| Peak number in Fig 7 | Gene ID | Peak category | THAP11 WT | Fold change (3) | RNA-seq log2(RPKM) THAP11 WT (4) | RNA-seq log2(RPKM) THAP11 F80L (4) | log2 fold change THAP11 WT vs THAP11 F80L |
|---------------------|---------|---------------|-----------|-----------------|--------------------------------|
| 1                   | ZNF691  | 107           | 3.39      | 3.41            | 0.00                            | 0.44                            | 1.02                        |
| 2                   | IPO13   | 196           | 4.04      | 4.06            | 0.00                            | 0.44                            | ND                          |
| 3                   | DPH2    | 277           | 4.76      | 4.81            | 0.03                            | 1.02                            | ND                          |
| 4                   | ATP6V0B | -262          | 6.69      | 6.61            | -0.13                           | 1.02                            | ND                          |
| 5                   | MUTYH   | 113           | 6.27      | 6.08            | 0.19                            | 1.02                            | ND                          |
| 6                   | RNF220  | 53            | 6.04      | 6.17            | 0.08                            | 1.02                            | ND                          |
| 7                   | BTBD19  | NA            | ND        | ND              | ND                              | ND                              | ND                          |
| 8                   | TOE1    | NA            | 0.19      | 0.19            | 0.19                            | 1.02                            | ND                          |
| 9                   | MMACHC  | -176          | 3.32      | 1.22            | -2.17                           | 1.02                            | ND                          |
| 10                  | TMEM69  | 73            | 4.77      | 5.03            | 0.15                            | 1.02                            | ND                          |

1. See Materials and Methods for the description of score calculation
2. S gene indicate the closest gene (+/-250 bp) that is a sense transcript; A-S gene indicate anti sense transcripts.
3. Distance between the gene transcription start site and the peak maximum
4. Mean between the two biological replicates
5. gene which transcription start site is within a region extending 250 bp on each side of the peak boundaries
   * gene which transcription start site is outside the aforementioned region
   NA non-applicable, meaning no such gene relative to the peak
   ND non-determined, meaning gene not expressed in our dataset