



Duplicated pairs:

Both reads have the same relative orientation and the 5' end positions map to the same positions.

Same internal:

Both reads map to the same fragment and the reads are pointing inwards.

F1R2 R1 R2 F2R1 R2 R1

Self-ligation:

As same internal, but reads are pointing outwards. Such pairs are kept, because they cannot be distinguished from read pairs that emerged from interactions within the same fragment.

R1F2 R1 R2 R2F1 R2 R1

Inadequately mapped:

At least one read is unmapped or ambiguously mapped.

Same dangling ends:

Both reads map to the same fragment, the 5' end position of at least one read has a distance of less than 7 to the next restriction cutting site.

Wrong size:

The calculated size of the hybrid fragment is smaller or greater than specified thresholds, e.g. 50 to 1000 bp.

Unique valid pair:

All remaining pairs are assumed to be the result of valid ligation events. The pairs may have all possible relative orientations.

F1R2 R1 R2 F2R1 R2 R1
 R1F2 R1 R2 R2F1 R2 R1
 F1F2 R1 R2 F2F1 R2 R1
 R1R2 R1 R2 R2R1 R2 R1