Supplementary material

Figure S1. siRNA microarrays analysis flowchart

Figure S2. Box-plot presentation of *ID2* mRNA expression in all tissues and skin tissues present in the *in silico* transcriptomics database (Kilpinen *et al*., Genome Biol. 2008). The box refers to the quartile distribution (25-75%) range, with the median shown as a vertical line (green in all tissues samples, blue in skin). In addition, the 95% range and individual outlier samples are shown.

Figure S3. (**A**) Expression of ID2 in A431 human skin cells, both in the nucleus and the cytoplasm. Cells were stained with fluorescent ID2-specific pAb (Green), DAPI for the nucleus (Blue), and anti-tubulin antibody as internal control and marker of microtubules (Red). These images were extracted from the Human Protein Atlas database (www.proteinatlas.org) (**B**) Sections of frozen breast skin biopsies were stained with ID2 specific-mAb (Red). Scale bar is 100 µm. Contrary to Figure 5A which was obtained from paraffin-embedded skin section, this frozen skin section was thicker and improved monitoring of the stratification of ID2 expression.

Table S1: List of all 220 genes screened with the siRNA microarrays. This excel file summarizes all the siRNAs analyzed by siRNA microarrays. For each siRNA, the HUGO gene symbol, Genbank accession number, Locuslink id and name of to the target gene are reported.

Table S2: Putative regulators of *ID2*. The screen enabled identification of 14 putative repressors of *ID2*. For each gene, the gene symbol, Genbank accession number and siRNA ID number corresponding to the position of the siRNA sequence within the targeted transcript were reported. The rank computed for the most efficient siRNA (capacity to induce the highest *ID2* GFP expression) is indicated. As each siRNA was processed independently, even when they targeted the same gene, the ranking obtained with a second siRNA was also indicated in between brackets.

Table S3: List of the primers used in the study. All primers used in this study are listed in the table.

Figure S1

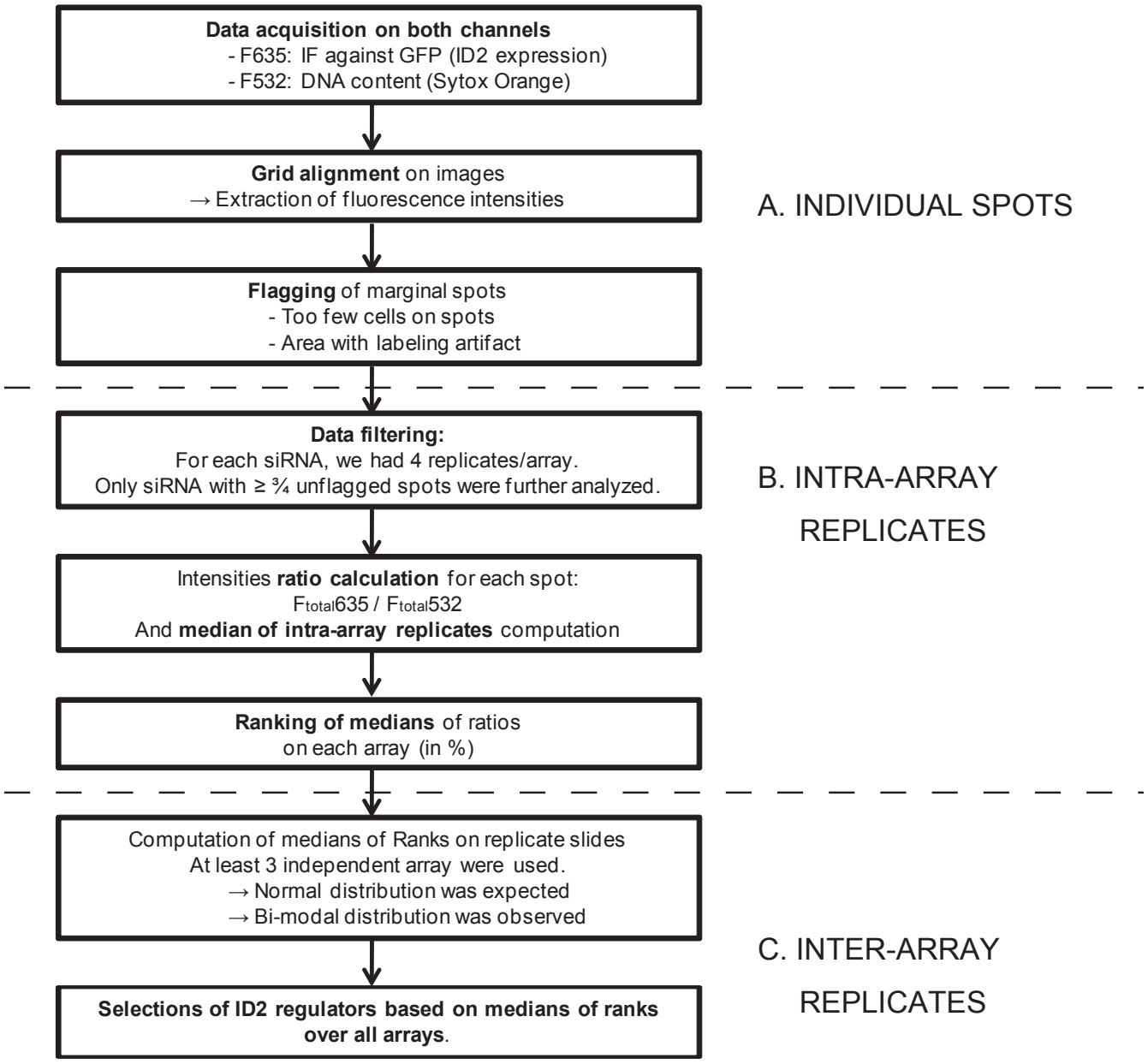

Data acquisition on both channels
- F635: IF against GFP (ID2 expression)
- F532: DNA content (Sytox Orange)
Grid alignment on images
→ Extraction of fluorescence intensities
A. INDIVIDUAL SPOTS
Flagging of marginal spots
- Too few cells on spots
- Area with labeling artifact
Data filtering:
For each siRNA, we had 4 replicates/array.
Only siRNA with ≥ ¾ unflagged spots were further analyzed.
B. INTRA-ARRAY REPLICATES
Intensities ratio calculation for each spot:
Ftotal635 / Ftotal532
And median of intra-array replicates computation
Ranking of medians of ratios
on each array (in %)
Computation of medians of Ranks on replicate slides
At least 3 independent array were used.
→ Normal distribution was expected
→ Bi-modal distribution was observed
C. INTER-ARRAY REPLICATES
Selections of ID2 regulators based on medians of ranks over all arrays.

Figure S2

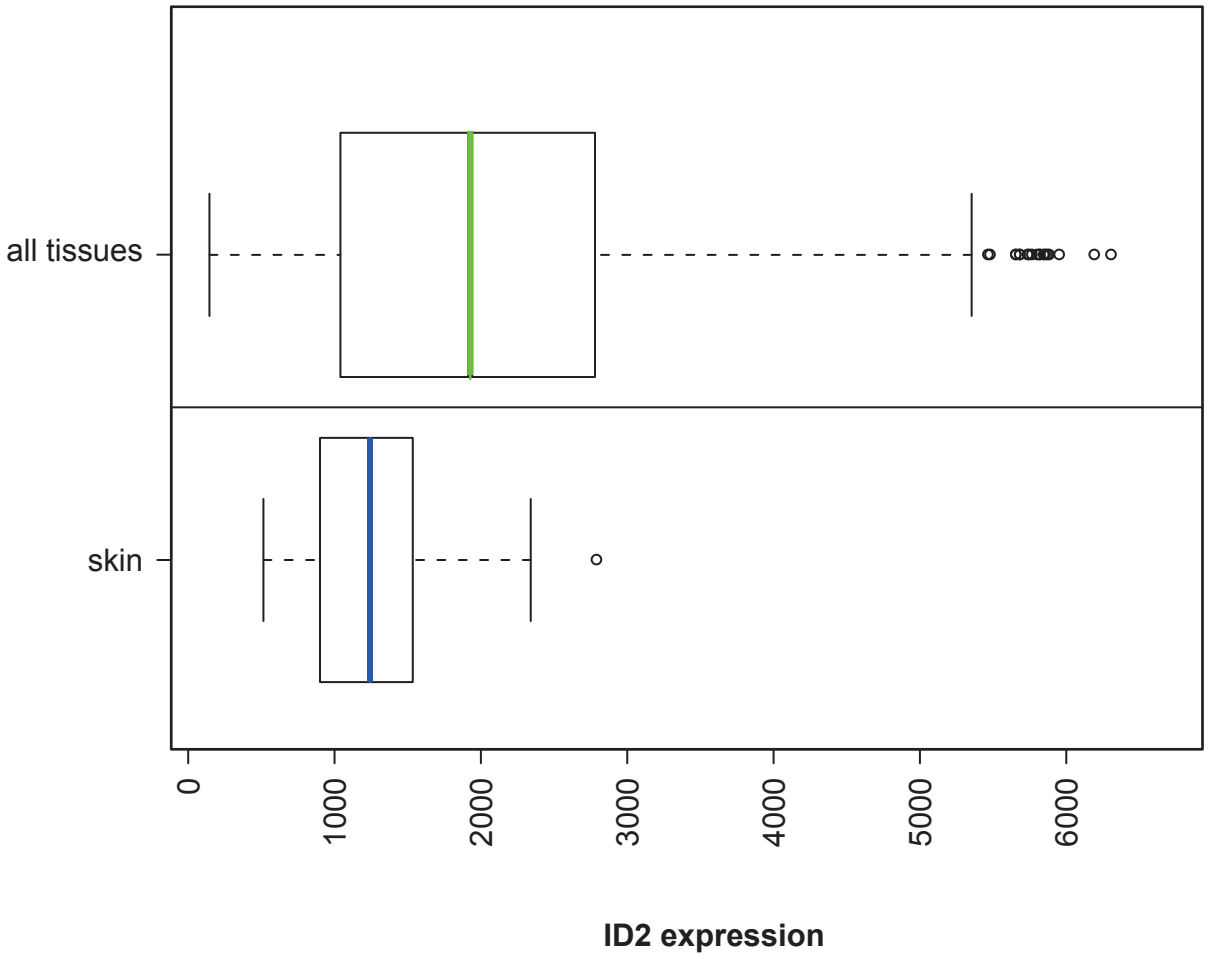
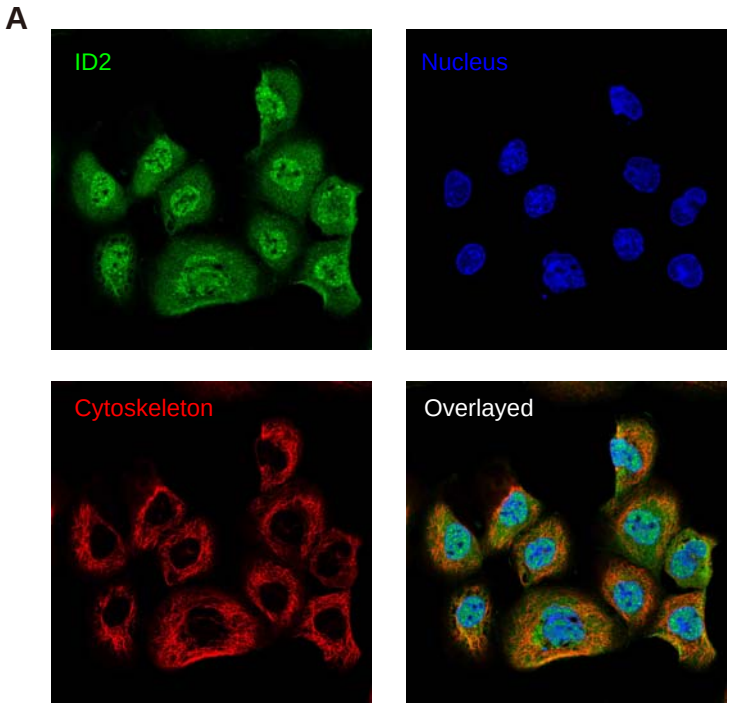

all tissues
skin
0
1000
2000
3000
4000
5000
6000
ID2 expression

Figure S3



	Symbol	Acc	LLID	Name
1	ACAT2	NM_005891	39	Acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)
2	ADAM17	NM_003183	6868	ADAM metallopeptidase domain 17 (tumor necrosis factor, alpha, converting enzyme)
3	ANAPC1	NM_022662	64682	Anaphase promoting complex subunit 1
4	ANAPC10	NM_014885	10393	Anaphase promoting complex subunit 10
5	ANAPC2	NM_013366	29882	Anaphase promoting complex subunit 2
6	ANAPC4	NM_013367	29945	Anaphase promoting complex subunit 4
7	ANAPC5	NM_016237	51433	Anaphase promoting complex subunit 5
8	ANAPC7	NM_016238	51434	Anaphase promoting complex subunit 7
9	ANLN	NM_018685	54443	Anillin, actin binding protein
10	ANP32E	NM_030920	81611	Acidic (leucine-rich) nuclear phosphoprotein 32 family, member E
11	APC	NM_000038	324	Adenomatosis polyposis coli
12	APC2	NM_005883	10297	Adenomatosis polyposis coli 2
13	ARTS-1	NM_016442	51752	Type 1 tumor necrosis factor receptor shedding aminopeptidase regulator
14	ASPM	NM_018136	259266	Asp (abnormal spindle) homolog, microcephaly associated (Drosophila)
15	ATAD2	NM_014109	29028	ATPase family, AAA domain containing 2
16	ATM	NM_000051	472	Ataxia telangiectasia mutated
17	ATR	NM_001184	545	Ataxia telangiectasia and Rad3 related
18	AURKB	NM_004217	9212	Aurora kinase B
19	BARD1	NM_000465	580	BRCA1 associated RING domain 1
20	BIRC5	NM_001168	332	Baculoviral IAP repeat-containing 5 (survivin)
21	BRCA1	NM_007294	672	Breast cancer 1, early onset
22	BRCA2	NM_000059	675	Breast cancer 2, early onset
23	BRMS1	NM_015399	25855	Breast cancer metastasis suppressor 1
24	BRMS1L	NM_032352	84312	Breast cancer metastasis-suppressor 1-like
25	BUB1	NM_004336	699	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)
26	BUB1B	NM_001211	701	BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)
27	BUB3	NM_004725	9184	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)
28	C14orf156	NM_031210	81892	Chromosome 14 open reading frame 156
29	C14orf173	BC006173	64423	Chromosome 14 open reading frame 173
30	CALM1	NM_006888	801	Calmodulin 1 (phosphorylase kinase, delta)
31	CAV1	NM_001753	857	Caveolin 1, caveolae protein, 22kDa
32	CAV2	NM_001233	858	Caveolin 2
33	CCDC86	NM_024098	79080	Coiled-coil domain containing 86
34	CCNA1	NM_003914	8900	Cyclin A1
35	CCNA2	NM_001237	890	Cyclin A2
36	CCNB2	NM_004701	9133	Cyclin B2
37	CCND2	NM_001759	894	Cyclin D2
38	CCND3	NM_001760	896	Cyclin D3
39	CCNF	NM_001761	899	Cyclin F
40	CCNG2	NM_004354	901	Cyclin G2
41	CCNH	NM_001239	902	Cyclin H
42	CCNK	NM_003858	8812	Cyclin K
43	CCNT1	NM_001240	904	Cyclin T1
44	CD320	NM_016579	51293	CD320 molecule
45	CDC14A	NM_003672	8556	CDC14 cell division cycle 14 homolog A (S. cerevisiae)
46	CDC14B	NM_003671	8555	CDC14 cell division cycle 14 homolog B (S. cerevisiae)
47	CDC73	NM_024529	79577	Cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)
48	CDH1	NM_004360	999	Cadherin 1, type 1, E-cadherin (epithelial)
49	CDH19	NM_021153	28513	Cadherin 19, type 2
50	CDH20	NM_031891	28316	Cadherin 20, type 2
51	CDK2AP2	NM_005851	10263	CDK2-associated protein 2
52	CDKN1A	NM_000389	1026	Cyclin-dependent kinase inhibitor 1A (p21, Cip1)
53	CDKN1B	NM_004064	1027	Cyclin-dependent kinase inhibitor 1B (p27, Kip1)
54	CDKN1C	NM_000076	1028	Cyclin-dependent kinase inhibitor 1C (p57, Kip2)
55	CDKN2A	NM_000077	1029	Cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)
56	CDKN2B	NM_004936	1030	Cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)
57	CDKN2C	NM_001262	1031	Cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)
58	CDKN3	NM_005192	1033	Cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)
59	CENPM	NM_024053	79019	Centromere protein M
60	CENPN	NM_018455	55839	Centromere protein N
61	CEP55	NM_018131	55165	Centrosomal protein 55kDa
62	CNKSR1	NM_006314	10256	Connector enhancer of kinase suppressor of Ras 1
63	CYB561D2	NM_007022	11068	Cytochrome b-561 domain containing 2
64	CYLD	NM_015247	1540	Cylindromatosis (turban tumor syndrome)
65	DAPK1	NM_004938	1612	Death-associated protein kinase 1
66	DBF4	NM_006716	10926	DBF4 homolog (S. cerevisiae)
67	DMC1	NM_007068	11144	DMC1 dosage suppressor of mck1 homolog, meiosis-specific homologous recombination (yeast)
68	DPH1	NM_080822	1801	DPH1 homolog (S. cerevisiae)
69	DTL	NM_016448	51514	Denticleless homolog (Drosophila)
70	E2F1	NM_005225	1869	E2F transcription factor 1
71	ECD	NM_007265	11319	Ecdysoneless homolog (Drosophila)
72	FAT	NM_005245	2195	FAT tumor suppressor homolog 1 (Drosophila)
73	FAT2	NM_001447	2196	FAT tumor suppressor homolog 2 (Drosophila)
74	GADD45A	NM_001924	1647	Growth arrest and DNA-damage-inducible, alpha
75	GADD45B	NM_015675	4616	Growth arrest and DNA-damage-inducible, beta
76	GADD45G	NM_006705	10912	Growth arrest and DNA-damage-inducible, gamma
77	GINS2	NM_016095	51659	GINS complex subunit 2 (Psf2 homolog)
78	GLTSCR1	NM_015711	29998	Glioma tumor suppressor candidate region gene 1
79	GLTSCR2	NM_015710	29997	Glioma tumor suppressor candidate region gene 2
80	GMNN	NM_015895	51053	Geminin, DNA replication inhibitor
81	GPS1	NM_004127	2873	G protein pathway suppressor 1
82	GPS2	NM_004489	2874	G protein pathway suppressor 2
83	GSTO1	NM_004832	9446	Glutathione S-transferase omega 1
84	GTSE1	NM_016426	51512	G-2 and S-phase expressed 1
85	HEY1	NM_012258	23462	Hairy/enhancer-of-split related with YRPW motif 1
86	HIC1	NM_006497	3090	Hypermethylated in cancer 1
87	HIF1A	NM_001530	3091	Hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
88	HMGA2	NM_003483	8091	High mobility group AT-hook 2
89	HMGB2	NM_002129	3148	High-mobility group box 2
90	HPRT1	NM_000194	3251	Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)
91	HRASLS	NM_020386	57110	HRAS-like suppressor
92	HRASLS2	NM_017878	54979	HRAS-like suppressor 2
93	HRASLS3	NM_007069	11145	HRAS-like suppressor 3
94	HSP90B1	NM_003299	7184	Heat shock protein 90kDa beta (Grp94), member 1
95	HSPC111	NM_016391	51491	Hypothetical protein HSPC111
96	HUS1	NM_004507	3364	HUS1 checkpoint homolog (S. pombe)
97	INCENP	NM_020238	3619	Inner centromere protein antigens 135/155kDa
98	IPO7	NM_006391	10527	Importin 7
99	ITGA6	NM_000210	3655	Integrin, alpha 6
100	KIAA0101	NM_014736	9768	KIAA0101
101	KIAA1524	NM_020890	57650	KIAA1524
102	KIF11	NM_004523	3832	Kinesin family member 11
103	KIF15	NM_020242	56992	Kinesin family member 15
104	KIF20A	NM_005733	10112	Kinesin family member 20A
105	KIF22	NM_007317	3835	Kinesin family member 22
106	KIF3B	NM_004798	9371	Kinesin family member 3B
107	KIF4A	NM_012310	24137	Kinesin family member 4A
108	KISS1	NM_002256	3814	KiSS-1 metastasis-suppressor
109	KNTC1	NM_014708	9735	Kinetochore associated 1
110	KSR2	NM_173598	283455	Kinase suppressor of ras 2
111	LATS1	NM_004690	9113	LATS, large tumor suppressor, homolog 1 (Drosophila)

112	LATS2	NM_014572	26524	LATS, large tumor suppressor, homolog 2 (Drosophila)
113	LLGL1	NM_004140	3996	Lethal giant larvae homolog 1 (Drosophila)
114	LLGL2	NM_004524	3993	Lethal giant larvae homolog 2 (Drosophila)
115	LUZP4	NM_016383	51213	Leucine zipper protein 4
116	LZTS1	NM_021020	11178	Leucine zipper, putative tumor suppressor 1
117	LZTS2	NM_032429	84445	Leucine zipper, putative tumor suppressor 2
118	MAD2L1	NM_002358	4085	MAD2 mitotic arrest deficient-like 1 (yeast)
119	MAD2L2	NM_006341	10459	MAD2 mitotic arrest deficient-like 2 (yeast)
120	MAPRE1	NM_012325	22919	Microtubule-associated protein, RP/EB family, member 1
121	MAPRE1	NM_012325	22919	Microtubule-associated protein, RP/EB family, member 1
122	MAPRE2	NM_014268	10982	Microtubule-associated protein, RP/EB family, member 2
123	MASTL	NM_032844	84930	Microtubule associated serine/threonine kinase-like
124	MCM2	NM_004526	4171	Minichromosome maintenance complex component 2
125	MELK	NM_014791	9833	Maternal embryonic leucine zipper kinase
126	MKI67	NM_002417	4288	Antigen identified by monoclonal antibody Ki-67
127	MOBKL1B	NM_018221	55233	MOB1, Mps One Binder kinase activator-like 1B (yeast)
128	MRPL23	NM_021134	6150	Mitochondrial ribosomal protein L23
129	MRPS17	NM_015969	51373	Mitochondrial ribosomal protein S17
130	MRPS28	NM_014018	28957	Mitochondrial ribosomal protein S28
131	MRTO4	NM_016183	51154	MRNA turnover 4 homolog (S. cerevisiae)
132	MTHFD1	NM_005956	4522	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase
133	MYH10	NM_005964	4628	Myosin, heavy chain 10, non-muscle
134	MYH9	NM_002473	4627	Myosin, heavy chain 9, non-muscle
135	NBN	NM_002485	4683	Nibrin
136	NCAPG	NM_022346	64151	Non-SMC condensin I complex, subunit G
137	NDC80	NM_006101	10403	NDC80 homolog, kinetochore complex component (S. cerevisiae)
138	NEK2	NM_002497	4751	NIMA (never in mitosis gene a)-related kinase 2
139	NF1	NM_000267	4763	Neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease)
140	NF2	NM_000268	4771	Neurofibromin 2 (bilateral acoustic neuroma)
141	NKTR	NM_005385	4820	Natural killer-tumor recognition sequence
142	NUDCD1	NM_032869	84955	NudC domain containing 1
143	OPCML	NM_002545	4978	Opioid binding protein/cell adhesion molecule-like
144	ORC6L	NM_014321	23594	Origin recognition complex, subunit 6 like (yeast)
145	PA2G4	NM_006191	5036	Proliferation-associated 2G4, 38kDa
146	PAICS	NM_006452	10606	Phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase
147	PDGFRL	NM_006207	5157	Platelet-derived growth factor receptor-like
148	PI4KB	NM_002651	5298	Phosphatidylinositol 4-kinase, catalytic, beta
149	PLK1	NM_005030	5347	Polo-like kinase 1 (Drosophila)
150	PPP1CC	NM_002710	5501	Protein phosphatase 1, catalytic subunit, gamma isoform
151	PPP1R12A	NM_002480	4659	Protein phosphatase 1, regulatory (inhibitor) subunit 12A
152	PRDX4	NM_006406	10549	Peroxiredoxin 4
153	PRDX6	NM_004905	9588	Peroxiredoxin 6
154	PRIM1	NM_000946	5557	Primase, DNA, polypeptide 1 (49kDa)
155	PRKCA	NM_002737	5578	Protein kinase C, alpha
156	PSMB3	NM_002795	5691	Proteasome (prosome, macropain) subunit, beta type, 3
157	PSMB6	NM_002798	5694	Proteasome (prosome, macropain) subunit, beta type, 6
158	PTEN	NM_000314	5728	Phosphatase and tensin homolog (mutated in multiple advanced cancers 1)
159	PTTG1	NM_004219	9232	Pituitary tumor-transforming 1
160	PTTG1IP	NM_004339	754	Pituitary tumor-transforming 1 interacting protein
161	PTTG2	NM_006607	10744	Pituitary tumor-transforming 2
162	RAB6C	NM_032144	84084	RAB6C, member RAS oncogene family
163	RACGAP1	NM_013277	29127	Rac GTPase activating protein 1
164	RAD21	NM_006265	5885	RAD21 homolog (S. pombe)
165	RAD51AP1	NM_006479	10635	RAD51 associated protein 1
166	RAD54L	NM_003579	8438	RAD54-like (S. cerevisiae)
167	RAD9A	NM_004584	5883	RAD9 homolog A (S. pombe)
168	RASSF1	NM_007182	11186	Ras association (RalGDS/AF-6) domain family 1
169	RASSF4	NM_032023	83937	Ras association (RalGDS/AF-6) domain family 4
170	RB1	NM_000321	5925	Retinoblastoma 1 (including osteosarcoma)
171	RB1CC1	NM_014781	9821	RB1-inducible coiled-coil 1
172	RBAK	NM_021163	57786	RB-associated KRAB zinc finger
173	RBBP4	NM_005610	5928	Retinoblastoma binding protein 4
174	RBBP7	NM_002893	5931	Retinoblastoma binding protein 7
175	RBL1	NM_002895	5933	Retinoblastoma-like 1 (p107)
176	RBL2	NM_005611	5934	Retinoblastoma-like 2 (p130)
177	RHOA	NM_001664	387	Ras homolog gene family, member A
178	RIT1	NM_006912	6016	Ras-like without CAAX 1
179	ROCK1	NM_005406	6093	Rho-associated, coiled-coil containing protein kinase 1
180	ROCK2	NM_004850	9475	Rho-associated, coiled-coil containing protein kinase 2
181	ROD1	NM_005156	9991	ROD1 regulator of differentiation 1 (S. pombe)
182	RSU1	NM_012425	6251	Ras suppressor protein 1
183	RTDR1	NM_014433	27156	Rhabdoid tumor deletion region gene 1
184	SACM1L	NM_014016	22908	SAC1 suppressor of actin mutations 1-like (yeast)
185	SEL1L	NM_005065	6400	Sel-1 suppressor of lin-12-like (C. elegans)
186	SOD2	NM_000636	6648	Superoxide dismutase 2, mitochondrial
187	STEAP4	NM_024636	79689	STEAP family member 4
188	SUFU	NM_016169	51684	Suppressor of fused homolog (Drosophila)
189	SUHW1	NM_080740	129025	Suppressor of hairy wing homolog 1 (Drosophila)
190	SUHW2	NM_080764	140883	Suppressor of hairy wing homolog 2 (Drosophila)
191	TP53	NM_000546	7157	Tumor protein p53 (Li-Fraumeni syndrome)
192	TP53BP1	NM_005657	7158	Tumor protein p53 binding protein 1
193	TP53BP2	NM_005426	7159	Tumor protein p53 binding protein, 2
194	TP53I11	NM_006034	9537	Tumor protein p53 inducible protein 11
195	TP53I3	NM_004881	9540	Tumor protein p53 inducible protein 3
196	TP53INP1	NM_033285	94241	Tumor protein p53 inducible nuclear protein 1
197	TP63	NM_003722	8626	Tumor protein p63
198	TP73	NM_005427	7161	Tumor protein p73
199	TRIM59	NM_173084	286827	Tripartite motif-containing 59
200	TSG101	NM_006292	7251	Tumor susceptibility gene 101
201	TSPYL2	NM_022117	64061	TSPY-like 2
202	TSSC1	NM_003310	7260	Tumor suppressing subtransferable candidate 1
203	TSSC4	NM_005706	10078	Tumor suppressing subtransferable candidate 4
204	TUSC2	NM_007275	11334	Tumor suppressor candidate 2
205	TUSC3	NM_006765	7991	Tumor suppressor candidate 3
206	TUSC4	NM_006545	10641	Tumor suppressor candidate 4
207	UBE2T	NM_014176	29089	Ubiquitin-conjugating enzyme E2T (putative)
208	VBP1	NM_003372	7411	Von Hippel-Lindau binding protein 1
209	VHL	NM_000551	7428	Von Hippel-Lindau tumor suppressor
210	WIT1	NM_015855	51352	Wilms tumor upstream neighbor 1
211	WT1	NM_000378	7490	Wilms tumor 1
212	WTAP	NM_004906	9589	Wilms tumor 1 associated protein
213	ZNF197	NM_006991	10168	Zinc finger protein 197
214		NM_015438		Data not found
215		NM_021000		Data not found
216		XM_061871		Data not found
217		XM_290793		Data not found
218		XM_371813		Data not found
219		XM_372031		Data not found
220		XM_374860		Data not found

Table S2.

Target Gene	Accession Number	siRNA ID	Rank
ANAPC4	NM_013367	2201	**4** -(24)
AURKB	NM_004217	495	**1** -(50)
BRMS1L	NM_032352	443	**5** -(53)
BUB1B	NM_001211	357	**5** -(20)
CYLD	NM_015247	2473	**1** -(43)
DTL	NM_016448	4077	**6** -(md)
ECD	NM_007265	1924	**3** -(91)
HIC1	NM_006497	245	**2** -(67)
LATS2	NM_014572	3443	**4** -(18)
LZTS2	NM_032429	2478	**6** -(94)
NBN	NM_002485	990	**5** -(87)
RAD21	NM_006265	1502	**1** -(md)
RIT1	NM_006912	301	**3** -(119)
TP63	NM_003722	2442	**6** -(28)

Table S3. Primers for cloning, qRT-PCR and ChIP-PCR analysis.

Primers for qRT-PCR analysis	
ID2 F	5'- GACCCGATGAGCCTGCTATAC -3'
ID2 R	5'- AATAGTGGGATGCGAGTCCAG -3'
NBN F	5'- TCTGTAACCAACCTGAGTCAAAC -3'
NBN R	5'- TCAAAGTTCGGGAAAAGCCATT -3'
RAD21 F	5'- GGATAAGAAGCTAACCAAAGCCC -3'
RAD21 R	5'- CTCCCAGTAAGAGATGTCCTGAT -3'
18S F	5'- CGATGCGCCGGCGTTATT -3'
18S R	5'- CCTGGTGGTGCCCTTCCGT -3'
pan-P63 F	5'- GACAGGAAGGCGGATGAAGATAG -3'
pan-P63 R	5'- TGTTTCTGAAGTAAGTGCTGGTGC -3'

Primers for RT-PCR analysis	
GAPDH F	5’-GCCTCAAGATCATCAGCAATGC-3’
GAPDH R	5’-CACGATACCAAAGTTGTCATGG-3’
ID2 F	5’-TGACCACCCTCAACACGGATA-3’
ID2 R	5’-CACCGCTTATTCAGCCACACA-3’
ΔNp63 F	5’-GAAGAAAGGACAGCAGCATTGAT-3’
ΔNp63 R	5’-GGGACTGGTGGACGAGGAG-3’
TAp63 F	5’-GGACTGTATCCGCATGCAG-3’
TAp63 R	5’-GAGCTGGGCTGTGCGTAG-3’

Primers for ChIP-PCR analysis	
ID2-2500 F	5’-CTAGCTGGGGCCGTTTGAACT-3’
ID2-2500 R	5’-AAATTGCTTTCGTGGGGGAAA-3’
ID2-800 F	5’-GCCCTGCCTCCTTCTTGAAAA-3’
ID2-800 R	5’-CGCGGGAGGCATTACTGTAAAC-3’
ID2-TSS F	5’-CGCCCGCTCGTCTTGATAGA-3’
ID2-TSS R	5’-GCTGAGCTAGCTGCGCTTGG-3’

Cloning Primers	
pID2-GFP	
Forward:	5'- GCGGGATCCCAGTATCGAAGAGCTGCAATGT -3’
Reverse:	5'- GGGGTACCGGCTCGGCTCAGAATGAA -3’
pID2-2.7K	
Forward:	5'- GGGGTACCCGTTTGAACTTTGGAGGC -3’
Reverse:	5'- GCGGGATCCCGAGGGAAGGCGAGAC -3’
pID2-980	
Forward:	5'- TTTCAAGGGCAGTGTATG -3’
Reverse:	5'- GCGGGATCCCGAGGGAAGGCGAGAC -3’
pID2-329	
Forward:	5'- TCTTCCTCCTCCCTCCT -3’
Reverse:	5'- GCGGGATCCCGAGGGAAGGCGAGAC -3’