

Cancer susceptibility genes

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Genome-wide association studies (GWASs) have identified hundreds of genetic "risk" variants for human cancers. The vast majority likely contribute to cancer development by regulating the expression of other genes, but these target genes remain largely unexplored.

Xingyi Guo, PhD, Zhishan Chen, PhD, and colleagues have now systematically evaluated 294 GWAS-associated variants for six types of

cancer—colorectal, lung, ovary, prostate, pancreas and melanoma—using gene expression data from multiple public resources.

They identified 270 candidate target genes, including 99 genes with previously unreported associations. Combined with the group's previous data from breast cancer, 24 genes were shared by at least two cancer types.

The researchers found that 33 [target genes](#) were associated with specific mutational signatures and 66 were associated with tumor mutational burden in cancer tissues.

The findings, reported in the *American Journal of Human Genetics*, sharpen understanding of how GWAS-identified risk variants might contribute to carcinogenesis: by regulating target susceptibility genes that in turn promote the generation of somatic gene mutations.

More information: Zhishan Chen et al. Identifying Putative Susceptibility Genes and Evaluating Their Associations with Somatic Mutations in Human Cancers, *The American Journal of Human Genetics* (2019). [DOI: 10.1016/j.ajhg.2019.07.006](https://doi.org/10.1016/j.ajhg.2019.07.006)

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