Indel-SNP

Pipeline steps

All variants: 36,140,217

1. Min. variant read count (x=3).

2. Indels only.

1,193,870

3. Indel size >3 bp.

208,460

4. Critical indel presence: all HD-16.

7,199

5. Identify indel-SNP pairs in HD-16:
“critical” indel coupled to marker SNP.

13,301 Pairs (6,640 critical indels)

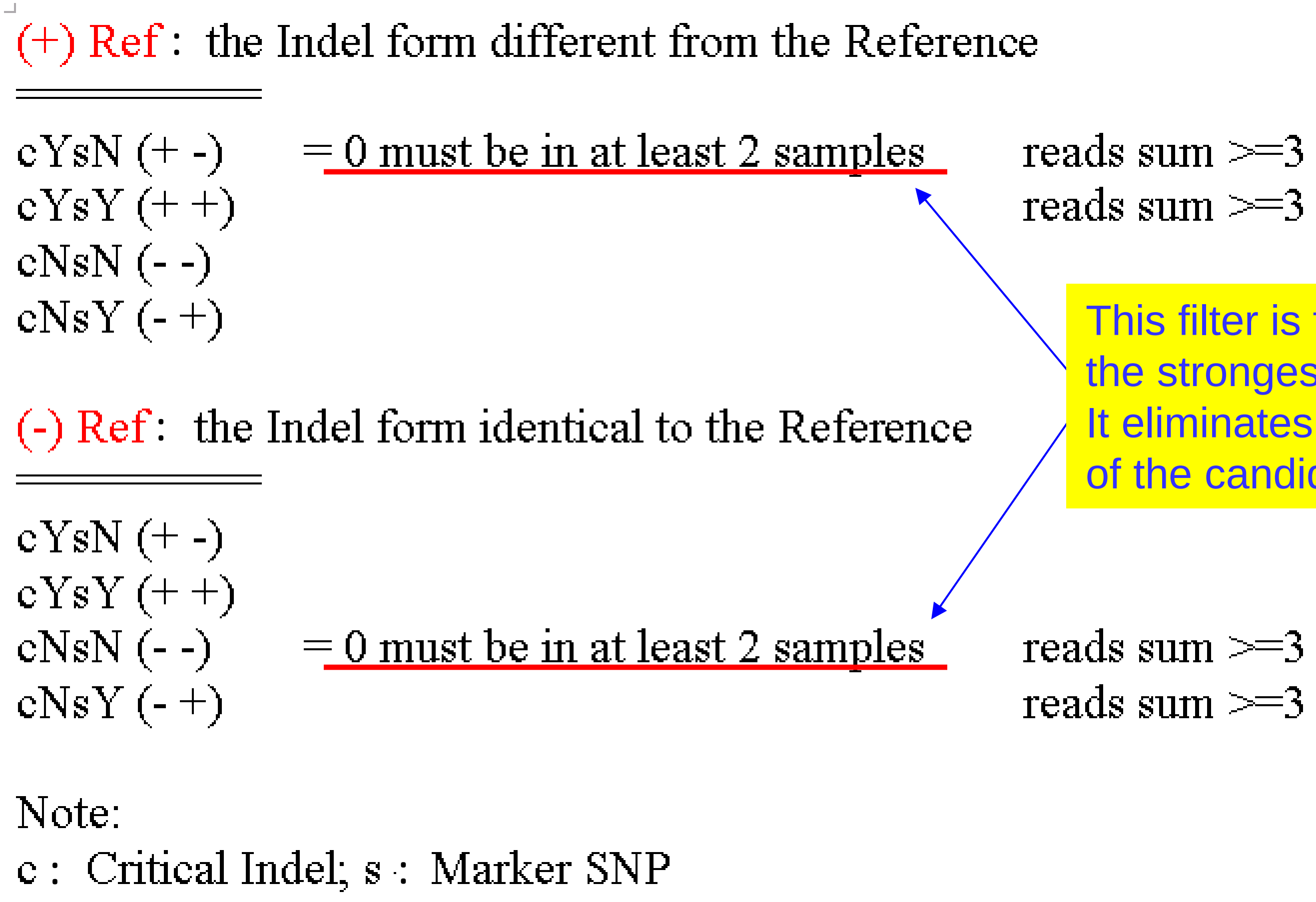
6. Critical indel presence/absence check.

12,753

7. Indel-SNP association check.

Candidates submitted: 2,937

The Indel-SNP Association Check



(+) Ref : the Indel form different from the Reference

cYsN (+ -) = 0 must be in at least 2 samples reads sum >=3
cYsY (+ +) reads sum >=3
cNsN (- -)
cNsY (- +)

(-) Ref : the Indel form identical to the Reference

cYsN (+ -)
cYsY (+ +)
cNsN (- -) = 0 must be in at least 2 samples reads sum >=3
cNsY (- +) reads sum >=3

Note:
c : Critical Indel; s : Marker SNP

This filter is found to be the strongest constraint. It eliminates the majority of the candidates.

A less stringent setting is used:
2 samples → 1 samples