

Tetraploid wheat exome sequencing with the hexaploid RefSeq-derived myBaits® target enrichment kit



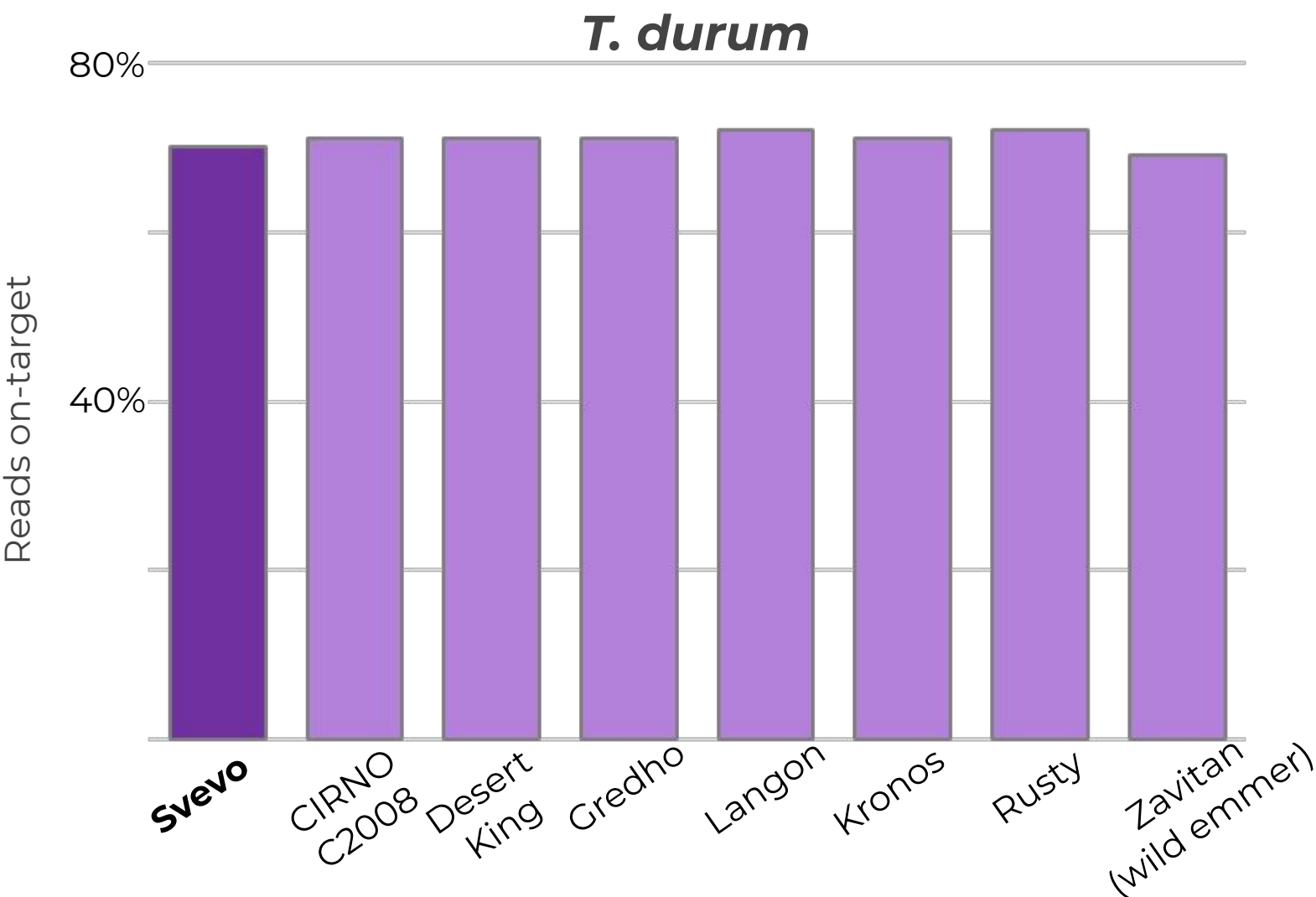
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Hybridization capture technology for targeted sequencing is highly tolerant of sequence variation between probes and targets. The user can tune experimental conditions to balance specificity and sensitivity, so that probes designed from one taxon can be used to enrich DNA from closely related taxa with high efficiency. Here we demonstrate how the Arbor Biosciences myBaits Wheat Exome V1 capture kit, developed in collaboration with the IWGSC using the hexaploid Chinese Spring bread wheat reference assembly, successfully enriches exomes of a broad range of wheat cultivars, including tetraploid varieties. We anticipate that large portions of the exomes of other cereal crops, including rye and barley, can also be obtained with this wheat-derived probe set under even default experimental conditions. This translates to inexpensive and logistically simple exome sequencing for projects of any cultivar composition, stage or scale.

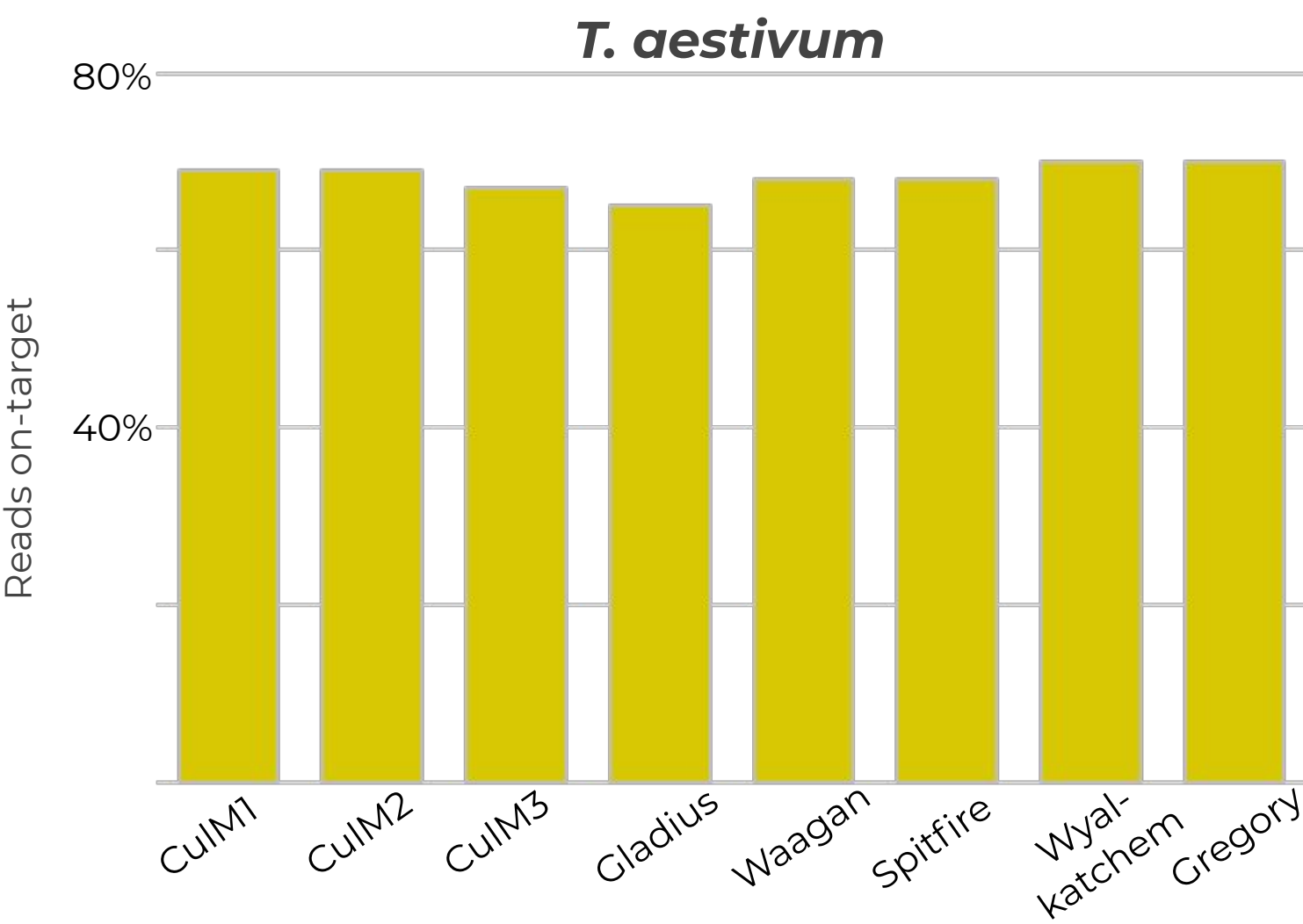
EXAMPLE READ COVERAGE AND PROBE SITES Svevo Cultivar Exome Capture Data

Comparable performance to bread wheat

Target enrichment of tetraploid cultivars using the hexaploid-derived Wheat Exome V1 enrichment kit yields **high specificity to the target space**. Below, the reads were mapped to all three subgenomes (A, B, and D) of the Chinese Spring hexaploid reference.



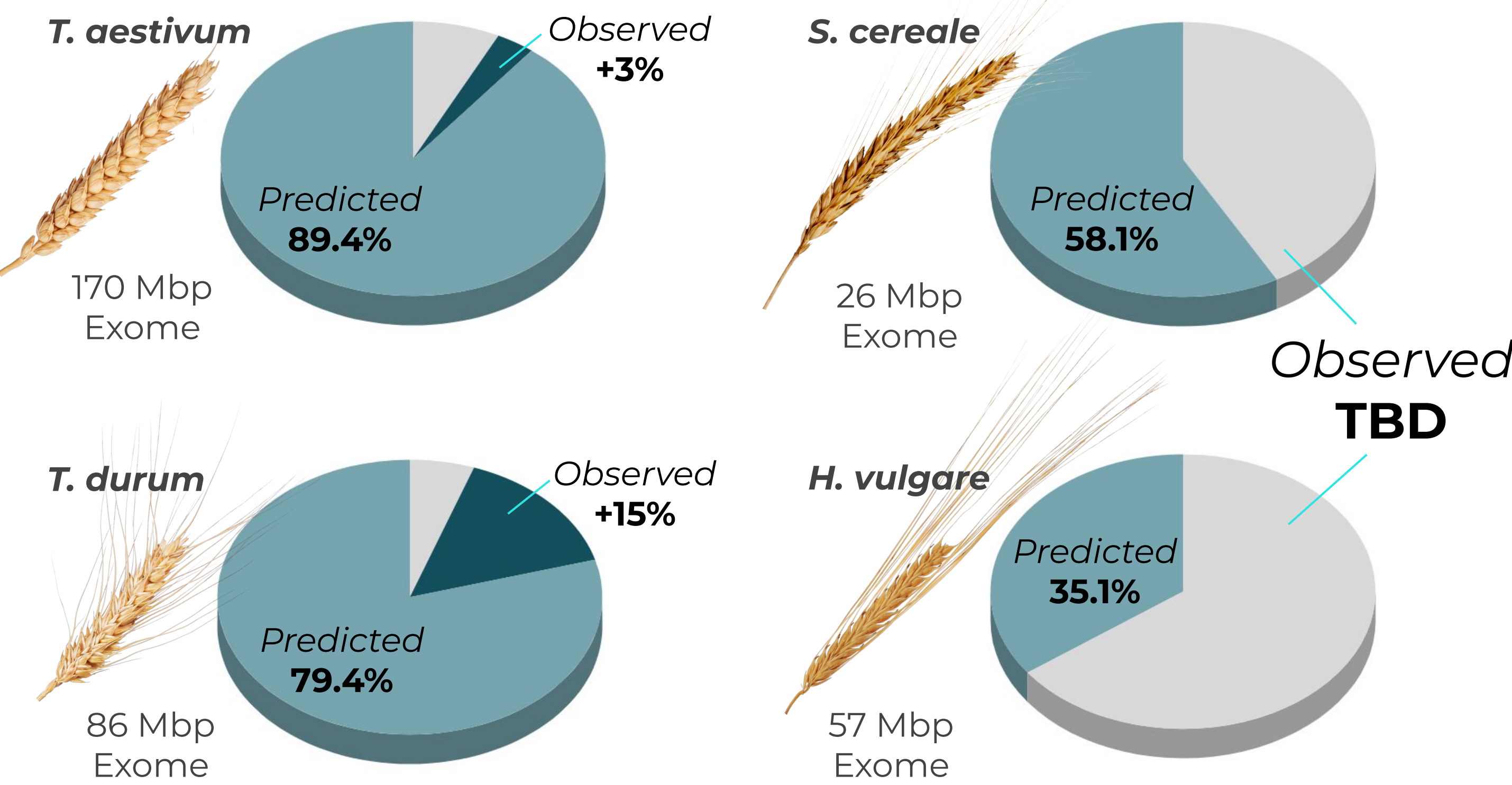
This performance compares favorably to the already consistently-high specificity obtainable for hexaploid varieties, even for those with a high frequency of radiation-induced indels.



Multi-taxon compatibility

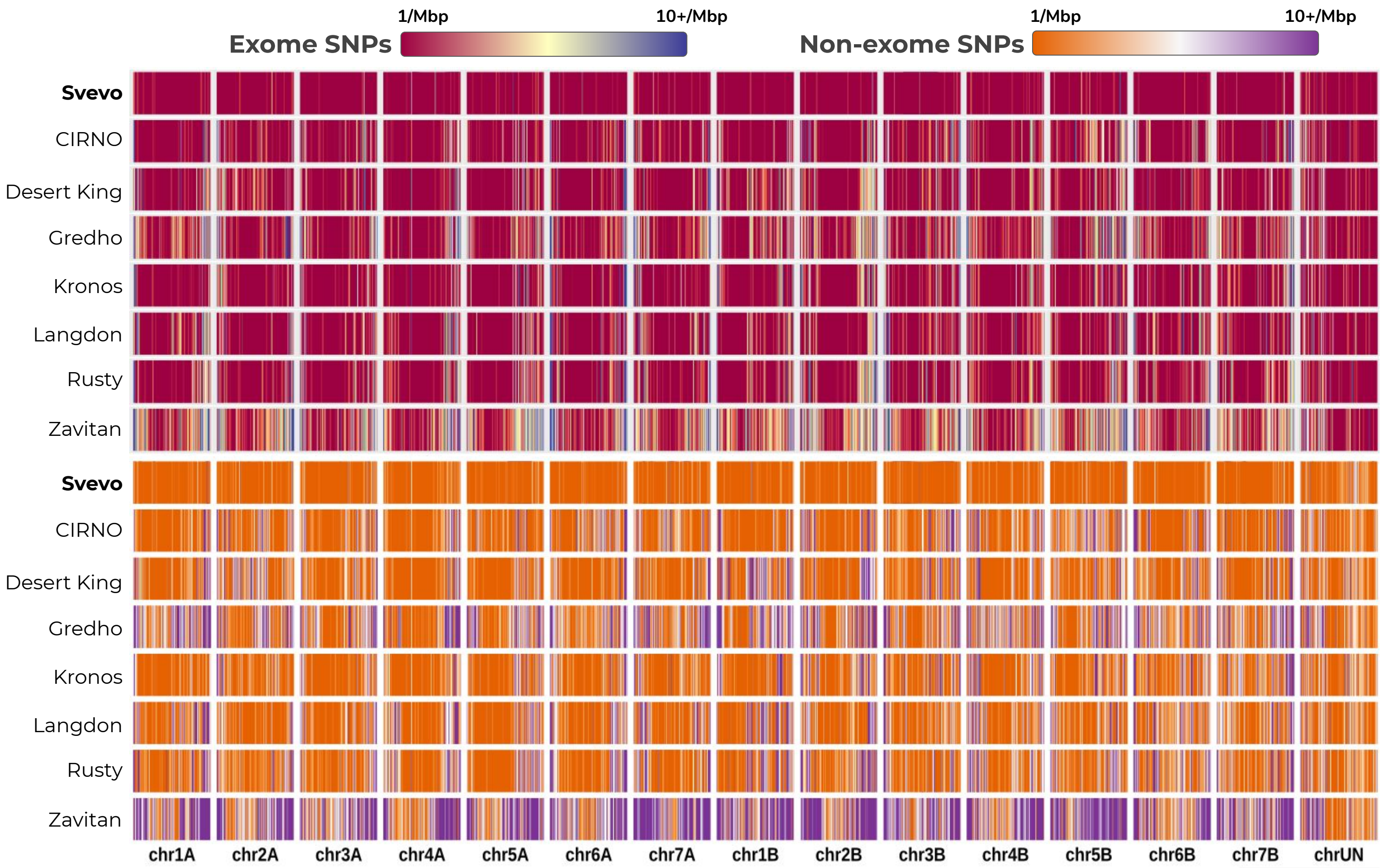
Cereal genomes are among the most complex in crops, and can be highly divergent from one another. However, the Wheat Exome V1 kit can serve as a **versatile general-purpose cereal exome and genotyping kit**. By modeling the likely hybridization sites of the probes against existing gene annotations, this hexaploid wheat-derived probe set is likely cross-compatible with significant proportions of other cereal exomes.

Predicted vs. observed capturable portions of exomes



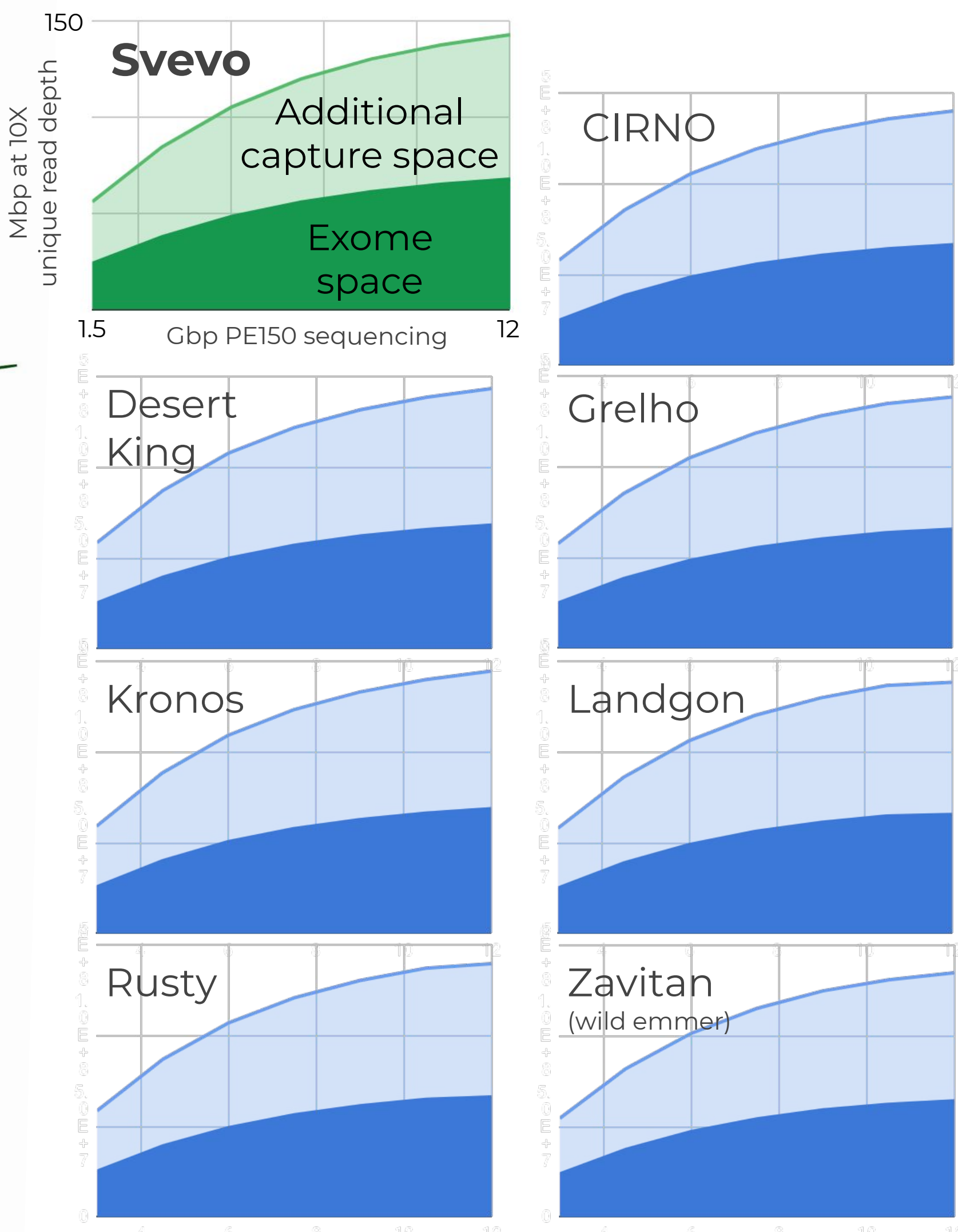
Capture variation across cultivars

The combination of exonic and non-exonic coverage obtained with the Wheat Exome V1 kit enables it to serve as an effective **hexaploid and tetraploid genotyping tool**. Even for highly divergent wild emmer wheat (Zavitan), it is easy to achieve high coverage depth at regions of enhanced SNV density.



Expanded discovery potential

A majority (56-61%) of tetraploid reads following exome capture align to annotated exons of the Svevo reference genome assembly. However, the kit **consistently retrieves substantial additional non-annotated** genome space with high sequence similarity to the hexaploid exome probes. And because the tetraploid genome 33% smaller than hexaploid, less sequencing is required to retrieve the space at high coverage depth.



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