

Emma Caunt

From: Justin Howes [REDACTED]
Sent: Wednesday, 2 October 2013 3:19 PM
To: Emma Caunt; Kylie Rika; Matthew Hunt; Rhys Parry
Subject: Re: Fwd: amp differences
Attachments: DNA template input amount & pk ht chart.doc

Hi all

The example here was sent to Al and he wrote to me with some info on this topic that comes from the full-vol sens data (attached). Some of his words relating to this are:

The fundamental assumption that template input = peak height is flawed as, on average the relationship is somewhat linear, the std deviation is quite broad. The variance parameters in STRmix accounts for it somewhat, but they are only as good as the data you put in ...

attached is a simple word document that is the full-volume sensitivity data as a chart on the first page, and the data table on the second - so a limited set of what is essentially pristine reference samples with the average (across all loci) and 2 standard deviation values shown. Now if you think of casework samples where the DNA is of variable quality, well I think you get the picture -

He wrote to say that he would be happy to talk about it at a FRIT meeting even though it isn't new, or completely exclusive to PP21, so I am mulling over this offer.

jah

>>> Emma Caunt Wednesday, 2 October 2013 3:00 pm >>>

we do see this quite often. This is why we can't use pk ht to direct us on homozygotes and is the general issue with PP21 as STRmix works on pk hts.

>>> Kylie Rika 2/10/2013 2:54 pm >>>

further to my email re 150pg and homozygotes....