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Data Article

# Dataset for the proteomic inventory and quantitative analysis of the breast cancer hypoxic secretome associated with osteotropism

Thomas R. Cox [a,*,1], Erwin M. Schoof [b,1,2], Alison Gartland [c], Janine T. Erler [a], Rune Linding [a,b,**]

[a] Biotech Research and Innovation Centre (BRIC), University of Copenhagen (UCPH), Copenhagen DK-2200, Denmark
[b] Cellular Signal Integration Group (C-SIG), Technical University of Denmark (DTU), Lyngby DK-2800, Denmark
[c] The Mellanby Centre for Bone Research, The University of Sheffield, Sheffield S10 2RX, UK

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ABSTRACT

The cancer secretome includes all of the macromolecules secreted by cells into their microenvironment. Cancer cell secretomes are significantly different to that of normal cells reflecting the changes that normal cells have undergone during their transition to malignancy. More importantly, cancer secretomes are known to be active mediators of both local and distant host cells and play an important role in the progression and dissemination of cancer. Here we have quantitatively profiled both the composition of breast cancer secretomes associated with osteotropism, and their modulation under normoxic and hypoxic conditions. We detect and quantify 162 secretome proteins across all conditions which show differential hypoxic induction and association with osteotropism. Mass Spectrometry proteomics data have been deposited to the ProteomeXchange Consortium with the dataset identifier PXD000397 and the complete proteomic, bioinformatic and biological analyses are reported in Cox et al. (2015) [1].



* Corresponding author.
** Corresponding author.
*E-mail addresses:* coxthomasr@gmail.com (T.R. Cox), linding@lindinglab.org (R. Linding).
[1] These authors contributed equally.
[2] Current address: Princess Margaret Cancer Centre, University Health Network, Toronto, ON, Canada M5G 1L7.

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**Specifications table**

| Subject area | Biology |
|---|---|
| More specific subject area | Breast Cancer, Bone Metastasis, Secretome |
| Type of data | Mass Spectrometry RAW files |
| How data was acquired | LC-MS/MS on a Q-Exactive Mass Spectrometer (Thermo Fisher Scientific) |
| Data format | .RAW files |
| Experimental factors | None applied |
| Experimental features | The project profiled the expression patterns in hypoxia induced secretomes between MDA-MB-231 parental and MDA-MB-231 Bone Tropic (BT) breast cancer cell lines which have been previously generated by Massague and colleagues (Kang et al. Cancer Cell 2003). |
| Data source location | Copenhagen, Denmark |
| Data accessibility | The Mass Spectrometry proteomics data for the article "The hypoxic cancer secretome induces pre-metastatic bone lesions through lysyl oxidase" doi:10.1038/nature14492 [1] have been deposited to the ProteomeXchange Consortium (http://proteomecentral.proteomexchange.org) via the PRIDE partner repository [2] with the dataset identifier PXD000397 |

***Value of the data***

- This data set will be of value to the scientific community wanting to determine which proteins are secreted from breast cancer cells that metastasize to bone, and those that are regulated by hypoxia.
- The dataset includes quantitative global proteome (Label-free and SILAC) analysis of hypoxic induced secretomes of parental and bone tropic human breast cancer cell lines.
- Differential analysis of secretome changes associated with bone tropism in breast cancer.
- Response of the cancer secretome to hypoxic induction.

## 1. Data, experimental design, materials and methods

### 1.1. Cell lines

The MDA-MB-231 Bone Tropic (BT) 1833 subclone cell line was obtained from J. Massagué at the Memorial Sloan-Kettering Cancer Center. The MDA-MB-231 parental cell line was obtained from the American Type Culture Collection (ATCC) (distributed by LGC Standards). All cell lines were routinely tested for mycoplasma and tested negative for murine pathogens by IMPACT I testing (IDEXX Laboratories).

### 1.2. Collection of hypoxia induced conditioned medium (CM)

For label-free Mass Spectrometry analysis, the MDA-MB-231 parental (wt) cell line and the MDA-MB-231 Bone Tropic (BT) (1833 sub clone derived in Kang et al. [3]) (a kind gift from J. Massagué) were routinely cultured in high glucose Dulbecco's Modified Essential Media (DMEM)+GlutaMAX (Gibco 31966-021) with 100 U/ml penicillin and 100 μg/ml streptomycin (Gibco 15140-122), plus 10% dialysed Fetal Bovine Serum (FBS) (Gibco 26400). For conditioned media (CM) collection, cells were