# **Request for bed file creation**

**Instructions:**

1. **Add genes symbols and/or transcripts to a panel in Moka**
2. **Add panel description to Moka**
3. **Answer following questions:**
4. **Pan number of bed file to be created:**

|  |  |  |
| --- | --- | --- |
| NGSEQ3 Exon+Intron CNV | -50/+50, 5UTR -50/+50,+ Pan657 | Pan1973 |
| NGSEQ3 variant | -10/+10. 5UTR +/-10bp | Pan1159 |
| SNP\_ID | Inclusion of LGC SNP ID assay | Pan659 |

1. **Panel description/name**

NGSEQ3

1. **Purpose of BED files:** (delete as appropriate)

* Calculating coverage Pan1159 + Pan659
* Performing CNV analysis using RPKM Pan1973

1. **Should specific transcripts be used to create the bed file?** (delete as appropriate)

* Yes - use specified transcripts (see question 4a)
* ~~No - use gene symbol to include all refseq transcripts~~

**4a) If transcripts are to be used have you provided multiple transcripts for the same gene?**

* Yes ~~/ No (If yes, please state any genes with multiple transcripts)~~

1. **If bed file is to be used for coverage:**

* Exon padding: 10bp

1. **If bed file is to be used for CNV RPKM analysis:**

* Control sites to include: Pan657
* Exon padding: 50bp

1. **Inclusion of UTRs**:

* Include 5’ and 3’ UTRs for all genes: No – 5UTR only
* Padding of UTRs: Yes 10bp for Pan1159, 50bp for Pan1973
* If UTRs are only required for a subset of genes please see section 8

1. **Any additional sites to be included:**

* Please provide genomic coordinates for target regions (without padding)
* Please describe region eg UTR, intronic site.
* Padding will be added as specified above

Eg: Chr1:123456-234567 5’ UTR for Gene ABC

**Requested by: Michael Yau Requested date: 04/11/2019**

**I only need Pan1973 to be done as Pan1159 has already been done. Please inactivate Pan1457**