Additional Guidelines
myBaits Expert Wheat Exome Capture

1. Ensure the starting genomic DNA extract is free from color and/or viscosity prior to library prep
2. Final insert length of the indexed library prior to enrichment should be no shorter than 400bp and no longer than 700bp (these are lengths without adapter)
3. Library should be quantified with Qubit or similar
4. Use 1 microgram per library in pools of 8 libraries per capture reaction (i.e., total 8ug per capture) as per the current manual
5. For pools of starting volume > 50 uL, concentrate first to 30 uL (or less) using SPRI or similar buffer exchange system; then vacuum centrifuge to the volume in the manual
6. Hybridize overnight for at least 18 hours
7. When performing the wash steps, remove bead aliquots from hot block before adding hot wash buffer; then return to hot block for incubation.
8. Following 10 cycles of post-capture amplification, insert lengths should average 325 bp or longer; if shorter, this is a likely failure
9. Following post-capture amplification, enriched library mass should be more than 100 ng by qubit. If lower, this is likely a failure.
10. Screen-sequence; if raw reads on-target is 66-72% and post-capture mass is >100ng, then sequence to 18Gbp per library (hexaploids); 12Gbp per library (tetraploids); etc.
11. If raw reads on-target is <66% but mass is >200ng, sequence deeper.

catalog numbers:

309108.V5	myBaits Wheat Exome 8 Rxn
309148.V5	myBaits Wheat Exome 48 Rxn
309196.V5	myBaits Wheat Exome 96 Rxn

To be used in combination with the Wheat Exome Manual

Per Daicel Arbor Biosciences R&D

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