

## **Identifying Regions of Genome Linked to Cancer**

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Data from a tiling array indicated 357 regions of the human genome are potentially linked to breast cancer. Comparative analysis was performed on these regions using the UCSC Genome Browser to tentatively investigate and identify regions best conserved across different species of animals. We found regions that are well conserved in mammals and regions that are well conserved across vertebrates, suggesting that these regions might be relevant to human biology. We hope to further find that some of these regions partially match cancer related genes. Our analysis should provide a focused set of novel gene regions to facilitate the experimental validation of previously missed genes in breast cancer studies.