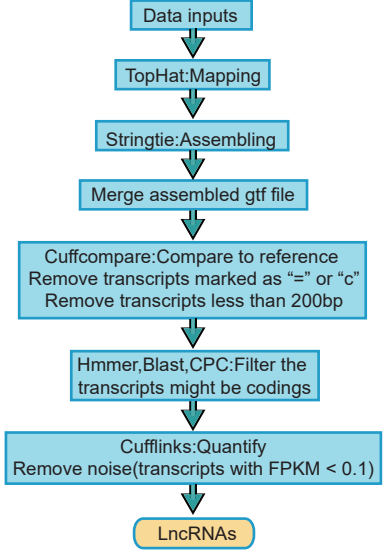


Data inputs



```
graph TD; A[Data inputs] --> B[TopHat:Mapping]; B --> C[Stringtie:Assembling]; C --> D[Merge assembled gtf file]; D --> E["Cuffcompare:Compare to reference<br/>Remove transcripts marked as '=' or 'c'<br/>Remove transcripts less than 200bp"]; E --> F["Hmmer,Blast,CPC:Filter the<br/>transcripts might be codings"]; F --> G["Cufflinks:Quantify<br/>Remove noise(transcripts with FPKM < 0.1)"]; G --> H(LncRNAs);
```

TopHat:Mapping

Stringtie:Assembling

Merge assembled gtf file

Cuffcompare:Compare to reference  
Remove transcripts marked as "=" or "c"  
Remove transcripts less than 200bp

Hmmer,Blast,CPC:Filter the  
transcripts might be codings

Cufflinks:Quantify  
Remove noise(transcripts with FPKM < 0.1)

LncRNAs