

Human Whole Genome Phasing Analysis Service

Informatics Pipeline Release Notes

Version 1.1.0

NEW FEATURES:

- General stability and robustness improvements.
- Gene stats now calculated only on autosomes for consistency.
- Change in the calculation of number of aligned reads. Affects the %mapped reads metric displayed in the PDF file.

DEFECT REPAIRS:

A fix was made in the calculation of the percent of genes phased which was counting the number of genes to considered for phasing estimation (denominator) inconsistently

KNOWN ISSUES:

None

Version 1.0.0

FIRST RELEASE