# **Request for bed file creation**

Use this form to request the creation of a single BED file (one Pan number). If RPKM and coverage bedfiles are required please submit these on seperate forms.

**Instructions:**

* **Add genes symbols and/or transcripts to a panel in Moka**
* **Add panel description to Moka**
* **Answer following questions:**

1. **Pan number of bed file to be created:**   
   Pan3610
2. **Panel description/name**

|  |  |  |
| --- | --- | --- |
| Category | SubCategory | Panel |
| VCP2\_Intron\_CNV\_v2p1 | Intronic Sites for CNV | VCP2\_Intron\_CNV\_v2p1 - Intronic Sites for CNV |

1. **Is this BED file for RPKM?** (delete as appropriate)

Yes

chr5 112181806 112181966 APC\_3UTR

chr11 108239696 108239856 ATM\_3UTR

chr10 88684815 88684975 BMPR1A\_3UTR

chr17 41196280 41196440 BRCA1\_3UTR

chr17 41234663 41234823 BRCA1\_IN11\_1

chr17 41235012 41235172 BRCA1\_IN11\_2

chr17 41234197 41234357 BRCA1\_IN12\_1

chr17 41233848 41234008 BRCA1\_IN12\_2

chr17 41281042 41281202 BRCA1\_PM\_5\_1

chr17 41286238 41286398 BRCA1\_PM\_5\_2

chr17 41297651 41297811 BRCA1\_PM\_5\_3

chr17 41322636 41322796 BRCA1\_PM\_5\_4

chr13 32973679 32973839 BRCA2\_3UTR

chr17 59756516 59756676 BRIP1\_3UTR

chr16 68869315 68869475 CDH1\_3UTR

chr2 47614038 47614198 EPCAM\_3UTR

chr15 33037312 33037472 GREM1\_3UTR

chr3 37092207 37092367 MLH1\_3UTR

chr2 47710227 47710387 MSH2\_3UTR

chr2 47668813 47670238 MSH2\_INV1

chr2 38120922 38121392 MSH2\_INV2

chr5 80172503 80172663 MSH3\_3UTR

chr2 48034020 48034180 MSH6\_3UTR

chr8 90945564 90945764 NBN\_3UTR

chr16 23614453 23614613 PALB2\_3UTR

chr7 6010344 6010503 PMS2\_3UTR

chr19 50921296 50921456 POLD1\_3UTR

chr12 133200317 133200477 POLE\_3UTR

chr10 89728402 89728562 PTEN\_3UTR

chr17 33426780 33426940 RAD51D\_3UTR

chr17 56429831 56429991 RNF43\_3UTR

chr18 48611281 48611441 SMAD4\_3UTR

chr19 1228304 1228464 STK11\_3UTR

chr17 7571689 7571849 TP53\_3UTR

1. **Is this BED file exclusively based on coordinates provided by a supplier** (e.g SNP identity kits).

No

* 1. If yes, does this need further padding?

N/A

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

No

* 1. **If specific transcripts are to be used have you provided multiple transcripts for the same gene?** (if Yes please state)

No

1. **What padding is required around the exons?**

None

1. **Should UTRs be included for ALL genes?** (delete as appropriate)

N/A

* 1. **Should UTRs be padded?**

N/A

1. **Are UTRs required for SOME genes?** (delete as appropriate)

Not required

* 1. **Please list genes/transcripts.**
  2. **Should UTRs be padded?**

N/A

1. **Any additional BED files to be included in this BED file?**

None

1. **Are any further regions required to be added?**

None

**Requested by:** Michael Yau

**Requested date:** 21/04/2020