

NUMBER_OF_READS:

The number of reads underlying the sequence. 1 for singletons, >1 for consensus

TARGET_REGION_FIRST_POS:

First position of target region in the sequence

TARGET_REGION_LENGTH_IN_BP:

Length of the target region in base pairs. If there is only one microsatellite targeted, the target region covers the microsatellite (compound or pure). Otherwise the target includes the two most distant target microsatellites and the sequence between them.

TARGET_MS_LENGTH_IN_REPEAT_NUMBER:

Length of the target microsatellite in repeat number. If microsatellite is compound, it is the number of repetition in the longest uninterrupted stretch.

If there are more than one microsatellites in the target region, target MS info refers to the longest (in repeat numbers) of the target microsatellites.

NUMBER_OF_MS:

The number of microsatellites in the target region. 1 for one pure microsatellite, 1.5 for one compound microsatellite, >1.5 the number of microsatellites (regardless whether pure and compound)

MOT_TRANS:

Repeat motif type, where circular permutations and their reverse complementary sequences are pooled (e.g. AC refers to AC, CA, TG, GT).

If there are more than one microsatellite in the target region, it refers to the longest (in repeat numbers) of the target microsatellites.

TARGET_REGION_SEQ:

Sequence of the target region as found in the read/consensus

POLYMORPH:

If polymorphism is detected, then the repeat motif and its position is indicated. NA for singletons, NO if the MS has the same length in all reads of a consensus.

ONE_PRIMER_FOR_EACH_SEQ:

Only one primer is selected for each sequence. Selecting lines with 1 in this column gives the total number of sequences with primers. The selection between the “best primer pairs” of each target region

is based on the number of microsatellites in the target region (NUMBER_OF_MS; the lowest the better) and the length of the microsatellite (TARGET_MS_LENGTH_IN_REPEAT_NUMBER; the highest the better).

This ordering is based on lab tests of PCR success rate and polymorphism of different primers (Meglecz et al. Submitted).

ONE_PRIMER_FOR_EACH_TARGET_REGION:

Only one primer is selected for each target region. Selecting lines with 1 in this column gives the total number of target regions with primers. There can be more than one

target region per sequence, so some of the markers are strongly linked. The selection is based on the alignment score between the primers and the amplicon (PCR_PRIMER_ALIGNSCORE; the lowest the better),

on the distance between primer and the target region (MIN_PRIMER_TARGET_DIST; the highest the better) and the size of the PCR product (PCR_PRODUCT_SIZE; the lowest the better).

this ordering is based on lab tests of PCR success rate of different primers (Meglecz et al. Submitted)

PCR_PRIMER_ALIGNSCORE:

The maximum alignment score between the primers and the sequence (excluding primers; from version 3.1.2) The maximum alignment score between the primers and the amplicon excluding primers (versions 3.1 and 3.1.1)

MIN_PRIMER_TARGET_DIST:

The smallest distance between the 3' end of the two primers and the target region. If primer(s) match more than once the sequence, the distance is calculated for the annealing site closer to the target region.

PCR_PRODUCT_SIZE:

PCR product size in bp including primers. If primer(s) match more than once the sequence, the size of the longest PCR product size is given here.

PCR_PRODUCT_SEQ:

Sequence of amplicon including primers. If primer(s) match more than once the sequence, the longest PCR product is given here.

PRIMER_LEFT_DIST_FROM_MS:

Distance between the target MS and the left primer in bp.

PRIMER_RIGHT_DIST_FROM_MS:

Distance between the target MS and the right primer in bp

PRIMER_LEFT_FIRST_POS:

5' end position of the left primer in the sequence

PRIMER_LEFT_LENGTH:

in bp

PRIMER_RIGHT_FIRST_POS:

5' end position of the right primer in the sequence

PRIMER_RIGHT_LENGTH:

in bp

PRIMER_LEFT_TM:

Annealing temperature of the left primer; see documentation of Primer3

PRIMER_RIGHT_TM

Annealing temperature of the right primer; see documentation of Primer3

PRIMER_LEFT_END_STABILITY:

see documentation of Primer3

PRIMER_RIGHT_END_STABILITY:

see documentation of Primer3

PRIMER3_PENALTY:

Primer pair penalty (see documentation of Primer3)

DESIGN:

guides for target region complexity

SEQUENCE_LENGTH:

Length of the read or consensus

SEQUENCE:

the whole sequence with homopolymers micro- and nanosatellites printed in lower case

CONTIG_CODE (If contig = 1):

id of the contig

FIRST_POS_ON_CONTIG (If contig = 1):

First position of the extracted fragment on its contig. These last two columns help to avoid choosing markers too close to each other on the same contig