Genome sequencing furthers understanding of multiple myeloma.

Printed from https://www.cancerquest.org/newsroom/2011/04/genome-sequencing-furthers-understanding-multiple-myeloma on 11/01/2026



Genome sequencing offers a unique and compelling approach to cancer research. Because cancer is a condition when normal cell functions break down, studying gene patterns may reveal specific mutations that lead to specific diseases. A recent study published in *Nature* documents the gene sequencing of 38 different cases of multiple myeloma. This research uncovered several notable parallels. Almost half of the cases had mutations in genes involving protein translation. There were also significant instances of gene mutations involving histone methylation, blood coagulation or NF-κB signaling. These findings demonstrate the power afforded by DNA sequencing as a way to understand cancer development and improve cancer treatment.

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