Washington University in St. Louis
Office of Technology Management

VARSCAN

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arScan is a Java-based, platform-independent, software tool that can detect variants in next-generation sequencing (NGS) data. It employs a robust statistical approach to call variants and is able to handle germline variants, multi-sample variants, somatic mutations and somatic copy number alterations.

In continuous development at the one of the world's leading genome centers, and with an ever-growing community of users, VarScan remains the premium variant caller in the market. It has many uses, including indicating genetic variants between cancer and normal tissue samples or genetic variants for a patient relative to a reference genome.

For more information, including licensing info, please click **here**.