

Analyses of non-coding somatic drivers in 2,658 cancer whole genomes

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Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing

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The landscape of viral associations in human cancers

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Pan-cancer analysis of whole genomes

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Pathway and network analysis of more than 2500 whole cancer genomes

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The transcriptional repressor domain of Gli3 is intrinsically disordered

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