STAR alignment types	Output classification	
1. nonligated, no gap	cont.sam continuous, failed proximity ligation	
2. short gap, span < window.	gap1.sam and cont.sam continuous if one segment failed filter	
3. long gap, span > window	gap1.sam and cont.sam continuous if one segment failed filter	cont.sam gap1.sam gapm.sam homo.sam trans.sam
4. same chr, back arranged	gap1.sam and cont.sam continuous if one segment failed filter	
5. chimeric, overlap arms	homo.sam likely to be RNA homodimers	
6. same chr, opposite strand	trans.sam and cont.sam continuous if one segment failed filter	
7. different chr, strand ignored	trans.sam and cont.sam continuous if one segment failed filter	
8. gap>1. chr or strand ignored	gapm.sam, gap1.sam or trans.sam. depending on strand, chrom or filter	