

# Generating a library with reads which are specific to one locus

Hello,

I am attempting to generate reads to test the ability of different alignment software (and various options associated with individual software) to accurately map reads to pseudogenes and their parent genes. A real RNAseq experiment would contain both a) reads which map equally well to the pseudogene and parent, as well as, b) reads which should map better to the pseudogene or the parent (due to the reads sequence similarity being higher to one or the other). To make software testing more straight forward, it would be helpful if I could use the flux simulator to only produce reads which are unique to either the pseudogene or parent (as is the case in b) thus knowing in advance the expected reads which should align to each locus. Is there a way to accomplish this? Thanks in advance for any help which you can offer!