

**Supplementary Table 1. Prerank GSEA analysis for 26 published stemness-associated gene sets.**

| Term  | No. of genes | NES <sup>a</sup> | FDR q-value <sup>b</sup> | Tag % <sup>c</sup> |
|---|--------------|------------------|--------------------------|--------------------|
| Yan, underexpressed in CD133+ GBM cells <sup>5</sup>                  | 125          | 2.5830           | 0                        | 76/116             |
| Kim, core human <sup>6</sup>  | 75           | 2.1563           | 0                        | 30/73              |
| Bhattacharya, hESC <sup>7</sup>                                       | 88           | 2.1081           | 0                        | 60/87              |
| Wong, core ESC-like module <sup>8</sup>                               | 335          | 2.1033           | 0                        | 182/315            |
| Benporath, ES1 <sup>7</sup>   | 379          | 2.0494           | 0                        | 171/352            |
| Wong, human ESC-like module <sup>8</sup>                              | 1192         | 2.0275           | 0                        | 559/1110           |
| Benporath, Nanog <sup>7</sup>   | 360          | 1.9690           | 0                        | 140/351            |
| Palmer, Stem cell gene set <sup>9</sup>                               | 189          | 1.9622           | 0                        | 72/176             |
| Shats, consensus <sup>7</sup>   | 80           | 1.9609           | 0                        | 47/80              |
| Shats, iPSC <sup>7</sup>  | 86           | 1.9550           | 7.92E-05                 | 47/71              |
| Kim, PrC_Human <sup>6</sup>   | 451          | 1.9484           | 7.39E-05                 | 168/434            |
| Kim, Myc <sup>7</sup>   | 325          | 1.9291           | 6.93E-05                 | 126/325            |
| Benporath, Sox2 <sup>7</sup>  | 360          | 1.8909           | 6.52E-05                 | 146/353            |
| Zhang, Stem.sig <sup>10</sup>   | 454          | 1.8874           | 6.16E-05                 | 134/390            |
| Kim, Myc Human <sup>6</sup>   | 355          | 1.8549           | 5.84E-05                 | 128/337            |
| Kim, core factors <sup>11</sup>                                       | 8            | 1.8280           | 1.66E-04                 | 5/8                |
| Benporath, proliferative genes <sup>7</sup>                           | 1035         | 1.7447           | 6.86E-04                 | 278/849            |
| Sato, HESC and MESC overlap genes <sup>12</sup>                       | 20           | 1.7382           | 7.06E-04                 | 6/9                |
| Smith, human epithelial ASC <sup>7</sup>                              | 49           | 1.6495           | 3.13E-03                 | 15/47              |
| Yuan, CancerSEA <sup>13</sup>   | 62           | 1.6173           | 4.57E-03                 | 21/55              |
| Miranda, Curated withouth immune and proliferative genes <sup>7</sup> | 109          | 1.6135           | 4.52E-03                 | 46/103             |
| Kim, Myc-related factors <sup>11</sup>                                | 11           | 1.5951           | 5.50E-03                 | 7/11               |
| Benporath, ES2 <sup>7</sup>   | 40           | 1.4576           | 2.29E-02                 | 11/37              |
| Yan, overexpressed in CD133+ GBM cells <sup>5</sup>                   | 89           | 1.3691           | 4.63E-02                 | 28/87              |
| Kim, polycomb related factors <sup>11</sup>                           | 7            | 1.2885           | 8.41E-02                 | 4/7                |
| Sato, HESC-related genes <sup>12</sup>                                | 16           | 1.2306           | 1.23E-01                 | 6/9                |

<sup>a</sup>NES: Normalized enrichment score, the enrichment score for the gene set after it has been normalized across analyzed gene sets.

<sup>b</sup>FDR q-value: False discovery rate, the estimated probability that the normalized enrichment score represents a false positive finding.

<sup>c</sup>Tag %: The percentage of gene hits before (for positive ES) or after (for negative ES) the peak in the running enrichment score. This gives an indication of the percentage of genes contributing to the enrichment score.