**SUPLEMENTARY DATA FILES**

1. **Nimblegen experiments:**

The data for each hybridization is provided in two formats:

1. Raw PM values: which were extracted from the NImblegen pair files without any processing.
2. Wiggle file containing indexed normalized log (S/G1) ratio smoothed using 50 kb Gaussian convolution. In the wiggle file all control probes (random fiduciaries etc..) are eliminated and all repetitive probes are averaged to allow viewing in UCSC genome browser.

**File Rawdata\_chip1 and Rawdata\_chip2** contain for each hybridization:

MATCH\_INDEX: another identifier

PROBE\_ID: an identifier for each probe

PROBE\_CLASS: describes the type of probes

PROBE-SEQUENCE: the sequence of the probe

CHROMOSOME: the chromosomal location of the probe

POSITION: the genomic position of the probe (HG18 coordinate)

XXX\_PM: the PM values for each hybridization

The wiggle files (XXX\_wig.txt) contain

Column 1: chromosomal position

Column 2: position of the first base of the probe

Column3: position of the first base of the probe plus 1

Column 4: Indexed normalized gaussed Log(S/G1)

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Column | hybridization | Sample | Cell type | Wiggle file | chip |
| 194272\_635\_PM | 37 | S (cy5) | Erythroid cells replicate 1 | 37Ery\_wig | chip 2 |
| 194272\_532\_PM | 37 | G1 (cy3) | Erythroid cells replicate 1 | 37Ery\_wig | chip 2 |
|  |  |  |  |  |  |
| 226091\_635\_PM | 39 | S (cy5) | Erythroid cells replicate 2 | 39Ery\_wig | chip 2 |
| 226091\_532\_PM | 39 | G1 (cy3) | Erythroid cells replicate 2 | 39Ery\_wig | chip 2 |
|  |  |  |  |  |  |
| 226089\_635\_PM | 38 | S2 (cy3) | Erythroid cells | 38Ery\_wig | chip 2 |
| 226089\_532\_PM | 38 | G1 (cy5) | Erythroid cells | 38Ery\_wig | chip 2 |
|  |  |  |  |  |  |
| 233815\_635\_PM | 45 | S1 (cy5) | Erythroid cells | 45Ery\_wig | chip 2 |
| 233815\_532\_PM | 45 | G1 (cy3) | Erythroid cells | 45Ery\_wig | chip 2 |
|  |  |  |  |  |  |
| 233914\_635\_PM | 46 | S3 (cy5) | Erythroid cells | 46Ery\_wig | chip 2 |
| 233914\_532\_PM | 46 | G1 (cy3) | Erythroid cells | 46Ery\_wig | chip 2 |
|  |  |  |  |  |  |
| 178412\_635\_PM | 30 | S (cy5) | Mesenchymal cells replicate 1 | 30MS\_wig | chip 2 |
| 178412\_532\_PM | 30 | G1 (cy3) | Mesenchymal cells replicate 1 | 30MS\_wig | chip 2 |
|  |  |  |  |  |  |
| 148457\_635\_PM | 28 | S (cy5) | Mesenchymal cells replicate 2 | 28MS\_wig | chip 2 |
| 148457\_532\_PM | 28 | G1 (cy3) | Mesenchymal cells replicate 2 | 28MS\_wig | chip 2 |
|  |  |  |  |  |  |
|  |  |  |  |  |  |
| 140789\_635\_PM | 31 | S (cy5) | Human Embryonic Stem cells replicate 1 | 31hES\_wig | chip 2 |
| 140789\_532\_PM | 31 | G1 (cy3) | Human Embryonic Stem cells replicate 1 | 31hES\_wig | chip 2 |
|  |  |  |  |  |  |
| 226071\_532\_PM | 41 | S (cy3) | Human Embryonic Stem cells replicate 2 | 41hES\_wig | chip 2 |
| 226071\_635\_PM | 41 | G1 (cy5) | Human Embryonic Stem cells replicate 2 | 41hES\_wig | chip 2 |
|  |  |  |  |  |  |
| 98731\_635\_PM | 27 | G1 (cy3) | Mesenchymal cells | 27MS\_wig | chip 1 |
| 98731\_532\_PM | 27 | G1 (cy5) | Mesenchymal cells | 27MS\_wig | chip 1 |
|  |  |  |  |  |  |
| 101320\_635\_PM | 26 | S (cy5) | Mesenchymal cells amplified | 26MS\_wig | chip 1 |
| 101320\_532\_PM | 26 | G1 (cy3) | Mesenchymal cells amplified | 26MS\_wig | chip 1 |
|  |  |  |  |  |  |
| 92676\_635\_PM | 25 | S (cy5) | Mesenchymal cells replicate 1 | 25MS\_wig | chip 1 |
| 92676\_532\_PM | 25 | G1 (cy3) | Mesenchymal cells replicate 1 | 25MS\_wig | chip 1 |

1. **Massively parallel sequencing**

We provide wiggle files with the calculated TimEX value for:

1. Erythroids-Experimental-TimEX-W5Kb-S100Kb.txt (13 million reads)
2. ES-Experimental-TimEX-W5Kb-S100Kb.txt (13 million reads)

We also provide wiggle files for the predicted TimEX values

1. U133-3UTR-ES-PredictedTimex-Reciprocal-1-ON-13.3-0.8-Gaussed.txt (Simulation\_hES.txt)
2. U133-3UTR-Erythroids-PredictedTimex-Reciprocal-1-ON-0.5-0.005-Gaussed.txt (Simulation\_Erythroblast.txt)

The raw data (fasta files with sequence of every reads obtained from the SoliD and Solexa sequencer) is available on request and will be deposited in appropriate repository at NCBI

1. **Expression data:**

File Affy-ER-ES-RMA-ProbeSet.txt contains averaged RMA normalized values U133 chip hybridized with human in vitro-derived erythroblasts (3 hybridizations) and hESCs (2 hybridizations)

Cel files for all hybridizations are available on requests