

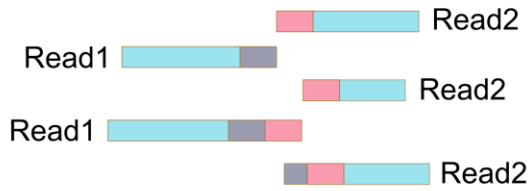
Splicing site identification



Two splicing sites with genomic sequence in between were concatenated



PE reads mapped to concatenated reference



Assemble PE reads with backsplicing sites



Identifying overlapping contigs to generate full-length circRNA candidates



Assess ORF length and quality
BLASTX validation of protein-coding transcript

Machine learning prediction of coding circRNAs based on ORF and BLASTX evaluation

Fig.S14. Flow chart showing the method used to identify circRNAs and to evaluate their coding potential.