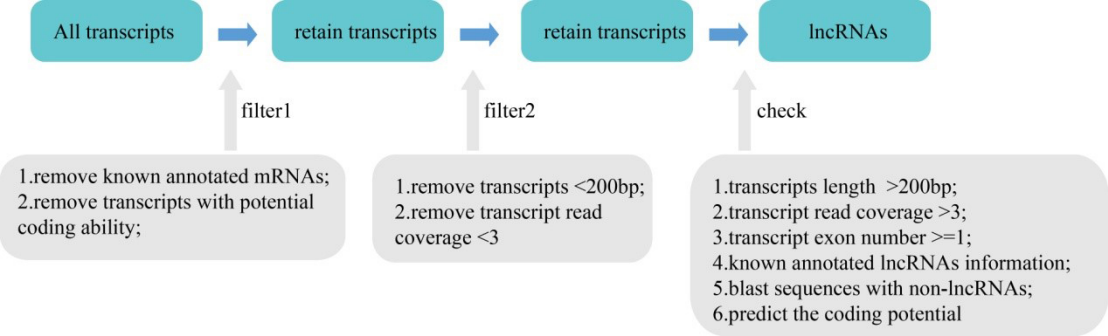
All transcripts
retain transcripts
retain transcripts
lncRNAs
filter1
filter2
check
1.remove known annotated mRNAs;
2.remove transcripts with potential coding ability;
1.remove transcripts <200bp;
2.remove transcript read coverage <3
1.transcripts length >200bp;
2.transcript read coverage >3;
3.transcript exon number >=1;
4.known annotated lncRNAs information;
5.blast sequences with non-lncRNAs;
6.predict the coding potential