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Transcriptome-wide Characterization of Alternative Splicing Variants in Drug Resistant AML

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Abstract

Abnormal splicing events can promote drug resistance in a variety of cancer types, however, the full extent of genome-wide splicing in therapy-resistant AML is not fully characterized. Further, expression changes of splice variants do not occur independently, but rather in a coordinated fashion in order to maintain proper cellular function. Therefore, in order to understand how aberrant splicing confers drug resistance in AML, alternative splicing needs to be studied on a systems-wide level. This research utilizes a network-based approach to characterize coordinated alternative splicing variation and identify potential splicing event signatures of drug response in AML.