Supplementary Data

Supplementary Table S1. Human Putative Candidate Oocyte Reprogramming Factors (CORFs)

Gene ID	*Gene identifier*	*UG cluster*	*Fold change*	*p value*
A1CF	NM_014576	Hs.499643	9.83	0.007813
AFAP1L2	AW138743	Hs.501106	5.54	0.009327
AFF4	AV652437	Hs.519313	4.54	0.016167
AKIRIN2	BC000764	Hs.485915	9.13	5.20E-10
AOF1	BE348688	Hs.709336	121.98	1.10E-05
ARID2	AI692432	Hs.317304	19.15	0.009654
ARID5B	BU171496	Hs.535297	8.95	0.020919
ASF1A	NM_014034	Hs.292316	6.57	0.012035
ASF1B	NM_018154	Hs.26516	3.95	0.027946
ASXL1	AI829840	Hs.374043	13.26	0.002342
ASZ1	BC034963	Hs.352412	15.05	0.00918
ATXN1	BF438383	Hs.712106	4.76	0.021963
BACH1	NM_001186	Hs.154276	14.99	0.001947
BANP	NM_017869	Hs.461705	8.67	1.34E-05
BATF2	AW083820	Hs.124840	12.92	0.008916
BAZ1A	NM_013448	Hs.509140	29.62	0.00716
BCL11B	AA918317	Hs.709690	12.35	0.015048
BHLHE40	NM_003670	Hs.719093	31.29	5.43E-06
BNC1	NM_001717	Hs.459153	18.24	0.031192
BRD1	NM_014577	Hs.127950	3.59	2.04E-05
BRDT	NM_001726	Hs.482520	7.6	0.033059
BRPF1	NM_004634	Hs.1004	7.54	0.019201
BTRC	BC006204	Hs.643802	3.37	0.037096
C17orf79	AJ272196	Hs.462729	4.38	0.000202
C1orf149	NM_022756	Hs.17118	3.97	0.001208
C1orf59	BE502436	Hs.7962	24.14	0.000361
C21orf45	AW151538	Hs.190518	6.74	0.005698
CAMK2A	NM_015981	Hs.716391	7.84	0.049556
CAMTA1	AF111804	Hs.397705	5.01	0.016866
CBFA2T3	NM_005187	Hs.513811	5.32	0.004634
CBX8	NM_020649	Hs.387258	8.28	0.016357
CBY1	NM_015373	Hs.334911	3.26	0.003414
CCNE1	AI671049	Hs.244723	17.62	0.001994
CDC45L	NM_003504	Hs.474217	5.08	0.028999
CDK7	L20320	Hs.184298	12.23	4.30E-05
CDKN2A	NM_000077	Hs.512599	4.14	0.044969
CENPP	AA766264	Hs.713775	5.52	0.018495
CIITA	U31931	Hs.701991	4.19	0.036814
CLOCK	NM_004898	Hs.436975	8.21	0.038533
CNOT6	AA633196	Hs.654984	10.74	5.87E-06
CNOT6L	AW514857	Hs.592519	14.69	0.005453
CNOT7	W94952	Hs.719129	4.09	0.003765
CNOT8	NM_004779	Hs.26703	4.39	0.000414
CPEB2	AI202327	Hs.656937	17.37	0.043742
CREB5	NM_004904	Hs.437075	14.74	0.0002
CRKRS	NM_016507	Hs.416108	5.58	0.018682
CSDE1	AA167775	Hs.69855	4.8	0.005164
CTCFL	NM_080618	Hs.131543	55.82	0.002403
CUX1	BE046521	Hs.654389	15.75	2.87E-05
CYLD	BE046443	Hs.578973	6.06	0.038044
DAB2	BC026261	Hs.481980	5.87	0.020987
DAB2IP	AB051530	Hs.522378	4.11	0.002471
DLX4	NM_001934	Hs.591167	3.13	0.011546
DLX6	NM_005222	Hs.249196	6.66	0.000565
DMRT1	NM_021951	Hs.98586	3.91	0.010175
DMRT2	AF284225	Hs.59506	3.71	0.015309
DMRTB1	AI198850	Hs.131654	205.78	0.000701
DND1	AI949010	Hs.591262	5.86	0.001094

(*continued*)

Supplementary Table S1. (Continued)

Gene ID	*Gene identifier*	*UG cluster*	*Fold change*	*p value*
DNMT1	NM_001379	Hs.202672	12.69	0.000558
DPF3	AI125562	Hs.162868	3.74	0.021744
DPPA3	AI066520	Hs.131358	369.73	6.06E-06
DPPA5	AI365263	Hs.125331	457.32	4.65E-09
DVL2	AW016304	Hs.118640	10.49	0.013597
EBF1	AF208502	Hs.573143	129.58	0.011163
EDA	AF061193	Hs.105407	17.39	0.009245
EHF	AI763378	Hs.653859	14.55	0.022372
EIF3B	AW207523	Hs.371001	3.7	0.047909
EIF5B	AB018284	Hs.158688	5.92	0.04986
ELA1	NM_001971	Hs.348395	8.91	0.000454
ELK3	AW575374	Hs.46523	3.35	0.006433
EN1	NM_001426	Hs.271977	7.63	0.028205
EPAS1	AF052094	Hs.468410	56.07	5.75E-05
EPB41L5	AI652872	Hs.654802	14.18	2.33E-05
ERCC6	BF433475	Hs.654449	11.44	0.005305
ERG	M21535	Hs.473819	6.63	0.001026
ESR1	AF258450	Hs.208124	11.2	0.013301
ESR2	AF051428	Hs.660607	3.29	0.036548
ESRRB	AK096020	Hs.435845	3.68	0.035991
ETV5	AW206458	Hs.43697	57.01	0.009912
EVI1	AI458437	Hs.719216	5.43	0.046048
EVX1	NM_001989	Hs.369879	3.26	0.023439
EYA2	U71207	Hs.472877	5.81	0.004916
FOSB	NM_006732	Hs.590958	14.38	0.003192
FOSL2	N36408	Hs.220971	4.63	0.030959
FOXA2	AI693985	Hs.155651	5.2	0.048186
FOXD2	NM_004474	Hs.166188	7.08	0.012445
FOXF2	NM_001452	Hs.484423	4.38	0.048442
FOXK1	AW007319	Hs.708095	3.35	0.007514
FOXK2	N49941	Hs.591140	14.4	0.011654
FOXN4	AF425597	Hs.528316	3.13	0.014351
FOXO3	BE888885	Hs.220950	6.97	0.001127
FOXP2	AF493430	Hs.656280	10.3	0.004578
FOXP4	BE504097	Hs.131436	3.25	0.039341
FOXQ1	AI676059	Hs.591352	17.26	0.00426
FOXR1	AA669512	Hs.116679	206.91	0.003052
FTSJD2	D43949	Hs.520102	6.94	1.33E-05
GAS7	BE439987	Hs.462214	12.54	0.028999
GATA2	BC002557	Hs.367725	3.22	0.036318
GATA4	D78260	Hs.243987	4.65	0.011957
GCM1	AB026493	Hs.28346	3.81	0.028867
GFI1	NM_005263	Hs.73172	19.22	0.014098
GFI1B	AI097490	Hs.553160	4.91	0.020104
GLP-1	AI923985	Hs.709296	5.31	0.042809
GRIP1	BE672408	Hs.505946	6.42	0.024859
GRM5	D60132	Hs.719168	3.87	0.011318
GTF2A1L	NM_006873	Hs.44385	150.01	0.000623
GTF2B	NM_001514	Hs.481852	10.48	0.006302
H1FOO	NM_153833	Hs.97358	318.44	0.026501
H2AFB2	AI218431	Hs.534498	3.03	0.025565
H2AFY	BI560542	Hs.599225	3.55	0.026797
HBP1	AF019214	Hs.162032	3.97	0.002576
HBZ	NM_005332	Hs.585357	4.45	0.031805
HCFC2	AW956392	Hs.506558	6.38	0.000475
HDAC9	BM726008	Hs.196054	56.05	0.001492
HES6	AW249678	Hs.42949	10.48	0.044439
HEY2	AF232238	Hs.144287	6.09	0.004236
HHEX	Z21533	Hs.118651	40.15	0.006371
HIC2	AI912206	Hs.632767	7.7	0.000121
HIPK2	AF207702	Hs.397465	3.86	0.042114
HIST1H1A	NM_005325	Hs.150206	71.47	0.017859

(*continued*)

Supplementary Table S1. (Continued)

Gene ID	*Gene identifier*	*UG cluster*	*Fold change*	*p value*
HIST1H1T	NM_005323	Hs.533293	3.53	0.030618
HLF	M95585	Hs.196952	4.02	0.01924
HMBOX1	NM_024567	Hs.591836	5.24	0.040897
HMX1	AI939402	Hs.104134	10.07	0.015528
HNF4G	NM_004133	Hs.241529	5.91	0.014972
HOPX	AB059408	Hs.654864	5.03	0.026112
HOXA13	BG289306	Hs.592172	7.64	0.032162
HOXA3	AW137982	Hs.659337	5.45	0.002327
HOXA4	NM_002141	Hs.533357	6.69	0.027229
HOXA6	NM_024014	Hs.679517	3.05	0.040474
HOXA7	AI492051	Hs.660918	140.96	0.007791
HOXB6	AA527340	Hs.98428	3.47	0.009142
HOXB7	AW102783	Hs.436181	5.14	0.007402
HOXC6	NM_018953	Hs.549040	3.02	0.007553
HOXD1	NM_024501	Hs.83465	7.02	0.02978
HOXD11	NM_021192	Hs.421136	4.96	0.016094
HOXD4	NM_014621	Hs.591609	3.72	0.03288
HOXD8	BF057634	Hs.301963	13.84	0.014693
HOXD9	AI432470	Hs.709219	7.83	0.01301
HSF2BP	NM_007031	Hs.406157	87.35	0.022817
HSF5	AL137385	Hs.380061	31.41	0.005726
HSFY1	AF332227	Hs.662281	3.61	0.033518
IFNAR2	L41944	Hs.708195	15.82	0.000879
IKZF1	S80876	Hs.435949	7.4	0.036962
IL26	NM_018402	Hs.272350	3.73	0.020981
ING3	NM_019071	Hs.489811	10.72	0.015899
ING5	AI971618	Hs.645460	5.38	0.037401
IRAK3	BC029493	Hs.369265	3.03	0.002287
IRF6	NM_006147	Hs.719361	4.22	0.03557
IRF8	AI073984	Hs.137427	58.99	7.79E-06
ISL1	NM_002202	Hs.505	13.13	0.000583
JMJD6	NM_015167	Hs.514505	3.91	0.038449
KCNH1	NM_002238	Hs.553187	6.4	0.018718
KCNH7	AF032897	Hs.657413	3.51	0.031955
KCNH8	NM_144633	Hs.475656	3.28	0.007587
KCNIP3	AK025847	Hs.437376	5.73	0.024237
KDM3A	AA524505	Hs.557425	9.03	0.000412
KDM6B	AI830331	Hs.223678	20.85	0.008573
KLF11	AF028008	Hs.12229	5.96	0.000634
KLF2	NM_016270	Hs.715677	61.53	9.84E-05
KLF5	AF132818	Hs.508234	14.49	0.034933
LCOR	AW663968	Hs.500695	6.25	0.030339
LEF1	AF288571	Hs.719332	60.54	0.008292
LHX2	NM_004789	Hs.696425	6.33	0.046111
LHX8	BC040321	Hs.403934	132.4	0.000802
LHX9	AJ296272	Hs.442578	4.58	0.022008
LOC730092	AI919493	Hs.658149	4.02	0.039829
LPIN2	U55968	Hs.132342	3.66	0.011224
LRCH4	AI660075	Hs.125742	3.86	0.022102
LRRFIP1	AV648843	Hs.471779	3.08	0.003847
LSM11	AI492353	Hs.631954	8.11	0.006564
LZTS1	AF123656	Hs.521432	3.12	0.015838
MAEL	AA446073	Hs.651245	218.11	0.001463
MAFG	NM_002359	Hs.252229	4.56	0.004604
MAFK	BG231691	Hs.520612	11.51	0.002855
MAGOH	AF067173	Hs.421576	4.82	2.46E-06
MAPRE3	NM_012326	Hs.515860	101.82	0.025037
MAT2B	NM_013283	Hs.54642	4.27	0.00034
MAX	BC003525	Hs.285354	5.31	1.20E-06
MBD2	NM_003927	Hs.25674	3.05	0.046642
MBIP	NM_016586	Hs.368647	3.37	0.023521
MED13	AB011165	Hs.282678	4.77	0.016316

(*continued*)

Supplementary Table S1. (Continued)

Gene ID	*Gene identifier*	*UG cluster*	*Fold change*	*p value*
MED13L	BG426689	Hs.603766	4.33	0.028355
MED19	BE781103	Hs.43619	6.89	0.027492
MED21	AI688580	Hs.286145	5.81	0.002051
MED30	AI026938	Hs.492612	4.65	0.000239
MED8	BG230758	Hs.301756	13.17	8.71E-05
MESP1	BC006219	Hs.447531	14.77	0.006322
MGA	BF438227	Hs.187569	7.71	0.00299
MITF	AL117653	Hs.166017	23.79	0.000796
MIXL1	AF211891	Hs.710576	10.85	0.042906
MLL3	BE962679	Hs.647120	20.92	0.00104
MLL4	NM_014727	Hs.92236	4.8	0.014748
MLLT1	AW962605	Hs.10095	3.81	6.86E-05
MLLT11	BC006471	Hs.75823	5.65	0.001975
MLX	N40555	Hs.714749	5.83	1.18E-06
MSI2	BE000929	Hs.658922	8.19	0.008127
MSL1	AI800794	Hs.532786	5.09	0.020338
MSL3	NM_006800	Hs.655288	4.41	0.009071
MSX1	AI421295	Hs.424414	7.44	0.035532
MSX2	D89377	Hs.89404	8.18	0.004802
MTERFD1	NM_015942	Hs.308613	8.97	5.83E-05
MUSK	AI341265	Hs.521653	5.29	0.02576
MXD1	AI188653	Hs.468908	141.31	1.01E-05
MXI1	NM_005962	Hs.719185	7.53	0.001169
MYNN	NM_018657	Hs.507025	4.46	0.006123
MYPOP	AA307731	Hs.515478	8.97	0.018575
MYT1L	BE671048	Hs.434418	6.25	0.035909
NANOS1	AW970089	Hs.591918	12.9	0.009298
NARG1	AF327722	Hs.715706	6.3	0.021327
NCOA3	AI761748	Hs.592142	4.48	0.001021
NCOA6	AF128458	Hs.368971	9.84	9.67E-05
NEUROG3	NM_020999	Hs.532682	4.25	0.011428
NFATC1	U08015	Hs.534074	8.7	0.023009
NFATC2	U43342	Hs.713650	10.37	0.027008
NFATC3	NM_004555	Hs.632209	5.19	0.000118
NFIC	AW134798	Hs.170131	3.26	0.02342
NFKBIA	AI078167	Hs.81328	24.67	0.009999
NFYA	AL137443	Hs.10441	3.67	0.025955
NFYC	NM_014223	Hs.233458	4.13	0.024371
NKX2-5	NM_004387	Hs.54473	3.92	0.03935
NKX3-1	AF247704	Hs.55999	34.21	0.009917
NLRC5	AA005023	Hs.528836	4.83	0.0038
NPAS2	AI743090	Hs.156832	8.06	0.001001
NPAS3	AL079281	Hs.657892	8.37	0.005381
NPM2	AI016313	Hs.131055	15.91	0.043543
NR1H4	NM_005123	Hs.282735	25.63	0.002325
NR2C1	M21985	Hs.108301	3.43	0.016047
NR2E1	AF220532	Hs.157688	354.22	0.004543
NR2F2	M64497	Hs.657455	15.01	0.014552
NR3C2	NM_000901	Hs.163924	4.87	0.028272
NR4A3	NM_006981	Hs.279522	7.21	0.016921
NR5A2	BC027893	Hs.33446	3.58	0.037019
NTRK3	AI140305	Hs.410969	11.22	0.010788
NUFIP1	NM_012345	Hs.525006	3.19	0.00313
OLIG1	AL355743	Hs.56663	41.67	0.003045
OTP	BC001800	Hs.202247	3.66	0.010687
OTX2	NM_021728	Hs.288655	6.68	0.032022
PADI4	AF229067	Hs.522969	18.83	0.005636
PAPD4	AI434509	Hs.418198	4.08	0.017454
PAX2	AW769732	Hs.155644	3.3	0.019616
PAX8	BC001060	Hs.469728	6.87	0.026598
PAXIP1	AI357401	Hs.443881	5.41	0.002475
PCMT1	NM_005389	Hs.279257	3.59	0.000315

(*continued*)

Supplementary Table S1. (Continued)

Gene ID	*Gene identifier*	*UG cluster*	*Fold change*	*p value*
PCNA	NM_002592	Hs.147433	4.74	2.96E-06
PDE8A	NM_002605	Hs.9333	3.24	0.011325
PDE8B	AK023913	Hs.584830	182.56	0.0025
PEG3	NM_015363	Hs.719209	44.98	0.023218
PER2	NM_022817	Hs.58756	15.92	1.09E-07
PER3	NM_016831	Hs.162200	3.06	0.001114
PHOX2A	AI469991	Hs.707879	3.12	0.041952
PHTF1	AW517261	Hs.655824	13.59	2.14E-05
PIAS1	NM_016166	Hs.162458	3.97	0.016942
PIAS4	AK022481	Hs.105779	3.53	0.012471
PITX1	NM_002653	Hs.84136	6.54	0.035271
POLR1D	N32181	Hs.507584	5.87	0.000119
POU2AF1	BC022056	Hs.654525	4.47	0.029639
POU4F1	L20433	Hs.654522	12.75	0.015087
PPARA	BG426657	Hs.103110	7.76	0.000374
PPM1A	NM_021003	Hs.130036	9.48	5.73E-09
PRDM16	NM_022114	Hs.99500	3.69	0.006687
PRDM4	NM_012406	Hs.506655	3.08	0.035952
PRDM5	BC030136	Hs.669312	8.65	0.041362
PRMT1	AF085918	Hs.20521	4.14	0.011829
PRMT2	AI928367	Hs.154163	7.12	0.00637
PROP1	AF076215	Hs.158301	6.55	0.044637
PTGER3	NM_000957	Hs.445000	3.58	0.039988
PTH	NM_000315	Hs.37045	4.01	0.039333
PTTG1	NM_004219	Hs.350966	7.41	3.41E-06
RAB6A	BC003617	Hs.503222	4.67	0.015953
RAD54L2	AU159543	Hs.105399	8.82	0.013932
RBBP5	NM_005057	Hs.519230	4.67	0.023139
RBL2	X76061	Hs.513609	9.04	0.00854
RCAN1	NM_004414	Hs.282326	21.37	7.76E-05
RELA	NM_021975	Hs.502875	3.17	0.039562
RERE	AK096094	Hs.463041	4.48	0.021114
RFC1	BE504689	Hs.507475	3.79	0.037032
RFX6	NM_173560	Hs.352276	6.24	0.044325
RHEBL1	NM_144593	Hs.159013	7.25	0.025008
RNF10	NM_014868	Hs.442798	4.37	0.000176
RNF14	AB022663	Hs.483616	16.89	0.001545
RORA	BC035094	Hs.655155	13.47	0.036045
RORC	AI218580	Hs.256022	4.36	0.038153
RPL26L1	NM_016093	Hs.546390	4.16	0.000262
RPL38	BC000603	Hs.380953	4.21	0.04764
RPS11	BF680255	Hs.433529	3.51	0.048496
RPS6KA5	AF074393	Hs.510225	9.6	0.005491
RPS8	AA976278	Hs.512675	4.88	0.007717
RRN3	AL110238	Hs.460078	3.86	0.015649
RUNX1	D43967	Hs.149261	14.17	0.002855
RUNX1T1	X79990	Hs.368431	48.56	0.016062
RXRG	NM_006917	Hs.26550	4.66	0.037446
S100A1	NM_006271	Hs.515715	3.44	0.035529
SAP30	NM_003864	Hs.591715	7.3	0.000514
SCML1	NM_006746	Hs.109655	34.52	1.93E-06
SEC14L2	AI571796	Hs.335614	7.66	0.015625
SETD8	AI813938	Hs.443735	3.97	0.028496
SFRS17A	BC001620	Hs.522572	3.21	0.01472
SHOX2	NM_006884	Hs.55967	8.1	0.0245
SIN3A	AI433017	Hs.513039	7.21	9.71E-09
SIRT7	NM_016538	Hs.514636	3.66	0.032429
SLA2	AA305476	Hs.713578	5.56	0.003619
SMAD1	AU146891	Hs.604588	8.84	0.003362
SMARCA2	AV725365	Hs.298990	15.42	0.020349
SMARCC2	NM_003075	Hs.236030	3.54	0.040336
SMARCD3	AW026975	Hs.647067	3.73	0.004012

(*continued*)

Supplementary Table S1. (Continued)

Gene ID	*Gene identifier*	*UG cluster*	*Fold change*	*p value*
SMYD2	AW135582	Hs.66170	6.7	0.013551
SNAPC1	NM_003082	Hs.179312	3.88	0.000301
SOX1	NM_005986	Hs.202526	26.31	0.030659
SOX13	AF116571	Hs.201671	3.07	0.000904
SOX15	NM_006942	Hs.95582	21.6	0.000321
SOX18	NM_018419	Hs.8619	3.64	0.041842
SOX30	NM_007017	Hs.716685	286.24	0.002013
SOX5	NM_006940	Hs.657542	3.14	0.018024
SOX7	AI808807	Hs.709543	6.73	0.025222
SP2	D28588	Hs.514276	3.19	0.009484
SPDEF	AI307915	Hs.485158	3.3	0.004024
SUDS3	AK024460	Hs.416630	21.87	0.004211
TACC3	NM_006342	Hs.104019	5.64	0.017536
TADA2L	BC001172	Hs.500066	5.32	0.020987
TAF2	AK001618	Hs.122752	5.37	0.029035
TAF4	AI744029	Hs.18857	5.17	0.002343
TAF4B	AI366784	Hs.369519	21.2	0.017582
TAF5	AW138827	Hs.96103	15.13	0.001655
TAX1BP1	NM_006024	Hs.34576	5.75	0.011349
TBL1Y	AF332222	Hs.664560	3.19	0.015028
TBPL1	NM_004865	Hs.486507	4.15	0.001469
TBR1	NM_006593	Hs.210862	4.01	0.014674
TBX1	AF012130	Hs.173984	3.66	0.031661
TBX20	AJ237589	Hs.404167	5.21	0.013597
TBX3	NM_016569	Hs.714737	9.37	0.005353
TBX5	AW269421	Hs.381715	212.87	0.017223
TBX6	NM_004608	Hs.198301	3.2	0.03287
TCEANC	NM_152634	Hs.222855	9.02	0.010137
TCEB3C	NM_145653	Hs.515381	4.5	0.043816
TCF7	NM_003202	Hs.573153	3.52	0.015075
TCL1A	X82240	Hs.2484	421.02	0.000203
TDRD9	AI989706	Hs.21454	57.41	0.007348
TFAP2B	NM_003221	Hs.33102	22.69	0.001278
TGIF2LY	AF332223	Hs.112148	4.1	0.04231
TLK2	AU151689	Hs.445078	3.45	0.011165
TP63	AF091627	Hs.137569	85.83	0.005082
TRAK1	AI633774	Hs.535711	32.1	0.002952
TSC22D2	NM_014779	Hs.715600	19.29	0.001459
TSHZ1	AF039698	Hs.284217	15.05	0.016956
TSSK6	AF348077	Hs.532711	11.9	0.020932
TULP3	AK024246	Hs.655333	13.41	0.045277
TWIST1	X99268	Hs.66744	166.94	0.012464
UHRF1	AK025578	Hs.108106	22.1	5.12E-07
USP2	AW274034	Hs.524085	22.28	0.018275
VAV1	NM_005428	Hs.116237	3.13	0.026631
VDR	AA454701	Hs.524368	6.44	0.012965
VEZF1	AU146275	Hs.463569	5.45	0.025283
VPS72	NM_005997	Hs.2430	3.32	0.04353
VSX1	AF251033	Hs.274264	3.79	0.044198
WAPAL	D87450	Hs.203099	4.73	0.003541
WHSC2	AF101434	Hs.21771	11.81	0.005111
WNT9A	BE220265	Hs.149504	9.65	0.037812
WT1	S75264	Hs.591980	6.41	0.044741
XRN1	BG534738	Hs.435103	6.4	0.006576
YBX2	NM_015982	Hs.567494	4.06	0.012094
YEATS2	BC032368	Hs.632575	3.89	0.026498
ZBTB17	AW082221	Hs.433764	3.61	0.005148
ZC3H8	AF334161	Hs.418416	3.79	0.040659
ZCCHC6	AW070776	Hs.655162	4.52	0.018594
ZFHX3	NM_006885	Hs.598297	3.02	0.027848
ZHX1	AI123518	Hs.612084	13.14	0.013161
ZHX2	NM_014943	Hs.719079	6.86	0.029497

(*continued*)

Supplementary Table S1. (Continued)

Gene ID	*Gene identifier*	*UG cluster*	*Fold change*	*p value*
ZNF131	BE972394	Hs.535804	3.1	0.005278
ZNF136	NM_003437	Hs.479874	5.1	0.034258
ZNF148	NM_021964	Hs.592591	4.76	0.03178
ZNF155	NM_003445	Hs.502127	13.34	0.031716
ZNF214	NM_013249	Hs.445849	6.18	0.038319
ZNF215	NM_013250	Hs.523457	7.37	1.14E-06
ZNF229	AF192979	Hs.709348	3.24	0.019127
ZNF235	NM_004234	Hs.298089	3.88	0.013727
ZNF25	N32599	Hs.499429	9.37	0.003137
ZNF257	AF070651	Hs.283900	17.01	0.019162
ZNF285A	AW513227	Hs.709428	6.66	0.019309
ZNF343	NM_024325	Hs.516846	6.89	0.010471
ZNF397	AW291411	Hs.591061	5.89	0.011607
ZNF404	AI393706	Hs.76561	6.81	0.038963
ZNF436	AB051497	Hs.293798	11.44	0.024662
ZNF443	BI830259	Hs.631623	5.81	0.01881
ZNF449	AI888786	Hs.28780	5.43	7.86E-05
ZNF479	AF277624	Hs.616660	4.48	0.049942
ZNF506	AI559570	Hs.351906	9.17	0.003976
ZNF529	N62934	Hs.708146	3.33	0.010278
ZNF540	BE466117	Hs.121283	4.27	0.026231
ZNF546	AA130174	Hs.709400	6.84	0.046006
ZNF552	AK023769	Hs.560727	4	0.01283
ZNF555	BF435923	Hs.47712	3.22	0.01978
ZNF556	NM_024967	Hs.287433	11.34	0.049657
ZNF558	AW119060	Hs.659797	3.36	0.038294
ZNF560	NM_152476	Hs.631613	24.42	0.001516
ZNF585A	AA203136	Hs.390568	7.45	0.008089
ZNF599	AI222019	Hs.590961	11.39	0.038477
ZNF610	AA776810	Hs.357663	6.48	0.008189
ZNF641	BF541598	Hs.23492	6.59	0.002412
ZNF677	AK026366	Hs.20506	11.06	0.000993
ZNF689	W80378	Hs.454685	6.57	0.00809
ZNF76	NM_003427	Hs.388024	4.8	0.00648
ZNF786	N30616	Hs.31743	7.13	0.006703
ZNF93	BC020837	Hs.301059	14.29	0.000725

Supplementary Table S2. Rhesus Monkey Putative Candidate Oocyte Reprogramming Factors (CORFs)

Gene ID	*Gene identifier*	*UG cluster*	*Ratio*	p *value*
ABL1	NM_005157	Hs.431048	7.97	0.000136
AFAP1L2	AW138743	Hs.501106	155.48	0.002011
AFF1	BF575588	Hs.480190	60.81	2.37E-05
AHCTF1	AI138934	Hs.300887	4.79	0.000366
ALKBH2	AI865555	Hs.374458	36.39	0.009836
ANKRD49	NM_017704	Hs.29052	20.44	0.002137
AOF1	BE348688	Hs.709336	11.93	0.016487
ARID2	AW104509	Hs.317304	8.17	0.000161
ARID4B	BF058966	Hs.575782	5.94	0.008563
ARIH2	BC000422	Hs.633601	5.2	0.01783
ASCL1	AW950513	Hs.704281	6.65	0.037991
ASCL2	AI393930	Hs.152475	4.91	0.011745
ASF1A	AB028628	Hs.292316	16.75	0.000213
ASF1B	NM_018154	Hs.26516	12.36	0.010311
ASXL1	AI829840	Hs.374043	13.58	0.00965
ASZ1	BC034963	Hs.352412	75.94	8.12E-05
ATF5	BC005174	Hs.9754	9.95	0.015325
ATF7IP2	AV716964	Hs.513343	77.75	0.043632
ATXN1	NM_000332	Hs.434961	5.19	1.81E-05
BACH1	NM_001186	Hs.154276	7.1	0.02418
BANP	NM_017869	Hs.461705	30.03	0.025058
BAZ1A	AA102574	Hs.509140	6.75	0.028695
BCL6B	AB076580	Hs.22575	5.12	0.019288
BCORL1	NM_021946	Hs.496748	11.39	0.032508
BRD4	BF718610	Hs.187763	7.09	0.000345
BRDT	NM_001726	Hs.482520	123.68	0.015027
BRPF1	NM_004634	Hs.1004	20.75	0.016919
C17orf49	AV759602	Hs.511801	13.86	0.002594
C1orf59	BE502436	Hs.7962	324.61	0.002106
C21orf45	NM_018944	Hs.190518	52.69	0.005675
C2orf65	Y12839	Hs.348645	74	3.96E-05
CAMTA1	AF111804	Hs.397705	44.96	0.00292
CAND2	AB014567	Hs.343664	281.69	0.012719
CAPRIN2	AF326778	Hs.234355	4.8	0.018162
CBX2	BE514414	Hs.368410	117.52	0.000834
CCNA1	NM_003914	Hs.417050	18.52	0.002389
CCNE1	AI671049	Hs.244723	43.73	0.001157
CDC45L	NM_003504	Hs.474217	14.63	0.000301
CDK7	L20320	Hs.184298	10.67	0.000325
CDX4	NM_005193	Hs.553488	22.38	0.037579
CDYL	AL050164	Hs.269092	9.85	0.026793
CEBPG	BE622659	Hs.429666	4.8	0.017737
CENPI	BF793446	Hs.348920	11.55	0.000928
CENPQ	NM_018132	Hs.88663	7.17	0.000371
CHAF1A	BF000239	Hs.79018	54.76	0.015053
CHD4	AI761771	Hs.162233	4.71	0.008192
CHD7	AI870918	Hs.20395	174.94	0.025683
CNBP	BF063728	Hs.518249	6.89	0.001063
CNOT6L	AW514857	Hs.592519	30.12	0.000498
CREB5	NM_004904	Hs.437075	4.88	0.035017
CRYM	NM_001888	Hs.924	61.99	0.034099
CSDE1	AA167775	Hs.69855	5.76	0.001114
CSTF2	NM_001325	Hs.132370	5.49	0.012157
CTCFL	NM_080618	Hs.131543	193.66	0.001519
CTDP1	NM_004715	Hs.465490	19.11	0.003461
CUX1	BE046521	Hs.654389	13.93	0.017428
CYLD	AK024212	Hs.578973	5.92	0.030656
CYP2C9	M15331	Hs.282624	13.27	0.008216
CYP3A5	NM_000777	Hs.695915	32.49	0.024635
DAB2IP	AB051530	Hs.522378	77.69	0.005003
DBP	U79283	Hs.414480	4.52	0.028339
DCP2	BE896137	Hs.443875	36.18	0.003064

(*continued*)

Supplementary Table S2. (Continued)

Gene ID	*Gene identifier*	*UG cluster*	*Ratio*	p *value*
DIP2A	BC033718	Hs.189585	30.41	0.025575
DLX6	T65128	Hs.249196	29.13	0.002253
DMRTB1	AI198850	Hs.131654	4.67	0.021338
DNMT1	NM_001379	Hs.202672	12.89	0.000888
DNMT3A	NM_022552	Hs.515840	84.94	0.020524
DPPA3	AI066520	Hs.131358	654.65	3.36E-05
DPPA5	AI365263	Hs.125331	235.34	0.027331
DRD3	NM_000796	Hs.121478	10.36	0.002048
DVL3	U49262	Hs.388116	6.99	0.027624
E2F1	NM_005225	Hs.654393	7.24	0.003169
EDA	AF061193	Hs.105407	6.53	0.042164
EDNRB	NM_003991	Hs.82002	11.75	0.023909
EGR1	AV733950	Hs.326035	7.47	0.014859
EIF1B	NM_005875	Hs.315230	6.52	0.024615
EIF4E3	AI935522	Hs.581355	11.47	0.000628
ELF1	AL559590	Hs.135646	6.11	0.000307
ELF5	AF115403	Hs.11713	65.73	0.029769
EMX1	AW196403	Hs.516090	20.96	0.036375
EPB41L5	AI652872	Hs.654802	30.27	0.041944
ERG	AA296657	Hs.473819	65.6	0.036131
ERI1	AL137679	Hs.20000	7	0.000465
ESR2	AB006589	Hs.660607	6.26	0.030952
ESRRB	AK096020	Hs.435845	13.08	0.029342
FBXO5	AK026197	Hs.520506	10.12	0.003444
FOXE3	NM_012186	Hs.112968	20.27	0.001848
FOXH1	NM_003923	Hs.708365	5.15	0.011397
FOXK2	AI798846	Hs.591140	6.53	0.029617
FOXN4	AF425597	Hs.528316	33.42	0.023576
FOXO1	AW117498	Hs.370666	30.79	0.000427
FOXO3	BE888885	Hs.220950	4.84	0.019727
FOXP4	AI673539	Hs.131436	6.75	0.0067
FOXR1	AA669512	Hs.116679	518.51	3.21E-05
FRZB	NM_001463	Hs.128453	21.21	0.008573
FTSJD2	D43949	Hs.520102	7.66	0.009591
FZD3	NM_017412	Hs.40735	207.21	0.016627
FZD4	NM_012193	Hs.591968	12.72	0.010388
GAS7	BE439987	Hs.462214	51.17	0.000168
GATA4	AV700724	Hs.243987	23.02	0.002759
GATAD2A	NM_017660	Hs.709287	4.85	0.005977
GCM1	AB026493	Hs.28346	26.93	0.007438
GRM5	D60132	Hs.719168	6.93	0.040593
GSG2	AB039834	Hs.534059	11.98	0.000493
GTF2A2	NM_004492	Hs.512934	4.91	0.044354
GTF2B	NM_001514	Hs.481852	6.8	0.003709
H1FOO	NM_153833	Hs.97358	18.04	0.007651
H3F3B	AW138159	Hs.180877	12.42	0.006075
HAND1	NM_004821	Hs.152531	5.05	0.024513
HBP1	AF019214	Hs.162032	5.32	0.0018
HCFC1	AA703045	Hs.83634	12.46	0.029827
HDAC10	AL022328	-	7.78	0.005599
HEXIM2	AI972367	Hs.56382	6.76	0.001711
HEY2	NM_012259	Hs.144287	81.82	0.000142
HHEX	Z21533	Hs.118651	193.39	0.0114
HIC2	AI912206	Hs.632767	8.86	0.012104
HIF3A	AK021881	Hs.420830	50.61	0.014219
HIRIP3	NM_003609	Hs.592046	6.19	0.000434
HIST1H1A	NM_005325	Hs.150206	83.49	0.000565
HIST1H1E	NM_005321	Hs.248133	17.84	0.023504
HJURP	NM_018410	Hs.532968	23.37	6.08E-05
HLF	W60800	Hs.196952	4.98	0.04791
HOXD8	BF057634	Hs.301963	14.69	0.009945
HSF2BP	NM_007031	Hs.406157	1832.78	0.002541

(*continued*)

Supplementary Table S2. (Continued)

Gene ID	*Gene identifier*	*UG cluster*	*Ratio*	p *value*
HSF4	AB029348	Hs.512156	4.54	0.044092
HSPC152	NM_016404	Hs.333579	7.69	0.001975
IKZF1	NM_006060	Hs.488251	4.92	0.002398
IKZF4	BF115531	Hs.553221	5.18	0.002842
ING3	NM_019071	Hs.489811	14.08	0.026072
IRF6	BC014852	Hs.719361	94.22	0.023502
IRF8	AI073984	Hs.137427	644.49	0.001428
IWS1	AW451291	Hs.469879	7.82	0.002721
JARID2	AW445218	Hs.630189	9	0.006468
JAZF1	AI990891	Hs.368944	13.55	0.031216
JDP2	BF109959	Hs.196482	15.21	0.030972
JHDM1D	BE217882	Hs.308710	8.45	0.0006
KCNH5	BC043409	Hs.27043	5.26	0.009909
KCNIP3	AF367022	Hs.437376	5.15	0.023719
KDM3A	AA524505	Hs.557425	14.75	7.04E-06
KDM4A	BC002558	Hs.155983	7.01	0.013588
KDM4D	AI467798	Hs.503598	17.08	0.002535
KDM5C	BE503653	Hs.631768	6.86	0.021104
KDM6B	AI830331	Hs.223678	10.42	0.023441
KLF11	AF028008	Hs.12229	38.39	0.024335
KLF2	NM_016270	Hs.715677	34	0.010672
LASS2	AK001105	Hs.713103	4.61	0.000876
LEF1	AF294627	Hs.719332	45.27	0.004022
LHX8	BC040321	Hs.403934	13	0.039359
LIN28B	AL039884	Hs.23616	186.99	2.02E-05
LMO4	AI824831	Hs.436792	8.99	0.025066
LOC705735	AF230103	Mmu.3517	5.99	0.0278
LOC706737	CN804008	Mmu.1429	6.78	0.010373
LRCH4	NM_002319	Hs.125742	8.29	0.031995
LSM11	AW014922	Hs.631954	11	0.002235
LZTFL1	NM_020347	Hs.30824	7.89	0.010814
MAEL	AA446073	Hs.651245	206.2	0.000104
MAZ	AI318120	Hs.23650	6.03	0.011023
MBD2	AI827820	Hs.25674	1097.44	0.003356
MBTD1	AL133577	Hs.656803	4.48	0.041026
MED12L	AF388364	Hs.58561	50.02	0.030953
MED13	AF151055	Hs.282678	5.8	0.003862
MED19	BE781103	Hs.43619	8.9	0.006889
MED20	AK023092	Hs.278434	5.75	0.017758
MED6	BF434383	Hs.497353	5.2	0.012016
MED8	BG230758	Hs.301756	5.67	0.010683
MESP1	AL357535	Hs.447531	207.89	0.025916
MESP2	AL360139	Hs.37311	9.76	0.030075
METTL3	BC001650	Hs.168799	4.63	0.002262
MGA	AU149225	Hs.187569	5.29	0.009866
MKL2	AK093577	Hs.49143	10.88	0.004501
MKRN1	AF117233	Hs.490347	6.94	0.029037
MLL2	AI742164	Hs.120228	11.59	0.029082
MLL3	AK025911	Hs.647120	31.27	0.001437
MLLT1	AW962605	Hs.10095	6.63	0.007381
MLLT10	N64035	Hs.30385	7.18	0.005673
MLLT6	BE677453	Hs.91531	8.37	0.008081
MPHOSPH8	BF678375	Hs.718457	5.32	0.022991
MSI2	AA521410	Hs.658922	46.08	0.037267
MSL3	R10150	Hs.655288	56.46	0.013725
MSX2	D89377	Hs.89404	28.04	0.015681
MTA3	BC004227	Hs.435413	12.21	0.003086
MTERFD1	NM_015942	Hs.308613	7.01	0.005054
MTF1	NM_005955	Hs.471991	23.39	0.0007
MTF2	AI566096	Hs.31016	19.77	0.008512
MXD1	AI188653	Hs.468908	63.56	5.11E-05
MYOCD	AI452798	Hs.567641	14.83	0.0421

(*continued*)

Supplementary Table S2. (Continued)

Gene ID	*Gene identifier*	*UG cluster*	*Ratio*	p *value*
MYST3	AJ251844	-	8.88	0.028587
NANOS1	AW970089	Hs.591918	124.74	2.79E-05
NASP	AW003362	Hs.319334	11.74	0.030982
NCOA3	AI438999	Hs.592142	9.17	0.014894
NCOA6	AF128458	Hs.368971	9.54	0.007692
NEUROG1	NM_006161	Hs.248149	7.56	0.001295
NFATC2	U43342	Hs.713650	39.05	0.002192
NFATC3	NM_004555	Hs.632209	12.25	0.000188
NFE2L3	NM_004289	Hs.404741	13.05	0.001385
NFKBIA	AI078167	Hs.81328	33.39	0.005916
NFXL1	AI743731	Hs.646325	10.05	0.004362
NFYC	NM_014223	Hs.233458	5.93	0.000142
NIPBL	AW272262	Hs.481927	17.75	0.009947
NKX3-1	AF249671	Hs.55999	12.12	0.038114
NPAS1	U51628	Hs.79564	194.29	0.007678
NPAT	U58852	Hs.171061	7.62	0.005861
NPM2	AI016313	Hs.131055	131.65	0.006961
NR2C1	M21985	Hs.108301	18.33	0.008423
NR5A2	AF228413	Hs.33446	94.22	8.92E-07
NRL	M81840	Hs.652297	7.83	0.015495
NUFIP1	AW593143	Hs.525006	18.35	0.011497
OLIG1	AL355743	Hs.56663	3545.32	0.005001
ONECUT2	H49805	Hs.194725	29.55	0.047819
OTX1	AI813505	Hs.445340	6.24	0.020738
OTX2	BE779765	Hs.288655	2949.14	0.005881
OVOL1	AA588400	Hs.134434	21.81	0.011979
PABPN1	BF675004	Hs.707712	7.25	0.032429
PAPD4	AI434509	Hs.418198	4.69	0.014726
PAPD5	AU146704	Hs.514342	7.91	0.002885
PAPOLA	AV683473	Hs.719187	16.15	0.005373
PAX8	NM_013952	Hs.469728	8.09	0.041566
PDE8B	AB085825	Hs.584830	10.52	0.000253
PDLIM1	BC000915	Hs.368525	29.65	0.001411
PEG3	NM_015363	Hs.719209	4.5	0.002366
PGR	AL137566	Hs.32405	150.93	0.045289
PHF12	AL161953	Hs.714975	7.17	0.0341
PIAS4	NM_015897	Hs.105779	29.07	0.004183
PITX1	NM_002653	Hs.84136	356.66	0.003516
PITX3	NM_005029	Hs.137568	4.81	0.04069
PKNOX2	AK023792	Hs.719275	12.23	0.008233
PLA2G1B	NM_000928	Hs.992	214.64	0.018305
PLAG1	NM_002655	Hs.14968	8.37	0.007633
PLAGL2	NM_002657	Hs.154104	6.94	0.001682
POLR1D	N32181	Hs.507584	5.63	0.007052
POLR2A	NM_000937	Hs.270017	9.37	0.02759
POLR2F	AK026327	Hs.436578	4.92	0.015017
POLR2H	U37689	Hs.432574	4.48	0.00719
POLR3E	AK023160	Hs.460298	7.38	0.038259
POU2F1	BF511210	Hs.493649	5.58	0.042384
POU3F1	NM_002699	Hs.1837	156.53	0.033108
POU4F1	MmuSTS.2078.1.S1_at	-	251.56	0.003
POU4F3	NM_002700	Hs.553499	8.92	0.001946
POU5F1	MmuSTS.2285.1.S1_at	-	93.63	0.010468
PPM1A	NM_021003	Hs.130036	4.75	0.021625
PRDM15	AL109788	Hs.473893	15.8	0.024444
PRDM2	AI681013	Hs.371823	12.82	5.97E-05
PRDM6	AF272898	Hs.135118	10.12	0.005436
PREB	AK001976	Hs.279784	6.85	0.008362
PRKD2	AF309082	Hs.466987	19.38	0.013671
PRMT8	NM_019854	Hs.504530	10.19	0.007113
PROX1	AK025453	Hs.585369	11.44	0.026479
PTGER3	AW242315	Hs.445000	19.36	0.033621

(*continued*)

Supplementary Table S2. (Continued)

Gene ID	*Gene identifier*	*UG cluster*	*Ratio*	p *value*
PTTG1	NM_004219	Hs.350966	5.92	0.001665
RAB3B	BC005035	Hs.123072	16.02	0.020596
RAB6A	AI805050	Hs.707804	38.65	0.016504
RBAK	AW138835	Hs.396178	23.56	0.003596
RBBP5	NM_005057	Hs.519230	5.87	0.00325
RBM15	NM_022768	Hs.435947	13.38	0.000136
RCOR1	D31888	Hs.510521	12.04	0.005182
RERE	NM_012102	Hs.463041	10.72	0.003529
RFC3	BC000149	Hs.115474	21.83	0.000533
RFX1	BF507952	Hs.655215	12.32	0.015063
RHEBL1	BC014155	Hs.159013	36.64	0.044465
RIPPLY1	BC007652	Hs.334726	5.64	0.046585
RNF10	NM_014868	Hs.442798	6.41	0.0012
RORA	BC035094	Hs.655155	104.48	0.03739
RPL15	AF279903	Hs.381219	5.25	0.011281
RPS6KA5	AF074393	Hs.510225	89.46	0.008359
RUNX1T1	X79990	Hs.368431	18.25	0.013221
RYBP	NM_012234	Hs.7910	8.2	0.000833
SAP30	BF247098	Hs.591715	6.63	0.017556
SET	AV702810	Hs.436687	46.73	0.000156
SFRP4	AW089415	Hs.658169	37.83	0.000658
SFRS17A	BC001620	Hs.522572	202.94	0.000382
SIN3A	AI433017	Hs.513039	30.13	0.002772
SIN3B	AB014600	Hs.13999	6.02	0.006181
SIVA1	NM_006427	Hs.112058	7.77	0.014483
SIX2	AF332197	Hs.101937	20.48	0.000964
SLBP	NM_006527	Hs.298345	8.24	0.000151
SMAD2	U65019	Hs.12253	5.15	0.000717
SMARCA2	X72889	Hs.298990	11.31	0.040111
SMARCA4	AI684141	Hs.327527	8.64	0.00058
SMARCD1	AI869240	Hs.79335	14.46	0.014809
SNAPC2	NM_003083	Hs.631860	10.41	0.003241
SNAPC4	AK023513	Hs.113265	4.63	0.034515
SNAPC5	BE259395	Hs.30174	13.92	0.024364
SOLH	BF433759	Hs.632219	27.85	0.008641
SOX5	NM_006940	Hs.657542	127.36	0.000127
SUB1	BE784583	Hs.229641	24.31	0.005214
SUDS3	AK024460	Hs.416630	4.91	0.001348
SUV39H2	NM_024670	Hs.554883	9.72	0.020715
TACC3	NM_006342	Hs.104019	17.19	0.012513
TADA2L	BC001172	Hs.500066	4.69	0.02556
TAF4	AI744029	Hs.18857	21.26	0.000797
TAF4B	AI366784	Hs.369519	9.19	0.001867
TAF5	AW138827	Hs.96103	20.55	0.03202
TAF5L	R60550	Hs.270621	5.39	0.030441
TAF8	AF086309	Hs.520122	6.32	0.01387
TBP	NM_003194	Hs.590872	5.88	0.003124
TBX19	NM_005149	Hs.716656	4.94	0.014923
TBX5	BC011028	Hs.381715	14.61	0.021817
TCEA2	NM_003195	Hs.505004	17.23	0.010976
TCEA3	AI675780	Hs.446354	32.47	0.01777
TCEANC	NM_152634	Hs.222855	42.14	6.53E-05
TCF3	M31523	Hs.371282	9.54	0.00823
TEAD2	BE888180	Hs.515534	6.93	0.049037
TESC	NM_017899	Hs.525709	73.9	0.003166
TFEC	NM_012252	Hs.125962	12.03	0.042017
TGIF2LY	AF332223	Hs.112148	27.55	0.016908
TOX4	BE783632	Hs.555910	4.52	0.014419
TP63	NM_003722	Hs.137569	173.59	0.008469
TRAK1	NM_014965	Hs.535711	11.91	0.018708
TRERF1	AJ277276	Hs.485392	10.31	0.018184
TRIM29	NM_012101	Hs.504115	41.65	0.031393

(*continued*)

Supplementary Table S2. (Continued)

Gene ID	*Gene identifier*	*UG cluster*	*Ratio*	p *value*
TRIM66	AI632106	Hs.130836	6.11	0.039553
TRMT61B	NM_017910	Hs.468026	4.65	8.76E-06
TTF1	AI632304	Hs.54780	10.62	0.015087
U2AF2	NM_007279	Hs.528007	6.55	0.01719
UBE2N	BG290646	Hs.524630	8.77	0.000136
UHRF1	AK025578	Hs.108106	4.74	0.011503
UPF1	D86988	Hs.515266	6.61	0.001774
USP2	NM_004205	Hs.524085	514.28	3.36E-05
USP21	AF217979	Hs.8015	8.86	0.03351
USP7	AI160440	Hs.706830	8.47	0.008899
VANGL2	AB033041	Hs.99477	21.85	0.01041
VAV1	NM_005428	Hs.116237	32.29	0.004781
WAPAL	D87450	Hs.203099	5.08	0.003399
WBSCR22	NM_017528	Hs.647063	5.73	0.001649
WHSC1	AI770166	Hs.113876	5.9	0.001203
YBX2	NM_015982	Hs.567494	186.55	0.021388
ZFP36L1	AI344045	Hs.85155	8.75	0.017369
ZKSCAN2	AK026852	Hs.513451	52.78	0.000277
ZMYND11	BC034784	Hs.292265	5.17	0.001031
ZNF12	AF505656	Hs.431471	10.07	0.011053
ZNF131	BE972394	Hs.535804	13.75	0.016666
ZNF141	NM_003441	Hs.654355	4.5	0.045097
ZNF174	NM_003450	Hs.155204	6.19	0.001123
ZNF195	AI476267	Hs.386294	23.31	0.005205
ZNF202	N46430	Hs.112556	7.62	0.048987
ZNF211	NM_006385	Hs.590977	52.9	0.00021
ZNF215	NM_013250	Hs.523457	17.19	0.006708
ZNF227	BF739795	Hs.371335	11.79	0.000159
ZNF235	NM_004234	Hs.298089	4.75	0.004051
ZNF250	BE350026	Hs.532277	9.57	0.000871
ZNF253	NM_021047	Hs.659321	5.86	0.046462
ZNF254	AI983886	Hs.434406	12.99	0.012259
ZNF256	BC001438	Hs.596242	37.63	7.50E-05
ZNF257	AF070651	Hs.283900	336.34	0.003157
ZNF26	NM_019591	Hs.489608	5.24	0.033689
ZNF281	AU150752	Hs.59757	4.82	0.002143
ZNF324	NM_014347	Hs.515660	5.07	0.001532
ZNF354A	NM_005649	Hs.484324	5.8	0.00853
ZNF394	AK022360	Hs.386324	7.14	0.000936
ZNF420	AI339586	Hs.444992	39.61	0.03739
ZNF44	AL137602	Hs.693933	7.44	0.023608
ZNF449	AI888786	Hs.28780	11.26	0.001883
ZNF540	AA013398	Hs.121283	9.57	0.001197
ZNF544	BF510451	Hs.438994	13.21	0.033723
ZNF548	AK057494	Hs.657353	8.08	0.017347
ZNF554	BC000113	Hs.307043	11.86	0.010149
ZNF555	NM_152791	Hs.47712	16.03	0.033708
ZNF571	NM_016536	Hs.590944	17.97	0.001514
ZNF582	BG432829	Hs.244391	4.68	0.002586
ZNF585A	BE550717	Hs.659236	4.89	0.015371
ZNF597	AI825587	Hs.88630	14.18	0.005717
ZNF599	BC033354	Hs.590961	9.04	0.000354
ZNF607	BC005085	Hs.116622	21.91	0.029129
ZNF641	BF541598	Hs.23492	18.34	0.001923
ZNF658	AW874634	Hs.522147	7.36	0.014319
ZNF669	NM_024804	Hs.163754	5.32	0.020289
ZNF671	NM_024833	Hs.180402	9.37	0.0057
ZNF689	W80378	Hs.454685	34.43	0.006791
ZNF708	BF223715	Hs.466296	11.98	0.005103
ZNF747	NM_023931	Hs.592032	5.01	0.009018
ZNF749	BE892698	Hs.695781	9.96	0.008318
ZNF765	BC001610	Hs.433293	14.51	0.019317

(*continued*)

Supplementary Table S2. (Continued)

Gene ID	*Gene identifier*	*UG cluster*	*Ratio*	p *value*
ZNF766	AA081007	Hs.439662	5.05	0.005964
ZNF792	AV758821	Hs.50405	5.75	0.009694
ZNF829	BF439163	Hs.124047	15.22	0.001575
ZNF93	NM_031218	Hs.301059	56.48	0.038554
ZNHIT3	AI131008	Hs.2210	7.86	0.004579
ZRANB2	AF065392	Hs.194718	4.72	0.018793
ZSCAN21	AL136865	Hs.632294	9.03	0.004912
ZSCAN22	BE794668	Hs.388162	5.77	0.004186
ZSCAN23	AL833347	Hs.376873	13.54	0.00651
ZSCAN4	NM_152677	Hs.469663	54.25	0.046847

Supplementary Table S3. Mouse Putative Candidate Oocyte Reprogramming Factors (CORFs)

Gene ID	*Gene identifier*	*UG cluster*	*Ratio*	p *value*
Adnp2	BC024969	Mm.26594	4.68	0.001195
Afap1l2	BG068103	Mm.226284	131.94	0.005781
Ahr	BE989096	Mm.341377	26.75	0.025319
Alx1	BB366930	Mm.19287	10.29	0.013207
Aof1	BM243793	Mm.31259	20.51	0.002424
Apitd1	AU043467	Mm.260893	5.87	0.040013
Arhgef11	BE957000	Mm.287267	3.84	0.010446
Arid2	AK014481	Mm.17166	12.87	0.001748
Arnt	AU022700	Mm.250265	9.21	0.012298
Arntl2	AY014836	Mm.442075	3.16	0.001469
Asf1a	AK007804	Mm.272989	4.82	0.022009
Asf1b	BC003428	Mm.29680	8.75	0.029764
Asxl1	BI648411	Mm.330677	9.6	0.007106
Atf1	NM_007497	Mm.676	5.55	0.004929
Atf2	BM119623	Mm.209903	6.29	0.006742
Atf6	BB129063	Mm.377046	6.78	0.044734
Atf7ip2	AI429259	Mm.108729	17.24	0.015527
Axin2	NM_015732	Mm.71710	22.47	0.004318
Bap1	AK009033	Mm.3779	4.18	0.011875
Baz1b	BE943572	Mm.40331	10.63	0.029781
Bmi1	M64279	Mm.289584	21.59	0.002906
Bnc1	U88064	Mm.243802	34.83	0.003454
Bnc2	BB482899	Mm.190774	13.46	0.000242
Bptf	AA867746	Mm.343986	11.56	0.003348
Brd1	AA930693	Mm.254438	14.45	0.015242
Brd7	NM_012047	Mm.5400	3.2	0.010271
Brd8	AV341197	Mm.45602	13.19	0.038399
Brdt	BG070923	Mm.182836	284.62	0.007165
Brwd1	BM230348	Mm.240871	16.87	0.008162
Btf3l4	AK011367	Mm.379178	4.32	0.000102
C79407	BB540053	Mm.21144	3.57	0.023611
Camta1	BB558154	Mm.318846	40.05	0.037939
Cand1	BB380335	Mm.203965	15.6	0.02748
Caprin2	BE951890	Mm.150568	4.33	0.005106
Casp8ap2	NM_011997	Mm.22279	11.98	0.00021
Cbfa2t3	NM_009824	Mm.194339	4.53	0.010288
Cbx2	BI693188	Mm.14547	5.94	0.014069
Ccar1	AW538049	Mm.196371	3.55	0.000462
Ccdc76	BG085812	Mm.259648	13.54	0.008103
Ccdc79	BG067871	Mm.249775	27.66	0.001083
Ccnl2	AK008585	Mm.23492	6	0.042259
Cdca8	AV307110	Mm.28038	8.99	0.007016
Cdk8	BC025046	Mm.260576	9.36	0.003395
Cdyl	AF081260	Mm.29002	4.78	0.002345
Cebpg	AB012273	Mm.273090	4.6	0.001246
Chd4	BM502696	Mm.333388	11.17	0.000358
Chd7	BB127276	Mm.138792	134.24	0.000567
Chd8	BB409788	Mm.289934	5.28	0.000195
Clock	BB203106	Mm.3552	3.39	0.001001
Cnot2	AA967305	Mm.351553	9.71	0.003154
Cnot4	AI448404	Mm.214525	8.69	0.000743
Cnot6l	BC018506	Mm.28374	21.09	0.012255
Cnot7	BC006021	Mm.272551	13.96	6.24E-06
Creb3l4	BC022605	Mm.299952	19.8	0.044357
Crebbp	BG069466	Mm.132238	9.01	0.00325
Crtc1	BE986758	Mm.227767	3.94	0.016505
Cry1	BG069864	Mm.26237	21.11	0.0031
Crym	NM_016669	Mm.9114	6.11	0.016212
Csrp2bp	C86984	Mm.227925	3.24	0.004005
Ctbp2	BG072903	Mm.246240	3.55	0.000621
Ctcf	BB836888	Mm.269474	6.32	0.045165
Ctnnbip1	BF457754	Mm.299735	4.4	0.016796

(*continued*)

Supplementary Table S3. (Continued)

Gene ID	*Gene identifier*	*UG cluster*	*Ratio*	p *value*
Dcp1a	BG069232	Mm.28733	69.15	0.038137
Dedd	AK006814	Mm.270139	3.24	9.93E-05
Dip2b	BB795504	Mm.243658	4.12	0.004202
Dmrtc1a	AK014934	Mm.29672	4.83	0.001346
Dnajb6	AK005680	Mm.290110	9.68	0.00648
Dnajc1	NM_007869	Mm.246674	3.02	0.022831
Dnmt1	BB116018	Mm.128580	11.03	0.019468
Dnmt3a	BB795491	Mm.5001	74.05	0.007655
Dnmt3b	NM_010068	Mm.89772	15.95	0.019794
Dnmt3l	AF220524	Mm.13433	9.76	0.018424
Dpf1	AW553317	Mm.101885	3.97	0.019418
Dppa2	AK010743	Mm.27857	71.29	0.045383
Dppa3	AY082485	Mm.27982	112.33	0.011139
Dppa5a	NM_025274	Mm.139314	3.32	0.027336
Dpy30	BC002240	Mm.28536	4.3	0.035017
E2f1	NM_007891	Mm.18036	11.99	0.003049
E2f2	BB543028	Mm.307932	83.03	0.006327
E2f5	BC003220	Mm.153415	21.07	0.001358
Eed	U97675	Mm.380914	6.49	0.000925
Efcab6	AK016516	Mm.196288	8.41	0.008019
Egln1	BE995700	Mm.140619	7.21	0.001585
Ehf	BC008249	Mm.10724	320.79	0.014531
Elf5	BC012424	Mm.20888	4.32	0.012088
Ell	BB139475	Mm.271973	6.1	0.003537
Ell3	BI660702	Mm.330522	8.2	0.01571
Elof1	BC024488	Mm.29801	20.37	0.006257
Ep400	AU023439	Mm.270487	14.5	0.000305
Erg	AV329219	Mm.164531	119.46	0.001123
Ern1	BG075179	Mm.340943	58.88	0.001795
Esrrg	BM120846	Mm.89989	23.25	0.043777
Etv1	NM_007960	Mm.4866	4.83	0.001164
Eya1	BB760085	Mm.250185	7.09	0.002376
Eya3	BB428881	Mm.227733	3.32	0.039402
Eya4	BB476944	Mm.332128	6.38	0.0349
Ezh1	NM_007970	Mm.5027	8.33	0.026131
Ezh2	NM_007971	Mm.246688	17.11	0.000302
Fam175a	AK014420	Mm.221269	3.35	0.041077
Figla	NM_012013	Mm.8024	3.71	0.040215
Foxj3	BM240405	Mm.259227	19.48	0.021178
Foxk1	BB794583	Mm.24214	6.43	0.018354
Foxk2	BM206907	Mm.209750	4.49	0.042737
Foxn3	BM196962	Mm.341972	9.4	0.012734
Foxo1	AW121569	Mm.29891	25.54	0.028746
Foxo3	NM_019740	Mm.338613	11.58	0.000838
Foxp2	AV322952	Mm.332919	3.06	0.002568
Ftsjd1	BC025546	Mm.275341	8.83	0.000462
Gata3	NM_008091	Mm.313866	119.22	0.000165
Gata4	NM_008092	Mm.247669	4.22	0.037061
Gatad2b	AF411837	Mm.270999	31.3	0.00102
Gbx2	L39770	Mm.204730	6.36	0.000863
Gcm2	AF081556	Mm.1399	18.8	0.001656
Gli2	AW546128	Mm.273292	3.11	0.017472
Gmcl1	AF163665	Mm.321452	6.41	0.025595
Gmeb1	BM935323	Mm.103489	4.4	0.00118
Gmnn	NM_020567	Mm.12239	3.71	0.012029
Gpbp1	BE912643	Mm.57286	3.9	0.007456
Grhl1	BC013080	Mm.263068	457.5	0.019777
Gsg2	BE457839	Mm.42045	15.14	0.001594
Gtf2a1	BI689897	Mm.275728	8.3	0.002376
Gtf2a1l	NM_023630	Mm.61330	23.11	0.002396
Gtf2b	BC016637	Mm.271756	12.39	2.07E-06
Gtf3c2	AV297256	Mm.271923	3.85	0.002939

(*continued*)

Supplementary Table S3. (Continued)

Gene ID	*Gene identifier*	*UG cluster*	*Ratio*	p *value*
Gzf1	AV231413	Mm.136913	4.1	0.006587
H1foo	NM_138311	Mm.21899	482.95	0.036366
Hdac6	NM_010413	Mm.29854	3.46	0.011104
Hdac9	BB750646	Mm.310551	226.99	0.00256
Hells	NM_008234	Mm.57223	3.88	0.003441
Hhex	AK014111	Mm.33896	7.38	0.006713
Hic2	BB292220	Mm.261602	17.58	0.019234
Hif3a	C87687	Mm.135110	69.55	0.02542
Hipk2	AK016742	Mm.23790	6.76	0.02285
Hivep1	NM_007772	Mm.4808	4.86	0.003348
Hlcs	AB066227	Mm.30921	5.07	0.028782
Hmg20a	NM_025812	Mm.150856	5.01	0.022216
Hnf1b	AB008174	Mm.7226	4.58	0.036009
Hnmt	NM_080462	Mm.33120	105.3	0.013629
Hoxa7	NM_010455	Mm.294826	4.55	0.005396
Hsf2bp	AK016553	Mm.75856	34.03	0.007395
Hsf5	BG075885	Mm.390371	6.46	0.009743
Huwe1	BM248615	Mm.27372	13.67	0.001159
Ikzf2	NM_011770	Mm.106343	11.77	0.000359
Ikzf4	BG071647	Mm.358648	459.05	0.002234
Ilf3	NM_010561	Mm.440026	15.71	0.005163
Ing1	BC016573	Mm.25709	7.71	8.50E-05
Ing3	BB020556	Mm.39999	13.21	0.004807
Ino80	BM238259	Mm.330496	7.65	0.001432
Irf8	BG069095	Mm.334861	20.13	0.001452
Jarid2	NM_021878	Mm.25059	21.17	0.004008
Jhdm1d	BG067970	Mm.293175	16.94	0.003536
Kcnh1	BM120185	Mm.4489	18.59	0.000517
Kdm1	AK007763	Mm.28540	3.29	0.009208
Kdm2b	AF176524	Mm.86406	4.33	0.006101
Kdm5b	BB361206	Mm.28995	3.21	0.014655
Kdm5c	BB376389	Mm.142655	3.64	0.006948
Kdm6a	AJ002730	Mm.257498	15.63	0.00586
Kdm6b	BG228765	Mm.261201	16.75	2.09E-05
Khsrp	BB332580	Mm.34296	3.69	0.009369
Klf11	BB137387	Mm.9616	3.35	0.006963
Klf17	AU022735	Mm.3848	445.92	0.011848
Kpna2	NM_010655	Mm.12508	4.98	0.02677
L3mbtl3	BB022070	Mm.338439	5.26	0.000662
Lass5	AY029533	Mm.390821	5.02	0.000874
Lbx1	BB248430	Mm.116815	8.46	0.033968
Lef1	AV156352	Mm.255219	6.91	0.027006
Lhx2	NM_010710	Mm.142856	32.18	0.024023
Lhx8	D49658	Mm.15530	25.91	0.045533
Lin28	BB706377	Mm.302567	231.01	0.003235
Lin54	BG073348	Mm.212568	5.7	0.000221
Lmo1	NM_057173	Mm.360145	25.94	0.018273
Lpin2	AK021389	Mm.227924	11.49	0.023615
Lrch4	BC012525	Mm.200763	37.06	0.001293
Lrrfip1	BG069059	Mm.45039	9.07	0.000137
Lztfl1	NM_033322	Mm.378263	6.44	0.016538
Mael	AV279061	Mm.26189	81.61	0.045031
Maf1	AU042856	Mm.289680	3.1	0.024332
Mapk8	AW909414	Mm.21495	44.56	0.002863
Max	AA617392	Mm.268548	3.23	0.012398
Mbd5	BB086698	Mm.440436	7.56	0.015688
Mbtd1	NM_134012	Mm.210334	23.51	0.017349
Mbtps2	BB264953	Mm.37577	5.24	0.008133
Mcm5	NM_008566	Mm.5048	14.24	0.002723
Mcm7	BB464359	Mm.378965	4.02	0.018174
Mdm4	BQ173933	Mm.472773	48.69	0.000256
Med12l	BG071747	Mm.240059	25.58	0.016864

(*continued*)

Supplementary Table S3. (Continued)

Gene ID	*Gene identifier*	*UG cluster*	*Ratio*	p *value*
Med14	AB019028	Mm.17616	8.21	8.67E-05
Med23	AK013854	Mm.28020	3.22	0.016307
Med31	NM_026068	Mm.159496	12.63	0.025216
Med4	NM_026119	Mm.282888	4.92	0.001734
Med7	NM_025426	Mm.24159	15.58	0.013913
Med8	AI506534	Mm.259567	4.24	0.018895
Meis2	U68384	Mm.247566	11.94	0.020312
Mesp2	NM_008589	Mm.31472	16.03	0.02065
Mett5d1	AK002682	Mm.330451	3.09	0.02079
Mettl3	AW556332	Mm.271759	5.76	0.020874
Mettl4	BB701076	Mm.139146	16.89	0.003527
Mettl7a1	AV171622	Mm.477986	21.55	0.003749
Mier2	BC005748	Mm.334193	7.87	0.021342
Mkrn1	AA717142	Mm.270484	7.56	0.000618
Mlf1ip	BB667813	Mm.22108	4.94	0.002622
Mll2	BG922679	Mm.425955	40.47	0.000119
Mll3	AV297525	Mm.332268	40.95	0.00329
Mllt10	BB353133	Mm.209175	17.84	0.002284
Mllt3	AK011386	Mm.288898	13.67	0.002333
Mlxip	AF265663	Mm.83277	3.31	0.020845
Morf4l1	BM115860	Mm.477470	3.63	0.032867
Mospd1	BC018329	Mm.476015	6.22	0.018488
Msl1	AW495537	Mm.258352	4.3	0.023389
Msl2	BB745314	Mm.436586	34.2	0.009533
Msl3	NM_010832	Mm.475716	7.2	0.004095
Mta3	BC022124	Mm.277668	8.71	0.030631
Mtf1	BE980297	Mm.272397	11.38	0.004056
Musk	U37709	Mm.16148	22.56	0.016678
Mybl1	L35261	Mm.479	3.3	0.04941
Mybl2	AV095095	Mm.4594	9	0.015199
Mycbp2	AW107633	Mm.6478	461.56	0.002968
Mynn	AK019238	Mm.200378	56.66	0.013545
Myt1l	BM116113	Mm.253067	7.68	0.027529
Nap1l3	NM_138742	Mm.477865	9.63	0.002228
Nap1l4	NM_008672	Mm.294625	4.68	0.022026
Nat14	BB702376	Mm.42652	20.69	0.009898
Ncoa1	NM_010881	Mm.301039	3.06	0.000819
Ncoa2	BM234716	Mm.2537	26.1	0.049665
Ncoa3	AI428254	Mm.476883	16.16	0.0114
Neo1	BB350308	Mm.42249	10.98	0.005348
Nfatc2	AF289078	Mm.116802	8.09	0.032137
Nfatc2ip	U76759	Mm.1389	5.83	0.022827
Nfkbiz	AB026551	Mm.247272	5.55	0.001783
Nfxl1	NM_133921	Mm.187453	27.03	0.006861
Nfya	D78642	Mm.4929	6.42	0.000471
Nfyc	BC020117	Mm.435590	3.21	0.009894
Ngdn	BB559925	Mm.21214	6.58	0.007305
Nobox	AY061761	Mm.17715	9.16	0.006981
Npas2	BG070037	Mm.2380	13.36	0.013451
Npas3	BB391772	Mm.247044	10.38	0.036745
Nr2e1	BB280339	Mm.287100	118.25	0.001935
Nr5a2	NM_030676	Mm.16794	26.31	0.006235
Nr6a1	AK007201	Mm.439703	27.42	0.001826
Nsd1	BM945177	Mm.168965	3.54	0.00283
Nsun4	AW701004	Mm.282560	26.14	0.021743
Nsun5	C80273	Mm.281189	3.79	0.002203
Ogt	AF363030	Mm.474838	3.79	0.033663
Onecut1	BG067274	Mm.303355	110.39	0.002802
Ovol1	BC021411	Mm.280225	3.38	0.02566
Papolg	BC019635	Mm.61064	36.57	0.044854
Pbx2	NM_017463	Mm.390957	62.79	0.001471
Pcbd1	NM_025273	Mm.39473	47.68	0.002421

(*continued*)

Supplementary Table S3. (Continued)

Gene ID	*Gene identifier*	*UG cluster*	*Ratio*	p *value*
Pcgf1	BG068910	Mm.12261	7.17	0.015034
Pcgf6	BC016195	Mm.35413	7.9	0.017254
Pcid2	BB309550	Mm.103427	9.36	0.016658
Pdcd7	NM_016688	Mm.476827	17.99	0.024397
Pde8a	BB220000	Mm.458069	3.29	0.019708
Per3	NM_011067	Mm.121361	16.7	0.000105
Phf1	NM_009343	Mm.258953	6.22	0.025406
Phf15	BI663145	Mm.259996	18.43	0.01406
Phf20	BB308157	Mm.427078	8.68	0.000518
Phf8	BB042885	Mm.17156	5.48	0.0303
Phtf2	BM228625	Mm.86410	35.94	0.001047
Pias1	BM246045	Mm.478010	32.76	0.00773
Pias4	BI412631	Mm.34428	5.9	0.016759
Plag1	NM_019969	Mm.331467	42.33	0.021761
Pnn	AV135835	Mm.22347	9.88	0.015623
Pole4	BF577544	Mm.195753	21.09	0.000321
Polr2c	NM_009090	Mm.292492	5.65	0.017569
Pou2f1	X56230	Mm.245261	3.23	0.024733
Pou2f2	X57939	Mm.208700	3.74	0.024982
Pou4f1	BB465134	Mm.246550	143.01	0.006493
Pou5f1	NM_013633	Mm.17031	44.28	0.003049
Ppara	AV282267	Mm.212789	12.41	0.007474
Ppargc1b	NM_133249	Mm.415302	10.21	0.013955
Ppp1r10	BC004771	Mm.29385	13.06	0.007988
Prdm4	AK013393	Mm.25307	3.93	0.045252
Prkcb	BF660388	Mm.207496	6.33	0.017058
Prmt2	NM_133182	Mm.32020	4.64	0.00661
Prpf6	BB085604	Mm.292001	9.41	0.021756
Psip1	NM_133948	Mm.105331	10.38	0.000545
Rb1	NM_009029	Mm.273862	9.24	0.000543
Rbak	BB446066	Mm.320419	3.77	0.007524
Rbbp7	BC003785	Mm.270186	4.91	1.69E-05
Rbm14	BB730281	Mm.276338	5.04	0.013448
Rbm15	AV277021	Mm.27966	3.4	0.040391
Rbm38	NM_019547	Mm.3865	69.16	0.008988
Rfx2	BC004654	Mm.102	17.12	0.01605
Rfx5	BB392192	Mm.24308	17.98	0.038045
Rif1	AK018316	Mm.254530	16.09	0.001253
Rnf141	AV024351	Mm.96867	20.27	0.000163
Rnf2	BC020122	Mm.441344	5.46	0.001589
Rnf20	AW540162	Mm.24765	5.99	9.80E-05
Rnf8	BC021778	Mm.305994	9.13	0.000394
Rnmt	AK015403	Mm.27544	6.24	0.002949
Rps6ka5	BE946999	Mm.220417	8.44	0.021579
Rreb1	BG143502	Mm.132634	14.4	0.023482
Rsc1a1	NM_023544	Mm.478119	7.06	0.019131
Runx1t1	BG072085	Mm.4909	13.89	0.01273
Sall4	BG064756	Mm.434054	1074.28	0.000749
Sap30	NM_021788	Mm.118	40.45	0.005816
Sap30l	BI152383	Mm.340083	3.36	0.017956
Scap	BI412871	Mm.288741	6.61	0.006234
Setd6	AK010304	Mm.261321	4.03	0.030773
Setdb1	AY091600	Mm.477473	29.84	0.005981
Sfmbt1	AV214764	Mm.294662	11.51	0.005824
Sfpq	BF224766	Mm.257276	3.4	0.000905
Shprh	BB539406	Mm.133101	5.66	0.000833
Sin3a	AW553200	Mm.15755	42.43	0.033658
Siva1	AF033112	Mm.289812	4.73	0.01379
Six6os1	BB282393	Mm.242892	3.74	0.048089
Skap1	BG075562	Mm.395840	21.45	0.017905
Smad3	BI646741	Mm.7320	17.94	3.27E-05
Smad4	AK004804	Mm.100399	6.2	0.011286

(*continued*)

Supplementary Table S3. (Continued)

Gene ID	*Gene identifier*	*UG cluster*	*Ratio*	*p value*
Smarcd2	NM_031878	Mm.21772	7.28	0.003483
Smyd1	C78565	Mm.234274	8.23	0.041016
Snapc1	AK012317	Mm.25937	3.11	0.006163
Snw1	C79000	Mm.271174	3.49	0.045683
Sox6	AJ010605	Mm.323365	7.56	2.02E-05
Sox8	AV345303	Mm.258220	3.72	0.013202
Ssbp2	NM_024186	Mm.343095	4.1	0.01757
St18	BB178719	Mm.234612	82.18	0.001635
Stat4	NM_011487	Mm.1550	8.92	0.002174
Stk36	AK007188	Mm.310974	11.4	0.034527
Sufu	AJ308624	Mm.41210	4.33	0.004401
Suv39h2	BB440055	Mm.128273	60.51	0.006916
Suz12	AW536442	Mm.283410	5.55	0.015031
Tada2l	BB440612	Mm.45159	3.08	0.009601
Taf13	NM_025444	Mm.24431	5.85	0.000323
Taf1a	NM_021466	Mm.383556	14.52	0.034871
Taf3	AV316700	Mm.86343	23.59	0.010549
Taf4a	BE632382	Mm.235542	4.71	0.000649
Taf4b	AV373814	Mm.312233	4.18	0.041154
Taf5	AV117817	Mm.301522	21.08	0.001493
Taf7	BB551747	Mm.236009	39.03	0.000208
Taf9b	AW555571	Mm.19440	15.73	0.005007
Tarbp2	BE373492	Mm.291485	3.27	0.041752
Tax1bp1	C85320	Mm.389757	22.44	0.001261
Tbl1xr1	NM_030732	Mm.202966	4.93	0.017565
Tbx19	BG069348	Mm.190649	7.99	0.035397
Tbx4	AV226212	Mm.275336	305.37	0.001024
Tcea3	BC010807	Mm.112	12.36	0.023147
Tcf20	AW552808	Mm.252156	28.99	0.002594
Tcf7	AI323642	Mm.31630	6.36	0.002121
Tcfap2c	BC003778	Mm.3629	89.75	0.004598
Tcfap2e	C88013	Mm.331881	234.79	0.012458
Tcl1	NM_009337	Mm.18154	86.75	0.003363
Tesc	NM_021344	Mm.273285	599.57	0.021338
Timeless	BM230269	Mm.6458	11.21	0.022736
Tlk2	NM_011903	Mm.126976	4.11	0.006536
Top1	BG068053	Mm.217233	7.73	5.02E-05
Trim27	NM_009054	Mm.314056	3.84	0.001735
Trim33	BE915274	Mm.195036	3.71	0.005918
Trp53bp1	AJ414734	Mm.215389	58.21	0.002002
Trp63	NM_011641	Mm.20894	6.03	0.003756
Trps1	NM_032000	Mm.30466	33.89	0.026943
Tsc22d1	AF201285	Mm.153272	6.09	0.000877
Tshz2	AW556161	Mm.315789	11.83	0.000618
Tspyl4	BC017540	Mm.21485	23.04	0.002219
Ttll5	AK009255	Mm.132172	4.37	0.010882
Txnip	AF173681	Mm.410189	23.45	0.000583
Uba3	AW210753	Mm.277626	4.03	0.007187
Ubn1	BB463209	Mm.66356	10.92	0.026559
Ubp1	BB550053	Mm.28052	7.45	0.002779
Uhrf1	BB702754	Mm.42196	8.43	0.002038
Usp2	AI553394	Mm.272770	37.1	0.00202
Usp7	BB354576	Mm.295330	38.12	0.005227
Wapal	BM230523	Mm.27957	5.76	0.011936
Wasl	BF466143	Mm.1574	34.2	0.000314
Wbp7	AK011392	Mm.168688	14.8	8.26E-06
Wdr5	AV095579	Mm.28265	8.84	0.005362
Wdr92	BB017703	Mm.298132	14.15	0.017381
Wwp2	AK004087	Mm.390058	14.4	0.011423
Yap1	NM_009534	Mm.221992	8	0.00177
Ywhab	NM_018753	Mm.477730	8.31	0.003045
Zbtb10	BG068032	Mm.103262	7.21	0.009237

(*continued*)

Supplementary Table S3. (Continued)

Gene ID	*Gene identifier*	*UG cluster*	*Ratio*	p *value*
Zbtb24	BM232143	Mm.258475	3.58	0.017186
Zbtb46	BG073185	Mm.307728	10.34	0.011814
Zbtb8b	BQ175933	Mm.458339	42.99	0.000438
Zc3h8	NM_020594	Mm.11675	7.69	0.019609
Zfp318	BM114753	Mm.439916	6.28	0.003447
Zfp354b	AF184112	Mm.74670	7.68	0.002919
Zfp449	BE993413	Mm.207345	3.72	0.022055
Zfp451	BC024435	Mm.289103	4.7	0.003716
Zfp46	BC006587	Mm.1504	4.62	0.005758
Zfp473	AV277242	Mm.382935	15.19	0.037032
Zfp518	AK018187	Mm.313523	16.37	0.034232
Zfp541	BF018747	Mm.290718	28.93	0.027185
Zfp57	BB549686	Mm.305561	92.65	3.69E-05
Zfp574	BF318389	Mm.455807	6.31	0.010371
Zfp592	BB478535	Mm.29525	12.67	0.013745
Zfp60	NM_009560	Mm.66913	62.31	0.014712
Zfp654	BC027760	Mm.25960	10.32	3.89E-05
Zfp664	BE980596	Mm.138617	5.17	0.01194
Zfp667	BF467246	Mm.276279	3.08	0.024185
Zfp710	AK017247	Mm.290925	15.04	0.026793
Zfp844	NM_023266	Mm.478044	36.76	0.018472
Zfp93	NM_018791	Mm.459431	17.11	0.004769
Zhx3	BB795614	Mm.471766	21.32	0.001546
Zkscan16	BQ175781	Mm.463942	30.29	0.002963
Zkscan5	U62907	Mm.332842	15.6	0.029968
Zkscan6	NM_026107	Mm.340052	6.62	0.000836
Zscan21	AI326272	Mm.2760	21.3	0.004807

Supplementary Table S4. Cross-Specific Putative Candidate Oocyte Reprogramming Factors (CORFs)

CORF	Gene (aka)	*Fold change in expression[a] compared to fibroblasts in:*			Function	Ref.
		Human oocytes	*Rhesus oocytes*	*Mouse oocytes*		
1	*AFAP1L2 (XB130)*	5.54	155.48	131.94	Contributes to SRC-regulated transcriptional activation[1]	1
-	*AOF1 (KDM1B)*	121.98	11.93	20.51	Histone H3K4 demethylase required to establish maternal genomic imprints in oocytes.	2, 3
2	*ARID2 (BAF200)*	19.15	8.17	12.87	Plays a key role in activating gene expression through the PBAF chromatin remodeling complex.	4
3	*ASF1A (CIA)*	6.57	16.75	4.82	Histone chaperone that facilitates histone deposition and histone exchange and removal during nucleosome assembly and disassembly. Cooperates with chromatin assembly factor 1 (CAF-1) which plays a key role in remodeling chromatin in pluripotent embryonic cells[5]	2, 5
4	*ASF1B (CIA-II)*	3.95	12.36	8.75	Histone chaperone that facilitates histone deposition and histone exchange and removal during nucleosome assembly and disassembly. Cooperates with chromatin assembly factor 1 (CAF-1) which plays a key role in remodeling chromatin in pluripotent embryonic cells[5]	2, 5
-	*ASXL1*	13.26	13.58	9.6	Involved in polycomb based repression; anti-transformative	2
5	*BRDT*	7.6	123.68	284.62	Role in the reorganization of acetylated chromatin in germ cells	6
-	*CAMTA1*	5.01	44.96	40.05	Tumor suppressor than inhibits proliferation and induces differentiation	7
-	*CNOT6L*	14.69	30.12	21.09	Involved in degradation of mRNA	
-	*DNMT1*	12.69	12.89	11.03	Maintains DNA methylation	
6	*DPPA3*	369.73	654.65	112.33	Critical component involved with altering chromatin structure in the oocyte	8
7	*DPPA5*	457.32	235	3.32	Pluripotency associated factor	9
8	*ERG*	6.63	65.6	119.46	Transformation-specific transcriptions factors that promotes and maintains leukemia	10
9	*FOXK2*	14.4	6.53	4.49	Promotes activation protein-1 (AP-1)-mediated transcriptional regulation throughout genome	11
-	*FOXO3*	6.97	4.84	11.58	Tumor suppressor that suppresses MYC	12
-	*GATA4*	4.65	23.02	4.22	Induces differentiation towards extraembryonic endoderm	13
-	*GTF2B*	10.48	6.8	12.39	Component of basal transcription complex	2
10	*H1FOO*	318.44	18.04	482.95	The somatic type linker histone H1c is rapidly replaced by H1oo in a donor nucleus transplanted into an oocyte. The greater mobility of H1oo as compared to H1c may contribute to this rapid replacement and increased instability of the embryonic chromatin structure. The rapid replacement of H1c with H1oo may play an important role in nuclear remodeling. The higher-order structure of chromatin *in vivo* is critically dependent on architectural chromatin proteins, with the family of linker histone proteins among the most critical structural determinants. Although somatic cells contain numerous linker histone variants, only one, H1FOO, is present in oocytes. Upon fertilization, H1FOO rapidly populates the introduced paternal genome and replaces sperm-specific histone-like proteins. The same dynamic replacement occurs upon introduction of a nucleus during somatic cell nuclear transfer. Although both histones associate readily with chromatin in nuclei of somatic cells, only	14

(*continued*)

CORF	Gene (aka)	Fold change in expression[a] compared to fibroblasts in: Human oocytes	Rhesus oocytes	Mouse oocytes	Function	Ref.
					H1FOO is capable of correct chromatin association in oocyte nuclei.	
11	*HHEX*	40.15	193.39	7.38	Transcription factor important for embryonic development	2
-	*HIC2*	7.7	8.86	17.58	Transcriptional repressor	2
-	*HSF2BP*	87.35	1832.78	34.03	Modulates heat shock factor (HSF)2 activation	2
12	*ING3*	10.72	14.08	13.21	Component of the NuA4 histone acetyltransferase (HAT) complex, which is involved in transcriptional activation of select genes principally by acetylation of nucleosomal histones H4 and H2A. This modification may both alter nucleosome–DNA interactions and promote interaction of the modified histones with other proteins which positively regulate transcription. This complex may be required for the activation of transcriptional programs associated with oncogene and proto-oncogene-mediated growth induction.	2
-	*IRF8*	58.99	644.49	20.13	Modulates expression of IFN-alpha and IFN-beta-regulated genes	2
13	*KDM6B*	20.85	10.42	16.75	Histone demethylase that specifically demethylates 'Lys-27' of histone H3. Polycomb group (PcG) proteins complex PRC1 recognizes methyl-H3K27 to form repressive chromatin. Therefore KDM6B removes repressive chromatin and opening up chromatin for reprogramming.	15
-	*KLF11 (TIEG2)*	5.96	38.39	3.35	Transcription factor. Represses promoters containing SP1-like binding inhibiting cell growth. Represses transcription of SMAD7, which enhances TGF-beta signaling. Induces apoptosis.	2
14	*LEF1*	60.54	45.27	6.91	Transcriptionally activates MYC and CCND1 expression and enhances cell proliferation	2
-	*LHX8*	132.4	13	25.91	Involved in differentiation	16
-	*LRCH4*	3.86	8.29	37.06	Regulator of the innate immune response	2
-	*MAEL*	218.11	206.2	81.61	Represses transposable elements in the germline	2
-	*MED8*	13.17	5.67	4.24	Component of the general transcriptional mediator complex	2
15	*MLL3*	20.92	31.27	40.95	Methylates 'Lys-4' of histone H3. H3 'Lys-4' methylation represents a specific tag for epigenetic transcriptional activation. Essential in maintaining hematopoietic stem cell state.	17
16	*MSL3*	4.41	56.46	7.2	Component of the MSL complex, which is responsible for the majority of histone H4 acetylation at 'Lys-16' implicated in the formation of higher-order chromatin structure. The incorporation of this modified histone into nucleosomal arrays inhibits the formation of compact 30-nanometer–like fibers and impedes the ability of chromatin to form cross-fiber interactions. H4-K16Ac also inhibits the ability of the adenosine triphosphate–utilizing chromatin assembly and remodeling enzyme ACF to mobilize a mononucleosome, indicating that this single histone modification modulates both higher-order chromatin structure and functional interactions between a nonhistone protein and the chromatin fiber.	18
17	*NCOA3*	4.48	9.17	16.16	Nuclear receptor coactivator that directly binds nuclear receptors and stimulates the transcriptional activities in a hormone-dependent fashion. Plays a central role in creating a multisubunit coactivator	2

(*continued*)

Supplementary Table S4. (Continued)

CORF	*Gene (aka)*	*Fold change in expression*[a] *compared to fibroblasts in:*			*Function*	*Ref.*
		Human oocytes	*Rhesus oocytes*	*Mouse oocytes*		
					complex, which probably acts via remodeling of chromatin. Involved in the coactivation of different nuclear receptors, such as for steroids (GR and ER), retinoids (RARs and RXRs), thyroid hormone (TRs), vitamin D3 (VDR), and prostanoids (PPARs). Displays HAT activity. Also involved in the coactivation of the NF-kappa-B pathway via its interaction with the NFKB1 subunit. Interacts with PSMB9.	
18	*NFATC2*	10.37	39.05	8.09	Induces lymphocyte proliferation	19
-	*NFYC*	4.13	5.93	3.21	Corepressor of agonist-bound mineralocorticoid receptor	20
19	*NR5A2*	3.58	94.22	26.31	Transcription factor that can replace OCT4 in reprogramming	21
-	*PIAS4*	3.53	29.07	5.9	Involved in gene silencing	2
20	*POU4F1*	12.75	251.56	143.01	Transcription factor associated with cancer (acute myeloid leukemia)	22
21	*RPS6KA5*	9.6	89.46	8.44	Contributes to gene activation by histone phosphorylation	2
-	*RUNX1T1*	48.56	18.25	13.89	Facilitate transcriptional repression.	2
-	*SAP30*	7.3	6.63	40.45	Capable of transcription repression by N-CoR. Active in deacetylating core histone octamers (when in a complex) but inactive in deacetylating nucleosomal histones	2
-	*SIN3A*	7.21	30.13	42.43	Transcriptional repressor.	2
22	*TADA2L*	5.32	4.69	3.08	Component of the ATAC complex, a complex with HAT activity on histones H3 and H4.	2
23	*TAF4B*	21.2	9.19	4.18	Function as a gene-selective coactivator in certain cells and is involved in the activation of antiapoptotic genes	2
-	*TAF5*	15.13	20.55	21.08	Component of transcription factor IID (TFIID) complex	2
-	*UHRF1*	22.1	4.74	8.43	Links the histone code and DNA methylation to ensure faithful epigenetic memory inheritance	23
-	*USP2*	22.28	514.28	37.1	Involved in myogenic differentiation	2
-	*WAPAL*	4.73	5.08	5.76	Regulator of sister chromatid cohesion in mitosis	2

[a] All fold changes in gene expression represented a statistically significant (p less than sign 0.05) three-fold or greater increase in detected gene expression in the relevant species metaphase II oocytes compared to their adult dermal fibroblasts.

Supplementary References

1. Xu, J., et al. (2007). XB130, a novel adaptor protein for signal transduction. J. Biol. Chem. 282, 16401–16412.
2. The GeneCards Human Gene Database. 2012. Available at www.genecards.org/
3. Ciccone, D.N., et al. (2009). KDM1B is a histone H3K4 demethylase required to establish maternal genomic imprints. Nature 461, 415–418.
4. Xu, F., Flowers, S., and Moran, E. (2012). Essential role of ARID2 protein-containing SWI/SNF complex in tissue-specific gene expression. J. Biol. Chem. 287, 5033–5041.
5. Houlard, M., et al. (2006). CAF-1 is essential for heterochromatin organization in pluripotent embryonic cells. PLoS Genet. 2, e181.
6. Pivot-Pajot, C., et al. (2003). Acetylation-dependent chromatin reorganization by BRDT, a testis-specific bromodomain-containing protein. Mol. Cell. Biol. 23, 5354–5365.
7. Henrich, K.O., et al. (2011). CAMTA1, a 1p36 tumor suppressor candidate, inhibits growth and activates differentiation programs in neuroblastoma cells. Cancer Res. 71, 3142–3151.
8. Liu, Y.J., Nakamura, T., and Nakano, T. (2012). Essential role of DPPA3 for chromatin condensation in mouse oocytogenesis. Biol. Reprod. 86, 40.
9. Kim, S.K., et al. (2005). Identification of developmental pluripotency associated 5 expression in human pluripotent stem cells. Stem Cells 23, 458–462.
10. Tsuzuki, S., Taguchi, O., and Seto, M. (2011). Promotion and maintenance of leukemia by ERG. Blood 117, 3858–3868.
11. Ji, Z., et al. (2012). The forkhead transcription factor FOXK2 promotes AP-1-mediated transcriptional regulation. Mol. Cell. Biol. 32, 385–398.
12. Bouchard, C., et al. (2007). FoxO transcription factors suppress Myc-driven lymphomagenesis via direct activation of Arf. Genes Dev. 21, 2775–2787.
13. Fujikura, J., et al. (2002). Differentiation of embryonic stem cells is induced by GATA factors. Genes Dev. 16, 784–789.
14. Becker, M., et al. (2005). Differential in vivo binding dynamics of somatic and oocyte-specific linker histones in oocytes and during ES cell nuclear transfer. Mol. Biol. Cell 16, 3887–3895.
15. Aoto, T., et al. (2008). Polycomb group protein-associated chromatin is reproduced in post-mitotic G1 phase and is required for S phase progression. J. Biol. Chem. 283, 18905–18915.
16. Manabe, T., et al. (2007). L3/Lhx8 is a pivotal factor for cholinergic differentiation of murine embryonic stem cells. Cell Death Differ. 14, 1080–1085.
17. Jude, C.D., et al. (2007). Unique and independent roles for MLL in adult hematopoietic stem cells and progenitors. Cell Stem Cell 1, 324–337.
18. Shogren-Knaak, M., et al. (2006). Histone H4-K16 acetylation controls chromatin structure and protein interactions. Science 311, 844–847.
19. Caetano, M.S., et al. (2002). NFATC2 transcription factor regulates cell cycle progression during lymphocyte activation: Evidence of its involvement in the control of cyclin gene expression. FASEB J. 16, 1940–1942.
20. Murai-Takeda, A., et al. (2010). NF-YC functions as a corepressor of agonist-bound mineralocorticoid receptor. J. Biol. Chem. 285, 8084–8093.
21. Heng, J.C., et al. (2010). The nuclear receptor Nr5a2 can replace Oct4 in the reprogramming of murine somatic cells to pluripotent cells. Cell Stem Cell 6, 167–174.
22. Fortier, J.M., et al. (2010). POU4F1 is associated with t(8;21) acute myeloid leukemia and contributes directly to its unique transcriptional signature. Leukemia 24, 950–957.
23. Uekawa, A., et al. (2009). Change of epigenetic control of cystathionine beta-synthase gene expression through dietary vitamin B12 is not recovered by methionine supplementation. J. Nutrigenet. Nutrigenomics. 2, 29–36.