Building a community menagerie of automated variant validations

Brad Chapman
Bioinformatics Core, Harvard Chan School
http://j.mp/bcbiolinks

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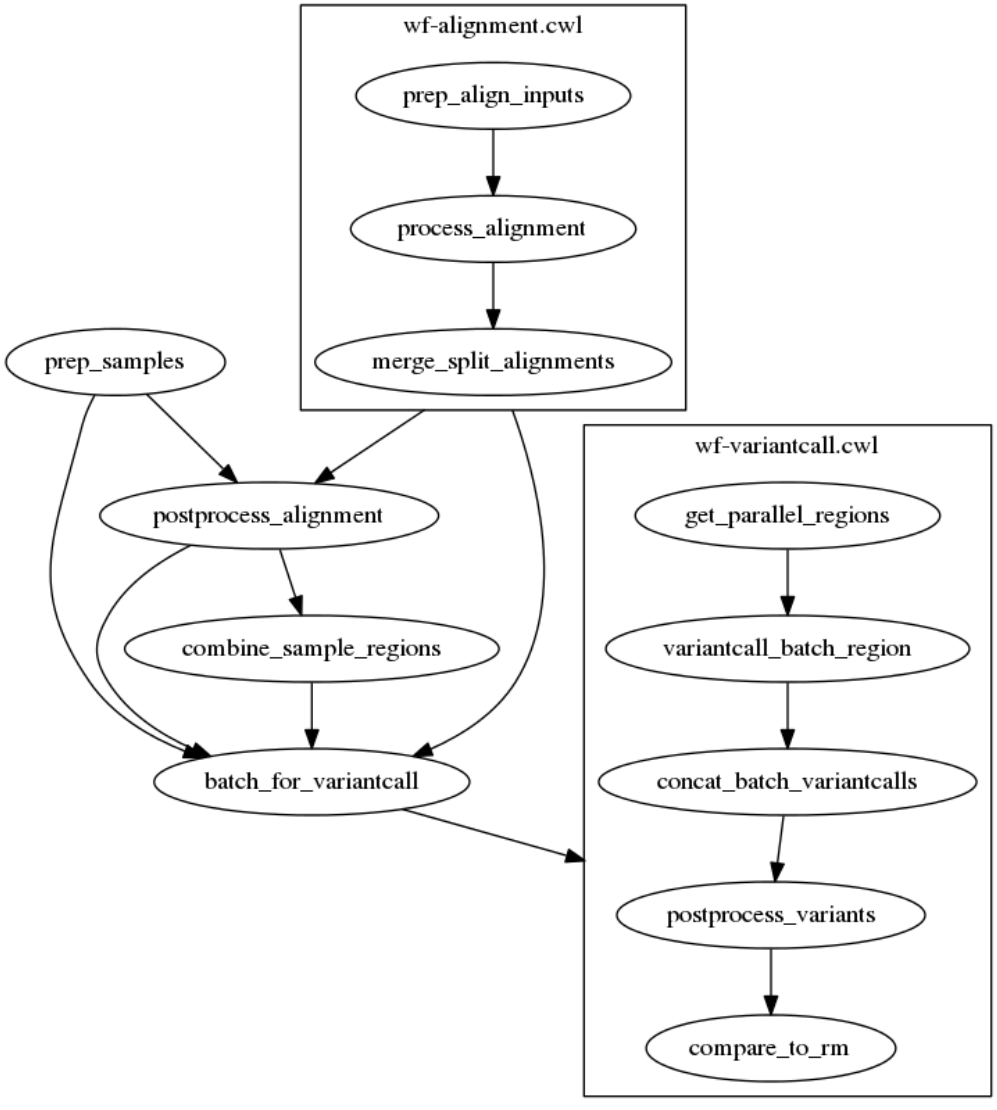
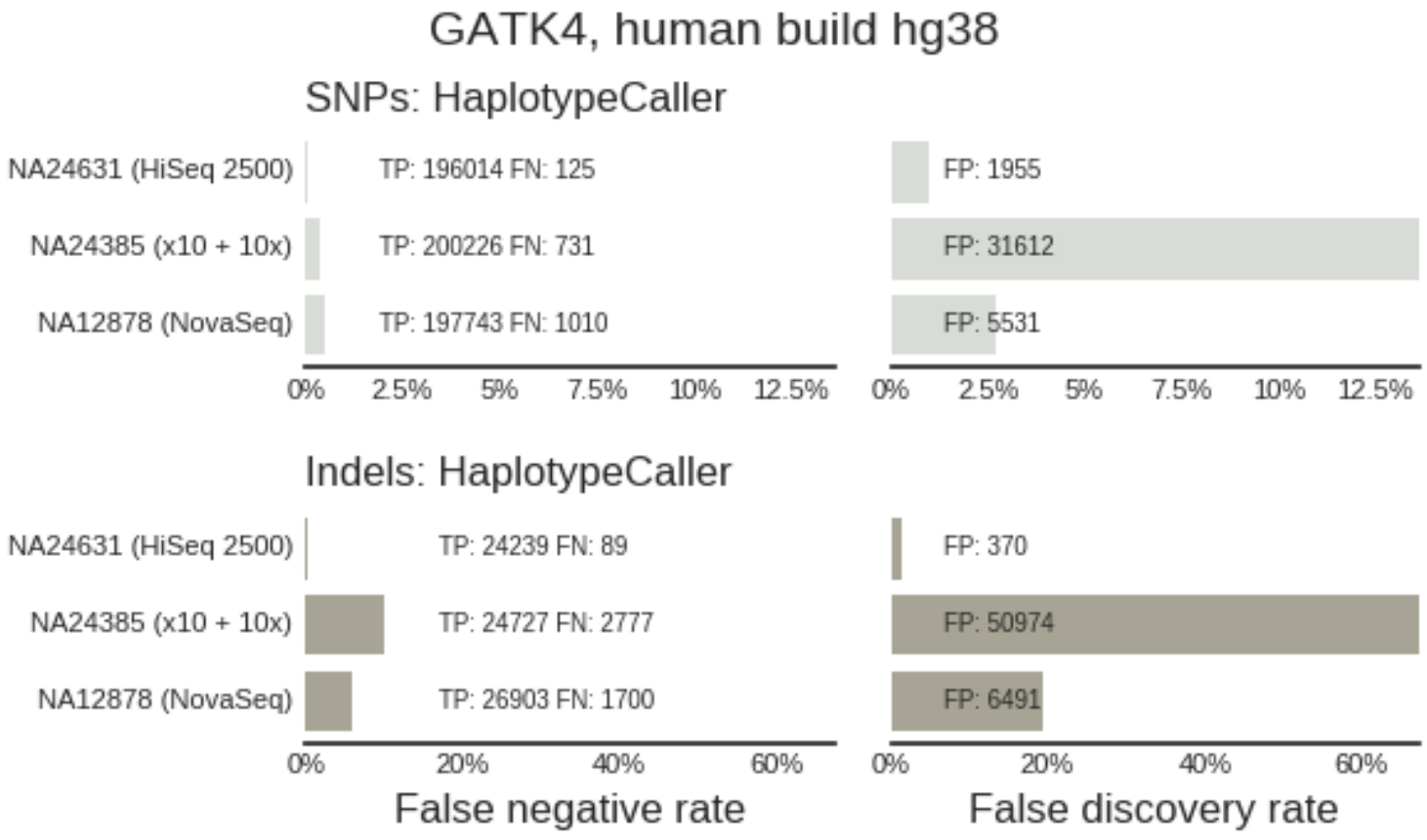
You have a variant calling pipeline



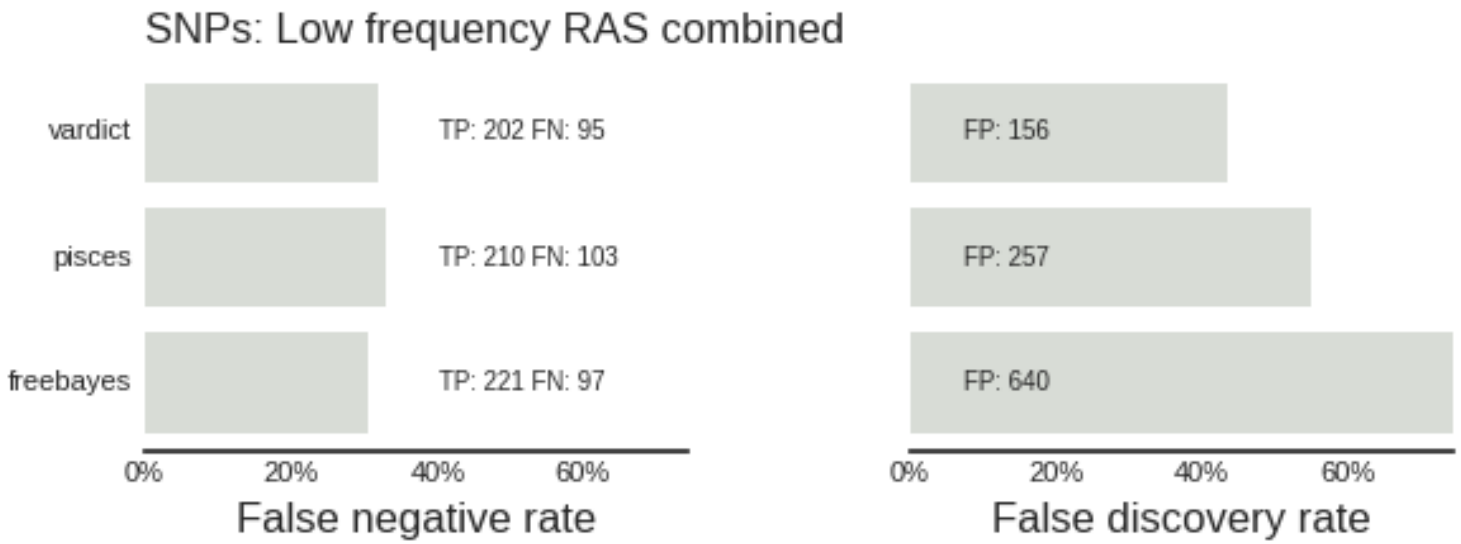
https://github.com/bcbio/bcbio-nextgen

Is it good? How good? What data types?

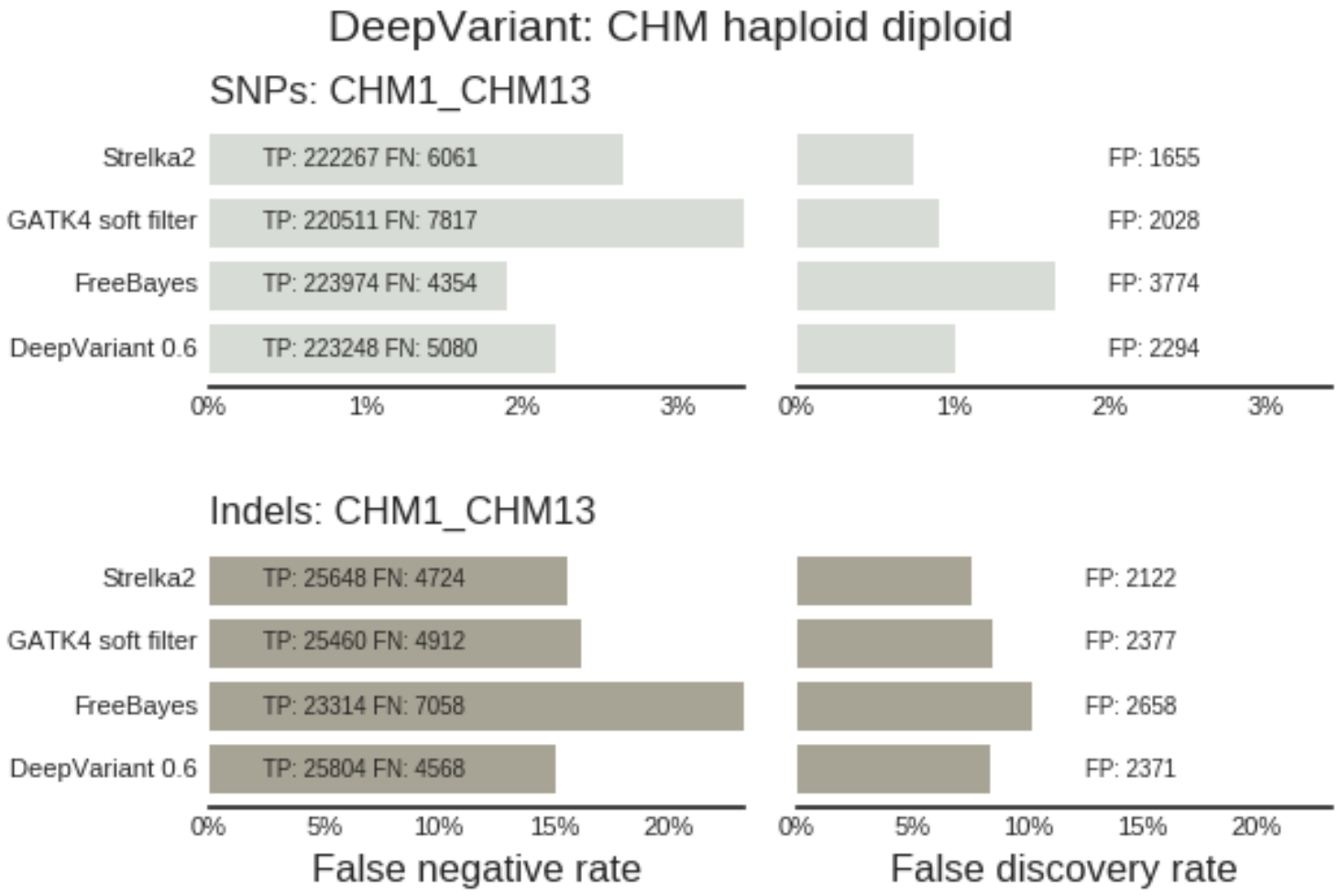


Does it work on my difficult samples?

Somatic tumor-only FFPE



Can I use it to improve callers?



Will it run correctly on my platform?

- Local machines and HPC: Cromwell, Toil
- AWS, GCP, Azure
- Arvados
- DNAnexus
- SevenBridges

http://bcbio-nextgen.readthedocs.io/en/latest/contents/cwl.html

Automated validations for everything

- Workflows

https://github.com/bcbio/bcbio_validation_workflows

- Analyses

https://github.com/bcbio/bcbio_validations

- Help us build a community

https://github.com/bcbio/bcbio-nextgen