

Lung cancer genetics mapped

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Genomics: Profiling lung cancer

A comprehensive analysis of the lung cancer genome is reported this week in *Nature*. By finding genes that are mutated in cancer cells compared with healthy cells, scientists are beginning to build a picture of what goes wrong to cause disease.

In a large multicentre study, Richard Wilson and colleagues examined genetic mutations associated with lung adenocarcinoma in 188 patient samples. Over 600 genes with known or potential links to the disease were sequenced, of which 26 were mutated at high frequencies.

The research identifies several genes that were not previously thought to be involved in lung cancer, roughly tripling the number of genes associated with this disease. These include genes that regulate the cell cycle and cell proliferation — ATM, APC, ERBB4 and FGFR4.

Overall the findings provide a road map of the signalling pathways gone awry in lung cancer, the leading cause of cancer death, and expand the range of potential therapeutic options.
