Faculty 09: Agricultural Sciences, Nutritional Sciences, and Environmental Management

Pangenome Analysis of Haplotypes Associated with Root Dry Mass in Wheat

Thesis of the Master of Science (MSc.) in Agrobiotechnology

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1. GENERAL INTRODUCTION

1.1. Wheat. Relevance, evolution and genomics

Wheat is a staple crop that feeds over 40% of the world's population, providing 20% fo the daily protein and food calories and whose production requires around 218 million hectars (Giraldo et al., 2019). Wheat originated in the fertile crescent around 7000 years ago and was one of the first cereals to be domesticated and has been the main food of the major civilizations of Europe, West Asia and North Africa. Modern bread wheat (Triticum aestivum L.) is an allohexaploid species (2n = 6x = 42 chromosomes, genomic composition AABBDD) that evolved through two polyploidization events between wild relative species (Fig. 1). Hibridization has been an important source of diversity in wheat (Warschefsky et al., 2014).

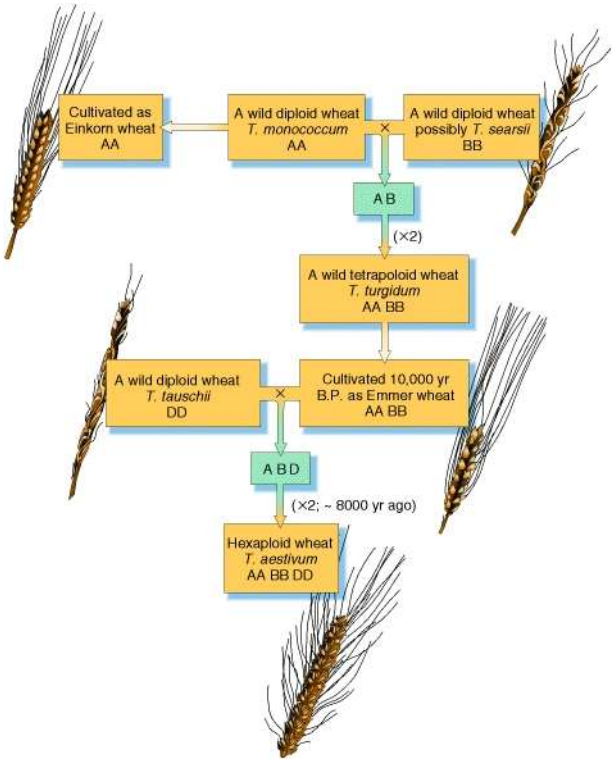

Figure 1: Hybridization events involved in the evolution of bread wheat, Triticum aestivum. The 'X2' refers to the doubling of the chromosome complement which gives rise in fertile hybrids. Source: https://www.cerealsdb.uk.net/cerealgenomics/WheatBP/Documents/DOC_Evolution.php

1.2. Increasing global wheat yield is required to meet future demand

Germany is one of the top European wheat producers, mainly bread wheat. In 2019, the last year of record, yield in Germany was nearly 7.4 tons of wheat per hectar, which doubled the average yield across the world (Fig. 2).

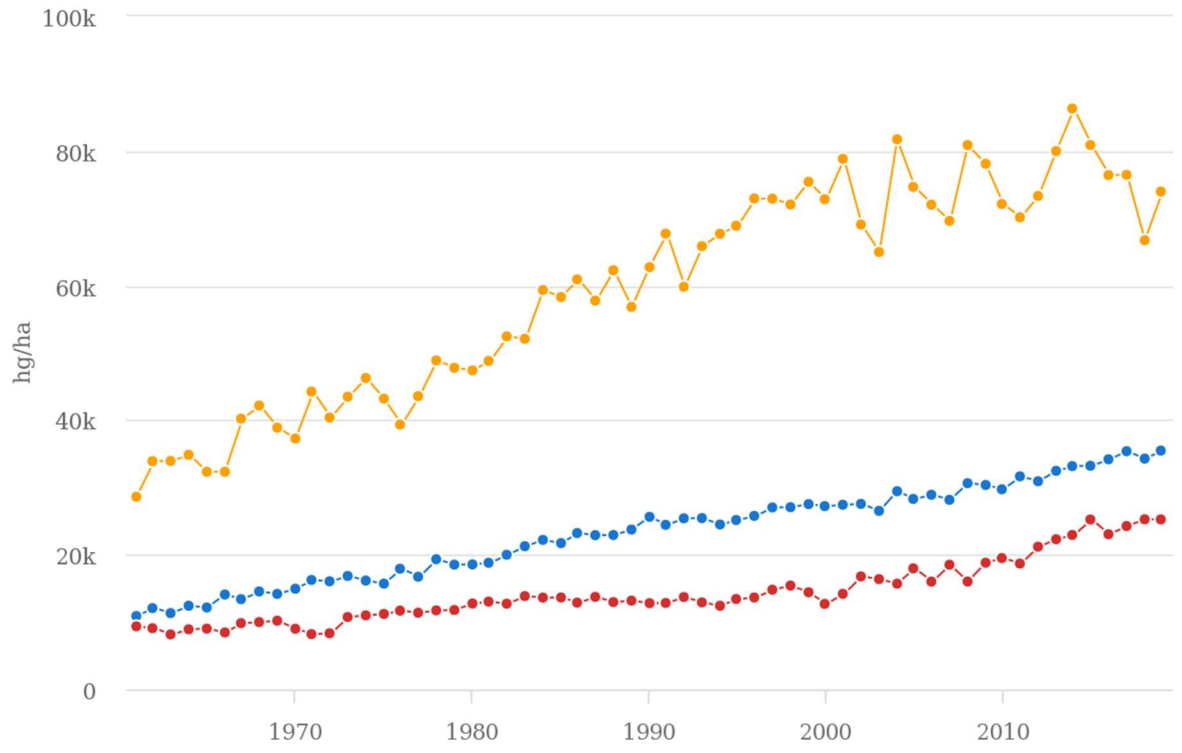

Figure 2: Evolution of wheat yield (hg/ha) between 1961 and 2019. Data is shown for the world average (blue), least developed countries (red) and Germany (orange). Source: FAOSTATS (2021).

The rapidly growing demand for food, feed and fuel due to the world population expansion, which is predicted to surpass nine billion by 2050, will require further increase in crop yields (ca. 2% per annum). However, wheat yield seems to have begun stagnating since the mid 1990s, especially in the biggest wheat-producing countries as Germany, France, United Kingdom or United States (Brisson et al., 2010). On the other hand, the world wheat yields follow a positive trend, although this seems to be due to the growing wheat yields in least developed countries and yet their annual growth is not bigger than 1% (FAOSTATS). According to Reynolds et al. (2012), current genetic gains are not enough to meet the food demands by 2050. Yield increases need to be increased in the future mainly through genetic yield improvement for temperate

regions in Europe with high wheat yields as Germany (Ewert et al., 2005). The "Green Revolution" in the 1960s set an example of the importance of genetic improvement in wheat production, with the introgression of dwarfing genes into modern high-yielding cultivars. Semi-dwarf wheat is easier to harvest and less prone to lodge in fertile and humid conditions and the fast-growing high yields achieved in the following decades were acknowledged to this trait (Casebow et al., 2016).

1.3. Plant breeding

Plant breeding has been used for thousands of years to stack benefitial plant traits and has a great value to human nutrition, feeding of farm animals or fibre production. The realization that many traits are controlled by genes led to the evolution from traditional plant breeding, aimed towards the selection and cross of plants with superior traits, to modern plant breeding, which incorporates molecular biology techniques to select specific genes involved in desired traits (Hartung and Schiemann, 2014). This is the purpose of marker-assisted selection (MAS), which is based on the use of DNA markers in plant breeding.

DNA markers are DNA sequences with known location in a genome. DNA markers can be linked by proximity with locus, e.g. specific position of a gene or DNA sequence on a chromosome, which can at the same time be associated with specific traits. In this case, we say that there is a marker-trait association (MTA). Collard and Mackill (2008) established the requirements that DNA markers should meet for their implementation in MAS: reliability; quantity and quality, technical procedure for marker assay, level of polymorphism and cost. The reliability of DNA markers depends on how close their location is to the target loci, since DNA markers are often not causal but simply associated with the trait of interest (Brinton et al., 2020). Also, higher polymorphism is a positive characteristic of DNA markers, since multiallelic markers can discriminate between more genotypes.

1.4. Role of single-nucleotide polymorphisms in wheat breeding and limitations

A single nucleotide polymorphism (SNP) is a single position in DNA that varies between individuals. SNPs are usually biallelic, e.g. one of two different nucleotides can be found in the SNP, each one representing a different allele. SNPs can be DNA markers when they show linkage disequilibrium with traits, e.g. when the allele distribution of a SNP is not random. Currently, SNPs markers represent the most common DNA marker because they occur abundantly in plant genomes and are easy to detect (Qian et al., 2017). SNPs can be discovered by pan-genome diversity analysis based on assemblies of wheat thanks to the availability of a chromosome-level reference assembly, Chinese Spring (IWGSC, 2014), plus the recent publication of further 9 reference-quality chromosome-level assemblies and 5 scaffold-level assemblies by the 10+ Wheat Genome Project (Walkowiak et al., 2020). These breakthroughs were enabled by the next-generation sequencing (NGS) technologies, despite the high complexity of wheat genome due to its enormous (~17,000 Mbp) repetitive (80% consistent of repetitive sequences) genome (IWGSC, 2014). NGS also allows SNP discovery without reference genome through genotyping-by-sequencing (GBS) methods. Poland et al. (2012) or Lin et al. (2015) provide examples of SNP discovery by GBS. The genetic diversity that SNPs provide can be exploited by high-density SNP genotyping arrays that allow high throughput analysis of large wheat populations. Wheat counts with 9k, 35 k, 90 k and 800 k SNPs platforms (Voss-Fels and Snowdon, 2015) that can be used in genome-wide association studies (GWAS) to link SNP markers with complex genetic traits controlled by quantitative trait loci (QTL). However, once marker-trait associations are established, SNP technologies can also be implemented with only one or a few markers to select lines carrying the diagnostic markers as in competitive allele specific PCR (KASP), which is a very common cost-effective technique in MAS (He, Holme and Anthony, 2014).

Nevertheless, SNP markers also have limitations. First, each SNP can only discriminate between two genotypes due to their biallelic nature. To overcome this issue SNPs tend to be clustered into haploblocks based on linkage disequilibrium (Qian et al., 2017). Bernardo (2010) defined haplotypes as two or more SNP alleles that tend to be inherited as a unit. Multiallelic SNP combinations are therefore capable of calling more than two genotypes and the resulting haploblocks are effective units of recombination by breeders (Walkowiak et al., 2020). Secondly, the non-causality of the SNPs identified in QTL analysis by GWAS towards the traits they are in LD with (Platten et al., 2019) can lead to the selection of false positive or negative individuals during the breeding process (Walkowiak et al., 2020). Also, SNP arrays lack of resolution to detect underrepresented rare alleles (Voss-Fels et Snowdon, 2016). Finally, SNP arrays are not exempt of genotyping errors. To avoid the difficulties related with these errors, maximum level of diversity (1-3%) are implemented to account for genotyping arrays, grouping together highly similar haploblocks (Brinton et al., 2020).

1.5. Potential impact of sequence-based haploblocks in wheat breeding

Despite SNPs being the traditional method to define haploblocks, these can also be defined by different methods to overcome the limitations of SNPs. The abovementioned new wheat assemblies allowed Brinton et al. (2020) to define wheat haploblocks based on full DNA sequence comparison between assemblies. First, data was generated by pairwise alignments between wheat assemblies, followed by alignment filtering by length to get rid of repetitive non-syntenic transposons. Next, alignments were clustered into bins by position to finally call haploblocks in those bins whose median percentage of identity was ≥99.99, to account for sequencing errors. Bins had a fixed size, which provided different resolutions to haploblock detection. This sequence-based approach to call haploblocks has been implemented more often on monoploid or diploid genomes as humans (Rizzi et al., 2019; Matsumoto and Kiryu, 2013; Barrett et al., 2005) or some human pathogens (Hong et al., 2019; Boose et al., 2011; Zheng et

al., 2004), especially by targeting specific loci by Sanger sequencing. Nevertheless, the rapid advancement of wheat pangenomics explained by the implementation of NGS technologies enabled the development of this new method. Brinton et al. (2020) displayed the sequence-based wheat haploblocks across the 15 assemblies on the website crop-haplotypes.com. This website is available for free and provides the opportunity to understand genetic diversity across the wheat pangenome. One potential application would be the redefinition of SNP-based haploblocks discovered by SNP arrays into sequence-based haploblocks. This would facilitate the exploration of conserved genomic regions between assemblies to develop new more precise SNP markers to discriminate between more genotypes with higher sensibility than is usually possible with the markers obtained from GWAs.

1.6. Aim of the master thesis

This master thesis focuses on the analysis of SNP-based haploblocks involved in higher root dry mass (Voss Fels et al., 2017) with bioinformatic methods, as the sequence-based method developed by Brinton to call haplotypes in wheat or variant calling from Illumina short reads. Root-related trait breeding is often discrimated in favor of shoot-related traits due to the difficulty of measuring root phenotypic indicators, despite of roots being essential for absorbing nutrients and maintaining physical stability in wheat (Voss Fels et al., 2017). Selection for shoot-related traits could have eroded below-ground traits meanwhile having higher root dry mass could support the adaptation of wheat to challenging environments (Voss-Fels, Snowdon and Hickey (2018). At the time of the discovery of these SNP markers by GWAS, pan-genomic diversity analysis was not possible since only the reference genome Chinese Spring (IWGSC, 2014) was available. The bioinformatic methods applied for this study have in common the use of pangenomic resources in wheat to analyze genomic diversity.

2. PANGENOME ANALYSIS OF HAPLOTYPES ASSOCIATED WITH ROOT DRY MASS

2.1. INTRODUCTION

Haplotypes are combinations of conserved allele sequences that are located in genome regions known as haploblocks or haplotype blocks, which have not been disrupted significantly by recombination events. Therefore, haplotypes have diverged from each other by random mutations and each haploblock contains at least a few haplotypes (Gabriel et al., 2002). Since gene combinations tend not to be inherited independently but in genetic linkage as haplotype blocks, haplotypes are important targets for trait selection and haploblocks can facilitate marker development for applied breeding (Walkowiak et al., 2020).

Haploblocks have been defined in the past by SNP markers because these markers occur frequently in the genome and are easy to detect (Qian et al., 2017). Bernardo (2010) describes a haplotype as "two or more SNP alleles that tend to be inherited as a unit." However, the method used for defining haplotype blocks changes between studies and the term 'haploblock' might seem ambiguous (Wall and Pritchard, 2003). The most common method is to assign polymorphic sites together into haplotype blocks based on linkage disequilibrium between markers showing little or no evidence of historical recombination and a joint inheritance in the same chromosomal block (Gabriel). Hereafter, we will refer to haplotypes and haploblocks defined by this method as SNP-haplotypes and SNP-haploblocks to avoid confusion with those defined by other methods.

One example of the discovery of SNP-haploblocks in allohexaploid wheat (*Triticum aestivum*) was provided by Voss-Fels et al. (2017), who defined two adjacent haploblocks associated with root dry mass (RDM) in chromosome 5B, Hap-5B-RDMa and Hap-5B-RDMb (hereafter shortened to RDMa and RDMb). These blocks were defined upon pairwise linkage

disequilibrium between 9 and 6 SNP markers, respectively from the 90k SNP Illumina Infinium wheat genotyping array in a genome-wide association study (GWAS) with 215 homozygous wheat accessions. After the application of locus-specific KASP markers designed from the original SNP chips by Makhoul et al. (2020), 2 and 4 haplotypes were identified among the tested population for either RDMa (h1 and h2) and RDMb (h1, h2, h3 and h8). A small group of wheat accessions carrying the combination of favourable haplotype variants RDMa-h2 and RDMb-h3 had significantly higher root dry mass than the rest of the accessions (Voss-Fels et al., 2017).

SNP-haploblocks are a popular target in marker-assisted selection (MAS) to improve the efficiency and speed of the breeding process in many crops. MAS is based on the correlation between the marker and the trait, but this correlation is not direct, since most SNP markers are not causal for phenotypes but are rather linked with the quantitative trait loci (QTL), e.g. genetic regions associated with specific phenotypic traits, which can result in selection of false-positive and false-negative individuals and hampers the use of SNP markers in breeding programs (Platten et al., 2019).

Other methods to define haploblocks are those based on sequence comparisons and have been exploited mainly in research about human genomics (Rizzi et al., 2019; Matsumoto and Kiryu, 2013; Barrett et al., 2005) and population genetics studies of pathogens (Hong et al., 2019; Boose et al., 2011; Zheng et al., 2004). However, these methods are difficult to apply in *Triticum aestivum* because of its large genome size, high sequence similarity between homoeologous chromosomes and abundance of repetitive elements (IWGSC, 2014).

The release of new assemblies helped Brinton et al. (2020) to detect haploblocks across wheat genome by sequence comparison between assemblies. They reported the shared haplotypes on the website crop-haplotypes.com. Brinton's method defined haplotype blocks as physical

regions with ≥99.99% sequence identity (across a fixed bin size of 5-, 2.5- or 1-Mbp) between pairwise comparisons of wheat lines in the 10+ Wheat Genome Project, which included 15 assemblies: 10 chromosome-level assemblies (CLA), including the IWGSC Chinese Spring reference genome plus reference-quality pseudomolecules (ArinaLrFor, Jagger, Julius, Lancer, Landmark, Mace, Norin61, Stanley, SY-Mattis) and 5 scaffold-level assemblies (SLA; Cadenza, Claire, Paragon, Robigus and Weebill). These 14 additional non-reference genomes were published by Walkowiak et al. to expand the reference genome assembly. Brinton and colleagues intended to develop a systematic haplotype-led approach to identify genetic diversity and enable its exploitation. The advantage of this method to the traditional SNP-based methods are increased precision in haplotype definition, since SNP markers tend not to be causal for traits and can cause false positives, and increased sensibility, being capable of differentiating 'identical-by-state' haplotypes from 'near-identical' sequences. Brinton and colleagues provided evidence of the importance of this sensibility for plant breeding that can be relevant in some cases.

The aim of this master thesis was to analyze the SNP-haploblocks RDMa and RDMb using the new sequence-based method of haplotype detection developed by Brinton et al. (2020). It was considered that the new wheat pangenome could help to validate the haplotypes and redefine the haplotype blocks to a more precise location for increased correlation marker-trait. Additionally, this could lead to the discovery of further SNP markers to discriminate between varieties carrying the RDM haplotypes and those carrying nearly-identical alleles. Results suggest that Brinton et al. reported inaccurate haploblock predictions mainly due to lower alignment coverage in comparisons using scaffolds as query. Considering the necessity of good-quality alignment properties in haploblock predictions, a new bioinformatic pipeline was developed to include additional information about alignment properties in haploblock predictions obtained by sequence comparisons. This tool was applied in RDMa-h2 to redefine

the SNP-haploblock to a new sequence-based haploblock in a more precise way, which could help increasing the correlation marker-trait. The new pipeline is user-friendly and can be applied to any input file containing alignments.

2.2. MATERIALS AND METHODS

2.2.1. BLAST calling of SNP-based RDM haplotypes among wheat assemblies

BLASTN, version 2.6.0+ (Zhang et al., 2000) was used with each of the 101 bp flanking sequences that Makhoul et al. (2020) used to develop KASP markers as query (Table 1) and the 15 publicly available wheat genome assemblies described in introduction as database in order to extract the SNP allele sequences from these blocks in each of the genotypes. These databases are available at the BLAST tool from EnsemblPlants, on the recently-released BLAST server IPK, Galaxy Blast Suite (https://galaxy-web.ipk-gatersleben.de), and can be downloaded at https://webblast.ipk-gatersleben.de/downloads/wheat/pseudomolecules/. Default parameters were applied.

For chromosome-level assemblies, hits were selected if their BLAST location was in chromosome 5B or in chromosome 7B in case of ArinaLrFor and SY Mattis, since these lines suffered a translocation in this chromosome arm between these two chromosomes (Miura et al., 1992). If there were more than one hit in these chromosomes, only the hit with the highest score was retained. For scaffold-level assemblies, the BLAST location of the hits were checked by blasting the context region against the Chinese Spring reference genome.

Haploblock	SNP marker	neg log p-value	Genomic location in IWGSC chr5B	101 bp SNP-flanking sequence	SNP	Positive allele	Effect on RDM (%)
Hap-5B-RDMa	Kukri_c46570_214	5,88	663079864-663079925	aggaaggagatcaacgaactcgcgcttaaaagatatcttcattttccagcRcgcttcggattcctggagcgttgcaagatcacgctcaagtccgtggagag	A/G	G	2,0056
	RAC875_c24226_1356	5,77	663136894-663136904	ggggctcaaaacagtgattgttaggccgaactctttaatgacaaagctggMgttgaacgcctttagagtgagcacgccgcaccctcatgccggatcacca	A/C	C	1,9988
	RAC875_c18088_2222	5,82	663509618-663509679	acttcaaaataaaactcaccaggcggtggttcataatttttgggaagatRccagcaaaaatatcagctgatgagccgaaggtcttggagcccctccatac	A/G	A	2,0056
	RAC875_c18088_950	5,79	663512943-663512982	acctgaccatcagttttgataggaacaacgtcctagggcgaaatatgtaYgctccagaagcctgaggatcatctccgcctccatcttgtcctatgtaata	T/C	T	2,0014
	BobWhite_c43_86	5,8	663516513-663516613	attgctattcacaactcattcgagttcagcttcaacaatacaacattctgRttcaaaattacaaaaaagttacaatgtcggcgatcatcgccatggcgcct	A/G	A	2,0039
	Excalibur_c25522_755	5,91	663523031-663523131	gcacccgcatgggagtagatcgccgatgcggctccttcagcactggactgYgtagtttcaccggttgcaccctcactgcctgggcgtacccatagtgcat	T/C	T	2,0056
	RAC875_c12293_588	5,87	664021529-664021555	ccttggatcatctcatcatcgactccttcaatgaaggactcgaattcatcRcccgtcctgctgatgggtccagttgaatggttgactaatctccatcca	A/G	A	2,0056
	GENE-2890_482	5,92	664025433-664025529	aggtagtaaagagrcaaccagataatcataaatgccacataataatRgagctaacacgagctaattgatgtgattcatgactggtgattggtgaaga	A/G	A	2,0085
	Excalibur_c60554_394	5,76	664026373-664026473	tcaatgacgcrgacagtgacgtcaggcacggaggagcgaagagcggcagcKagacaagctgcagcctctgacttgccgctgcacggctgcccgcacatcac	T/G	T	1,9960
Hap-5B-RDMb	BS00022477_51	-	652632762-652632862	tcacagtccgggcacttcttctccggctccacaggaacgatcacctcagcRcagctgtggcaccagtacctgctttcctgaccttcttccatcttgtgact	A/G	-	.
	BS00029852_51	-	652634893-652634993	caagctggcagcttatgatcccacaatcaacaaactgtgacagcagatccKtctcatgttcctcaagacccctgcaaataacaagaaaatggcagcaaact	T/G	-	.
	Tdurum_con48959_1172	5,7	653432974-653433074	gggatcagaatcagcaccaaaccaatcaatcaatcaatcaaagcagcaggKatctgaaaatcagaaccaaatcaaccaggagtagtaaccaatcgatcaaa	T/G	T	2,2923
	BS00110293_51	-	653655509-653655609	gtgttgcctgcagccaaaaagcagaatatcccatacacaaactattttcaRaagcagcagtacaatgttcagagtaaagccagtacaaattctccacaaca	A/G	-	.
	BS00022231_51	-	653655578-653655673	caacgcagagtaaagccagtacaaatttctccacaacaacaagtggcccctRttaagcaaccagagaccacaatggtcagcaatcataaattcaagaaacct	A/G	-	.
	IACX6288	-	653704379-653704498	tctttgctgcattcaaggagatctaatttcgatgataccttacagtatgctgtgtttgacYgccttcgctagagtcctgtaatatgatttgtcgtgatttctgtcgatttatccaaacc	T/C	-	.

Table 1: **Information about the SNP markers in RDM haploblocks discovered by Voss-Fels et al. (2017).** Markers were considered significantly associated with RDM if their -log(p-value) was over the arbitrary threshold 4 and markers with the symbol – in this column were added to construct the block RDMb, where only one marker, Tdurum_con48959_1172, was found in LD with RDM. Notice that the marker Kukri_c46570_214 presents another homologous target upstream in the IWGSC chromosome 5B.

2.2.2. Identification of sequence-based haploblock predictions with crop-haplotypes.com

The website crop-haplotypes.com provides a graphical visualization of the shared sequence-based haploblock that were called from a combination of whole-chromosome NUCmer and gene-based BLAST pairwise alignments between wheat assemblies by Brinton et al. (2020). Each NUCmer alignment compared one reference against one query genome. However, scaffold-level assemblies could only be queries in the chromosome comparisons since their genomes are not organized in chromosomes so only NUCmer pairwise comparisons between chromosomes (CLA-CLA) or chromosome-scaffold (CLA-SLA) were conducted by Brinton and colleagues. Consequently, gene-based BLAST pairwise alignments were performed

between any two lines to allow for SLA-SLA comparisons and the genes compared with this method needed to be consistent with the expected chromosomes and have only one projection. Delta files were output of nucmer using the option -mum, to avoid repeats by keeping only maximal unique matches between the reference and the query, and alignments of length under 20 Kbp were filtered out with delta-filter (-l 20000) and specifying additionally -r -q, to retain only the longest consistent set of alignments for the reference and query. After the NUCmer pairwise comparisons, delta files were imported to R (R Core Team, 2021) where alignments were clustered into bins of fixed size (5-, 2.5- and 1-Mbp) across chromosomes (Brinton et al, 2020). Median percentage of identity was calculated across bins, which were assigned to haploblocks if their median percentage of identity was ≥99.99. Consecutive assigned bins were assigned to the same haploblock and two errors (<99.99% identity) in a row within each haploblock were allowed. Regarding the BLAST-based method, alignments containing Ns were discarded and haploblocks were assigned by using a 25-gene sliding window. The 3 alignments with the lowest percentage of identity were also discarded in the windows and the mean percentage of identity was calculated across windows. Only 100% identical windows were assigned to blocks. Both sets of haploblocks defined from NUCmer or BLAST were combined and the longest predictions were selected in haploblocks called by both methods.

The RDMa block position (coordinates in chromosome 5B: Chinese Spring, 663,100,000-664,000,000 base pairs; Lancer, 655,700,000-656,600,000 bp) was searched on the website (crop-haplotypes.com/Wheat/haplotype/5B). All assemblies were compared at the RDMa region by selecting each of the available bin size views ('Haplotypes for 5Mbp', '[…] 2.5Mbp' and '[…] 1-Mbp'). The SNP-based RDMa block position was selected as the main highlighted bin, shown as dark grey boxes. If haploblocks were found in this bin, the haplotypes were analyzed throughout their whole length, meanwhile if no haploblock was found, other haploblocks were checked in the nearest bins. Notice that coordinates might differ between

identical regions in different assemblies due to insertion/deletion events. Finally, tables showing the haploblock coordinates in the lines sharing RDMa-h2 were produced (Fig. 3a).

2.2.3. Validation and redefinition of haploblocks

To assess the accuracy of the haploblock predictions called on crop-haplotypes.com, the scripts and files reported in Brinton *et al.* (2020) that were used for the creation of crop-haplotypes.com were applied. These original scripts are named 'assign_mummer_blocks_whole_genome.r' and 'assign_BLAST_blocks_whole_genome.r' and can be found at https://github.com/Uauy-Lab/pangenome-web. The original scripts were edited to create a new script in R (R Core Team, 2016), called 'Haplotype-based Pangenome Analysis' (hereafter referred to as HBPA).

Brinton´s method produced information on sequence-based haploblocks from bins of fixed size across wheat chromosomes but does not consider alignment properties during the haploblock calling process that could be essential to obtain accurate predictions. This is because, when clustering alignment into bins, the median percentage of identity was the only criterium used to assign bins into blocks. As a result, some predictions meeting the cutoff percentage of identity criterium could be based on poor number of alignments and therefore potential false positive or negative calls. HBPA provides adds new opportunities to Brinton's method. First, HBPA performs a chromosome-scale analysis that checks for alignment properties across the whole target chromosome chromosome. The alignment properties considered in the analysis are (1) percentage of coverage of the reference chromosome by alignments (hereafter referred to as alignment coverage), e.g. the sum of the lenghts of all alignments in a pairwise comparison divided by the chromosome length of the reference assembly, (2) average alignment length, (3) number of alignments and (4) average expected number of alignment per bin, e.g. total number of alignments divided by the number of bins of a fixed bin size that fit in the chromosome, supposing homogeneous alignment distribution. Alignment coverage depends is proportional to the next two properties, which makes it the most important indicator. These properties

provide an overview of the alignment quality of the pairwise comparison. Secondly, HBPA conducts a 'target-scale' analysis to validate haploblock predictions based on their alignment properties in chromosome regions of interest. For this, HBPA produces dotplots using the function 'plot_aln_and_bins', which contain graphical and numerical information on the haploblock predictions made in a selected region and its alignment coverage, as can be appreciated in Figure 5 and Figure 6. In this graph, the x axis marks the position of individual alignments, the y axis shows the alignment percentage of identity against the query and dot color indicates alignment length. Graphs are generated for the self-defined bin size and the bins are shown as the area between two consecutive vertical lines, for which the number of alignments is shown. Simultaneously, haploblock predictions from crop-haplotypes.com are highlighted in green and areas of interest, for example SNP-haploblocks, can also be highlighted on the graph. Therefore, this dotplot assists with haploblock validation and redefinition. Finally, HBPA extracts a list of the genes, e.g. projections and sources in IWGSC RefSeq v1.0, contained in haploblocks of interest. HBPA can be found at https://github.com/MonteroJLU/Haplotype-based-Pangenome-Wheat-Analysis, where several scripts that allow the replication of this project analyses or the personalized used of this method are hosted. The script containing the analysis of this study is named 'demonstration_rdma_hbpa.r'. Any person interested in applying a similar analysis with personal data can use the script 'template_hbpa.r'. However, reading the file 'ReadMe.txt' is recommended before downloading any of these resources.

HBPA is structured in three sections: (1) calling haploblocks from NUCmer pairwise comparisons, (2) Extracting a list of genes located within a haploblock and (3) calling haploblocks from BLAST pairwise comparisons. Notice the BLAST-based method was deemed insufficient to fully differenciate between haplotypes, with haplotypes called by NUCmer not being called by BLAST and viceversa.

For the analysis of the RDMa haplotype 2 shared between LongReach Lancer and Paragon, the raw data about alignments was imported into the script from a RDS file containing all filtered delta files from all NUCmer pairwise comparisons in chromosome 5B. This file is available at https://opendata.earlham.ac.uk/wheat/under_license/toronto/Brinton_etal_2020-05-20-Haplotypes-for-wheat-breeding/nucmer/. The target-scale analysis was conducted on a target region between 655,000,000 and 665,000,000 in Lancer's chromosome 5B where the SNP-haploblock is located. For the gene identification, files were downloaded from https://webblast.ipk-gatersleben.de/downloads/wheat/gene_projection/. These included 'geneid_2_chinese.sourceid.txt', that matches gene model projections in assemblies with their source in the reference genome and 'projectedGenes__Triticum_aestivum_LongReach_Lancer_v1.0.gff', containing gene model projections in Lancer genome. For the third section, 'varieties_all_identities_2000bp.tab.gz' was downloaded from https://opendata.earlham.ac.uk/wheat/under_license/toronto/Brinton_etal_2020-05-20-Haplotypes-for-wheat-breeding/pairwise_blast/ and ' iwgsc_refseq_v1.2_gene_annotation.zip' from https://urgi.versailles.inrae.fr/download/iwgsc/IWGSC_RefSeq_Annotations/v1.2/. These files contain the haploblock predictions obtained by Brinton and colleagues from gene-based BLAST pairwise alignments and the gene annotation in the reference genome respectively.

2.2.4. Statistical analysis of the differences in alignment coverage

To verify differences in alignment coverage caused by using scaffolds or chromosomes as query assemblies, two data groups were made based on the type of comparison, which is a relevant feature for Brinton's method: comparisons in which both reference and query are chromosome-level assemblies (CLA-CLA) and comparisons in which the reference is a chromosome- and the query is a scaffold-level assembly (CLA-SLA). To prove if there were significant

differences in alignment coverage between chromosomes, data was split into the 21 chromosomes of allohexaploid wheat (7x3). Functions were generated to calculate alignment coverage and can be found in the script 'functions_hbpa.r' at the github repository. The script generated for the data generation and statistical analysis can be found at this repository under the name 'alignment_props_supplementary_hbpa.r'.

The percentage of coverage by alignment of the reference chromosome was calculated for the groups CLA-CLA and CLA-SLA as the alignment coverage mean values from all possible NUCmer pairwise comparison within each group and chromosome: 90 bidirectional pairwise comparisons for CLA-CLA (10 CLA x 10-1 CLA, as assemblies cannot act both as reference and query) and 50 unidirectional comparisons for CLA-SLA (10 CLA x 5 SLA). From the data relative to chromosomes, the average alignment coverage between the 21 chromosomes was calculated and compared between the CLA-CLA and CLA-SLA groups. Regarding the statistical analysis of the second hypothesis, only data from comparisons CLA-CLA was used and chromosome alignment coverage was compared between the 21 chromosomes.

Boxplots were generated plotting either the comparison type (CLA-CLA or CLA-SLA) or the analyzed chromosome against the percentage of coverage (Fig. 4). Analysis of residuals was conducted among the data to check prerequisites of the analysis of variance (ANOVA). Given the heteroscedasticity and non-normal distribution of the data, the Wilcoxon rank sum exact test was applied to the first hypothesis and Kruskal-Wallis to the second. To check differences in alignment coverage between chromosome 5B and the rest of the chromosomes, the Wilcoxon test was used.

2.2.5. Search for KASP marker targeting the haplotype RDMa-h2

The platform 'Search sequence capture probes' (https://www.cerealsdb.uk.net/cerealgenomics/CerealsDB/sequence_capture.php) was

consulted to search for all codominant SNP marker probes in chromosome 5B on the database. After selecting options and clicking on submit form, the website returned the names, sequences and the SNP positions of 497 probes. After that, a fasta was displayed and used as query for BLAST search with IWGSC Chinese Spring reference genome as database. Probes seemed to be clearly specific to chromosome 5B and the alignment bitscores in this chromosome tended to be higher than in its homoeologues. The BLAST output was generated in tabular format 6 and the table was read in RStudio, where only probes with chr5B alignments within the synonymous region in Chinese Spring chromosome 5B between 663,000,000 and 671,000,000 (equivalent to Lancer 655,000,000-663,000,000) were kept. These remaining probes were afterwards BLASTed against the pseudomolecules to filter out non-diagnostic markers (markers with alleles that differ between LongReach Lancer and Paragon). Locus-specificity was also pre-analyzed as recommended in Makhoul et al. (2020) by selecting the markers whose alignments in chromosome 5B showed a higher bitscore value than its counterparts in the homoeologous chromosomes in IWGSC Chinese Spring.

2.2.6. Identification of SNPs through high-stringency variant calling from Illumina paired-end short reads

The forward and reverse raw fastq files containing Illumina paired-end short reads generated by whole-genome shotgun (WGS) from three Chinese accessions reported to contain the RDM-positive allele T of the SNP marker Tdurum_con48959_1172 (Table 1) were downloaded from the website of the Genome Sequence Archive in BIG Data Center, accession number CRA001870 (Hao et al., 2020) The accession numbers of the three cultivars are: Guangtoushanmai, CRR062160; Yanmai 5, CRR062073 and Jimai 20, CRR062080.

Subsequently, a pipeline was developed on Ubuntu bash for variant calling from Illumina paired-end short reads and applied to each pair of forward and reverse fastq files. Pre-processing was performed with the tool cutadapt (Kechin et al., 2017). Reads under 30 bp, quality treshold

30 and more than 10% N were removed. The adaptor sequences of the kit TruSeq kit used for library preparation were found on the official Illumina webpage, 'Illumina Adapter Sequences' (https://support-docs.illumina.com/SHARE/AdapterSeq/Content/SHARE/AdapterSeq/TruSeq/CDIndexes.htm). Minimap2 (Li, 2018) was selected to map illumina paired-end reads against a fasta file containing the region between 652634893 and 653655509 bp on chromosome 5B of Chinese Spring RefSeq v1.0, region located between the SNP markers BS00029852_51 and BS00110293_51 (Table 1). The output SAM file was converted to BAM and quality-filtered with threshold 50 using samtools view (Li et al., 2019). To get rid of duplicated reads, these were first collated, e.g. grouped together by names, using samtools collate; followed by samtools fixmate to fill in mate coordinates and size fields; samtools sort to order reads and finally samtools markdup to mark duplicate alignments. After duplicate marking, the BAM file was filtered positively for paired reads (-f 1) and negatively for unmapped reads and mates (-F 12) using samtools view and refiltered for quality using the threshold 50. Alignment coverage was checked with mosdepth (Pedersen and Quinlan, 2018). Before variant calling, RG tags were added to the BAM file with picard AddOrReplaceReadGroups (http://broadinstitute.github.io/picard/) and a sequence dictionary was created with gatk-launch CreateSequenceDictionary for the fasta reference file. These steps were necessary for the next step involving gatk HaplotypeCaller (Ren et al., 2019) to call variants between the bam file generated from the short reads and the fasta file of the chromosome 5B fragment in Chinese Spring RefSeqv 1.0. Output was generated in GVCF format and the SNP marker Tdurum_con48959_1172 was found successfully when searching in each GVCF file by position (Table 1).

Each of the three individual GVCF files contained around 250k recorded variants. After merging the files, the number decreased to 413302, from which 139919 were SNPs. Multiallelic

SNPs were filtered out and only SNPs were retained in the merged file with bcftools view (Li, 2018), option --min-af 1:alt1 (minimum frequence of the alternative allele 1) --types=snps (only keep SNPs). This step reduced the number of SNPs to 7311. Minimum quality and read depth thresholds were set to 10000 and 100 respectively after thorough analysis applying intervals of values and checking the outcome number of SNPs. This filtering step produced 6105 SNPs. Output was cleared out of sites that had not been called in each of the Chinese varieties with grep, -v "./.", producing 568 SNPs. Finally, the same was conducted to eliminate SNPs with indels as alleles, leaving 542 SNPs.

The 101 bp flanking sequences of each SNP were extracted from the reference genome with samtools faidx. To generate the command lines for this operation, an R script (R Core Team, 2021) was generated that took in the text file and calculated the intervals between the sites located 50 bp downstream and upstream each SNP, printing these intervals inside the command lines that were later executed in Ubuntu. The 542 flanking sequences were merged and used as query for BLAST (Zhang et al., 2000) with each of the RDMb-h2-carrying assemblies as database (Julius, Norin, Stanley). The maximum number of hits per alignment was set to one so that only one hit with the maximum bitscore was produced on chromosome 5B for each SNP. Output tables were edited with grep to get rid of hits off chromosome 5B. Most of the aligned sequences between the SNP 101 bp flanking sequences from Chinese Spring genome and targets in chromosome 5B from these RDMb-h2-carrying assemblies were 100% identical.

The text files files were imported to R and merged into a single table. SNP flanking sequences that had produced <100% identical alignments were re-BLASTed to check if the missaligned nucleotide was located in the SNP allele. 4 SNPs were different in the allele position containing the allele for RDMb-h3 so finally 538 SNPs were exported to a table (Supplementary File 2).

2.3. RESULTS AND DISCUSSION

2.3.1. Two wheat assemblies contain a SNP-haplotype that increases root dry mass

In order to retrieve genomic information from genotypes carrying favorable RDM haplotypes, the flanking sequences of the 9 and 6 SNP chip markers in Table 1 that define each of two RDM haploblocks, RDMa and RDMb respectively, were searched in wheat genome databases. BLAST revealed that the RDM-associated haplotype h2 in RDMa was present in the assemblies LongReach Lancer and Paragon, meanwhile Hap-5B-RDMa-h1 was carried by the remaining

Hap-5B-RDMa haplotypes	ALLELES									ASSEMBLIES
	Kukri_c46570_214	RAC875_c24226_1356	RAC875_c18088_2222	RAC875_c18088_950	BobWhite_c43_86	Excalibur_c25522_755	RAC875_c12293_588	GENE-2890_482	Excalibur_c60554_394	
RDMa-h1	A	A	G	C	G	C	G	G	G	ARI, JAG, JUL, LDM, MAC, NOR, STA, MAT, CSP, CAD, CLA, ROB, WEE
RDMa-h2	G	C	A	T	A	T	A	A	A	LAC, PAR

Hap-5B-RDMb haplotypes	ALLELES						ASSEMBLIES
	BS00022477_51	BS00029852_51	Tdurum_con48959_1172	BS00110293_51	BS00022231_51	IACX6288	
RDMb-h1	A	G	G	A	G	T	ARI, JUL, LAC, LDM, MAC, MAT, CAD, CLA, PAR, ROB, WEE
RDMb-h2	G	T	G	G	A	C	CSP, JAG, NOR, STA
RDMb-h3	G	T	T	G	G	C	
RDMb-h8	A	G	T	G	G	C	

Table 2: SNP-haplotype pattern for the RDM haploblocks among the 15 wheat genome assemblies: ARI, ArinaLrFor; JAG, Jagger; JUL, Julius; LAC, Lancer; LDM, Landmark; MAC, Mace; NOR, Norin61; STA, Stanley; MAT, SY-Mattis; CSP, Chinese Spring; CAD, Cadenza; CLA, Claire; PAR, Paragon; ROB, Robigus; WEE, Weebill. Haplotypes with positive effects on RDM are filled in green. Haplotype RDMb-h3 was not found to be present in any of the assemblies.

13 lines. Regarding the adjacent haplotype block RDMb, the RDM-associated haplotype h3 was not found in any of the assemblies, which contained RDMb-h1 or h2 instead (Table 2).

2.3.2. A sequence-based haplotype matches with the SNP-based RDMa-h2 according to crop-haplotypes.com

To confirm if the SNP-haplotypes identified by BLAST match with the sequence-based haplotypes produced by Brinton et al. among the 15 wheat assemblies, crop-haplotypes.com was used. Shared haplotypes were predicted by the website between the RDMa-h2-carrying assemblies, Lancer and Paragon in the proximity of the SNP-haploblock RDMa at the three different bin sizes (5-, 2.5- and 1-Mbp), as shown in Figure 3a and 3b. However, the first two predictions did not overlap with the SNP-haploblock and only the prediction at 1-Mbp did, as it started from 656 Mbp in Lancer's chromosome 5B. Haploblock length increased at 1-Mbp compared with 5- and 2.5-Mbp as an effect of the increase in resolution. Between 5- and 2.5-Mbp, the lengths remains identical although the haploblock position changes, which can be seen in Figure 1b with the green bar moving to the right from 5- to 2.5-Mbp. Therefore, the reported sequence-based haplotype was hypothesized to be the same as the SNP-haplotype RDMa-h2. It was also considered that the haploblock could be larger than the original SNP-haploblock. Nevertheless, since only one of the three predictions overlapped the SNP-haploblock, it was considered convenient to validate this hypothesis following the original Brinton's method.

Regarding the 13 assemblies carrying RDMa-h1, the website revealed a complex haplotype pattern in this block. This means that many different shared and unique haplotypes, e.g. haplotypes that are not shared between at least two lines, were observed around the RDMb block position (Chinese Spring, 652,600,000-653,700,000 bp), as can be appreciated in Figure 3c. If the RDMa-h1 is actually conserved between the assemblies, it could have been undetected because of (1) its length under the minimum bin size, 1-Mbp, or (2) that the small region is not

identical-by-state (≥ 99.99% median sequence identity) between these assemblies but nearly-identical (<99.99%). The latter hypothesis would correspond with the higher sensibility of Brinton's method to detect small differences between alleles, although in this case, these differences would not be relevant for breeding, since this haplotype is not associated with RDM.

a

Bin size (Mbp)	Block number	Start	End	Length
5	5165	660,000,000	665,000,000	5,000,000
2.5	7063	657,500,000	662,500,000	5,000,000
1	13794	656,000,000	663,000,000	7,000,000

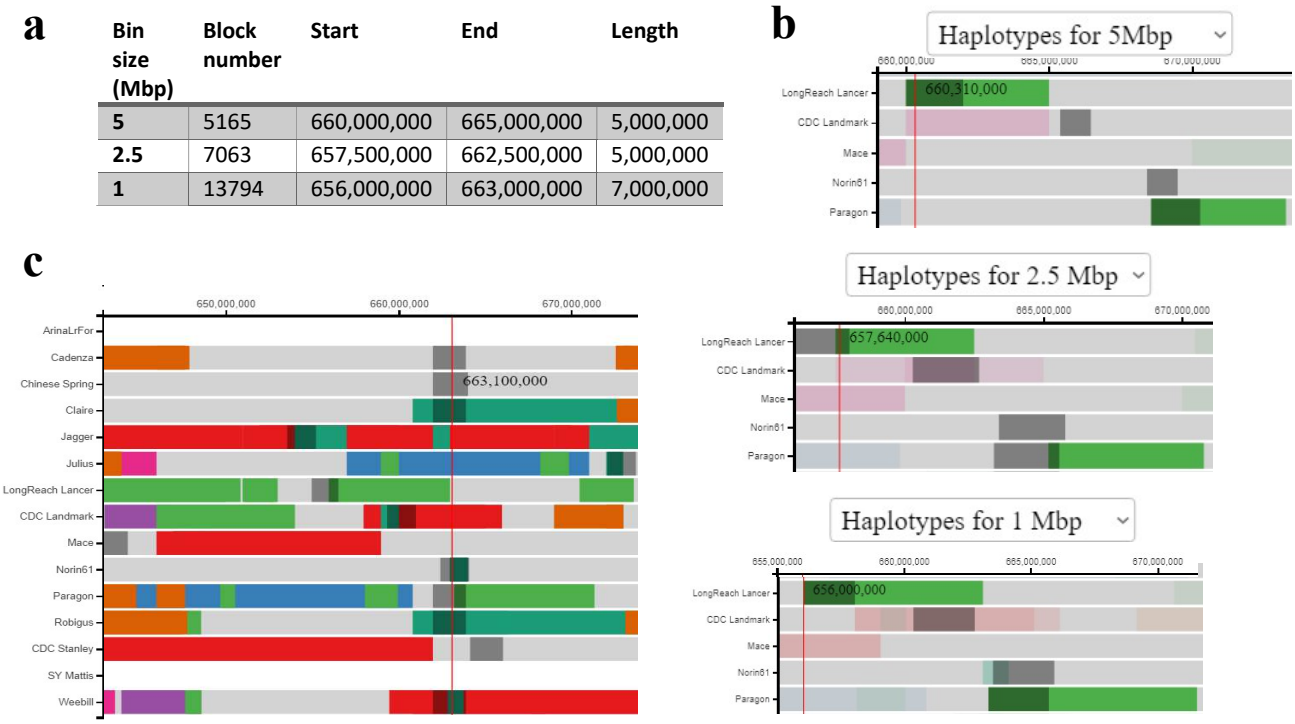

Figure 3: **Haploblock predictions on crop-haplotypes.com.** (a) Haplotype shared between LongReach Lancer and Paragon in chromosome 5B near the SNP-haploblock RDMa. Coordinates relative to Lancer. (b) Graphical visualization from the data in a. Only the haploblock prediction at bin size 1-Mbp includes part of the SNP-haploblock RDMa (655,700,000-656,600,000). Coordinates relative to Lancer. (c) Haplotypes among the 15 wheat genome assemblies under 1-Mbp bin size at the start position of RDMa in IWGSC Chinese Spring (663,100,000). The highlighted dark grey boxes are the homologous of the region around 663 Mbp in Chinese Spring in every assembly.

2.3.3. Using scaffolds as query in NUCmer pairwise alignments reduces alignment coverage

The observations during the analysis of the RDMa haploblock raised two questions: (1) whether using scaffold-level assemblies as query had a negative effect on alignment coverage by NUCmer pairwise comparisons, which could affect the reliability of haploblock predictions and (2) if the differences in alignment coverage depend on the analyzed chromosome.

Regarding the first hypothesis, the boxplot showed an apparently much lower alignment coverage in comparisons CLA-SLA than in comparisons CLA-CLA (Fig. 4a). This observation

was proved significant using the Wilcoxon rank sum exact test (p-value 7.431e-12). Two reasons explaining why using scaffolds in NUCmer pairwise comparisons produces low alignment coverage and thus inaccurate predictions are: (1) lower sequencing quality than their chromosome-level counterparts and (2) the lack of chromosome-level organization, since this would facilitate the aligner to find the right target, which would otherwise be challenged to find the this sequence among homologous sequences in the whole scaffold set without any indication. This problem is not indicated in Brinton et al. and they only rely on the gene-based BLAST pairwise comparisons to alleviate it despite their reported insufficiency to fully differenciate between haplotypes. Some solutions to improve the alignment quality of these comparisons would be: (1) to further assemble the scaffold-level genomes to the chromosome-level or (2) to sort out the scaffolds into chromosomes by for example BLASTing them against the reference genome.

Regarding the second hypothesis, the boxplot was sort by increasing median value and chromosome 5B was observed to have the lowest median, so the hypothesis was reshaped to ask if alignment coverage in chromosome 5B differed to those from other chromosomes (Fig. 4b). The analyzed chromosome seemed to have a signficant effect on alignment coverage (p-value 2.2e-16), according to Kruskal-Wallis test. Additionally, the alignment coverage of chromosome 5B in NUCmer comparisons between chromosomes was significantly lower than in every other chromosome (p-value 0.0325), as Wilcoxon test revealed. These differences in alignment coverage between chromosomes could be due to differences in sequencing efforts

that could translate in some chromosomes having presenting more sequencing errors or Ns that difficult the aligning process.

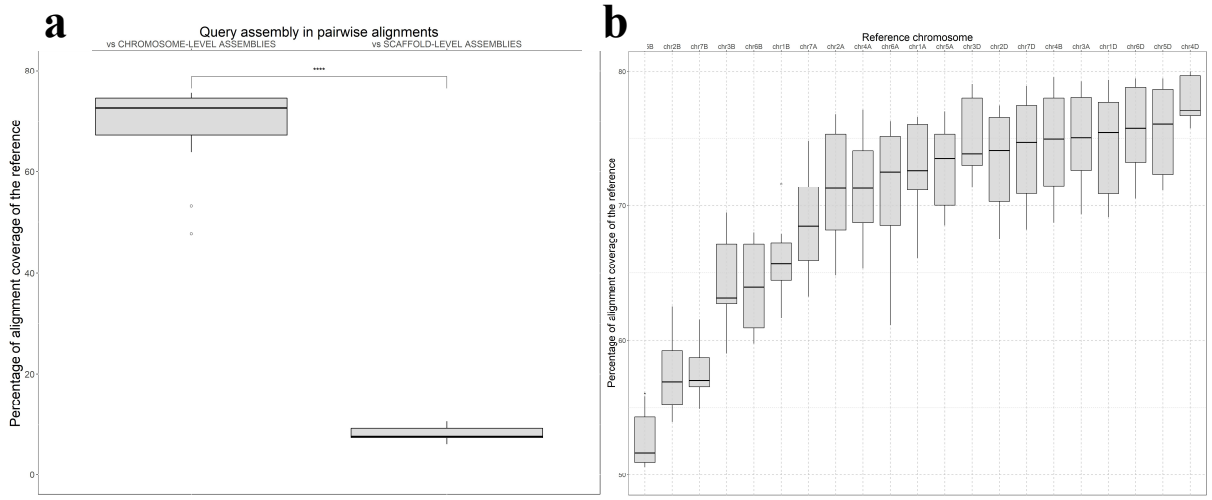

Figure 4: **Boxplots showing differences in the percentage of alignment coverage of the reference chromosome,** between (a) comparisons in which the query is a chromosome-level assembly (left) or a scaffold-level assembly (right), which have very significantly lower alignment coverage (p-value X, ****), and between (b) comparisons chromosome-chromosome in different analyzed chromosomes, among which the chromosome 5B has a significantly lower alignment coverage than any of them (p value X, *). Significance thresholds: * (P = 0.05), ** (P = 0.01), *** (P = 0.001), **** (P = 0.0001).

2.3.4. Checking alignment properties is essential for accurate haploblock prediction

When analyzing the dotplot generated with the R function 'plot_aln_and_bins', a large discontinuity at 663.0-664.5 Mbp containing only two <90.0% identical alignments was noticeable (Fig. 5a). Despite of this, the region between 660 and 665 Mbp had been assigned to a haploblock at 5-Mbp bin size given that the median percentage of identity of the 5-Mbp bin where it is located laid over the cut-off 99.99%. Discontinuities contain missing information from alignments and can increase false positive and negative haplotype predictions affecting the power to detect haploblocks and the precision to make right predictions, since the algorithm from Brinton's method does not take low alignment coverage into account.

This negative situation could be common in NUCmer pairwise alignments with low alignment coverage, as reported previously about the comparisons between chromosome- and scaffold-level assemblies. In this case, discontinuities could be due to sequencing gaps or alignment errors due to the difficulty of aligning assemblies with different coordinate systems

(chromosome vs scaffolds). The latter would explain why these discontinuities are often associated with alignments of relatively low percentage of identity. However, given the differences in alignment coverage between analyzed chromosomes, these discontinuities could be also expected in comparisons between reference-quality assemblies, especially under heterogeneous distribution.

Despite this wrong assignment at 5-Mbp bin size, reducing bin size to 2.5-Mbp can overturn this error by excluding the segment between 662.5 and 665.0 Mbp containing this discontinuity (Fig. 5b). However, this prediction extends over another discontinuity between 658,0 and 659,0 Mbp containing only one alignment of 99.75% identity that remains when the bin size is further decreased to 1-Mbp (Fig. 5a), due to the 'two consecutive errors' rule by Brinton et al. (2020) discussed in the introduction. It seems difficult to assess if this error is actually a false positive, e.g. a wrong haploblock assignation in a region that differs between the compared assemblies, or if the low coverage and identity are simply due to technical factors such as sequencing errors.

A different scenario in which considering alignment properties is relevant would be when haplotypes are called based on only a few alignments in comparisons in which haploblocks are not expected, illustrated by one case in Norin61's chromosome 5B (Fig. 6). Here, this assembly mainly shares haplotypes only with Mace at bin sizes 5- and 2.5-Mbp, but at 1-Mbp, many new haplotypes appear mainly in comparisons with scaffold-level assemblies. One of these blocks, at 537-538 Mbp (Norin61) was called due to the presence of only one alignment with ≥99.99% identity in a 1-Mbp bin meanwhile the region around this bin contains many empty bins or alignments with low percentage of identity. Furthermore, Norin61 is with Chinese Spring one of the pre-1950 line and thus clearly different to the rest of the assemblies (Brinton et al., 2020). These factors lead to think that this is a false positive prediction, which was probably caused by misalignment with a very similar off-target region

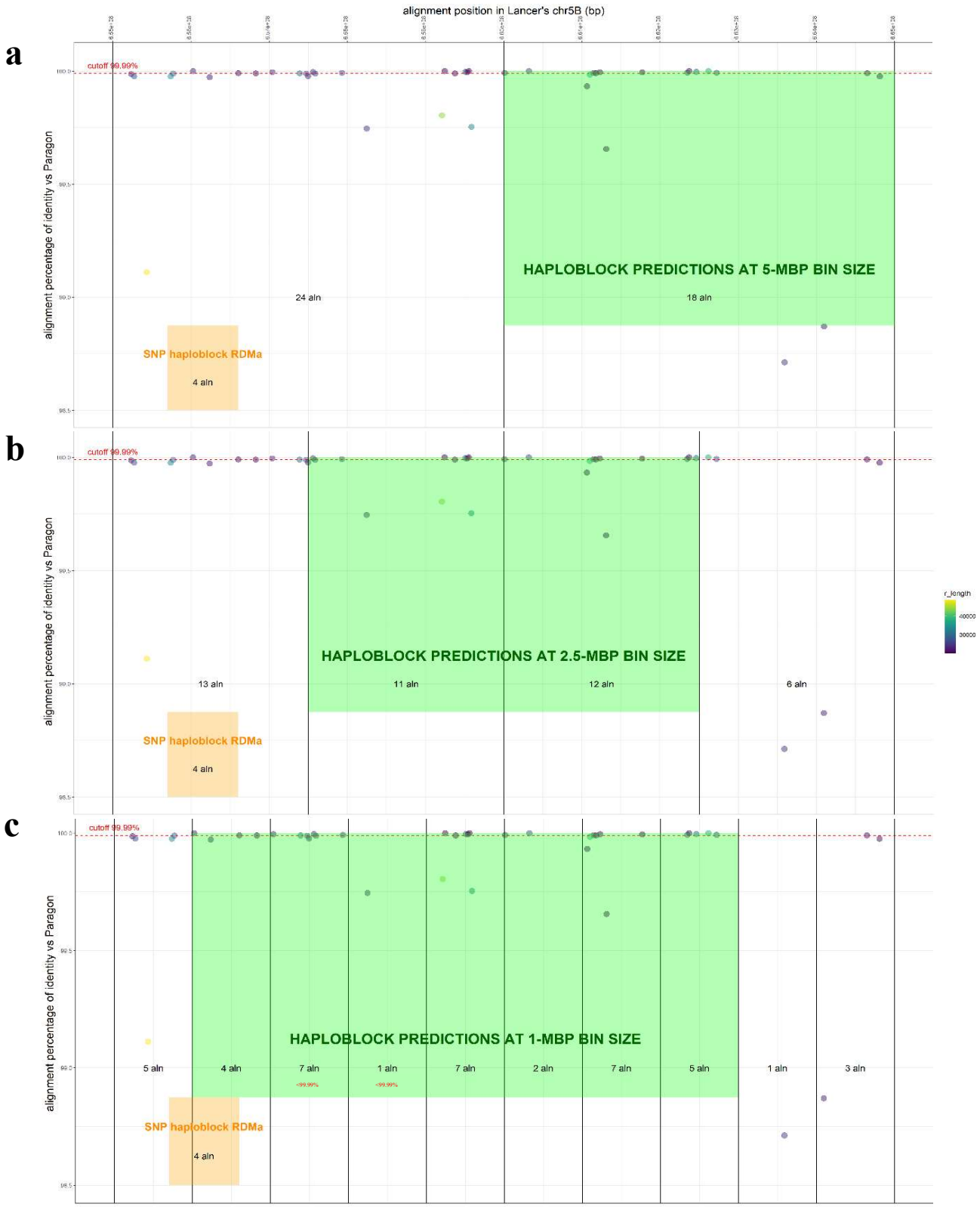

Figure 5: Effects of changing bin size on haploblock predictions on crop-haplotypes.com in the region between 655 and 665 Mbp of Lancer's chromosome 5B, at (a) 5-Mbp, (b) 2.5-Mbp and (c) 1-Mbp bin size. Dots indicate Lancer's alignment position in the x axis and percentage of identity against Paragon's scaffolds in the y axis. Simultaneouly, the bins of fixed size used in Brinton's method for haplotype detection are marked with vertical lines and the number of alignments within each bin is shown between consecutive lines. Haploblock predictions generated by Brinton's method and that can be observed on crop-haplotypes.com are highlighted in green and titled and the SNP-haploblock where RDMa-h2, shared between Lancer and Paragon, is located is also highlighted in orange. This graph was generated by the function 'plot_aln_and_bins' in the R script 'functions_hbpa.R'.

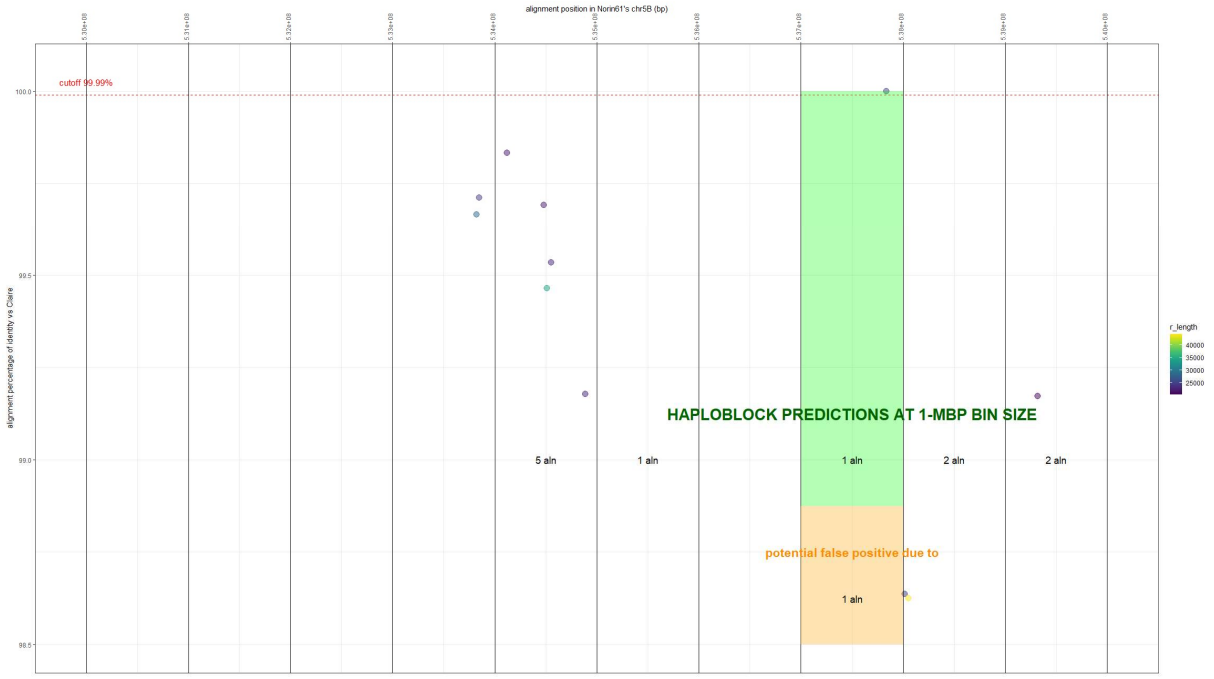

Figure 6: **Potential wrong assignment of the Norin's chromosome 5B region between 537 and 538 Mbp to a 1-Mbp-long haploblock at 1-Mbp bin size on crop-haplotypes.com.** Dots indicate Norin's alignment position in the x axis and percentage of identity against Claire's scaffolds in the y axis. Simultaneouly, the bins of fixed size used in Brinton's method for haplotype detection are marked with vertical lines and the number of alignments within each bin is shown between consecutive lines (no message is printed if bins are empty). Haploblock predictions generated by Brinton's method and that can be observed on crop-haplotypes.com is highlighted in green and titled and the same haploblock is also highlighted in orange. This graph was generated by the function 'plot_aln_and_bins' in the R script 'functions_hbpa.R'.

2.3.5. Low alignment coverage and discontinuities hamper validation and redefinition of the haploblock RDMa

The chromosome-scale analysis pointed out that the NUCmer pairwise comparison between Lancer and Paragon was defined by low-quality alignment properties. Only 11.64% of the 702438406 bp of Lancer's chromosome 5B are covered by alignments against the scaffolds from Paragon, which is very low in comparison with its average coverage 55.81% in alignments between Lancer and any chromosome-level assembly. This lower alignment coverage was due to shorter alignment average lengths (~31 Kbp versus ~47 Kbp) and lower number of alignments (~2.7 K vs ~8.3 K) when Lancer is aligned versus Paragon than when it is aligned versus any CLA. From these values, the average number of alignments that we can expect in 1-Mbp bins was 3.8 in Lancer-Paragon, compared with 11.9 in Lancer against any chromosome.

As reported previously, these features are characteristic not only of this comparison but generally of any comparison between chromosomes and scaffolds.

When the region between 655,000,000 and 665,000,000 bp in Lancer's chromosome 5B was analyzed with the function 'plot_aln_and_bins', the existence of two discontinuities at 658,0-659,0 Mbp and 663,0-664,5 Mbp was evident. At 1-Mbp bin size, the haploblock prediction avoids the second discontinuity and overlaps with the SNP-haploblock RDMa (655,700,000-656,600,000). However, the haploblock prediction still span across the first disconuity, which cuts it into the two regions at 656-658 and 659-663 Mbp, which seem to have a good balance between alignment density and high percentage of identity.

Therefore, in order to redefine haploblock RDMa based on the information obtained from sequence comparison, we could adopt one of the following four approaches (Fig. 7):

1. To completely invalidate the haploblock predictions due to their low-quality alignment properties and therefore to not attempt to redefine it. This conservative approach would suppose to keep the SNP-haploblock RDMa as the target region for RDM breeding in wheat: 655,700,000-656,600,000.
2. To consider discontinuities within haploblocks as wrong assignations explained by differences between the lines. This would mean to expand the haploblock in upstream direction but stopping before the first discontinuity: 656,000,000-658,000,000.
3. To redefine the haploblock as the region after the discontinuity, considering that this might be were the causal gene actually lies and that the SNP-haploblock RDMa is only linked by proximity with this region: 659,000,000-663,000,000.
4. To understand discontinuities within haploblocks as identical regions that are incorrectly reported as non-identical due to sequencing or alignment errors. This less conservative

approach would mean to completely validate the prediction at 1-Mbp bin size: 656,000,000-663,000,000.

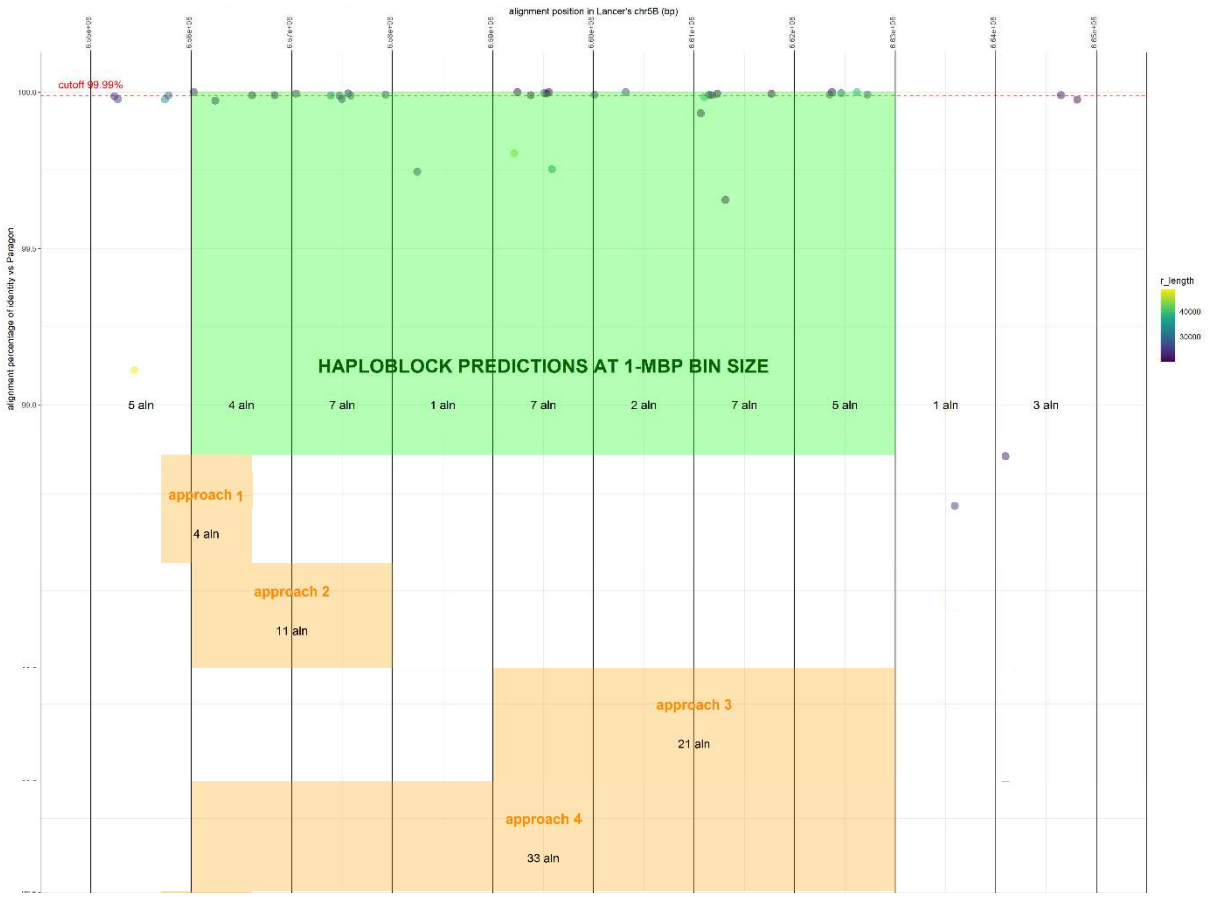

Figure 7: **Comparison between the four approaches for haploblock redefinition.** This graph was edited from four dotplots generated by the function 'plot_aln_and_bins', in the script 'funtions_hbpa.R'.

2.3.6. New KASP markers from an array could target the potentially larger haploblock RDMa-h2

Since RDMa could be larger than the original SNP region (0.9-Mbp-long), as found out in previous steps, molecular markers were searched to target a new region that could be associated with the haploblock. 5 codominant SNP probes were discovered among a raw list of 39 Axiom SNP probes flanking a region between 658,499,200 and 662,451,059 in LongReach Lancer's chromosome 5B following these restrictive search criteria (Table 3). 34 more probes were added to a raw list of markers located in the candidate region. Ideally, these probes could be

used to develop KASP markers to genotype wheat plants for association studies, which could help by increasing trait-marker correlation for the haplotype Hap-5B-RDMa-h2.

Axiom SNP marker name	AX-94878590_116_Co-dominant_pos-61_v1	AX-95255236_263_Co-dominant_pos-61_v1	AX-95173034_464_Co-dominant_pos-61_v1	AX-94636419_373_Co-dominant_pos-61_v1	AX-94994996_195_Co-dominant_pos-61_v1
SNP probe	ATGTCTCTACATGATTGCCCTTG AAGATAATGATCCTTTGGGCAT TGCCATTTGATGAAYGAGAAGC GGTTTGCATCGCGTGTTCTGTTG AAGAGGTGTACTGACGAGGAG GCCTTTA	TGCTGGCGCAAATGCTTCTCAAT CCGGCAGATCTCCACGCGCCGA GTCGTGGCTTTCGCAARTTGCCTT TCAAATCCTTTTGGCATAAGAAA ACTGGCAGTTCTTGACATCATCA GTTTGG	TGTGCCTCTTGTGCTATTTTATGT CGTTTTTCAATGTGTTCAACGGT GTCAGTTCGAATCNCTGTTAATT AAGTACTCCGATGTAAAGAAAT TGATAGCTTTTAGATCATTCGTG AATG	GTGCACTACTTTAAGCTGCTGAA ATGGCTTGTGGTTCTGCCGATGC TCGGGATGTTCCTTRTCCTCGTC CACCGTTGCCATCGTTTTCGCGG AACAAC	GGTACTGGATTCATCTGCAGAGG ATGTCATTGCTACTCTGCGAGGT GTGCACCCCGAGTCRATTCAATA CCTTTGTTCCAGCGGCTGAGAGAC TAAGCCAAGAACTAGGACCTAC GCTCT
BLAST position (IWGSC)	666.209.099	666.209.246	667.839.964	668.473.987	670.831.214
BLAST position (Lancer)	658.499.200	658.499.347	659.290.270	659.893.416	662.451.059
LONGREACH LANCER	C	G	T	G	G
PARAGON	C	G	T	G	G
ArinaLrFor	C	G	T	C	T
Jagger	C	G	C	G	T
Mace	C	G	C	G	T
Norin61	C	G	C	G	G
Julius	C	G	T	C	T
Stanley	T	A	-	C	G
CDC Landmark	C	G	C	G	T
SY Mattis	C	G	C	G	T
Claire	C	G	C	G	G
Weebill	C	G	C	G	T
Cadenza	C	G	C	G	T
Robigus	C	G	C	G	G
IWGSC - chr5B	T	A	T	C	G
IWGSC - Chr5A	c	g	-	g	g
IWGSC - Chr5D	c	g	-	g	g

Table 3: Candidate codominant SNP markers to target the redefined potential RDMa haploblock. Identifier, SNP probe, position in Lancer and Chinese Spring and allele sequences in 15 wheat genome assemblies are provided in the table. SNP probes were obtained from the Axiom Pannel at cerealsdb.uk.net. Notice that the RDMa-h2-carrying lines Lancer and Paragon share the same allele sequence and among the other lines, some of them share the same allele (red) and some of them possess the other allele (green) of the same markers. In the last three rows, the allele sequence is displayed for Chinese Spring in its three homoeologues chromosomes 5 (5A, 5B, 5D), showing how alleles differ between chromosome 5B and the other two off-target chromosomes. Lower case indicates that this hit does not have the highest bitscore among the three hits in the homoeologous chromosomes.

2.3.7. Genome sequences of RDMb-h3-carrying varieties were identified and provided new SNP markers

As the RDM haplotype RDMb-h3 was not detected in any of the available wheat genome assemblies, it needed to be searched in public databases. In 2020, Hao et al. conducted the resequencing of 145 Chinese cultivars and captured more than 60.92 million SNPs, based on Chinese Spring RefSeq v1.0. Upon request, the SNP marker Tdurum_con48959_1172 was search and found among the raw SNP set generated in the experiment in three Chinese varieties: one landrace, Guangtoushanmai and two modern cultivars, Yangmai 5, Jimai 20. However, this SNP was not found among the highly reliable SNP set, unlike the other 5 markers that define RDMb. This finding provided for the first time genome sequences of the very infrequent haplotype RMDb-h3 (Voss Fels et al., 2017). Furthermore, high-stringency mapping of the Illumina paired-end short reads and variant calling between Chinese Spring (RDMb-h2) and the three Chinese varieties (RDMb-h3) provided 538 SNPs in the highly-reliable SNP set (Supplementary File 2) obtained with very stringent filtering. Tdurum_con48959_1172 was found in all raw GVCF files but removed after filtering due to lower quality and read depth. These SNP sequences could be confirmed by Sanger sequencing to develop diagnostic KASP markers to select RDMb-h3. Furthermore, these genome sequences could be further analyzed to identify the underlying genes causing higher RDM or to find out if any of these accessions also carries the haplotype RDMa-h2, since the combination RDMa-h2/RDMb-h3 is associated with the highest phenotypic effects (Voss-Fels et al., 2017). Also, it could be studied if the sequence similarity between RDMb-h2 and RDMb-h3 is due to a recombination event between the markers Tdurum_con48959_1172 and BS00029852_51. This could have been possible in this study if long reads had been available for these three varieties since assemblying these sequences enables the analysis by comparison of potential recombination breakpoints between RDMb-h2 and h3.

3. GENERAL DISCUSSION

Pangenomics provide a groundbreaking opportunity to understand and harness genetic diversity in wheat. According to Rasheed et al. (2017), genetic resources should be prioritized in the post-genomics era for the improvement of wheat production in order to double yield by 2050.

The on-going international efforts on wheat pan-genome sequencing succeeded with the publication of reference-quality wheat assemblies and scaffold-level assemblies (Walkowiak et al., 2020). The sequence-based haploblock prediction method developed by Brinton et al. (2020) will contribute to increasing precision of wheat breeding by redefining traditional SNP-based haploblocks. This breakthrough could not have been possible without the recent abovementioned wheat pangenomic resources.

In this master thesis, new contributions were made to Brinton's method after the realization that alignment properties must be considered for calling haploblocks from sequence comparison. The newly-developed R script allows target-scale analysis of shorter chromosome fragments of interest and provides graphic and numeric information about the alignment properties in this region that can be used for the validation of the haploblock predictions observed in crop-haplotypes.com. Furthermore, it enables the simple manipulation of parameters, such as bin size or cutoff, to personalize the analysis given the clear usage instructions provided along the script and the high degree of detail provided by the graphs. The script is not only constricted to the original raw data but can instead be used to analyze new data sets. Since wheat pangenomics does not have a long history and there are still not enough available resources, these tools could be very important for precision breeding.

Furthermore, this work achieved to find genome sequences for the haploblock RDMb-h3 for the first time. The genomic resources were used to identify new diagnostic SNP markers that

could potentially be used for breeding wheat with higher root dry mass and are still subject to further interesting analyses.

4. SUMMARY

Haploblocks can be defined by comparing DNA sequences in wheat instead of by following the traditional method based on SNP markers. Sequence-based methods have the advantage of higher precision in finding regions that are causal for traits and higher accuracy in detecting small differences between highly identical alleles. SNP-based haplotypes can be redefined to sequence-based haplotypes if sequence information from the haplotype-carrying varieties is available. In this article, a SNP-based haploblock associated with higher root dry mass was analyzed among 15 wheat genome assemblies. To achieve this, a new method based on pairwise alignments between assemblies was used to confirm that two wheat lines carrying one of the favorable SNP-based haplotype also share a sequence-based haplotype at this region. Subsequently, the fundaments of this method were explored in an attempt to redefine the SNP-based haploblock to a more precise sequence-based region. The relevance of alignment properties in haploblock predictions was highlighted and bioinformatic resources were developed to include the analysis of these properties into the method to detect haplotype from pairwise alignments with increased precision. Additionally, genome sequences were found in public databases for another favorable haplotype and used to identify new SNPs to target this haplotype.

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6. APPENDIX

The following pages contain the supplementary files 1 and 2

Haplotype-based Pangenome Analysis in Wheat

As the writer of this script I would like to express appreciation and give all credit to the authors of the following article for creating original raw data and scripts required for this R script:

Brinton, J., Ramirez-Gonzalez, R. H., Simmonds, J., Wingen, L., Orford, S., Griffiths, S., 10 Wheat Genome Project, Haberer, G., Spannagl, M., Walkowiak, S., Pozniak, C., & Uauy, C. (2020). A haplotype-led approach to increase the precision of wheat breeding. *Communications biology*, 3(1), 712. https://doi.org/10.1038/s42003-020-01413-2 (https://doi.org/10.1038/s42003-020-01413-2)

This script was written in R 4.1.0 by Jose Antonio Montero Tena as part of his master thesis in 2021. Free use and modification of this script for personal interest is encouraged.

Introduction

SNP-haplotypes discovered from marker arrays can be redefined as sequence-based haplotypes, which are identical-by-state sequences sharing 100 percentage of identity between the genomes and discovered by sequence comparison. Brinton et al developed a method in 2020 that mainly defined haploblocks as physical regions with >= 99.99 pident across fixed-size bins of 5-, 2.5- or 1-Mbp between NUCmer pairwise comparisons of the assemblies in the 10+ Wheat Genome Project. This method will subsequently be referred to as the Brinton's method. The resulting sequence-based haplotypes can be either shared haplotypes or unique haplotypes, e.g. alleles that are carried by one single assembly. Additionally, Brinton and colleagues published crop-haplotypes.com, a website that provides an interactive graphic visualization of the shared haplotypes between the wheat genome assemblies. These assemblies were chromosome-level genome assemblies of nine wheat assemblies (ArinaLrFor, Jagger, Julius, Lancer, Landmark, Mace, Norin61, Stanley, SY-Mattis) and the Chinese Spring RefSev1.0 assembly alongside scaffold-level assemblies of five additional assemblies (Cadenza, Claire, Paragon, Robigus and Weebill).

Aim

The aim of this script is to use Brinton's method and resources to conduct both a chromosome-scale and small-scale analysis of the pairwise comparisons between assemblies. The small-scale analysis option is original to this script and allows the analysis of target regions within chromosomes. The aim of the small-scale analysis is to assist with mapping physical start and end coordinates of the predicted haploblock both in the reference and query genomes after considering alignment coverage, in other words to avoid false positive haplotype predictions. Also, this script aims to identify the genes contained in mapped haploblock, both in the haplotype-carrying genomes and in the IWGSC Chinese Spring Ref v1.1. Brinton et al called haplotypes both from mummer and gene-based BLAST pairwise alignments and selected for matching positions the longer predictions. Both types of analysis are provided in this script, although haplotype predictions obtained these two methods, NUCmer and BLAST, do not always match.

Background

The SNP-haplotype Hap-5B-RDMa-h2, associated with increased root dry mass (RDM), is taken as an example. This haplotype was first found by GWAS upon 9 SNP marker alleles located in the wheat chromosome 5B and matched with the assemblies of the assemblies LongReach Lancer and Paragon by BLAST. SNP-RDMa-h2 BLAST position in Lancer's chromosome 5B (655760000-656600000 bp) was observed in crop-haplotypes.com in order to determine if the SNP-haploblock region matched with the region of any sequence-based haploblock, discovered with Brinton's method, in this area. The following blocks were observed in the pairwise comparison Lancer-Paragon under each bin size (bin size - start - end - length): 5-Mbp - 660.000.000 - 665.000.000 - 5.000.000 // 2.5-Mbp - 657.500.000 - 662.500.000 - 5.000.000 // 1-Mbp - 656.000.000 - 663.000.000 - 7.000.000 (start and end according to Lancer's coordinate system as Lancer acts as the reference in this comparison). Data from the website suggested that there might be a match between the SNP-based haplotype and a sequence-based haplotype in Lancer and Paragon. Despite of this, Brinton's method must be applied on this redefined region to understand if the prediction made on crop-haplotypes.com is reliable. Additionally, other research questions as the exact start and end position of the sequence-based haploblock or the underlying genes can be answered in this script.

Running the script

The script is designed so that you only have to edit only the upcoming parameters. You can run the script by lines (recommended for first time) or simply pressing 'Source' in the upper right corner of this window. The running time is expected to be between 5 and 7 minutes. Please, be patient and only look for solutions if error messages interrupt the pipeline. If errors do not stop coming up, you can contact the script editor at the e-mail adress jmonterotena@gmail.com (mailto:jmonterotena@gmail.com).

Defining parameters

On which chromosome are your haploblocks located? Copy the same format

```
chromosome <- "5B"
```

Which is the reference assembly in the pairwise comparison that you are using? Alignment coordinates will apply for this assembly's chromosome. Can NEVER be a scaffold-level assembly (Cadenza, Claire, Paragon, Robigus, Weebil). Follow the next naming guidelines: "arinalrfor", "jagger", "julius", "lancer", "landmark", "mace", "norin61", "stanley", "sy_mattis", "chinese" (works with capital letters)

```
reference_assembly <- "Lancer"
```

Which is the query assembly? This genome is aligned against the reference chromosome. Can be a scaffold-level assembly. Follow the next naming guidelines: "cadenza", "claire", "paragon", "robigus", "weebil" (works with capital letters)

```
query_assembly <- "Paragon"
```

Specify a start of the region highlighted in the small-scale analysis to look for haploblocks after this position. ADVICE: use multiples of 5 so that the bins match with those on crop-haplotypes

```
zoom_start <- 655000000
```

Specify an end of the region highlighted in the small-scale analysis to look for haploblocks before this position. ADVICE: use multiples of 5 so that the bins match with those on crop-haplotypes

```
zoom_end <- 665000000
```

Do you have previous information on haploblock locations in this region (e.g. SNP-based haploblocks from SNP chips)? If you have evidence of a haplotype within your zoom region that you want to compare with the sequence-based haplotypes obtained in this script, write its start coordinate in the reference chromosome. If not, simply write NA. The target region must be within the zoom region

```
target_start <- 655700000
```

Do you have previous information on haploblock locations in this region (e.g. SNP-based haploblocks from SNP chips)? If you have evidence of a haplotype within your zoom region that you want to compare with the sequence-based haplotypes obtained in this script, write its end coordinate in the reference chromosome. If not, simply write NA. The target region must be within the zoom region

```
target_end <- 656600000
```

You do not need to worry about the next step yet. Complete section one and then come back to define the **new coordinates of your haploblocks**. Genes will be extracted from this position. If you have no interest in redefining your region, simply write 'target_start' or 'zoom_start', to keep with the previous coordinates

```
selected_start <- 655760000
```

You do not need to worry about the next step yet. Complete section one and then come back to define the **new coordinates of your haploblocks**. Genes will be extracted until this position. If you have no interest in redefining your region, simply write 'target_end' or 'zoom_end', to keep with the previous coordinates

```
selected_end <- 662740000
```

Running functions

Source the script 'functions.hbpa.r' to read the packages and functions required for this script.

1. Calling haplotypes from raw data containing >= 20-Kbp-long NUCmer pairwise alignments between Lancer and Paragon

Requirements:

- Raw delta files in 'all_20_kb_filtered_delta_CHROMOSOME_tables.rds'; in this case the chromosome is 5B (downloadable from https://opendata.earlham.ac.uk/wheat/under_license/toronto/Brinton_etal_2020-05-20-Haplotypes-for-wheat-breeding/nucmer/ (https://opendata.earlham.ac.uk/wheat/under_license/toronto/Brinton_etal_2020-05-20-Haplotypes-for-wheat-breeding/nucmer/)). Brinton et al filtered out alignments under 20000Kbp of length in order to get rid of non-syntenic retrotransposons
- Script 'functions.hbpa.r' (downloadable from https://github.com/MonteroJLU/Haplotype-based-Pangenome-Wheat-Analysis.git (https://github.com/MonteroJLU/Haplotype-based-Pangenome-Wheat-Analysis.git))
- Text file 'table_assembly_chr_length.txt' (downloadable from https://github.com/MonteroJLU/Haplotype-based-Pangenome-Wheat-Analysis.git (https://github.com/MonteroJLU/Haplotype-based-Pangenome-Wheat-Analysis.git))

1.1. Chromosome-scale analysis

1.1.1. Download and save the required documents in the working directory

1.1.2. Run the script 'functions_hbpa.r'

1.1.3. Read the rds file into a data frame:

```
aln_library <- readRDS(file = paste0("all_20_kb_filtered_delta_", chromosome,"_tables.rds"))
```

1.1.4. Create a subset of the data frame containing only the alignments from the pairwise comparison Lancer-Paragon, where Lancer acts as the the reference genome:

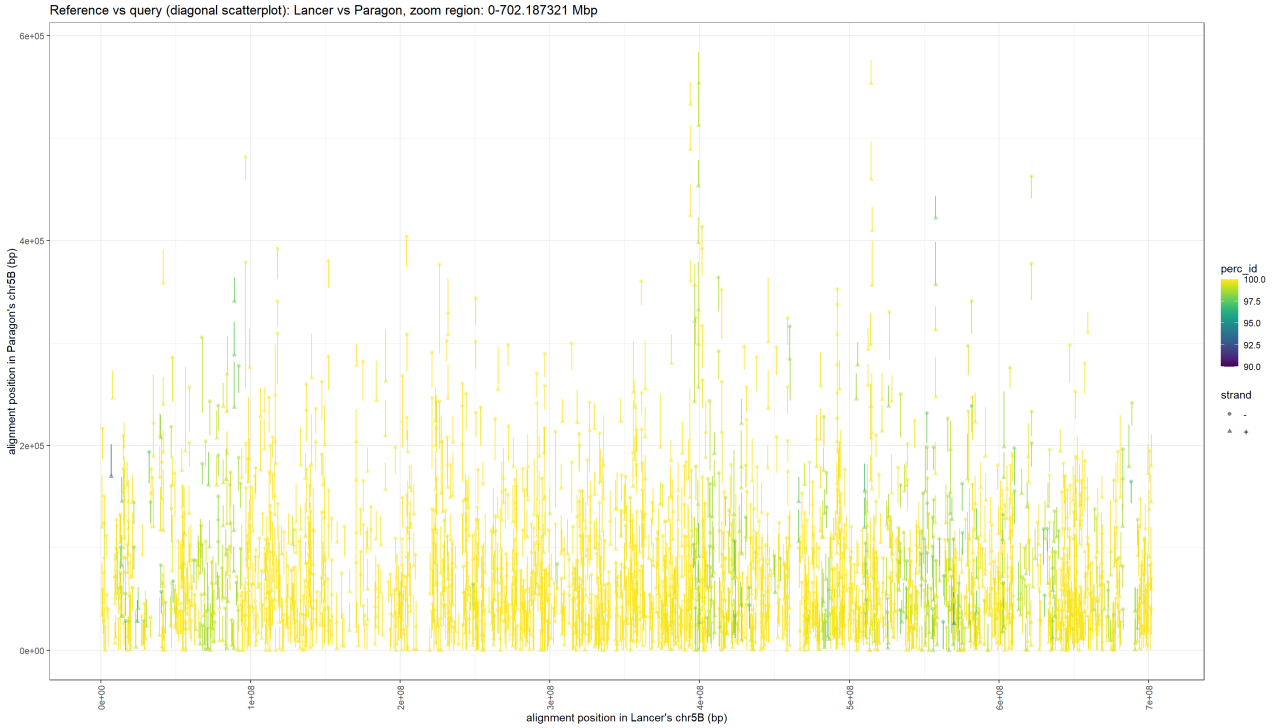
```
aln_subset <- aln_library[grepl(paste0("^", tolower(reference_assembly), sep = ""), aln_library$comparison) & grepl(tolower
(query_assembly), aln_library$comparison),]
head(aln_subset, 3)
```

```
##               rs        re     qs     qe error                qid        rid
## 110088 398797814 398831949    527  34667   454 par_scaffold_000027 chr5B__lac
## 210074 398846085 398881400  48451  83752   257 par_scaffold_000027 chr5B__lac
## 310044 398885774 398923047 104871 142145   268 par_scaffold_000027 chr5B__lac
##        strand r_length  perc_id perc_id_factor     r_mid    q_mid
## 110088      +    34135 98.66999           <100 398814882  17597.0
## 210074      +    35315 99.27226           <100 398863743  66101.5
## 310044      +    37273 99.28098           <100 398904411 123508.0
##                                    comparison chrom
## 110088 lancer_v_paragon.5B_filtered_L20Kb_rq.delta    5B
## 210074 lancer_v_paragon.5B_filtered_L20Kb_rq.delta    5B
## 310044 lancer_v_paragon.5B_filtered_L20Kb_rq.delta    5B
```

Description of the column headers: rs: reference start, re: reference end, qs: query start, qe: query end, error: number of unmatches, qid: query identification, rid: reference identification, strand: forward or reverse strand, r_length: length of the alignment in the reference, perc_id: percentage of identity, perc_id_factor: factor that summarises perc_id, r_mid: midpoint the alignment in reference ((r_end-r_start)/2), q_mid: query midpoint, comparison: assemblies compared, chrom: chromosome.

1.1.5. Scatter-plot the alignment midpoints (X: r_mid, Y: q_mid)

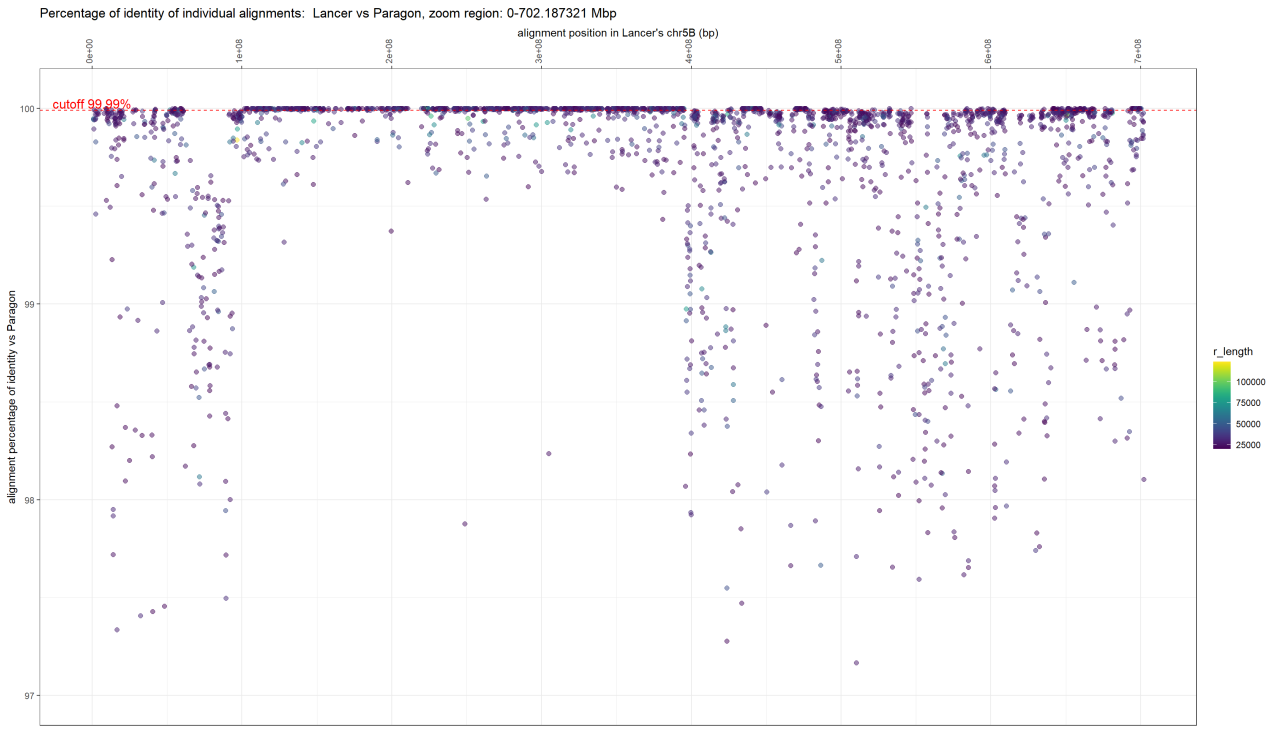
```
plot_diagonal_scatterplot(aln_subset, cap_lower = 90.00, cap_upper = 100, reference_name = reference_assembly, query_name =
 query_assembly , x_label_gap = 100000000)
```



Notice unexpected vertical lines in the scatter-plot due to the use of a scaffold-level assembly as query (CLA-SLA comparison). However, this function works well for CLA-CLA comparisons.

1.1.6. Dot-plot the alignments to show percentage of identity and alignment length (X: r_mid, Y: perc_id)

```
plot_aln_pid_and_length(aln_subset, reference_name = reference_assembly, query_name = query_assembly , x_label_gap = 1000000
00, dot_size = 2)
```



1.1.7. Check for alignment properties in the data frame (percentage of alignment coverage of reference chromosome, average aln length and av aln number)

Chromosome length

```
table_chrlength_v_assembly <- read.table(file = "table_assembly_chr_length.txt", sep = "\t", header = TRUE)
chr_length <- table_chrlength_v_assembly$sequence_length[grepl(tolower(reference_assembly), table_chrlength_v_assembly$assembly_name) & grepl(paste0("chr", unique(aln_subset$chrom)), table_chrlength_v_assembly$sequence_name)]
print(paste0("chr", unique(aln_subset$chrom), " is ", chr_length, " bp-long in ", reference_assembly))
```

```
## [1] "chr5B is 702438406 bp-long in Lancer"
```

Average alignment length in this pairwise comparison

```
print(paste0(round(mean(aln_subset$r_length), 0), " is the average alignment length in ", reference_assembly, "-", query_assembly, paste0(" chr", unique(aln_subset$chrom)), " comparison"))
```

```
## [1] "30858 is the average alignment length in Lancer-Paragon chr5B comparison"
```

Number of alignments in this pairwise comparison

```
print(paste0(nrow(aln_subset), " is the number of alignments in ", reference_assembly, "-", query_assembly, paste0(" chr", unique(aln_subset$chrom)), " comparison"))
```

```
## [1] "2650 is the number of alignments in Lancer-Paragon chr5B comparison"
```

Alignment coverage in this pairwise comparison

```
print(paste0(round((sum(aln_subset$r_length)/chr_length*100), 0), "% is the alignment coverage in ", reference_assembly, "-", query_assembly, paste0(" chr", unique(aln_subset$chrom)), " comparison"))
```

```
## [1] "12% is the alignment coverage in Lancer-Paragon chr5B comparison"
```

Alignment coverage overview in different comparisons by reference assembly and comparison type (with/without scaffold-level assemblies)

```
coverage <- COV(aln_library, chr_length = table_chrlength_v_assembly)
print(coverage)
```

```
## $`Average % coverage with CHROMOSOME-LEVEL ASSEMBLIES as query`
## [1] 47.74529
##
## $`(By assembly)`
## arinalrfor     jagger     julius     lancer   landmark       mace    norin61
##   28.44218   50.59484   51.33529   55.81078   50.99109   55.28362   53.99118
##    stanley  sy_mattis    chinese
##   51.89199   28.44447   50.66749
##
## $`Average % coverage with SCAFFOLD-LEVEL ASSEMBLIES as query`
## [1] 9.390724
##
## $`(By assembly)`
## arinalrfor     jagger     julius     lancer   landmark       mace    norin61
##   4.216677  10.113839  10.478023  12.165450   9.566494  11.940812  11.252819
##    stanley  sy_mattis    chinese
##  10.103706   4.302350   9.767073
```

Average alignment length overview in different comparisons by reference assembly and comparison type (with/without scaffold-level assemblies)

```
length <- LENGTH(aln_library)
print(length)
```

```
## $`Average aln length with CHROMOSOME-LEVEL ASSEMBLIES as query`
## [1] 45635.03
##
## $`(By assembly)`
## arinalrfor     jagger     julius     lancer   landmark       mace    norin61
##   50573.98   42245.55   43894.80   46985.47   42621.59   46726.19   45787.59
##    stanley  sy_mattis    chinese
##   44081.69   50841.05   42592.41
##
## $`Average aln length with SCAFFOLD-LEVEL ASSEMBLIES as query`
## [1] 30425.71
##
## $`(By assembly)`
## arinalrfor     jagger     julius     lancer   landmark       mace    norin61
##   31092.67   29791.85   30193.23   31045.12   29593.04   30915.88   30557.44
##    stanley  sy_mattis    chinese
##   29983.10   31462.44   29622.29
```

Average number of alignments overview in different comparisons by reference assembly and comparison type (with/without scaffold-level assemblies)

```
number <- NUMBER(aln_library)
print(number)
```

```
## $`Average aln number with CHROMOSOME-LEVEL ASSEMBLIES as query`
## [1] 7253.244
##
## $`(By assembly)`
## arinalrfor     jagger     julius     lancer   landmark       mace    norin61
##   2703.778   8426.556   8480.333   8343.778   8500.111   8172.778   8399.667
##    stanley  sy_mattis    chinese
##   8404.222   2617.667   8483.556
##
## $`Average aln number with SCAFFOLD-LEVEL ASSEMBLIES as query`
## [1] 2129.46
##
## $`(By assembly)`
## arinalrfor     jagger     julius     lancer   landmark       mace    norin61
##      652.0     2388.6     2516.4     2752.6     2296.8     2668.0     2623.2
##    stanley  sy_mattis    chinese
##     2405.8      639.8     2351.4
```

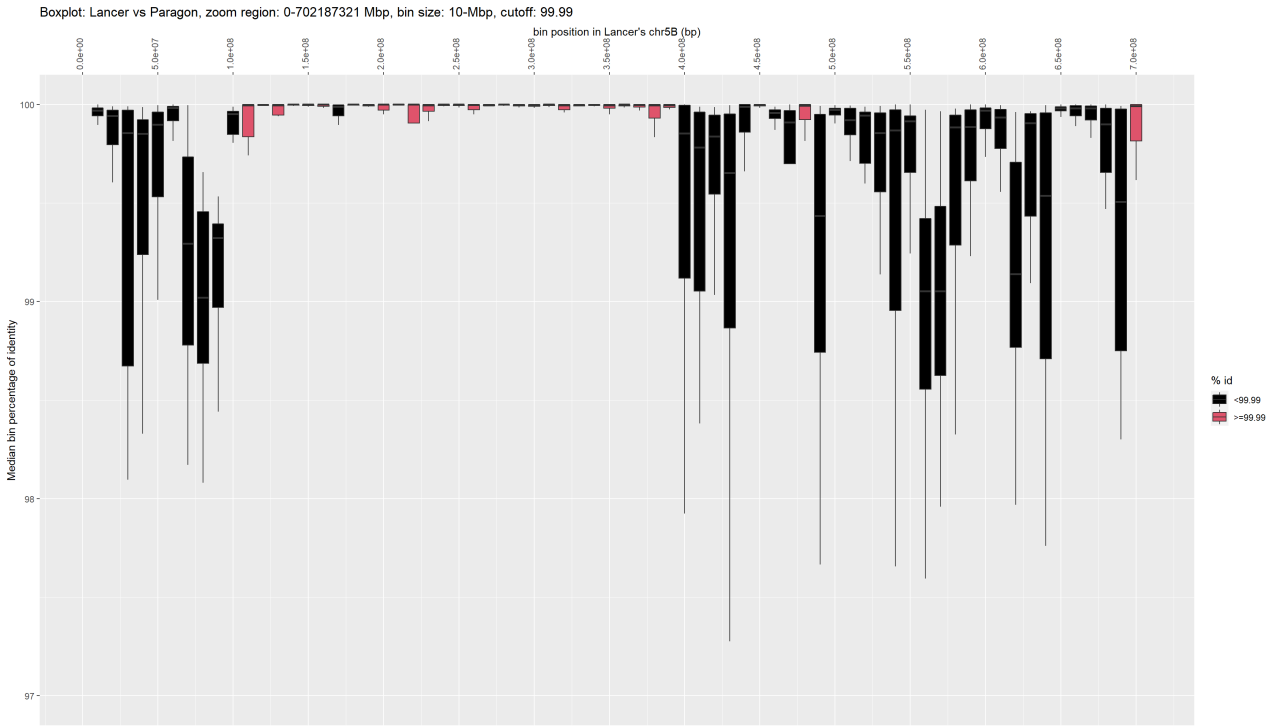
Expected number of alignments per bin in this pairwise comparison at different bin sizes

```
bin_size <- c(5000000, 2500000, 1000000)
names(bin_size) <- c("bin size: 5-Mbp", "bin size: 2.5-Mbp", "bin size: 1-Mbp")
for (i in 1:3){
  print("average expected number of alignments per bin across the chromosome")
  print(round(nrow(aln_subset)/(chr_length/bin_size[i]), 1))
}
```

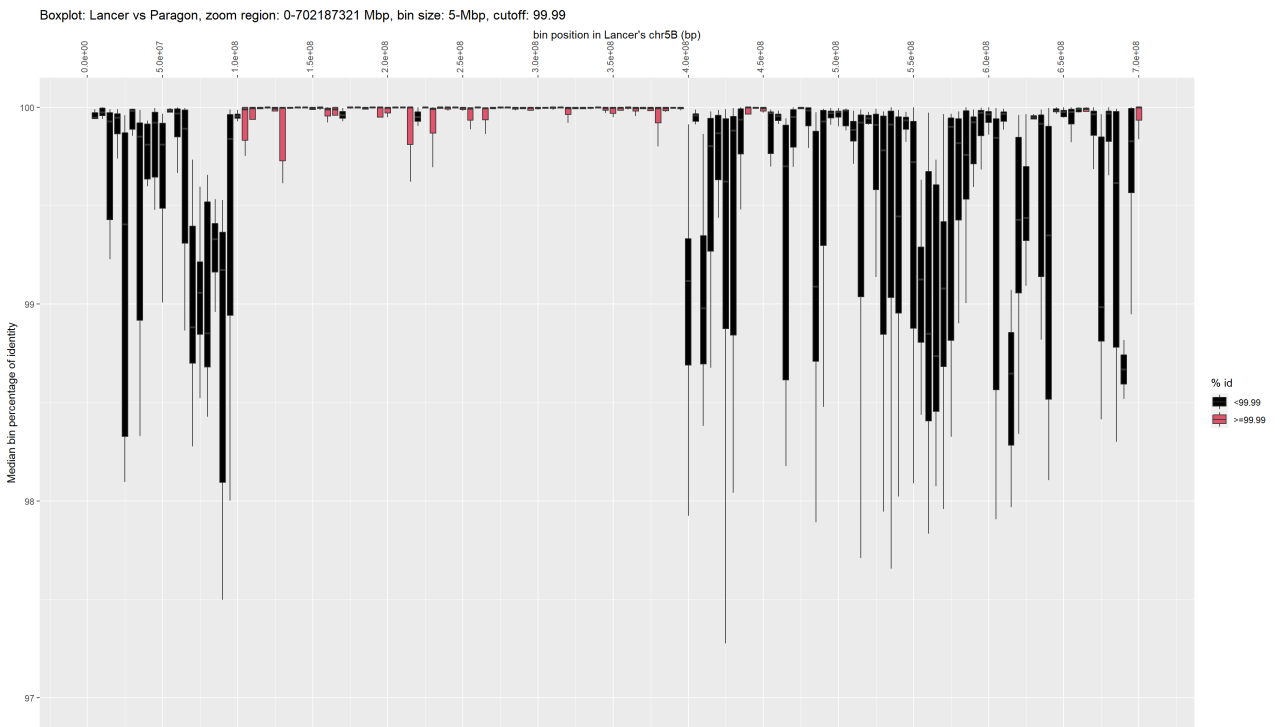
```
## [1] "average expected number of alignments per bin across the chromosome"
## bin size: 5-Mbp
##           18.9
## [1] "average expected number of alignments per bin across the chromosome"
## bin size: 2.5-Mbp
##              9.4
## [1] "average expected number of alignments per bin across the chromosome"
## bin size: 1-Mbp
##            3.8
```

1.1.8. Boxplot the alignments (X: bin, Y: perc_id_median)

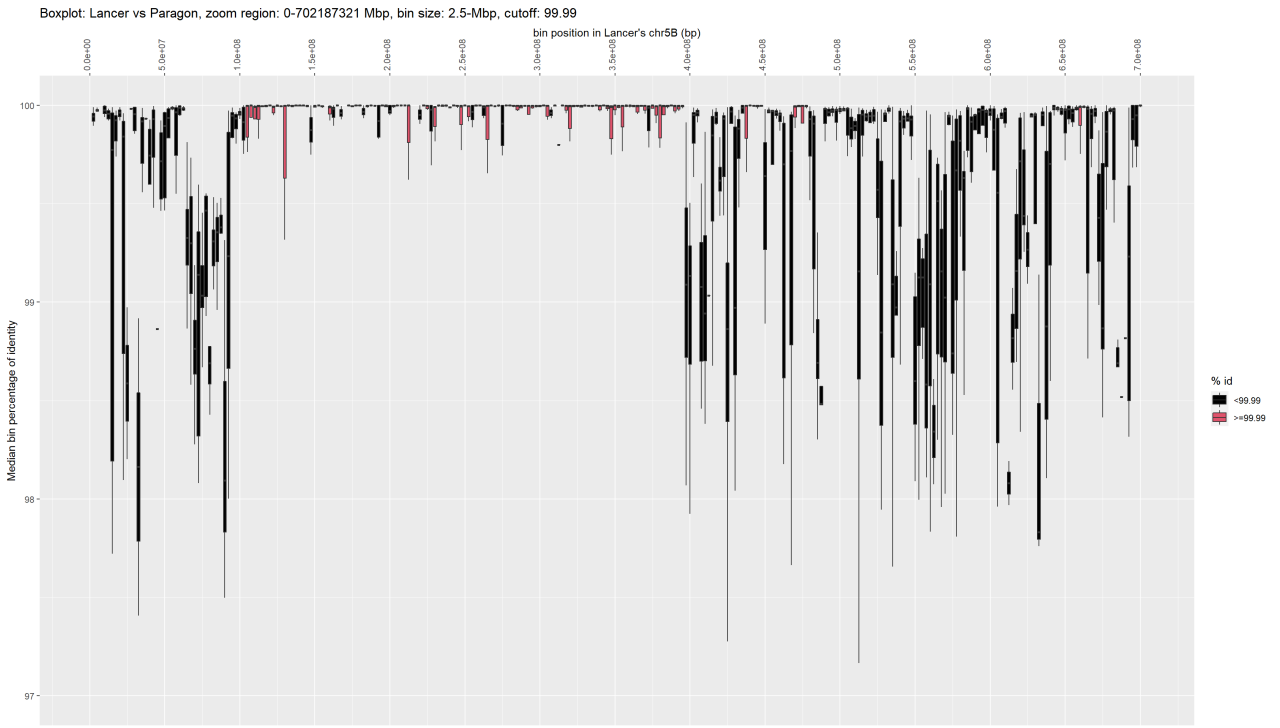
```
plot_boxplots_bin_median(aln_subset, bin_size = 10000000, bin_start = 0, bin_end = max(aln_subset$re), cut_off = 99.99, refe
rence_name = reference_assembly, query_name = query_assembly , x_label_gap = 50000000, show_outliers = FALSE)
```



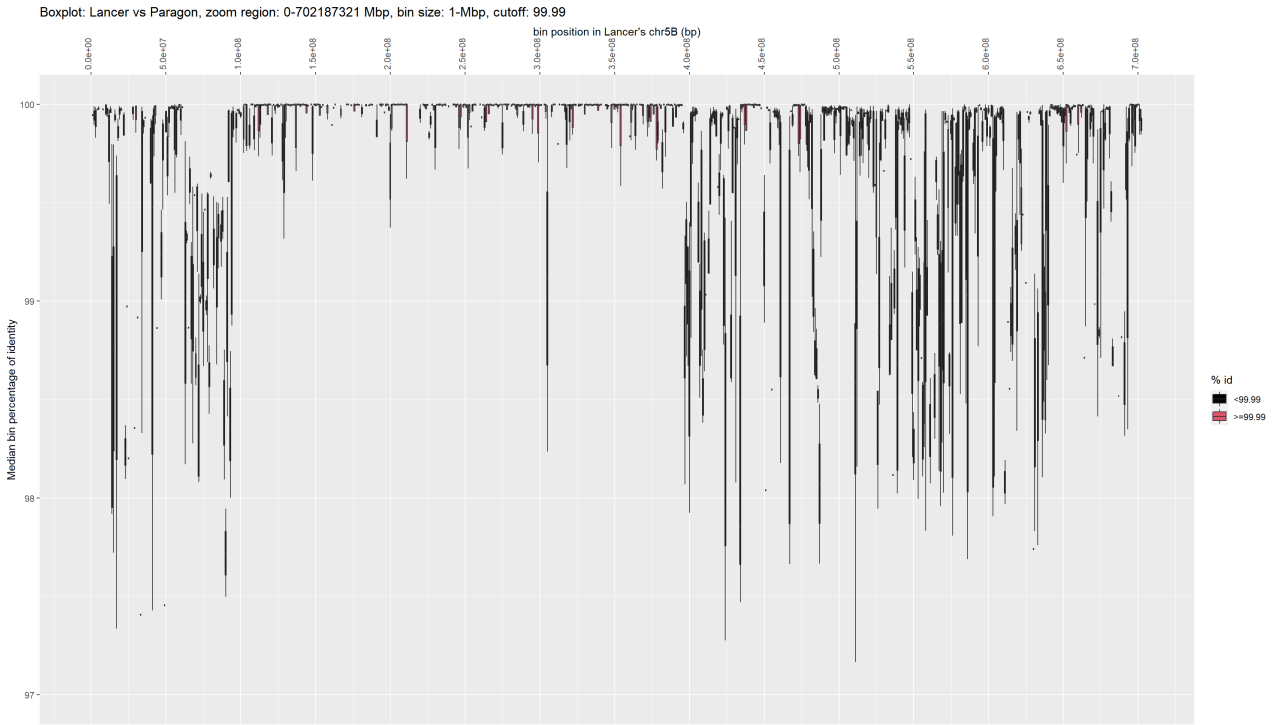

```
plot_boxplots_bin_median(aln_subset, bin_size = 5000000, bin_start = 0, bin_end = max(aln_subset$re), cut_off = 99.99, refer
ence_name = reference_assembly, query_name = query_assembly , x_label_gap = 50000000, show_outliers = FALSE)
```




```
plot_boxplots_bin_median(aln_subset, bin_size = 2500000, bin_start = 0, bin_end = max(aln_subset$re), cut_off = 99.99, refer
ence_name = reference_assembly, query_name = query_assembly , x_label_gap = 50000000, show_outliers = FALSE)
```

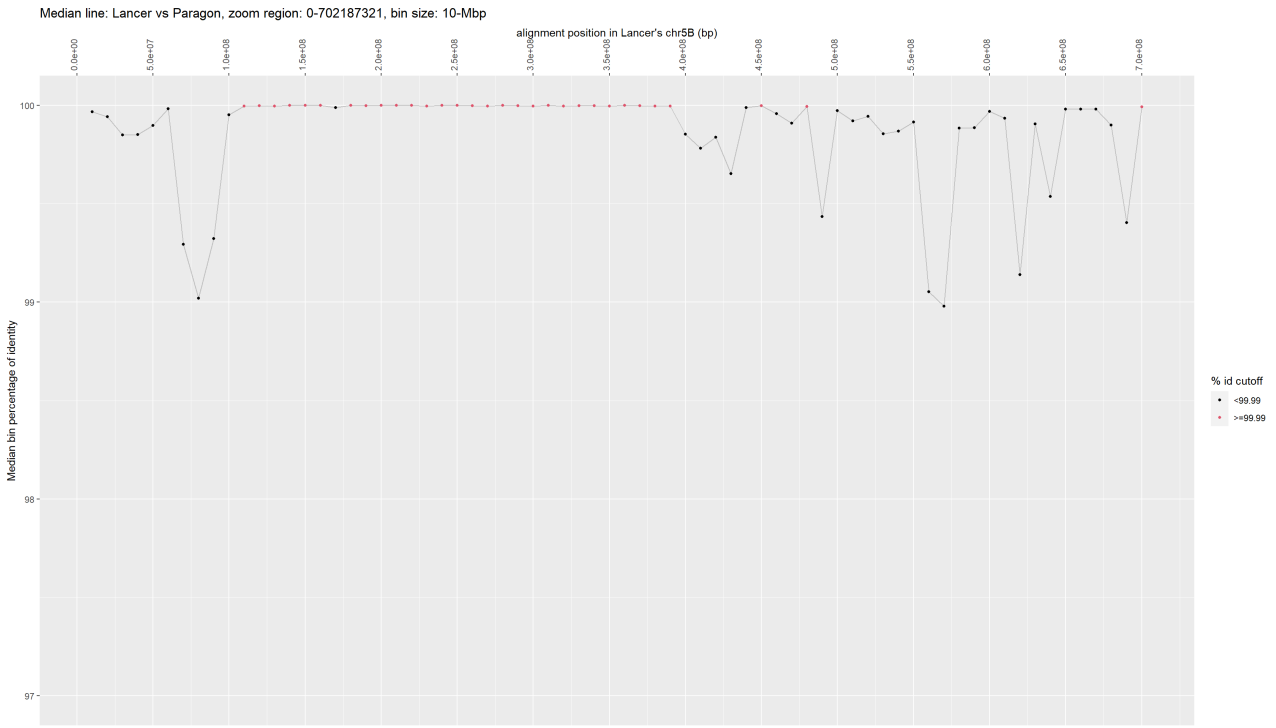



```
plot_boxplots_bin_median(aln_subset, bin_size = 1000000, bin_start = 0, bin_end = max(aln_subset$re), cut_off = 99.99, refer
ence_name = reference_assembly, query_name = query_assembly , x_label_gap = 50000000, show_outliers = FALSE)
```

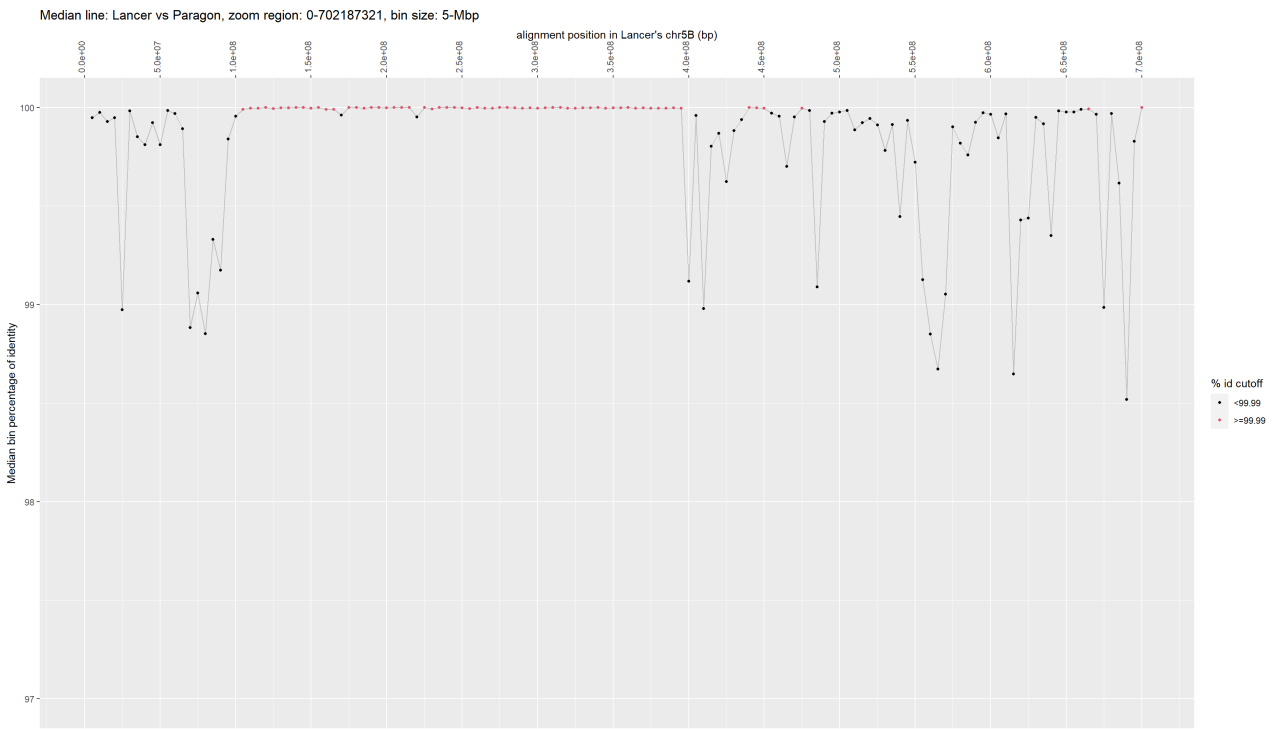


1.1.9. Plot the median percentage of identity across the chromosome or median line (X: r_mid, Y: perc_id_median)

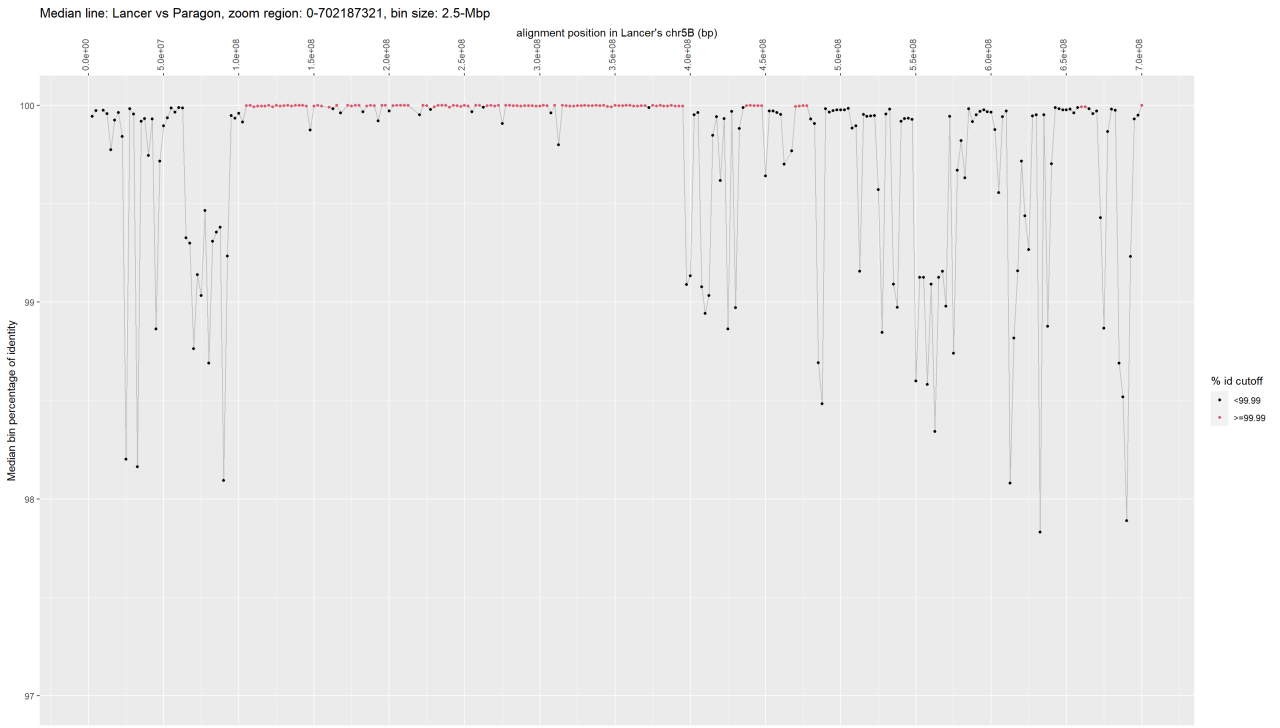
```
medians_aln_subset_10Mbp <- plot_line_bin_median(aln_subset, bin_size = 10000000, bin_start = 0, bin_end = max(aln_subset$r
e), cut_off = 99.99, reference_name = reference_assembly, query_name = query_assembly , x_label_gap = 50000000)
medians_aln_subset_10Mbp
```



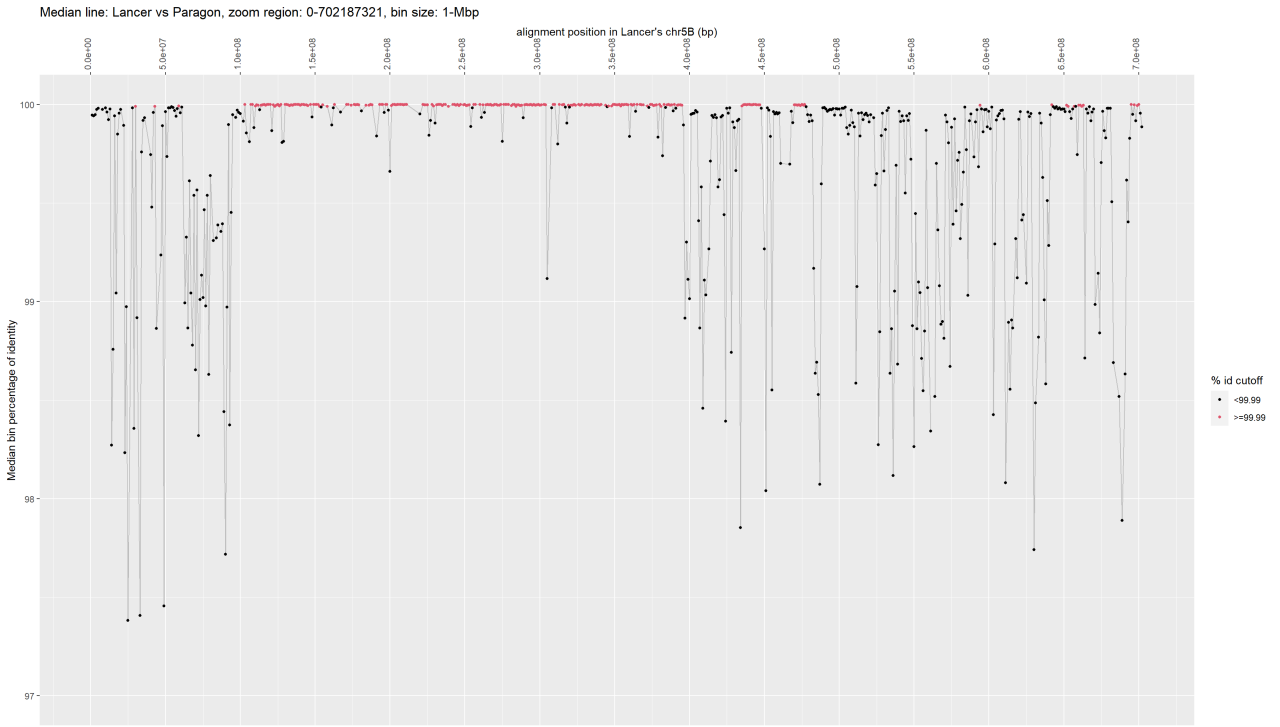

```
medians_aln_subset_5Mbp <- plot_line_bin_median(aln_subset, bin_size = 5000000, bin_start = 0, bin_end = max(aln_subset$re), cut_off = 99.99, reference_name = reference_assembly, query_name = query_assembly , x_label_gap = 50000000)
medians_aln_subset_5Mbp
```




```
medians_aln_subset_2.5Mbp <- plot_line_bin_median(aln_subset, bin_size = 2500000, bin_start = 0, bin_end = max(aln_subset$re), cut_off = 99.99, reference_name = reference_assembly, query_name = query_assembly , x_label_gap = 50000000)
medians_aln_subset_2.5Mbp
```




```
medians_aln_subset_1Mbp <- plot_line_bin_median(aln_subset, bin_size = 1000000, bin_start = 0, bin_end = max(aln_subset$re),
cut_off = 99.99, reference_name = reference_assembly, query_name = query_assembly , x_label_gap = 50000000)
medians_aln_subset_1Mbp
```



1.1.10. Print information about the haploblock predictions in the pairwise comparison across the reference chromosome

```
medians_aln_subset_10Mbp_bin_info <- assign_blocks_mummer(median_cutoffs = medians_aln_subset_10Mbp[["data"]], original_file
= aln_subset)
medians_aln_subset_5Mbp_bin_info <- assign_blocks_mummer(median_cutoffs = medians_aln_subset_5Mbp[["data"]], original_file =
aln_subset)
medians_aln_subset_2.5Mbp_bin_info <- assign_blocks_mummer(median_cutoffs = medians_aln_subset_2.5Mbp[["data"]], original_fi
le = aln_subset)
medians_aln_subset_1Mbp_bin_info <- assign_blocks_mummer(median_cutoffs = medians_aln_subset_1Mbp[["data"]], original_file =
aln_subset)
medians_aln_subset_10Mbp_block_summary <- block_summary(medians_aln_subset_10Mbp_bin_info, bin_size = 10000000, reference_na
me = reference_assembly, query_name = query_assembly )
medians_aln_subset_5Mbp_block_summary <- block_summary(medians_aln_subset_5Mbp_bin_info, bin_size = 5000000, reference_name
 = reference_assembly, query_name = query_assembly )
medians_aln_subset_2.5Mbp_block_summary <- block_summary(medians_aln_subset_2.5Mbp_bin_info, bin_size = 2500000, reference_n
ame = reference_assembly, query_name = query_assembly )
medians_aln_subset_1Mbp_block_summary <- block_summary(medians_aln_subset_1Mbp_bin_info, bin_size = 1000000, reference_name
 = reference_assembly, query_name = query_assembly )
print(medians_aln_subset_10Mbp_block_summary)
```

```
##   bin_size      comparison block_no block_start block_end
## 1   10-Mbp Lancer->Paragon        1     1.0e+08   3.9e+08
## 2   10-Mbp Lancer->Paragon        2     4.4e+08   4.8e+08
## 3   10-Mbp Lancer->Paragon        3     6.9e+08   7.0e+08
```

```
print(medians_aln_subset_5Mbp_block_summary)
```

```
##   bin_size      comparison block_no block_start block_end
## 1    5-Mbp Lancer->Paragon        1    1.00e+08  3.95e+08
## 2    5-Mbp Lancer->Paragon        2    4.35e+08  4.50e+08
## 3    5-Mbp Lancer->Paragon        3    4.70e+08  4.75e+08
## 4    5-Mbp Lancer->Paragon        4    6.60e+08  6.65e+08
## 5    5-Mbp Lancer->Paragon        5    6.95e+08  7.00e+08
```

```
print(medians_aln_subset_2.5Mbp_block_summary)
```

```
##   bin_size      comparison block_no block_start block_end
## 1  2.5-Mbp Lancer->Paragon        1   102500000 395000000
## 2  2.5-Mbp Lancer->Paragon        2   435000000 447500000
## 3  2.5-Mbp Lancer->Paragon        3   467500000 477500000
## 4  2.5-Mbp Lancer->Paragon        4   657500000 662500000
## 5  2.5-Mbp Lancer->Paragon        5   697500000 700000000
```

```
print(medians_aln_subset_1Mbp_block_summary)
```

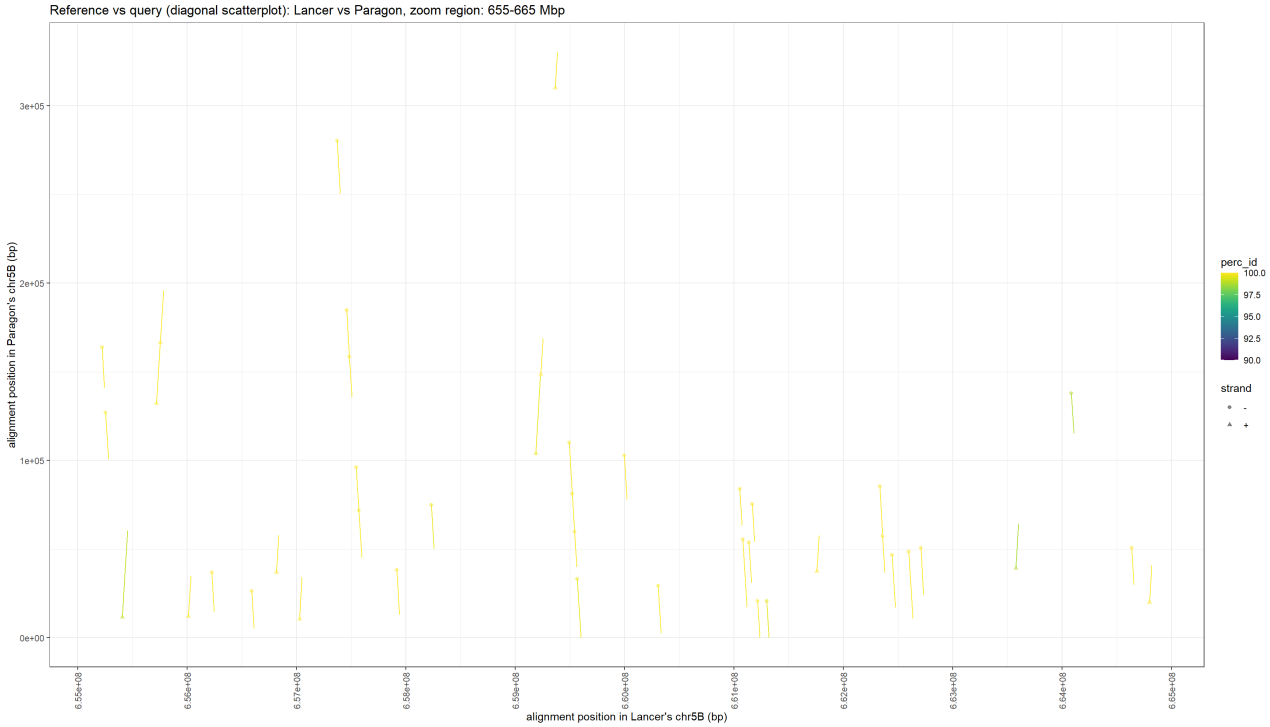
```
##    bin_size      comparison block_no block_start block_end
## 1     1-Mbp Lancer->Paragon        1    2.90e+07  3.00e+07
## 2     1-Mbp Lancer->Paragon        2    4.20e+07  4.30e+07
## 3     1-Mbp Lancer->Paragon        3    5.80e+07  5.90e+07
## 4     1-Mbp Lancer->Paragon        4    1.02e+08  3.95e+08
## 5     1-Mbp Lancer->Paragon        5    4.34e+08  4.47e+08
## 6     1-Mbp Lancer->Paragon        6    4.69e+08  4.77e+08
## 7     1-Mbp Lancer->Paragon        7    5.93e+08  5.94e+08
## 8     1-Mbp Lancer->Paragon        8    6.41e+08  6.42e+08
## 9     1-Mbp Lancer->Paragon        9    6.51e+08  6.53e+08
## 10    1-Mbp Lancer->Paragon       10    6.56e+08  6.63e+08
## 11    1-Mbp Lancer->Paragon       11    6.94e+08  7.00e+08
```

Block number 10 reveals the haplotype prediction obtained at crop-haplotypes.com at 1-Mbp bin size between Lancer and Paragon that could match with the SNP-based haplotype discovered previously. This information can be contrasted with other haplotypes shared between Lancer and Paragon graphically with different graphs (boxplot, median line…) back in this script.

1.2. Small-scale analysis

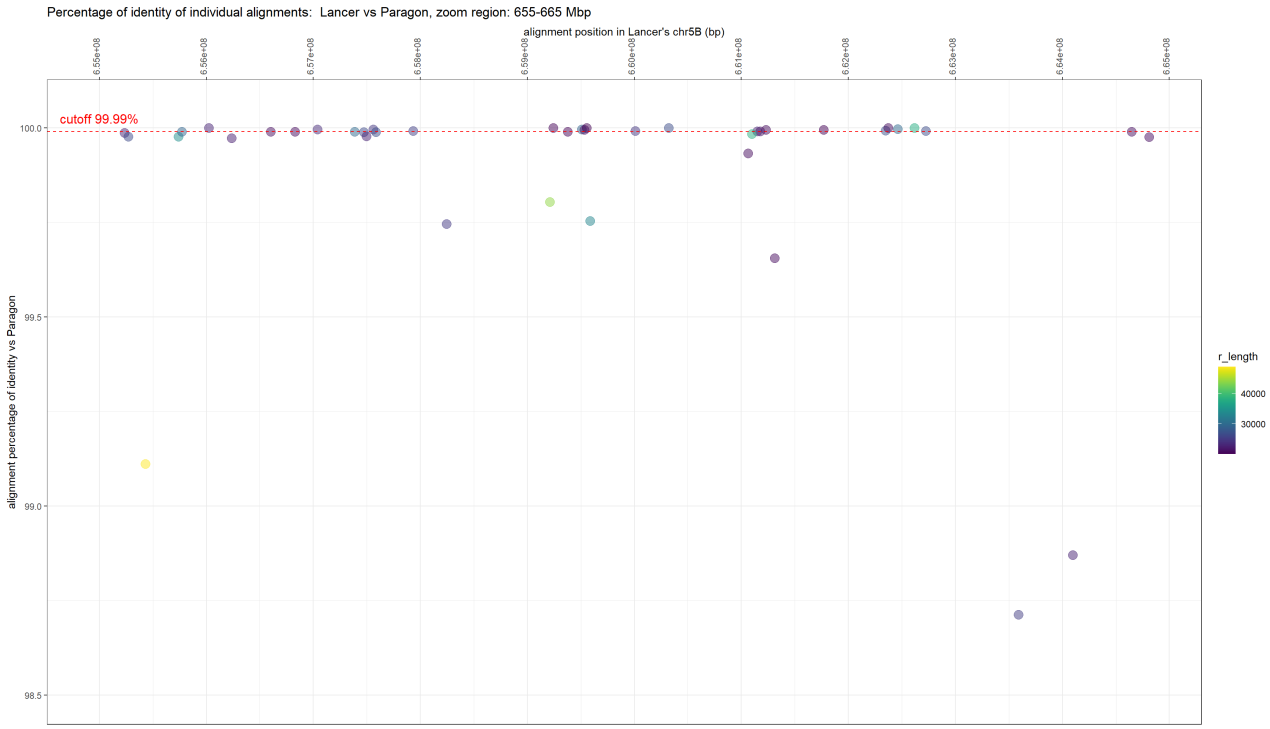
1.2.1. Scatter-plot the alignment midpoints across the zoom region (X: r_mid, Y: q_mid)

```
plot_diagonal_scatterplot(aln_subset, xmin = zoom_start, xmax = zoom_end, cap_lower = 90.00, cap_upper = 100, reference_name
= reference_assembly, query_name = query_assembly , x_label_gap = 1000000)
```



1.2.2. Dot-plot the alignments to show percentage of identity and alignment length in the zoom region (X: r_mid, Y: perc_id)

```
graph <- plot_aln_pid_and_length(data = aln_subset, xmin = zoom_start, xmax = zoom_end, ymin = 98.5, reference_name = refere
nce_assembly, query_name = query_assembly , x_label_gap = 1000000, dot_size = 4)
graph
```



1.2.3. Check for alignment properties in the zoom region

Average alignment length in the target region

```
aln_target <- aln_subset[(aln_subset$r_mid >= target_start) & (aln_subset$r_mid <= target_end),]
print(paste0(round(mean(aln_target$r_length), 0), " is the average alignment length for the target region between ", target_
start/1e06, " and ", target_end/1e06, " Mbp in ", reference_assembly, "-", query_assembly, paste0(" chr", unique(aln_target
$chrom)), " comparison"))
```

```
## [1] "27206 is the average alignment length for the target region between 655.7 and 656.6 Mbp in Lancer-Paragon chr5B comp
arison"
```

Number of alignments in the target region

```
print(paste0(nrow(aln_target), " is the number of alignments for the target region between ", target_start/1e06, " and ", ta
rget_end/1e06, " Mbp in ", reference_assembly, "-", query_assembly, paste0(" chr", unique(aln_target$chrom)), " comparison"
))
```

```
## [1] "4 is the number of alignments for the target region between 655.7 and 656.6 Mbp in Lancer-Paragon chr5B comparison"
```

Alignment coverage in the target region

```
print(paste0(round((sum(aln_target$r_length)/(target_end-target_start)*100), 0), "% is the alignment coverage for the target
region between ", target_start/1e06, " and ", target_end/1e06, " Mbp in ", reference_assembly, "-", query_assembly, paste0("
chr", unique(aln_target$chrom)), " comparison") )
```

```
## [1] "12% is the alignment coverage for the target region between 655.7 and 656.6 Mbp in Lancer-Paragon chr5B comparison"
```

Average alignment length in the zoom region

```
aln_zoom <- aln_subset[(aln_subset$r_mid >= zoom_start) & (aln_subset$r_mid <= zoom_end),]
print(paste0(round(mean(aln_zoom$r_length), 0), " is the average alignment length for the zoom region between ", zoom_start/
1e06, " and ", zoom_end/1e06, " Mbp in ", reference_assembly, "-", query_assembly, paste0(" chr", unique(aln_subset$chrom)),
" comparison"))
```

```
## [1] "25963 is the average alignment length for the zoom region between 655 and 665 Mbp in Lancer-Paragon chr5B compariso
n"
```

Number of alignments in the zoom region

```
print(paste0(nrow(aln_zoom), " is the number of alignments for the zoom region between ", zoom_start/1e06, " and ", zoom_en
d/1e06, " Mbp in ", reference_assembly, "-", query_assembly, paste0(" chr", unique(aln_subset$chrom)), " comparison"))
```

```
## [1] "42 is the number of alignments for the zoom region between 655 and 665 Mbp in Lancer-Paragon chr5B comparison"
```

Alignment coverage in the zoom region

```
print(paste0(round((sum(aln_zoom$r_length)/(zoom_end-zoom_start)*100), 0), "% is the alignment coverage for the zoom region
 between ", zoom_start/1e06, " and ", zoom_end/1e06, " Mbp in ", reference_assembly, "-", query_assembly, paste0(" chr", uni
que(aln_subset$chrom)), " comparison"))
```

```
## [1] "11% is the alignment coverage for the zoom region between 655 and 665 Mbp in Lancer-Paragon chr5B comparison"
```

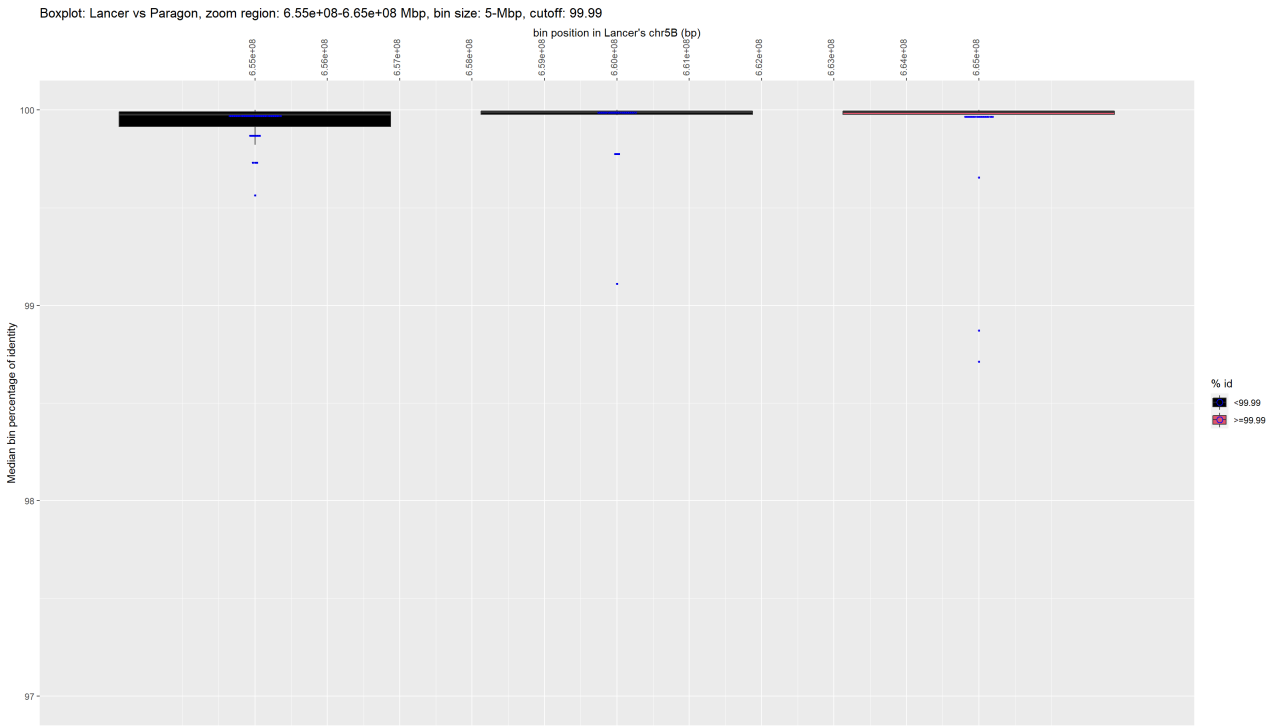
Expected number of alignments per bin across the zoom region

```
bin_size <- c(5000000, 2500000, 1000000)
names(bin_size) <- c("bin size: 5-Mbp", "bin size: 2.5-Mbp", "bin size: 1-Mbp")
for (i in 1:3){
  print("average expected number of alignments per bin across zoom region")
  print(nrow(aln_zoom)/((zoom_end-zoom_start)/bin_size[i]))
}
```

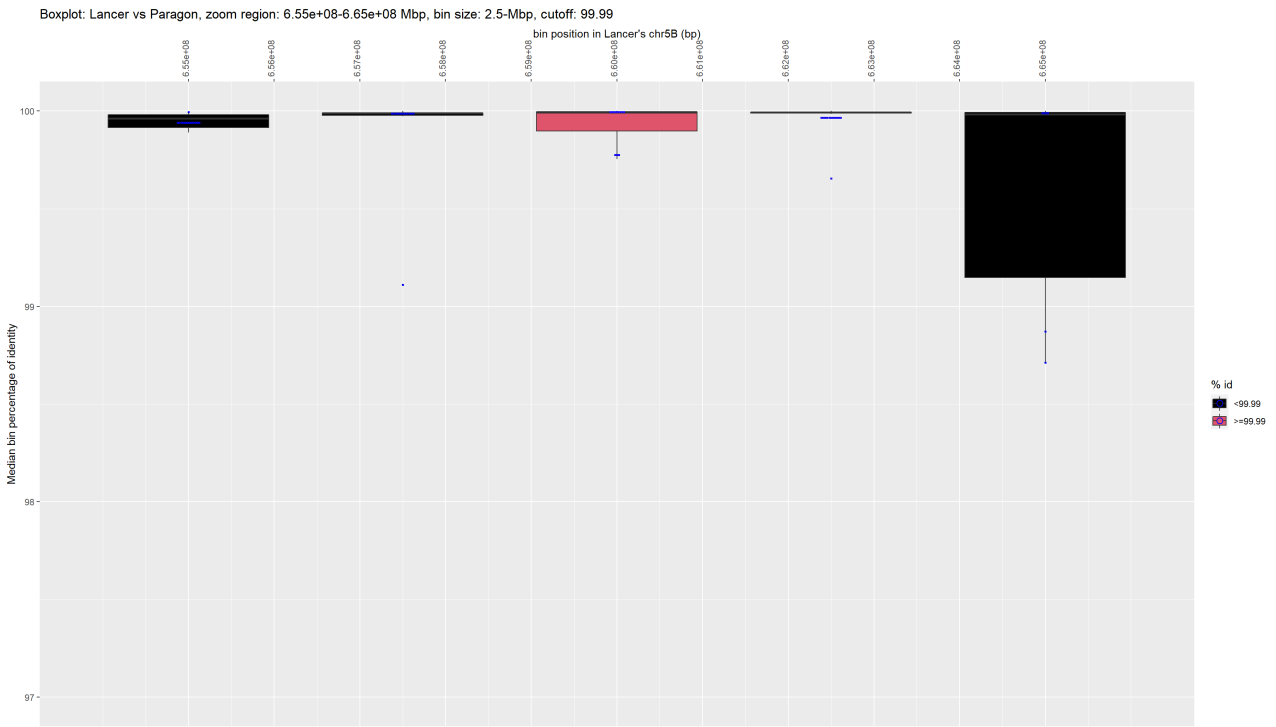
```
## [1] "average expected number of alignments per bin across zoom region"
## bin size: 5-Mbp
##              21
## [1] "average expected number of alignments per bin across zoom region"
## bin size: 2.5-Mbp
##              10.5
## [1] "average expected number of alignments per bin across zoom region"
## bin size: 1-Mbp
##             4.2
```

1.2.4. Boxplot the bin median percentage of identity in the zoom region to check for outliers

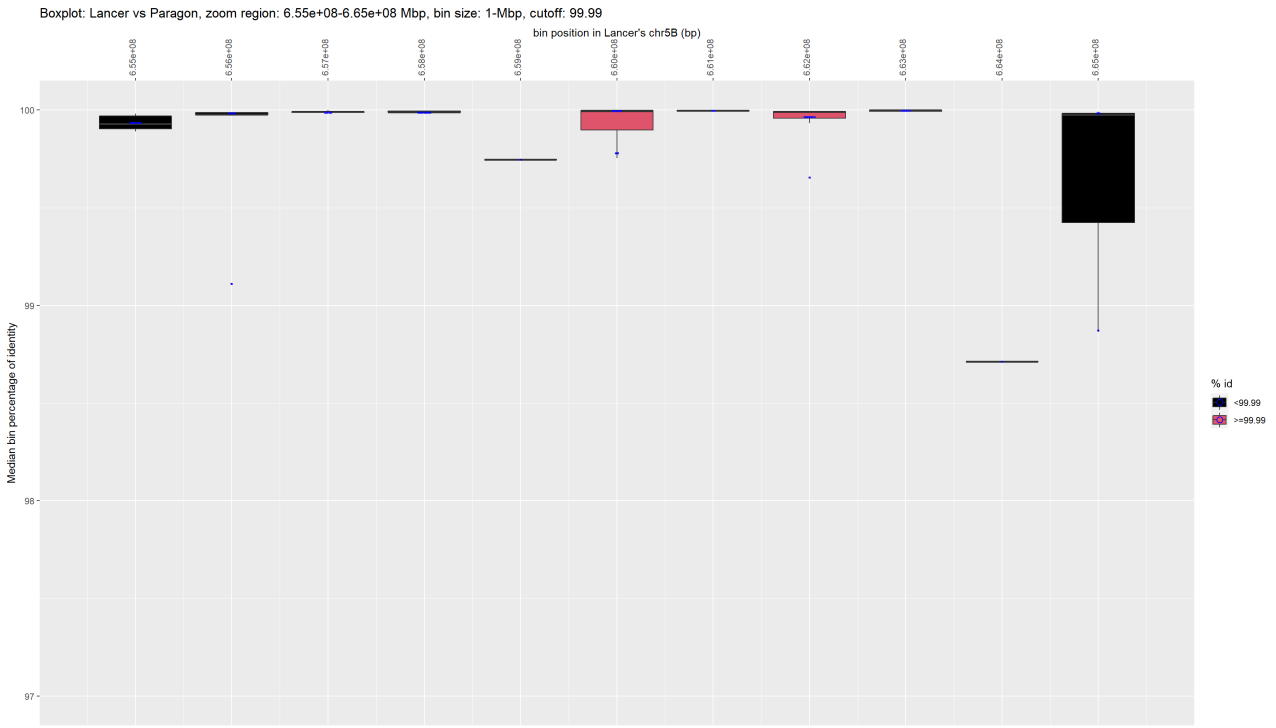
```
plot_boxplots_bin_median(aln_subset, bin_size = 5000000, bin_start = zoom_start, bin_end = zoom_end, cut_off = 99.99, refere
nce_name = reference_assembly, query_name = query_assembly , x_label_gap = 1000000, show_outliers = TRUE)
```




```
plot_boxplots_bin_median(aln_subset, bin_size = 2500000, bin_start = zoom_start, bin_end = zoom_end, cut_off = 99.99, refere
nce_name = reference_assembly, query_name = query_assembly , x_label_gap = 1000000, show_outliers = TRUE)
```

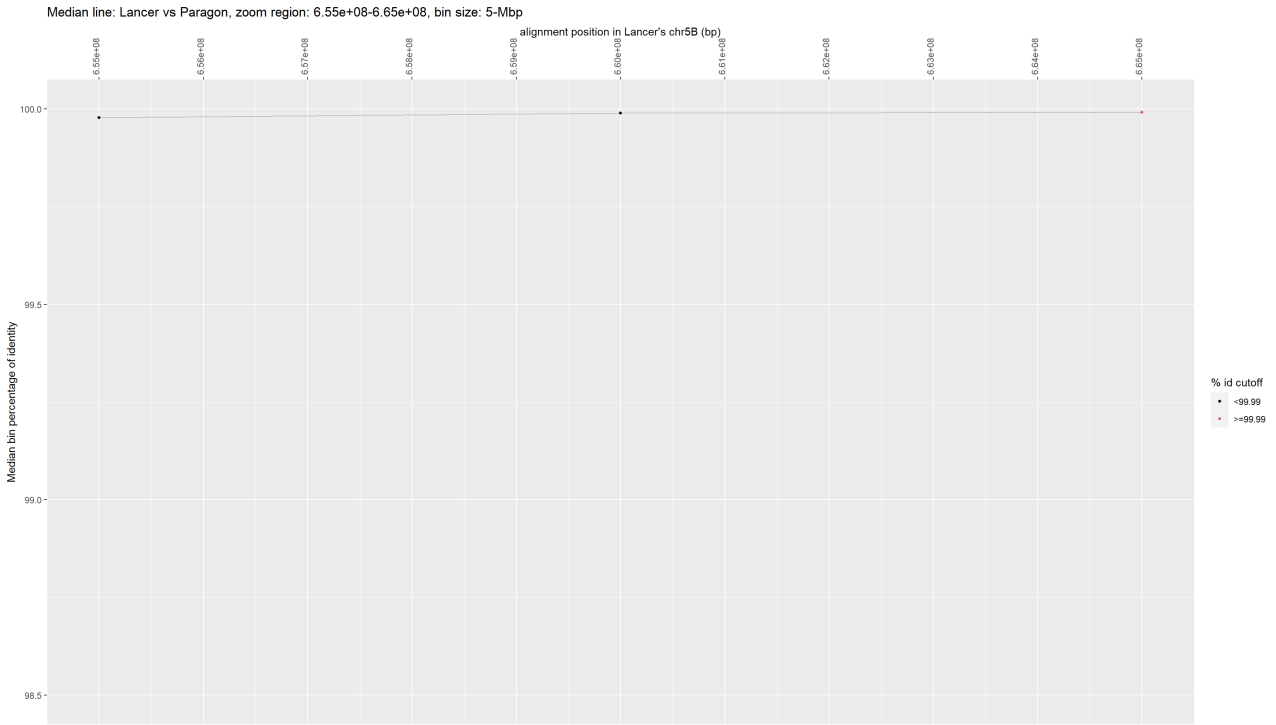



```
plot_boxplots_bin_median(aln_subset, bin_size = 1000000, bin_start = zoom_start, bin_end = zoom_end, cut_off = 99.99, refere
nce_name = reference_assembly, query_name = query_assembly , x_label_gap = 1000000, show_outliers = TRUE)
```

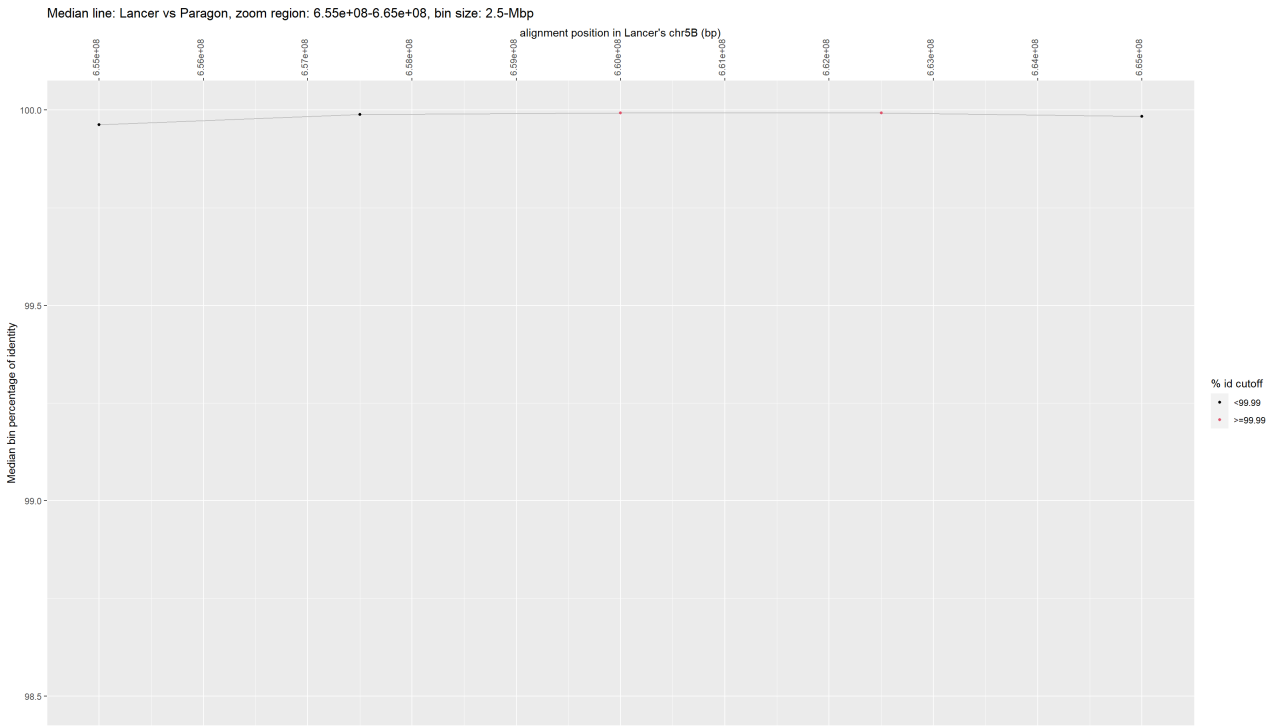


1.2.5. Plot the median line in the zoom region to see the haploblock predictions at different bin sizes

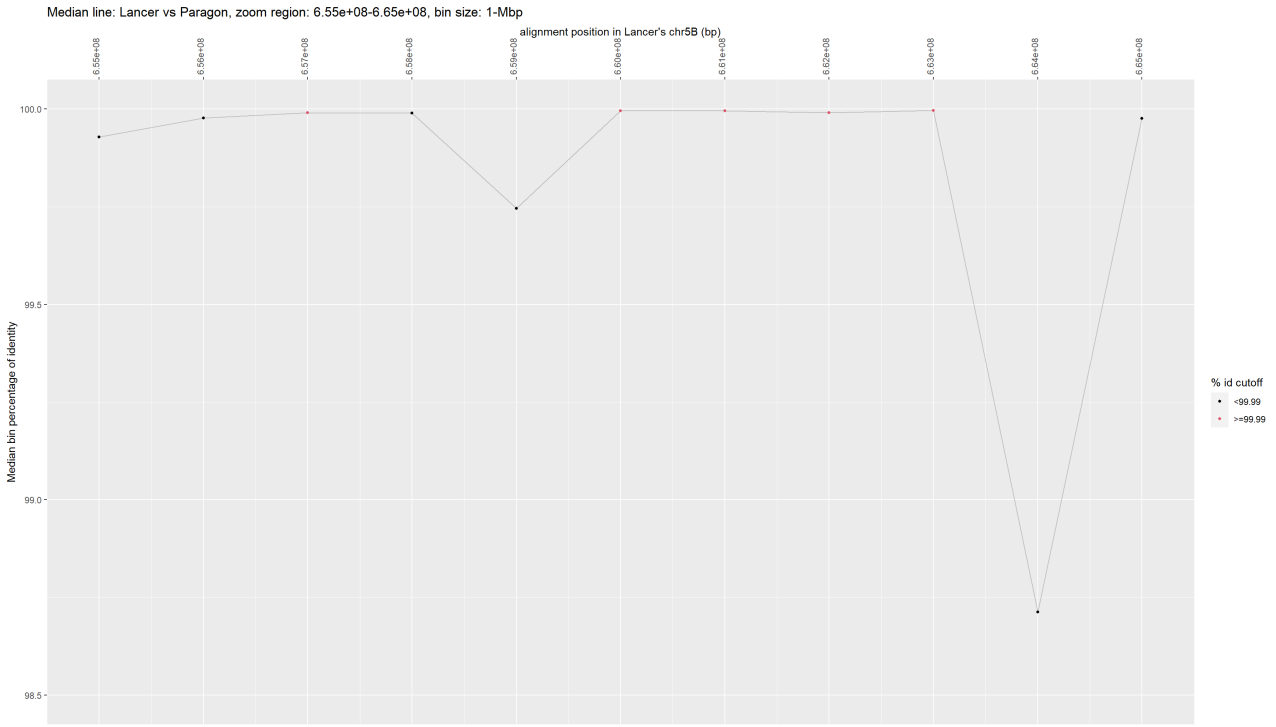
```
plot_line_bin_median(aln_subset, bin_size = 5000000, bin_start = zoom_start, bin_end = zoom_end, ymin = 98.5, cut_off = 99.99, reference_name = reference_assembly, query_name = query_assembly , x_label_gap = 1000000)
```




```
plot_line_bin_median(aln_subset, bin_size = 2500000, bin_start = zoom_start, bin_end = zoom_end, ymin = 98.5, cut_off = 99.99, reference_name = reference_assembly, query_name = query_assembly , x_label_gap = 1000000)
```



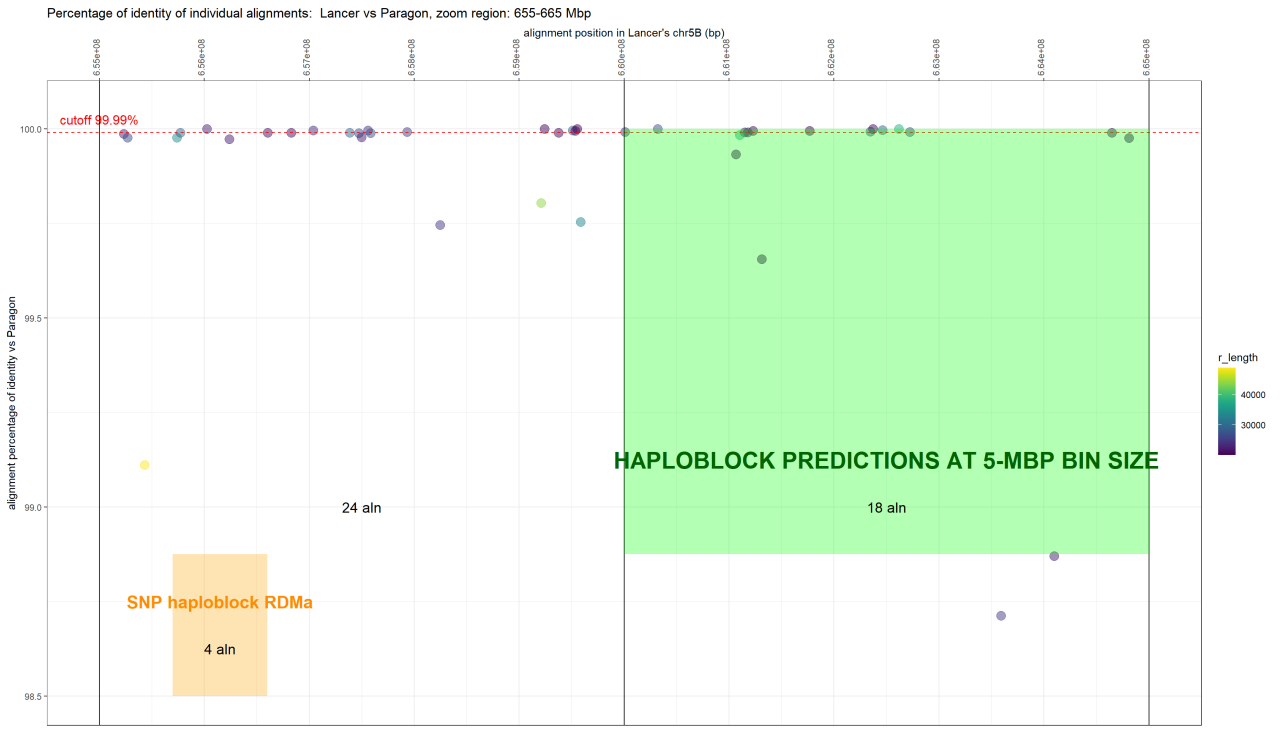

```
plot_line_bin_median(aln_subset, bin_size = 1000000, bin_start = zoom_start, bin_end = zoom_end, ymin = 98.5, cut_off = 99.9
9, reference_name = reference_assembly, query_name = query_assembly , x_label_gap = 1000000)
```



1.2.6. Dot-plot the zoom region with the haploblock predictions and the target region and make decisions regarding the start and end limits of the sequence-based haploblock

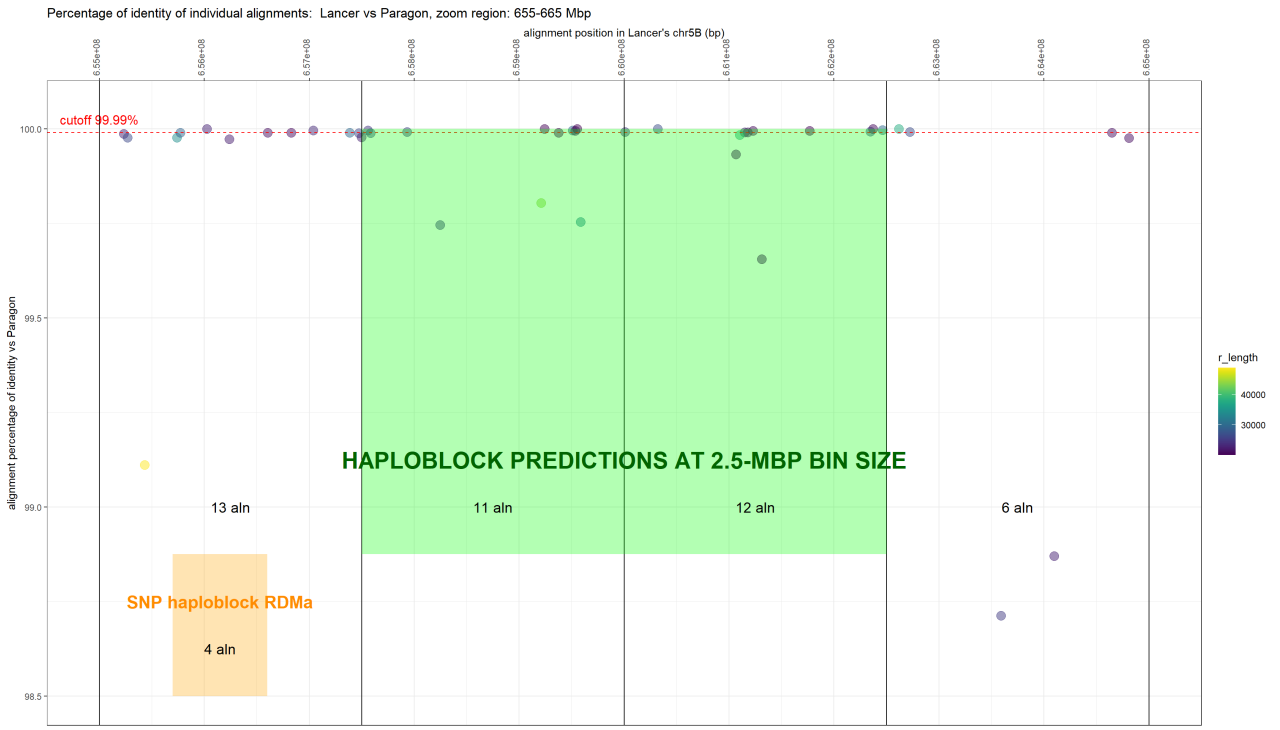
```
target <- data.frame(target_start, target_end)
plot_aln_and_bins(aln_subset = aln_subset, bin_size = 5000000, zoom_start = zoom_start, zoom_end = zoom_end, highlighted_tar
get = target, target_text = "SNP haploblock RDMa", fill_target = "orange", color_target_text = "darkorange", fill_prediction
s = "green", color_prediction_text = "darkgreen", ymin = 98.5, cut_off = 99.99, reference_name = reference_assembly, query_n
ame = query_assembly, dot_size = 4, x_label_gap = 1000000)
```

```
## [1] "BINS AT 5-MBP BIN SIZE"
##        bin perc_id_median cut_off block_no bin_start  bin_end aln_number
## 1 6.55e+08       99.97763  <99.99 NO_BLOCK  6.50e+08 6.55e+08         37
## 2 6.60e+08       99.98986  <99.99 NO_BLOCK  6.55e+08 6.60e+08         24
## 3 6.65e+08       99.99159 >=99.99        1  6.60e+08 6.65e+08         18
## [1] "BLOCK SUMMARY AT 5-MBP BIN SIZE"
##   bin_size      comparison block_no block_start block_end
## 1    5-Mbp Lancer->Paragon        1     6.6e+08  6.65e+08
```



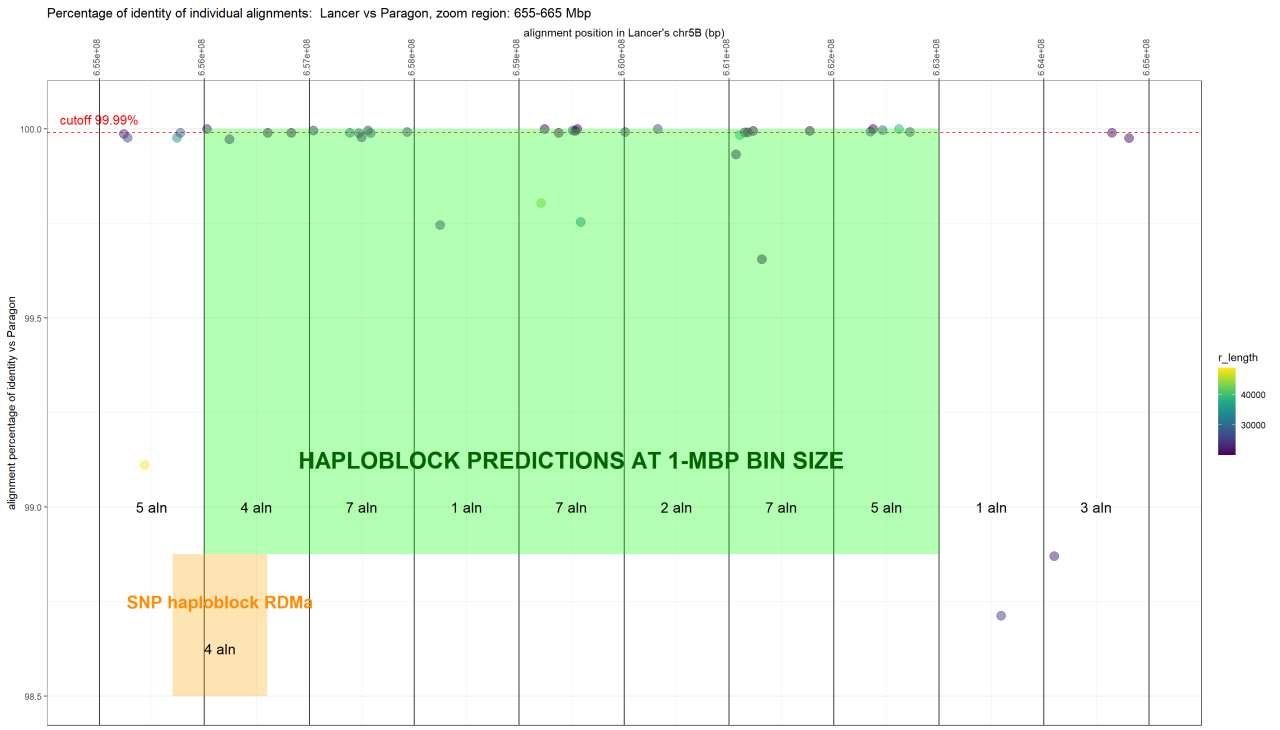

```
plot_aln_and_bins(aln_subset = aln_subset, bin_size = 2500000, zoom_start = zoom_start, zoom_end = zoom_end, highlighted_tar
get = target, target_text = "SNP haploblock RDMa", fill_target = "orange", color_target_text = "darkorange", fill_prediction
s = "green", color_prediction_text = "darkgreen", ymin = 98.5, cut_off = 99.99, reference_name = reference_assembly, query_n
ame = query_assembly, dot_size = 4, x_label_gap = 1000000)
```

```
## [1] "BINS AT 2.5-MBP BIN SIZE"
##         bin perc_id_median cut_off block_no bin_start   bin_end aln_number
## 1 655000000       99.96227  <99.99 NO_BLOCK 652500000 655000000         13
## 2 657500000       99.98867  <99.99 NO_BLOCK 655000000 657500000         13
## 3 660000000       99.99211 >=99.99        1 657500000 660000000         11
## 4 662500000       99.99228 >=99.99        1 660000000 662500000         12
## 5 665000000       99.98336  <99.99 NO_BLOCK 662500000 665000000          6
## [1] "BLOCK SUMMARY AT 2.5-MBP BIN SIZE"
##   bin_size      comparison block_no block_start block_end
## 1  2.5-Mbp Lancer->Paragon        1   657500000 662500000
```




```
plot_aln_and_bins(aln_subset = aln_subset, bin_size = 1000000, zoom_start = zoom_start, zoom_end = zoom_end, highlighted_tar
get = target, target_text = "SNP haploblock RDMa", fill_target = "orange", color_target_text = "darkorange", fill_prediction
s = "green", color_prediction_text = "darkgreen", ymin = 98.5, cut_off = 99.99, reference_name = reference_assembly, query_n
ame = query_assembly, dot_size = 4, x_label_gap = 1000000)
```

```
## [1] "BINS AT 1-MBP BIN SIZE"
##         bin perc_id_median cut_off block_no bin_start  bin_end aln_number
## 1  6.55e+08       99.92852  <99.99 NO_BLOCK  6.54e+08 6.55e+08          6
## 2  6.56e+08       99.97730  <99.99 NO_BLOCK  6.55e+08 6.56e+08          5
## 3  6.57e+08       99.99048 >=99.99        1  6.56e+08 6.57e+08          4
## 4  6.58e+08       99.98996  <99.99 NO_BLOCK  6.57e+08 6.58e+08          7
## 5  6.59e+08       99.74574  <99.99 NO_BLOCK  6.58e+08 6.59e+08          1
## 6  6.60e+08       99.99528 >=99.99        1  6.59e+08 6.60e+08          7
## 7  6.61e+08       99.99595 >=99.99        1  6.60e+08 6.61e+08          2
## 8  6.62e+08       99.99072 >=99.99        1  6.61e+08 6.62e+08          7
## 9  6.63e+08       99.99664 >=99.99        1  6.62e+08 6.63e+08          5
## 10 6.64e+08       98.71248  <99.99 NO_BLOCK  6.63e+08 6.64e+08          1
## 11 6.65e+08       99.97621  <99.99 NO_BLOCK  6.64e+08 6.65e+08          3
## [1] "BLOCK SUMMARY AT 1-MBP BIN SIZE"
##   bin_size      comparison block_no block_start block_end
## 1    1-Mbp Lancer->Paragon        1    6.56e+08  6.63e+08
```



Define new parameters:

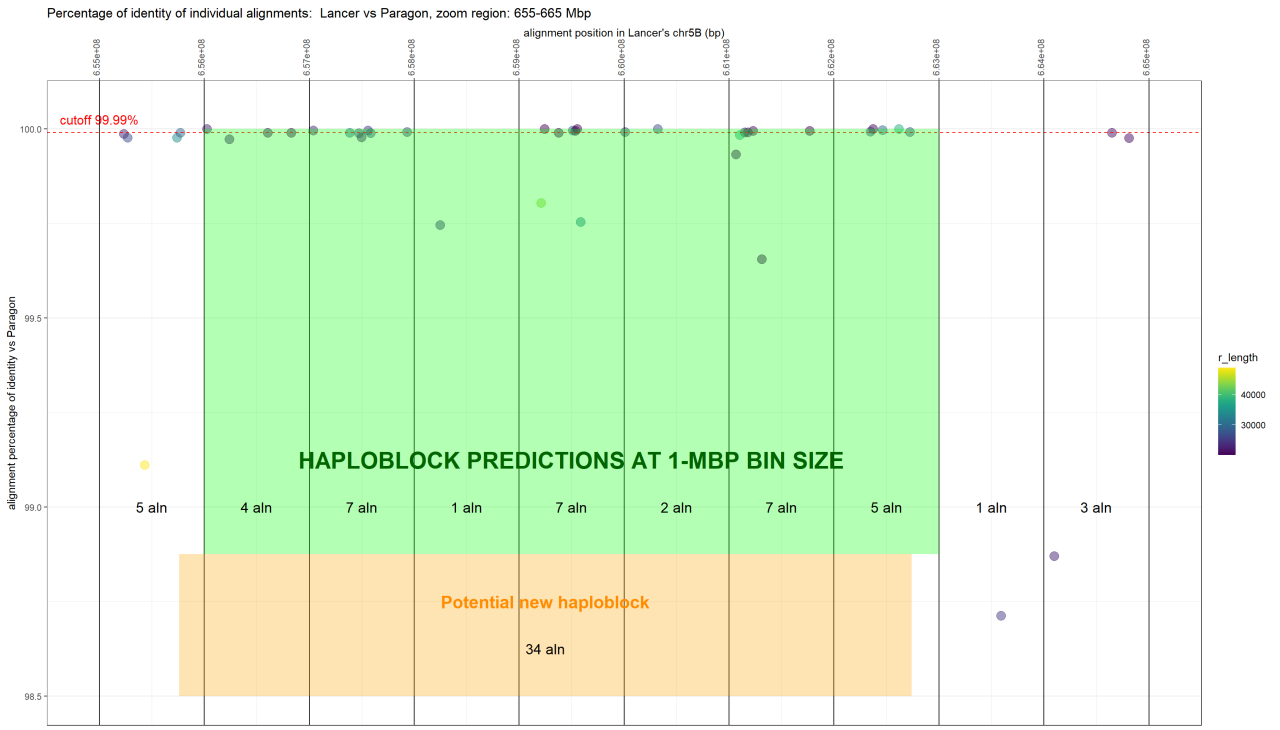
```
selected_start <- 655760000 # Genes will be extracted from this position. If you have no interest in redefining your region, simply write 'target_start' or 'zoom_start', to keep with the previous coordinates
selected_end <- 662740000 # Genes will be extracted until this position. If you have no interest in redefining your region, simply write 'target_end' or 'zoom_end', to keep with the previous coordinates
target_text <- "Potential new haploblock" # Text to print on the selected region

selected_haploblock <- data.frame(selected_start, selected_end)
print(selected_haploblock)
```

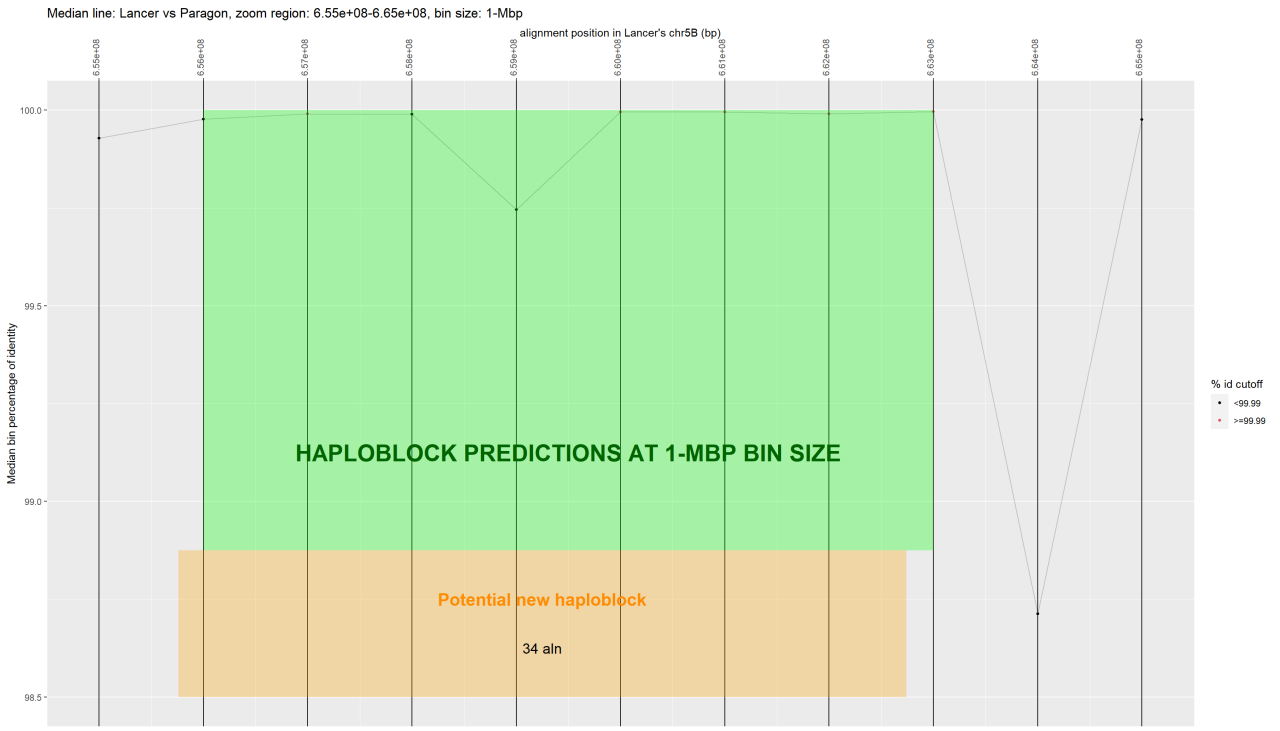
```
##   selected_start selected_end
## 1      655760000    662740000
```

1.2.7. Plot summary graphs

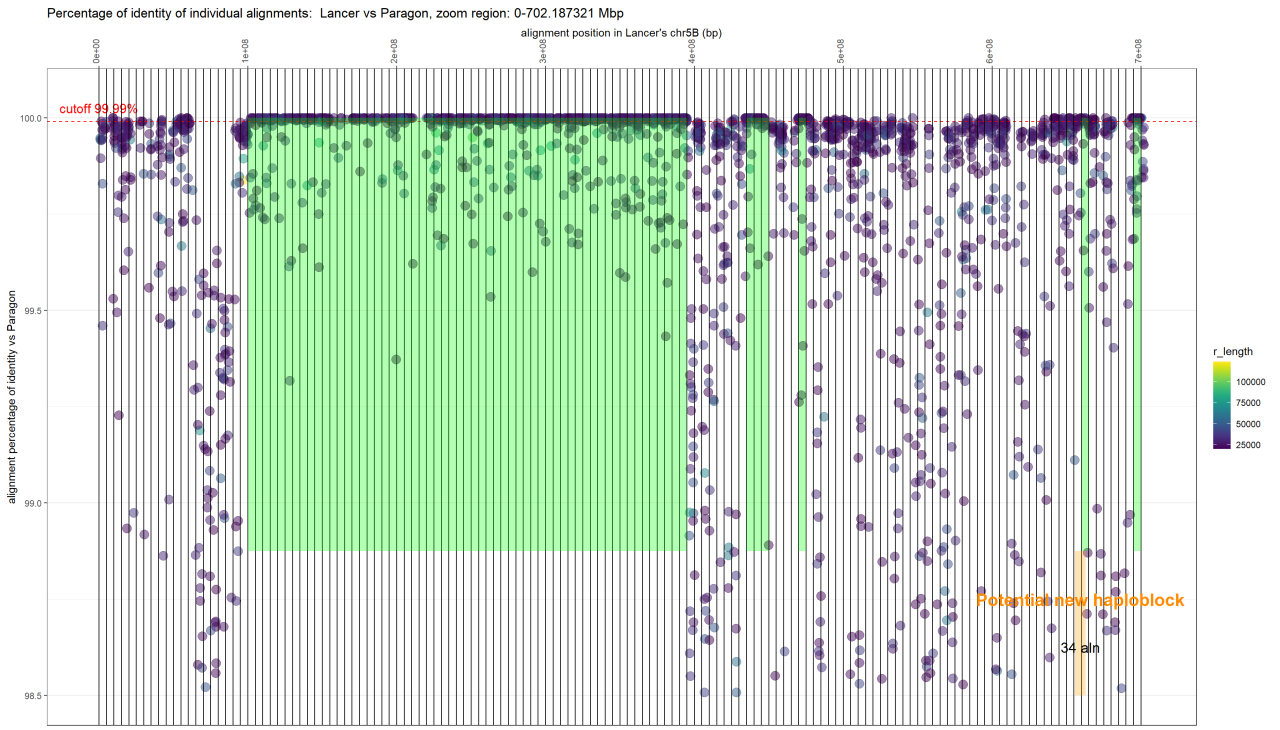
```
plot_aln_and_bins(print_tables = FALSE, aln_subset = aln_subset, bin_size = 1000000, zoom_start = zoom_start, zoom_end = zoom_end, highlighted_target = selected_haploblock, target_text = target_text, fill_target = "orange", color_target_text = "darkorange", fill_predictions = "green", color_prediction_text = "darkgreen", ymin = 98.5, cut_off = 99.99, reference_name = reference_assembly, query_name = query_assembly, dot_size = 4, x_label_gap = 1000000)
```



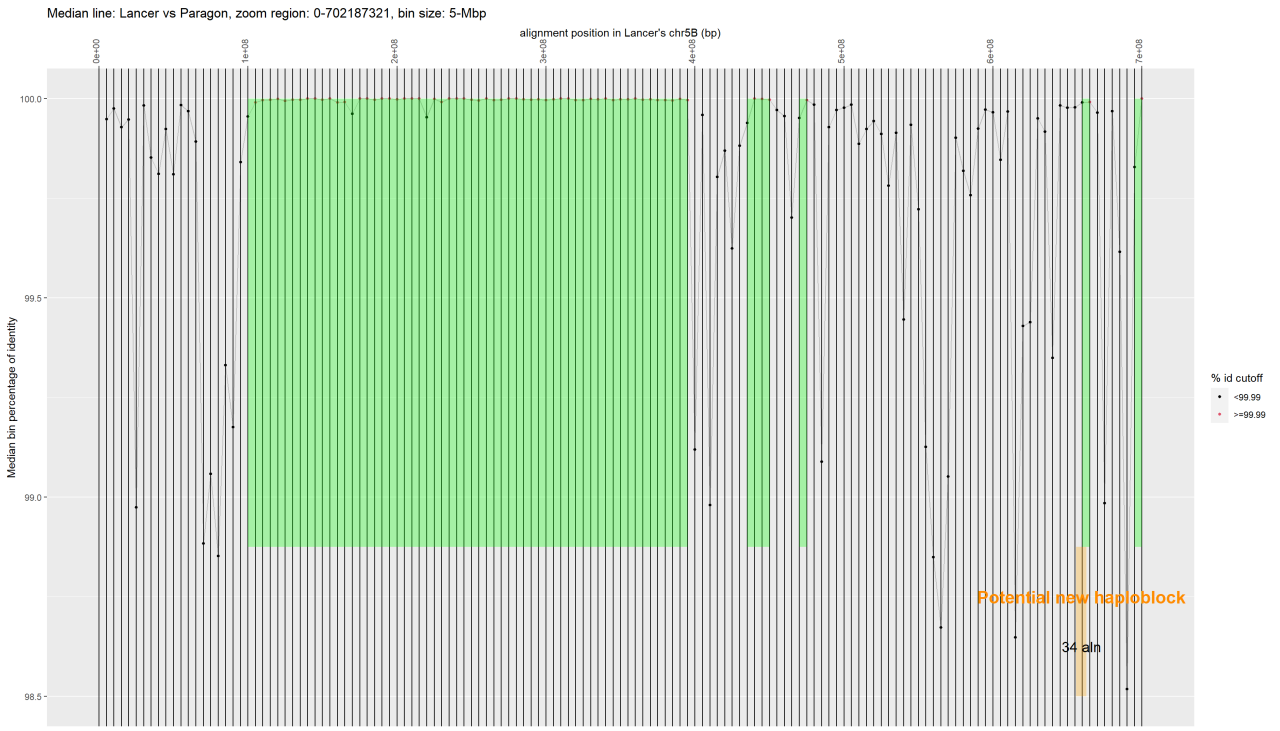

```
plot_bins_and_selected_region(print_tables = FALSE, aln_subset = aln_subset, bin_size = 1000000, zoom_start = zoom_start, zoom_end = zoom_end, highlighted_target = selected_haploblock, target_text = target_text, fill_target = "orange", color_target_text = "darkorange", fill_predictions = "green", color_prediction_text = "darkgreen", ymin = 98.5, cut_off = 99.99, reference_name = reference_assembly, query_name = query_assembly, dot_size = 4, x_label_gap = 1000000)
```




```
plot_aln_and_bins(print_tables = FALSE, aln_subset = aln_subset, bin_size = 5000000, zoom_start = 0, zoom_end = max(aln_subset$re), highlighted_target = selected_haploblock, target_text = target_text, fill_target = "orange", color_target_text = "darkorange", fill_predictions = "green", ymin = 98.5, cut_off = 99.99, reference_name = reference_assembly, query_name = query_assembly, dot_size = 4, x_label_gap = 100000000, prediction_text = FALSE, aln_text = F)
```




```
plot_bins_and_selected_region(print_tables = FALSE, aln_subset = aln_subset, bin_size = 5000000, zoom_start = 0, zoom_end =
 max(aln_subset$re), highlighted_target = selected_haploblock, target_text = target_text, fill_target = "orange", color_targ
et_text = "darkorange", fill_predictions = "green", color_prediction_text = "darkgreen", ymin = 98.5, cut_off = 99.99, refer
ence_name = reference_assembly, query_name = query_assembly, dot_size = 4, x_label_gap = 100000000, prediction_text = FALSE)
```



2. Identify genes in the haploblock

Requirements:

- File 'projectedGenes__Triticum_aestivum_REFERENCEassembly_v1.0.gff', in this case the reference is LongReach Lancer (downloadable from https://webblast.ipk-gatersleben.de/downloads/wheat/gene_projection/ (https://webblast.ipk-gatersleben.de/downloads/wheat/gene_projection/))
- File 'geneid_2_chinese.sourceid.txt' (downloadable from https://webblast.ipk-gatersleben.de/downloads/wheat/gene_projection/ (https://webblast.ipk-gatersleben.de/downloads/wheat/gene_projection/))

2.1. Download the files and save them in the working directory

2.2. Read the gff file containing the gene model projection for the reference assembly

```
ref_gff <- read.table ( file = "projectedGenes__Triticum_aestivum_LongReach_Lancer_v1.0.gff", sep = "\t" , header = F, strin
gsAsFactors = F)
```

2.3. Create subsets for gene projections only and edit the table

```
ref_gff_gene_only <- ref_gff[ref_gff$V3 == "gene",]
colnames(ref_gff_gene_only) <- c("chr", "annotation", "biotype", "start", "end", "score", "strand", "info", "ref_id")
ref_gff_gene_only$var_id <- gsub("ID=", "", ref_gff_gene_only$ref_id)
```

2.4. Create a subset for the haploblock

```
my_genes <- ref_gff_gene_only[grep(chromosome, ref_gff_gene_only$chr),]
my_genes <- my_genes[(my_genes$start >= selected_start) & (my_genes$end <= selected_end),]
```

2.5. Download 'geneid_2_chinese.sourceid.txt' from the last link and read the table

```
cs_id <- read.table(file = "geneid_2_chinese.sourceid.txt", sep="\t", header=T, stringsAsFactors = F)
```

2.6. Add a column to the subset with the IDs of the gene sources in Chinese Spring for each of Lancer's genes

```
my_genes <- cs_id_filler(data = my_genes, library = cs_id, chr = chromosome, ref.var = tolower(reference_assembly))
```

2.7. Extract the names of the genes in chromosome 5B separated by commas

```
my_gene_sources <- as.character(my_genes$cs_id[!grepl("^source", my_genes$cs_id)])
my_gene_sources_text <- paste(my_gene_sources, collapse = ", ")
write.table(x = my_gene_sources_text, file = "my_gene_sources.txt", sep = "", row.names = F, col.names = F, quote = F)

my_variety_genes <- as.character(my_genes$var_id[!grepl("^source", my_genes$cs_id)])
my_variety_genes_text <- paste(my_variety_genes, collapse = ", ")
write.table(x = my_variety_genes_text, file = "my_variety_genes.txt", sep = "", row.names = F, col.names = F, quote = F)

print_my_genes <- data.frame( "var_id" = my_genes$var_id, "chinese_id" = my_genes$cs_id)
write.csv2(x = print_my_genes, file = "my_genes_and_sources.csv", row.names = F, quote = F)

head(print_my_genes, 10)
```

```
##                 var_id         chinese_id
## 1  TraesLAC5B01G535100 TraesCS5B02G495900
## 2  TraesLAC5B01G535200 TraesCS5B02G496000
## 3  TraesLAC5B01G535300 TraesCS5B02G496100
## 4  TraesLAC5B01G535400 TraesCS5B02G496200
## 5  TraesLAC5B01G535500 TraesCS5B02G496300
## 6  TraesLAC5B01G535600 TraesCS5B02G496400
## 7  TraesLAC5B01G535700 TraesCS5B02G496600
## 8  TraesLAC5B01G535800 TraesCS5B02G496700
## 9  TraesLAC5B01G535900 TraesCS5B02G496900
## 10 TraesLAC5B01G536000 TraesCS5B02G497100
```

3. Check if the haplotype prediction was also made by gene-based BLAST pairwise alignments

Requirements:

- File 'varieties_all_identities_2000bp.tar.gz' (downloadable from https://opendata.earlham.ac.uk/wheat/under_license/toronto/Brinton_etal_2020-05-20-Haplotypes-for-wheat-breeding/pairwise_blast/ (https://opendata.earlham.ac.uk/wheat/under_license/toronto/Brinton_etal_2020-05-20-Haplotypes-for-wheat-breeding/pairwise_blast/))
- File 'iwgsc_refseq_v1.2_gene_annotation.zip' (downloadable from https://urgi.versailles.inrae.fr/download/iwgsc/IWGSC_RefSeq_Annotations/v1.2/ (https://urgi.versailles.inrae.fr/download/iwgsc/IWGSC_RefSeq_Annotations/v1.2/))

3.1. Download the zip file, decompress it in the working directory and read the tables

```
HC_gtf <- read.table("IWGSC_v1.2_HC_20200615.gff3", sep = "\t", header = FALSE, stringsAsFactors = FALSE)
LC_gtf <- read.table("IWGSC_v1.2_LC_20200615.gff3", sep = "\t", header = FALSE, stringsAsFactors = FALSE)
ALL_gtf <- rbind(HC_gtf, LC_gtf)
```

3.2. Extract the BLAST alignments and put them in table with Chinese Spring genes and their location in the IWGSC genome (long process)

```
BLAST_library <- read_pairwise_position(blast_path_gz = "varieties_all_identities_2000bp.tab.gz", gtf = ALL_gtf, write_table
= "BLAST_library.tab")
```

3.3. Extract a subset with Lancer-Paragon comparison in chr5B

```
BLAST_subset <- BLAST_library[grepl(paste0(tolower(reference_assembly), "->", tolower(query_assembly), sep = ""), BLAST_libr
ary$aln_type) & grepl(chromosome, BLAST_library$chr),]
```

3.4. Use the vector with the genes identified in the previous step to extract another subset with only the genes in our haploblock

```
BLAST_subset <- BLAST_subset[grepl(paste(my_gene_sources, collapse = "|"), BLAST_subset$transcript),]
write.csv2(x = BLAST_subset, file = "BLAST_subset.csv", row.names = F, quote = F)
```

Brinton et al (2020) only retained only gene projections consistent with the expected chromosome. This explains why this subset contains less genes that the total amount of annotated genes in our region.

```
colnames(BLAST_subset)[1] <- "cs_transcript"
colnames(BLAST_subset)[14] <- "cs_start"
colnames(BLAST_subset)[15] <- "cs_end"

BLAST_subset$var_transcript <- my_genes$var_id[grepl(paste(BLAST_subset$cs_transcript, collapse = "|"), my_genes$cs_id)]
BLAST_subset$var_start <- my_genes$start[grepl(paste(BLAST_subset$var_transcript, collapse = "|"), my_genes$var_id)]
BLAST_subset$var_end <- my_genes$end[grepl(paste(BLAST_subset$var_transcript, collapse = "|"), my_genes$var_id)]
```

Notice that some genes were filtered out if they contained more than one projection in the expected chromosome, so the amount of genes shown in this table is expected to be smaller than those found in lancer's projected genes in the region. The genes that were excluded can be seen here:

```
my_gene_sources[my_gene_sources %in% BLAST_subset$cs_transcript == FALSE]
```

```
##  [1] "TraesCS5B02G496400" "TraesCS5B02G496700" "TraesCS5B02G497300"
##  [4] "TraesCS5B02G497500" "TraesCS5B02G500500" "TraesCS5B02G500600"
##  [7] "TraesCS5B02G500700" "TraesCS5B02G502700" "TraesCS5B02G503400"
## [10] "TraesCS5B02G503500" "TraesCS5B02G504400" "TraesCS5B02G552700"
```

```
my_genes$var_id[grepl(paste(my_gene_sources[my_gene_sources %in% BLAST_subset$cs_transcript == FALSE], collapse = "|"), my_g
enes$cs_id)]
```

```
##  [1] "TraesLAC5B01G535600" "TraesLAC5B01G535800" "TraesLAC5B01G536100"
##  [4] "TraesLAC5B01G536300" "TraesLAC5B01G539700" "TraesLAC5B01G539800"
##  [7] "TraesLAC5B01G539900" "TraesLAC5B01G542300" "TraesLAC5B01G542700"
## [10] "TraesLAC5B01G542900" "TraesLAC5B01G543700" "TraesLAC5B01G544200"
```

We can extract another list containing only the genes that were present among the BLAST alignments

```
my_gene_sources_filtered_by_Brinton <- my_gene_sources[my_gene_sources %in% BLAST_subset$cs_transcript == TRUE]
my_variety_genes_filtered_by_Brinton <- my_genes$var_id[grepl(paste(my_gene_sources [my_gene_sources %in% BLAST_subset$cs_tr
anscript == TRUE], collapse = "|"), my_genes$cs_id)]
my_gene_sources_filtered_by_Brinton_text <- paste(my_gene_sources_filtered_by_Brinton, collapse = ", ")
write.table(x = my_gene_sources_filtered_by_Brinton_text, file = "my_gene_sources_filtered_by_Brinton_text.txt", sep = "", r
ow.names = F, col.names = F, quote = F)

my_variety_genes_filtered_by_Brinton_text <- paste(my_variety_genes_filtered_by_Brinton, collapse = ", ")
write.table(x = my_variety_genes_filtered_by_Brinton_text, file = "my_variety_genes_filtered_by_Brinton_text.txt", sep = "",
row.names = F, col.names = F, quote = F)

print_blast <- data.frame( "var_id" = my_variety_genes_filtered_by_Brinton_text, "chinese_id" = my_gene_sources_filtered_by_
Brinton_text)
write.csv2(x = print_blast, file = "my_genes_and_sources_filtered_by_Brinton.csv", row.names = F, quote = F)
```

3.5. Calculate the percentage of identity in windows of 20 genes where genes containing Ns are filtered out

```
BLAST_subset <- BLAST_subset[ BLAST_subset$Ns_total == 0, ]

window_BLAST_subset <- edited_calculate_pid_windows(aln_data = BLAST_subset)
blocks_BLAST_subset <- assign_blocks(window_BLAST_subset)
```

```
## [1] "less than 100%"
## [1] "less than 100%"
## [1] "less than 100%"
## [1] "less than 100%"
## [1] "less than 100%"
## [1] "less than 100%"
## [1] "less than 100%"
## [1] "less than 100%"
## [1] "less than 100%"
## [1] "less than 100%"
## [1] "less than 100%"
## [1] "less than 100%"
## [1] "less than 100%"
## [1] "less than 100%"
## [1] "less than 100%"
## [1] "less than 100%"
## [1] "less than 100%"
## [1] "less than 100%"
## [1] "less than 100%"
## [1] "less than 100%"
## [1] "less than 100%"
## [1] "less than 100%"
## [1] "less than 100%"
## [1] "less than 100%"
```

```
blocks_BLAST_subset
```

```
##    start end  cs_start    cs_end var_start   var_end pident_mean
## 1      1  20 663134978 666196835 655761539 658486203    99.99828
## 2      2  21 663234734 666207172 656020702 658496928    99.99761
## 3      3  22 663796017 666209291 656553758 658499392    99.99761
## 4      4  23 664022132 666372136 656600250 658525735    99.99742
## 5      5  24 664672987 668463343 657035254 659882405    99.99742
## 6      6  25 664682920 668474547 657044824 659893484    99.99609
## 7      7  26 664726808 668519308 657104030 659938479    99.99609
## 8      8  27 664949927 668583715 657329620 660019299    99.99498
## 9      9  28 664979682 669217640 657359517 660818003    99.99587
## 10    10  29 664998106 669232964 657377616 660827247    99.99460
## 11    11  30 665016776 669292146 657396273 660884339    99.99254
## 12    12  31 665024295 669306368 657403038 660900818    99.99387
## 13    13  32 665170918 669452267 657534486 661060959    99.99280
## 14    14  33 665539582 669483645 657903967 661091774    99.99280
## 15    15  34 665560612 669898631 657925163 661273027    99.99280
## 16    16  35 665719477 669909637 658082849 661430757    99.99382
## 17    17  36 665767971 670099306 658131416 661722411    99.99146
## 18    18  37 665938590 670116476 658242152 661739162    99.99146
## 19    19  38 665939237 670118309 658242780 661741296    99.99146
## 20    20  39 666195640 670130079 658485922 661752676    99.99146
## 21    21  40 666202129 670246635 658492724 661761415    99.99146
## 22    22  41 666207065 670305619 658497166 661773746    99.99213
## 23    23  42 666371429 670694936 658525028 662378160    99.99213
## 24    24  43 668461124 670716758 659880577 662400081    99.99449
##           aln_type start_cs_transcript  end_cs_transcript start_var_transcript
## 1  lancer->paragon  TraesCS5B02G495900 TraesCS5B02G500000  TraesLAC5B01G535100
## 2  lancer->paragon  TraesCS5B02G496300 TraesCS5B02G500100  TraesLAC5B01G535500
## 3  lancer->paragon  TraesCS5B02G496600 TraesCS5B02G500200  TraesLAC5B01G535700
## 4  lancer->paragon  TraesCS5B02G497100 TraesCS5B02G500300  TraesLAC5B01G536000
## 5  lancer->paragon  TraesCS5B02G497700 TraesCS5B02G501100  TraesLAC5B01G536500
## 6  lancer->paragon  TraesCS5B02G497800 TraesCS5B02G501200  TraesLAC5B01G536600
## 7  lancer->paragon  TraesCS5B02G497900 TraesCS5B02G501300  TraesLAC5B01G536700
## 8  lancer->paragon  TraesCS5B02G498000 TraesCS5B02G501400  TraesLAC5B01G537100
## 9  lancer->paragon  TraesCS5B02G498100 TraesCS5B02G501600  TraesLAC5B01G537200
## 10 lancer->paragon  TraesCS5B02G498200 TraesCS5B02G501800  TraesLAC5B01G537300
## 11 lancer->paragon  TraesCS5B02G498300 TraesCS5B02G501900  TraesLAC5B01G537400
## 12 lancer->paragon  TraesCS5B02G498400 TraesCS5B02G502100  TraesLAC5B01G537500
## 13 lancer->paragon  TraesCS5B02G498500 TraesCS5B02G502200  TraesLAC5B01G537600
## 14 lancer->paragon  TraesCS5B02G498700 TraesCS5B02G502300  TraesLAC5B01G537800
## 15 lancer->paragon  TraesCS5B02G498800 TraesCS5B02G503200  TraesLAC5B01G537900
## 16 lancer->paragon  TraesCS5B02G498900 TraesCS5B02G503300  TraesLAC5B01G538000
## 17 lancer->paragon  TraesCS5B02G499100 TraesCS5B02G503700  TraesLAC5B01G538200
## 18 lancer->paragon  TraesCS5B02G499300 TraesCS5B02G503800  TraesLAC5B01G538400
## 19 lancer->paragon  TraesCS5B02G499400 TraesCS5B02G503900  TraesLAC5B01G538500
## 20 lancer->paragon  TraesCS5B02G500000 TraesCS5B02G504000  TraesLAC5B01G539000
## 21 lancer->paragon  TraesCS5B02G500100 TraesCS5B02G504100  TraesLAC5B01G539100
## 22 lancer->paragon  TraesCS5B02G500200 TraesCS5B02G504200  TraesLAC5B01G539200
## 23 lancer->paragon  TraesCS5B02G500300 TraesCS5B02G504600  TraesLAC5B01G539300
## 24 lancer->paragon  TraesCS5B02G501100 TraesCS5B02G504700  TraesLAC5B01G540400
##     end_var_transcript block_no
## 1  TraesLAC5B01G539000       NA
## 2  TraesLAC5B01G539100       NA
## 3  TraesLAC5B01G539200       NA
## 4  TraesLAC5B01G539300       NA
## 5  TraesLAC5B01G540400       NA
## 6  TraesLAC5B01G540500       NA
## 7  TraesLAC5B01G540600       NA
## 8  TraesLAC5B01G540700       NA
## 9  TraesLAC5B01G541300       NA
## 10 TraesLAC5B01G541500       NA
## 11 TraesLAC5B01G541600       NA
## 12 TraesLAC5B01G541800       NA
## 13 TraesLAC5B01G541900       NA
## 14 TraesLAC5B01G542000       NA
## 15 TraesLAC5B01G542400       NA
## 16 TraesLAC5B01G542600       NA
## 17 TraesLAC5B01G543100       NA
## 18 TraesLAC5B01G543200       NA
## 19 TraesLAC5B01G543300       NA
## 20 TraesLAC5B01G543400       NA
## 21 TraesLAC5B01G543500       NA
## 22 TraesLAC5B01G543600       NA
## 23 TraesLAC5B01G543800       NA
## 24 TraesLAC5B01G543900       NA
```

According to the previous data, no haplotype is predicted by BLASTing the gene sequences from this set between Lancer and Paragon (block_no = NA). In this case, the NUCmer-based prediction should be taken as the reference, as Brinton et al. (2020) explained that genic sequence alone was insufficient to fully differentiate between haplotypes.

Supplementary file 2: List of potential SNP markers to target the haplotype RDMb-h3, associated with higher root dry mass. SNPs were identified by high-stringency mapping of Illumina paired-end short reads and variant calling against Chinese Spring from three resequenced Chinese varieties by Hao et al. (2020). The SNP flanking sequence corresponds to those of the h2-carrying assemblies. The alleles expected for the RDMb-h2 and RDMb-h3 blocks are indicated alongside with the start and end coordinates in each of the h2-carrying assemblies.

ID	SNP flanking seq	h2 allele	h3 allele	Cspring start	Cspring end	Jagger start	Jagger end	Norin start	Norin end	Stanley start	Stanley end
RDMb-h3:SNP_1	ATAAAACTCGGATGACAACATTTTCTCAAAACAATCATAATATGATATATCAAGATGGTATCTCGCTAGCCCTTTCTGGTACCGCAAAACATAAATGCAGG	T	A	652643873	652643973	643924029	643924129	652943359	652943459	654512701	654512801
RDMb-h3:SNP_2	CCACAAGTGCCTAGAGACCATATCATGCATTAGAACTACTTGGGACCAAGTAAAATTGACATGCAAGCTCAAGAATAGGGACACCTTAGCAGCAAGAATTT	G	A	652646778	652646878	643926934	643927034	652946264	652946364	654515606	654515706
RDMb-h3:SNP_3	AGTGCCTAGAGACCATATCATGCATTAGAACTACTTGGGACCAAGTAAAATTGACATGCAAGCTCAAGAATAGGGACACCTTAGCAGCAAGAATTTGCAAT	A	T	652646783	652646883	643926939	643927039	652946269	652946369	654515611	654515711
RDMb-h3:SNP_4	CAACACCTGCAATATTCAAAAAGGGTCTACCAAGGATAATCGACATACTGTCGTCCCCGGGAATATCAAGAATGACAAAGTCTGTTAAGATAGTAACGTTT	G	A	652647345	652647445	643927501	643927601	652946831	652946931	654516173	654516273
RDMb-h3:SNP_5	GTCTACCAAGGATAATCGACATACTGTCGTCCCCGGGAATATCAAGAATGACAAAGTCTGTTAAGATAGTAACGTTTGCAACAACAACATGCACGTCTTCA	G	A	652647369	652647469	643927525	643927625	652946855	652946955	654516197	654516297
RDMb-h3:SNP_6	CGGGAATATCAAGAATGACAAAGTCTGTTAAGATAGTAACGTTTGCAACAACAACATGCACGTCTTCACAAATACCGATAGGTATAGCAGTTGATTTATCG	A	C	652647402	652647502	643927558	643927658	652946888	652946988	654516230	654516330
RDMb-h3:SNP_7	TTCACAAATACCGATAGGTATAGCAGTTGATTTATCGGCCATTTGCAAAAATATTTCAGTCGGTGTCAACTTATTTAATTCAAATCTCCGATATAAAGAGA	A	G	652647466	652647566	643927622	643927722	652946952	652947052	654516294	654516394
RDMb-h3:SNP_8	CGATAGGTATAGCAGTTGATTTATCGGCCATTTGCAAAAATATTTCAGTCGGTGTCAACTTATTTAATTCAAATCTCCGATATAAAGAGAGAGGCATAACA	C	A	652647477	652647577	643927633	643927733	652946963	652947063	654516305	654516405
RDMb-h3:SNP_9	TTGATTTATCGGCCATTTGCAAAAATATTTCAGTCGGTGTCAACTTATTTAATTCAAATCTCCGATATAAAGAGAGAGGCATAACACTAACATCAGTTCCA	T	C	652647492	652647592	643927648	643927748	652946978	652947078	654516320	654516420
RDMb-h3:SNP_10	TCGGCCATTTGCAAAAATATTTCAGTCGGTGTCAACTTATTTAATTCAAATCTCCGATATAAAGAGAGAGGCATAACACTAACATCAGTTCCAAGATCACA	A	G	652647500	652647600	643927656	643927756	652946986	652947086	654516328	654516428
RDMb-h3:SNP_11	CCATTTGCAAAAATATTTCAGTCGGTGTCAACTTATTTAATTCAAATCTCCGATATAAAGAGAGAGGCATAACACTAACATCAGTTCCAAGATCACATAAA	C	A	652647504	652647604	643927660	643927760	652946990	652947090	654516332	654516432
RDMb-h3:SNP_12	CTTATTTAATTCAAATCTCCGATATAAAGAGAGAGGCATAACACTAACATCAGTTCCAAGATCACATAAAGCAGTTTTAACATAGTTTCTTTTAATGGAGC	T	C	652647535	652647635	643927691	643927791	652947021	652947121	654516363	654516463
RDMb-h3:SNP_13	TTTAATTCAAATCTCCGATATAAAGAGAGAGGCATAACACTAACATCAGTTCCAAGATCACATAAAGCAGTTTTAACATAGTTTCTTTTAATGGAGCATGA	T	C	652647539	652647639	643927695	643927795	652947025	652947125	654516367	654516467
RDMb-h3:SNP_14	CCAAGATCACATAAAGCAGTTTTAACATAGTTTCTTTTAATGGAGCATGATATAGTTGGTATTCCTGGATCTCCAAGTTTCTTAGGTATTCCACCCTTAAA	A	G	652647590	652647690	643927746	643927846	652947076	652947176	654516418	654516518
RDMb-h3:SNP_15	AGACTCAGATCAAATACCAAGATCTCGTTAAGCGTGTTATTATGAAGTAACCGTGGACGCCGACCAGGGCCAGGCCCACCTGTCTCCTAGGTGGTCTCAAC	A	T	652649846	652649946	643930002	643930102	652949332	652949432	654518674	654518774
RDMb-h3:SNP_16	TCAGATCAAATACCAAGATCTCGTTAAGCGTGTTATTATGAAGTAACCGTGGACGCCGACCAGGGCCAGGCCCACCTGTCTCCTAGGTGGTCTCAACCTGC	T	C	652649850	652649950	643930006	643930106	652949336	652949436	654518678	654518778
RDMb-h3:SNP_17	AGATCAAATACCAAGATCTCGTTAAGCGTGTTATTATGAAGTAACCGTGGACGCCGACCAGGGCCAGGCCCACCTGTCTCCTAGGTGGTCTCAACCTGCCA	G	A	652649852	652649952	643930008	643930108	652949338	652949438	654518680	654518780
RDMb-h3:SNP_18	AGGTACACAACGTCTAATAACACCATCTACTCCTTCTTTATAAAGGTGTCGGTCATCCCAAAAGTAATGTCTTAAATCATAAAAGAACTTTTTCTTTTGCT	C	G	652661522	652661622	643941851	643941951	652960915	652961015	654530201	654530301
RDMb-h3:SNP_19	AGAGTTTTCAATAATCTTTCTTCTTGCTCTGAAAGGTTAGCACTAAAAATAACAGGATATATTTTCTTTTCATCAAGATAAGCATACTTAAGATTATC	A	T	652663176	652663276	643943505	643943605	652962569	652962669	654531855	654531955
RDMb-h3:SNP_20	TTTAACACAATCGAACTTAGGTGTCATACCTGACTCCTTACCATCGTCGAAACCCCAGTCTTCAAAGTTGCGTTTAATTCTTTCCAATAAGTCCCATTTGA	A	G	652664378	652664478	643944707	643944807	652963771	652963871	654533057	654533157
RDMb-h3:SNP_21	AATCGAACTTAGGTGTCATACCTGACTCCTTACCATCGTCGAAACCCCAGTCTTCAAAGTTGCGTTTAATTCTTTCCAATAAGTCCCATTTGAAATCAATA	G	A	652664386	652664486	643944715	643944815	652963779	652963879	654533065	654533165
RDMb-h3:SNP_22	CTTAGGTGTCATACCTGACTCCTTACCATCGTCGAAACCCCAGTCTTCAAAGTTGCGTTTAATTCTTTCCAATAAGTCCCATTTGAAATCAATAGTCTTCA	A	G	652664393	652664493	643944722	643944822	652963786	652963886	654533072	654533172
RDMb-h3:SNP_23	GTTGCGAAACTATTCTGCATTGTTTCAAATGTAAACCAAACTCGTAACTGAAATATTCTCCTCCACGATCAGATCGTAGAAACTTTATTTTCTTGTTACGC	G	C	652699197	652699297	643979241	643979341	652998215	652998315	654567865	654567965
RDMb-h3:SNP_24	AATATTCTCCTCCACGATCAGATCGTAGAAACTTTATTTTCTTGTTACGCTGATTTTCCACTTCACTCTGAAATTCTTTGAACTTTCAAATGTTTCAGAC	C	A	652699248	652699348	622332218	622332118	630262053	630261953	632994990	632994890
RDMb-h3:SNP_25	CTAAGCCTAGCACAAAGATCGTGTAGTTCGTATGCTAAAGCTTTTCTAACGTCAAGTATCTTTTCTGTAGACCATGAGATTGTGCAACTCCCGGATGCCGT	C	T	652699856	652699956	643979900	643980000	652998874	652998974	654568524	654568624
RDMb-h3:SNP_26	CGCTTCCGCTTAGCGATCTACAAGGGTATGTAGATGCACTCTCCTTCCCGTCGTTGTTGGTTTCTCCATAGATAGATCTTGGTGACACGTAGGAAAATTTT	G	C	652701211	652701311	643981255	643981355	653000229	653000329	654569879	654569979
RDMb-h3:SNP_27	TGATAGTAGCAATTATGCGGACTGGGTCCGTGAACTGAGGATTGTCCTCGTTGCTTCGTAGAAGGCTTATGTCCTTAATGCACCGCTCGGTGTGCTTGACC	G	A	652702669	652702769	643982714	643982814	653001687	653001787	654571338	654571438
RDMb-h3:SNP_28	TAGCAATTATGCGGACTGGGTCCGTGAACTGAGGATTGTCCTCGTTGCTTCGTAGAAGGCTTATGTCCTTAATGCACCGCTCGGTGTGCTTGACCTCGAAC	T	G	652702675	652702775	643982720	643982820	653001693	653001793	654571344	654571444
RDMb-h3:SNP_29	GCAATTATGCGGACTGGGTCCGTGAACTGAGGATTGTCCTCGTTGCTTCGTAGAAGGCTTATGTCCTTAATGCACCGCTCGGTGTGCTTGACCTCGAACGT	G	A	652702677	652702777	643982722	643982822	653001695	653001795	654571346	654571446
RDMb-h3:SNP_30	CAATTATGCGGACTGGGTCCGTGAACTGAGGATTGTCCTCGTTGCTTCGTAGAAGGCTTATGTCCTTAATGCACCGCTCGGTGTGCTTGACCTCGAACGTA	T	C	652702678	652702778	643982723	643982823	653001696	653001796	654571347	654571447
RDMb-h3:SNP_31	TCGTTGCTTCGTAGAAGGCTTATGTCCTTAATGCACCGCTCGGTGTGCTTGACCTCGAACGTAGTCTGTGGATGTTGTGAACATCTGACATACACGTTTTG	T	G	652702716	652702816	643982761	643982861	653001734	653001834	654571385	654571485
RDMb-h3:SNP_32	CGTTGCTTCGTAGAAGGCTTATGTCCTTAATGCACCGCTCGGTGTGCTTGACCTCGAACGTAGTCTGTGGATGTTGTGAACATCTGACATACACGTTTTGA	G	A	652702717	652702817	643982762	643982862	653001735	653001835	654571386	654571486
RDMb-h3:SNP_33	CGTAGAAGGCTTATGTCCTTAATGCACCGCTCGGTGTGCTTGACCTCGAACGTAGTCTGTGGATGTTGTGAACATCTGACATACACGTTTTGATAACTACG	A	G	652702725	652702825	643982770	643982870	653001743	653001843	654571394	654571494
RDMb-h3:SNP_34	TCTGACATACACGTTTTGATAACTACGTGATAGTTCAATTAAATGGTTTCGAGTAGAGGCACCAAAGACATTTTCGAAACATCACGGAACATATGAGATGT	C	A	652702799	652702899	643982844	643982944	653001817	653001917	654571468	654571568
RDMb-h3:SNP_35	GACATACACGTTTTGATAACTACGTGATAGTTCAATTAAATGGTTTCGAGTAGAGGCACCAAAGACATTTTCGAAACATCACGGAACATATGAGATGTTTC	G	A	652702802	652702902	643982847	643982947	653001820	653001920	654571471	654571571
RDMb-h3:SNP_36	CATACACGTTTTGATAACTACGTGATAGTTCAATTAAATGGTTTCGAGTAGAGGCACCAAAGACATTTTCGAAACATCACGGAACATATGAGATGTTTCGA	A	T	652702804	652702904	643982849	643982949	653001822	653001922	654571473	654571573
RDMb-h3:SNP_37	TACACGTTTTGATAACTACGTGATAGTTCAATTAAATGGTTTCGAGTAGAGGCACCAAAGACATTTTCGAAACATCACGGAACATATGAGATGTTTCGAGG	A	T	652702806	652702906	643982851	643982951	653001824	653001924	654571475	654571575
RDMb-h3:SNP_38	AACTACGTGATAGTTCAATTAAATGGTTTCGAGTAGAGGCACCAAAGACATTTTCGAAACATCACGGAACATATGAGATGTTTCGAGGGCTGAAATTGGGA	A	G	652702819	652702919	643982864	643982964	653001837	653001937	654571488	654571588
RDMb-h3:SNP_39	GAACATCATAGTTGCACCCTATTGGATATGGTGCGTACCATGATGTCTCCTATCAAATTACCACTATCGTTCATGGGTTAGGCATTAGAGACAACCGCACT	C	T	652704440	652704540	643984485	643984585	653003458	653003558	654573109	654573209
RDMb-h3:SNP_40	TATTACTCATATAAATAGAACAACCATTATTCTCTGATTTAAATGAATATCCGTCTCGCATCAAACAAGATCCAGATATAATGTTCATGCTTAACACTGGC	T	A	652708344	652708444	643988389	643988489	653007362	653007462	654577013	654577113
RDMb-h3:SNP_41	TGAAGGCTATCTTTCTGAAACTAGTGATGATGAATCAGGTGATGAATTTTTCCCCAGCTATGTCAAACTTGCTTCCCTTGCCACTGAACAACAAAGAGCTT	T	G	652714063	652714163	643994108	643994208	653013081	653013181	654582732	654582832
RDMb-h3:SNP_42	GAAGGCTATCTTTCTGAAACTAGTGATGATGAATCAGGTGATGAATTTTTCCCCAGCTATGTCAAACTTGCTTCCCTTGCCACTGAACAACAAAGAGCTTT	T	G	652714064	652714164	643994109	643994209	653013082	653013182	654582733	654582833
RDMb-h3:SNP_43	AGGTGATGAATTTTTCCCCAGCTATGTCAAACTTGCTTCCCTTGCCACTGAACAACAAAGAGCTTTGGAAAAGATTCAAAACATGCTTAGTAAGAGCGATG	G	A	652714099	652714199	643994144	643994244	653013117	653013217	654582768	654582868
RDMb-h3:SNP_44	GGCGAAGAAATGGATCAGTCAAAAGCTTTGGCTGATAGTCTTCAGAGACATCACTCCAAGTTTGATGCCCTTCAAGATCAACATAATGCTCTCTTATCTGA	A	T	652714208	652714308	643994253	643994353	653013226	653013326	654582877	654582977
RDMb-h3:SNP_45	AGTCAAAAGCTTTGGCTGATAGTCTTCAGAGACATCACTCCAAGTTTGATGCCCTTCAAGATCAACATAATGCTCTCTTATCTGATCATGAGAAACTTTCT	T	C	652714224	652714324	643994269	643994369	653013242	653013342	654582893	654582993
RDMb-h3:SNP_46	AAGCCTGAGCAGTATCCCAAAACCACATGGGTTGCTGCAAAGGAACCTTTAGTGGATCCATCTACTTTATCTGGATTTACCTGTGCTAATCCTATTATCAT	T	C	652714745	652714845	413478945	413479045	653013763	653013863	654583414	654583514
RDMb-h3:SNP_47	CTCTCTTTGATGTGGCCATCATCCACAATTTCATTGATGAGTGGTTCGATACCCCAAACGTCAGCTTTGAAGACTTACAGCTTCCAATTGGCCTCATCGTC	T	C	652721108	652721208	644001150	644001250	653020136	653020236	654589774	654589874
RDMb-h3:SNP_48	ACAATTTCATTGATGAGTGGTTCGATACCCCAAACGTCAGCTTTGAAGACTTACAGCTTCCAATTGGCCTCATCGTCTCTTTCAATGGCGCCATTGCTTCT	C	T	652721132	652721232	644001174	644001274	653020160	653020260	654589798	654589898
RDMb-h3:SNP_49	GATACCCCAAACGTCAGCTTTGAAGACTTACAGCTTCCAATTGGCCTCATCGTCTCTTTCAATGGCGCCATTGCTTCTGAGCTGGCTCTCGCTCAGCGAAT	T	G	652721155	652721255	644001197	644001297	653020183	653020283	654589821	654589921
RDMb-h3:SNP_50	TGACTATCATGTTGAGCATAGGCCTCAAGTCCAGAAGCCCAAGCCAAGATTGCCAAGGTTTCCAGGTACTGCAAACTCAGCAGGGTCCTTCAATGCAAATG	T	C	652722732	652722832	644002774	644002874	653021760	653021860	654591398	654591498
RDMb-h3:SNP_51	ACTCTATGGCCTATCAAAGGACATTCATCAGCGGCAAAGCTTGAAGGAGTTATGAAGACTTTGGTCTTCTACATTTTCAATGGCATCAACTTCAATGCACA	T	C	652723429	652723529	644003471	644003571	653022457	653022557	654592095	654592195
RDMb-h3:SNP_52	CCATTGGCTGGAAATACTCGTCTGCCTCATCGAGCACCTACCGAAGCCATTGAAAGCACCATTGCCCAAAGGCCTCAGAAGCATTCTCGTGTTCTCAATGA	T	C	652723801	652723901	644003843	644003943	653022829	653022929	654592467	654592567
RDMb-h3:SNP_53	TGTCAATCGCATTCGCAACCTTGCCACCAAGAATGCCTTTGTTGCTCACAAAACTTGTCGGCGATCATGGAAGAGTTTGACCCTGCTTAGTGCTGAAGCAG	A	G	652723986	652724086	644004028	644004128	653023014	653023114	654592652	654592752
RDMb-h3:SNP_54	GCATTCGCAACCTTGCCACCAAGAATGCCTTTGTTGCTCACAAAACTTGTCGGCGATCATGGAAGAGTTTGACCCTGCTTAGTGCTGAAGCAGATCTTCAA	T	C	652723994	652724094	644004036	644004136	653023022	653023122	654592660	654592760

RDMb-h3:SNP_55	TCGGATGAACCACGATGTCGGGGATTCAATCAATCCCGTATACAATTCCATTTTTCCATCGGTATGTTACTTGCCCGAGATTCGATCGTCGGTATCCCCGT	A	C	652733715	652733815	644013751	644013851	653032742	653032842	654602375	654602475
RDMb-h3:SNP_56	ATGAACCACGATGTCGGGGATTCAATCAATCCCGTATACAATTCCATTTTTCCATCGGTATGTTACTTGCCCGAGATTCGATCGTCGGTATCCCCGTACCT	T	G	652733719	652733819	644013755	644013855	653032746	653032846	654602379	654602479
RDMb-h3:SNP_57	TTTTTCCATCGGTATGTTACTTGCCCGAGATTCGATCGTCGGTATCCCCGTACCTCATTCAATCTCGTTACCGGCAAGTCTCTTTACTCGTTCCGTAAAGC	G	A	652733765	652733865	644013801	644013901	653032792	653032892	654602425	654602525
RDMb-h3:SNP_58	ATCGGTATGTTACTTGCCCGAGATTCGATCGTCGGTATCCCCGTACCTCATTCAATCTCGTTACCGGCAAGTCTCTTTACTCGTTCCGTAAAGCATGATCC	A	G	652733772	652733872	644013808	644013908	653032799	653032899	654602432	654602532
RDMb-h3:SNP_59	AGTCTCTTTACTCGTTCCGTAAAGCATGATCCCGTGGCTAACTCCTTAGACACATTGAGCTCATTATTATGATGCATTACCGAGTGGGCCCAGAGATACCT	A	T	652733841	652733941	644013877	644013977	653032868	653032968	654602501	654602601
RDMb-h3:SNP_60	GTAAAGCATGATCCCGTGGCTAACTCCTTAGACACATTGAGCTCATTATTATGATGCATTACCGAGTGGGCCCAGAGATACCTCTCCGTCATACGGAGTGA	T	G	652733859	652733959	644013895	644013995	653032886	653032986	654602519	654602619
RDMb-h3:SNP_61	GGTAAGAGAAATCATAGATCGCACCATATCCAATAGAGTGCGATTACGATGTACGGACACACCATTTCGCTGAGGTGTTCCATGCGGCGTGAGTAGTCAAA	T	C	652736594	652736694	644016630	644016730	653035621	653035721	654605254	654605354
RDMb-h3:SNP_62	AAGAGAAATCATAGATCGCACCATATCCAATAGAGTGCGATTACGATGTACGGACACACCATTTCGCTGAGGTGTTCCATGCGGCGTGAGTAGTCAAAAAA	A	T	652736597	652736697	644016633	644016733	653035624	653035724	654605257	654605357
RDMb-h3:SNP_63	TAGAGTGCGATTACGATGTACGGACACACCATTTCGCTGAGGTGTTCCATGCGGCGTGAGTAGTCAAAAAATTCCACATTTTTTTAAGTGTGTGCCAAACG	T	G	652736627	652736727	644016663	644016763	653035654	653035754	654605287	654605387
RDMb-h3:SNP_64	ACGATGTACGGACACACCATTTCGCTGAGGTGTTCCATGCGGCGTGAGTAGTCAAAAAATTCCACATTTTTTTAAGTGTGTGCCAAACGTGTGACTCAAAT	A	T	652736639	652736739	644016675	644016775	653035666	653035766	654605299	654605399
RDMb-h3:SNP_65	ATGTACGGACACACCATTTCGCTGAGGTGTTCCATGCGGCGTGAGTAGTCAAAAAATTCCACATTTTTTTAAGTGTGTGCCAAACGTGTGACTCAAATATT	C	G	652736642	652736742	644016678	644016778	653035669	653035769	654605302	654605402
RDMb-h3:SNP_66	ACGGACACACCATTTCGCTGAGGTGTTCCATGCGGCGTGAGTAGTCAAAAAATTCCACATTTTTTTAAGTGTGTGCCAAACGTGTGACTCAAATATTCTCC	A	C	652736646	652736746	644016682	644016782	653035673	653035773	654605306	654605406
RDMb-h3:SNP_67	TTCGCTGAGGTGTTCCATGCGGCGTGAGTAGTCAAAAAATTCCACATTTTTTTAAGTGTGTGCCAAACGTGTGACTCAAATATTCTCCTCCACGGTTTGAT	T	C	652736659	652736759	644016695	644016795	653035686	653035786	654605319	654605419
RDMb-h3:SNP_68	ATTTTTTTAAGTGTGTGCCAAACGTGTGACTCAAATATTCTCCTCCACGGTTTGATCATAAGAACTTTATTTTCCTGTCACGTTGATTCTCTACCTCGCTC	G	A	652736704	652736804	644016740	644016840	653035731	653035831	654605364	654605464
RDMb-h3:SNP_69	TTTTTTAAGTGTGTGCCAAACGTGTGACTCAAATATTCTCCTCCACGGTTTGATCATAAGAACTTTATTTTCCTGTCACGTTGATTCTCTACCTCGCTCTG	T	C	652736706	652736806	644016742	644016842	653035733	653035833	654605366	654605466
RDMb-h3:SNP_70	AAGTGTGTGCCAAACGTGTGACTCAAATATTCTCCTCCACGGTTTGATCATAAGAACTTTATTTTCCTGTCACGTTGATTCTCTACCTCGCTCTGAAATTC	A	G	652736712	652736812	644016748	644016848	653035739	653035839	654605372	654605472
RDMb-h3:SNP_71	AGCTCCAGCAACTGGTGGTAGACTCGAACACTCCATTGTATGATGGTTGTAATCCTGAGGTGGCTCGCTTGAGTTTCATGCTCCAACTCCTGAAGACAAAG	T	C	652738888	652738988	644018924	644019024	653037915	653038015	654607548	654607648
RDMb-h3:SNP_72	GGTGGTAGACTCGAACACTCCATTGTATGATGGTTGTAATCCTGAGGTGGCTCGCTTGAGTTTCATGCTCCAACTCCTGAAGACAAAGGATAAAAACAAAT	G	A	652738901	652739001	644018937	644019037	653037928	653038028	654607561	654607661
RDMb-h3:SNP_73	GTAATCCTGAGGTGGCTCGCTTGAGTTTCATGCTCCAACTCCTGAAGACAAAGGATAAAAACAAATGGACCGACACTAGCCTCGATGATCATCTCAAGTAC	A	G	652738936	652739036	644018972	644019072	653037963	653038063	654607596	654607696
RDMb-h3:SNP_74	CCTGAGGTGGCTCGCTTGAGTTTCATGCTCCAACTCCTGAAGACAAAGGATAAAAACAAATGGACCGACACTAGCCTCGATGATCATCTCAAGTACCTAAA	A	C	652738941	652739041	644018977	644019077	653037968	653038068	654607601	654607701
RDMb-h3:SNP_75	TCCTGAAGACAAAGGATAAAAACAAATGGACCGACACTAGCCTCGATGATCATCTCAAGTACCTAAAGGATGTTCTTCCCGCGAGGAATCTATGTCCTACT	T	G	652738975	652739075	644019011	644019111	653038002	653038102	654607635	654607735
RDMb-h3:SNP_76	TGGCACCTGGCAAGTTTGAGCCATTAGAGCCGGAAGAACCTCACAAGTGATATGGGAACCAAGTAGGATGCATCCTACCGGAATGCGCGAGCATCAACGAC	A	C	652741317	652741417	644021354	644021454	653040344	653040444	654610138	654610238
RDMb-h3:SNP_77	CGGAATGCGCGAGCATCAACGACAATGACTTAAGGAGTAAAGAACATTTCAGGCAGTTTCTCCTGATGAAGATGCACAAGGGATTCAAGTTCCCCCACCGG	C	G	652741395	652741495	644021432	644021532	653040422	653040522	654610216	654610316
RDMb-h3:SNP_78	CGAGCATCAACGACAATGACTTAAGGAGTAAAGAACATTTCAGGCAGTTTCTCCTGATGAAGATGCACAAGGGATTCAAGTTCCCCCACCGGGATGATAGC	T	G	652741404	652741504	644021441	644021541	653040431	653040531	654610225	654610325
RDMb-h3:SNP_79	AACGACAATGACTTAAGGAGTAAAGAACATTTCAGGCAGTTTCTCCTGATGAAGATGCACAAGGGATTCAAGTTCCCCCACCGGGATGATAGCATAGAGCA	T	C	652741412	652741512	644021449	644021549	653040439	653040539	654610233	654610333
RDMb-h3:SNP_80	CAATGACTTAAGGAGTAAAGAACATTTCAGGCAGTTTCTCCTGATGAAGATGCACAAGGGATTCAAGTTCCCCCACCGGGATGATAGCATAGAGCAACCGT	A	T	652741417	652741517	644021454	644021554	653040444	653040544	654610238	654610338
RDMb-h3:SNP_81	AAGGAGTAAAGAACATTTCAGGCAGTTTCTCCTGATGAAGATGCACAAGGGATTCAAGTTCCCCCACCGGGATGATAGCATAGAGCAACCGTGGGATGATC	G	A	652741426	652741526	644021463	644021563	653040453	653040553	654610247	654610347
RDMb-h3:SNP_82	CTCCTGATGAAGATGCACAAGGGATTCAAGTTCCCCCACCGGGATGATAGCATAGAGCAACCGTGGGATGATCCGAAGGTGAAATTGATTAACAATTACGC	G	A	652741454	652741554	644021491	644021591	653040481	653040581	654610275	654610375
RDMb-h3:SNP_83	TGAAGATGCACAAGGGATTCAAGTTCCCCCACCGGGATGATAGCATAGAGCAACCGTGGGATGATCCGAAGGTGAAATTGATTAACAATTACGCCATGGGC	G	A	652741461	652741561	644021498	644021598	653040488	653040588	654610282	654610382
RDMb-h3:SNP_84	GTTCCCCCACCGGGATGATAGCATAGAGCAACCGTGGGATGATCCGAAGGTGAAATTGATTAACAATTACGCCATGGGCATGTTCAGCAATGATTTGGCCT	G	A	652741483	652741583	644021520	644021620	653040510	653040610	654610304	654610404
RDMb-h3:SNP_85	TAGCATAGAGCAACCGTGGGATGATCCGAAGGTGAAATTGATTAACAATTACGCCATGGGCATGTTCAGCAATGATTTGGCCTCTTGGAAAGGGAGGGTGA	T	C	652741501	652741601	644021538	644021638	653040528	653040628	654610322	654610422
RDMb-h3:SNP_86	TCTAGGGAGTACCTCCAAAACTTCATGGTACAGAATAAGGACCAGGAAACTGTCCTCCTACCTTATCATCCAGTTAGTTCCGGACAACCCTTTCATACATT	C	T	652745657	652745757	644025689	644025789	653044684	653044784	654614473	654614573
RDMb-h3:SNP_87	GCCGTGTATTTGGACCCTACCATAAACTACGAGAAGAAGGACTACACCCTCATAATGAATATTCTAGATGATACTCTCCAAGGCTTCAGCATTAGGGGTGG	T	A	652745860	652745960	644025892	644025992	653044887	653044987	654614676	654614776
RDMb-h3:SNP_88	AATGGGGTCTCGGGCGCCATCCATAAAGGCTTCAAAAGTAGACAAGAAGCAGAAGCTAGTTACTTGAGGTTCACGCTAGCGCGAGAGGACTTGTAACCGCC	C	G	652746746	652746846	644026778	644026878	653045773	653045873	654615562	654615662
RDMb-h3:SNP_89	CAAGAAGCAGAAGCTAGTTACTTGAGGTTCACGCTAGCGCGAGAGGACTTGTAACCGCCACCTCATGTACTGCATAGTTCCGCTCTCACTTATAGTGATAG	T	C	652746788	652746888	644026820	644026920	653045815	653045915	654615604	654615704
RDMb-h3:SNP_90	AGAGGACTTGTAACCGCCACCTCATGTACTGCATAGTTCCGCTCTCACTTATAGTGATAGCTCTTCTCGCGTATATCATTGTTTAGATGGATAACGATGTA	T	C	652746829	652746929	644026861	644026961	653045856	653045956	654615645	654615745
RDMb-h3:SNP_91	GTTGTCATACTCATCAACATGCAAGTCGTGATTCCTATTACAAGAACATAATCAATCTCATACATCTCATATATAATTCATCACATCCTTTTGGACATATC	A	G	652749318	652749418	644029350	644029450	653048345	653048445	654618134	654618234
RDMb-h3:SNP_92	GTTACCACCATGGCAACTCATGTGGGTCTCATACCCATCTCCCTCGATGGACTATCTATCACAACACATGATAGCCCTTTTGTAAATGGATCTGCCAGATT	G	C	652761473	652761573	644041624	644041724	653060560	653060660	654630166	654630266
RDMb-h3:SNP_93	CATGTGGGTCTCATACCCATCTCCCTCGATGGACTATCTATCACAACACATGATAGCCCTTTTGTAAATGGATCTGCCAGATTCTTAGCCATATGGTCATA	A	G	652761491	652761591	644041642	644041742	653060578	653060678	654630184	654630284
RDMb-h3:SNP_94	TCTCCCTCGATGGACTATCTATCACAACACATGATAGCCCTTTTGTAAATGGATCTGCCAGATTCTTAGCCATATGGTCATACTCCAATGCTATCACTCCG	T	G	652761510	652761610	644041661	644041761	653060597	653060697	654630203	654630303
RDMb-h3:SNP_95	CACAACACATGATAGCCCTTTTGTAAATGGATCTGCCAGATTCTTAGCCATATGGTCATACTCCAATGCTATCACTCCGGAGTTTCTCAATTTTCTAACAG	A	G	652761532	652761632	644041683	644041783	653060619	653060719	654630225	654630325
RDMb-h3:SNP_96	ACATGATAGCCCTTTTGTAAATGGATCTGCCAGATTCTTAGCCATATGGTCATACTCCAATGCTATCACTCCGGAGTTTCTCAATTTTCTAACAGCTTTTA	T	A	652761538	652761638	644041689	644041789	653060625	653060725	654630231	654630331
RDMb-h3:SNP_97	ATAGCCCTTTTGTAAATGGATCTGCCAGATTCTTAGCCATATGGTCATACTCCAATGCTATCACTCCGGAGTTTCTCAATTTTCTAACAGCTTTTAATCTC	C	G	652761543	652761643	644041694	644041794	653060630	653060730	654630236	654630336
RDMb-h3:SNP_98	CTTTTGTAAATGGATCTGCCAGATTCTTAGCCATATGGTCATACTCCAATGCTATCACTCCGGAGTTTCTCAATTTTCTAACAGCTTTTAATCTCATTCTT	T	C	652761549	652761649	644041700	644041800	653060636	653060736	654630242	654630342
RDMb-h3:SNP_99	GATTCTTAGCCATATGGTCATACTCCAATGCTATCACTCCGGAGTTTCTCAATTTTCTAACAGCTTTTAATCTCATTCTTATGTGTTTTGGACTTCATGTT	C	T	652761570	652761670	644041721	644041821	653060657	653060757	654630263	654630363
RDMb-h3:SNP_100	CCATATGGTCATACTCCAATGCTATCACTCCGGAGTTTCTCAATTTTCTAACAGCTTTTAATCTCATTCTTATGTGTTTTGGACTTCATGTTGTCCTTTGA	A	G	652761579	652761679	644041730	644041830	653060666	653060766	654630272	654630372
RDMb-h3:SNP_101	ACGCGATGTCACGCCTTGTTGCGCTCGCTAGGTACATCAGTGAACCAATAATTTGAGAGTATCTCAGTTGATCTTTAGCCGTGCCTTCGAACTTTCGAATC	A	G	652762096	652762196	644042247	644042347	653061183	653061283	654630789	654630889
RDMb-h3:SNP_102	GTTGCGCTCGCTAGGTACATCAGTGAACCAATAATTTGAGAGTATCTCAGTTGATCTTTAGCCGTGCCTTCGAACTTTCGAATCAACACGCTAGGATCATA	G	A	652762113	652762213	644042264	644042364	653061200	653061300	654630806	654630906
RDMb-h3:SNP_103	AGTGAACCAATAATTTGAGAGTATCTCAGTTGATCTTTAGCCGTGCCTTCGAACTTTCGAATCAACACGCTAGGATCATATTTTGTTTGAGATGGTGTGCA	C	T	652762134	652762234	644042285	644042385	653061221	653061321	654630827	654630927
RDMb-h3:SNP_104	ATCTTTAGCCGTGCCTTCGAACTTTCGAATCAACACGCTAGGATCATATTTTGTTTGAGATGGTGTGCAGTCTAAATATCCAAAATGACTCAACACCTTCT	T	G	652762166	652762266	644042317	644042417	653061253	653061353	654630859	654630959
RDMb-h3:SNP_105	TCTTTAGCCGTGCCTTCGAACTTTCGAATCAACACGCTAGGATCATATTTTGTTTGAGATGGTGTGCAGTCTAAATATCCAAAATGACTCAACACCTTCTC	T	G	652762167	652762267	644042318	644042418	653061254	653061354	654630860	654630960
RDMb-h3:SNP_106	TTCGAATCAACACGCTAGGATCATATTTTGTTTGAGATGGTGTGCAGTCTAAATATCCAAAATGACTCAACACCTTCTCAACATAATGGGATTGCAGAAGT	T	C	652762189	652762289	644042340	644042440	653061276	653061376	654630882	654630982
RDMb-h3:SNP_107	TCGAATCAACACGCTAGGATCATATTTTGTTTGAGATGGTGTGCAGTCTAAATATCCAAAATGACTCAACACCTTCTCAACATAATGGGATTGCAGAAGTG	A	G	652762190	652762290	644042341	644042441	653061277	653061377	654630883	654630983
RDMb-h3:SNP_108	GAGTTGTATTAAACTTATCATGCCATTACTTAGGTGCTTGCTTCAGGCCGTATAAAAATTTCAGCAACCTACACACCTTTCTTTCCTGACCATCTATCACA	G	A	652762528	652762628	644042679	644042779	653061615	653061715	654631221	654631321
RDMb-h3:SNP_109	ATTAAACTTATCATGCCATTACTTAGGTGCTTGCTTCAGGCCGTATAAAAATTTCAGCAACCTACACACCTTTCTTTCCTGACCATCTATCACAAAGCCAT	A	G	652762535	652762635	644042686	644042786	653061622	653061722	654631228	654631328
RDMb-h3:SNP_110	TTCAGCAACCTACACACCTTTCTTTCCTGACCATCTATCACAAAGCCATTTGGTTGTTGCACATAGATTTCCTTGTTTAGCTCTCCATTTAGAAAAGTCGT	T	C	652762587	652762687	644042738	644042838	653061674	653061774	654631280	654631380
RDMb-h3:SNP_111	GCAACCTACACACCTTTCTTTCCTGACCATCTATCACAAAGCCATTTGGTTGTTGCACATAGATTTCCTTGTTTAGCTCTCCATTTAGAAAAGTCGTCTTA	T	C	652762591	652762691	644042742	644042842	653061678	653061778	654631284	654631384
RDMb-h3:SNP_112	CACACCTTTCTTTCCTGACCATCTATCACAAAGCCATTTGGTTGTTGCACATAGATTTCCTTGTTTAGCTCTCCATTTAGAAAAGTCGTCTTAACATCCAT	C	T	652762599	652762699	644042750	644042850	653061686	653061786	654631292	654631392
RDMb-h3:SNP_113	ATTTCCTTGTTTAGCTCTCCATTTAGAAAAGTCGTCTTAACATCCATCTAGTGAACGAGAAGACCGTGCAAGGCCGCCAACAAGAGTAATACTCGAATAGT	A	G	652762653	652762753	644042804	644042904	653061740	653061840	654631346	654631446
RDMb-h3:SNP_114	CCTTGTTTAGCTCTCCATTTAGAAAAGTCGTCTTAACATCCATCTAGTGAACGAGAAGACCGTGCAAGGCCGCCAACAAGAGTAATACTCGAATAGTGGTC	A	G	652762657	652762757	644042808	644042908	653061744	653061844	654631350	654631450
RDMb-h3:SNP_115	CAGGCTCAGGAGTCTCCTCAGATTCCTGTCTAGAAGTGCTTTGCATATCCCTCATAGGAAAAACATCCTCAAAGAATGTAGCATCCTTACACTCCATAGTT	C	T	652763170	652763270	644043321	644043421	653062257	653062357	654631863	654631963
RDMb-h3:SNP_116	TCCTCAGATTCCTGTCTAGAAGTGCTTTGCATATCCCTCATAGGAAAAACATCCTCAAAGAATGTAGCATCCTTACACTCCATAGTTGTACCGACCTTCTG	C	T	652763184	652763284	644043335	644043435	653062271	653062371	654631877	654631977
RDMb-h3:SNP_117	TTGCATATCCCTCATAGGAAAAACATCCTCAAAGAATGTAGCATCCTTACACTCCATAGTTGTACCGACCTTCTGGTTAGGTACCTCAGATTTAACTACTA	C	G	652763210	652763310	644043361	644043461	653062297	653062397	654631903	654632003
RDMb-h3:SNP_118	CCTCATAGGAAAAACATCCTCAAAGAATGTAGCATCCTTACACTCCATAGTTGTACCGACCTTCTGGTTAGGTACCTCAGATTTAACTACTAGAAATCTAT	G	A	652763219	652763319	644043370	644043470	653062306	653062406	654631912	654632012

RDMb-h3:SNP_119	TCAAAGAATGTAGCATCCTTACACTCCATAGTTGTACCGACCTTCTGGTTAGGTACCTCAGATTTAACTACTAGAAATCTATAGCCAACGCTGTTCTTAGC	T	C	652763238	652763338	644043389	644043489	653062325	653062425	654631931	654632031
RDMb-h3:SNP_120	CCTTACACTCCATAGTTGTACCGACCTTCTGGTTAGGTACCTCAGATTTAACTACTAGAAATCTATAGCCAACGCTGTTCTTAGCGTAGCCCAAATTAACG	A	C	652763254	652763354	644043405	644043505	653062341	653062441	654631947	654632047
RDMb-h3:SNP_121	CTTAGCGTAGCCCAAATTAACGCAGTCCACAGTCTTGGGTCCAAGCTTATGCTTTTTGGGGATCGGCACATTGACTTTCGCCAAACAGCCCCAAGTACGCA	T	C	652763333	652763433	644043484	644043584	653062420	653062520	654632026	654632126
RDMb-h3:SNP_122	CAGATACACATAGCAATATCTAGTGGAATCATCTATCAATGTCATGAAGCATTTCTTTCCACCTTTAGTCAACACACCATTCATCTCACAAAGATCAGAAT	C	T	652763818	652763918	644043969	644044069	653062905	653063005	654632511	654632611
RDMb-h3:SNP_123	ATGAGTTCTAATGGTGCCAAGTGTCTCTCCTCCGCAGCCTTGTGAGGCTGGCGAGGTTTCTTAGCTTGCACACATGAAAGGCACTTAGAACCTTTGGCTAA	G	T	652763921	652764021	644044072	644044172	653063008	653063108	654632614	654632714
RDMb-h3:SNP_124	AATGGTGCCAAGTGTCTCTCCTCCGCAGCCTTGTGAGGCTGGCGAGGTTTCTTAGCTTGCACACATGAAAGGCACTTAGAACCTTTGGCTAAGTGAAACTC	T	G	652763930	652764030	644044081	644044181	653063017	653063117	654632623	654632723
RDMb-h3:SNP_125	AGGCACTTAGAACCTTTGGCTAAGTGAAACTCGGGATTAAATCCAACTTAGCTAGCCGCGTCATAACACTGAAACTTATGTGACAAAGACGTGAACGCCAA	A	G	652763999	652764099	644044150	644044250	653063086	653063186	654632692	654632792
RDMb-h3:SNP_126	TAAGTGAAACTCGGGATTAAATCCAACTTAGCTAGCCGCGTCATAACACTGAAACTTATGTGACAAAGACGTGAACGCCAAACTTCATATTCACTAAAACT	T	C	652764019	652764119	644044170	644044270	653063106	653063206	654632712	654632812
RDMb-h3:SNP_127	CTTAGCTAGCCGCGTCATAACACTGAAACTTATGTGACAAAGACGTGAACGCCAAACTTCATATTCACTAAAACTCGAATGAATATGGTTCATGACTTTAT	C	T	652764045	652764145	644044196	644044296	653063132	653063232	654632738	654632838
RDMb-h3:SNP_128	CGTCATAACACTGAAACTTATGTGACAAAGACGTGAACGCCAAACTTCATATTCACTAAAACTCGAATGAATATGGTTCATGACTTTATTACAGAAATCTG	T	G	652764057	652764157	644044208	644044308	653063144	653063244	654632750	654632850
RDMb-h3:SNP_129	AACACTGAAACTTATGTGACAAAGACGTGAACGCCAAACTTCATATTCACTAAAACTCGAATGAATATGGTTCATGACTTTATTACAGAAATCTGCGAGGG	C	T	652764063	652764163	644044214	644044314	653063150	653063250	654632756	654632856
RDMb-h3:SNP_130	CGTGAACGCCAAACTTCATATTCACTAAAACTCGAATGAATATGGTTCATGACTTTATTACAGAAATCTGCGAGGGAAAGGCGGAACATCCCTCCGCTCTT	T	C	652764088	652764188	644044239	644044339	653063175	653063275	654632781	654632881
RDMb-h3:SNP_131	ACTCGCGCCATTCCCCATCAATACGGACCCGTGGCCTGTGACCTGGTAATAAGAAAATAATGAAATGTCAGCACATACATGAACGCCTGCACCTATATCCA	T	G	652764390	652764490	644044541	644044641	653063477	653063577	654633083	654633183
RDMb-h3:SNP_132	CGCCATTCCCCATCAATACGGACCCGTGGCCTGTGACCTGGTAATAAGAAAATAATGAAATGTCAGCACATACATGAACGCCTGCACCTATATCCACAAAC	A	G	652764395	652764495	644044546	644044646	653063482	653063582	654633088	654633188
RDMb-h3:SNP_133	CATTCCCCATCAATACGGACCCGTGGCCTGTGACCTGGTAATAAGAAAATAATGAAATGTCAGCACATACATGAACGCCTGCACCTATATCCACAAACTAA	T	C	652764398	652764498	644044549	644044649	653063485	653063585	654633091	654633191
RDMb-h3:SNP_134	ACCCGTGGCCTGTGACCTGGTAATAAGAAAATAATGAAATGTCAGCACATACATGAACGCCTGCACCTATATCCACAAACTAATCGGTGGGCTGAAACACT	T	C	652764416	652764516	644044567	644044667	653063503	653063603	654633109	654633209
RDMb-h3:SNP_135	CTGTGACCTGGTAATAAGAAAATAATGAAATGTCAGCACATACATGAACGCCTGCACCTATATCCACAAACTAATCGGTGGGCTGAAACACTGAAAAAACA	G	A	652764425	652764525	644044576	644044676	653063512	653063612	654633118	654633218
RDMb-h3:SNP_136	GTAATAAGAAAATAATGAAATGTCAGCACATACATGAACGCCTGCACCTATATCCACAAACTAATCGGTGGGCTGAAACACTGAAAAAACAGTAAATAAAT	A	G	652764435	652764535	644044586	644044686	653063522	653063622	654633128	654633228
RDMb-h3:SNP_137	AAAATAATGAAATGTCAGCACATACATGAACGCCTGCACCTATATCCACAAACTAATCGGTGGGCTGAAACACTGAAAAAACAGTAAATAAATTACCGTAC	A	C	652764443	652764543	644044594	644044694	653063530	653063630	654633136	654633236
RDMb-h3:SNP_138	TAATGAAATGTCAGCACATACATGAACGCCTGCACCTATATCCACAAACTAATCGGTGGGCTGAAACACTGAAAAAACAGTAAATAAATTACCGTACCCAA	T	C	652764447	652764547	644044598	644044698	653063534	653063634	654633140	654633240
RDMb-h3:SNP_139	GACGGTTTTCAACCATCTTGTAATCTTGGAACTGCTCTATAATATACATTTCGCTCCCAGCGTCAGTGGCCCCAAATTTAGATTCGAGCGCCTCCCACAAG	T	C	652765042	652765142	644045193	644045293	653064129	653064229	654633735	654633835
RDMb-h3:SNP_140	CCATCTTGTAATCTTGGAACTGCTCTATAATATACATTTCGCTCCCAGCGTCAGTGGCCCCAAATTTAGATTCGAGCGCCTCCCACAAGTCCTTGGCGACA	G	A	652765054	652765154	644045205	644045305	653064141	653064241	654633747	654633847
RDMb-h3:SNP_141	TCTTGTAATCTTGGAACTGCTCTATAATATACATTTCGCTCCCAGCGTCAGTGGCCCCAAATTTAGATTCGAGCGCCTCCCACAAGTCCTTGGCGACACGC	A	G	652765057	652765157	644045208	644045308	653064144	653064244	654633750	654633850
RDMb-h3:SNP_142	TTGTAATCTTGGAACTGCTCTATAATATACATTTCGCTCCCAGCGTCAGTGGCCCCAAATTTAGATTCGAGCGCCTCCCACAAGTCCTTGGCGACACGCAC	T	C	652765059	652765159	644045210	644045310	653064146	653064246	654633752	654633852
RDMb-h3:SNP_143	CTTGGAACTGCTCTATAATATACATTTCGCTCCCAGCGTCAGTGGCCCCAAATTTAGATTCGAGCGCCTCCCACAAGTCCTTGGCGACACGCACATGTAAA	A	G	652765066	652765166	644045217	644045317	653064153	653064253	654633759	654633859
RDMb-h3:SNP_144	AGTGGCCCCAAATTTAGATTCGAGCGCCTCCCACAAGTCCTTGGCGACACGCACATGTAAATATGCGTGGACCAACTTATCTCCGATCATGCTAAGTACTG	C	T	652765106	652765206	644045257	644045357	653064193	653064293	654633799	654633899
RDMb-h3:SNP_145	TCGAGCGCCTCCCACAAGTCCTTGGCGACACGCACATGTAAATATGCGTGGACCAACTTATCTCCGATCATGCTAAGTACTGCTCCGAGGAACACGACGGT	G	C	652765125	652765225	644045276	644045376	653064212	653064312	654633818	654633918
RDMb-h3:SNP_146	GCCTCCCACAAGTCCTTGGCGACACGCACATGTAAATATGCGTGGACCAACTTATCTCCGATCATGCTAAGTACTGCTCCGAGGAACACGACGGTGGCTTC	A	G	652765131	652765231	644045282	644045382	653064218	653064318	654633824	654633924
RDMb-h3:SNP_147	TGAATACCTTCTCCTGTTCAGGAGCAATCGTCCCCGAAGGGACACCGATAACCCAAAACACGTTCATAACCGTGAGCCGTAAGGTGTTCTTTGTCTGCCAA	A	G	652765234	652765334	644045385	644045485	653064321	653064421	654633927	654634027
RDMb-h3:SNP_148	AGGGACACCGATAACCCAAAACACGTTCATAACCGTGAGCCGTAAGGTGTTCTTTGTCTGCCAATGCTTAAAATATGTACCGGTAAACTTATCCGGTTTCA	T	G	652765271	652765371	644045422	644045522	653064358	653064458	654633964	654634064
RDMb-h3:SNP_149	TGATCTAAACATGCACGTACTAAGCAAACAGTAGACAAATCTACACATAGTTCTAGTACTGCTAATACCAAAATAAACAGGAGCGGGATAAACGTGTTATA	G	C	652765513	652765613	644045664	644045764	653064600	653064700	654634206	654634306
RDMb-h3:SNP_150	ACTAAGCAAACAGTAGACAAATCTACACATAGTTCTAGTACTGCTAATACCAAAATAAACAGGAGCGGGATAAACGTGTTATACCCTCCAGTAGGACAGGC	C	T	652765531	652765631	644045682	644045782	653064618	653064718	654634224	654634324
RDMb-h3:SNP_151	ACAGTAGACAAATCTACACATAGTTCTAGTACTGCTAATACCAAAATAAACAGGAGCGGGATAAACGTGTTATACCCTCCAGTAGGACAGGCAGAAGCCGC	A	T	652765540	652765640	644045691	644045791	653064627	653064727	654634233	654634333
RDMb-h3:SNP_152	ATTTGTGTTTAGAGTTGTGTTGTGATATCTTCCCGTGAGTCCCTGATCTCGATCGTACACATTTGCGTGTATGATTAGTGTACGATTGAATTGGGGGCGTC	C	T	652785411	652785511	644065383	644065483	653084441	653084541	654654020	654654120
RDMb-h3:SNP_153	CTCATTGGATGAAAAAGATGAGGAGGAGAGCGAAGAACAAAAGGAGGAAAAGCGGATTAGCTACCCGTGCCCACCTTCTAGTGAGAGTAACTCTTCAACTC	A	G	652791423	652791523	644071346	644071446	653090195	653090295	654659784	654659884
RDMb-h3:SNP_154	TACATTCCGATGATGGGCTTCCTCAAACGCCCGAGGTCTTCATGAGCAAACAAGTTGGATGCACACCCACTTAGTTTTAGTTTGAGCTTTCATACACTTAT	A	G	652794482	652794582	644074405	644074505	653093254	653093354	654662843	654662943
RDMb-h3:SNP_155	TACACGGCATTGCATACATGATAGAGCCTATGGCTGAAGCATAGGGAACTTCTTTCATTTTCTCTCTATCTTCTGCAGTGGTCGGGCATTGAGTCTGACTC	T	A	652810656	652810756	644090583	644090683	653109428	653109528	654679021	654679121
RDMb-h3:SNP_156	ACTTCTTTCATTTTCTCTCTATCTTCTGCAGTGGTCGGGCATTGAGTCTGACTCAATTTCACACCTTGTATTACAGGCAAGAACCTTTCTTTGCTTGATCC	G	T	652810703	652810803	644090630	644090730	653109475	653109575	654679068	654679168
RDMb-h3:SNP_157	TATCAAATATACCTTTCACTTTGCCATCCTTCTTATCCGCCAAATACTTAGGGTAGTTCCGCTTCCAGTGACCAGTCCCTTTGTAGTAGAAGCACTTAGTTT	A	G	652832267	652832367	644112028	644112128	653131039	653131139	654700466	654700566
RDMb-h3:SNP_158	AAATATACCTTTCACTTTGCCATCCTTCTTATCCGCCAAATACTTAGGGTAGTTCCGCTTCCAGTGACCAGTCCCTTTGTAGTAGAAGCACTTAGTTTCAG	T	C	652832271	652832371	644112032	644112132	653131043	653131143	654700470	654700570
RDMb-h3:SNP_159	GCGTTTGAGTTTTTGGATGCTTATTCTGGTTATCATCAGATCAAGATGTCAGTTAAGGACGAGGAGAAGACGGCTTTTATTACTCCATTTGGAGCCTTCT	T	G	652844511	652844611	644124272	644124372	653143283	653143383	654712710	654712810
RDMb-h3:SNP_160	ATTCGTCCAAGCATAATTTTGAGGATTGCAACATGTTTCGTCAAATAGTCAAATCGGCCATTGAAAAAGGACGATTGAAGTTTGTTGAAACACCAAGAGAT	C	T	652849662	652849762	356838158	356838058	365268219	365268119	367765728	367765628
RDMb-h3:SNP_161	TCATACTAACTTATCGATGTTCGAGAGCACAAAGACTCACGTAAGTCGGCGGAGGAGACCCGCCGGCCGTGGAATATCGCTCATCTTCGGCCTTACTACAC	C	A	652854101	652854201	644133861	644133961	653152873	653152973	654722299	654722399
RDMb-h3:SNP_162	TGCTGAGAATGCTTCATATTTATGCTTCAAGAAATAAGGCCAAACTTTTTGCGAATAATCATCAATAATAGTCAGCATGTAACTTGCACCACCTAATGACT	T	C	652883420	652883520	644163180	644163280	653182193	653182293	654751618	654751718
RDMb-h3:SNP_163	GCTGAGAATGCTTCATATTTATGCTTCAAGAAATAAGGCCAAACTTTTTGCGAATAATCATCAATAATAGTCAGCATGTAACTTGCACCACCTAATGACTT	G	T	652883421	652883521	644163181	644163281	653182194	653182294	654751619	654751719
RDMb-h3:SNP_164	TTGTGCTTGCCGAAGATACAATGCTCACAAAATTTCAATTTACCAGGTTAATATCCATCAAGAAGACCTCTCTTATTTAACTCTGCTAAACCAAGTTCACT	A	C	652883607	652883707	644163367	644163467	653182380	653182480	654751805	654751905
RDMb-h3:SNP_165	ATCCATCAAGAAGACCTCTCTTATTTAACTCTGCTAAACCAAGTTCACTGATATGTCCAAGACGCATATGCCAAAGGTTAGCAGCATCACAATCAGAATTC	G	C	652883659	652883759	644163419	644163519	653182432	653182532	654751857	654751957
RDMb-h3:SNP_166	TGTTATAGAATGATTTGGTGCAATGTCTTGTCAGTTTCGAGTTGGTGTTTCCACCATCCTTCTTCAACATCATGACGCACGTCCTAGTTCACCTATGCGAA	T	C	652891176	652891276	644170936	644171036	653189949	653190049	654759374	654759474
RDMb-h3:SNP_167	TCATGTTGCTAGACAACAATGAACCTACGAGCTATGGAGAAGCGATGGTGGGCCCGGATTCCGATAAATGGCTTGAGGCCATAAAATCCGAGAGAGGATCC	A	G	652905289	652905389	5269382	5269482	653204016	653204116	10807758	10807858
RDMb-h3:SNP_168	GAGGATCCATGTATGAAAACAAAGTGTAGACTTTGGCAGAACGGCTCGACGGTCGTAAGGCTAATGAGTACAGATGGATTTCAAAAGGAAGACGGACAATG	C	T	652905382	652905482	644185186	644185286	653204109	653204209	654773491	654773591
RDMb-h3:SNP_169	TTAGGTGTTTCATATATTGTGTTACCTAGCTAATTAATAGAGAGAAGTGCCCTCTCTTATGTCCGTGCTTGGTCGACGCTACGTACTATATATACATAAGT	C	T	652913430	652913530	644198768	644198868	653212102	653212202	654781540	654781640
RDMb-h3:SNP_170	GGCCAATCGTTGATGGTCACGAAACATCAACGCCTTTAGGTTAAATTCCTTCTGTTTGTGCTCATCCCACGTACGTACACCGTTTCCATTCCACAGCTGTAA	T	C	652918921	652919021	644204057	644204157	653217350	653217450	654786686	654786786
RDMb-h3:SNP_171	GTGCTCATCCCACGTACGTACACCGTTTCCATTCCACAGCTGTAAAAGTATTTCAACTAATGGCCTTAGGTACACATCAATGTCGTTGCCGGGTTGCTTAG	A	T	652918977	652919077	644204113	644204213	653217406	653217506	654786742	654786842
RDMb-h3:SNP_172	TGCTCATCCCACGTACGTACACCGTTTCCATTCCACAGCTGTAAAAGTATTTCAACTAATGGCCTTAGGTACACATCAATGTCGTTGCCGGGTTGCTTAGG	T	C	652918978	652919078	644204114	644204214	653217407	653217507	654786743	654786843
RDMb-h3:SNP_173	GCAGCAATTCCAGTACGGTACCGAGCTTTGTGTTGCCATCTTCGCAATTAGGGTACAATGACCCGGCGAAGATCATCATCATCGGGCACATCGTCTGGTTC	A	G	652919723	652919823	644204859	644204959	653218152	653218252	654787488	654787588
RDMb-h3:SNP_174	TCCTCCTCTCCTTGTTTTCCTCAATCTTGTTACCCTCCTCATCGAATTTTTTGTATTCCGGAGGTAGAACGAAATGTTCCATAAGCTTTTTGAAGCAATCT	T	G	652940188	652940288	275640578	275640478	653238616	653238716	285996924	285996824
RDMb-h3:SNP_175	GCATGATGTACTGATCGTTTTCTTATCTTTCCGTTTCCTCGGTTTGCTATTCATGTCCTTCACATAGAAAACCTGAGCGACATCTTTCGCTAGGACGAATG	T	C	652942624	652942724	644227428	644227528	653241178	653241278	6479564	6479464
RDMb-h3:SNP_176	TCCCTTTATATTGGACGAGAATCCAGACGGGACCTTCATACTGCTCAGGTATTCAAAAAAGATGACCTTCTCTTCTTTGGTCAGAGCGTAGCCGGCACGAC	T	C	652943797	652943897	644228601	644228701	653242351	653242451	654814231	654814331
RDMb-h3:SNP_177	CTCAGGTATTCAAAAAAGATGACCTTCTCTTCTTTGGTCAGAGCGTAGCCGGCACGACCTTGAAACCATTCCGGATGCCGGTCATCAGGGTCTTTCAAACG	C	T	652943840	652943940	644228644	644228744	653242394	653242494	654814274	654814374
RDMb-h3:SNP_178	ATCCATTGCCGATTCATCTGCATTATTATAATATAAAATATATAATTAATCATCATGCATTTGTTAAAGTAACTAGCTATAAACAATAGAAATTAAACAAT	T	C	652945775	652945875	690191512	690191612	24186547	24186447	285990080	285989980
RDMb-h3:SNP_179	GCGAGGAAACGAACCCTCCGCAACCTTGCCGAAGTCTATCAAGTAGCAATAATAAACCCATGGACTGACACAGCTATTACTTTTAATGCCAGTGACGAACC	T	C	652964190	652964290	644248989	644249089	653262740	653262840	654834643	654834743
RDMb-h3:SNP_180	CTCCGCAACCTTGCCGAAGTCTATCAAGTAGCAATAATAAACCCATGGACTGACACAGCTATTACTTTTAATGCCAGTGACGAACCTAAATTCCGGACAGC	C	G	652964205	652964305	644249004	644249104	653262755	653262855	654834658	654834758
RDMb-h3:SNP_181	GGCTAAGAGAATCGTCGGAGGTCTTATACCTCTTGACGTGCGCACGAGCCATGAAATCCCAATTTCAGCCCTCGAAACATCTCATATGTTCCGCGATGTTTC	A	C	652976251	652976351	644261050	644261150	653274801	653274901	654846704	654846804
RDMb-h3:SNP_182	TTTGGGGATACGCTCTAGAGACAGCTACATTCACTTTAAATAGGGCACCATCTAAATCCGTTGAGACGACACCGTATGAATTATGGTTTGGGAAGAAACCT	A	G	652981715	652981815	21192283	21192383	9083827	9083727	8620290	8620190

RDMb-h3:SNP_183	TATGCGGTTTGACCGATAAAGATCTTCGTAGAATATGTAGGAACCAATACGGGCATCCAGGTCCCGCTATTGGTTATTGACCAGAGATGTGTCTCAGTCAT	C	T	652984127	652984227	644268926	644269026	653282677	653282777	654854580	654854680
RDMb-h3:SNP_184	TTTCAGAGTGAAGTAGAAAATCATCGTAACAAGAAAATAAAGTTTCTACAATCTGATCGTGGAGGAGAATATTTGAGTTACGAGTTTGGTTTACATTTGAA	A	G	652988071	652988171	255060363	255060263	264425279	264425179	265446667	265446567
RDMb-h3:SNP_185	TTCCTAATACTAGTACTCTTTCCTTCCCCCTCCAAATAAGATAAGGAAAGGAGAGGGAAACCTACTTGGAGTAGGTTTCCCCCTCCTCATGGCGCGCCCCC	G	A	652991647	652991747	644276446	644276546	653290197	653290297	654869120	654869220
RDMb-h3:SNP_186	AAGGCCAGTCTTCGGACGCCTTCTTCGGGGTTCCGGATAGATATCCGGTTCCGGCGATGCGCCACAGTTCGGCTCCGTCCACTTGATATATTGACCCCTCA	T	C	652997312	652997412	644282112	644282212	653295862	653295962	654874786	654874886
RDMb-h3:SNP_187	ACGCCTTCTTCGGGGTTCCGGATAGATATCCGGTTCCGGCGATGCGCCACAGTTCGGCTCCGTCCACTTGATATATTGACCCCTCATGAGAACGGGGTACG	C	T	652997327	652997427	644282127	644282227	653295877	653295977	654874801	654874901
RDMb-h3:SNP_188	ACGGGGTACGATGCAGAATAATCTTTTCCACAGCGCAAAATGAGCCTCGGCGCCCAAGAACAGCTCGCAAAGGGCCACGAAGCCCGCGATGTGCAGAATGG	G	A	652997418	652997518	644282218	644282318	653295968	653296068	654874892	654874992
RDMb-h3:SNP_189	CGAGGACCCCTTAATCCAGGACTCCCTCAGTAGCCCCTGAACCAGGCTTTAATGACGATGAGTCCTGCGCGCAGATTGTCTTCGGCATTGCAAGGCGGGTT	T	C	653034831	653034931	644319029	644319129	653332751	653332851	654911782	654911882
RDMb-h3:SNP_190	CTATGCTGTTGATGTAGAAGCCCTCCATGGTCGATTCCCCCTCTGGCGGGGCACCGGCGAAGGCTCCAAGATGGGATCTCGCGGATACAGAAGGTTACAAC	G	A	653048331	653048431	644332531	644332631	653346251	653346351	654925284	654925384
RDMb-h3:SNP_191	AAATTGGGTTGCCTCCCAACTAGCGCTATCGTTTAACGCCCCTAGCTAGATATAAAAGCGAAGATAGATCTAAGTAGTGCCATCTTTGGCACTCAATTCAT	A	G	653051660	653051760	644335860	644335960	653349580	653349680	654928613	654928713
RDMb-h3:SNP_192	AATTGGGTTGCCTCCCAACTAGCGCTATCGTTTAACGCCCCTAGCTAGATATAAAAGCGAAGATAGATCTAAGTAGTGCCATCTTTGGCACTCAATTCATA	T	C	653051661	653051761	644335861	644335961	653349581	653349681	654928614	654928714
RDMb-h3:SNP_193	ATTTACTGTTTCTTCCCCCTCTTCTCTCCGGTAGACTACGAGACCGACGTTGCTGCTGCCCAGTTCGACTACGGAGTTGATAACCCCTCCTTCTTGCCAGA	T	C	653079761	653079861	644363959	644364059	653377681	653377781	654956714	654956814
RDMb-h3:SNP_194	TAGACTACGAGACCGACGTTGCTGCTGCCCAGTTCGACTACGGAGTTGATAACCCCTCCTTCTTGCCAGAGCAACCAGGCAAGCCCCCCCTTGATCACCAG	T	C	653079792	653079892	644363990	644364090	653377712	653377812	654956745	654956845
RDMb-h3:SNP_195	ACCGACGTTGCTGCTGCCCAGTTCGACTACGGAGTTGATAACCCCTCCTTCTTGCCAGAGCAACCAGGCAAGCCCCCCTTGATCACCAGATATTGCCTTT	T	A	653079803	653079903	644364001	644364101	653377723	653377823	654956756	654956856
RDMb-h3:SNP_196	CGTCGCCGGAGAATAACAAAGGGTGTGGGTGAGTAGAGGGATGGCTAGGACAGCGATGGGAGTACGATGGGGCAGTGAGGCCTACGCGGCAGCATAGCCGG	A	C	653102166	653102266	644386127	644386227	653399832	653399932	654979024	654979124
RDMb-h3:SNP_197	AAAGGGTGTGGGTGAGTAGAGGGATGGCTAGGACAGCGATGGGAGTACGATGGGGCAGTGAGGCCTACGCGGCAGCATAGCCGGCCGCGGGGAGGAGGGAG	A	G	653102183	653102283	644386144	644386244	653399849	653399949	654979041	654979141
RDMb-h3:SNP_198	CCCCATATGTCCAACCATTAGGAGGAACCATATTTTTGGGCTTGTAGTACTGAGACACTTGCTTGTGTACTGCCATGATGCTGGTGGGTCCCTACTGTCAT	C	T	653103185	653103285	644387144	644387244	653400851	653400951	654980041	654980141
RDMb-h3:SNP_199	TATGTCCAACCATTAGGAGGAACCATATTTTTGGGCTTGTAGTACTGAGACACTTGCTTGTGTACTGCCATGATGCTGGTGGGTCCCTACTGTCATCCTCT	A	G	653103190	653103290	644387149	644387249	653400856	653400956	654980046	654980146
RDMb-h3:SNP_200	ATTAGGAGGAACCATATTTTTGGGCTTGTAGTACTGAGACACTTGCTTGTGTACTGCCATGATGCTGGTGGGTCCCTACTGTCATCCTCTCCATGTACGGC	T	C	653103201	653103301	644387160	644387260	653400867	653400967	654980057	654980157
RDMb-h3:SNP_201	CGGTTTGGGCGGCTGGAGGAAGAAGACAAGAGATAGAAGATACATGACAAATGTTGGATGTCAATCCAACGGCTGGTAGGCAGAATCGTTTGTTGACT	A	G	653103648	653103748	644387607	644387704	653401314	653401414	654980504	654980601
RDMb-h3:SNP_202	CATAATGCACAAACCTCAAAACACAAGCACTTCTCCTTTGTTCTAGAATATTCTGTATTATAATTGTTTTTTCCCTAAATGAATTGCCATTATTTGTTTTT	A	C	653111796	653111896	644395614	644395714	653409437	653409537	654988786	654988886
RDMb-h3:SNP_203	CAAACCTCAAAACACAAGCACTTCTCCTTTGTTCTAGAATATTCTGTATTATAATTGTTTTTTCCCTAAATGAATTGCCATTATTTGTTTTTTACTTTATG	T	C	653111805	653111905	644395623	644395723	653409446	653409546	654988795	654988895
RDMb-h3:SNP_204	ATGGCTACCTTTGTTTCAATATCTACAAGGGTTGGATGAAGAGCAAGAGTCAAGTGTGCGGTTCAAGCAAAGAAGTATCGGCCAAGAGGAAGAGGGACAAG	T	C	653115630	653115730	644399448	644399548	653413271	653413371	654992620	654992720
RDMb-h3:SNP_205	GACAAGGACGAAGTCGAGGACGTGGACGAGGACTCCTCCGAGTGAGTAACGTGTCAGTATTGTTGCTCATGGTGGTTCTAACGCAGTGTCTATCGGATTAG	C	G	653115725	653115825	644399543	644399643	653413366	653413466	654992715	654992815
RDMb-h3:SNP_206	AGGACGAAGTCGAGGACGTGGACGAGGACTCCTCCGAGTGAGTAACGTGTCAGTATTGTTGCTCATGGTGGTTCTAACGCAGTGTCTATCGGATTAGTTGC	T	G	653115729	653115829	644399547	644399647	653413370	653413470	654992719	654992819
RDMb-h3:SNP_207	GAAGTCGAGGACGTGGACGAGGACTCCTCCGAGTGAGTAACGTGTCAGTATTGTTGCTCATGGTGGTTCTAACGCAGTGTCTATCGGATTAGTTGCATAGT	A	G	653115734	653115834	644399552	644399652	653413375	653413475	654992724	654992824
RDMb-h3:SNP_208	CAGGTGTGCTTAGTTGAATTTGAGGGGTGTGTTGTGCTGAGCCCCAGCAAAACTATGTTATGTTTCTTCTCGTTACTTTAACTCCTCAGTATGATACATAC	A	G	653115842	653115942	644399660	644399760	653413483	653413583	654992832	654992932
RDMb-h3:SNP_209	AGAATTTAGCACCCCAATTAAGCACGTACTAGCTTTTTAATAGTAATATGTGCATAATTTGGCGACGAGTGCTCTCTATATGTACCACCTTTTTTTTAAT	G	A	653115961	653116061	644399779	644399879	653413602	653413702	654992951	654993051
RDMb-h3:SNP_210	TTGTGGCAGAGCGTCAGGGCAGGTTGAGACCGCCTAGGAGAGAGGTGGGTCTGACCCTGTTCGGCATTCGCGGATACTTAACACGCTTAACGAGATCCTGG	T	C	653118835	653118935	644402507	644402607	653416330	653416430	654995679	654995779
RDMb-h3:SNP_211	GGCAGAGCGTCAGGGCAGGTTGAGACCGCCTAGGAGAGAGGTGGGTCTGACCCTGTTCGGCATTCGCGGATACTTAACACGCTTAACGAGATCCTGGTATT	A	G	653118839	653118939	644402511	644402611	653416334	653416434	654995683	654995783
RDMb-h3:SNP_212	GGGCAGGTTGAGACCGCCTAGGAGAGAGGTGGGTCTGACCCTGTTCGGCATTCGCGGATACTTAACACGCTTAACGAGATCCTGGTATTTGATCTGAGTTG	A	G	653118851	653118951	644402523	644402623	653416346	653416446	654995695	654995795
RDMb-h3:SNP_213	GTCTGACCCTGTTCGGCATTCGCGGATACTTAACACGCTTAACGAGATCCTGGTATTTGATCTGAGTTGGTTACGAGCCTATACGCACTAACCATCTACGC	C	T	653118883	653118983	644402555	644402655	653416378	653416478	654995727	654995827
RDMb-h3:SNP_214	GCGGATACTTAACACGCTTAACGAGATCCTGGTATTTGATCTGAGTTGGTTACGAGCCTATACGCACTAACCATCTACGCAGGAGTAGTTATGGGTATCCC	T	C	653118904	653119004	644402576	644402676	653416399	653416499	654995748	654995848
RDMb-h3:SNP_215	GTTATGGGTATCCCGGCGTCGTGGTATCAGCCGAAGCACTTCGTGACGTTAGCGACTGAGCGGCGCGCCGGATTGGACTGGAACGCCACTAGGCTAGGT	T	C	653118991	653119091	644402663	644402763	653416486	653416586	654995835	654995935
RDMb-h3:SNP_216	GTAACCACCGATGGACGAGAACTTCGCCTATTGGTCCGCCTCGTCCTAAAGAGCAGGAAAATGGTTCTCTTCGTCCCTCGCCCTTGGTACCGACGTTGTTG	A	C	653123533	653123633	644407218	644407318	653421028	653421128	655000390	655000490
RDMb-h3:SNP_217	GAGCCTATACGCACTAACCATCTACGCGGGAGTAGTTATGGGTATCCCGGCGTCGTGGTATCAGCCGAAGCACTTCGTGACGTCAGCGACTGAGCGGTGCG	G	A	653126693	653126793	644410506	644410606	653424171	653424271	655003854	655003954
RDMb-h3:SNP_218	GGCGTCGTGGTATCAGCCGAAGCACTTCGTGACGTCAGCGACTGAGCGGTGCGCGCCGGATTGGACTGGAACGCCACTAGGCTAGGTCTGCTTCCTGCCGC	T	C	653126741	653126841	644410554	644410654	653424219	653424319	655003902	655004002
RDMb-h3:SNP_219	CGGTGCGCGCCGGATTGGACTGGAACGCCACTAGGCTAGGTCTGCTTCCTGCCGCGTATGCAACGTGCAGGTGTGCTCAGGGCGATGGGCCCAGACCCCTG	T	G	653126787	653126887	644410600	644410700	653424265	653424365	655003948	655004048
RDMb-h3:SNP_220	AATATTGGCGACCCTTTTGTCCACCGGTGCCTTTGCCACCGATGAACGAAGAATGACTCGGGTGCTCATGCTGTCATGCATCCTCCAGCGCGCATGTTGGA	A	G	653129822	653129922	644413635	644413735	653427300	653427400	655006983	655007083
RDMb-h3:SNP_221	GGCGACCCTTTTGTCCACCGGTGCCTTTGCCACCGATGAACGAAGAATGACTCGGGTGCTCATGCTGTCATGCATCCTCCAGCGCGCATGTTGGAGATGAG	A	G	653129828	653129928	644413641	644413741	653427306	653427406	655006989	655007089
RDMb-h3:SNP_222	GACTCGGGTGCTCATGCTGTCATGCATCCTCCAGCGCGCATGTTGGAGATGAGCTCGCACGAGCTGTGTTTTTTGTCCCACAACGCCACTCAAGCCACCCG	T	C	653129876	653129976	644413689	644413789	653427354	653427454	655007037	655007137
RDMb-h3:SNP_223	TTGACGCAAACACATAGACAAACTGATATTTCATATAAACAACGATGGAGATCATATAAAATACTGGATTTTCATACAAACATGACGGATTTCATTACATT	G	A	653130023	653130123	644413836	644413936	653427501	653427601	655007184	655007284
RDMb-h3:SNP_224	TTTCATACAAACATGACGGATTTCATTACATTCAAATGAACTACGCGATACTAGTTCTGGACAGCACAGATATATAATACCTGGCCTAAATGGTCGCCCGC	A	G	653130092	653130192	644413905	644414005	653427570	653427670	655007253	655007353
RDMb-h3:SNP_225	TTTCATTACATTCAAATGAACTACGCGATACTAGTTCTGGACAGCACAGATATATAATACCTGGCCTAAATGGTCGCCCGCCGATCGATTTGTGTTCCTCA	A	G	653130112	653130212	644413925	644414025	653427590	653427690	655007273	655007373
RDMb-h3:SNP_226	CCTGGCCTAAATGGTCGCCCGCCGATCGATTTGTGTTCCTCATGTCCGGTAGCACGATAACCGGACTGCTGGGAGCCCTGGAGGTATATGCTTCGGCGCAA	T	C	653130171	653130271	644413984	644414084	653427649	653427749	655007332	655007432
RDMb-h3:SNP_227	AATGGTCGCCCGCCGATCGATTTGTGTTCCTCATGTCCGGTAGCACGATAACCGGACTGCTGGGAGCCCTGGAGGTATATGCTTCGGCGCAAAGGACGGCT	A	C	653130180	653130280	644413993	644414093	653427658	653427758	655007341	655007441
RDMb-h3:SNP_228	GCCGATCGATTTGTGTTCCTCATGTCCGGTAGCACGATAACCGGACTGCTGGGAGCCCTGGAGGTATATGCTTCGGCGCAAAGGACGGCTTGCTCCCCCAC	T	C	653130191	653130291	644414004	644414104	653427669	653427769	655007352	655007452
RDMb-h3:SNP_229	CCGGTAGCACGATAACCGGACTGCTGGGAGCCCTGGAGGTATATGCTTCGGCGCAAAGGACGGCTTGCTCCCCCACTGCCTAACTGATATCATTGGCTGGT	G	A	653130216	653130316	644414029	644414129	653427694	653427794	655007377	655007477
RDMb-h3:SNP_230	CGGACTGCTGGGAGCCCTGGAGGTATATGCTTCGGCGCAAAGGACGGCTTGCTCCCCCACTGCCTAACTGATATCATTGGCTGGTGCTAAAGATGATGGTG	T	C	653130232	653130332	644414045	644414145	653427710	653427810	655007393	655007493
RDMb-h3:SNP_231	CTGCTGGGAGCCCTGGAGGTATATGCTTCGGCGCAAAGGACGGCTTGCTCCCCCACTGCCTAACTGATATCATTGGCTGGTGCTAAAGATGATGGTGGCCG	C	T	653130236	653130336	644414049	644414149	653427714	653427814	655007397	655007497
RDMb-h3:SNP_232	CCTGGAGGTATATGCTTCGGCGCAAAGGACGGCTTGCTCCCCCACTGCCTAACTGATATCATTGGCTGGTGCTAAAGATGATGGTGGCCGGCACCAGTTTG	T	C	653130247	653130347	644414060	644414160	653427725	653427825	655007408	655007508
RDMb-h3:SNP_233	GGCGGTGGACGCGGAGGCGCTGGCCACCGACTCATCGCTCTCCGCACACTTGGCTTCTATCGCTGCTTGCATGGAGCGGCCGCCGGCATGGGAGTCTCGGC	T	C	653130563	653130663	644414376	644414476	653428041	653428141	655007724	655007824
RDMb-h3:SNP_234	GGGGTTTCGAAGATTCAAATTCATAGGAAGTGCATTCATCTATTTGAACTCGAGATAATGGCATTTGTAAGTCAGATGTAAAAGGGGGCATCAATCTTTGTT	T	C	653134123	653134223	644418186	644418286	653431602	653431702	655011284	655011384
RDMb-h3:SNP_235	CATAGGAAGTGCATTCATCTATTTGAACTCGAGATAATGGCATTTGTAAGTCAGATGTAAAAGGGGGCATCAATCTTTGTTGTGAGTTTGAACATGCTATA	G	A	653134144	653134244	644418207	644418307	653431623	653431723	655011305	655011405
RDMb-h3:SNP_236	ATCTTTGTTGTGAGTTTGAACATGCTATATATATTCATACGCATATCTAGCTTTTTATTTTTTGCAACCAAGGAGATTATATCTGGAACCATGCATGAACT	G	A	653134216	653134316	644418279	644418379	653431695	653431795	655011377	655011477
RDMb-h3:SNP_237	ACTTCACCAAGACGCCAGTCTCAACCGCCTCCGAGAAGCATTCATACGCTGTGAGCGCCTAAACACCCATGCGCTCGGTCGAAATCTATCCCGCCCACATT	T	C	653134631	653134731	644418694	644418794	653432110	653432210	655011792	655011892
RDMb-h3:SNP_238	TCCGAGAAGCATTCATACGCTGTGAGCGCCTAAACACCCATGCGCTCGGTCGAAATCTATCCCGCCCACATTTGGGACACCTGACATGACTGTCCTACCCC	T	C	653134660	653134760	644418723	644418823	653432139	653432239	655011821	655011921
RDMb-h3:SNP_239	TCTGCTGGTACTTATAGTGCAGTAGAAGGTCCAAGTCCACCGGCTAAATATACAAACACGGTATCACCTGCTCCACCAGCTGCAACATCCGCTTCAACTGT	A	C	653140935	653141035	644424998	644425098	653438414	653438514	655018096	655018196
RDMb-h3:SNP_240	CTTATAGTGCAGTAGAAGGTCCAAGTCCACCGGCTAAATATACAAACACGGTATCACCTGCTCCACCAGCTGCAACATCCGCTTCAACTGTACCAACATCT	G	A	653140945	653141045	644425008	644425108	653438424	653438524	655018106	655018206
RDMb-h3:SNP_241	TGCGTAATTCTGGGTTGGTTGTCAAGGTAACCCCTCGTCCAAATCGCCTTCTGAACAAAATCTTCCTGCTAGACAGAGTGATATATTTGTGCTCCAGACAC	T	A	653142845	653142945	644426908	644427008	653440324	653440424	655020006	655020106
RDMb-h3:SNP_242	CACTCAGGTCAAATGATATGTGCTTCTATACATCTGATGGTGCTTTTATTTGGAAGGACTGTAAACTTTATGCCAACAGGCCTTTTGTTGTATGGTTGGAA	T	C	653143123	653143223	644427186	644427286	653440602	653440702	655020284	655020384
RDMb-h3:SNP_243	AAGAGAGTAGATGGGGAGAAACATCATAAGATCCAACTATAATAGCAAATCTCGTGATACATCAAGATCGTATCACCTCAAGAACACAAGAGAGAGAGAGA	T	G	653146639	653146739	644430702	644430802	653444118	653444218	655023800	655023900
RDMb-h3:SNP_244	AGTAGATGGGGAGAAACATCATAAGATCCAACTATAATAGCAAATCTCGTGATACATCAAGATCGTATCACCTCAAGAACACAAGAGAGAGAGAGATCA	T	C	653146644	653146744	644430707	644430807	653444123	653444223	655023805	655023905
RDMb-h3:SNP_245	GAGGAAGGAAACGGTCCCATATAATCAAAGCCCCAAACATCAAATGGTTTAATAACAAGAGAATAATTCATAGGCATTTCTTGATGTCTACTAATATTACC	T	C	653153793	653153893	644437857	644437957	653451272	653451372	655030955	655031055
RDMb-h3:SNP_246	GATACATCTACTAGCCAGAGCAAACAGAAGAAACCACAAGAATACCAAGGCTGGGATGACATGTAGAGAGTGAGTACTAAGTACCACATTTGATTAGACAT	G	A	653157198	653157298	644441262	644441362	653454677	653454777	655034360	655034460

RDMb-h3:SNP_247	ATGTCCCCAAGAGTAAAGATATGCAATGAATTTAAATGATTTCTTTCCCATAGATGCCTTGCTCCCCTGAATCTAGCATGGGATATTGGGAGAAGATAGGG	A	T	653157297	653157397	644441361	644441461	653454776	653454876	655034459	655034559
RDMb-h3:SNP_248	CAAGAGTAAAGATATGCAATGAATTTAAATGATTTCTTTCCCATAGATGCCTTGCTCCCCTGAATCTAGCATGGGATATTGGGAGAAGATAGGGAACAGAA	C	T	653157304	653157404	644441368	644441468	653454783	653454883	655034466	655034566
RDMb-h3:SNP_249	CATCACAGAGAAAACACTTGTCACCTCAGCTCACTAGACTAATAAGATCGCACAAAGATTTGCAAGGAATTTACTGAATGATATGCAATGAATTGGATGCA	G	T	653157925	653158025	644441989	644442089	653455404	653455504	655035087	655035187
RDMb-h3:SNP_250	ATGTTAGAGTATATTGACTTAGGAGTCAAGTGAGATCACTTGATCATAGATCATACTCATCGTTTAAGCTCAAAATGGGGTTGCCATATTTCGTTTAAGCA	A	G	653158165	653158265	644442229	644442329	653455644	653455744	655035327	655035427
RDMb-h3:SNP_251	CTTGATCATAGATCATACTCATCGTTTAAGCTCAAAATGGGGTTGCCATATTTCGTTTAAGCATCTTGGTGTATTCTCATCTTGTCGAGTTGCTTTAGCTC	A	T	653158203	653158303	644442267	644442367	653455682	653455782	655035365	655035465
RDMb-h3:SNP_252	CATCGTTTAAGCTCAAAATGGGGTTGCCATATTTCGTTTAAGCATCTTGGTGTATTCTCATCTTGTCGAGTTGCTTTAGCTCATGACTTGGGGTAAAGCTT	G	A	653158222	653158322	644442286	644442386	653455701	653455801	655035384	655035484
RDMb-h3:SNP_253	AAGCTCAAAATGGGGTTGCCATATTTCGTTTAAGCATCTTGGTGTATTCTCATCTTGTCGAGTTGCTTTAGCTCATGACTTGGGGTAAAGCTTCTCTAAGA	T	A	653158230	653158330	644442294	644442394	653455709	653455809	655035392	655035492
RDMb-h3:SNP_254	CATCTTGGTGTATTCTCATCTTGTCGAGTTGCTTTAGCTCATGACTTGGGGTAAAGCTTCTCTAAGATGGAATAACATACCTTGGTTGGTGGTGATGTCCA	G	A	653158264	653158364	644442328	644442428	653455743	653455843	655035426	655035526
RDMb-h3:SNP_255	TAAGCTCATGTCTTGCATGTATCCAATGGAGTTTCTACTCCAAGTTTGAGGCATCAATGATGTTCAATTCTCCTCTTAACCTGCAAAACAGTTTCTCATCA	G	A	653158740	653158840	644442804	644442904	653456219	653456319	655035902	655036002
RDMb-h3:SNP_256	AAGTTTGAGGCATCAATGATGTTCAATTCTCCTCTTAACCTGCAAAACAGTTTCTCATCAAGAGGTTTAGTGAATATATCCGCTAATTGCTTTTCGGTGCG	G	C	653158781	653158881	644442845	644442945	653456260	653456360	655035943	655036043
RDMb-h3:SNP_257	ATGTCACCCTTAGCAACATGATCTCGAATGAAATGATGACGAACTTCAACATGCTTAGTTCGAGAATGTTACACAGGATTATGACCAATTTTGATAGCACT	C	T	653158898	653158998	644442962	644443062	653456377	653456477	655036060	655036160
RDMb-h3:SNP_258	TCTCGAATGAAATGATGACGAACTTCAACATGCTTAGTTCGAGAATGTTACACAGGATTATGACCAATTTTGATAGCACTTTCATTGTCACAAAGCAATGG	A	G	653158919	653159019	644442983	644443083	653456398	653456498	655036081	655036181
RDMb-h3:SNP_259	TAATCTTTAAGAGTTTGGGTCATCCAAAGTAATTGAGCACAACATGAACTAGCGGCAATGTATTCCGCTTCGGCAGTGGATAAGGATACCGAGTTTTGTTT	T	C	653159042	653159142	644443106	644443206	653456521	653456621	655036204	655036304
RDMb-h3:SNP_260	TAAGGATAATAATGGTTACTCTGTTTATTTGAATAATACCTTCAATGGTATTGCACCTAAAATTAATGGTTTATTGAATCTCGATTGTAGTGATACACATG	A	C	653163571	653163671	644447691	644447791	653461050	653461150	655040735	655040835
RDMb-h3:SNP_261	CATGATGTTCTTCACGGGATGCCTTCCTCCAACATGTTTACCTTCTTGATAAGCACTGCAAAGTCTATCCTTATCAAATATGACATTGTTAACACCAAGGA	T	C	653170170	653170270	644454292	644454392	653467649	653467749	655047336	655047436
RDMb-h3:SNP_262	ATTTATTGCATTATGGGCTGTTATTACACATTATGTCACAATACTTATGGATATTCTCTCTTATTTTACAAGGTTTATCATGAAGAGGGAGAATGCCGGCA	G	C	653181091	653181191	644465213	644465313	653478570	653478670	655058257	655058357
RDMb-h3:SNP_263	TTTATTGCATTATGGGCTGTTATTACACATTATGTCACAATACTTATGGATATTCTCTCTTATTTTACAAGGTTTATCATGAAGAGGGAGAATGCCGGCAG	A	C	653181092	653181192	644465214	644465314	653478571	653478671	655058258	655058358
RDMb-h3:SNP_264	AGATATGATCCATGTATGAGAACAAAGTATGGACTTTGATTGACTTGCTTGATGATCAGCAAGCCATGTTAAATAAATGGATTTTCAAGAGGAAGACGGAC	T	C	653188607	653188707	644472730	644472830	653486086	653486186	655065774	655065874
RDMb-h3:SNP_265	AATCCTAGGGGATCCTCCTCCACCCAAGGGTGATCCCGTGTTTGAGCTACAACCATTACCTGATAATCTTAAATATGCTTATCTTGATGAAAAGAAGATAT	C	A	653192903	653193003	644477027	644477127	653490381	653490481	655070070	655070170
RDMb-h3:SNP_266	CTCCGTATAAGATGGTTTATGGAAAACCATGTCACTTACCTCTTGAACTTGAACATAAAGCATATTGGGCTATTAAAGAGCTCAACTATGACTTCAAACTT	T	A	653195374	653195474	644479498	644479598	653492852	653492952	655072541	655072641
RDMb-h3:SNP_267	AGATGGTTTATGGAAAACCATGTCACTTACCTCTTGAACTTGAACATAAAGCATATTGGGCTATTAAAGAGCTCAACTATGACTTCAAACTTGCCGGTGAG	A	G	653195383	653195483	644479507	644479607	653492861	653492961	655072550	655072650
RDMb-h3:SNP_268	AAGAGGGTAACTTCATCTACGCAAAACATACCACTCGCCAGTGCCGGCTTTTAATCCAGCAGTGTCAAGGAAAACAGCCCAAGGACAAAGAGAAGGAGTCG	T	C	653199218	653199318	644483342	644483442	653496696	653496796	655076385	655076485
RDMb-h3:SNP_269	ATCTACGCAAAACATACCACTCGCCAGTGCCGGCTTTTAATCCAGCAGTGTCAAGGAAAACAGCCCAAGGACAAAGAGAAGGAGTCGGACAAGGCCGAGGA	G	T	653199232	653199332	644483356	644483456	653496710	653496810	655076399	655076499
RDMb-h3:SNP_270	TGCTCATTATTTCTCTGATCATGACATTACAGTCGTCAGCGACGCACCACTGTCAGATATTCTGCACAACAGAGATGCAACTGGTCGAGTGGCTAAATGGG	C	T	653201369	653201469	644485493	644485593	653498847	653498947	655078536	655078636
RDMb-h3:SNP_271	GCATCCGTCGCCTCATGGTTTATGGCGACTCAGATTTGGTATTCAATCATGTGATGAAGGAGTGGGACGTTAGAAGCCCAACCATGACTGGATACTGCAAT	T	G	653201770	653201870	644485894	644485994	653499248	653499348	655078937	655079037
RDMb-h3:SNP_272	AGATTTGGTATTCAATCATGTGATGAAGGAGTGGGACGTTAGAAGCCCAACCATGACTGGATACTGCAATGCAGTGAGGAAGCTTGAAAAGAAATTCGAAG	A	G	653201801	653201901	644485925	644486025	653499279	653499379	655078968	655079068
RDMb-h3:SNP_273	AGCTTGAAAAGAAATTCGAAGGGTTAGAGCTCCACCATATACCCCGACTAAAAAATCAAGCGGCTGATGATTTGGCGAAGATAGGGTCTAAGAGAGAAGCC	A	G	653201881	653201981	644486005	644486105	653499359	653499459	655079048	655079148
RDMb-h3:SNP_274	TACCCCGACTAAAAAATCAAGCGGCTGATGATTTGGCGAAGATAGGGTCTAAGAGAGAAGCCATTCCCAGTGATGTGTTCTTGGAGCATATCCATACTCCA	T	C	653201920	653202020	644486044	644486144	653499398	653499498	655079087	655079187
RDMb-h3:SNP_275	ACAACTCAGTGGTGGCCTGACAGACAACGAAACAAGACAAAGGTCAATCAACCAATTTGCAGTGAAGCAGAATGAATAAAGCAAGATTACAACCGAGGATA	A	G	653207553	653207653	644491407	644491507	653506078	653506178	655084722	655084822
RDMb-h3:SNP_276	GCAGCCTGATATGAGCGAGGCTCAGAAGATGGATCCGCAACAGCAGCAGTCAAACAAGCAGCCAACCAAGCAACCGTACCATCCTTACGTTTCTTAGGTTT	T	C	653235113	653235213	644518967	644519067	653533638	653533738	655112282	655112382
RDMb-h3:SNP_277	GCAGCAGTCAAACAAGCAGCCAACCAAGCAACCGTACCATCCTTACGTTTCTTAGGTTTGAAAATGCCACTGCGACTGCGTGTATGTGGTCGGGACACAGG	T	C	653235155	653235255	644519009	644519109	653533680	653533780	655112324	655112424
RDMb-h3:SNP_278	GCCAAGACCAAGGAAGCTTCGCTGGAAGCGCTTATGACACTTGGAGGCCTAGTGCCCATCGCGGCCACAAAGCTGACACACACGTGGACCGCCAGCCCCCG	T	C	653237264	653237364	644521118	644521218	653535789	653535889	655114433	655114533
RDMb-h3:SNP_279	GCCCCGTCCAGACGCGATGGGCCGGATTGTAGACCGGACCGTGCACGCTATCTACCAGCGCGGGTGGGCAGGGAAGCGATCCGTCGACGTAGCCTAGCAGG	A	G	653237902	653238002	644521756	644521856	653536427	653536527	655115071	655115171
RDMb-h3:SNP_280	CTAGCAGGTAGTGACTCCCCAAGAGCGGGAGAACCTGCGCACGCCAGAATATGTAGTTGTCGGCCGAGAGCTTGATGGTGATGAGATGACCGAAGTGAAAC	T	G	653237995	653238095	644521849	644521949	653536520	653536620	655115164	655115264
RDMb-h3:SNP_281	ACCGTGGCCCTCTTGTGGAGCAAGACTCTTAAAGTAGCCTTTGTTGGGCTTGTCTAGAACGGTCTTTATGTGATTAACTTTTCGGAGCGACCCACTAAGAC	T	A	653244478	653244578	644528330	644528430	653543004	653543104	655121645	655121745
RDMb-h3:SNP_282	GGCCCTCTTGTGGAGCAAGACTCTTAAAGTAGCCTTTGTTGGGCTTGTCTAGAACGGTCTTTATGTGATTAACTTTTCGGAGCGACCCACTAAGACCGCGA	T	G	653244483	653244583	644528335	644528435	653543009	653543109	655121650	655121750
RDMb-h3:SNP_283	AGCCGCAGCCTCAGGAGGGTGAGTGCGTTCTTCTGGCCACCCACGTCGATCGTGGGTTTTCTTTGCCACCCCACCCTTTCTTTCGGGGTTTTTTTGAATTT	T	C	653246867	653246967	644530719	644530819	653545393	653545493	655124034	655124134
RDMb-h3:SNP_284	GTGAGTGCGTTCTTCTGGCCACCCACGTCGATCGTGGGTTTTCTTTGCCACCCCACCCTTTCTTTCGGGGTTTTTTTGAATTTCTTTGGGGCACAACTCCA	A	G	653246885	653246985	644530737	644530837	653545411	653545511	655124052	655124152
RDMb-h3:SNP_285	TGGCCACCCACGTCGATCGTGGGTTTTCTTTGCCACCCCACCCTTTCTTTCGGGGTTTTTTTGAATTTCTTTGGGGCACAACTCCACCACTTCACGCCCAA	T	C	653246900	653247000	644530752	644530852	653545426	653545526	655124067	655124167
RDMb-h3:SNP_286	GCCGAGGTGGAGTCCCAAAAGGGACTAAACCAGGAGGAGGTGGTCCTGGGGGCGCCGCAAGGTGACCTCCCAGACTCCAGGCCCAAAGGGGGTAAAGCCCC	G	A	653250655	653250755	644534507	644534607	653549181	653549281	655127822	655127922
RDMb-h3:SNP_287	CCCAAAAGGGACTAAACCAGGAGGAGGTGGTCCTGGGGGCGCCGCAAGGTGACCTCCCAGACTCCAGGCCCAAAGGGGGTAAAGCCCCAGAGGGATCTAAG	T	C	653250668	653250768	644534520	644534620	653549194	653549294	655127835	655127935
RDMb-h3:SNP_288	TGCTTGTTGCGACGTGACCTGCCCTTGTTGTCCTTGGTATCCGAATTGCTAGGGCTCTTGGTTATGTTATTGCTACGAGCTAGCTAGCTGTCTTCTCCCGC	T	C	653254447	653254547	644538299	644538399	653552973	653553073	655131614	655131714
RDMb-h3:SNP_289	GCGAGTTTGTGTGGCTTCTGTTGGTCCACTCGGAGGACCAAGTCTCCTTATTTGAAGGCTCGGCTCTTCACATTTCTGGCGTAGAATCGGCGCAAGTCTTG	A	C	653264571	653264671	644548546	644548646	653562839	653562939	655141892	655141992
RDMb-h3:SNP_290	AGTTTGTGTGGCTTCTGTTGGTCCACTCGGAGGACCAAGTCTCCTTATTTGAAGGCTCGGCTCTTCACATTTCTGGCGTAGAATCGGCGCAAGTCTTGCTG	T	G	653264574	653264674	644548549	644548649	653562842	653562942	655141895	655141995
RDMb-h3:SNP_291	CTTCACATTTCTGGCGTAGAATCGGCGCAAGTCTTGCTGATAGATGGTCAATCGGATCATGGCCATCTCTCTTTCTTCCTCAGAAGGTCGACTGTGTCCT	A	G	653264636	653264736	644548611	644548711	653562904	653563004	655141957	655142057
RDMb-h3:SNP_292	GTCAATCGGATCATGGCCATCTCTCTTTCTTCTTCCAGAAGGTCGACTGTGTCCTGCCGGGCTTGCTCCGCTTTGACTTCAGAGTAGAGCTCGACTCGCGG	T	C	653264682	653264782	644548657	644548757	653562950	653563050	655142003	655142103
RDMb-h3:SNP_293	CTTTAGGAGTCCACTCAAACTTCTCTGAGTTCTTCATCAGTCGGTAAAGGAGTAATGCCTTCTCACCGAGACGAGAGATGAATCGACTTAAAGCGGCCAAG	G	A	653266714	653266814	644550689	644550789	653564982	653565082	655144035	655144135
RDMb-h3:SNP_294	CGACTTAAAGCGGCCAAGCAACCAGTAAGCTTCTGAACATCGTGCACACACACAAATCGTTTCATTCGGAGTATAGTCCCCACTTTCTCTGGGTTTGCGTC	A	G	653266797	653266897	644550772	644550872	653565065	653565165	655144118	655144218
RDMb-h3:SNP_295	TCGTTTCATTCGGAGTATAGTCCCCACTTTCTCTGGGTTTGCGTCGATTACTCGTTCGGAAACGAGAAAACCGAGTAACTTTCTGCCAGGAACTCCAAATG	A	C	653266853	653266953	644550828	644550928	653565121	653565221	655144174	655144274
RDMb-h3:SNP_296	CTCTTCCTCACCATTGGCATATTTGGTGGCTATCTCCATCATTCGACTCTGAGACATGTCTCCGGTTCGACCGAATTTCAGGCTTAGCTCTCTGTACTTAA	T	A	653268818	653268918	644552793	644552893	653567086	653567186	655146139	655146239
RDMb-h3:SNP_297	CATTCTCTACAGTGTGATGCAATGTGATCCATCTCTGGATGTAATCTCTTAAAGTCTCATTCGACTTCTGCACACAAGATTGCAGCTCTGTCAGTCCTGCT	T	C	653268958	653269058	644552933	644553033	653567226	653567326	655146279	655146379
RDMb-h3:SNP_298	ACTCTTGTGGAGCCATCACCAACCCAAGACCCACACGCTTCCGAAGAACGAAGTGAAGGCCCTCAATCTCATGAACAAGATCAAGGGCAAGATCAACCTCAAGATGGTGGTGAACCAC	G	A	653271274	653271374	644555249	644555349	653569542	653569642	655148595	655148695
RDMb-h3:SNP_299	ACCAACCCAAGACCCACACGCTTCCGAAGAACGAAGTGAAGGCCCTCAATCTCATGAACAAGATCAAGGGCAAGATCAACCTCAAGATGGTGGTGAACCAC	T	C	653271291	653271391	644555266	644555366	653569559	653569659	655148612	655148712
RDMb-h3:SNP_300	ATAACCTTGCAGATATTTTCAGGAAGCCCTTGGATGAAGCAAGATTTCGTGAGTTAAGTCATGAGCTAAATATCATTGATTCGAGCAATGTGGTTTGAATC	T	C	653273111	653273211	644557086	644557186	653571379	653571479	655150432	655150532
RDMb-h3:SNP_301	CAGATATTTTCAGGAAGCCCTTGGATGAAGCAAGATTTCGTGAGTTAAGTCATGAGCTAAATATCATTGATTCGAGCAATGTGGTTTGAATCCTTGCACAC	T	G	653273120	653273220	644557095	644557195	653571388	653571488	655150441	655150541
RDMb-h3:SNP_302	GAGTTAAGTCATGAGCTAAATATCATTGATTCGAGCAATGTGGTTTGAATCCTTGCACACTCCACCATACTCATCATGCTATCTTGTCTAGGTGTAGGCAT	T	C	653273161	653273261	644557136	644557236	653571429	653571529	655150482	655150582
RDMb-h3:SNP_303	CGGTCTACTTGTCACGGACGTGATGCCTATATACATGATCATGCCTAGACAATCTCATAATTATTCGATTTTCTATCAATTGCTCGACAGTAATTTGTTCA	C	T	653275729	653275829	644559704	644559804	653573997	653574097	655153050	655153150
RDMb-h3:SNP_304	CTAAAACTGGCCCAAGAGAACTTGACGAAGGCGAAGGAGGAAGCTAAAGTTATGCTTGGTGAGGCCTTTGACGATTGCCTTTGCCTCTCACTTGTTTCCGA	T	G	653286068	653286168	644570013	644570113	653584065	653584165	655163273	655163373
RDMb-h3:SNP_305	CGAAGGCGAAGGAGGAAGCTAAAGTTATGCTTGGTGAGGCCTTTGACGATTGCCTTTGCCTCTCACTTGTTTCCGAATCTAATCTTCACTGTAACTTTGCA	T	C	653286093	653286193	644570038	644570138	653584090	653584190	655163298	655163398
RDMb-h3:SNP_306	CTCCCTCTCTTCCTCTAACAGGTCGACTACATCCTGCCGCGCTTGTTCTACTTCTGCTTCAGTGTAGAGCTCGACTCGGGGAGCATTGTGGAGAAGGTCAC	A	G	653289586	653289686	644572812	644572912	653586864	653586964	655166072	655166172
RDMb-h3:SNP_307	AGAAGGTCACTCGGTAAGACTGCTTCAGCCCCGTAGACCAAGAAGAATGAAGTTCTCCTAGTCGACCGGTTGGGCGTGGTCCTTAAGCCCCAAAGCACCGA	A	G	653289677	653289777	644572903	644573003	653586955	653587055	655166163	655166263
RDMb-h3:SNP_308	TCTTGATGGGTTTAGCTTCGATCCACTTAGTGAACTTGTCGACTGCTACTAGCACATGGGTAAAACCGCTTCTGCCTGTTCTCAAAGGACCGACCATATCC	T	C	653290055	653290155	644573281	644573381	653587333	653587433	655166541	655166641
RDMb-h3:SNP_309	CAAGGAGTCGAGCCACTTCCTCGTCAATGGCTTTTTTCTTCTGAACGGCAGACCGTCGAAGATGTTCCTTAACAGGTTTTGCTTTTGAATCGACTCTAAGG	A	G	653297328	653297428	644580577	644580677	653594274	653594374	655173482	655173582
RDMb-h3:SNP_310	AAAAAATGACGTTGCAGGTGCTGCCGGACAAGATCCGGACAGGCAAGAATTTCTGCGCCAACTGAAGGCCGGCGAGAGGGTGCTGCAAAAGGTGCAGCAAG	T	C	653313108	653313208	644596357	644596457	653610054	653610154	655189262	655189362

RDMb-h3:SNP_311	ACAGGCAAGAATTTCTGCGCCAACTGAAGGCCGGCGAGAGGGTGCTGCAAAAGGTGCAGCAAGAAAGGAACAAGCTCCAGGATGCCCATGCCCAGCTTGGA	A	T	653313146	653313246	644596395	644596495	653610092	653610192	655189300	655189400
RDMb-h3:SNP_312	AGTTCGCCAACGTTGTAAGTCTTGGCCCGTACTTCTCTGCTTTGGTATCGTCGAGCCTGCTGCTGATAAAATGCGGAACGAGCCTTGGCGACGTCGCGTTC	G	T	653314807	653314907	644598056	644598156	653611753	653611853	655190961	655191061
RDMb-h3:SNP_313	TCCATGGGGCGATTACTGCCATTATGTCGTGAGCTGAGGGTGTTGTTTCATCGGCTGGAACGCCGGTTATGTCAGATTGTTCTGCGGCTGCCTCCGGTTTG	A	G	653315862	653315962	644599111	644599211	653612808	653612908	655192016	655192116
RDMb-h3:SNP_314	GAGGCAACGGCGGAGGTGACCCGTCGCACGACCATGAGGAGTACCGTCCTGAGCCCCTCGACTCACAGCAGAGGGAAGAGCTTCGCCGCCGGAACATGGAT	T	C	653321007	653321107	644604256	644604356	653617953	653618053	655197161	655197261
RDMb-h3:SNP_315	CCGTGAGAACTGGGACATCTTCGCATGGAAACCTTCTGACATGCCGGGTTTACCCAGGGGACTGGCTGAGCATCGTCTACGAGTCGACTCGAAGGCAAAAC	T	G	653323546	653323646	644606795	644606895	653620492	653620592	655199700	655199800
RDMb-h3:SNP_316	TTTACCACTCCGAGTGGCTCGCCAATGTCGTCATGGTCCCCAAAAAGGATAATTCTCTTCGCATGTGCACCGATTTCAAGCATATCAATCGGGCCTGCCCGAAAGATTATTTTCCTCTTCC	T	C	653323743	653323843	644606992	644607092	653620689	653620789	655199897	655199997
RDMb-h3:SNP_317	GCCAATGTCGTCATGGTCCCCAAAAAGGATAATTCTCTTCGCATGTGCACCGATTTCAAGCATATCAATCGGGCCTGCCCGAAAGATTATTTTCCTCTTCC	C	T	653323763	653323863	644607012	644607112	653620709	653620809	655199917	655200017
RDMb-h3:SNP_318	TCGCATGTGCACCGATTTCAAGCATATCAATCGGGCCTGCCCGAAAGATTATTTTCCTCTTCCCCGCATCGACCAAATAGTCGACTCAACTGCGGGATGTG	T	C	653323801	653323901	644607050	644607150	653620747	653620847	655199955	655200055
RDMb-h3:SNP_319	TTCATCACCCCATTCGGGTGCTTCTGTTATGTCACCATGCCATTCGGCCACAAGAATGCCGGAGCCACGTTCATGAGGATGATTCAGAAGTGTTTGCTCAC	A	T	653323979	653324079	644607228	644607328	653620925	653621025	655200133	655200233
RDMb-h3:SNP_320	GTGCGTGTGCACGATGTCCAGAAACTTACTGGATGCTTGGCCGCATTAATTCGATTCATCTCTCGCCTTGGTGAAAAGGCATTGCCTCTTTACCGACTGAT	T	G	653324324	653324424	644607573	644607673	653621270	653621370	655200478	655200578
RDMb-h3:SNP_321	AGAAACTTACTGGATGCTTGGCCGCATTAATTCGATTCATCTCTCGCCTTGGTGAAAAGGCATTGCCTCTTTACCGACTGATGAAGAAGTCAGACAAGTTC	T	C	653324343	653324443	644607592	644607692	653621289	653621389	655200497	655200597
RDMb-h3:SNP_322	TGGATCAGCAGAAACCACACAAGCTTGCTCCTACTTGGGAAGGTCCCTTAATCGTCACCAAAGTTCTCCATAATGGGGCATACCGCCTTTACAATGTCGAG	A	C	653326547	653326647	644609796	644609896	653623493	653623593	655202701	655202801
RDMb-h3:SNP_323	GCGATGAAGGTCTCCATGAAAGAGCGGAAGTCATGCTTCCTAGTGTTGGTCACCTTGAGAGACACTAGCTTGTCTTCTCTCGCTTCTTTGCAGTGGACGCGGACCAAGGACAGAGCG	T	C	653328292	653328392	644611558	644611658	653625238	653625338	655204446	655204546
RDMb-h3:SNP_324	TGAAAGAGCGGAAGTCATGCTTCCTAGTGTTGGTCACCTTGAGAGACACTAGCTTGTCTTCTCTCGCTTCTTTGCAGTGGACGCGGACCAAGGACAGAGCG	T	C	653328308	653328408	644611574	644611674	653625254	653625354	655204462	655204562
RDMb-h3:SNP_325	TGCAGTGGACGCGGACCAAGGACAGAGCGACATCAGCACCGCACCTGGCCGAAGACTTCTTCCACTCTTGCACTCGACTCGGAATCTCGTTCAGTCGAGTC	C	A	653328380	653328480	644611646	644611746	653625326	653625426	655204534	655204634
RDMb-h3:SNP_326	TGCTTGGCTGGCGGTTCGGATCGCCTTCACCTGCTCCATCATAATCCCGACCTGGCGTGTGGCTTCCTTAGCAGCGCTTGCTTGGTCCTCCGGGACTGGTAGGTGGAGAA	A	G	653329764	653329864	644613030	644613130	653626710	653626810	655205918	655206018
RDMb-h3:SNP_327	GGCGGTTCGGATCGCCTTCACCTGCTCCATCATAATCCCGACCTGGCGTGTGGCTTCCTTAGCAGCGCTTGCTTGGTCCTCCGGGACTGGTAGGTGGAGAA	G	A	653329773	653329873	644613039	644613139	653626719	653626819	655205927	655206027
RDMb-h3:SNP_328	CCGTTGGGCATCGAGTACAACTCAGTGGTTTCCTGAAACACAGCAAGCAGGACAAAGGTCAATCGACTGATTTACGACGAAACAGAATAGAAGGAGCAGTC	G	A	653330643	653330743	644613909	644614009	653627589	653627689	655206797	655206897
RDMb-h3:SNP_329	CAGCTCAACTGGGGCGCAATCGCAGTGGTTCTCCCAGTGCTACCTTAGCTGATAAAATGGAACGTAAGGTACCAAAACATGGGAGCCGGGCAAACCCAACT	T	C	653338187	653338287	644621453	644621553	653635133	653635233	655214341	655214441
RDMb-h3:SNP_330	CTGGGGCGCAATCGCAGTGGTTCTCCCAGTGCTACCTTAGCTGATAAAATGGAACGTAAGGTACCAAAACATGGGAGCCGGGCAAACCCAACTATTGACCC	T	C	653338195	653338295	644621461	644621561	653635141	653635241	655214349	655214449
RDMb-h3:SNP_331	CGGGTCATGAGTGATGTAAGGGCTGCCATGGATTTAGGCTTTTCCTGTCGCAGGTGCCGGGCCAGCCACTCGTCGCGGATGTTATGCTTGAAGGCCGCGAG	G	C	653340084	653340184	644623350	644623450	653637030	653637130	655216238	655216338
RDMb-h3:SNP_332	ATGTAAGGGCTGCCATGGATTTAGGCTTTTCCTGTCGCAGGTGCCGGGCCAGCCACTCGTCGCGGATGTTATGCTTGAAGGCCGCGAGGGCCTCGGCATCC	C	A	653340097	653340197	644623363	644623463	653637043	653637143	655216251	655216351
RDMb-h3:SNP_333	CGGATGTTATGCTTGAAGGCCGCGAGGGCCTCGGCATCCGGACAGTCGATGATTTGGTTTTTCTTGGTTAAGAACCGTGTCCAGAATTGTCTGGCCGATTC	T	C	653340159	653340259	314195309	314195409	15029270	15029370	324938575	324938675
RDMb-h3:SNP_334	AGCGGGATCATATGCCTCCACCTCTAATCGGGGGAGCAGCTTACGTTTGAGGTAGCTTTTGGAGGGTCGTTCGAGTTCATGCTCTTTGGCCGCGAGGACTT	A	G	653340902	653341002	644624168	644624268	653637848	653637948	655217056	655217156
RDMb-h3:SNP_335	CCACCTCTAATCGGGGGAGCAGCTTACGTTTGAGGTAGCTTTTGGAGGGTCGTTCGAGTTCATGCTCTTTGGCCGCGAGGACTTCAGTCCATCTGTCAGCT	T	G	653340919	653341019	644624185	644624285	653637865	653637965	655217073	655217173
RDMb-h3:SNP_336	AGCAGATCTTGATCAGCTCTAAGCTGCTGCTGCTTTTTCTTGAGGCTGTCTGCCATGGCCATAAGCCTGCGTTTGAAATGCTCCTGTTCGACGGGATCCTC	C	T	653341020	653341120	644624286	644624386	653637966	653638066	655217174	655217274
RDMb-h3:SNP_337	ATCTTGATCAGCTCTAAGCTGCTGCTGCTTTTTCTTGAGGCTGTCTGCCATGGCCATAAGCCTGCGTTTGAAATGCTCCTGTTCGACGGGATCCTCCGGCA	A	G	653341025	653341125	644624291	644624391	653637971	653638071	655217179	655217279
RDMb-h3:SNP_338	CTTTATTAATATTGATGATGTGGGTTACAAGAGTAGATCTACCACGAGAGCAAGGAGGCTAAACCCTAGAAGCTAGCCTATGGTATGATTGTTGTTCGTCC	G	T	653342402	653342502	644625668	644625768	653639348	653639448	655218556	655218656
RDMb-h3:SNP_339	TATTCCCCTTGAGCTAAGGACACACAGTCCTCGCCCAATCACTCTGGTAGGTCTTCAAGGTAGACTTCTGAACCTTCACAGACTTCGTTCACCGTCGATCC	G	A	653344415	653344515	644627680	644627780	653641360	653641460	655220568	655220668
RDMb-h3:SNP_340	TCCCAAGCCAAAGTTCTCAGATGCTGCACTTAGACTCATTGCTTCTAAGACACCCCTGAAGATGTGGGTGGTGAAGAAGAATTAACTTCTCTTGCAGGGCA	A	C	653348853	653348953	644632118	644632218	653645798	653645898	655225006	655225106
RDMb-h3:SNP_341	CTGCACTTAGACTCATTGCTTCTAAGACACCCCTGAAGATGTGGGTGGTGAAGAAGAATTAACTTCTCTTGCAGGGCAAGGTCTCCAGCCGGAAAGCAAAA	G	T	653348876	653348976	644632141	644632241	653645821	653645921	655225029	655225129
RDMb-h3:SNP_342	GTGGTTGAAACTGTGGATGTGCAGTTCGATGAGACTAACGGCTCGCAAACAGAGCACCTGCCAAATGTGCTAGATGAAGCTACACTAGGTGAAGCTATCAA	C	G	653350436	653350536	644633701	644633801	653647381	653647481	655226589	655226689
RDMb-h3:SNP_343	TGGTAGGAAAAGACCATCGCTCGTCCCCGACTACAACTCATAAGGAAGATAATCAATAAATAAAATTGTGCTCCGACTTCATCACAAAGCGGTTCACCATA	T	C	653358999	653359099	644642264	644642364	653655944	653656044	655235152	655235252
RDMb-h3:SNP_344	TTCTGTTTTTCAGCAGAATCAAAACAACTATCATCATAGCTTATCCTATGGGTTCTACTTGGCACAAACACTAATTAAAACATAAAACCACATCTAAACAG	G	A	653360235	653360335	644643500	644643600	653657180	653657280	655236388	655236488
RDMb-h3:SNP_345	CAAACCAAACGGATAATTCGAAGAGACTTGCAAAGATAACTCAATCATATATAAAAGAATTCAGAGAAGAATCAAATATTATTCATAGATAAGCTGGATCA	T	C	653362270	653362370	644645535	644645635	653659215	653659315	655238423	655238523
RDMb-h3:SNP_346	GAATCAAATATTATTCATAGATAAGCTGGATCATAAACCCACAATTCATTGGTCTCAAGAAACACACCGCAAAAAGAAGATTACATCGAATAGATCTCCAC	T	C	653362338	653362438	644645603	644645703	653659283	653659383	655238491	655238591
RDMb-h3:SNP_347	ATTATTCATAGATAAGCTGGATCATAAACCCACAATTCATTGGTCTCAAGAAACACACCGCAAAAAGAAGATTACATCGAATAGATCTCCACAAGAGAGGG	G	C	653362347	653362447	644645612	644645712	653659292	653659392	655238500	655238600
RDMb-h3:SNP_348	ACCTGCAACTGTTGTTGTAGTAATCTGTGAGCCACGAGGACTCAGCAATACCATTACCATGGGTAACAAGACTAGCAAAGCTTAATGGGAAAGGAAGGGGT	A	C	653375163	653375263	644658584	644658684	653672109	653672209	655251452	655251552
RDMb-h3:SNP_349	GTAGTAATCTGTGAGCCACGAGGACTCAGCAATACCATTACCATGGGTAACAAGACTAGCAAAGCTTAATGGGAAAGGAAGGGGTAAAGTGGTGAGGTTGC	A	T	653375179	653375279	644658600	644658700	653672125	653672225	655251468	655251568
RDMb-h3:SNP_350	CGATCAGTCTCGGAATCCCGGTTTACAAGACATTTCGACAATGGTAAAATAAGACCAGCAAGACCGCCCGATGTGTCGACAATCCCGATAGGAGTCGCACG	T	C	653375650	653375750	644659071	644659171	653672596	653672696	655251939	655252039
RDMb-h3:SNP_351	TTCTCCAAAGAAAGAACACTGTCATGCAGACTCCGCATAGCACCGGTTGAAGCATTGAGGAGAATAGTCGGTAGCATCGGCCTACCCGCCACATGCACCCTCCTCGAGATA	A	C	653398930	653399030	644682353	644682453	653695876	653695976	655275221	655275321
RDMb-h3:SNP_352	AAAGAACACTGTCATGCAGACTCCGCATAGCACCGGTTGAAGCATTGAGGAGAATAGTCGGTAGCATCGGCCTACCCGCCACATGCACCCTCCTCGAGATA	G	C	653398940	653399040	644682363	644682463	653695886	653695986	655275231	655275331
RDMb-h3:SNP_353	AACACTGTCATGCAGACTCCGCATAGCACCGGTTGAAGCATTGAGGAGAATAGTCGGTAGCATCGGCCTACCCGCCACATGCACCCTCCTCGAGATATCCT	A	T	653398944	653399044	644682367	644682467	653695890	653695990	655275235	655275335
RDMb-h3:SNP_354	CAAAGGCAAGGAGATGAAGTCATCGGCCGAGAGGCTTAGTTACCGTGATAGCGTCGAGCCCGGCTAATGTCGAGGCACCGCCAACGGCGGGCGTGCAAGTG	A	G	653399885	653399985	644683308	644683408	653696831	653696931	655276176	655276276
RDMb-h3:SNP_355	GAGATGAAGTCATCGGCCGAGAGGCTTAGTTACCGTGATAGCGTCGAGCCCGGCTAATGTCGAGGCACCGCCAACGGCGGGCGTGCAAGTGACGGAGGGGC	C	T	653399895	653399995	644683318	644683418	653696841	653696941	655276186	655276286
RDMb-h3:SNP_356	AGGCCTTGCTCGGCACGCTCCGCGTCCTCCTTGTCCCATATAGGTTCCGGCACTCTGTAACCGCCGGGACCGAGTTTGTGGACCCCTAAGTTCAAGTCCCG	G	C	653400740	653400840	644684163	644684263	653697686	653697786	655277031	655277131
RDMb-h3:SNP_357	GCATTTATTTCCCCCACTGACTTGATTCCGCGGATGGCTTGCTCCTGCACTTGATCTTGAACTCCCGGTAGTTAGCTTCGCTGATCGAAGGATTTTTCTCC	C	A	653400840	653400940	644684263	644684363	653697786	653697886	655277131	655277231
RDMb-h3:SNP_358	CCCACTGACTTGATTCCGCGGATGGCTTGCTCCTGCACTTGATCTTGAACTCCCGGTAGTTAGCTTCGCTGATCGAAGGATTTTTCTCCTTGATCTTCTCA	C	G	653400852	653400952	644684275	644684375	653697798	653697898	655277143	655277243
RDMb-h3:SNP_359	GATTCCGCGGATGGCTTGCTCCTGCACTTGATCTTGAACTCCCGGTAGTTAGCTTCGCTGATCGAAGGATTTTTCTCCTTGATCTTCTCATAACTATCACC	T	C	653400863	653400963	644684286	644684386	653697809	653697909	655277154	655277254
RDMb-h3:SNP_360	TTCCGCGGATGGCTTGCTCCTGCACTTGATCTTGAACTCCCGGTAGTTAGCTTCGCTGATCGAAGGATTTTTCTCCTTGATCTTCTCATAACTATCACCAC	G	T	653400865	653400965	644684288	644684388	653697811	653697911	655277156	655277256
RDMb-h3:SNP_361	GGATGGCTTGCTCCTGCACTTGATCTTGAACTCCCGGTAGTTAGCTTCGCTGATCGAAGGATTTTTCTCCTTGATCTTCTCATAACTATCACCACGTAGAA	C	G	653400871	653400971	644684294	644684394	653697817	653697917	655277162	655277262
RDMb-h3:SNP_362	AATGGACTAAAGAAACTGACAAGAAAATTAATCAAGCTAGGACACAACATGGCAAAATGTATACTATAAACAGGGGATAGTCGACATATCTGCATCTCCAG	T	C	653409218	653409318	644692640	644692740	653706164	653706264	655285508	655285608
RDMb-h3:SNP_363	TTGATATCGTACGCCTCATACGTCATCAGGTTGTGCTCGGCGCCCTGTGGCAAGGTGAATATGAGTTGTTCTTCCGCGGAAGAATCCTCATGTAAAGGGTA	G	A	653411853	653411953	644695329	644695429	653708798	653708898	655288013	655288113
RDMb-h3:SNP_364	TCGTACGCCTCATACGTCATCAGGTTGTGCTCGGCGCCCTGTGGCAAGGTGAATATGAGTTGTTCTTCCGCGGAAGAATCCTCATGTAAAGGGTACGACAG	T	C	653411859	653411959	644695335	644695435	653708804	653708904	655288019	655288119
RDMb-h3:SNP_365	GGACCAGAAGATGCACCATAACATCGAAGAATGCGGGCGGGAAGTACATGTCAAGCTCGCATAGTATCACCACGATCTCTTCCTGTAGCCTTCTGAGTTGC	G	C	653412403	653412503	644695879	644695979	653709348	653709448	655288563	655288663
RDMb-h3:SNP_366	GGAATCCGGGTCTATAAGGCTCTTCAGCTTGCATCTTCGACACGGACATTTTATCTCCGTCTTGTTCTTTTGAAGCATCTCGGCCTTCACGGAGCTCAAAAA	T	C	653414684	653414784	644698160	644698260	653711629	653711729	655290844	655290944
RDMb-h3:SNP_367	ATAAGGCTCTTCAGCTTGCATCTTCGACACGGACATTTTATCTCCGTCTTGTTCTTTTGAAGCATCTCGGCCTTCACGGAGCTCAAAAACCTATTCATGAT	T	C	653414697	653414797	644698173	644698273	653711642	653711742	655290857	655290957
RDMb-h3:SNP_368	ACACGGACATTTTATCTCCGTCTTGTTCTTTTGAAGCATCTCGGCCTTCACGGAGCTCAAAAACCTATTCATGATGCCTTCGGTCATTGTGCGGACCATGG	A	G	653414723	653414823	644698199	644698299	653711668	653711768	655290883	655290983
RDMb-h3:SNP_369	GCGGACCATGGTCGCCTGCGGGGGTAGAGCAAAACGATATTTTAGAACCCAAAAAAATTGGCATGACTTTGCCTAAAAATAGGACCAAAAAGAATGCATAG	C	A	653414813	653414913	644698289	644698389	653711758	653711858	655290973	655291073
RDMb-h3:SNP_370	TTGATTATTGTTCCCACAAGTTGTTTGCTCACAAAATCCCTATGCATAGTAAGTGGGTTAGACTTAAATGTGCTAGTCATATTCTTCATGATGCTCTCTTT	T	G	653419064	653419164	644702540	644702640	653716009	653716109	332453147	332453047
RDMb-h3:SNP_371	ATTGCTCATGTAGCAACTAGGGGCTGTCAGTGTCTTCCATGCTAGGTGGATTATTCTCAAGAGGAGTGGACTCCGCTCCTCATTCACGAGAAAGGGGCGGT	A	G	653421456	653421556	644704932	644705032	653718401	653718501	655297612	655297712
RDMb-h3:SNP_372	GTGGATTATTCTCAAGAGGAGTGGACTCCGCTCCTCATTCACGAGAAAGGGGCGGTAACCGGGATGCCCAGTCCCATGAGCAAATAAAACTCCCCCAGGTT	G	T	653421501	653421601	644704977	644705077	653718446	653718546	655297657	655297757
RDMb-h3:SNP_373	AGTTGGAGGCACCCGTTGTTTCGGGCAAGCCATGGATTGATGATTGTTGATGGAGGGGGAGTAAAAACTTTTACCATTCTGTTTGGGAACCGCCTATAATG	A	G	653421609	653421709	644705085	644705185	653718554	653718654	655297765	655297865
RDMb-h3:SNP_374	ATGTATGTAGTATGGAAGATATTGGGAACTCTTGGTTGTTATGTTGACATTGAGATCATACCTCTCAAAATTATTTATCTCTATTTCAAAATCGAGCTCTG	T	A	653421707	653421807	234399464	234399364	243565508	243565408	244586551	244586451

RDMb-h3:SNP_375	TGCTTCCCTCTGCGAAGGGCCTATCTTTTACTTTATGTCATTTACTTTACGCAAGAGTCAAGGTGATCTTCACCTTTCCCTTTTTCATTTTATCCTTTGGA	C	T	653421825	653421925	644705301	644705401	653718770	653718870	655297981	655298081
RDMb-h3:SNP_376	TTTTGGTGATCAACTTGCGGGTTCCGCCCATGAACCTATGCATAGGGGTGGGCACGCGTTTTCATCTTGACTCTCCGGTAGAAACTTTGGGGCACTCTTTG	G	T	653423290	653423390	644706766	644706866	653720235	653720335	655299446	655299546
RDMb-h3:SNP_377	TGATCAACTTGCGGGTTCCGCCCATGAACCTATGCATAGGGGTGGGCACGCGTTTTCATCTTGACTCTCCGGTAGAAACTTTGGGGCACTCTTTGAAGTAC	G	A	653423296	653423396	644706772	644706872	653720241	653720341	655299452	655299552
RDMb-h3:SNP_378	TGATCATCTTACATTCCAAGTTATCCATTACATTCTATATTTCTATGTCAGAATCTTATCATCCTGGACTAAACCATTGTCTTGTTTTCCCTAGGATGGTC	A	G	653442810	653442910	644726692	644726792	653739602	653739702	655319424	655319524
RDMb-h3:SNP_379	CCATTACATTCTATATTTCTATGTCAGAATCTTATCATCCTGGACTAAACCATTGTCTTGTTTTCCCTAGGATGGTCAACACCCGCAACAACCCTGCTCTC	C	T	653442834	653442934	644726716	644726816	653739626	653739726	655319448	655319548
RDMb-h3:SNP_380	AGTCCTTGAAAAAGGGTTTCATCCGTCCTAGTTCGTCTCCATGGGCTTGTCCCGTTCTCTTCGTCAAGAAGAAGGATGGTACGGATCGGATGGTTGTAGAT	T	C	653444604	653444704	644728486	644728586	653741396	653741496	655321218	655321318
RDMb-h3:SNP_381	TGAAAAAGGGTTTCATCCGTCCTAGTTCGTCTCCATGGGCTTGTCCCGTTCTCTTCGTCAAGAAGAAGGATGGTACGGATCGGATGGTTGTAGATTATCGA	T	C	653444610	653444710	644728492	644728592	653741402	653741502	655321224	655321324
RDMb-h3:SNP_382	CAGTCAACCTGGTCACAATCAAGAACAAGTATCCGCTCCCCAGGATCAAGGATCTGTATGATCAGCTCGCTGGATCCTCATTCTTCTCCAAAATGGATTTG	G	C	653444712	653444812	644728594	644728694	653741504	653741604	655321326	655321426
RDMb-h3:SNP_383	ACATGAGGAGAATTATCCTACTCATGATCTAGAGCTTGCAGCTGTAGTCCATGCACTCAAAACCTGGCGACATTACCTCCTCGGTAATCATTGCAAAATCT	C	T	653445520	653445620	644729402	644729502	653742312	653742412	655322134	655322234
RDMb-h3:SNP_384	AGAATTATCCTACTCATGATCTAGAGCTTGCAGCTGTAGTCCATGCACTCAAAACCTGGCGACATTACCTCCTCGGTAATCATTGCAAAATCTTCACTGAT	C	T	653445528	653445628	644729410	644729510	653742320	653742420	655322142	655322242
RDMb-h3:SNP_385	GCTGTAGTCCATGCACTCAAAACCTGGCGACATTACCTCCTCGGTAATCATTGCAAAATCTTCACTGATCATCAAATTCTGAAGTACATATTCACCCAACC	A	G	653445560	653445660	644729442	644729542	653742352	653742452	655322174	655322274
RDMb-h3:SNP_386	AGTCCATGCACTCAAAACCTGGCGACATTACCTCCTCGGTAATCATTGCAAAATCTTCACTGATCATCAAATTCTGAAGTACATATTCACCCAACCGGATT	A	G	653445565	653445665	644729447	644729547	653742357	653742457	655322179	655322279
RDMb-h3:SNP_387	ATGCACTCAAAACCTGGCGACATTACCTCCTCGGTAATCATTGCAAAATCTTCACTGATCATCAAATTCTGAAGTACATATTCACCCAACCGGATTTGAAT	C	A	653445570	653445670	644729452	644729552	653742362	653742462	655322184	655322284
RDMb-h3:SNP_388	CCTGGCGACATTACCTCCTCGGTAATCATTGCAAAATCTTCACTGATCATCAAATTCTGAAGTACATATTCACCCAACCGGATTTGAATCTCAGGCAAAGA	T	C	653445582	653445682	644729464	644729564	653742374	653742474	655322196	655322296
RDMb-h3:SNP_389	CGACATTACCTCCTCGGTAATCATTGCAAAATCTTCACTGATCATCAAATTCTGAAGTACATATTCACCCAACCGGATTTGAATCTCAGGCAAAGACGTTG	T	G	653445587	653445687	644729469	644729569	653742379	653742479	655322201	655322301
RDMb-h3:SNP_390	ACCGGATTTGAATCTCAGGCAAAGACGTTGGGTCGAGTTGATCACAGATCTCGACTTAGGGATAACTTACACCCCAGGAAAAGCCAATGTCATGGCTGATG	C	T	653445658	653445758	644729540	644729640	653742450	653742550	655322272	655322372
RDMb-h3:SNP_391	ATCTCAGGCAAAGACGTTGGGTCGAGTTGATCACAGATCTCGACTTAGGGATAACTTACACCCCAGGAAAAGCCAATGTCATGGCTGATGTACTAAGTCGT	G	A	653445669	653445769	644729551	644729651	653742461	653742561	655322283	655322383
RDMb-h3:SNP_392	GGGTCGAGTTGATCACAGATCTCGACTTAGGGATAACTTACACCCCAGGAAAAGCCAATGTCATGGCTGATGTACTAAGTCGTAAATTTTATTGTAACAAT	A	G	653445687	653445787	644729569	644729669	653742479	653742579	655322301	655322401
RDMb-h3:SNP_393	TGATCACAGATCTCGACTTAGGGATAACTTACACCCCAGGAAAAGCCAATGTCATGGCTGATGTACTAAGTCGTAAATTTTATTGTAACAATCTGATGTTA	T	C	653445696	653445796	644729578	644729678	653742488	653742588	655322310	655322410
RDMb-h3:SNP_394	GACTTAGGGATAACTTACACCCCAGGAAAAGCCAATGTCATGGCTGATGTACTAAGTCGTAAATTTTATTGTAACAATCTGATGTTACAACAAAGTCAACC	T	C	653445710	653445810	644729592	644729692	653742502	653742602	655322324	655322424
RDMb-h3:SNP_395	ACTTAGGGATAACTTACACCCCAGGAAAAGCCAATGTCATGGCTGATGTACTAAGTCGTAAATTTTATTGTAACAATCTGATGTTACAACAAAGTCAACCG	A	G	653445711	653445811	644729593	644729693	653742503	653742603	655322325	655322425
RDMb-h3:SNP_396	TACACCCCAGGAAAAGCCAATGTCATGGCTGATGTACTAAGTCGTAAATTTTATTGTAACAATCTGATGTTACAACAAAGTCAACCGCTTCTCCATGAGGA	T	C	653445725	653445825	644729607	644729707	653742517	653742617	655322339	655322439
RDMb-h3:SNP_397	CTGATGTTACAACAAAGTCAACCGCTTCTCCATGAGGAATTTCGGAAGCCTAATCTTCACATCGTTCCTCAAGGATTTCTTTCCACCTTGGTGGCGAAACC	C	T	653445788	653445888	644729670	644729770	653742580	653742680	655322402	655322502
RDMb-h3:SNP_398	TGTTACAACAAAGTCAACCGCTTCTCCATGAGGAATTTCGGAAGCCTAATCTTCACATCGTTCCTCAAGGATTTCTTTCCACCTTGGTGGCGAAACCTACT	T	C	653445792	653445892	644729674	644729774	653742584	653742684	655322406	655322506
RDMb-h3:SNP_399	AAAGTCAACCGCTTCTCCATGAGGAATTTCGGAAGCCTAATCTTCACATCGTTCCTCAAGGATTTCTTTCCACCTTGGTGGCGAAACCTACTCTTATGAAT	C	T	653445801	653445901	644729683	644729783	653742593	653742693	655322415	655322515
RDMb-h3:SNP_400	ATCGTTCCTCAAGGATTTCTTTCCACCTTGGTGGCGAAACCTACTCTTATGAATCAAATCATCACTGCCCAAAAGCGAGATAAAGGGATATCTAGGATCAA	T	C	653445848	653445948	644729730	644729830	653742640	653742740	655322462	655322562
RDMb-h3:SNP_401	CGTTCCTCAAGGATTTCTTTCCACCTTGGTGGCGAAACCTACTCTTATGAATCAAATCATCACTGCCCAAAAGCGAGATAAAGGGATATCTAGGATCAAGG	A	G	653445850	653445950	644729732	644729832	653742642	653742742	655322464	655322564
RDMb-h3:SNP_402	AACCTACTCTTATGAATCAAATCATCACTGCCCAAAAGCGAGATAAAGGGATATCTAGGATCAAGGAGAACATTGCTAGAGGAGGTGCTAGATATTTCTCC	G	A	653445885	653445985	644729767	644729867	653742677	653742777	655322499	655322599
RDMb-h3:SNP_403	CTTATGAATCAAATCATCACTGCCCAAAAGCGAGATAAAGGGATATCTAGGATCAAGGAGAACATTGCTAGAGGAGGTGCTAGATATTTCTCCACAAATGA	G	A	653445893	653445993	644729775	644729875	653742685	653742785	655322507	655322607
RDMb-h3:SNP_404	CCCAAAAGCGAGATAAAGGGATATCTAGGATCAAGGAGAACATTGCTAGAGGAGGTGCTAGATATTTCTCCACAAATGATCATGGTGTTGTGTACTTTGAG	A	C	653445915	653446015	644729797	644729897	653742707	653742807	655322529	655322629
RDMb-h3:SNP_405	AAAGGGATATCTAGGATCAAGGAGAACATTGCTAGAGGAGGTGCTAGATATTTCTCCACAAATGATCATGGTGTTGTGTACTTTGAGAACCGTTTAGTGGT	A	G	653445929	653446029	644729811	644729911	653742721	653742821	655322543	655322643
RDMb-h3:SNP_406	TTGGAGTATGCGCCGTACTCTTTAGGGAGTTCGGCTTCGGTCCATTCAGTGACAAAGTCAGCCAAAACTTGTGACTTTATAGCTCGCCAAGGTTTGTAAGT	T	C	653452710	653452810	644736592	644736692	653749502	653749602	655329324	655329424
RDMb-h3:SNP_407	GTCCATTCAGTGACAAAGTCAGCCAAAACTTGTGACTTTATAGCTCGCCAAGGTTTGTAAGTTATATCAAATGGTAAGAGCTCAATGGCCCATTTTGCAAT	A	G	653452749	653452849	644736631	644736731	653749541	653749641	655329363	655329463
RDMb-h3:SNP_408	GGCGGTCATAAGAAAACCACCTAGCCGGATAGTTTGGCCGGCGGCCAAGACTCCTTTGGCGAAAATACCGTCCTTGAAGACGGGAGGAGGCATCCTTCCTA	A	G	653455927	653456027	644739809	644739909	653752719	653752819	655332541	655332641
RDMb-h3:SNP_409	CCGCATCTCTCCAGAGTCCACGATGTCTTCCACGTTTCTCAACTCAGGCATTGCTTCTCGGATCCTATCCATGGAGTGGACCACGAAACACTTGATCTTCA	A	G	653457087	653457187	644740969	644741069	653753879	653753979	655333701	655333801
RDMb-h3:SNP_410	GATGTCTTCCACGTTTCTCAACTCAGGCATTGCTTCTCGGATCCTATCCATGGAGTGGACCACGAAACACTTGATCTTCAAGATAACCTCACGTATCGAGA	A	G	653457108	653457208	644740990	644741090	653753900	653754000	655333722	655333822
RDMb-h3:SNP_411	AACTCAGGCATTGCTTCTCGGATCCTATCCATGGAGTGGACCACGAAACACTTGATCTTCAAGATAACCTCACGTATCGAGAGTACCCTGTTCGTATCCTC	A	G	653457127	653457227	644741009	644741109	653753919	653754019	655333741	655333841
RDMb-h3:SNP_412	ATTGCTTCTCGGATCCTATCCATGGAGTGGACCACGAAACACTTGATCTTCAAGATAACCTCACGTATCGAGAGTACCCTGTTCGTATCCTCGATCAAGCC	T	C	653457136	653457236	644741018	644741118	653753928	653754028	655333750	655333850
RDMb-h3:SNP_413	CGGATCCTATCCATGGAGTGGACCACGAAACACTTGATCTTCAAGATAACCTCACGTATCGAGAGTACCCTGTTCGTATCCTCGATCAAGCCGAGCGTACC	C	T	653457145	653457245	644741027	644741127	653753937	653754037	655333759	655333859
RDMb-h3:SNP_414	ACCACGAAACACTTGATCTTCAAGATAACCTCACGTATCGAGAGTACCCTGTTCGTATCCTCGATCAAGCCGAGCGTACCACTCGACGTCATAATATCAAG	T	C	653457166	653457266	644741048	644741148	653753958	653754058	655333780	655333880
RDMb-h3:SNP_415	CCACGAAACACTTGATCTTCAAGATAACCTCACGTATCGAGAGTACCCTGTTCGTATCCTCGATCAAGCCGAGCGTACCACTCGACGTCATAATATCAAGT	G	A	653457167	653457267	644741049	644741149	653753959	653754059	655333781	655333881
RDMb-h3:SNP_416	CCCAGTTATGTTGTGACGTTTGGTACACCCAAAGCACTCCTACGGTATCTAGGAGTTACACAATCTCATAGTCTAAGGAAAAGATACTTGACATTGGAAAA	T	C	653464236	653464336	644748119	644748219	653761028	653761128	655340851	655340951
RDMb-h3:SNP_417	TGGTACACCCAAAGCACTCCTACGGTATCTAGGAGTTACACAATCTCATAGTCTAAGGAAAAGATACTTGACATTGGAAAAGCTCTAGCAAACGAACTACA	A	G	653464256	653464356	644748139	644748239	653761048	653761148	655340871	655340971
RDMb-h3:SNP_418	CCAGTGTTCCATGCCAGGATTACTTTGGTACCTTCCTACCAAACTTACGACAAGGTTTACATCAGGTCTTGTACACAGCATGGCATACATAATAGACCCTA	A	G	653465240	653465340	644749123	644749223	653762032	653762132	655341855	655341955
RDMb-h3:SNP_419	TACTTTGGTACCTTCCTACCAAACTTACGACAAGGTTTACATCAGGTCTTGTACACAGCATGGCATACATAATAGACCCTATGGCCGAGGCATAGGGGATG	T	G	653465260	653465360	644749143	644749243	653762052	653762152	655341875	655341975
RDMb-h3:SNP_420	GTGAACATCTCCATGTTGATCGTATCTTCCATACGACTCATGTTCGACCATTCGGTCTCTTGTGTTCCGAGGCCATGCCTGTACATGCTAGGCTCGTCAAG	A	T	653468842	653468942	644752725	644752825	653765634	653765734	655345457	655345557
RDMb-h3:SNP_421	CCATACGACTCATGTTCGACCATTCGGTCTCTTGTGTTCCGAGGCCATGCCTGTACATGCTAGGCTCGTCAAGTTAACCTAAGTGTTTTGCATGTGTGAAT	C	T	653468870	653468970	644752753	644752853	653765662	653765762	655345485	655345585
RDMb-h3:SNP_422	TAAAGTGGGAGAGACAGACACCCGCTAGCCACCTTATGCAACTAGTGCACGTCAGTCAGTGGAACCAGTCTCACGTAAGCGTACGTGTAAGGTCGGTCCGG	C	T	653469711	653469811	644753594	644753694	653766503	653766603	655346326	655346426
RDMb-h3:SNP_423	GAGAGACAGACACCCGCTAGCCACCTTATGCAACTAGTGCACGTCAGTCAGTGGAACCAGTCTCACGTAAGCGTACGTGTAAGGTCGGTCCGGGCCGCTTC	A	G	653469719	653469819	644753602	644753702	653766511	653766611	655346334	655346434
RDMb-h3:SNP_424	TGAGACCTGCAGGAGCTGTACGCCATGTCGGAGGAGTCGGAGAGGCCAGCAGAGAAGAACTCGACGATGGTTGCGGCGCCAATCAGCGGGGGGCTGATGTC	C	T	653474381	653474481	644758264	644758364	653771173	653771273	655350996	655351096
RDMb-h3:SNP_425	CCTGCAGGAGCTGTACGCCATGTCGGAGGAGTCGGAGAGGCCAGCAGAGAAGAACTCGACGATGGTTGCGGCGCCAATCAGCGGGGGGCTGATGTCGCCAA	A	T	653474386	653474486	644758269	644758369	653771178	653771278	655351001	655351101
RDMb-h3:SNP_426	GTCCCACGTGTCAGTCACTCGGAAGCGACCCTTTTAAGGTGACGGGACTGAGGCGTCCGCACTGTGCACGCCGTTTCCTCCTTCTCCCTTCTCCGCTCCTCCGTCGCAC	T	C	653475796	653475896	644759501	644759601	653772556	653772656	655352233	655352333
RDMb-h3:SNP_427	GTCAGTCACTCGGAAGCGACCCTTTTAAGGTGACGGGACTGAGGCGTCCGCACTGTGCACGCCGTTTCCTCCTTCTCCCTTCTCCGCTCCTCCGTCGCAC	C	T	653475805	653475905	644759510	644759610	653772565	653772665	655352242	655352342
RDMb-h3:SNP_428	TGCCGGGCTGGATTCAGGGCGATTGGATCCAGTCTTCGATTCGGCAGGCAGATCTGGACGAGCTGGCGGAGTCTGGGCTAATCGCAAAGGGAGCGGCAAGG	A	G	653476045	653476145	644759750	644759850	653772805	653772905	655352482	655352582
RDMb-h3:SNP_429	ATATAGTCGTCCAATATATCGATCTTTACGTCTCGACCATTTTGAGACTTCTCGTCATGTCCCCGATCTCATCCGGGACTCCGAACTCCTTCGGTACATCA	T	C	653480310	653480410	644764014	644764114	653777070	653777170	655356746	655356846
RDMb-h3:SNP_430	TACGCCAACTGAACATGTACCTTCGGAGACACCTGTAGTACTCCTTTATCATCTCCCAGTTACGTTGTAACGTTTGGTAGTACCCAAAGTGTTCCTCCGGTAAAC	C	A	653480824	653480924	644764528	644764628	653777584	653777684	655357260	655357360
RDMb-h3:SNP_431	CCAACTGAACATGTACCTTCGGAGACACCTGTAGTACTCCTTTATCATCTCCCAGTTACGTTGTAACGTTTGGTAGTACCCAAAGTGTTCCTCCGGTAAAC	T	A	653480828	653480928	644764532	644764632	653777588	653777688	655357264	655357364
RDMb-h3:SNP_432	CCTTCGGAGACACCTGTAGTACTCCTTTATCATCTCCCAGTTACGTTGTAACGTTTGGTAGTACCCAAAGTGTTCCTCCGGTAAACGGGAGTTGCATAATC	A	G	653480843	653480943	644764547	644764647	653777603	653777703	655357279	655357379
RDMb-h3:SNP_433	CCAACAGTTTCCTTTGGGTATTCTATGAAGACGCACTTCTCCGATTTGGATTCGAGCTTATTAGGTTGAAAACCCTTTACATATAAGCATCGCAACTCCAAACTTTAAGAAAC	A	G	653483081	653483181	644766786	644766886	653779841	653779941	655359518	655359618
RDMb-h3:SNP_434	TTTGGGTATTCTATGAAGACGCACTTCTCCGATTTGGATTCGAGCTTATTAGGTTGAAAACCCTTTACATATAAGCATCGCAACTCCAAACTTTAAGAAAC	T	C	653483093	653483193	644766798	644766898	653779853	653779953	655359530	655359630
RDMb-h3:SNP_435	TGAAGACGCACTTCTCCGATTTGGATTCGAGCTTATTAGGTTGAAAACCCTTTACATATAAGCATCGCAACTCCAAACTTTAAGAAACGACAGCTTAGGTT	C	T	653483106	653483206	644766811	644766911	653779866	653779966	655359543	655359643
RDMb-h3:SNP_436	GACGCACTTCTCCGATTTGGATTCGAGCTTATTAGGTTGAAAACCCTTTACATATAAGCATCGCAACTCCAAACTTTAAGAAACGACAGCTTAGGTTTATT	A	T	653483110	653483210	644766815	644766915	653779870	653779970	655359547	655359647
RDMb-h3:SNP_437	TTGCCGATAACTTCAACAAAACATGATCATCTCATACAACAACTTATATTTCATCACGTCTTGACCATATCACATCACAACATGCCCTGCAAAAACAAGTT	T	C	653485920	653486020	623450216	623450316	631365670	631365770	634119695	634119795
RDMb-h3:SNP_438	TTTTAACCTTCGCAAGGACCGGGTGTAGCCACACTCGATTCAGCTAAAGGGAGAGAGACAGACACCCACCGGCCACCTTTAAGCACAAGTGCTTGTAACGG	G	T	653486133	653486233	644769838	644769938	653782893	653782993	655362570	655362670

RDMb-h3:SNP_439	TAAAGGGAGAGAGACAGACACCCACCGGCCACCTTTAAGCACAAGTGCTTGTAACGGTAAAACCAGTCTCGCGTAAGCGTACGCGTAATGTCGGTCCGGGC	T	C	653486177	653486277	644769882	644769982	653782937	653783037	655362614	655362714
RDMb-h3:SNP_440	AGAGACAGACACCCACCGGCCACCTTTAAGCACAAGTGCTTGTAACGGTAAAACCAGTCTCGCGTAAGCGTACGCGTAATGTCGGTCCGGGCCACTTCATC	A	G	653486186	653486286	644769891	644769991	653782946	653783046	655362623	655362723
RDMb-h3:SNP_441	AATTTATTGACGGTTAGCAAGCATTGTATTGGTCATTTGAACAATTCATAAAATAATATTGAAGGAAGAGAGATTTCACATATAAATATACTATCCTAGAC	A	G	653495001	653495101	644778706	644778806	653791761	653791861	655371438	655371538
RDMb-h3:SNP_442	TATTGACGGTTAGCAAGCATTGTATTGGTCATTTGAACAATTCATAAAATAATATTGAAGGAAGAGAGATTTCACATATAAATATACTATCCTAGACATCT	T	G	653495005	653495105	644778710	644778810	653791765	653791865	655371442	655371542
RDMb-h3:SNP_443	TGCTACCCAAAAATTCCTAGCACCAAGTAGAGATACTACTTGTGCTTCCCAATATCCTTAAACCCAGTTTTGCCATGAGAATCCACCATATCTACCTATGG	C	A	653495256	653495356	644778961	644779061	653792016	653792116	655371693	655371793
RDMb-h3:SNP_444	CATGAGAATCCACCATATCTACCTATGGATTGAGTAAGATCCTTCAAGTGAGTTGTCATCGGTGCGAGCAATAAAAATTGCTCTCTAAATATGCATGACTTATTAGTGTGGAGAAAA	G	A	653495329	653495429	644779034	644779134	653792089	653792189	655371766	655371866
RDMb-h3:SNP_445	ATCTACCTATGGATTGAGTAAGATCCTTCAAGTGAGTTGTCATCGGTGCGAGCAATAAAAATTGCTCTCTAAATATGCATGACTTATTAGTGTGGAGAAAA	G	A	653495345	653495445	644779050	644779150	653792105	653792205	655371782	655371882
RDMb-h3:SNP_446	TGGAGGCAACATTATAAGCCCCAATCTTTCTCTGTGTCTGATTAAAACTCCGTAACCACAAGTACTGCGTGAGTGTTAGCAATTGTAGAAGACTATATGAT	C	T	653495785	653495885	644779490	644779590	653792545	653792645	655372222	655372322
RDMb-h3:SNP_447	GAGGCAACATTATAAGCCCCAATCTTTCTCTGTGTCTGATTAAAACTCCGTAACCACAAGTACTGCGTGAGTGTTAGCAATTGTAGAAGACTATATGATAG	G	A	653495787	653495887	644779492	644779592	653792547	653792647	655372224	655372324
RDMb-h3:SNP_448	CTTGGCGATCCGGATATTATATTTCCTTCCTTGTAACCGACTCCATGTAGACCCTTGCTCTCCGGTGTCTATATAAGCTGGAGAGGATGGTCCTTAGAAGT	G	A	653496841	653496941	644780546	644780646	653793601	653793701	655373278	655373378
RDMb-h3:SNP_449	GCACTCGCCTTTTGGCGACATGCTGAACTCATTAAAGTCTCTCTCTTTGCCAGGAGGCTCTGGGCCGAACTATGTCCGGCTTGAGTGGGAAGCAGGCGACG	C	T	653497761	653497861	644781466	644781566	653794521	653794621	655374198	655374298
RDMb-h3:SNP_450	TCTGGGCCGAACTATGTCCGGCTTGAGTGGGAAGCAGGCGACGAAGGAAGTCGCTGCCCACCCACCACCCACTTTGTCGCCACGATCGATGATTTGACCGA	G	T	653497819	653497919	644781524	644781624	653794579	653794679	655374256	655374356
RDMb-h3:SNP_451	GAAGTCGCTGCCCACCCACCACCCACTTTGTCGCCACGATCGATGATTTGACCGACGTGCTCGACTTTGACTTCGAAGACATCGACGGTATGGCCAACGAT	G	A	653497865	653497965	644781570	644781670	653794625	653794725	655374302	655374402
RDMb-h3:SNP_452	ACGGTGGACAGCCACCTCTTCATACGATATATACATGGTGGACACTCTGCAAGAAACCAATGGCGATGAGGCAATGGAGGATAACCCCTCCAAGAAGAAAG	C	A	653497998	653498098	644781703	644781803	653794758	653794858	655374435	655374535
RDMb-h3:SNP_453	GATAAAGAGTGTCCAGGTTTTCCACGAACACCCCAGTACTAGTTACACGCGGGCGGAAGCCGACGACTGGCCTAGTTTCAAAATTTGATAAACAGGCGCAC	C	G	653501431	653501531	644785136	644785236	653798191	653798291	655377868	655377968
RDMb-h3:SNP_454	GAACACCCCAGTACTAGTTACACGCGGGCGGAAGCCGACGACTGGCCTAGTTTCAAAATTTGATAAACAGGCGCACAAAAGGTAATATTTTAAATAACAAA	G	C	653501456	653501556	644785161	644785261	653798216	653798316	655377893	655377993
RDMb-h3:SNP_455	CCCAGTACTAGTTACACGCGGGCGGAAGCCGACGACTGGCCTAGTTTCAAAATTTGATAAACAGGCGCACAAAAGGTAATATTTTAAATAACAAAAGCACT	A	G	653501462	653501562	644785167	644785267	653798222	653798322	655377899	655377999
RDMb-h3:SNP_456	ACGCGGGCGGAAGCCGACGACTGGCCTAGTTTCAAAATTTGATAAACAGGCGCACAAAAGGTAATATTTTAAATAACAAAAGCACTACATAGCGCAAGTAA	G	C	653501477	653501577	644785182	644785282	653798237	653798337	655377914	655378014
RDMb-h3:SNP_457	CGGAAGCCGACGACTGGCCTAGTTTCAAAATTTGATAAACAGGCGCACAAAAGGTAATATTTTAAATAACAAAAGCACTACATAGCGCAAGTAACTTCGTC	A	G	653501484	653501584	644785189	644785289	653798244	653798344	655377921	655378021
RDMb-h3:SNP_458	CAAGTAACTTCGTCTTTAAATTACAAACATGACAGAGGTGAATTCATTCGAAAATTATGTCTTTGGTACATTCATCGGCCACGAGGCAAGCACCCTTCATA	G	A	653501571	653501671	644785276	644785376	653798331	653798431	655378008	655378108
RDMb-h3:SNP_459	CATGGGGGAGGAGCTAGCCAAGCTACTTGAGGCCGGATTCATCAGAGATGTCAAAACATCTGGACTGGCTGGCGAACTTGGTAATGGTACCAAAGAAGGAC	G	A	653509287	653509387	644792992	644793092	653806047	653806147	655385724	655385824
RDMb-h3:SNP_460	AGCTAGCCAAGCTACTTGAGGCCGGATTCATCAGAGATGTCAAAACATCTGGACTGGCTGGCGAACTTGGTAATGGTACCAAAGAAGGACAAATCCTGGCG	T	C	653509298	653509398	644793003	644793103	653806058	653806158	655385735	655385835
RDMb-h3:SNP_461	AGCCAAGCTACTTGAGGCCGGATTCATCAGAGATGTCAAAACATCTGGACTGGCTGGCGAACTTGGTAATGGTACCAAAGAAGGACAAATCCTGGCGTCTG	C	T	653509302	653509402	644793007	644793107	653806062	653806162	655385739	655385839
RDMb-h3:SNP_462	GGCCCTTCGCGGTCTGGGGGTTGGATATGGTTGGACCCCTTAAAGGGGGGAGCTACAAGAAAAAATACTTATTGGTCATGGTAGAGAAGTTCACCAAATGG	G	A	653511495	653511595	644795200	644795300	653808255	653808355	655387932	655388032
RDMb-h3:SNP_463	CTTCGCGGTCTGGGGGTTGGATATGGTTGGACCCCTTAAAGGGGGGAGCTACAAGAAAAAATACTTATTGGTCATGGTAGAGAAGTTCACCAAATGGATAG	T	C	653511499	653511599	644795204	644795304	653808259	653808359	655387936	655388036
RDMb-h3:SNP_464	GTCTACCATCGTCAAACGAATGGCCAGGTTGAACGGGCAAACGGTCTCACCATGAGTGGCATCAAACCCACACTAGTGTGATCCTTAACAGAGTCGGATAC	C	T	653511773	653511873	644795478	644795578	653808533	653808633	655388210	655388310
RDMb-h3:SNP_465	GGATTCCTCTAGCTTGGCAACTGTGGCCCTCAGTTGGGTCTTGCACTCCCCTAGCTCCCGAGACAATTGCTCATTCTTATCTACAAGAACCTGCGTATAAA	C	T	653513972	653514072	644797677	644797777	653810732	653810832	655390409	655390509
RDMb-h3:SNP_466	TACAAGAACCTGCGTATAAATTGATACTTAAAACTGTTGTTTCAACCGTCTCAAGTCTCAGGGGCTACTAATATACATGCTCATCAAACTTTCTTACCCGT	C	T	653514053	653514153	644797758	644797858	653810813	653810913	655390490	655390590
RDMb-h3:SNP_467	TGGGCACTCTGTTGGATGCTTGCTCGAGGAGGGAGAGTGAGGTTTGGATATGGGAATCCCCGTCTCTTCCTATAGACGGTTAGCCCGAAGGACCGAGGGTG	A	C	653515968	653516068	644799673	644799773	653812728	653812828	655392405	655392505
RDMb-h3:SNP_468	TGCTCGAGGAGGGAGAGTGAGGTTTGGATATGGGAATCCCCGTCTCTTCCTATAGACGGTTAGCCCGAAGGACCGAGGGTGGCAAATGCAAAAATGCCTCG	C	A	653515988	653516088	644799693	644799793	653812748	653812848	655392425	655392525
RDMb-h3:SNP_469	ATCTGAGCTTGTCGCCTTTGGGAGAGGTGAGGACGATGCCGGCTCCCAAACTAGTGCGCATTTTGGATCCGTCAAAGTGCATCCGCCAATGGGTGGAGTCG	A	G	653520316	653520416	644804021	644804121	653817076	653817176	655396753	655396853
RDMb-h3:SNP_470	CTGAGCTTGTCGCCTTTGGGAGAGGTGAGGACGATGCCGGCTCCCAAACTAGTGCGCATTTTGGATCCGTCAAAGTGCATCCGCCAATGGGTGGAGTCGGG	T	C	653520318	653520418	644804023	644804123	653817078	653817178	655396755	655396855
RDMb-h3:SNP_471	CGCCTTTGGGAGAGGTGAGGACGATGCCGGCTCCCAAACTAGTGCGCATTTTGGATCCGTCAAAGTGCATCCGCCAATGGGTGGAGTCGGGTGCTGGTGGC	T	C	653520328	653520428	644804033	644804133	653817088	653817188	655396765	655396865
RDMb-h3:SNP_472	TGGGAGAGGTGAGGACGATGCCGGCTCCCAAACTAGTGCGCATTTTGGATCCGTCAAAGTGCATCCGCCAATGGGTGGAGTCGGGTGCTGGTGGCAAGTAC	T	C	653520334	653520434	644804039	644804139	653817094	653817194	655396771	655396871
RDMb-h3:SNP_473	TGCGCATTTTGGATCCGTCAAAGTGCATCCGCCAATGGGTGGAGTCGGGTGCTGGTGGCAAGTACTAGGTCTCGACCGAGTCGACGAGGAAGTCGGCCAGC	T	A	653520370	653520470	644804075	644804175	653817130	653817230	655396807	655396907
RDMb-h3:SNP_474	GCATTTTGGATCCGTCAAAGTGCATCCGCCAATGGGTGGAGTCGGGTGCTGGTGGCAAGTACTAGGTCTCGACCGAGTCGACGAGGAAGTCGGCCAGCACT	T	C	653520373	653520473	644804078	644804178	653817133	653817233	655396810	655396910
RDMb-h3:SNP_475	TTTTGGATCCGTCAAAGTGCATCCGCCAATGGGTGGAGTCGGGTGCTGGTGGCAAGTACTAGGTCTCGACCGAGTCGACGAGGAAGTCGGCCAGCACTTGG	T	C	653520376	653520476	644804081	644804181	653817136	653817236	655396813	655396913
RDMb-h3:SNP_476	TGGATCCGTCAAAGTGCATCCGCCAATGGGTGGAGTCGGGTGCTGGTGGCAAGTACTAGGTCTCGACCGAGTCGACGAGGAAGTCGGCCAGCACTTGGGAC	C	T	653520379	653520479	644804084	644804184	653817139	653817239	655396816	655396916
RDMb-h3:SNP_477	TCAAAGTGCATCCGCCAATGGGTGGAGTCGGGTGCTGGTGGCAAGTACTAGGTCTCGACCGAGTCGACGAGGAAGTCGGCCAGCACTTGGGACTTGATGGC	A	G	653520387	653520487	644804092	644804192	653817147	653817247	655396824	655396924
RDMb-h3:SNP_478	CATCCGCCAATGGGTGGAGTCGGGTGCTGGTGGCAAGTACTAGGTCTCGACCGAGTCGACGAGGAAGTCGGCCAGCACTTGGGACTTGATGGCGGTGTGAG	A	G	653520395	653520495	644804100	644804200	653817155	653817255	655396832	655396932
RDMb-h3:SNP_479	CCGCCAATGGGTGGAGTCGGGTGCTGGTGGCAAGTACTAGGTCTCGACCGAGTCGACGAGGAAGTCGGCCAGCACTTGGGACTTGATGGCGGTGTGAGGCT	G	C	653520398	653520498	644804103	644804203	653817158	653817258	655396835	655396935
RDMb-h3:SNP_480	GACCGAGTCGACGAGGAAGTCGGCCAGCACTTGGGACTTGATGGCGGTGTGAGGCTGATAGAAGATGGTATAAGGAGCCAGTGCAATGGCCCACTTTGCAA	T	C	653520443	653520543	644804148	644804248	653817203	653817303	655396880	655396980
RDMb-h3:SNP_481	AGTCGACGAGGAAGTCGGCCAGCACTTGGGACTTGATGGCGGTGTGAGGCTGATAGAAGATGGTATAAGGAGCCAGTGCAATGGCCCACTTTGCAACCCGG	C	T	653520448	653520548	644804153	644804253	653817208	653817308	655396885	655396985
RDMb-h3:SNP_482	CGGCCAGCACTTGGGACTTGATGGCGGTGTGAGGCTGATAGAAGATGGTATAAGGAGCCAGTGCAATGGCCCACTTTGCAACCCGGCTAGATGCATCCCGA	A	G	653520463	653520563	644804168	644804268	653817223	653817323	655396900	655397000
RDMb-h3:SNP_483	TGGGACTTGATGGCGGTGTGAGGCTGATAGAAGATGGTATAAGGAGCCAGTGCAATGGCCCACTTTGCAACCCGGCTAGATGCATCCCGACTTCCCATGAT	G	A	653520474	653520574	644804179	644804279	653817234	653817334	655396911	655397011
RDMb-h3:SNP_484	CGGTGTGAGGCTGATAGAAGATGGTATAAGGAGCCAGTGCAATGGCCCACTTTGCAACCCGGCTAGATGCATCCCGACTTCCCATGATCTCGGCAAGCGGG	C	T	653520487	653520587	644804192	644804292	653817247	653817347	655396924	655397024
RDMb-h3:SNP_485	TAGAAGATGGTATAAGGAGCCAGTGCAATGGCCCACTTTGCAACCCGGCTAGATGCATCCCGACTTCCCATGATCTCGGCAAGCGGGGAAGTGCAAACGAC	T	C	653520501	653520601	644804206	644804306	653817261	653817361	655396938	655397038
RDMb-h3:SNP_486	GAGCCAGTGCAATGGCCCACTTTGCAACCCGGCTAGATGCATCCCGACTTCCCATGATCTCGGCAAGCGGGGAAGTGCAAACGACCGTGATGGGGTGCTCT	T	G	653520517	653520617	644804222	644804322	653817277	653817377	655396954	655397054
RDMb-h3:SNP_487	ATCACCGTCCAGCAAGCCTACGATGGAATTACTCACGCACGGCGGTGAGTATCATGAAATTGGTGATGGAGGATGGTTGATGATGACGACGGCGACGAATC	T	C	653524946	653525046	644808651	644808751	653821706	653821806	655401383	655401483
RDMb-h3:SNP_488	ACCAACTCCTACGACATATTTGACTCACCAAATGAAGGAATTGGAAGATTCTTCATGGCCAAAGGTCCAAAGGTAACACATCCCGAGTATGTTGATTCAAT	T	G	653528424	653528524	644812129	644812229	653825184	653825284	655404861	655404961
RDMb-h3:SNP_489	GGTGATGATAATTTACTTGTTGACAACTCTAGTGATGAATACTATGATGGAACATCAATTAATCATGCTAAACAAGATAAAACGAATGACAATGATAAGGA	G	A	653528546	653528646	644812251	644812351	653825306	653825406	655404983	655405083
RDMb-h3:SNP_490	ATGATAATTTACTTGTTGACAACTCTAGTGATGAATACTATGATGGAACATCAATTAATCATGCTAAACAAGATAAAACGAATGACAATGATAAGGAAG	A	G	653528550	653528650	644812255	644812355	653825310	653825410	655404987	655405087
RDMb-h3:SNP_491	ACAACTCTAGTGATGAATACTATGATGGAACATCAATTAATCATGCTAAACAAGATAAAACGAATGACAATGATAAGGAGAAGATTGATCTTCTAACTAAA	A	T	653528568	653528668	644812273	644812373	653825328	653825428	655405005	655405105
RDMb-h3:SNP_492	ATCATGCTAAACAAGATAAAACGAATGACAATGATAAGGAGAAGATTGATCTTCTAACTAAAGAACTAAACACTCTTAAGTTAGCTCATGAAACTATCTTC	T	G	653528607	653528707	125112990	125113090	130858614	130858714	130680683	130680783
RDMb-h3:SNP_493	AGTGGGAAGAAGATCAATACCCCAAGACGAAGTTTGTTCCTCAACAAGATAAGTATGATCCTACTTCTTTCAAGGGAACACAAGCTCACGATGATCTTCCA	T	G	653529156	653529256	644812861	644812961	653825916	653826016	655405593	655405693
RDMb-h3:SNP_494	TCGGTGCCACCGAACTGTGACTCGGTCTGACCGAGTTCACTAGTTTAGGGTCCAAAACTACTTCGGTATCACCGAGTTTGAAAATCGGTAGATCTGGAATGCTTTTTGTGG	G	T	653530928	653531028	644814633	644814733	653827688	653827788	655407365	655407465
RDMb-h3:SNP_495	CGAACTGTGACTCGGTCTGACCGAGTTCACTAGTTTAGGGTCCAAAACTACTTCGGTATCACCGAGTTTGAAAATCGGTAGATCTGGAATGCTTTTTGTGG	A	G	653530938	653531038	644814643	644814743	653827698	653827798	655407375	655407475
RDMb-h3:SNP_496	TAGGGTCCAAAACTACTTCGGTATCACCGAGTTTGAAAATCGGTAGATCTGGAATGCTTTTTGTGGAAACTAAAACTAAGTTTTTGAATCATTCTTTTGCA	T	C	653530973	653531073	644814678	644814778	653827733	653827833	655407410	655407510
RDMb-h3:SNP_497	GGGTCCAAAACTACTTCGGTATCACCGAGTTTGAAAATCGGTAGATCTGGAATGCTTTTTGTGGAAACTAAAACTAAGTTTTTGAATCATTCTTTTGCAAA	G	A	653530975	653531075	644814680	644814780	653827735	653827835	655407412	655407512
RDMb-h3:SNP_498	ACTACTTCGGTATCACCGAGTTTGAAAATCGGTAGATCTGGAATGCTTTTTGTGGAAACTAAAACTAAGTTTTTGAATCATTCTTTTGCAAAAATCTCTGC	T	C	653530984	653531084	644814689	644814789	653827744	653827844	655407421	655407521
RDMb-h3:SNP_499	ACTAAGTTTTTGAATCATTCTTTTGCAAAAATCTCTGCATTTTGTGATGGTCATCCACTCTATCTCATCTATAACTATTCACAGGGTCAGCAGTCAGTGTT	G	C	653531047	653531147	644814752	644814852	653827807	653827907	655407484	655407584
RDMb-h3:SNP_500	ACTCCACAACACATTTCTATCCAGATGGCAGGATAGTTTGGATGTCTGACGGAACAAGATACCAGTCAACCATAGAGGAATGGGAAAGTCTGATCAATGCC	C	A	653532149	653532249	644815854	644815954	653828909	653829009	655408586	655408686
RDMb-h3:SNP_501	AGATGACTTGGATGTATATGCCAAGAAGAAGATGGGACACAATACTATGCCACATATGTACAAAGAGATCCCAGACAAAGCCCTTGAGACTATCTCGTTTG	C	T	653532264	653532364	644815969	644816069	653829024	653829124	655408701	655408801
RDMb-h3:SNP_502	TACTATGCCACATATGTACAAAGAGATCCCAGACAAAGCCCTTGAGACTATCTCGTTTGGGTCAGTCCATTTTCTTCTGTCAGGGCTGCCTACGATCAACT	A	T	653532306	653532406	644816011	644816111	653829066	653829166	655408743	655408843

RDMb-h3:SNP_503	CAGTCCATTTTCTTCTGTCAGGGCTGCCTACGATCAACTGGATCTTAAGAGACACTCTTTTGCCCAAATCAGGTGACCACAACATGATAAGAGGGCATGCA	A	G	653532368	653532468	644816073	644816173	653829128	653829228	655408805	655408905
RDMb-h3:SNP_504	TCTTGCTTCATGTGCTTAGTGATATGCTCCAAAACCCTCAACTACTTTCTCACATCCACATATGACCTAAACCTAAAGCCCAAATCGGTCACACCGATTCT	T	C	653534008	653534108	644809477	644809577	653822532	653822632	655402209	655402309
RDMb-h3:SNP_505	TGCTTCATGTGCTTAGTGATATGCTCCAAAACCCTCAACTACTTTCTCACATCCACATATGACCTAAACCTAAAGCCCAAATCGGTCACACCGATTCTTTC	C	T	653534011	653534111	644809480	644809580	653822535	653822635	655402212	655402312
RDMb-h3:SNP_506	AAACCCTCAACTACTTTCTCACATCCACATATGACCTAAACCTAAAGCCCAAATCGGTCACACCGATTCTTTCTATCCGGCGCCACCGAGTTCAGATGTCA	C	A	653534039	653534139	644809508	644809608	653822563	653822663	655402240	655402340
RDMb-h3:SNP_507	CCCTCAACTACTTTCTCACATCCACATATGACCTAAACCTAAAGCCCAAATCGGTCACACCGATTCTTTCTATCCGGCGCCACCGAGTTCAGATGTCATAG	A	C	653534042	653534142	644809511	644809611	653822566	653822666	655402243	655402343
RDMb-h3:SNP_508	CACAATGGTATCTCGCTAGCCCTTTCTGAGACCGCAAAACATAAATGCATAGAACCTTTAAAGATCAAGGACTGACTAAACATTGTAATCCATTGTAAAAG	T	G	653535699	653535799	644819406	644819506	653832459	653832559	655412137	655412237
RDMb-h3:SNP_509	ATAAATGCATAGAACCTTTAAAGATCAAGGACTGACTAAACATTGTAATCCATTGTAAAAGAGATCCAGTCAAGTCATACCCAATATAAACCAATAATAAT	C	T	653535739	653535839	644819446	644819546	653832499	653832599	655412177	655412277
RDMb-h3:SNP_510	ATGCATAGAACCTTTAAAGATCAAGGACTGACTAAACATTGTAATCCATTGTAAAAGAGATCCAGTCAAGTCATACCCAATATAAACCAATAATAATGAAT	T	G	653535743	653535843	644819450	644819550	653832503	653832603	655412181	655412281
RDMb-h3:SNP_511	TCCTCTTGAGAATAACCCACCTAGCATGGAAGATATAGGCAGCCCTAGTGGAAACATGAGCAGCTCGAGCATACAAAACAGAATTTCATTTGAAGGTTTAG	G	T	653536277	653536377	644819984	644820084	653833037	653833137	655412715	655412815
RDMb-h3:SNP_512	TAACCCACCTAGCATGGAAGATATAGGCAGCCCTAGTGGAAACATGAGCAGCTCGAGCATACAAAACAGAATTTCATTTGAAGGTTTAGAGTTTGGCACAT	A	T	653536289	653536389	644819996	644820096	653833049	653833149	655412727	655412827
RDMb-h3:SNP_513	AAAATCCCCAACAATAAGAATATCATACTTTTTCTTGACAGTAGGGAGACGAAATTCAAAACCTCCAATAATAATTGATGGAATTTTCTCAATAGTATTTA	C	G	653539349	653539449	644823056	644823156	653836109	653836209	655415787	655415887
RDMb-h3:SNP_514	ACGTCCTCACAAATGCCGACAGGTATAGCAGTTGATTTATCAGCCATTTACAAGGATATCTCAGTGGGTGTCAACTTACTCAATTCAAGTCTACGGTACAA	A	G	653539659	653539759	644823366	644823466	653836419	653836519	655416097	655416197
RDMb-h3:SNP_515	AGCCTCCCCCAAGCTTGTGGGAGACTCTCTTCTTTGATTTGCACAAAATCATATATTTCCCACAAGGCAGCTTGTTTCTTATGAGCAGGGAAATATTTAGC	C	T	653541264	653541364	644824971	644825071	653838024	653838124	655417702	655417802
RDMb-h3:SNP_516	TGGGGCTCTCCTAGGAGATAACACCCCTAGTCCTGCTCTGCGGGGTCTCTGCATGATCACTAAATCAGTGAGTTGCTACAGGAGGCTCCTTGAGCTGTTTT	T	C	653544423	653544523	644828131	644828231	653841183	653841283	655420862	655420962
RDMb-h3:SNP_517	TCATGTTGGCTTAATTCATGTTCGGTACTTTGATAATTTGATATGTGGGAGGACCGGTGCTTAGGTGCGGCTCTTACTTGAACAAACCTCCAACTTATGAT	A	T	653548424	653548524	644832132	644832232	653845184	653845284	655424863	655424963
RDMb-h3:SNP_518	TCGGTACTTTGATAATTTGATATGTGGGAGGACCGGTGCTTAGGTGCGGCTCTTACTTGAACAAACCTCCAACTTATGATTAATCCTCTCGCAAGCATCCG	C	T	653548445	653548545	644832153	644832253	653845205	653845305	655424884	655424984
RDMb-h3:SNP_519	CAACATACATATCATCAAAAAAATCGAATACATATCAAGTTCACATGATCACTTGCAACATGATTTCTCCTGTGACCTCAAGAACGAAAGTAACTACTCAC	C	T	653548761	653548861	644832469	644832569	653845521	653845621	655425200	655425300
RDMb-h3:SNP_520	CCTTGGGGTCGAAACTTGGAGTAAAAGCCTCCACAAAGTCGGTTTCACCTGAAAGGCAAGAGTCCTTCTCGGACTCCAGGGCCAGACGCCAGGGACCCTGG	T	C	653573984	653574084	644857883	644857983	653870527	653870627	31388458	31388358
RDMb-h3:SNP_521	TATTTGATTCAAGCCATTGTAATACCCAGACATTCTGAGCACATGCTCATTGGTTGAGCTATTATCCTCCATCTTGTAGGCAAAGTACTTTGTCAGAGGCC	T	C	653576912	653577012	644860811	644860911	653873455	653873555	655453296	655453396
RDMb-h3:SNP_522	TCGCACCGGAGGCGAGCCGGACTTCGATCTCTCCGCGCTCAGCTCCGACAAGGAAGAAGAAGAGTAAGATTCCTTGCTGTACTTGTAGTTCTTCAATTTTA	A	G	653588550	653588650	644872450	644872550	653885093	653885193	655464935	655465035
RDMb-h3:SNP_523	TTGAATATTCGCTTGACCTTTCTCCCCTCTTCGGTCGTCAGATCCACCTACCACGGAGCCGATGGAAACCGAGGCCGCCGGCGAGGAGAACGCGCGCGGCA	A	G	653589182	653589282	644873082	644873182	653885725	653885825	655465567	655465667
RDMb-h3:SNP_524	CAAGGCTGCCGCCGCAGAAGCGGGCGAGGGATCCGGCGATCGCACTGACAGCCCCGAGGCCGCAGGAGCGCCAGGCGCTACACCGACCGCCGATCCCTCCA	A	G	653589350	653589450	644873250	644873350	653885893	653885993	655465735	655465835
RDMb-h3:SNP_525	TAGCAGCCTGAAGACGGTCCTCCTCAAGGAGCAGCGCGTCATCTTGTCGTAGCTGCTCTTGCTCAAGCTCATCATAAGCGAGCACTTGAGGTGATCCGTAT	T	C	653591800	653591900	644875699	644875799	653888343	653888443	655468184	655468284
RDMb-h3:SNP_526	AACTGGCACGCTTCACACTTGGTTACTTGTGCAGTTGCATCCTGGAGGGTTGTCGGCCAAAAGAAACCTTGCCAGAACGCTTTGCCGGCAAGTGCTCTTGA	T	C	653592459	653592559	644876358	644876458	653889002	653889102	655468843	655468943
RDMb-h3:SNP_527	AGCACGTTGGCGTGCATGCTGGTCTTGAGCACCCCGAGATCCACCAGCTCGATCTTGTCCCAACGAACGTATGGTACTGCGAATACCATGACGCTGTCGGT	T	C	653597552	653597652	288843867	288843967	653894095	653894195	299619477	299619577
RDMb-h3:SNP_528	AGTCGATTCATCTCACGACTCGGTGAAAAGGCACTGCCTCTTTACCGACGGATGAAGAAGGCTGACAAGTTCGAGTGGACTCCAGAAGCTGATGCAGCGTT	G	T	653618097	653618197	644902184	644902284	653914286	653914386	655493951	655494051
RDMb-h3:SNP_529	CAGCTGATGATCTAGCAAAGATAGGTTCCAAGAGAGAAGCCATTCCGAGGGGTGTGTTCTTGGAGCATATACACACTCCGTCAGTCAAAGAAGATCCTTTC	G	T	653619025	653619125	644903112	644903212	653915214	653915314	655494879	655494979
RDMb-h3:SNP_530	GATCATGGAGGTTTTGGTGGTCATTCCCGACTGGACGATTCCGTATGTCACATATATCTTGAGGAAAGAGCTTCCGGAGGATGAGGAAGAGGCTTGACAGA	A	G	653619197	653619297	644903284	644903384	653915386	653915486	655495051	655495151
RDMb-h3:SNP_531	TGTCACATATATCTTGAGGAAAGAGCTTCCGGAGGATGAGGAAGAGGCTTGACAGATCGTCCATCGATCTAAGGCCTTTACCGTAATCAAAGGACAATTAT	T	C	653619242	653619342	644903329	644903429	653915431	653915531	655495096	655495196
RDMb-h3:SNP_532	ACGCAGTCGACCTTTTAGAGGAAGAAAGGGAGATGGCTCTGATCCGGTCAACCATCTACCAACAAGATTTGCGCCGTTTCCACGCCAGAAATGTGAGAGGT	A	G	653620165	653620265	586074136	586074036	653916354	653916454	655496019	655496119
RDMb-h3:SNP_533	CCCCTTACCACGTTCGGTCGAAGGGTCGTGGACAAGCTTCGACCGCCTTCCTGAGCGCGGTGGTACGACCTCCTCCTCCTCTTCTTCCTCGTCCTCGACGT	C	T	653624231	653624331	644907962	644908062	653919637	653919737	655500059	655500159
RDMb-h3:SNP_534	TGTCCGGCCAAATGGGATCGAGCGTGTTGGGTTATGTGGTGCACCCCTAGAGGGAAGTTTATCTATCTGAATAGCCGTGTCCCTCAATAAAAGGACGACGC	G	C	653639329	653639429	644922838	644922938	653934450	653934550	655514588	655514688
RDMb-h3:SNP_535	TCGAGCGTGTTGGGTTATGTGGTGCACCCCTAGAGGGAAGTTTATCTATCTGAATAGCCGTGTCCCTCAATAAAAGGACGACGCGGAGTTGTACCTTGACC	C	T	653639346	653639446	644922855	644922955	653934467	653934567	655514605	655514705
RDMb-h3:SNP_536	CGAGCGTGTTGGGTTATGTGGTGCACCCCTAGAGGGAAGTTTATCTATCTGAATAGCCGTGTCCCTCAATAAAAGGACGACGCGGAGTTGTACCTTGACCT	T	C	653639347	653639447	644922856	644922956	653934468	653934568	655514606	655514706
RDMb-h3:SNP_537	GTGCTTTAGTAAGAATATTGATGTTAAGGTTTGTGATTCCCTATGCAAGAACGAAAGTCAATAGATATGCAATGAAATTTATATCCTACTTATGGTGCATT	A	C	653641912	653642012	644925421	644925521	653937033	653937133	655517171	655517271
RDMb-h3:SNP_538	TATTGATGTTAAGGTTTGTGATTCCCTATGCAAGAACGAAAGTCAATAGATATGCAATGAAATTTATATCCTACTTATGGTGCATTATTCAGTGTTACTTA	A	T	653641927	653642027	644925436	644925536	653937048	653937148	655517186	655517286

7. DECLARATION OF AUTHORSHIP

I hereby confirm that this thesis and the work presented in it is entirely my own. Where I have consulted the work of others this is always clearly stated. All statements taken literally from other writings or referred to by analogy are marked and the source is always given. This paper has not yet been submitted to another examination office, either in the same or similar form. I agree that the present work may be verified with an anti-plagiarism software.

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Place, Date Original Signature

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