

Open Peer Review on Qeios

GISTIC

National Cancer Institute

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A statistical approach for identifying genomic regions of aberration that are more likely to drive cancer pathogenesis. The method identifies those regions of the genome that are aberrant more often than would be expected by chance, with greater weight given to high-amplitude events (high-level copy-number gains or homozygous deletions) that are less likely to represent random aberrations.

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