cells plus with single-cell RNA seq. in 3-6 patients.	Peter Van Loo, Thierry Voet Ongoing