# **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 2022\_\_\_\_\_\_\_

1. **Panel description/name**

CM\_CMD Variant -10+10 plus [COL6A1 chr21:47409881C>T]

Same as Pan1464 but change INPP5K transcript from NM\_001135642.1 to NM\_016532.3

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

* Calculating coverage

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

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

* Exon padding: \_+/-10\_\_\_bp

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

* ~~Control sites to include: Pan\_\_\_\_~~
* ~~Exon padding: \_\_\_\_bp~~

1. **Inclusion of UTRs**:

* Include 5’ and 3’ UTRs for all genes: No
* Padding of UTRs: No
* If UTRs are only required for a subset of genes please see section 8

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

COL6A1 chr21:47409881C>T

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