# **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 2023\_\_\_\_\_\_\_

1. **Panel description/name**

NGSEQ2 CNV +/-50, DMD 5'UTR-50+50, plus 5'UTR (chrX:149737047-149737112) for MTM1 NM\_000252.2, +Pan657

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?**

* Yes (If yes, please state any genes with multiple transcripts)

DMD

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:**

DMD 5'UTR

MTM1 promotor chrX:149737047-149737112

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