Tutorial – Designed Primers

The PolyMarker program was used to design primers on all the markers in the 2017_WeatCAP experiment. This table below gives a good summary of the results. PolyMarker automates the design of genome specific primers. Primer3 is used to pick candidates then PolyMarker selects a primer pair with the highest specificity.

SNP_type	primer_type	total	percentage
		32466	2.92920590
homoeologous		3778	0.34086552
homoeologous	chromosome_nonspecific	616	0.05557786
homoeologous	chromosome_semispecific	10575	0.95411669
homoeologous	chromosome_specific	5202	0.46934421
non-homoeologous		189269	17.07656843
non-homoeologous	chromosome_nonspecific	170574	15.38983448
non-homoeologous	chromosome_semispecific	436538	39.38611726
non-homoeologous	chromosome_specific	259337	23.39836966

In T3 Wheat you can access the designed primers in three ways.

1. Go to Reports => JBrowse => RefSeq_v1. Make sure the “Primers 2017_WheatCAP” is selected in available tracks. Navigate to the region of interest then click on an item in the “Primers 2017_WheatCAP” track to view primer information. Within the popup box there is a “T3_link” to more information on the associated SNP.
2. Go to Select => Markers. Select “Wheat CAP 2017” Map, then chromosome, then enter a range, then “show markers”. Highlight up to 10 markers and click on the “Select markers” button. Then go to Reports => Designed Primers.
3. Go to Analyze => BLAST. Enter a marker sequence, select “RefSeq_v1”, then select “Basic Search”. On the results page click on the best hit in the “T3 JBrowse” column. In JBrowse click on an item in the “Primers 2017_WheatCAP” track.