

## **High-Throughput Analysis of KASP Marker Data**

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Here we report on the development of a free web-based SNP calling application that rapidly analyzes results from fluorescence-based, allele-specific PCR markers (i.e. KASP or PACE). The application was developed in Python using Plotly Dash, deployed via Heroku, and can be accessed via [snp-caller.herokuapp.com](http://snp-caller.herokuapp.com). The SNP caller provides a simple, high-throughput method to convert the output file from any microplate reader to actionable genotypic data. It can be accessed anywhere with an internet connection without the need to purchase or install any additional software and will be continuously updated as needed.