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

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

[a]NES (normalized enrichment score): The enrichment score for a gene set after normalization across all analyzed gene sets.

[b]FDR q value: The false discovery rate, representing the estimated probability that the normalized enrichment score reflects a false-positive finding.

[c]Tag %: The percentage of genes contributing to the enrichment score, defined as the proportion of gene hits occurring before the peak of the running enrichment score for positive enrichment, or after the peak for negative enrichment.