(1)genotyping of SVDetect results:

A. SVs were detected and filtered in each of 115 accessions.

B. All these SVs were combined and clustered into an SV table. In this table, if an accession has a corresponding SV found by the SVdetect in the previous step, then this SV has a value of 1. Otherwise, the accession has a value of 0.

C. For an accession, if a deletion event has the value of 0, it will be converted to N if (i) there is none of normal reads that reside within the anchoring window and have same orientation as the abnormal read; AND (ii) less than 5% of deleted region is covered by normal reads.

For an accession, if an insertion event has the value of 0, it will be converted to N if (i) there is none of normal reads that reside within the anchoring window and have same orientation as the abnormal read.

For inversion and duplication, the value is either 0 or 1.

(2) genotyping of Pindel results:

A & B are same as SVdetect.

C. For an accession, if a deletion event has the value of 0, it will be converted to N if (i) less than 5% of deleted region is covered by normal reads.

PIndel only detects deletions.