# **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:**

Pan 1974\_\_\_\_\_\_

1. **Panel description/name**

CM\_CMD CNV; +/-50 + NGS CNV sites v2 (Pan657) plus 5'UTR (chrX:149737047-149737112) for MTM1 NM\_000252.2

Same as Pan1471 but;

change INPP5K transcript from NM\_001135642.1 to NM\_016532.3

and add in MTM1 promotor chrX:149737047-149737112

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

* Performing CNV analysis using RPKM

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

* Yes - use specified transcripts (see question 4a)

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

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

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

* ~~Exon padding: \_\_\_\_bp~~

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

* Control sites to include: Pan657\_\_\_\_
* Exon padding: \_50\_\_\_bp

1. **Inclusion of UTRs**:

* Include 5’ and 3’ UTRs for all genes: No
* Padding of UTRs: Yes / No
* 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

MTM1 promotor chrX:149737047-149737112

**Requested by: Rachael Mein, 13 March 2018 **