

# Annotated Data Sets

## ANNOVAR

This project demonstrates the use of ANNOVAR ([www.openbioinformatics.org/annovar](http://www.openbioinformatics.org/annovar)) to obtain gene annotations for VCF data. Details can be found in the User's Guide. The tool is designed to work with output as shown here:

*ANNOVAR Output File Assumptions:*

<i>FUNCTION</i>	<i>GENE</i>	<i>CHROM</i>	<i>START</i>	<i>END</i>	<i>REF</i>	<i>ALT</i>	<i>#VCF</i>	<i>HEADER</i>
			<i>NA00001</i>	<i>NA00002</i>				<i>NA00003</i>

*In the example above, the sample IDs are NA00001, NA00002 and NA00003.*