Is there any way to find out which exon is sequenced?

Hi,

I sequence some reads based on the Directional RNA-Seq Protocol by using the example .par file, and I notice that by checking the .pro file generated, I can know which transcript is sequenced, and by checking the .gtf file, I can know all the exons related to the transcript. However, sometimes the transcript is lowly sequenced(by checking the "Covered Fraction"), and some of the exons related to this transcript is not sequenced. So I want to know is there a way to check whether an exon is sequenced or not directly? Thank you very much.

Chong