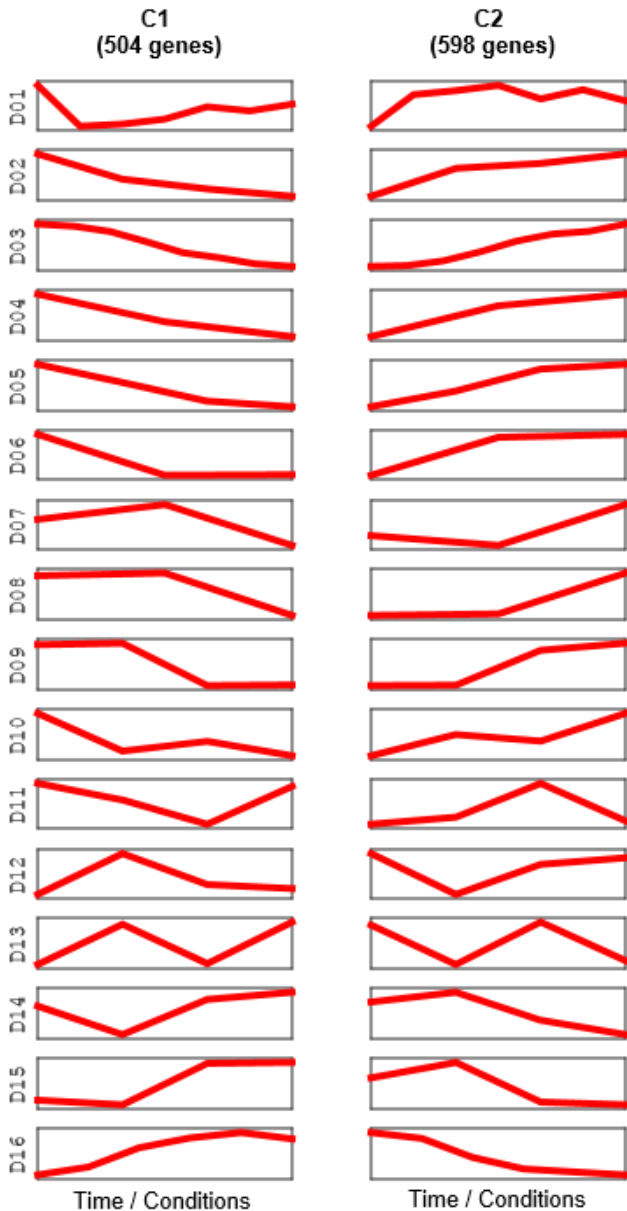


# Gene clusters offer better answers in breast cancer prognosis

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Breast cancer patients could get a more reliable idea of how long they will live now scientists have

linked a new group of genes to poor prognosis.

It could add a new layer of precision to [prognosis](#), helping doctors plan the most helpful treatments, and crucially, patients to plan their futures.

"It is very encouraging," said Professor Asoke Nandi at Brunel University London.

"The genes we have discovered can give prognosis which is as good as, and looking better than, what is currently available for prognosis. It could in future help develop a standard test to give a more accurate result."

How genes behave at low oxygen levels is a good pointer to cancer prognosis and a promising sphere for targeted treatment.

Brunel University London developed novel decision-making method, UNCLES, which blends results from multiple experiments and can answer questions current methods can't. Looking at data from 16 different [breast cancer](#) data sets at low oxygen levels identified two main subclusters of genes working in opposite ways. One gene subcluster makes cancer cells grow and multiply. The other is oxygen-sensitive.

A second study examined samples collected from the lab and from patients. Analysed together, these two opposite subclusters of growth and oxygen-leeching genes give the same quality prognosis as the current method which only looks at oxygen-sensitive genes. And there are strong signs that using the subclusters together can actually offer a far more precise prediction.

"Our discovery of two clusters of oppositely behaving [genes](#) from multiple experiments under hypoxia-related conditions came from an exploratory study – we weren't looking for anything specific," explained Professor Nandi. "And this could not have been achieved by any other existing

method. So this opens up amazing new opportunities – not just in genomics but in brain signal processing and, indeed, in any studies related to clustering.

"Prognosis is becoming increasingly important in breast [cancer](#) both for patients and for clinicians to prepare appropriate treatments as well as to offer appropriate support".

**More information:** Basel Abu-Jamous et al. UNCLES: method for the identification of genes differentially consistently co-expressed in a specific subset of datasets, *BMC Bioinformatics* (2015).  
[DOI: 10.1186/s12859-015-0614-0](https://doi.org/10.1186/s12859-015-0614-0)

Provided by Brunel University London

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