# **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:**

|  |  |  |
| --- | --- | --- |
| WES\_CNV\_v2 | see S0768212\_Covered file for co-ordinates | Pan3296 |

1. **Panel description/name**

WES\_CNV\_v2

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

* Performing CNV analysis using RPKM Pan3296

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

No **–** used specific co-ordinates in S0768212\_Covered

* ~~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:**

No

1. **If bed file is to be used for CNV RPKM analysis:** seePan3296

No – used specific co-ordinates in S0768212 covered

1. **Inclusion of UTRs**:

* No

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

* No

See attached excel – S0768212 covered

|  |  |  |
| --- | --- | --- |
| WES\_CNV\_v2 | used specific co-ordinates in S0768212 Covered | Pan3296 |

**Requested by: Michael Yau Requested date: 25/10/2019**