# Table S1

| | | Uniquely mapped tags | | | | Mappability (%) | | |
|---|---|---|---|---|---|---|---|---|
| | Tags | Eland | Bowtie | MAQ | Soap2 | Bowtie | MAQ | Soap2 |
| c−Myc | 26,507,905 | 6,637,404 | 10,706,401 | 11,570,815 | 12,359,761 | 63.26 | 62.10 | 63.48 |
| E2f1 | 29,877,423 | 6,026,155 | 10,354,841 | 10,938,919 | 11,680,246 | 52.18 | 51.14 | 52.53 |
| Esrrb | 25,284,321 | 3,609,843 | 11,831,415 | 12,698,806 | 13,351,007 | 65.92 | 65.12 | 66.23 |
| Klf4 | 19,658,061 | 3,807,970 | 6,688,461 | 7,105,939 | 7,573,812 | 51.42 | 50.89 | 52.63 |
| Nanog | 23,210,244 | 8,424,102 | 10,228,002 | 10,984,575 | 11,775,466 | 68.89 | 67.52 | 69.93 |
| n−Myc | 22,818,575 | 4,823,212 | 7,711,070 | 8,412,032 | 8,787,237 | 51.80 | 51.94 | 52.84 |
| Oct4 | 23,339,676 | 4,911,144 | 8,051,461 | 8,718,505 | 9,145,158 | 53.45 | 53.46 | 54.46 |
| Smad1 | 19,348,766 | 3,338,896 | 5,283,929 | 5,261,880 | 6,140,352 | 45.09 | 41.07 | 45.33 |
| Sox2 | 22,221,844 | 4,821,446 | 8,271,344 | 9,004,099 | 9,383,822 | 56.12 | 56.51 | 57.39 |
| Stat3 | 21,575,655 | 5,351,116 | 8,788,899 | 9,668,243 | 10,083,166 | 66.70 | 66.82 | 67.64 |
| Tcfcp2l1 | 30,624,944 | 8,787,961 | 11,073,220 | 11,685,125 | 12,476,979 | 52.45 | 51.40 | 52.77 |
| Zfx | 17,734,559 | 3,844,429 | 7,406,375 | 7,781,303 | 8,372,722 | 62.51 | 60.69 | 62.74 |

# Table S2

| | Fold Change | | | | Overlap (%) | | | |
|---|---|---|---|---|---|---|---|---|
| | Eland | Bowtie | MAQ | Soap2 | Eland | Bowtie | MAQ | Soap2 |
| c-Myc | 1.00 | 1.61 | 1.74 | 1.86 | 100.00 | 90.30 | 96.84 | 99.42 |
| E2f1 | 1.00 | 1.72 | 1.82 | 1.94 | 100.00 | 92.90 | 97.28 | 99.96 |
| Esrrb | 1.00 | 3.28 | 3.52 | 3.70 | 100.00 | 67.31 | 68.88 | 69.78 |
| Klf4 | 1.00 | 1.76 | 1.87 | 1.99 | 100.00 | 90.37 | 94.49 | 97.31 |
| Nanog | 1.00 | 1.21 | 1.30 | 1.40 | 100.00 | 90.56 | 96.22 | 98.46 |
| n-Myc | 1.00 | 1.60 | 1.74 | 1.82 | 100.00 | 90.11 | 96.22 | 98.12 |
| Oct4 | 1.00 | 1.64 | 1.78 | 1.86 | 100.00 | 90.99 | 96.08 | 98.43 |
| Smad1 | 1.00 | 1.58 | 1.58 | 1.84 | 100.00 | 86.89 | 90.71 | 97.43 |
| Sox2 | 1.00 | 1.72 | 1.87 | 1.95 | 100.00 | 90.91 | 96.07 | 98.26 |
| Stat3 | 1.00 | 1.64 | 1.81 | 1.88 | 100.00 | 91.10 | 97.44 | 99.22 |
| Tcfcp2l1 | 1.00 | 1.26 | 1.33 | 1.42 | 100.00 | 83.79 | 87.50 | 89.38 |
| Zfx | 1.00 | 1.93 | 2.02 | 2.18 | 100.00 | 91.41 | 96.50 | 99.99 |

- Table S1
  - Mapping result of high-quality 26-bp tags derived from ChIP-seq data (GSE11431). Eland has been done by Chen et. al. (Cell 2008, 133:1106-1117). Mappability is calculated by (unique hits + multiple hits) / total 26-bp tags.
- Table S2
  - Fold change of the number of mapped tags over that of Chen's data. Overlaps have been checked by that at least one base of 26-bp tags of Chen_Eland overlaps to any of tags mapped in this study.

# Table S3

| | Chen | FindPeaks | | | | Overlap of Chen's peaks | | | |
|---|---|---|---|---|---|---|---|---|---|
| | Eland | Eland | Bowtie | MAQ | Soap2 | Eland | Bowtie | MAQ | Soap2 |
| c-Myc | 3422 | 3441 | 11150 | 7708 | 11665 | 3255 | 2677 | 2653 | 2730 |
| E2f1 | 20699 | 21378 | 27834 | 28226 | 29036 | 17680 | 15455 | 15490 | 15670 |
| Esrrb | 21647 | 62309 | 67634 | 71211 | 84965 | 21452 | 19183 | 19267 | 19529 |
| Klf4 | 10875 | 24988 | 38763 | 38449 | 41619 | 10549 | 9968 | 9885 | 10057 |
| Nanog | 10343 | 10432 | 22219 | 18992 | 25005 | 10129 | 9095 | 9315 | 9483 |
| n-Myc | 7182 | 13348 | 23291 | 25813 | 25852 | 6851 | 6049 | 6156 | 6187 |
| Oct4 | 3761 | 9000 | 23349 | 25281 | 25505 | 3644 | 3169 | 3179 | 3294 |
| Smad1 | 1126 | 1683 | 3596 | 3643 | 3978 | 1031 | 851 | 899 | 919 |
| Sox2 | 4526 | 8257 | 19127 | 20764 | 21062 | 4452 | 4089 | 4099 | 4206 |
| Stat3 | 2546 | 4079 | 21614 | 12231 | 21211 | 2472 | 2062 | 2080 | 2155 |
| Tcfcp2l1 | 26910 | 28015 | 46466 | 41402 | 49798 | 23963 | 24433 | 24523 | 24953 |
| Zfx | 10338 | 27085 | 39361 | 40738 | 41935 | 9810 | 9063 | 9057 | 9141 |

# Table S4

| | Chen | FP4 (chr1, chr2, chr3, ..., chrX) | |
|---|---|---|---|
| | | Eland | Bowtie |
| c-Myc | 7 | 7, 7, 7, 7, 7, 8, 7, 8, 8, 7, 8, 7, 8, 7, 8, 7, 7, 7, 7, 6 | 8, 8, 8, 8, 8, 8, 8, 8, 9, 8, 9, 8, 8, 8, 8, 8, 8, 8, 8, 6 |
| E2f1 | 6 | 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 5 | 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 5 |
| Esrrb | 5 | 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 6, 5, 5, 5, 5, 5, 5, 5, 5, 5 | 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 7, 6, 6, 6, 6, 6, 7, 6, 6, 5 |
| Klf4 | 5 | 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 5 | 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 5 |
| Nanog | 7 | 8, 7, 7, 7, 7, 7, 7, 8, 8, 7, 8, 7, 7, 7, 8, 7, 7, 7, 8, 6 | 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 6 |
| n-Myc | 6 | 6, 6, 6, 6, 7, 6, 6, 7, 6, 6, 7, 6, 6, 6, 6, 6, 6, 6, 6, 5 | 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 5 |
| Oct4 | 6 | 7, 7, 6, 7, 7, 6, 7, 7, 7, 6, 7, 6, 7, 7, 7, 7, 7, 6, 7, 5 | 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 6 |
| Smad1 | 6 | 7, 6, 7, 6, 6, 6, 6, 7, 6, 6, 6, 6, 7, 6, 7, 6, 7, 7, 6, 5 | 8, 8, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 8, 7, 7, 7, 6 |
| Sox2 | 6 | 7, 7, 6, 7, 7, 6, 7, 7, 7, 6, 7, 7, 6, 6, 7, 6, 7, 7, 7, 5 | 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 6 |
| Stat3 | 6 | 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 6 | 8, 8, 7, 7, 7, 7, 7, 8, 7, 7, 8, 7, 7, 7, 7, 7, 7, 8, 7, 6 |
| Tcfcp2l1 | 6 | 7, 7, 6, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 5 | 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 5 |
| Zfx | 5 | 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 5 | 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 5 |

| | Chen | FP4 (chr1, chr2, chr3, ..., chrX) | |
|---|---|---|---|
| | | MAQ | Soap2 |
| c-Myc | 7 | 8, 9, 8, 8, 9, 8, 8, 9, 9, 9, 9, 8, 9, 8, 8, 8, 8, 9, 8, 6 | 9, 9, 8, 8, 9, 9, 8, 9, 9, 9, 9, 9, 9, 8, 8, 9, 8, 9, 9, 6 |
| E2f1 | 6 | 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 5 | 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 6 |
| Esrrb | 5 | 6, 6, 6, 6, 7, 6, 6, 7, 7, 6, 7, 6, 6, 6, 7, 6, 7, 6, 7, 5 | 6, 7, 6, 7, 7, 6, 7, 7, 7, 7, 7, 6, 6, 6, 6, 6, 7, 6, 7, 5 |
| Klf4 | 5 | 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 7, 6, 6, 6, 6, 6, 6, 6, 6, 5 | 6, 6, 6, 6, 6, 6, 6, 7, 6, 6, 7, 6, 6, 6, 6, 6, 6, 6, 6, 5 |
| Nanog | 7 | 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 6 | 8, 8, 8, 8, 8, 8, 8, 9, 8, 8, 9, 8, 8, 8, 8, 8, 8, 8, 8, 6 |
| n-Myc | 6 | 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 5 | 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 6 |
| Oct4 | 6 | 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 8, 7, 7, 7, 7, 7, 7, 7, 7, 6 | 7, 7, 7, 7, 7, 7, 7, 8, 8, 7, 8, 7, 7, 7, 7, 7, 7, 7, 8, 6 |
| Smad1 | 6 | 7, 7, 7, 7, 7, 7, 7, 8, 7, 8, 7, 7, 7, 7, 8, 7, 7, 8, 7, 6 | 8, 8, 8, 7, 7, 7, 7, 8, 8, 8, 8, 8, 8, 7, 8, 8, 7, 8, 8, 6 |
| Sox2 | 6 | 7, 7, 7, 7, 7, 7, 7, 8, 7, 7, 8, 7, 7, 7, 7, 7, 7, 7, 7, 6 | 7, 7, 7, 7, 7, 7, 7, 8, 8, 7, 8, 7, 7, 7, 7, 7, 7, 7, 8, 6 |
| Stat3 | 6 | 8, 8, 8, 7, 8, 7, 7, 8, 8, 8, 8, 7, 8, 8, 8, 8, 7, 8, 8, 6 | 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 6 |
| Tcfcp2l1 | 6 | 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 5 | 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 6 |
| Zfx | 5 | 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 7, 6, 6, 6, 6, 6, 6, 6, 6, 5 | 6, 6, 6, 6, 6, 6, 6, 7, 6, 6, 7, 6, 6, 6, 6, 6, 6, 6, 6, 5 |

- Table S3
  - Number of peaks. FP4 (FindPeaks 4.0) detected tag enrichments. Overlaps of Chen_Eland to ours have been checked by whether a Chen's peak center co-localizes with any of peak centers detected by FP4 within 200-bp window.
- Table S4
  - Thresholds used to detect significant peaks (FDR < 5). Chen et al. have determined thresholds by qPCR. We performed Monte Carlo simulations on each chromosome.