Supplementary Table S1: PAX3-FOXO1 candidate interactors

Total number of proteins: 230

Nuclear proteins : 201

Chromatin regulating complexes

Chromatin modifying complexes: 6 Proteins

Protein name	**Gen name**	**Exclusive unique peptide count** **RH4** **FLAG#1**	 **RMS** **FLAG#2**	 **RMS** **FLAG#3**	 **RMS** **FLAG#4**
SIN 3 complex					
Histone deacetylase complex subunit SAP18	SAP18	2	6	6	4
CoRESt complex					
REST corepressor 1	RCOR1	2	2	2	3
PRC1 complex					
E3 ubiquitin-protein ligase RING2	RNF2/RING1B	1	4	2	0
MLL1/MLL complex					
Isoform 14P-18B of Histone-lysine N-methyltransferase MLL	MLL/KMT2A	0	2	2	0
WD repeat-containing protein 5	WDR5	2	4	6	0
Isoform 2 of Menin	MEN1	3	0	2	1

Chromatin remodelling complexes: 22 Proteins

CHD4/NuRD complex					
Isoform 2 of Chromodomain-helicase-DNA-binding protein 4	CHD4	3	21	6	0
Isoform 2 of Lysine-specific histone demethylase 1A	KDM1A/LSD1[a]	3	5	6	8
Histone deacetylase 1	HDAC1[b]	3	3	2	2
Histone deacetylase 2	HDAC2[b]	9	6	7	10
Histone-binding protein RBBP4	RBBP4[b]	10	7	6	7
Histone-binding protein RBBP7	RBBP7[b]	2	1	0	3
Transcriptional repressor p66-alpha	GATAD2A	6	2	0	4
Metastasis-associated protein MTA2	MTA2	8	1	2	6
SWI/SNF complex BAF					
SMARCA4 isoform	SMARCA4/BRG1	6	13	10	0
AT-rich interactive domain-containing protein 1A	ARID1A/BAF250	2	6	1	0
SWI/SNF complex subunit SMARCC1	SMARCC1/BAF155[c]	6	11	8	0
SWI/SNF complex subunit SMARCC2	SMARCC2/BAF170[c]	2	2	0	0
Isoform 2 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1	SMARCD1/BAF60a[c]	2	0	0	4
Isoform 2 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 3	SMARCD3/BAF60c[c]	7	2	0	9
Isoform 2 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	SMARCE1/BAF57[c]	4	2	0	5
Actin-like protein 6A	ACTL6A/BAF53a[c]	7	7	0	0
SWI/SNF complex PBAF					
Isoform 2 of Protein polybromo-1	PBRM1/BAF180	0	5	3	0
ISWI complex NURF					
Uncharacterized protein GN=SMARCA1	SMARCA1/SNF2L	0	9	6	0
ISWI complex ACF					
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5/SNF2H[d]	22	30	26	0
Isoform 2 of Bromodomain adjacent to zinc finger domain protein 1A	BAZ1A/ACF1	0	5	2	0
ISWI complex WICH					
Isoform 2 of Tyrosine-protein kinase BAZ1B	BAZ1B/WSTF[e]	4	8	13	0
ISWI complex NoRC					
Isoform 1 of Bromodomain adjacent to zinc finger domain protein 2A	BAZ2A/Tip5	5	5	1	0

[a] also associates with the CoREST complex

[b] are also associated with RCOR1 or SAP18 in the SIN3 or CoREST complex

[c] are also associated with BAF180 to form the PBAF complex

[d] SNF2H also associates with BAZ2A to form the NoRC complex

[e] also associates with BRG1 to form the WINAC complex

Transcriptional Regulation: 62 Proteins

Transcription factor A, mitochondrial	TFAM	1	10	5	2
C-terminal-binding protein 1	CTBP1	9	4	7	8
Isoform 2 of C-terminal-binding protein 2	CTBP2	6	2	5	7
Zinc finger protein 326	ZNF326	6	12	8	13
Zinc finger protein 148	ZNF148	4	12	5	2
Isoform 2 of Zinc finger protein 384	ZNF384	3	4	1	5
Zinc finger protein 638	ZNF638	3	14	0	0
Zinc finger protein 281	ZNF281	2	3	1	0
Prospero homeobox protein 1	PROX1	21	4	7	14
Nuclear receptor coactivator 5	NCOA5	14	6	6	11
Isoform UBF2 of Nucleolar transcription factor 1	UBTF	18	7	4	5
Isoform 2 of Transcription factor AP-2-beta	TFAP2B	15	4	8	6
Isoform 2 of DNA-binding protein SATB1	SATB1	7	3	2	4
Putative uncharacterized protein SATB2	SATB2	12	3	2	4
Isoform B of Methyl-CpG-binding protein 2	MECP2	3	4	2	8
Isoform 2 of Nuclear transcription factor Y subunit gamma	NFYC	4	3	4	4
Transcriptional repressor CTCF	CTCF	4	6	2	2
SAFB-like transcription modulator	SLTM	2	14	4	0
Transcription factor AP-1	JUN	4	8	3	0
Transcription factor MafG	MAFG	1	8	2	2
Zinc finger RNA-binding protein	ZFR	4	9	6	0
Isoform 2 of Homeobox-containing protein 1	HMBOX1	3	3	1	5
Nuclear factor interleukin-3-regulated protein	NFIL3	8	0	2	2
Zinc finger protein ubi-d4	DPF2	2	2	0	6
Transcriptional enhancer factor TEF-1	TEAD1	0	3	2	3
Isoform 2 of Chromodomain-helicase-DNA-binding protein 1	CHD1	2	6	4	0
Chromodomain-helicase-DNA-binding protein 7	CHD7	13	35	0	0
Isoform 2 of Protein ELYS	AHCTF1	0	27	13	0
MHC class II regulatory factor RFX1	RFX1	1	12	10	0
Isoform 1 of RNA-binding protein 14	RBM14	0	0	11	11
Pinin	PNN	2	18	0	0
Isoform 2 of Zinc finger homeobox protein 4	ZFHX4	0	18	5	0
MICOS complex subunit MIC19	CHCHD3	0	8	6	0
Helix-loop-helix transcription factor 4 isoform c	TCF12	0	0	3	10
Actin-like protein 6A	ACTL6A	7	7	0	0
Cyclic AMP-dependent transcription factor ATF-3	ATF3	0	6	3	1
Isoform 1 of Core-binding factor subunit beta	CBFB	0	0	6	3
Isoform 2 of Ubinuclein-1	UBN1	1	6	6	0
Activity-dependent neuroprotector homeobox protein	ADNP	1	7	4	0
Isoform PTX2C of Pituitary homeobox 2	PITX2	0	3	4	0
Isoform 2 of ATP-binding cassette sub-family F member 1	ABCF1	4	0	0	3
Transcription factor AP-4	TFAP4	1	4	3	0
Isoform AML-1G of Runt-related transcription factor 1	RUNX1	2	6	10	6
Isoform 3 of Runt-related transcription factor 2	RUNX2	0	1	4	2
Myoblast determination protein 1	MYOD1	1	4	4	0
Myogenin	MYOG	2	5	4	0
Zinc finger E-box-binding homeobox 1	ZEB1	0	5	4	0
Zinc finger E-box-binding homeobox 2	ZEB2	2	4	1	0
Isoform 1 of Suppressor of fused homolog	SUFU	0	0	3	5
Isoform 1 of General transcription factor 3C polypeptide 5	GTF3C5	1	0	3	4
Homeobox protein SIX1	SIX1	0	4	3	0
Zinc finger and BTB domain-containing protein 7A	ZBTB7A	2	0	0	3
CREB-binding protein	CREBBP	0	4	4	0
Teashirt homolog 3	TSHZ3	0	2	5	0
Basonuclin 2	BNC2	0	3	3	0
Nascent polypeptide-associated complex subunit alpha	NACA	0	3	2	0

Isoform 2 of Protein CBFA2T2	CBFA2T2	2	0	0	2
Isoform 1 of Core histone macro-H2A.1	H2AFY	6	7	6	3
Histone H2A.Z	H2AFZ	3	3	3	1
Histone H2A type 2-B	HIST2H2AB	4	3	2	1
Isoform Short of Protein HIRA	HIRA	14	6	3	3
Histone chaperone ASF1B	ASF1B	0	2	2	0

Enzyme: 31 Proteins

Isoform Beta of Zinc finger protein RFP	TRIM27	4	1	3	3
E3 ubiquitin-protein ligase UBR5	UBR5	0	7	6	0
NAD-dependent deacetylase sirtuin-1	SIRT1	8	0	3	1
CAD protein	CAD	5	20	51	0
Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	PPP2CB	2	3	9	0
Isoform 2 of Serine/threonine-protein phosphatase 6 regulatory subunit 3	PPP6R3	8	0	2	0
Isoform 1 of Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A	ANKRD28	6	0	2	0
Aurora kinase B	AURKB	0	2	3	0
Casein kinase II subunit alpha	CSNK2A1	2	0	2	0
Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	PPP2R2A	12	5	13	7
Probable ATP-dependent RNA helicase DDX41	DDX41	4	3	3	4
Probable ATP-dependent RNA helicase DDX27	DDX27	5	3	0	3
ATP-dependent RNA helicase DDX1	DDX1	0	1	7	6
ATP-dependent RNA helicase DDX50	DDX50	3	1	1	5
Nucleolar RNA helicase 2	DDX21	16	6	0	0
Calcineurin-binding protein cabin-1	CABIN1	5	10	4	0
Inactive serine/threonine-protein kinase VRK3	VRK3	1	3	2	5
Isoform 2 of 5'-3' exoribonuclease 2	XRN2	2	1	2	3
Superkiller viralicidic activity 2-like 2	SKIV2L2	2	2	5	0
DNA-directed RNA polymerases I, II, and III subunit RPABC1	POLR2E	0	3	5	1
DNA-directed RNA polymerase	POLR2B	0	9	14	0
DNA ligase 3	LIG3	3	9	0	0
Isoform 3 of Apoptosis-inducing factor 1	AIFM1	2	1	7	5
DNA-directed RNA polymerases I, II, and III subunit RPABC1	POLR2E	0	3	5	1
N-acetyltransferase 10	NAT10	3	3	0	0
Apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	APOBEC3B	0	5	2	0
Transcription termination factor 2	TTF2	5	2	0	0
ATPase family AAA domain-containing protein 2	ATAD2	2	3	0	0
Isoform Complexed of Arginyl-tRNA synthetase, cytoplasmic	RARS	0	0	4	10
Peptidyl-prolyl cis-trans isomerase-like 1	PPIL1	3	3	2	0
Peptidyl-prolyl cis-trans isomerase H	PPIH	0	2	3	0

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Proliferating cell nuclear antigen	PCNA	2	7	10	0
Isoform Beta-1 of DNA topoisomerase 2-beta	TOP2B	13	21	16	0
Replication protein A 70 kDa DNA-binding subunit	RPA1	23	16	15	12
Isoform Short of DNA topoisomerase 3-alpha	TOP3A	11	13	8	7
DNA replication licensing factor MCM5	MCM5	7	5	3	17
Replication protein A 32 kDa subunit	RPA2	2	5	5	0
DNA repair protein XRCC1	XRCC1	0	6	2	3
Isoform 2 of DNA-dependent protein kinase catalytic subunit	PRKDC	63	114	109	0
Structural maintenance of chromosomes protein 5	SMC5	1	15	12	0
Structural maintenance of chromosomes protein 1A	SMC1A	1	13	3	0
Isoform 2 of Tumor suppressor p53-binding protein 1	TP53BP1	0	10	12	0
Melanoma-associated antigen G1	NDNL2	0	9	4	0
Replication factor C subunit 4	RFC4	1	5	3	0
DNA mismatch repair protein Msh2	MSH2	2	4	0	0
RecQ-mediated genome instability protein 2	RMI2	2	2	0	0
Bloom syndrome protein	BLM	2	13	8	0

Cell Cycle: 9

0

E3 SUMO-protein ligase RanBP2	RANBP2	4	76	39	0
Cell division protein kinase 4	CDK4	0	6	7	0
Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase	NOP2	2	6	2	4
Isoform 2 of Mediator of DNA damage checkpoint protein 1	MDC1	7	19	14	0
Isoform 2 of Pogo transposable element with ZNF domain	POGZ	2	8	10	0
MKI67 FHA domain-interacting nucleolar phosphoprotein	MKI67	2	35	0	0
Prohibitin	PHB	1	2	4	0
Borealin	CDCA8	0	2	2	0
Isoform 2 of Protein KIAA1967	KIAA1967	15	7	6	0

Transporter: 7

Nuclear RNA export factor 1	NXF1	5	16	11	9
Importin subunit alpha-1	KPNA1	3	2	7	5
Exportin-1	XPO1	1	4	4	4
THO complex subunit 4	THOC4	2	3	4	0
Importin subunit alpha-3	KPNA3	3	1	3	4
GTP-binding nuclear protein Ran	RAN	0	6	11	0
Isoform 2 of Transportin-1	TNPO1	4	0	1	3

1

Other: 48

Emerin	EMD	2	12	4	0
Kinesin-like protein KIF22	KIF22	7	2	1	5
PHD finger-like domain-containing protein 5A	PHF5A	2	0	2	0
Isoform 2 of Polypyrimidine tract-binding protein 2	PTBP2	5	2	4	4
Isoform 2 of Nuclear mitotic apparatus protein 1	NUMA1	16	72	81	1
14-3-3 protein zeta/delta	YWHAZ	3	5	7	0
DnaJ homolog subfamily A member 2	DNAJA2	3	6	1	3
Tigger transposable element-derived protein 2	TIGD2	0	4	2	4
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	0	5	7	0
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	12	18	14	16
A-kinase anchor protein 8-like	AKAP8L	2	4	5	10
LEM domain-containing protein 2	LEMD2	6	4	5	6
Aladin	AAAS	3	9	9	4
Kanadaptin	SLC4A1AP	2	6	6	2
Isoform 2 of Structural maintenance of chromosomes protein 6	SMC6	2	13	14	0
Transmembrane protein 43	TMEM43	2	7	6	0
U2 small nuclear ribonucleoprotein A'	SNRPA1	4	10	7	0
Coiled-coil domain-containing protein KIAA1826	KIAA1826	9	3	0	4
Isoform 2 of Protein CASC5	CASC5	2	6	2	0
Isoform 2 of Nesprin-3	C14orf49	2	6	1	2
Isoform 2 of Structural maintenance of chromosomes protein 2	SMC2	3	4	2	0
PH-interacting protein	PHIP	2	3	3	0
Isoform 2 of Protein LAS1 homolog	LAS1L	2	2	0	4
Isoform Alpha of Lamina-associated polypeptide 2, isoform alpha	TMPO	0	0	31	37
Isoform 2 of Remodeling and spacing factor 1	RSF1	0	17	9	0
Sickle tail protein homolog	KIAA1217	0	11	10	0
Isoform 2 of SPATS2-like protein	SPATS2L	10	3	0	0
KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	3	4	0	0
Ubinuclein-2	UBN2	3	5	0	0
Barrier-to-autointegration factor	BANF1	2	3	0	1
Isoform 2 of Structural maintenance of chromosomes protein 4	SMC4	1	4	2	0
Isoform Beta of Nucleolar and coiled-body phosphoprotein 1	NOLC1	0	5	3	1
DDB1- and CUL4-associated factor 7	DCAF7	0	4	5	0
DnaJ homolog subfamily B member 6	DNAJB6	0	3	4	0
Protein Red	IK	3	1	1	3

Nucleolar GTP-binding protein 1	GTPBP4	0	2	0	4
DNA-directed RNA polymerase II subunit RPB3	POLR2C	0	6	4	0
Protein Wiz	WIZ	2	3	0	0
PHD finger protein 14	PHF14	1	4	2	0
Glutamate-rich WD repeat-containing protein 1	GRWD1	1	0	3	2
Unc-84 homolog A (C. elegans)	UNC84A	2	4	0	0
AT-hook DNA-binding motif-containing protein 1	AHDC1	0	3	3	0
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	0	2	2	0
COP9 signalosome complex subunit 4	COPS4	3	0	3	0
Isoform 1 of Non-structural maintenance of chromosomes element 4 homolog A	NSMCE4A	0	0	2	3
WD repeat-containing protein 18	WDR18	2	0	2	0
Isoform 2 of Replication factor C subunit 1	RFC1	0	3	2	0
Eukaryotic translation initiation factor 6	EIF6	0	2	3	0

Transcriptional Regulation:	**63**
Enzyme:	**31**
Chromatin Modifying complexes	**27**
DNA Replication/Repair:	**16**
Cell Cycle:	**9**
Transporter:	**7**
Other:	**48**
Total	**201**

Proteins with exclusively non nuclear localisation: 29

Enzyme: 18

cAMP-dependent protein kinase type I-alpha regulatory subunit	PRKAR1A	3	5	3	4
Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B delta isoform	PPP2R2D	2	0	4	0
Glutaminyl-tRNA synthetase	QARS	0	4	3	13
Bifunctional aminoacyl-tRNA synthetase	EPRS	3	9	5	0
Isoleucyl-tRNA synthetase, cytoplasmic	IARS	3	10	7	0
Methionyl-tRNA synthetase, cytoplasmic	MARS	1	2	5	8
Chromosome 6 open reading frame 150	C6orf150	9	2	1	2
Fatty acid synthase	FASN	0	8	20	0
Leucyl-tRNA synthetase, cytoplasmic	LARS	1	10	13	0
Isoform Mitochondrial of Lysyl-tRNA synthetase	KARS	1	1	2	6
Multifunctional protein ADE2	PAICS	2	1	6	1
Isoform 2 of ATPase family AAA domain-containing protein 2B	ATAD2B	0	6	2	0
Hydroxymethylglutaryl-CoA synthase, cytoplasmic	HMGCS1	1	3	3	1
Vesicle-fusing ATPase	NSF	0	0	3	2
L-lactate dehydrogenase	LDHA	0	2	4	0
Isoform 2 of Putative ATP-dependent RNA helicase DHX30	DHX30	7	5	13	0
Isoform 2 of Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	13	9	46	0
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	3	1	4	2

Other: 11

Prolow-density lipoprotein receptor-related protein 1	LRP1	0	34	33	2
Charged multivesicular body protein 4b	CHMP4B	2	5	5	0
DnaJ homolog subfamily A member 1	DNAJA1	8	5	10	5
Programmed cell death 6-interacting protein	PDCD6IP	2	4	3	2
BAG family molecular chaperone regulator 2	BAG2	0	3	8	2
Isoform Short of 14-3-3 protein beta/alpha	YWHAB	2	6	8	0
DnaJ homolog subfamily C member 9	DNAJC9	1	9	10	0
Isoform 2 of Structural maintenance of chromosomes flexible hinge domain-containing protein 1	SMCHD1	0	3	4	0
Ribonuclease inhibitor	RNH1	1	1	3	3
14-3-3 protein gamma	YWHAG	1	3	5	0
Elongation factor 1-beta	EEF1B2	0	2	2	0

Enzyme:	**18**
Other:	**11**
Total:	**29**

Supplementary Table S2: Custom siRNA Library

RefSeq Accession Number	Gene Symbol	Full Gene Name	siRNA ID	Exon(s) Targeted	Sense siRNA Sequence	Antisense siRNA Sequence
NM_006015	ARID1A	AT rich interactive domain 1A (SWI-like)	s15784	11,11	GGAAACCUCUGGACCUCUAtt	UAGAGGUCCAGAGGUUUCCta
NM_006015	ARID1A	AT rich interactive domain 1A (SWI-like)	s15785	20,20	CGGUAUCACCGUUGAUGAAtt	UUCAUCAACGGUGAUACCGag
NM_006015	ARID1A	AT rich interactive domain 1A (SWI-like)	s15786	9,9	GGACAAGGGAUUAAUAGUAtt	UACUAUUAAUCCCUUGUCCat
NM_032408	BAZ1B	bromodomain adjacent to zinc finger domain, 1B	s17208	Not Determined	GAUCGAAACCAUAAUAGAUtt	AUCUAUUAUGGUUUCGAUCtg
NM_032408	BAZ1B	bromodomain adjacent to zinc finger domain, 1B	s17209	Not Determined	CCUUCGUAGUGAUCUCAUUtt	AAUGAGAUCACUACGAAGGaa
NM_032408	BAZ1B	bromodomain adjacent to zinc finger domain, 1B	s17210	Not Determined	CCUCAUUGCAUACUACAAAtt	UUUGUAGUAUGCAAUGAGGtg
NM_013449	BAZ2A	bromodomain adjacent to zinc finger domain, 2A	s22056	24	GAGAUAUCAUAUGAGAUCAtt	UGAUCUCAUAUGAUAUCUCtg
NM_013449	BAZ2A	bromodomain adjacent to zinc finger domain, 2A	s22057	28	GCAUCAUCAAAAAUCCUAUtt	AUAGGAUUUUUGAUGAUGCgc
NM_013449	BAZ2A	bromodomain adjacent to zinc finger domain, 2A	s22058	20	CAAGCACUCUGGUUUAACAtt	UGUUAAACCAGAGUGCUUGag
NM_000057	BLM	Bloom syndrome, RecQ helicase-like	s1997	21	CCCACUACUUUGCAAGUAAtt	UUACUUGCAAAGUAGUGGGaa
NM_000057	BLM	Bloom syndrome, RecQ helicase-like	s1998	5	GGAUGUUCUUAGCACAUCAtt	UGAUGUGCUAAGAACAUCCtc
NM_000057	BLM	Bloom syndrome, RecQ helicase-like	s1999	22	GAUAUCUUCCAAAACGAAAtt	UUUCGUUUUGGAAGAUAUCtt
NM_012295	CABIN1	calcineurin binding protein 1	s24000	9	GGAUUGAUUUGUCGGACUAtt	UAGUCCGACAAAUCAAUCCtt
NM_012295	CABIN1	calcineurin binding protein 1	s24001	7	GGAUUGCCGGUACAGCAAAtt	UUUGCUGUACCGGCAAUCCtt
NM_012295	CABIN1	calcineurin binding protein 1	s24002	19	GCGAUUCUAUGUGCGAGUAtt	UACUCGCACAUAGAAUCGCag
NM_001270	CHD1	chromodomain helicase DNA binding protein 1	s2974	18	GGUGAAUAUUUAUCGUCUAtt	UAGACGAUAAAUAUUCACCtg
NM_001270	CHD1	chromodomain helicase DNA binding protein 1	s2975	3	CAUCAAGCCUCAUCUAAUAtt	UAUUAGAUGAGGCUUGAUGtt
NM_001270	CHD1	chromodomain helicase DNA binding protein 1	s2976	26	GGGUCCAACAUUCCGAAUAtt	UAUUCGGAAUGUUGGACCCtt
NM_001273	CHD4	chromodomain helicase DNA binding protein 4	s2983	12	CUAUCGCUAUGGGAUAAAAtt	UUUUAUCCCAUAGCGAUAGaa
NM_001273	CHD4	chromodomain helicase DNA binding protein 4	s2984	29	GCAAUUAUGCGAUAUGGUAtt	UACCAUAUCGCAUAAUUGCat
NM_006015	CHD4	chromodomain helicase DNA binding protein 4	s2985	20	CACUCGAAAUUUUGAAGCAtt	UGCUUCAAAAUUUCGAGUGag
NM_006015	CHD7	chromodomain helicase DNA binding protein 7	s31140	15	CUAACGUACCUAACCUAUUtt	AAUAGGUUAGGUACGUUAGct
NM_006015	CHD7	chromodomain helicase DNA binding protein 7	s31141	31	GGAUGACGAUAAGUCGGAAtt	UUCCGACUUAUCGUCAUCCtc
NM_032408	CHD7	chromodomain helicase DNA binding protein 7	s31142	2	GGGAUUAGUUAACAAUACAtt	UGUAUUGUUAACUAAUCCCtg
NM_032408	COPS4	COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis)	s27533	4	GCAUCUUGCAUCUAUAUAUtt	AUAUAUAGAUGCAAGAUGCtg
NM_032408	COPS4	COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis)	s27534	3	CUUCCUAACUUGCCUGAUAtt	UAUCAGGCAAGUUAGGAAGat
NM_013449	COPS4	COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis)	s27535	5	CGAGCAUCGUUGCUUCAGAtt	UCUGAAGCAACGAUGCUCGat
NM_013449	CTBP1	C-terminal binding protein 1	s3698	8,7	CUCUGAAGGAUGCACCCAAtt	UUGGGUGCAUCCUUCAGAGgg
NM_013449	CTBP1	C-terminal binding protein 1	s3699	4,3	GGCAGUGGUUUUGACAACAtt	UGUUGUCAAAACCACUGCCaa
NM_000057	CTBP1	C-terminal binding protein 1	s3700	10,9	GUUUGUGACUGUAACCAUUtt	AAUGGUUACAGUCACAAACat
NM_000057	CTBP2	C-terminal binding protein 2	s3701	11,11,9	GGAAAAUCACAUUACUACAtt	UGUAGUAAUGUGAUUUUCCta
NM_000057	CTBP2	C-terminal binding protein 2	s3702	5,5,3	GGAAUUGCCGUGUGCAACAtt	UGUUGCACACGGCAAUUCCga
NM_012295	CTBP2	C-terminal binding protein 2	s56075	Not Determined	CAUCAAUGACUUUACCAUAtt	UAUGGUAAAGUCAUUGAUGag
NM_012295	CTCF	CCCTC-binding factor (zinc finger protein)	s20966	6	CAUUCGCUCUCAUACUGGAtt	UCCAGUAUGAGAGCGAAUGtg
NM_012295	CTCF	CCCTC-binding factor (zinc finger protein)	s20967	3	GGACGAUACCCAGAUUAUAtt	UAUAAUCUGGGUAUCGUCCac
NM_001270	CTCF	CCCTC-binding factor (zinc finger protein)	s20968	4	GCUUUGCAGUUACACGUGUtt	ACACGUGUAACUGCAAAGCtc
NM_001270	DDX1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	s4001	3	GAAUCUAUCCCAUUGAUCUtt	AGAUCAAUGGGAUAGAUUCag
NM_001270	DDX1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	s4002	10	GAUGUUACCUGGAUAUAGAtt	UCUAUAUCCAGGUAACAUCca
NM_001273	DDX1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	s4003	12	GGCACCGGAUGGUUACAUUtt	AAUGUAACCAUCCGGUGCCtt
NM_001273	DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	s17563	14	CUACCGCAUCAGUAACAGAtt	UCUGUUACUGAUGCGGUAGgt
NM_006015	DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	s17564	5	GGAGGUCAAUUUGAACGCAtt	UGCGUUCAAAUUGACCUCCat
NM_006015	DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	s17565	10	GGAAUUAAGUUCAAACGAAtt	UUCGUUUGAACUUAAUUCCcg
NM_006015	DDX27	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	s31194	Not Determined	GCAUCUCAGUACGAUGAAAtt	UUUCAUCGUACUGAGAUGCat
NM_032408	DDX27	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	s31196	Not Determined	GCAGAUACACUCAAAGUAAtt	UUACUUUGAGUGUAUCUGCtt
NM_032408	DDX27	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	s445946	Not Determined	GAAAGAAAAGGAAAACAGAtt	UCUGUUUUCCUUUUCUUUCga
NM_032408	DDX41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	s28120	8	GGAACAAGAGAAGAGGUUAtt	UAACCUCUUCUCUUGUUCCag
NM_013449	DDX41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	s28121	5	GGCUAAGGGCAUUACGUAUtt	AUACGUAAUGCCCUUAGCCat
NM_013449	DDX41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	s224203	8	GCCGUGACAUGAUAGGCAUtt	AUGCCUAUCAUGUCACGGCca
NM_013449	DDX50	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	s35415	13	GCCUAGAGGAAAUACAGGAtt	UCCUGUAUUUCCUCUAGGCtt
NM_000057	DDX50	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	s35416	5	GGUGGAACAUCAUAUCAAAtt	UUUGAUAUGAUGUUCCACCat
NM_000057	DDX50	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	s35417	6	GGAUCUUUCUAAACUGCGAtt	UCGCAGUUUAGAAAGAUCCaa
NM_006015	DHX30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	s22643	Not Determined	GGACCAUAGAUGUUACCGAtt	UCGGUAACAUCUAUGGUCCct
NM_006015	DHX30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	s22644	Not Determined	CUAGGGACCUAUUAAAAGAtt	UCUUUUAAUAGGUCCCUAGaa
NM_006015	DHX30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	s22645	Not Determined	GCAAUGUUAUCAUCACCCAtt	UGGGUGAUGAUAACAUUGCag
NM_032408	HDAC1	histone deacetylase 1	s73	2	CUAUGGUCUCUACCGAAAAtt	UUUUCGGUAGAGACCAUAGtt
NM_032408	HDAC1	histone deacetylase 1	s74	7	CCGGUCAUGUCCAAAGUAAtt	UUACUUUGGACAUGACCGGct
NM_032408	HDAC1	histone deacetylase 1	s75	10	CCAAUAUGACUAACCAGAAtt	UUCUGGUUAGUCAUAUUGGaa
NM_013449	HDAC2	histone deacetylase 2	s6493	8	GGGUUGUUUCAAUCUAACAtt	UGUUAGAUUGAAACAACCCag
NM_013449	HDAC2	histone deacetylase 2	s6494	7	GGCAGAUAUUUAAGCCUAUtt	AUAGGCUUAAAUAUCUGCCca
NM_013449	HDAC2	histone deacetylase 2	s6495	1	CUACGACGGUGAUAUUGGAtt	UCCAAUAUCACCGUCGUAGta
NM_000057	SAP18	Sin3A-associated protein, 18kDa	s20098	Not Determined	GAACUGACAAGCUUAGUAAtt	UUACUAAGCUUGUCAGUUCtt
NM_000057	SAP18	Sin3A-associated protein, 18kDa	s20099	Not Determined	UCGUUUUUACAGAUGUUAAtt	UUAACAUCUGUAAAAACGAtt
NM_000057	SAP18	Sin3A-associated protein, 18kDa	s20100	Not Determined	GAUCUACACUUGGAUGGAUtt	AUCCAUCCAAGUGUAGAUCtg
NM_012295	GATAD2A	GATA zinc finger domain containing 2A	s224320	Not Determined	CGUUCAGUCCGUCACCCAAtt	UUGGGUGACGGACUGAACGtg
NM_012295	GATAD2A	GATA zinc finger domain containing 2A	s29501	Not Determined	GCAAAACUCGUGUUGUUGAtt	UCAACAACACGAGUUUUGCtt
NM_012295	GATAD2A	GATA zinc finger domain containing 2A	s29502	Not Determined	GCGGCAGAGUCAAAUACAAtt	UUGUAUUUGACUCUGCCGCaa
NM_001270	HIRA	HIR histone cell cycle regulation defective homolog A (S. cerevisiae)	s14521	23	CGAAGGGUUUGAAUACCGAtt	UCGGUAUUCAAACCCUUCGtt
NM_001270	HIRA	HIR histone cell cycle regulation defective homolog A (S. cerevisiae)	s14522	15	CGUCCAAGAUCGAACCCAUtt	AUGGGUUCGAUCUUGGACGgg
NM_001270	HIRA	HIR histone cell cycle regulation defective homolog A (S. cerevisiae)	s445947	Not Determined	GAUAUUUCCUGGACUCUGAtt	UCAGAGUCCAGGAAAUAUCca
NM_001273	HMBOX1	homeobox containing 1	s35926	Not Determined	GUACUGGAAUGACUAAACAtt	UGUUUAGUCAUUCCAGUACgc
NM_001273	HMBOX1	homeobox containing 1	s35927	Not Determined	GGAGAAUAAUGAGCGAUUAtt	UAAUCGCUCAUUAUUCUCCct
NM_006015	HMBOX1	homeobox containing 1	s35928	Not Determined	CCAUGUCUCAUUAUACAGAtt	UCUGUAUAAUGAGACAUGGtt
NM_006015	AOF2	amine oxidase (flavin containing) domain 2	s617	Not Determined	GGUCUUGGAGGGAAUCCUAtt	UAGGAUUCCCUCCAAGACCtg
NM_006015	AOF2	amine oxidase (flavin containing) domain 2	s618	Not Determined	GAGCAAGAGUUUAACCGGUtt	ACCGGUUAAACUCUUGCUCta
NM_032408	AOF2	amine oxidase (flavin containing) domain 2	s619	Not Determined	CUGCAGUUGUGGUUGGAUAtt	UAUCCAACCACAACUGCAGtg
NM_032408	JUN	jun proto-oncogene	s7658	1	GGCACAGCUUAAACAGAAAtt	UUUCUGUUUAAGCUGUGCCac
NM_032408	JUN	jun proto-oncogene	s7659	1	CCAAGUGCCGAAAAAGGAAtt	UUCCUUUUUCGGCACUUGGag
NM_002228	JUN	jun proto-oncogene	s7660	1	GGAUCAAGGCGGAGAGGAAtt	UUCCUCUCCGCCUUGAUCCgc
NM_021174	KIAA1967	KIAA1967	s33736	9,9	CGCUUAUAGUUCGAAGGUAtt	UACCUUCGAACUAUAAGCGgg
NM_021174	KIAA1967	KIAA1967	s33737	19,19	GGCUCUACCUAGAGAACAAtt	UUGUUCUCUAGGUAGAGCCgg
NM_021174	KIAA1967	KIAA1967	s33738	14,14	GGCUAUAGAGUUUAUAAGAtt	UCUUAUAAACUCUAUAGCCaa
NM_004992	MECP2	methyl CpG binding protein 2 (Rett syndrome)	s8644	Not Determined	GGAAGCUCCUUGUCAAGAUtt	AUCUUGACAAGGAGCUUCCca
NM_004992	MECP2	methyl CpG binding protein 2 (Rett syndrome)	s8645	Not Determined	GACAUUGUUUCAUCCUCCAtt	UGGAGGAUGAAACAAUGUCtt
NM_004992	MECP2	methyl CpG binding protein 2 (Rett syndrome)	s8646	Not Determined	GCUUCCCGAUUAACUGAAAtt	UUUCAGUUAAUCGGGAAGCtt
NM_004739	MTA2	metastasis associated 1 family, member 2	s17629	13	GGAUCUACUGGAAGAAGUAtt	UACUUCUUCCAGUAGAUCCaa
NM_004739	MTA2	metastasis associated 1 family, member 2	s17630	10	GCAUAGUCCAGUUUUAUUAtt	UAAUAAAACUGGACUAUGCtg
NM_004739	MTA2	metastasis associated 1 family, member 2	s17631	10	CCACAGACCGGUAUAUUCAtt	UGAAUAUACCGGUCUGUGGtt
NM_002479	MYOG	myogenin (myogenic factor 4)	s9232	3	ACUUAUUUGGAUUUCCUUUtt	AAAGGAAAUCCAAAUAAGUta
NM_002479	MYOG	myogenin (myogenic factor 4)	s9233	3	CAAGGUCUCCUGUGCUGAAtt	UUCAGCACAGGAGACCUUGgt
NM_002479	MYOG	myogenin (myogenic factor 4)	s9234	3	CCUCAUCCAUGUAAGGUUAtt	UAACCUUACAUGGAUGAGGaa
NM_020967	NCOA5	nuclear receptor coactivator 5	s33688	3	GGACCACAGACAUAGUAGAtt	UCUACUAUGUCUGUGGUCCcg
NM_020967	NCOA5	nuclear receptor coactivator 5	s33689	4	CCGUUACAGAGAUAGCUUUtt	AAAGCUAUCUCUGUAACGGtc
NM_020967	NCOA5	nuclear receptor coactivator 5	s33690	3	GGAUUUUCGAGAUCAGCGAtt	UCGCUGAUCUCGAAAAUCCct
NM_014223	NFYC	nuclear transcription factor Y, gamma	s9534	Not Determined	GGAAUUUAACAGUGAAAGAtt	UCUUUCACUGUUAAAUUCCgg
NM_014223	NFYC	nuclear transcription factor Y, gamma	s9535	Not Determined	GGCUCGUAUUAAGAAGAUUtt	AAUCUUCUUAAUACGAGCCag
NM_014223	NFYC	nuclear transcription factor Y, gamma	s9536	Not Determined	GGCAGAUCAUCAUCGCACAtt	UGUGCGAUGAUGAUCUGCCca
NM_002592	PCNA	proliferating cell nuclear antigen	s10133	5,4	CGUAUAUGCCGAGAUCUCAtt	UGAGAUCUCGGCAUAUACGtg
NM_002592	PCNA	proliferating cell nuclear antigen	s10134	5,4	GGAGUGAAAUUUUCUGCAAtt	UUGCAGAAAAUUUCACUCCgt
NM_002592	PCNA	proliferating cell nuclear antigen	s10135	3,2	GAAGAUAUCAUUACACUAAtt	UUAGUGUAAUGAUAUCUUCat
NM_013374	PDCD6IP	programmed cell death 6 interacting protein	s19465	Not Determined	GAAGGAUGCUUUCGAUAAAtt	UUUAUCGAAAGCAUCCUUCca
NM_013374	PDCD6IP	programmed cell death 6 interacting protein	s19466	Not Determined	GCUAUAAUCCUUAUGCGUAtt	UACGCAUAAGGAUUAUAGCcc

NM_013374	PDCD6IP	programmed cell death 6 interacting protein	s19467	Not Determined	GAAUUACUGCAACGAAAUAtt	UAUUUCGUUGCAGUAAUUCag
NM_001009552	PPP2CB	protein phosphatase 2, catalytic subunit, beta isozyme	s10960	2	GGAUAUUAUUCAGUGGAGAtt	UCUCCACUGAAUAAUAUCCtc
NM_001009552	PPP2CB	protein phosphatase 2, catalytic subunit, beta isozyme	s10961	6	CAAUUACUGUUAUCGUUGUtt	ACAACGAUAACAGUAAUUGgg
NM_001009552	PPP2CB	protein phosphatase 2, catalytic subunit, beta isozyme	s10962	3	CAAUAUUGAGAGGAAAUCAtt	UGAUUUCCUCUCAAUAUUGta
NM_018312	SAPS3	SAPS domain family, member 3	s30657	Not Determined	GGUUACAUGGGACACCUAAtt	UUAGGUGUCCCAUGUAACCat
NM_018312	SAPS3	SAPS domain family, member 3	s30658	Not Determined	GAUGAAUCCUUGCUAAUGAtt	UCAUUAGCAAGGAUUCAUCtt
NM_018312	SAPS3	SAPS domain family, member 3	s445949	Not Determined	GGAAAACUGUUACCAGGAUtt	AUCCUGGUAACAGUUUUCCtc
NM_002734	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	s286	11,11,11	GGACCGACCUAGAUUUGAAtt	UUCAAAUCUAGGUCGGUCCag
NM_002734	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	s287	6,6,6	CUAUGUGAUUGAUCAAGGAtt	UCCUUGAUCAAUCACAUAGaa
NM_002734	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	s288	3,3,3	CGGCAUCCUAUGUUAGAAAtt	UUUCUAACAUAGGAUGCCGca
NM_001081640	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	s773	31,31	GCGUUGGAGUGCUACAACAtt	UGUUGUAGCACUCCAACGCgg
NM_001081640	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	s774	6,6	GCGCUUUUCUGGGUGAACUtt	AGUUCACCCAGAAAAGCGCgg
NM_001081640	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	s775	27,27	CAAGCGACUUUAUAGCCUUtt	AAGGCUAUAAAGUCGCUUGaa
NM_002763	PROX1	prospero homeobox 1	s11227	2	CCUGAAUCCUUAGACUUAAtt	UUAAGUCUAAGGAUUCAGGag
NM_002763	PROX1	prospero homeobox 1	s11228	2	GUUUGAUAUGGAUCGCUUAtt	UAAGCGAUCCAUAUCAAACtg
NM_002763	PROX1	prospero homeobox 1	s11229	3	CGACGUAAAGUUCAACAGAtt	UCUGUUGAACUUUACGUCGga
NM_005610	RBBP4	retinoblastoma binding protein 4	s11837	Not Determined	GGAUACUCGUUCAAACAAUtt	AUUGUUUGAACGAGUAUCCca
NM_005610	RBBP4	retinoblastoma binding protein 4	s11838	Not Determined	CUUGUAUCAUCGCAACAAAtt	UUUGUUGCGAUGAUACAAGgg
NM_005610	RBBP4	retinoblastoma binding protein 4	s11839	Not Determined	CAGUGGUACUGAUCGCAGAtt	UCUGCGAUCAGUACCACUGga
NM_002893	RBBP7	retinoblastoma binding protein 7	s11846	Not Determined	GCUUUAUGGGAUCUGCGUAtt	UACGCAGAUCCCAUAAAGCta
NM_002893	RBBP7	retinoblastoma binding protein 7	s11847	Not Determined	GGAAGAAGAAUACACCGUUtt	AACGGUGUAUUCUUCUUCCag
NM_002893	RBBP7	retinoblastoma binding protein 7	s11848	Not Determined	CUCACAUCAUUGCUACAAAtt	UUUGUAGCAAUGAUGUGAGga
NM_015156	RCOR1	REST corepressor 1	s23229	5	GAGUGGACUGUGGAAGAUAtt	UAUCUUCCACAGUCCACUCat
NM_015156	RCOR1	REST corepressor 1	s23230	8	GGAAUUGGUUUCAGUCAAAtt	UUUGACUGAAACCAAUUCCat
NM_015156	RCOR1	REST corepressor 1	s23231	6	CCAGAUAAAUCUAUAGCAAtt	UUGCUAUAGAUUUAUCUGGaa
NM_007212	RNF2	ring finger protein 2	s12067	5	GGCUAGAGCUUGAUAAUAAtt	UUAUUAUCAAGCUCUAGCCca
NM_007212	RNF2	ring finger protein 2	s12068	5	CAAACGGACCAAAACAUCUtt	AGAUGUUUUGGUCCGUUUGtt
NM_007212	RNF2	ring finger protein 2	s12069	3	GGAGUGUUUACAUCGUUUUtt	AAAACGAUGUAAACACUCCtt
NM_004348	RUNX2	runt-related transcription factor 2	s2455	4	CUUGAUGACUCUAAACCUAtt	UAGGUUUAGAGUCAUCAAGct
NM_004348	RUNX2	runt-related transcription factor 2	s2456	7	CCAAAUUUGCCUAACCAGAtt	UCUGGUUAGGCAAAUUUGGat
NM_004348	RUNX2	runt-related transcription factor 2	s2457	4	CAAGUCCUUUUAAUCCACAtt	UGUGGAUUAAAAGGACUUGgt
NM_001001890	RUNX1	runt-related transcription factor 1	s2458	5,8	CCAAUACCUGGGAUCCAUUtt	AAUGGAUCCCAGGUAUUGGta
NM_001001890	RUNX1	runt-related transcription factor 1	s2459	2,5	GAACCAGGUUGCAAGAUUUtt	AAAUCUUGCAACCUGGUUCtt
NM_001001890	RUNX1	runt-related transcription factor 1	s229351	4,4,7	GGCAGAAACUAGAUGAUCAtt	UGAUCAUCUAGUUUCUGCCga
NM_002971	SATB1	SATB homeobox 1	s12479	Not Determined	GGCUCGUAUCAACACCUAUtt	AUAGGUGUUGAUACGAGCCca
NM_002971	SATB1	SATB homeobox 1	s12480	Not Determined	CGAAUAUACCAGGACGAAAtt	UUUCGUCCUGGUAUAUUCGgt
NM_002971	SATB1	SATB homeobox 1	s12481	Not Determined	GCAUUGCUGUCUCUAGGUUtt	AACCUAGAGACAGCAAUGCca
NM_015265	SATB2	SATB homeobox 2	s23539	Not Determined	CCACAGUACUCCAAUCCGAtt	UCGGAUUGGAGUACUGUGGtg
NM_015265	SATB2	SATB homeobox 2	s23540	Not Determined	GUCCACAACUUGUAAGGCAtt	UGCCUUACAAGUUGUGGACta
NM_015265	SATB2	SATB homeobox 2	s223583	Not Determined	GCAUUACAGCCCAUCAUGAtt	UCAUGAUGGGCUGUAAUGCgg
NM_012238	SIRT1	sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae)	s23771	Not Determined	GGGUCUUCCCUCAAAGUAAtt	UUACUUUGAGGGAAGACCCaa
NM_012238	SIRT1	sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae)	s223591	Not Determined	CAACUAUACCCAGAACAUAtt	UAUGUUCUGGGUAUAGUUGcg
NM_012238	SIRT1	sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae)	s223592	Not Determined	CCCUCAAAGUAAGACCAGUtt	ACUGGUCUUACUUUGAGGGaa
NM_003072	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	s13139	Not Determined	GGAAUACCUCAAUAGCAUUtt	AAUGCUAUUGAGGUAUUCCtg
NM_003072	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	s13140	Not Determined	GGCUUGAUGGAACCACGAAtt	UUCGUGGUUCCAUCAAGCCtg
NM_003072	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	s13141	Not Determined	GUAGCUCCGAGGUCUGAUAtt	UAUCAGACCUCGGAGCUACtt
NM_003601	SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	s16081	7	GGAGAUACUUAGUAAUAGAtt	UCUAUUACUAAGUAUCUCCaa
NM_003601	SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	s16082	3	GGGCAAAUAGAUUCGAGUAtt	UACUCGAAUCUAUUUGCCCgg
NM_003601	SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	s16083	16	GGGCGAAAGUUCACUUAGAtt	UCUAAGUGAACUUUCGCCCat
NM_003074	SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	s13145	Not Determined	CCAACACCUGUACCCAAUAtt	UAUUGGGUACAGGUGUUGGgt
NM_003074	SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	s13146	Not Determined	CAAGAGUAUUUAACUAGCAtt	UGCUAGUUAAAUACUCUUGgg
NM_003074	SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	s13147	Not Determined	CCAUCUCGAAUGGAUCGUAtt	UACGAUCCAUUCGAGAUGGgt
NM_003079	SMARCE1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	s13160	6	GCAGAAAAGAUAGAGUACAtt	UGUACUCUAUCUUUUCUGCtt
NM_003079	SMARCE1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	s13161	7	GUACCUUGCUUACAUAAAUtt	AUUUAUGUAAGCAAGGUACgc
NM_003079	SMARCE1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	s13162	6	GACCUAAAGUUGUGGGAGAtt	UCUCCCACAACUUUAGGUCag
NM_001039590	USP9X	ubiquitin specific peptidase 9, X-linked	s15742	19,19	GAUGUAUUCUCAAUCGUAUtt	AUACGAUUGAGAAUACAUCgt
NM_001039590	USP9X	ubiquitin specific peptidase 9, X-linked	s15743	18,18	CAGUGUUAAUUGUGCAAGAtt	UCUUGCACAAUUAACACUGtc
NM_001039590	USP9X	ubiquitin specific peptidase 9, X-linked	s15744	33,33	GCCUGUUAAUCUGCGUGAAtt	UUCACGCAGAUUAACAGGCtc
NM_017588	WDR5	WD repeat domain 5	s225470	5,4	GCCUGGUCGUCAGAUUCUAtt	UAGAAUCUGACGACCAGGCta
NM_017588	WDR5	WD repeat domain 5	s21863	13,12	CGAAAGAGAUUGUACAGAAtt	UUCUGUACAAUCUCUUUCGtc
NM_017588	WDR5	WD repeat domain 5	s21864	4,3	GAUGGGAAAUUUGAGAAAAtt	UUUUCUCAAAUUUCCCAUCat
NM_001128128	ZEB1	zinc finger E-box binding homeobox 1	s229971	7,7	GGUAGAUGGUAAUGUAAUAtt	UAUUACAUUACCAUCUACCgc
NM_001128128	ZEB1	zinc finger E-box binding homeobox 1	s229972	7,7	GGACAGCACAGUAAAUCUAtt	UAGAUUUACUGUGCUGUCCtg
NM_030751	ZEB1	zinc finger E-box binding homeobox 1	s13883	6	CAGUCUGGGUGUAAUCGUAtt	UACGAUUACACCCAGACUGcg
NM_014795	ZEB2	zinc finger E-box binding homeobox 2	s19032	Not Determined	CCGGAGUUUUUGUUGAUAAtt	UUAUCAACAAAAACUCCGGct
NM_014795	ZEB2	zinc finger E-box binding homeobox 2	s19033	Not Determined	GGAAUGGUUUGAACAACGAtt	UCGUUGUUCAAACCAUUCCtt
NM_014795	ZEB2	zinc finger E-box binding homeobox 2	s19034	Not Determined	CCACAACAGUGUUACGAAUtt	AUUCGUAACACUGUUGUGGag
NM_021964	ZNF148	zinc finger protein 148	s15207	9	GCAUAGUAGUACUAAUUAUtt	AUAAUUAGUACUACUAUGCac
NM_021964	ZNF148	zinc finger protein 148	s15208	9	GUAUUGAAACAUAAACGUAtt	UACGUUUAUGUUUCAAUACac
NM_021964	ZNF148	zinc finger protein 148	s15209	6	GAACUAUCACUUACAGAGAtt	UCUCUGUAAGUGAUAGUUCgt
NM_001039916	ZNF384	zinc finger protein 384	s46887	7,8,7,7,7,8	CCACACUGGUGAUAGACCAtt	UGGUCUAUCACCAGUGUGGat
NM_001039916	ZNF384	zinc finger protein 384	s46888	9,10,9,9,9,10	CAGUGUUCCUUUGACCUGAtt	UCAGGUCAAAGGAACACUGgg
NM_001039916	ZNF384	zinc finger protein 384	s46889	9,10,9,9,9,10	CAUACCUUAUGAAACAUAUtt	AUAUGUUUCAUAAGGUAUGtt
NM_181781	ZNF326	zinc finger protein 326	s195971	Not Determined	GGAUCGUGAUUAUGGCCCUtt	AGGGCCAUAAUCACGAUCCat
NM_181781	ZNF326	zinc finger protein 326	s195972	Not Determined	UAUCAGGGCUUUAAUGGAAtt	UUCCAUUAAAGCCCUGAUAag
NM_181781	ZNF326	zinc finger protein 326	s195973	Not Determined	AUACUUAUCAGGGCUUUAAtt	UUAAAGCCCUGAUAAGUAUtc
NM_006510	TRIM27	tripartite motif containing 27	s11959	2	GCUGAACUCUUGAGCCUAAtt	UUAGGCUCAAGAGUUCAGCtc
NM_006510	TRIM27	tripartite motif containing 27	s11960	5	CAAAAAUGUCUAUUCUUGAtt	UCAAGAAUAGACAUUUUUGgg
NM_006510	TRIM27	tripartite motif containing 27	s11961	3	GCAGCUGUAUCACUCCUUAtt	UAAGGAGUGAUACAGCUGCtc

Supplementary Table S3: Leading edge subset

	Protein name	Gen name	RANK IN GENE LIST	RANK METRIC SCORE	RUNNING ES	CORE ENRICHMENT
1	Isochorismatase domain-containing protein 1	ISOC1	0	3.698696613	0.025464967	Yes
2	Sodium bicarbonate transporter 4	NBC4	35	2.496522188	0.041109372	Yes
3	Manosidase, enod-alpha	MANEA	66	2.140193939	0.054482136	Yes
4	Heart development protein with EGF-like domains 1	HEG1	93	1.947881818	0.06671248	Yes
5	Tripartit motiv containing	TRIM58	95	1.92384994	0.07991248	Yes
6	DTW domain-containing protein 1	DTWD1/MDS009	101	1.893535733	0.09272217	Yes
7	Interphotoreceptor mmatrix proteoglycan 1	IMPG1	117	1.822807193	0.10459085	Yes
8	Transmembrane protein 202	TMEM202	124	1.790550351	0.11664608	Yes
9	Analplastic lymphoma receptor tyrosine kinase	ALK	132	1.776676178	0.1285604	Yes
10	P-cadherin	CDH3	409	1.318120718	0.13671853	Yes
11	Tissue inhibitor of metalloproteinase 3	TIMP3	417	1.312698364	0.14543843	Yes
12	Pleiomorphic adenoma gene-like 1	PLAGL1	474	1.258885026	0.15156297	Yes
13	Fas apoptotic inhibitory molecule	FAIM	497	1.244239688	0.15913047	Yes
14	Tuftelin interacting protein 11	TFIP11	518	1.232141018	0.16670547	Yes
15	Leucine zipper putative tumor suppressor 3	LZTS3	522	1.229026198	0.17503092	Yes
16	Transricption factor E4TF1-60	E4TF1-60	530	1.224172235	0.18314132	Yes
17	Teneurin 3	TENM3	571	1.20076251	0.1895922	Yes
18	Hypoxia-inducible factor-2alpha	EPAS1	588	1.187447548	0.19704111	Yes
19	RNA-binding Protein 35B	RBM35B	607	1.179178596	0.21254866	Yes
20	Calcium channel, voltage-dependent, beta 2 subunit	CACNB2	690	1.123668432	0.22459577	Yes
21	Bone morphogenetic protein 5	BMP5	710	1.112659931	0.23139356	Yes
22	Plakophilin 1	PKP1	766	1.08441925	0.23636235	Yes
23	Spermidinespermine N1-acetyltransferase	SAT1	794	1.069862843	0.24250226	Yes
24	Tousled-like kinase 1	TLK1	1024	0.976659536	0.23882866	Yes
25	Coiled-coil domain containing 121	CCDC121	1113	0.947796762	0.24135846	Yes
26	Microtubule plus-end tracking protein TIP150	TIP150/MTUS2	1119	0.945643008	0.24764204	Yes
27	Synaptic Vesicle Glycoprotein 2a	SV2A	1121	0.945068359	0.2541033	Yes
28	Transcription factor AP2beta	TFAP2beta	1129	0.942483664	0.26027432	Yes
29	2-5oligoadenylate synthetase 2	OAS2	1232	0.907269478	0.26188943	Yes
30	F-box only protein 17	FBXO17	1353	0.873526156	0.2624549	Yes
31	Calcium-activated potassium channel SK3	KCNN3	1439	0.852016211	0.2644615	Yes
32	Glycine amidinotransferase	GATM	1470	0.844306111	0.26891226	Yes
33	Cytochrome P450 polypeptide 43	CYP3A43	1491	0.840080678	0.27378798	Yes
34	Centrosomal protein of 104 kDa	CEP104	1537	0.825581908	0.27742878	Yes
35	Disrupted in schizophrenia 1	DISC1	1785	0.776802301	0.2715619	Yes
36	Complement decay-accelerating factor for complement	CD55	1829	0.769265771	0.27490577	Yes
37	Serinethreonine kinase RICK	RICK	1885	0.758343697	0.27762955	Yes
38	Rho guanine nucleotide exchange factor 3	ARHGEF3	1949	0.745236158	0.2798999	Yes
39	Meiotic recombination protein DMC1/LIM15 homolog	HsLim15/DCM1	1968	0.741775393	0.2841896	Yes
40	Metallophosphoesterase 1	MPPE1	2040	0.725010157	0.28595743	Yes
41	Mitochondrial NAD(P)+ dependent malic enzyme	ME2	2158	0.70450604	0.28549546	Yes
42	Cyclin-dependent kinase 3	CDK3	2217	0.694423258	0.287643	Yes
43	Membrane metallo-endopeptidase	MME	2223	0.693363011	0.29218966	Yes
44	Ankyrin 2, neuronal	ANK2	2297	0.681526303	0.2935673	Yes
45	Adrenergic, beta-1-, receptor	ADRB1	2318	0.67876333	0.29733238	Yes
46	Ras supressor 1	RSU1	2345	0.673559248	0.3007892	Yes
47	Na+/K+ Transporting ATPase Interacting 1	NKAIN1	2379	0.668322086	0.30389214	Yes

Supplementary Methods

Plasmids, transfection methods and lentiviral transduction. FLAG-tagged PAX3-FOXO1 was generated by inserting the cDNA into pCMV-SC-NF or pCMV-SC-CF (N/C-terminal 3xFLAG, Stratagene, Agilent Technologies). FLAG-PAX3-FOXO1 was subcloned into pBABE puro (Addgene, no. 1764) using In-Fusion® HD Cloning Kit (Takara Bio Europe/Clontech) according to the manufacturer`s instructions. The vector pCMV-SC-CF-FLAG only was used as negative control for immunoprecipitation and was generated by introducing a start codon into the parental pCMV-SC-CF vector. RH4 and RMS13 cells were transfected using JetPrimeTM (Polyplus-Transfections) and 293T cells grown in 6 cm dishes were transfected with plasmid DNA by the $CaPO_4$ co-precipitation method. For transduction we used tet-inducible lentiviral shRNA expression vectors, containing indicated shRNAs (Cellecta, BioCat GmbH, Supplementary Table S4). Lentiviral packaging and envelope plasmids (pMDL, pREV and pVSV-G kindly provided by Oliver Pertz, Department of Biomedicine, University of Basel, Switzerland) were co-transfected into HEK293T cells using $CaPO_4$. After 48 hrs, we collected virions from supernatant cultures and concentrated these using Amicon Ultra tubes, (Ultracel 100k, Millipore). RH4, RMS, RD, MRC5 and myoblast cells were transduced for 24 hrs in the presence of 8ug/ml polybrene (Sigma-Aldrich). 72 hrs after transduction we started selection with puromycin with the exception of transduced myoblast cells, which were subjected to fluorescence activated cell sorting. For experiments shRNA expression was induced using 100ng/ml doxycycline (Sigma-Aldrich). Data were normalized to uninduced and related to scrambled shRNA expressing cells.

Supplementary Table S4: shRNA hairpin sequences

Name	**shRNA sequence 5`to 3`**
shscr	ACCGGCAACAAGATGGAGAGCACTAAGTTAATATTCATAGCTTGGTGCTCTTCATCTTGTTGTTTT
shLSD1#1	ACCGGGCTACATCTTACCTTAGTTATGTTAATATTCATAGCATGACTAAGGTAAGATGTAGCTTTT
shLSD1#2	ACCGGGGAAGTTGTCATTCAGTTATAGTTAATATTCATAGCTGTAACTGAATGACAACTTCCTTTT
shCHD4#1	ACCGGGCGGGAGTTTAGTACTAATAAGTTAATATTCATAGCTTATTGGTACTGAACTCCCGCTTTT
shCHD4#2	ACCGGCCTCGAGTGAGGGTGATGATTGTTAATATTCATAGCAGTCATCATCCTCACTCGAGGTTTT
shPAX3-FOXO1	ACCGGGGCCTCTCACCTCAGAATTCAGTTAATATTCATAGCTGAATTCTGAGGTGAGAGGCCTTTT

Mass spectrometry. Samples were analyzed on a LTQ-Orbitrap Classic mass spectrometer (Thermo Fischer Scientific) coupled to an Eksigent-Nano-HPLC system (Eksigent Technologies). Solvent composition at the two channels was 0.2% formic acid, 1% acetonitrile for channel A and 0.2% formic acid, 80% acetonitrile for channel B. Peptides were resuspended in 3% ACN and 0.2% formic acid and loaded on a self-made tip column (75µm × 70mm) packed with reverse phase C18 material (AQ, 3µm 200Å, Bischoff GmbH) and eluted with a flow rate of 200 nl per min by a gradient from 3 to 35% of B in 55 min, 48% B in 60min, 97% B in 68min. Full-scan MS spectra (300−2000 m/z) were acquired with a resolution of 60 000 at 400 m/z after accumulation to a target value of 500 000.

Collision induced dissociation (CID) MS/MS spectra were recorded in data dependent manner in the ion trap from the five most intense signals above a threshold of 500, using a normalized collision energy of 28% and an activation time of 30ms. Charge state screening was enabled and singly charge states were rejected. Precursor masses selected twice for MS/MS were excluded for further selection for 120s. The exclusion window was set to 20 ppm, while the size of the exclusion list was set to a maximum of 500 entries. Samples were acquired using internal lock mass calibration set on m/z 429.088735 and 445.120025.

Database search and protein identification. The raw-files from the mass spectrometer were converted into Mascot generic files (mgf) with Mascot Distiller software 2.4.2.0 (Matrix Science Ltd.,London, UK). The peak lists were searched using Mascot Server 2.3 against the forward UniProtKB/Swiss-Prot database for human, concatenated to a reversed decoyed FASTA database consisting of a total of 135,183 proteins with accessions in Gene Ontology compatible format and 260 common protein contaminants (NCBI taxonomy ID 9606, release date 2012-04-12). The protein sequence of PAX3-FOXO1 (gi|431254|gb|AAC50053.1|) was included in the database as in reference (1). The parameters for precursor tolerance and fragment ion tolerance were set to ± 5 ppm and ± 0.8 Da, respectively. Carbamidomethylation of cysteine was set as fixed modification, while phosphorylation (S, T, Y) and oxidation (M) were set as variable. The results were loaded into Scaffold 4.0

(Proteome Software, Portland, US) and filtered for peptides with a minimum mascot score of 20 and peptide probability higher than 95%, protein probability greater than 99% and minimum of 2 peptides per protein.

Quantitative Real Time PCR. Total RNA was extracted using the Qiagen RNeasy Kit and reverse transcription was carried out using high-capacity cDNA reverse transcription kit (Life Technologies) according to the manufacturer`s instructions. Quantitative Real Time PCR was performed using commercially available TaqMan gene expression master mix and assays (all Life Technologies, Supplementary Table S5). Reactions were run using standard conditions on an ABI 7900 HT Real Time PCR machine and the data were analyzed with SDS 2.3 software. C_T values were normalized to GAPDH and relative expression levels were calculated using the $\Delta\Delta C_T$ method based on experiments performed in triplicates. Data analysis was done with the GraphPad prism software, version 6.

Supplementary Table S5: TaqMan Gene Expression Assays

Name	Assay
CHD4	Hs00172349_m1
LSD1	Hs01002741_m1
PAX3-FOXO1	Hs03024825_ft
TFAP2B	Hs00231468_m1
CDH3	Hs00999918_m1
NMYC	Hs00232074_m1
PIPOX	Hs04188864_m1
MYL1	Hs00984899_m1
GAPDH	Hs02758991_g1
CB1	Hs01038522_s1
ALK	Hs00608284_m1

For ChIP-qPCR Taqman assays spanning recently identified PAX3-FOXO1 binding sites at regulatory regions of various direct target genes, or the GAPDH promoter region as negative control were designed (all Microsynth AG, Supplementary Table S6) (2). Quantity of purified ChIP-DNA was determined by absolute quantification using standard curves and normalized to the amount of input material. Fold enrichment was calculated relative to the shscr noninduced control.

Supplementary Table S6: Primer sets and TaqMan probes for ChIP-qPCR

Name	**Sequence 5`to 3`**
CDH3 fwd	ATGCTCCCGAGATACCAGAT
CDH3 rev	AGAAGCGTTGTAATCCTCCAA
CDH3 probe	TGCTCGTTGTACCCTCAGCCATG
GAPDH fwd	CCAATCTCAGTCCCTTCCC
GAPDH rev	GGTCTTGAGGCCTGAGCTAC
GAPDH probe	CCCAGTTGAACCAGGCGGCT
PIPOX fwd	GGGATTTCCACTGCATCTTT
PIPOX rev	CAGCGAGATAGCAACGAGAG
PIPOX probe	TGCCTCTTCGAAGCTCAACAGAGG
FGFR4 fwd	CCCTGAGAAGTGGTTGAGG
FGFR4 rev	GGAAAGCTGGGTGAGTTCAG
FGFR4 probe	CTGTTGGCGATTTCACGCCC
NMYC fwd	CAGGGTGGGTTACACCGT
NMYC rev	CTCATTACACCAATTCCTGGAG
NMYC probe	AACAGCTGCCACCGGCAAGA

FOXO1 silencing. Knockdown of FOXO1 prior immunoprecipitation was achieved by reverse transfection of 4x10^6 cells in 15cm plates using 8.6nM scrambled (4390846) or FOXO1 directed siRNAs (siscr: 4390846, siFOXO1#1: s456610, siFOXO1#2: s456611 all Ambion, Life Technologies) with INTERFERin^{TM} according to the manufacturer's protocol (Polyplus-Transfections). Cells were lysed 72 hours post transfection.

Antibodies. Western blot membranes were incubated with anti-FOXO1 (H-128) (sc-11350; 1:1000; Santa Cruz Biotechnology), anti-LSD1 (C69G12) (2184; 1:1000; Cell Signaling), anti-CHD4 (A301-082A, 1:1000; Bethyl Laboratories), anti-HDAC1 (10E2) (5356; 1:1000; Cell Signaling) anti-HDAC2 (3F3) (5113; 1:1000; Cell Signaling) anti-Cleaved Caspase-7 (Asp198) (9491; 1:1000; Cell Signaling) anti-PARP (9542; 1:1000; Cell Signaling) antibodies. Anti-β-Tubulin mouse mAb (1:40,000; Sigma-Aldrich), anti-β-Actin (13E5) rabbit mAb (4970; 1:1000; Cell Signaling) and anti-GAPDH (D16H11) XP^{TM} rabbit mAb (5174; 1:1000; Cell Signaling) were used as loading controls. Membranes were incubated with the secondary antibodies anti-mouse IgG HRP-linked antibody (7076; 1:2000; Cell Signaling), anti-rabbit IgG HRP-linked antibody (7074; 1:2000; Cell Signaling), EasyBlot anti-mouse IgG HRP-linked antibody (GTX221667-01; 1:1000; Genetex) or EasyBlot anti-rabbit IgG HRP-linked antibody (GTX221666-01; 1:1000; Genetex) for one hour at room temperature.

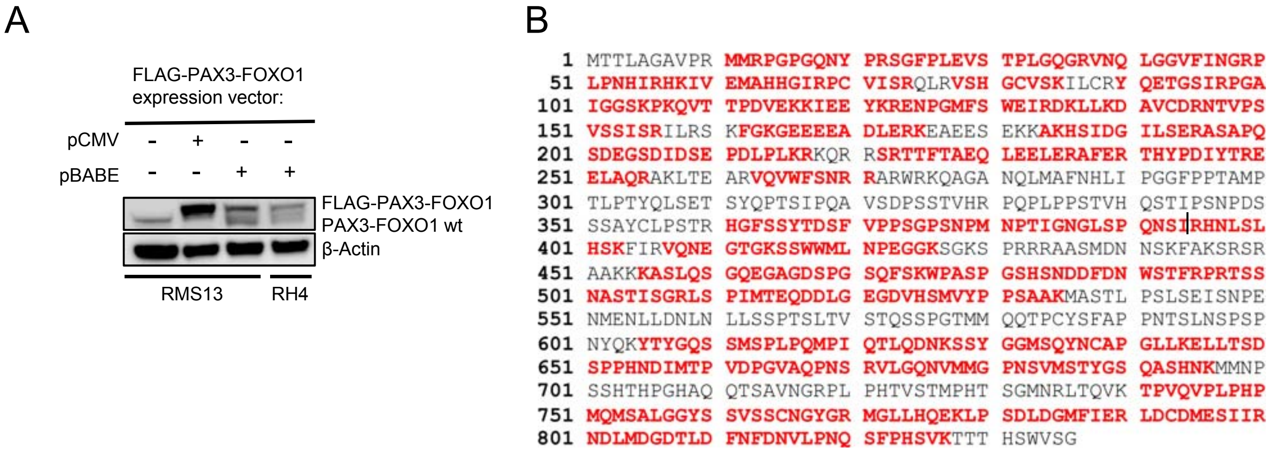
IP experiments were performed using anti-FOXO1 (C-20) (sc-9808; Santa Cruz Biotechnology) and monoclonal ANTI-FLAG® M2 antibody (F1804, Sigma-Aldrich). Reverse IP was performed with anti-CHD4 (A301-082A, polyclonal, rabbit, Bethyl Laboratories) and chromatin immunoprecipitations were performed using anti-CHD4 antibody (ab70469, [3F2/4] ChIP Grade, Abcam) and anti-Pax3/7 (N-19) (sc-7749X; goat, polyclonal, Santa Cruz Biotechnology).

Tissue arrays. Tissue arrays have been previously described (3). Briefly, three-micron thick sections of a tissue microarray representing formalin-fixed, paraffin-embedded tissues from 58 FP-RMS and 203 FN-RMS tumors were mounted on glass slides (SuperFrost Plus; Menzel, Braunschweig, Germany), deparaffinized, rehydrated and stained with hematoxylin and eosin (H&E) using standard histological techniques. Immunohistochemistry was performed with anti-CHD4 ChIP Grade (Abcam Limited, ab70469, dilution 1:500) as described in the immunohistochemistry section. For evaluation of stainability of individual tissue cores, a separate section of the tissue array was stained with the general RMS marker Desmin and only Desmin-positive tumors were selected for further analysis. Furthermore, only FP-RMS tumors for which PAX3-FOXO1 fusion status has been verified or which express TFAP2β, a marker of FP-RMS, have been included in the analyses (3).

1 Shapiro DN, Sublett JE, Li B, Downing JR, Naeve CW. Fusion of PAX3 to a member of the forkhead family of transcription factors in human alveolar rhabdomyosarcoma. Cancer research. 1993 Nov 1;**53**(21):5108-12.

2 Cao L, Yu Y, Bilke S, et al. Genome-wide identification of PAX3-FKHR binding sites in rhabdomyosarcoma reveals candidate target genes important for development and cancer. Cancer research. 2010 Aug 15;**70**(16):6497-508.

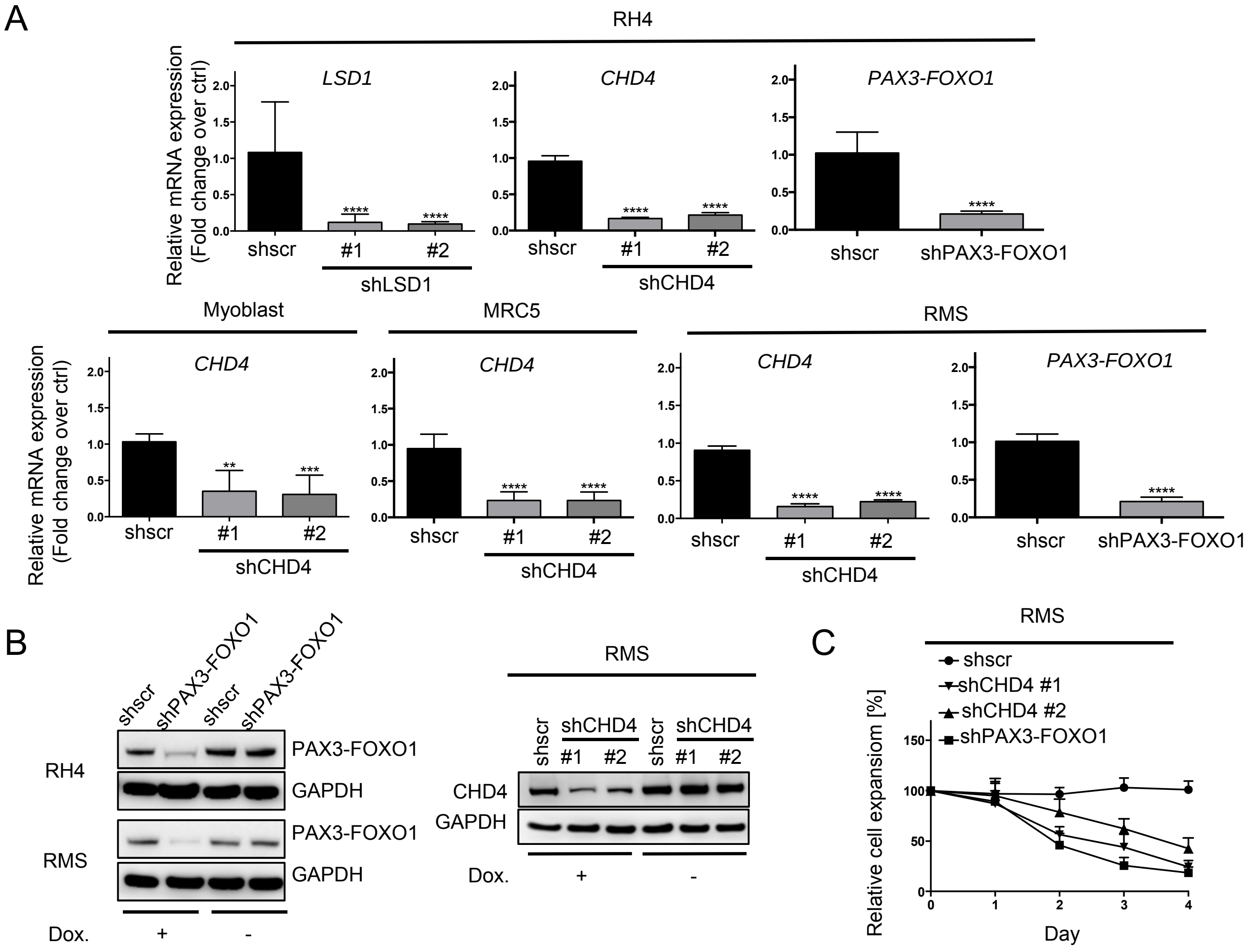
3 Wachtel M, Runge T, Leuschner I, et al. Subtype and prognostic classification of rhabdomyosarcoma by immunohistochemistry. Journal of clinical oncology : official journal of the American Society of Clinical Oncology. 2006 Feb 10;**24**(5):816-22.



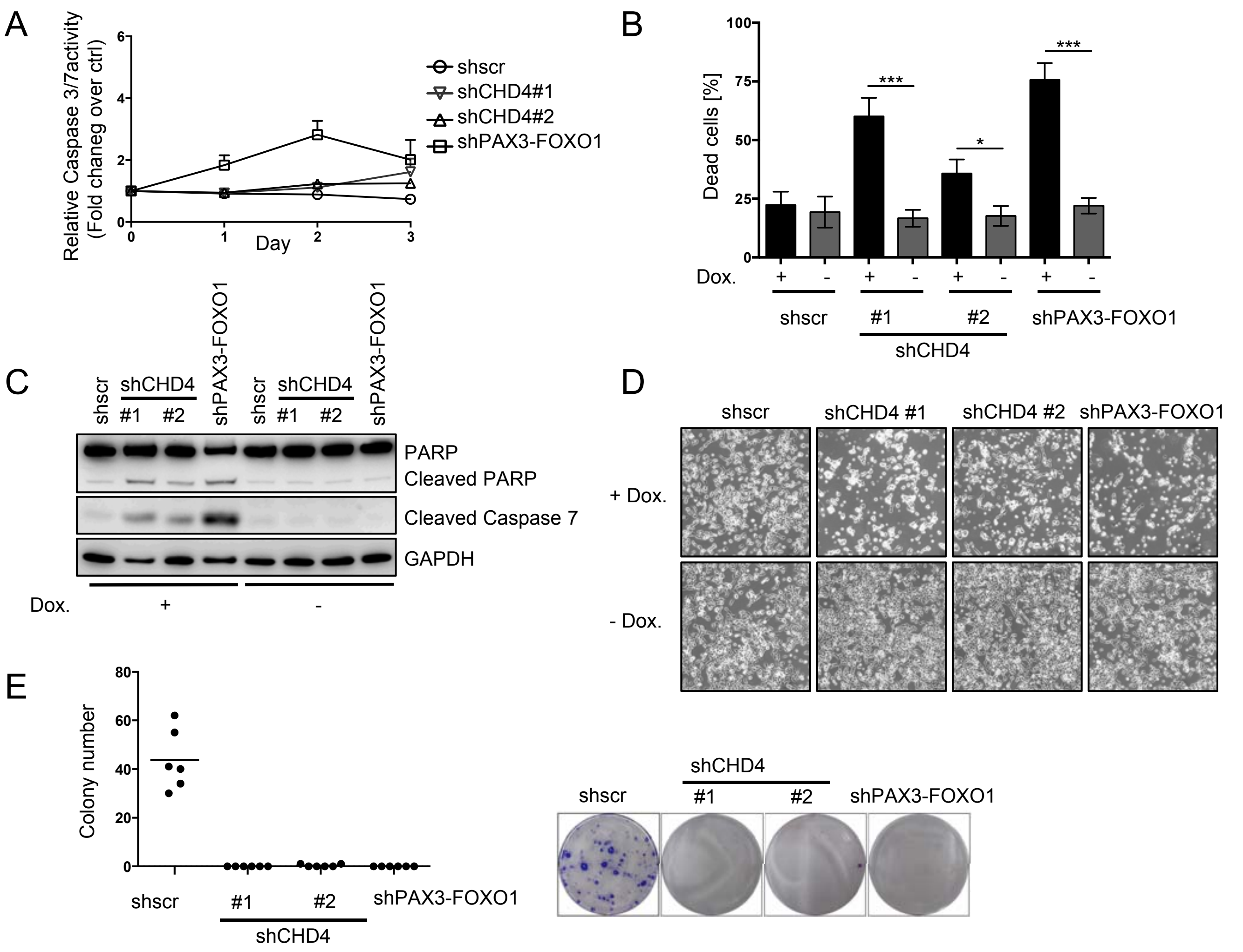
Supplementary Figure 1. Immunoprecipitation of FLAG-PAX3-FOXO1. (A) Qualitative comparison of different FLAG-PAX3-FOXO1 expression systems in RH4 and RMS13 cells. pCMV expression system for high over expression and pBABE for expression levels comparable to endogenous PAX3-FOXO1 expression level (wt). **(B)** Peptide sequence of the PAX3-FOXO1 fusion protein. Peptide sequences identified by mass spectrometry in RMS13 cells are marked in red and the break point of PAX3 and FOXO1 is indicated with a black vertical hatch mark.

Protein	Biological Role
RBBP4	Histone-binding, Scaffold protein in chromatin repressive complexes
CHD4	ATP-dependent chromatin remodeler, (CHD family)
LSD1	Histonedemethylase; Lysine-specific demethylation of H3 and proteins (e.g. p53)
BAZ1B/WSTF	Tyrosine kinase; phosphorylates H2AX during DNA damage response Essential component of WSTF-ISWI (WICH) chromatin remodeling complex
CHD1	ATP-dependent chromatin remodeler, (CHD family)
RCOR1	Component of the chromatin repressor complex CoREST
MYOG/MYF4	Muscle determination factor, bHLH transcription factor
ZNF148	Transcriptional repressor
CCAR2	Inhibitor of metalloenzymes (SIRT1, SUV39H1)

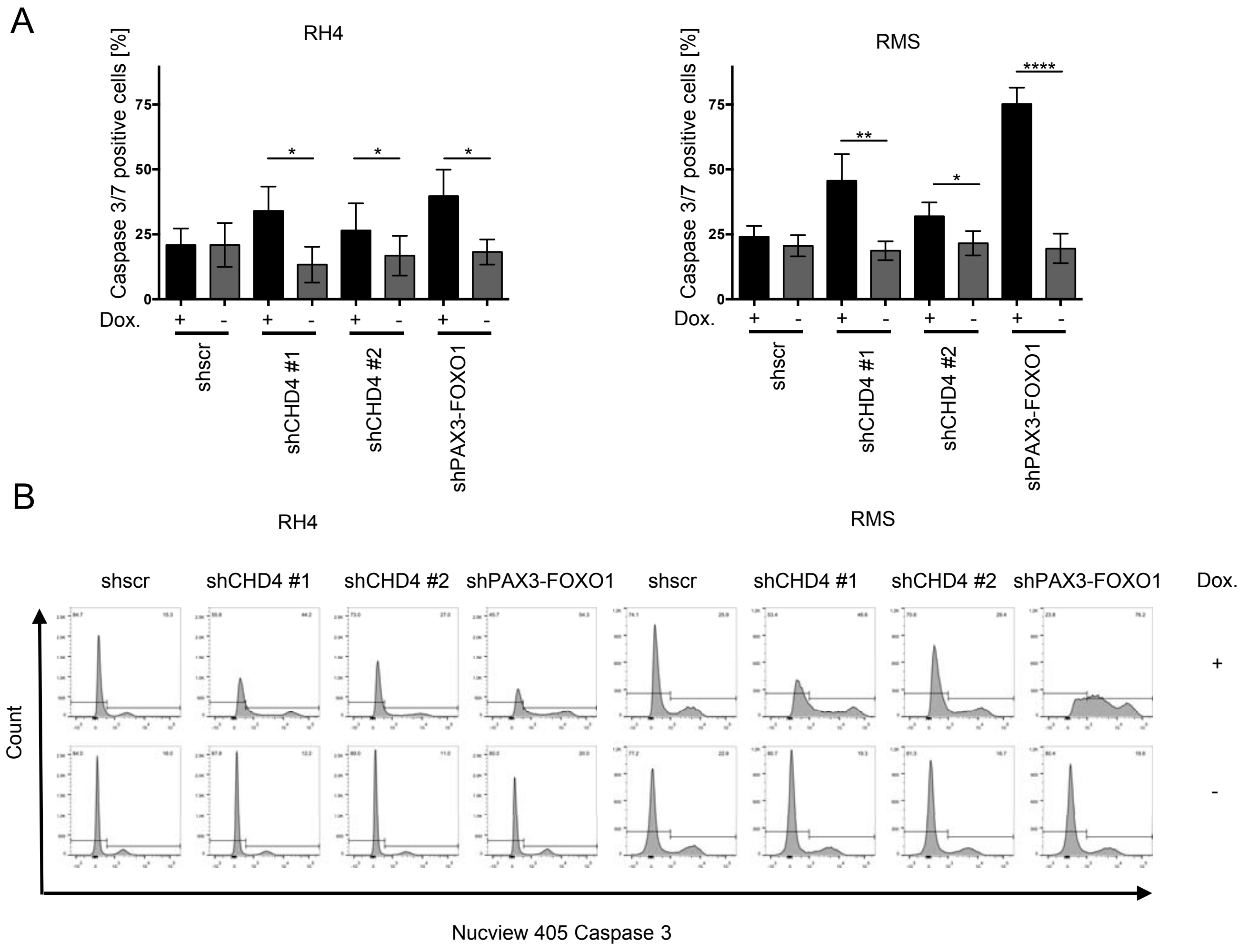
Supplementary Figure 2. Biological role of candidate interactors from siRNA screen



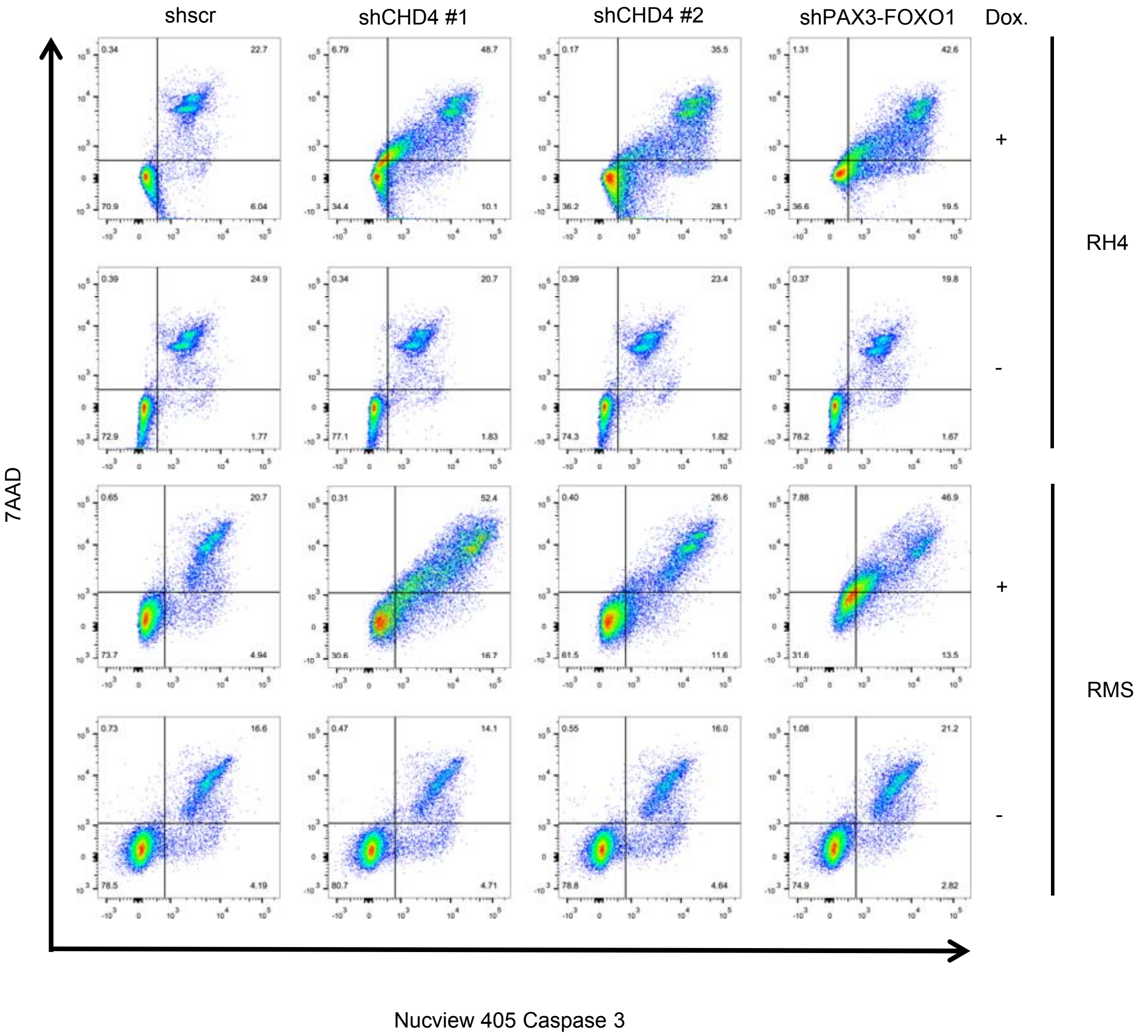
Supplementary Figure 3. Validation of LSD1, CHD4 and PAX3-FOXO1 silencing and effect on expansion of FP-RMS cell line RMS. (A) Knockdown of *CHD4*, *LSD1* or *PAX3-FOXO1* mRNA in indicated cell lines 72hrs after induction with doxycycline as measured by qRT-PCR. Bar charts are geometric means from three independent experiments with 95% CI (★★★★p< 0.0001 Dunnett`s multiple comparison test). Fold changes of mRNA expression are normalized to uninduced controls.. (B) Western blots after knockdown of PAX3-FOXO1 or CHD4 in indicated aRMS cell extracts 72hrs after induction with doxycycline (Dox.). Uninduced cells served as negative control and GAPDH was used as loading control. (C) Effect of CHD4 and PAX3-FOXO1 knockdown on expansion of the FP-RMS cell line RMS relative to uninduced control cells at indicated timepoints as measured by WST-assay.



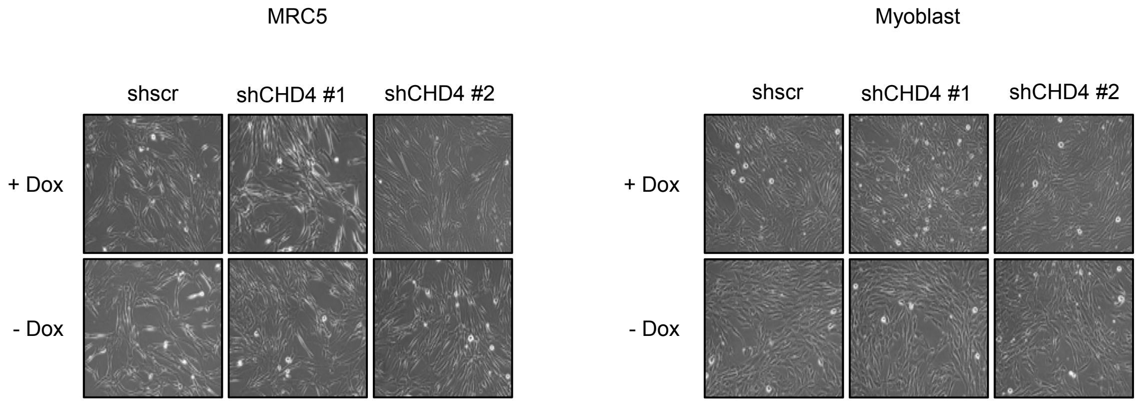
Supplementary Figure 4. CHD4 knockdown induces cell death of FP-RMS cell line RMS in vitro. (A) Caspase 3/7 activity in RMS cells 72hrs after induction of CHD4 silencing. Fold change of Caspase 3/7 activity was normalized to the uninduced control cells (ctrl). Shscr treated cells served as negative and PAX3-FOXO1 knockdown cells as positive control. Values are means ±SD of three independent experiments. (B) Percentage of dead cells 96hrs after treatment as in (A). Cells were stained with NucView caspase-3 substrate and 7-AAD and quantified by flow cytometry. Values are means ±SD of four independent experiments (★★★p< 0.001;★p< 0.05; Uncorrected Fisher`s LSD). (C) Western blot of PARP and cleaved Caspase 7 using extracts from the FP-RMS cell line RMS 72hrs after induction of CHD4 or PAX3-FOXO1 silencing and uninduced or shscr treated control cells. (D) Representative phase-contrast images of RMS cells 72h after induction of silencing with doxycycline (Dox.) in indicated cell lines and uninduced control cells, magnification 100x. (E) Clonogenic assays on RMS cells at 12 days after induction of CHD4 silencing. Representative images for crystal violet stains and quantitation of number of colonies. The black bars represent the means.



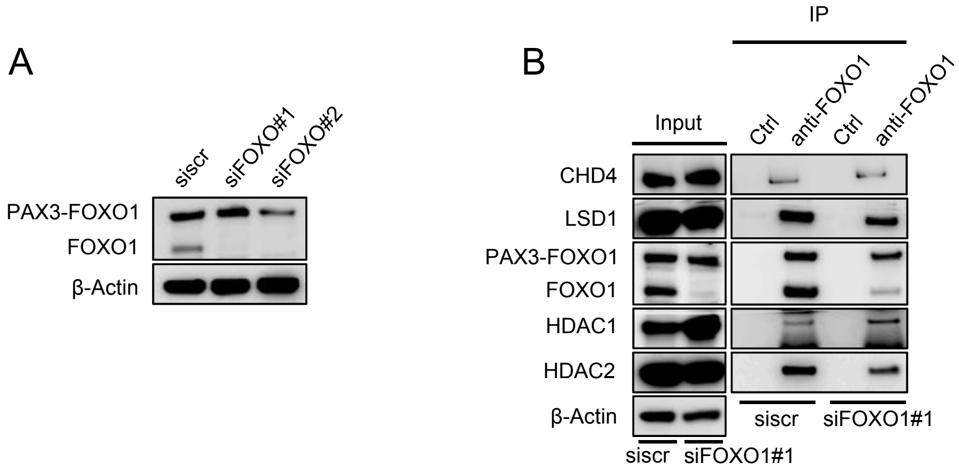
Supplementary Figure 5. Detection of Caspase 3/7 cleavage in individual cells by flow cytometry. (A) Percentage of Caspase 3/7 positive cells 72hrs after CHD4 knockdown in indicated FP-RMS cell lines and uninduced controls. Cells were stained with NucView 405 Caspase 3 substrate and quantified by flow cytometer. Values are means ±SD of four independent experiments (★★★★p< 0.0001; ★★p< 0.01, ★p< 0.05; Uncorrected Fisher`s LSD). (B) FACS histograms of cells from (A). Histograms show number of cells after exclusion of cell doublets gated on forward and side scatter characteristics and percentage of 3/7 positive and negative cells.



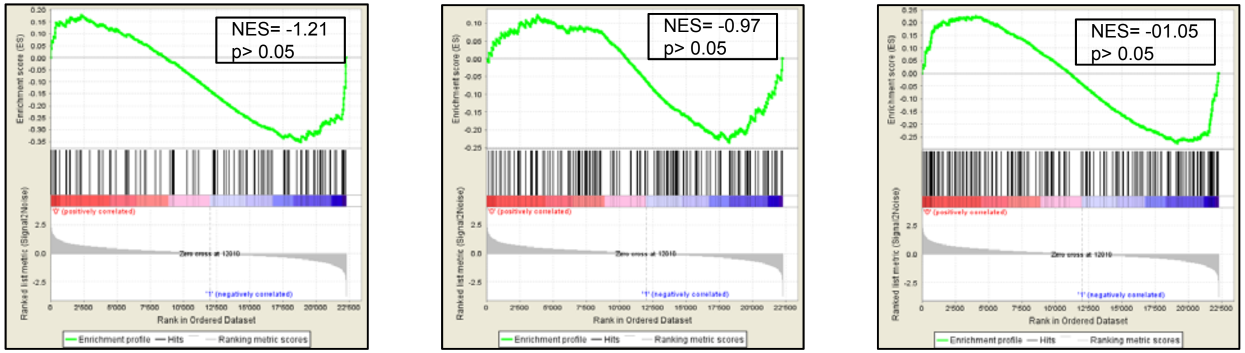
Supplementary Figure 6. Percentage of Caspase 3/7 and/or 7AAD positive FP-RMS cells. FACS histogram analysis of indicated cells 96hrs after induction of CHD4 silencing with doxycycline and uninduced controls stained with Nucview 405 Caspase 3 substrate and 7AAD. Plots show live and dead cells after exclusion of cell doublets gated on forward- and side scatter characteristics, and the percentage of DAPI and 7AAD positive or negative cells.



Supplementary Figure 7. CHD4 silencing does not affect normal human MRC5 or myoblast cells. Representative bright-field images of MRC5 and myoblast cells 72hrs after induction of CHD4 silencing with doxycycline (Dox) in indicated cell lines and uninduced control cells, magnification 100x.



Supplementary Figure 8. Interaction of PAX3-FOXO1 with NuRD complex components persists after FOXO1 silencing. (A) Western blots showing FOXO1 silencing efficiency and effect on PAX3-FOXO1 expression level after treatment of RH4 cells with indicated siRNAs. SiFOXO1#1, not affecting PAX3-FOXO1 expression level, was used in (B). (B) Representative western blots of endogenous PAX3-FOXO1 IPs and lysates from scrambled control and FOXO1 knockdown RH4 cells. PAX3-FOXO1 and FOXO1 were precipitated by the anti-FOXO1 antibody and uncoated beads served as negative control (ctrl).

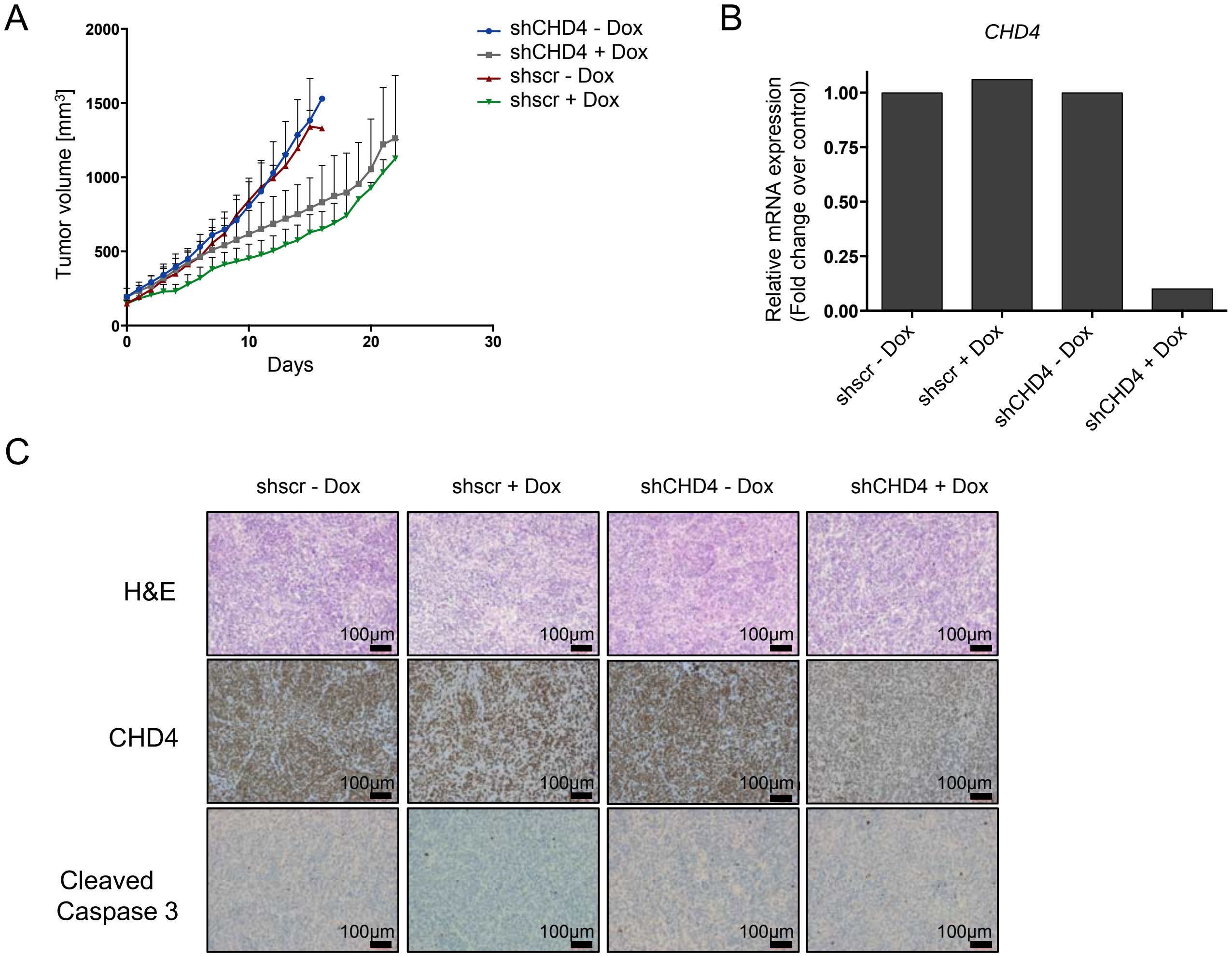


PAX3-FOXO1 directly downregulated geneset
shCHD4 rank ordered dataset

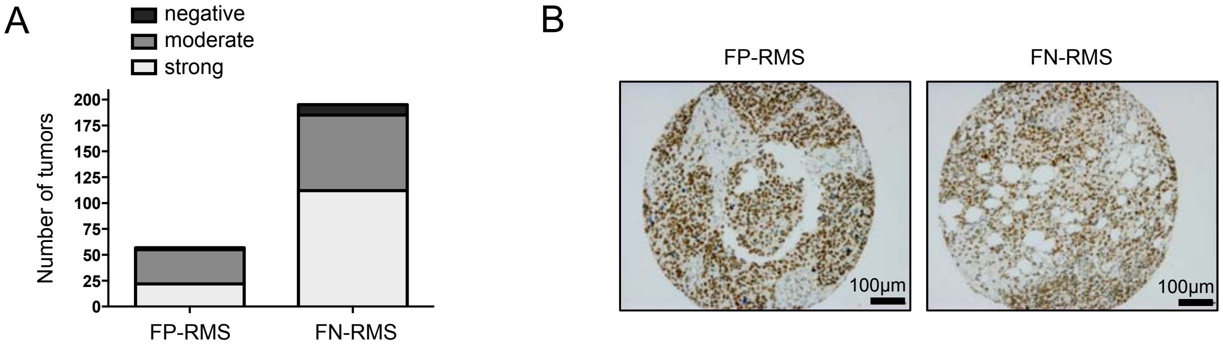
PAX3-FOXO1 indirectly upregulated geneset
shCHD4 rank ordered dataset

PAX3-FOXO1 indirectly downregulated geneset
shCHD4 rank ordered dataset

Supplementary Figure 9. CHD4 depletion does not affect PAX3-FOXO1 indirectly affected or directly repressed genes. Gene set enrichment analysis using CHD4 regulated genes in RH4 cells as the rank ordered data set and PAX3-FOXO1 targets as the geneset. Left panel: GSEA using 106 directly PAX3-FOXO1 downregulated genes as geneset (fold change> 1.7, p< 0.05). Middle panel: GSEA using 144 indirectly upregulated PAX3-FOXO1 targets as geneset. (fold change> 2.0, p< 0.05). Right panel: GSEA using the 191 indirectly downregulated PAX3-FOXO1 targets as geneset (fold change>, p< 0.05). Normalized enrichment score (NES) and p-value are shown.



Supplementary Figure 10. CHD4 inhibition in RD cell xenografts. *In vivo* treatment of NOD/Scid mice engrafted with RD cells containing stably integrated doxycycline inducible shCHD4#1 or shscr expression vectors. Mice bearing palpable tumors were treated intraperitonealy for two days with either vehicle control or doxycycline at a dose of 53.3 mg/kg. Additionally starting from the first day of treatment mice were fed with doxycycline supplemented food or control food. (A) Left panel: Absolute tumor volumes of xenografts upon treatment. Absolute tumor volume was measured by caliper. ShCHD4 groups consisted of 5 mice and shscr groups consisted of 4 mice. Right panel: *CHD4* mRNA levels in one representative tumor of each group after 4 days of doxycycline treatment. *CHD4* expression level of the treated tumor was normalized to the corresponding untreated tumor. (B) Immunohistochemical stainings of tumors with indicated antibodies. Tumors were excised four days after doxycycline treatment start.



Supplementary Figure 11. CHD4 is expressed in human FP-RMS and FN-RMS tumors. (A) Patient-derived tissue microarray immunohistochemically stained for CHD4 expression, FP-RMS (n = 57) and FN-RMS (n=195). Per patient only strongest staining tumor biopsy core was considered. Patients were grouped according the following semiquantitative scoring system into negative, moderate or strong CHD4 expression. The intensity of staining was classified as weak (1) or strong (2), and the staining pattern was classified as negative (0 : 0%), sporadic (1 : 1% to 25%), focal (2 : 26% to 50%) or diffuse (3 : ≥51%). An overall expression score was calculated by multiplying the intensity and positivity scores: 0 (negative, aRMS=2, eRMS=10), 1-3 (moderate, aRMS=33, eRMS=73), 4-6 (strong, aRMS=22, eRMS=112). (B) Representative FP-RMS and FN-RMS tumor core of CHD4 strong expression cohorts.