

| miR    | Ensembl Gene ID | Intronic  | Putative Pol-III Promoter | Intact A-Box | Intact B-Box | Transcript Length (Min) | Chr | Start     | End        |
|--------|-----------------|-----------|---------------------------|--------------|--------------|-------------------------|-----|-----------|------------|
| 7-2    | ENSG00000207703 | -         | AluJb                     | Y            | Y            | 593                     | 15  | 86956060  | 86956169   |
| 34a    | ENSG00000207865 | -         | MIR                       | Y            | Y            | 532                     | 1   | 9134314   | 9134423    |
| 297    | ENSG00000207823 | -         | AluJb                     | Y            | Y            | 215                     | 12  | 24038064  | 240381481  |
| 297    | ENSG00000207824 | GRID1     | AluSz                     | -            | Y            | 360                     | 10  | 88046488  | 88046570   |
| 297    | ENSG00000207822 | VWF       | AluYa1                    | Y            | Y            | 376                     | 12  | 5943647   | 5943729    |
| 549    | ENSG00000208003 | -         | MIRb                      | Y            | Y            | 288                     | 15  | 78921374  | 78921469   |
| 565-1  | ENSG00000207591 | -         | AluSx                     | Y            | Y            | 470                     | 6   | 27290934  | 272910181  |
| 565-2  | ENSG00000207592 | -         | AluSq                     | Y            | Y            | 378                     | 6   | 27289590  | 27289671   |
| 565-3  | ENSG00000207593 | -         | tRNA-Arg                  | Y            | Y            | 134                     | 3   | 45705468  | 45705564   |
| 566-1  | ENSG00000207919 | C10ORF104 | AluS                      | Y            | Y            | 229                     | 10  | 73665070  | 736651621  |
| 566-2  | ENSG00000207922 | Sema3F    | AluS                      | Y            | Y            | 230                     | 3   | 50185763  | 50185856   |
| 578    | ENSG00000207559 | CPE       | MIRb                      | -            | Y            | 367                     | 4   | 166526844 | 166526939  |
| 585    | ENSG00000207619 | SLIT3     | AluJo                     | Y            | Y            | 636                     | 5   | 168623183 | 168623276  |
| 594    | ENSG00000207796 | -         | tRNA-Arg                  | Y            | Y            | 118                     | 7   | 138675997 | 138676085  |
| 608    | ENSG00000207551 | Sema4     | AluJb                     | Y            | Y            | 274                     | 10  | 102724732 | 1027248311 |
| 633    | ENSG00000207552 | -         | MIRb                      | -            | Y            | 188                     | 1   | 9134314   | 9134423    |
| 642    | ENSG00000207773 | GIPR      | AluJb                     | Y            | Y            | 682                     | 19  | 50870026  | 508701221  |
| 181b-2 | ENSG00000207737 | ENSESTG   | MIRb                      | -            | Y            | 645                     | 9   | 126495810 | 1264958981 |

**Supplementary Table 3.** Human miRNAs with putative Pol-III promoters. Eighteen human microRNAs outside of the C19MC are potentially transcribed Pol-III transcription. Due to their small size, Pol-III promoters are difficult to identify unless identified in association with a larger sequence (e.g. tRNAs). Pol-III promoters were annotated as determined by the Censor Server (GIRINST) excepting tRNA-Arg elements which were identified using the Lowe Lab tRNA database. While the occurrence of a miRNA in an intron could be taken to suggest Pol-II transcription and processing via splicing, potentially, the occurrence of intronic miRNAs with intact upstream Pol-III promoters could suggest the production of these miRNAs both in parallel with their overlying genes (Pol-II) and a separate independent transcription. A-Box presence was not strictly required (B-boxes being sufficient for low level transcription). Sequences were filtered and removed if the Pol-III terminator (TTTT) was present. Importantly, while miR-7-2 is clearly not Alu-driven in other species, transposition events such as the one resulting in an Alu insertion just 5' of miR-7-2 may result in species-specific modulations of miRNA expression. "Transcript Length (min)" refers to the minimal transcript or difference between the 5' most promoter position and far 3' pre-miRNA nt. While Pol-III transcripts are commonly 200-400 bp in length, the lengths proposed are not seemingly beyond the capacity of Pol-III. Finally, it should be noted that the miR-297 hairpins have not been experimentally confirmed but were instead predicted and annotated by Ensembl based homology to rat miR-297 sequences.

#### References

1. E. Birney, *et al.*, Ensembl.Nucleic Acids Res. **34**, D556-D561 (2006)
2. Pavlicek, A., Kohany, O., Jurka, J. Repeat mining: basic tools for detection and analysis. In Analytical tools for DNA, genes and genomes nuts and bolts. (Markoff, A., ed). DNA Press, Eagleville (2005).
3. Jurka, J. *et. al.* Repbase Update, a database of eukaryotic repetitive elements. Cytogenetic and Genome Research **110**, 462-467 (2005).
4. Jurka, J. Repbase Update: a database and an electronic journal of repetitive elements. Trends Genet. **9**,418-420 (2000).
5. A Weber, *et al.* Total-Genome Analysis of BRCA1/2 -Related Invasive Carcinomas of the Breast Identifies Tumor Stroma as Potential Landscaper for Neoplastic Initiation. Am J Hum Genet. **78**,961-72 (2006).