# **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:**  
   Pan4290
2. **Panel description/name**

|  |  |  |
| --- | --- | --- |
| Category | SubCategory | Panel |
| DMD\_Intronic\_Variant\_v3 | +/-5bp\_Cryptic Splice Variants excl. chrX:32644478- 32644479, X:32274691-32274692 | DMD\_Intronic\_Variant\_v3 +/-5bp\_Cryptic Splice Variants excl. chrX:32644478- 32644479, X:32274691-32274692 |

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 – see attached 

|  |  |
| --- | --- |
| NC\_000023.10:g.32669100G>A | DMD c.961-5831C>T |
| NC\_000023.10:g.31279293T>C | DMD c.9225-160A>G |
| NC\_000023.10:g.31279418T>C | DMD c.9225-285A>G |
| NC\_000023.10:g.31393490C>A | DMD c.9085-26739G>T |
| NC\_000023.10:g.31995823T>A | DMD c.6439-9192A>T |
| NC\_000023.10:g.32042111dup | DMD c.6439-55480dup |
| NC\_000023.10:g.32479316T>C | DMD c.3432+2240A>G |
| NC\_000023.10:g.32479520T>C | DMD c.3432+2036A>G |
| NC\_000023.10:g.33192452C>T | DMD c.31+36947G>A |
| NC\_000023.10:g.31279780T>C | DMD c.9225-647A>G |
| NC\_000023.10:g.31382270C>A | DMD c.9085-15519G>T |
| NC\_000023.10:g.32756908T>C | DMD c.650-39498A>G |
| NC\_000023.10:g.32841967T>C | DMD c.265-463A>G |
| NC\_000023.10:g.32669194T>G | DMD c.961-5925A>C |
| NC\_000023.10:g.31983146C>A | DMD c.6614+3310G>T |
| NC\_000023.10:g.31226400T>C | DMD c.9563+1215A>G |
| NC\_000023.10:g.31627738T>C | DMD c.8217+18052A>G |
| NC\_000023.10:g.32407106A>T | DMD c.4518+512T>A |
| NC\_000023.10:g.32460274G>T | DMD c.3787-843C>A |
| NC\_000023.10:g.32591046T>C | DMD c.1812+601A>G |

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

5bp

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?**

5bp

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:** Natasha

**Requested date:** 01/02/21