

Building a Reference Panel and Assessing Imputation Methods for Low-Coverage Sequencing in Black Soldier Fly (*Hermetia illucens*)



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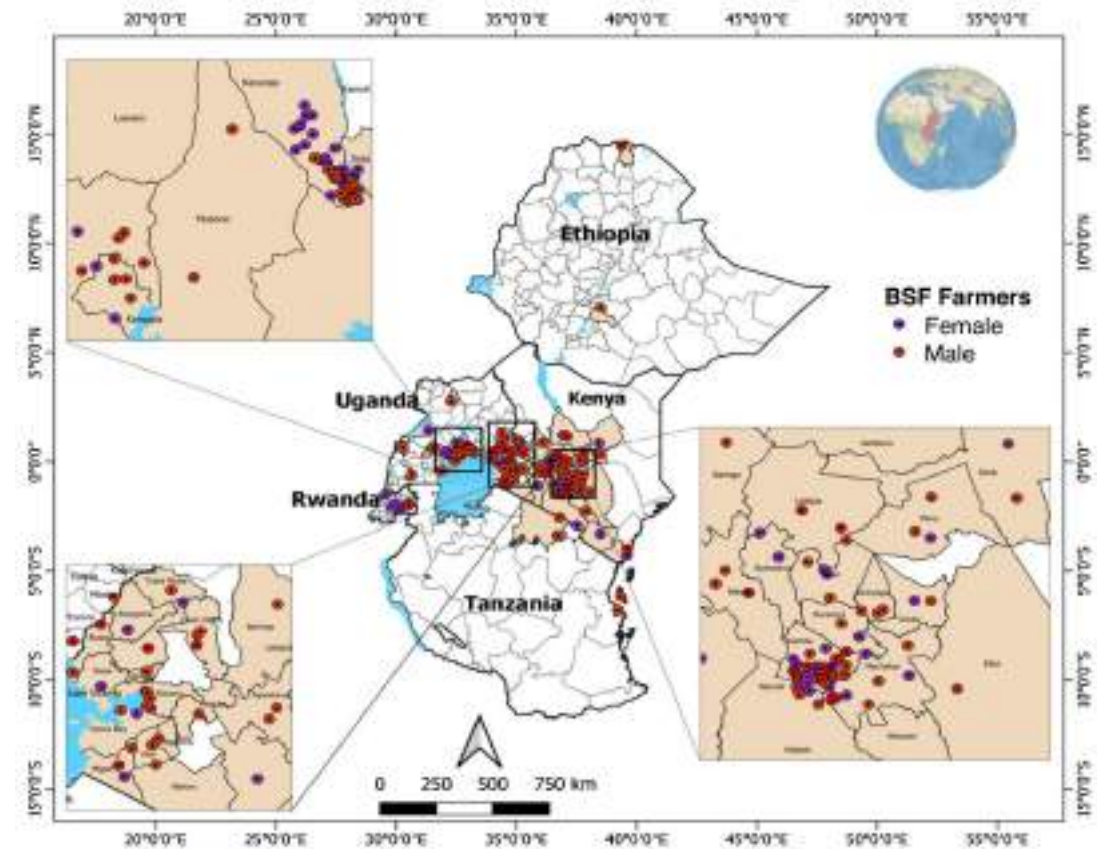
The Need for Genomic Resources

Importance of BSF:

- An alternative source of protein for animal feed.
- Organic waste bioconversion and environmental sustainability.

How Genomic Resources Can Help:

- Enhance understanding of BSF biology and population structure.
- Optimize desirable traits, e.g., growth rate, reproduction, and waste conversion efficiency through breeding programs.



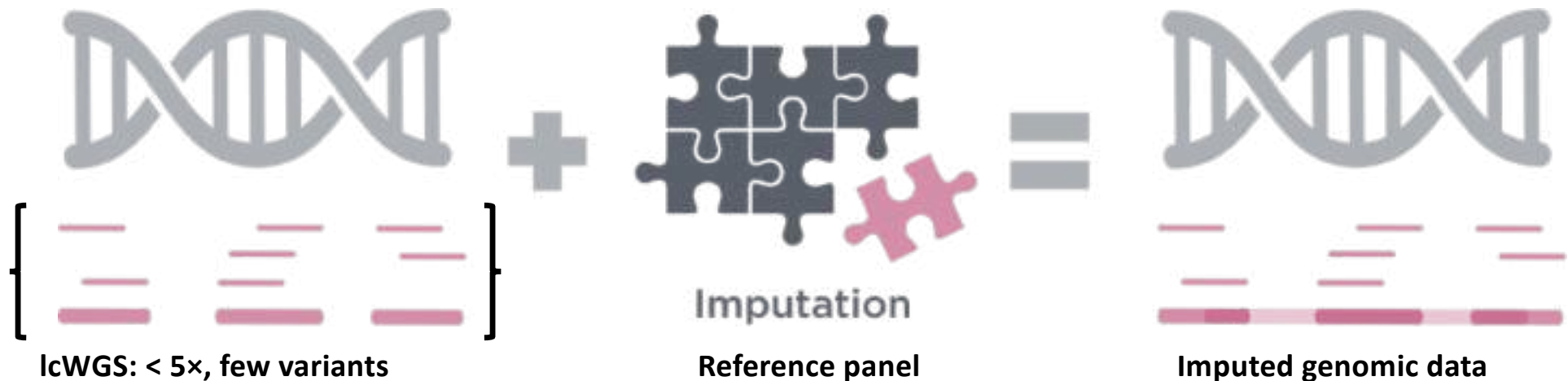
BSF Farming in East Africa: *Tanga et al., 2021*

Limitation

- Limited existing BSF genomic data
 - High sequencing cost
- Lack of standardized resources for BSF
 - Computational challenges

Alternative

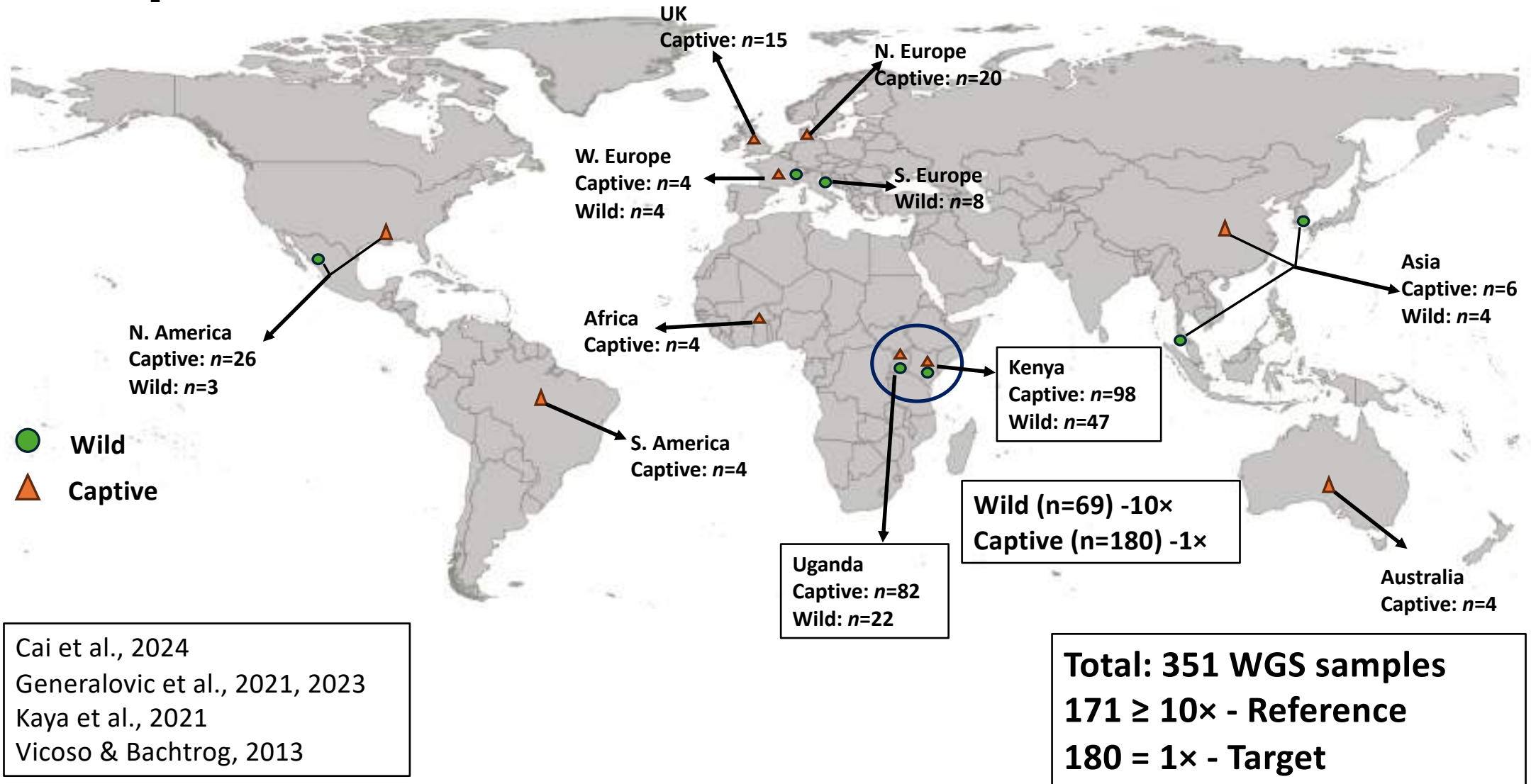
- Low-coverage sequencing followed by imputation using a reference panel



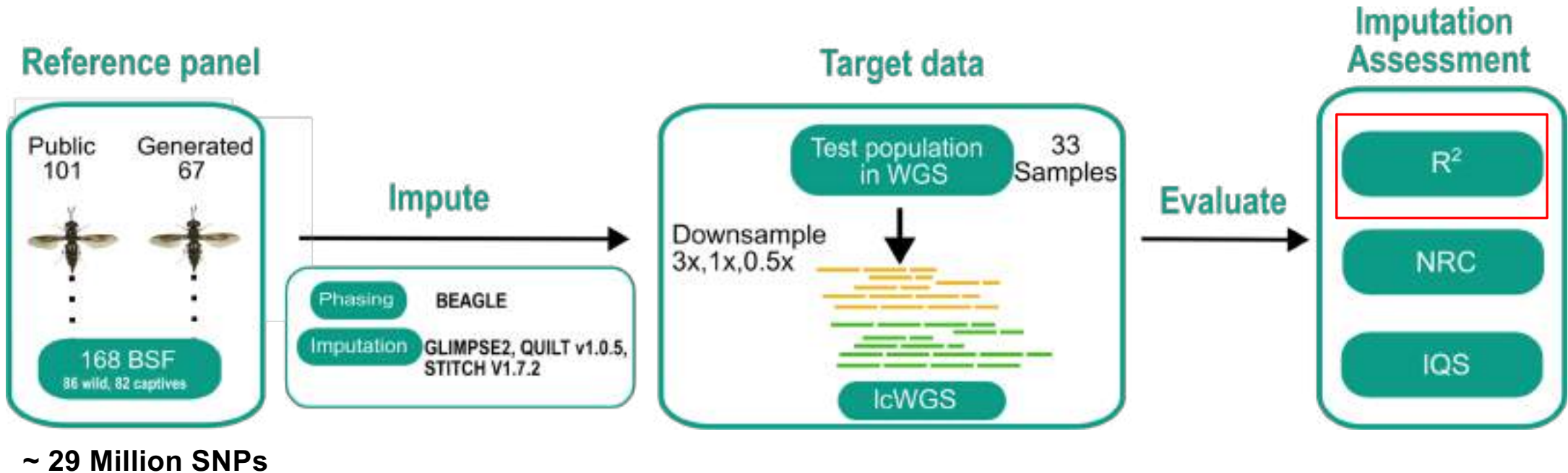
Objectives

- Build a reliable reference panel
- Test and optimize imputation tools that can handle low-coverage whole genome sequence (lcWGS) data
- Provide guidelines for implementing lcWGS imputation pipelines in BSF

Sample Collection

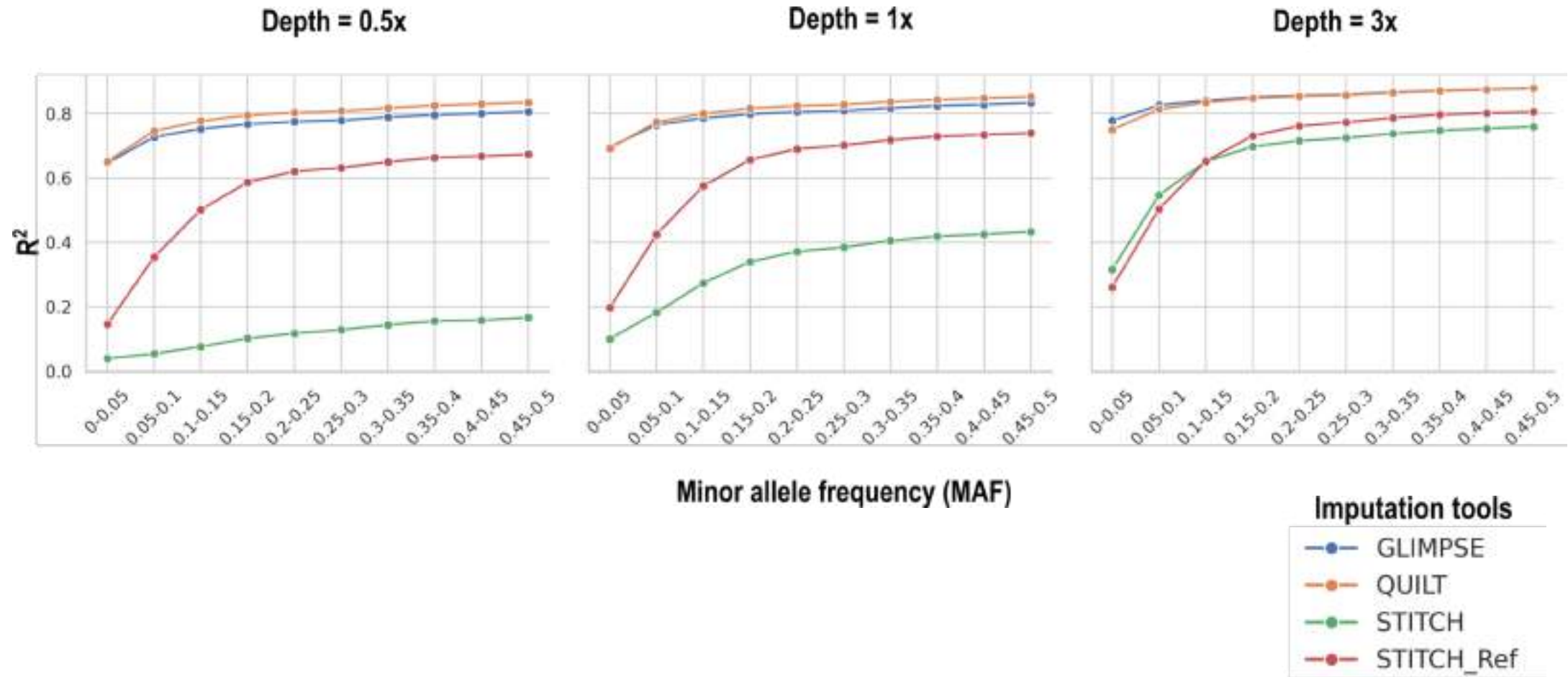


Study Design



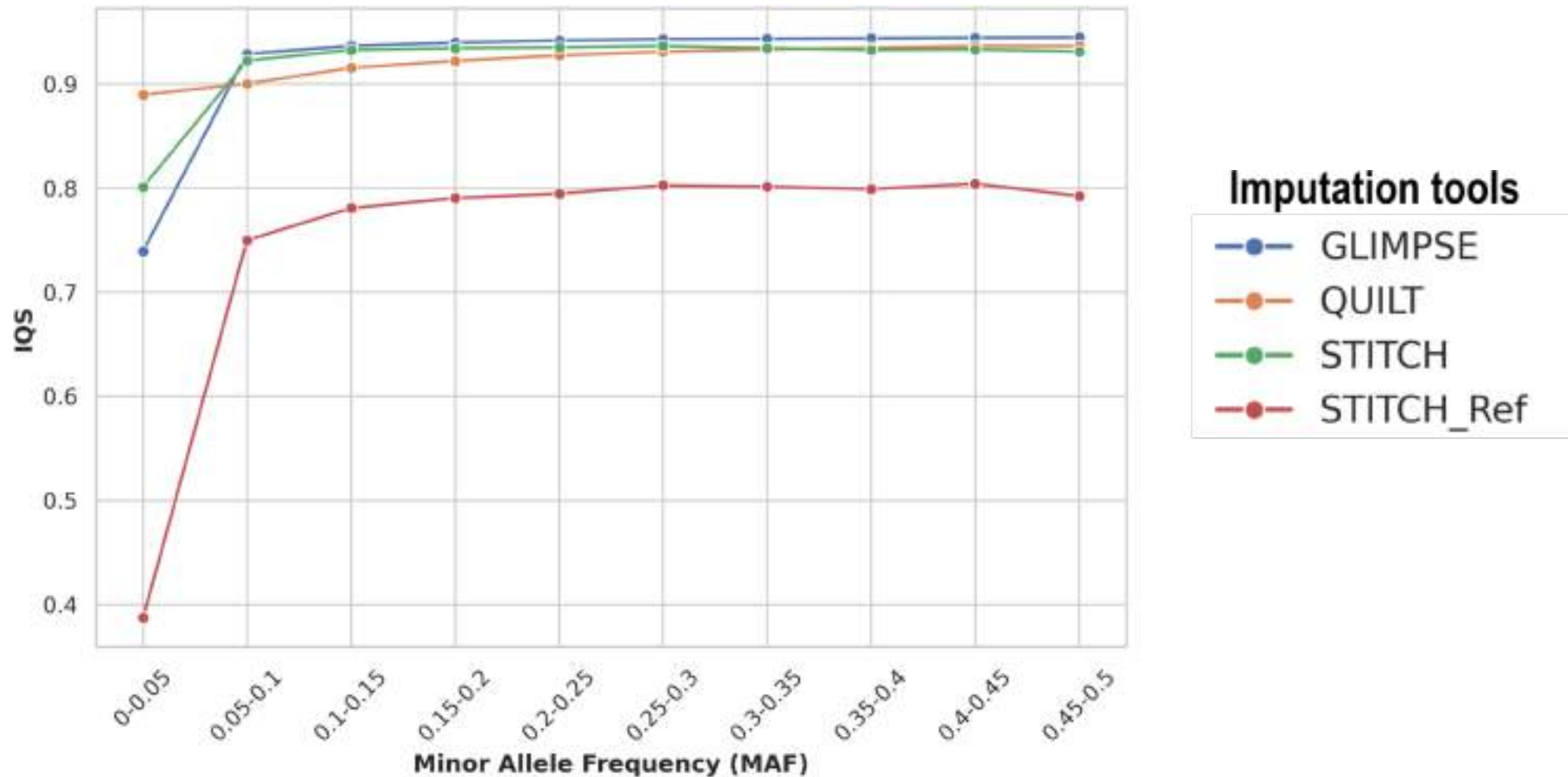
- R^2 indicates the correlation between the true genotype dosages (actual values) and the imputed genotype dosages.
- A higher R^2 (closer to 1) means better accuracy.

Test Dataset (n=33), ~ 29 Million SNPs

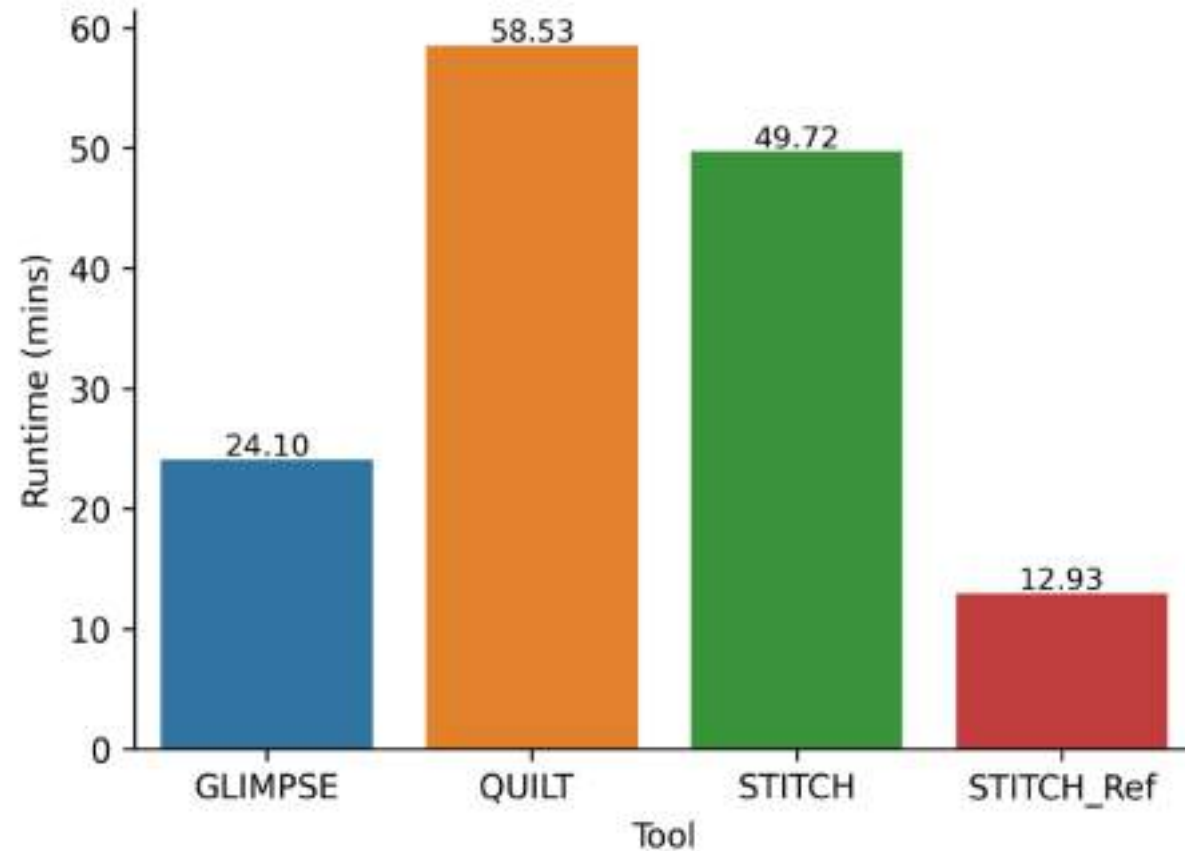


Imputation Quality Score (IQS)

Target Dataset - (n=180,1×), ~ 29 Million SNPs



Runtime – Chr1, ~ 6.9 Million SNPs



Linux cluster (Intel Xeon & AMD EPYC 9374F CPUs) with 35 computation nodes

Conclusion

- Built a reliable and robust reference panel for imputation.
- Tested and optimized the performance of low-coverage imputation tools.
- **QUILT** outperformed other tools in accuracy and reliability.
- Expanded the genomic dataset for future research.
- Code and data will be made publicly available to support reproducibility.

Acknowledgment



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Field Survey

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