# **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:**  
   Pan3612
2. **Panel description/name**

|  |  |  |
| --- | --- | --- |
| **Category** | **SubCategory** | **Panel** |
| Nimagen\_SNP\_ID\_v2 | Exome SNP Variants | Nimagen\_SNP\_ID\_v2 - Exome SNP Variants |

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

No

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

No - attached

NC\_000001.10:g.179520506G rs1410592

NC\_000001.10:g.67861520C rs2229546

NC\_000002.11:g.227896976C rs10203363

NC\_000003.11:g.4403767A rs2819561

NC\_000004.11:g.5749904T rs4688963

NC\_000005.9:g.82834630T rs309557

NC\_000008.10:g.94935937T rs4735258

NC\_000009.11:g.100190780A rs1381532

NC\_000010.10:g.100219314G rs10883099

NC\_000011.9:g.16133413A rs4617548

NC\_000012.11:g.993930C rs7300444

NC\_000013.10:g.39433606A rs9532292

NC\_000015.9:g.34528948G rs4577050

NC\_000017.10:g.71197748G rs1037256

NC\_000018.9:g.21413869T rs9962023

NC\_000020.10:g.6100088A rs10373

NC\_000021.8:g.44323590T rs4148973

NC\_000008.10:g.121228679A rs4870723

NC\_000008.10:g.124987478T rs7465584

NC\_000009.11:g.125391409A rs1536928

NC\_000009.11:g.104133628C rs1572983

NC\_000009.11:g.79321871C rs577993

NC\_000013.10:g.33703656T rs495680

NC\_000014.8:g.68042574A rs11158685

NC\_000017.10:g.71196809A rs1026128

NC\_000017.10:g.57963537A rs1292053

NC\_000017.10:g.14005439G rs2159132

NC\_000018.9:g.60027241C rs1805034

NC\_000018.9:g.61654463A rs3826616

NC\_000020.10:g.52786219G rs2296241

NC\_000022.10:g.39178701A rs760482

NC\_000023.10:g.109694685T rs2073787

NC\_000023.10:g.135431358C rs5930933

NC\_000023.10:g.111698036T rs6568050

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

No

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

N/A

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

N/A

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

N/A

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)

N/A

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

N/A

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

N/A

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

N/A

**Requested by:** Michael Yau

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