	Category 1 (only for deletions)	
1 2 3 4	Number of uniquely mapped reads (UMRs) overlapping the deletion candidate Number of error-free UMRs overlapping the deletion candidate Number of non uniquely mapped reads (N-UMRs) overlapping the deletion candidate Number of error-free N-UMRs overlapping the found deletion Category 2 (for all indels)	reference genome overlapping reads
5	Number of UMRs mapping 60bp upstream of the indel candidate	
6	Number of <i>error-free UMRs</i> mapping 60bp <i>upstream</i> of the indel candidate Number of <i>N-UMRs</i> mapping 60bp <i>upstream</i> of the indel	60 bp mapped reads indel candidate
7 8	candidate Number of <i>error-free N-UMRs</i> mapping 60bp <i>upstream</i> of the	reference genome upstream 60 bp
9	indel candidate Number of <i>UMRs</i> mapping 60bp <i>downstream</i> of the indel candidate	20.5-
10	Number of <i>error-free UMRs</i> mapping 60bp <i>downstream</i> of the indel candidate	mapped reads 60 bp
11	Number of <i>N-UMRs mapping</i> 60bp <i>downstream</i> of the indel candidate	reference genome downstream
12	Number of $\emph{error-free N-UMRs}$ mapping 60bp $\emph{downstream}$ of the indel candidate	•
	Category 3 (for all indels)	
13	Single position variation (SPV) from split read alignment confirmed by SPV from the mapping algorithm	SPV mapping supported SPV mapping not supported
14	SPV from split read alignment not confirmed by SPV from the mapping algorithm	reference genome indel candidate
15	SPV from mapping algorithm not conformed by SPV from the split read alignment	SPV split read alignment supported SPV split read alignment not supported
-	Category 4 (for all indels)	
16	Deletion/Insertion length	reference genome deletion candidate split read alignments
17	Number of splitted reads <i>supporting</i> the <i>same</i> indel location (split read alignment support)	reference genome insertion candidate