Supplementary Table S1: PAX3-FOXO1 candidate interactors

Total number of proteins: 230 Nuclear proteins : 201

Exclusive unique peptide count RH4 RMS RMS RMS FLAG#1 FLAG#2 FLAG#3 FLAG#4

Protein name Chromatin regulating complexes Gen name Chromatin modifying complexes: 6 Proteins

Chromatin modifying complexes. 0 Proteins					
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-Iysine 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°	6	11	8	0
SWI/SNF complex subunit SMARCC2	SMARCC2/BAF170°	2	2	0	0
Isoform 2 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1	SMARCD1/BAF60ac	2	0	0	4
Isoform 2 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 3	SMARCD3/BAF60cc	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 laso associates with RCOR1 to 2inc tinger domain protein 2A
 ^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

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 SATB1	SATB1	12	3	2	4
	MECP2		4		8
Isoform B of Methyl-CpG-binding protein 2		3		2	
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	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
			7	4	-
Activity-dependent neuroprotector homeobox protein	ADNP	1			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
Basonucin 2 Nascent polypeptide-associated complex subunit alpha	NACA	0	3	2	0
Nascent polypeptide-associated complex suburit alpha	INACA	U	3	4	U

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

T					
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					
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

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

Isoform 2 of Transportin-1	INPO1	4	0	1	3
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-diphosphooligosaccharideprotein 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: Other: Total: 18 11 29

Supplementary Table S2: Custom siRNA Library

		Custom SIRNA Library				
RefSeq Accession Number	Gene Symbol	Full Gene Name	siRNA ID	Exon(s)	Sense siRNA Sequence	Antisense siRNA Sequence
NM_006015	ARID1A	AT rich interactive domain 1A (SWI-like)	s15784	Targeted 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 NM_032408	BAZ1B BAZ1B	bromodomain adjacent to zinc finger domain, 1B bromodomain adjacent to zinc finger domain, 1B	s17209 s17210	Not Determined	CCUUCGUAGUGAUCUCAUUtt CCUCAUUGCAUACUACAAAtt	AAUGAGAUCACUACGAAGGaa UUUGUAGUAUGCAAUGAGGtg
NM_013449	BAZ16 BAZ2A	bromodomain adjacent to zinc finger domain, 18 bromodomain adjacent to zinc finger domain, 2A	s22056	Not Determined 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 NM 012295	BLM CABIN1	Bloom syndrome, RecQ helicase-like calcineurin binding protein 1	s1999 s24000	22	GAUAUCUUCCAAAACGAAAtt GGAUUGAUUUGUCGGACUAtt	UUUCGUUUUGGAAGAUAUCtt UAGUCCGACAAAUCAAUCCtt
NM_012295	CABIN1 CABIN1	calcineurin binding protein 1	s24000	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 NM_001273	CHD4 CHD4	chromodomain helicase DNA binding protein 4 chromodomain helicase DNA binding protein 4	s2983 s2984	12 29	CUAUCGCUAUGGGAUAAAAtt GCAAUUAUGCGAUAUGGUAtt	UUUUAUCCCAUAGCGAUAGaa UACCAUAUCGCAUAAUUGCat
NM_006015	CHD4 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 NM_013449	CTBP1 CTBP1	C-terminal binding protein 1 C-terminal binding protein 1	s3698 s3699	8,7 4,3	CUCUGAAGGAUGCACCCAAtt GGCAGUGGUUUUGACAACAtt	UUGGGUGCAUCCUUCAGAGgg UGUUGUCAAAACCACUGCCaa
NM_000057	CTBP1 CTBP1	C-terminal binding protein 1	s3699 s3700	4,3	GUUUGUGACUGUAACCAUUtt	AAUGGUUACAGUCACAAACat
NM_000057	CTBP1 CTBP2	C-terminal binding protein 2	s3700 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 NM_001270	CTCF DDX1	CCCTC-binding factor (zinc finger protein) DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	s20968	4	GCUUUGCAGUUACACGUGUtt GAAUCUAUCCCAUUGAUCUtt	ACACGUGUAACUGCAAAGCtc
NM_001270 NM_001270	DDX1 DDX1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1 DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	s4001 s4002	3 10	GAAUCUAUCCCAUUGAUCUtt GAUGUUACCUGGAUAUAGAtt	AGAUCAAUGGGAUAGAUUCag 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 NM_032408	DDX27 DDX27	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27 DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	s31196 s445946	Not Determined	GCAGAUACACUCAAAGUAAtt GAAAGAAAAGGAAAACAGAtt	UUACUUUGAGUGUAUCUGCtt UCUGUUUUCCUUUUCUUUCga
NM 032408	DDX27 DDX41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27 DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	s28120	Not Determined	GGAACAAGAGAGAGAGGGUUAtt	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 NM_006015	DHX30 DHX30	DEAH (Asp-Glu-Ala-His) box polypeptide 30 DEAH (Asp-Glu-Ala-His) box polypeptide 30	s22643 s22644	Not Determined Not Determined	GGACCAUAGAUGUUACCGAtt CUAGGGACCUAUUAAAAGAtt	UCGGUAACAUCUAUGGUCCct 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 NM_013449	HDAC2 HDAC2	histone deacetylase 2 histone deacetylase 2	s6494 s6495	1	GGCAGAUAUUUAAGCCUAUtt CUACGACGGUGAUAUUGGAtt	AUAGGCUUAAAUAUCUGCCca UCCAAUAUCACCGUCGUAGta
NM_000057	SAP18	Sin3A-associated protein, 18kDa	s0495 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 HIRA	GATA zinc finger domain containing 2A HIB histone cell cycle regulation defective homolog A /S, cerevisiae)	s29502	Not Determined 23	GCGGCAGAGUCAAAUACAAtt	UUGUAUUUGACUCUGCCGCaa UCGGUAUUCAAACCCUUCGtt
NM_001270 NM_001270	HIRA	HIR histone cell cycle regulation defective homolog A (S. cerevisiae) HIR histone cell cycle regulation defective homolog A (S. cerevisiae)	s14521 s14522	23 15	CGAAGGGUUUGAAUACCGAtt 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 AOF2	amine oxidase (flavin containing) domain 2 amine oxidase (flavin containing) domain 2	s617 s618	Not Determined Not Determined	GGUCUUGGAGGGAAUCCUAtt GAGCAAGAGUUUAACCGGUtt	UAGGAUUCCCUCCAAGACCtg ACCGGUUAAACUCUUGCUCta
NM_006015 NM_032408	AOF2 AOF2	amine oxidase (flavin containing) domain 2 amine oxidase (flavin containing) domain 2	s618 s619	Not Determined	GAGCAAGAGUUUAACCGGUtt CUGCAGUUGUGGUUGGAUAtt	UAUCCAACCACAACUGCUCta
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
NINA 004474	KIAA1967	KIAA1967	s33737	19,19	GGCUCUACCUAGAGAACAAtt	
NM_021174	1/14 * * * * * *		s33738	14,14	GGCUAUAGAGUUUAUAAGAtt	UCUUAUAAACUCUAUAGCCaa
NM_021174	KIAA1967 MECP2	KIAA1967 methyl CoG binding protein 2 (Rett syndrome)	s8644	Not Determined	GGAAGCUCCUUCUCAACAU#	AUCHUGACAAGGAGCUUCCoo
NM_021174 NM_004992	MECP2	methyl CpG binding protein 2 (Rett syndrome)	s8644 s8645	Not Determined Not Determined	GGAAGCUCCUUGUCAAGAUtt GACAUUGUUUCAUCCUCCAtt	AUCUUGACAAGGAGCUUCCca UGGAGGAUGAAACAAUGUCtt
NM_021174			s8644 s8645 s8646	Not Determined Not Determined Not Determined	GGAAGCUCCUUGUCAAGAUtt GACAUUGUUUCAUCCUCCAtt GCUUCCCGAUUAACUGAAAtt	AUCUUGACAAGGAGCUUCCca UGGAGGAUGAAACAAUGUCtt UUUCAGUUAAUCGGGAAGCtt
NM_021174 NM_004992 NM_004992	MECP2 MECP2	methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome)	s8645	Not Determined	GACAUUGUUUCAUCCUCCAtt GCUUCCCGAUUAACUGAAAtt GGAUCUACUGGAAGAAGUAtt	UGGAGGAUGAAACAAUGUCtt
NM_021174 NM_004992 NM_004992 NM_004992 NM_004939 NM_004739 NM_004739	MECP2 MECP2 MECP2 MTA2 MTA2	methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) metastasia sassociated 1 family, member 2 metastasia sassociated 1 family, member 2	s8645 s8646 s17629 s17630	Not Determined Not Determined 13 10	GACAUUGUUUCAUCCUCCAtt GCUUCCCGAUUAACUGAAAtt GGAUCUACUGGAAGAAGUAtt GCAUAGUCCAGUUUUAUUAtt	UGGAGGAUGAAACAAUGUCtt UUUCAGUUAAUCGGGAAGCtt UACUUCUUCCAGUAGAUCCaa UAAUAAAACUGGACUAUGCtg
NM_021174 NM_004992 NM_004992 NM_004992 NM_004739 NM_004739 NM_004739	MECP2 MECP2 MECP2 MTA2 MTA2 MTA2	methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) metastasis associated 1 family, member 2 metastasis associated 1 family, member 2 metastasis associated 1 family, member 2	s8645 s8646 s17629 s17630 s17631	Not Determined Not Determined 13	GACAUUGUUUCAUCCUCCAtt GCUUCCCGAUUAACUGAAAtt GGAUCUACUGGAAGAAGUAtt GCAUAGUCCAGUUUUAUUAtt CCACAGACCGGUAUAUUCAtt	UGGAGGAUGAAACAAUGUCit UUUCAGUUAAUCGGGAAGCit UACUUCUUCAGUAGAUCCaa UAAUAAAACUGGACUAGGig UGAAUAUACCGGUCUGUGGit
NM_021174 NM_004992 NM_004992 NM_004992 NM_004739 NM_004739 NM_004739 NM_004739 NM_004739 NM_004739	MECP2 MECP2 MECP2 MTA2 MTA2 MTA2 MTA2 MYOG	methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) metastasis associated 1 family, member 2 metastasis associated 1 family, member 2 metastasis associated 1 family, member 2 myogenin (myogenic factor 4)	s8645 s8646 s17629 s17630 s17631 s9232	Not Determined Not Determined 13 10	GACAUUGUUUCAUCCUCCAit GCUUCCCGAUUAACUGAAAtt GGAUCUACUGGAAGAAGUAit GCAUAGUCCAGUUUUAUUAIt CCACAGACGGUAUAUUCAit ACUUAUUUGGAUUUCCUUUit	UGGAGGAUGAAACAAUGUCtt UUUCAGUUAAUCGGGAAGCtt UACUUCUUCCAGUAGAUCCaa UAAUAAAACUGGACUAUGCtg UGAAUAUACCGGUCUGUGGtt AAAGGAAAUCCAAAUAAGUta
NM_021174 NM_004992 NM_004992 NM_004992 NM_004739 NM_004739 NM_004739 NM_002479 NM_002479	MECP2 MECP2 MECP2 MTA2 MTA2 MTA2 MYOG MYOG	methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) metastasia sasociated 1 family, member 2 metastasia sasociated 1 family, member 2 metastasia sasociated 1 family, member 2 myogenin (myogenic factor 4) myogenin (myogenic factor 4)	s8645 s8646 s17629 s17630 s17631 s9232 s9233	Not Determined Not Determined 13 10	GACAUUGUUUCAUCCUCAII GCUUCCCGAUUAACUGAAAI GCAUCUACUGAAGAAGAAGUAII GCAUCAACUGAAGAAGUAII CCACAGACCGGUAUAUUCAII ACUUAUUUGGAUUUCCUUUI CAAGGUCUCCUGUGCUGAAII	UGGAGGAUGAAACAAUGUCtt UUUCAGUUAAUCGGGAAGGtt UACUUCUUCCAGUAGUCCaa UAAUAAACUGGACUAUGCtg UGAAUAUACCGGUCUGUGGtt AAAGGAAAUCCAAUAAGUla UUCAGCACAGGAGACCUUGgt
NM_021174 NM_004992 NM_004992 NM_004992 NM_004739 NM_004739 NM_004739 NM_002479 NM_002479 NM_002479	MECP2 MECP2 MTA2 MTA2 MTA2 MTA2 MYOG MYOG MYOG	methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) metastasis associated 1 family, member 2 metastasis associated 1 family, member 2 metastasis associated 1 family, member 2 myogenin (myogenic factor 4)	s8645 s8646 s17629 s17630 s17631 s9232 s9233 s9234	Not Determined Not Determined 13 10	GACAUUGUUUCAUCCUCAII GCUUCCCGAUUAACUGAAAt GGAUCUACUGGAAGAAGAAGUAI GCAUAGUCCAGUUUUAUUAAt CCACAGACCGGUAUAUUCAI ACUUAUUUGGAUUUCCUUUI CAAGGUCUCCUGUGCUGAAAt CCUCAUCCAUGUAAGGUUAIt	UGGAGGAUGAAACAAUGUCtt UUUCAGUUAAUCGGGAAGCtt UACUUCUUCCAGUAGAUCCaa UAAUAAAACUGGACUAUGCtg UGAAUAAUACCGGUCUGUGGtt AAAGGAAUCCAAAUAAGUta UUCAGCACAGGACACCUUGgt UAACCUUACAUGGAUGAGGaa
NM_021174 NM_004992 NM_004992 NM_004739 NM_004739 NM_004739 NM_004739 NM_002479 NM_002479 NM_002479 NM_002479 NM_002479 NM_020867	MECP2 MECP2 MECP2 MTA2 MTA2 MTA2 MYOG MYOG	methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) metastasia sasociated 1 family, member 2 metastasia sasociated 1 family, member 2 metastasia sasociated 1 family, member 2 myogenin (myogenic factor 4) myogenin (myogenic factor 4) myogenin (myogenic factor 4)	s8645 s8646 s17629 s17630 s17631 s9232 s9233	Not Determined Not Determined 13 10	GACAUUGUUUCAUCCUCAII GCUUCCCGAUUAACUGAAAI GCAUCUACUGAAGAAGAAGUAII GCAUCAACUGAAGAAGUAII CCACAGACCGGUAUAUUCAII ACUUAUUUGGAUUUCCUUUI CAAGGUCUCCUGUGCUGAAII	UGGAGGAUGAAACAAUGUCtt UUUCAGUUAAUCGGGAAGGtt UACUUCUUCCAGUAGUCCaa UAAUAAACUGGACUAUGCtg UGAAUAUACCGGUCUGUGGtt AAAGGAAAUCCAAUAAGUla UUCAGCACAGGAGACCUUGgt
NM_021174 NM_004992 NM_004992 NM_004992 NM_004739 NM_004739 NM_004739 NM_004739 NM_002479 NM_002479 NM_002479	MECP2 MECP2 MTA2 MTA2 MTA2 MTA2 MYOG MYOG NCOA5	methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) metastasis associated 1 family, member 2 metastasis associated 1 family, member 2 metastasis associated 1 family, member 2 myogenin (myogenic factor 4) myogenin (myogenic factor 5)	\$8645 \$8646 \$17629 \$17630 \$17631 \$9232 \$9233 \$9233 \$9234 \$33688	Not Determined Not Determined 13 10	GACAUUGUUUCAUCCUCAII GCUUCCCGAUUAACUGAAAt GGAUCUACUGAAGAAGAAGIAI GGAUCUACUGAAGAAGAAGIAI CCACAGACCGGUAUUUAUUAIt CCACAGACCGGUAUUAAI ACUUAUUUGGAUUUCCUUUIt CAAGGUCUCCUGUGCUGAAIt CCUCAUCCAUGUAAGGUUAIt GGACCACAGACAUAGUAGaIt	UGGAGGAUGAAACAAUGUCtt UUUCAGUUAAUCGGGAAGCtt UACUUCUUCCAGUAGAUCCaa UAAUAAACUGGACUAUGCtg UGAAUAAUACCGGUCUGUGGtt AAAGGAAAUCCAAAUAAGUta UUCAGCACAGGAGACCUUGgt UAACCUUACAUGAUCAAGaa UCUACUAUGUCUGUGGUCCcg
NM_021174 NM_004992 NM_004992 NM_004992 NM_004739 NM_004739 NM_002479 NM_002479 NM_022479 NM_022479 NM_0226967 NM_020967 NM_0220967 NM_014223	MECP2 MECP2 MTA2 MTA2 MTA2 MTA2 MYOG MYOG MYOG NCOA5 NCOA5 NCOA5 NFYC	methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) metastasia sasociated 1 family, member 2 metastasia sasociated 1 family, member 2 metastasia sasociated 1 family, member 2 myogenin (myogenic factor 4) myogenin (myogenic factor 4) myogenin (myogenic factor 4) nuclear receptor coactivator 5 nuclear receptor coactivator 5 nuclear receptor factor Y, gamma	s8645 s8646 s17629 s17630 s17631 s9232 s9233 s9234 s33688 s33689 s33690 s9534	Not Determined Not Determined 13 10 3 3 3 4 3 Not Determined	GACAUUGUUUCAUCCUCCAII GCUUCCCGAUUAACUGAAAti GGAUCUACUGAAGAAGAAGAA GGAUACUCCAGUUUUAUUAIt CCACAGACCGGUAUUAAUUAIt ACUUAUUUGGAUUUCCUUUIt CAAGGUCUCCUGUGCUGAAti CCUCAUCCAUGUAAGGUUAIt GGACCACAGACAUAGUUAIt CCGUUACGACAUAGAUAGAIt CCGUUACGAGAUAGCUUUIt GGAUUUUCAGAGUCAGGAIt GGAUUUUAACAGUGAAAGAIt	UGGAGGAUGAAACAAUGUCtt UUUCAGUUAAUCGGGAAGCtt UACUUCUUCCAGUAGAUCCaa UAAUAAACUGGACUAUGCtg UGAAUAAUCCGGUCUGUGGtt AAAGGAAUCCAAAUAAGUta UUCAGCACAGGAGACCUUGgt UAACCUUACAUGGAUGAGGaa UCUACUUACAUGGUGGUCCcg AAAGCUAUCUCGAAAUGCct UCGUGAUCUCGAAAAUCCct UCUUUCACUGUUAAAUUCCgg
NM_021174 NM_004992 NM_004992 NM_004739 NM_004739 NM_004739 NM_002479 NM_002479 NM_022479 NM_020967 NM_020967 NM_020967 NM_014223	MECP2 MECP2 MECP2 MTA2 MTA2 MTA2 MYOG MYOG MYOG MYOG NCOA5 NCOA5 NCOA5 NFYC NFYC	methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) metastasis associated 1 family, member 2 metastasis associated 1 family, member 2 metastasis associated 1 family, member 2 myogenin (myogenic factor 4) myogenin (myogenic factor 4) myogenin (myogenic factor 4) myogenin (myogenic factor 4) muclear receptor coactivator 5 nuclear receptor coactivator 5 nuclear receptor coactivator 5 nuclear receptor coactivator 5 nuclear rancoription factor Y, gamma nuclear transcription factor Y, gamma	s8645 s8646 s17629 s17630 s17631 s9232 s9233 s9234 s33688 s33689 s33690 s9534 s9535	Not Determined Not Determined 13 10 10 3 3 4 3 3 Not Determined Not Determined	GACAUUGUUUCAUCCUCCAII GCUUCCCGAUUAACUGAAAI GCUUCCCGAUUAACUGAAAI GCAUCUACUGAAGAAGUAI CCACAGACCGGUAUAUUCAI ACUUAUUGGAAUCACUUUII CAAGGUCUCCUGUGCUGAAI CCUCAUCCAUGUAGGUUAI CCUCAUCCAUGAAGAI CCGUUACAGAGAUAGAAI CCGUUACAGAGAUAGCUUUII GGAUUUUCAGAGUCAAGAI GGAUUUAAGAGUGAAGAI GGCUCGUAUUAAGAAGAUUIII	UGGAGGAUGAAACAAUGUCtt UUUCAGUUAAUCGGGAAGGtt UACUUCUUCCAGUAGAUCCaa UAAUAAACUGGACUAUGCtg UGAAUAUACCGGUCUGUGGtt AAAGGAAUCCAAUAAGUa UUCAGCACAGGAGACCUUGgt UAACCUUACAUGGAUGAGGaa UCUCUCUGUCUGUGGUCCcg AAAGCUAUCUCUGUAACGGtc UCGUGAUCUGUAAACGGt UCGUGAUCUGUAAACGGt UCGUGAUCUGUAAACGGt
NM_021174 NM_004992 NM_004992 NM_004739 NM_004739 NM_004739 NM_002479 NM_002479 NM_002479 NM_020967 NM_020967 NM_020967 NM_02233 NM_014223 NM_014223	MECP2 MECP2 MECP2 MTA2 MTA2 MTA2 MYOG MYOG MYOG NCOA5 NCOA5 NCOA5 NCOA5 NFCC NFYC NFYC	methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) metastasia sasociated 1 family, member 2 metastasis associated 1 family, member 2 metastasis associated 1 family, member 2 myogenin (myogenic factor 4) myogenin (myogenic factor 4) myogenin (myogenic factor 4) muclear receptor coactivator 5 nuclear resciption factor Y, gamma nuclear transcription factor Y, gamma	s8645 s8646 s17629 s17630 s17631 s9232 s9233 s9234 s33688 s33689 s33690 s9534 s9535 s9536	Not Determined Not Determined 13 10 10 3 3 3 3 4 4 3 Not Determined Not Determined	GACAUUGUUUCAUCCUCCAH GCUUCCCGAUUAACUGAAAH GCAUCUACUGAAAA GCAUCUACUGAAAA GCAUCUACUGAAAAAAUUUAH GCAUCUACUGAGUUUUAUUAH CCAAGUUCCUUUH CAAGGUUCCUGUUGUGAAH CCUUACUACUAGAAAAAAH CCUUACUACUAGUAAH CCUCUAUCCUGUUGUGAAH CCUCUAUCAGAAAAAAH CCUUACAAGAAAAAAAAAAAAA GGAUUUUCGAGAUCAGCGAH GGAUUUUAGAAAAAAAH GGAUUUUAAGAAAAAAH GGAUUUUAAAAAAAAH GGAUUAUAAAAAAAAH GGAUCAUCAUCACAAAAAH	UGGAGGAUGAAACAAUGUCtt UUUCAGUUAAUCGGGAAGCtt UACUUCUUCCAGUGAUCCaa UAAUAAACUGGACUAUGCtg UGAAUAUACCGGUCUGUGGtt AAAGGAAAUCCAAAUAAGUta UUCACCACAGAGACCCUUGgt UUACCCUUACAUGGAUGAGGaa UCUACUUGUGUAGGGCCg AAAGCUAUCUCUGUAACGGtc UCGUGAUCUCGAAAAUCCcg UCUUCACUGUUAAAUGACCgg AAUCUUCUUAUAACGGCCgg UGUGCGAUGAUGAUCUGCCca
NM_021174 NM_004992 NM_004992 NM_004739 NM_004739 NM_002479 NM_002479 NM_002479 NM_020967 NM_020967 NM_020967 NM_014223 NM_014223 NM_015292	MECP2 MECP2 MECP2 MTA2 MTA2 MTA2 MTA2 MTA2 MYOG MYOG NCOA5 NCOA5 NCOA5 NCOA5 NCOA5 NCOA5 NCOA5 NFYC PCNA	methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) metastasia sasociated 1 family, member 2 metastasia sasociated 1 family, member 2 metastasia sasociated 1 family, member 2 myogenin (myogenic factor 4) myogenin (myogenic factor 4) myogenin (myogenic factor 4) nuclear receptor coactivator 5 nuclear receptor coactivator 5 nuclear receptor coactivator 5 nuclear transcription factor Y, gamma nuclear transcription factor Y, gamma nuclear transcription factor Y, gamma	s8645 s8646 s17629 s17630 s17631 s9232 s9233 s9234 s33688 s33689 s33690 s9535 s9536 s10133	Not Determined Not Determined 13 10 10 3 3 3 4 3 Not Determined Not Determined Not Determined 5,4	GACAUUGUUUCAUCCUCCAH GCUUCCCGAUUAACUGAAAtt GGAUCUACUGAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	UGGAGGAUGAAACAAUGUCtt UUUCAGUUAAUCGGGAAGCtt UACUUCUUCCAGUAGAUCCaa UAAUAAAACUGGACUAUGCtg UGAAUAACUGGACUAUGCtg UGAAUAACUGGACUAUGGt UUCAGCACAGGAGACUUGt UUCAGCACAGGAGACUUGt UAACCUUACUGGAUGAGGaa UCUACUUGUGUGGUCCcg AAAGCUAUCUCGGAAAUCCct UCCUGAUCUCGAAAAUCCct UCUUUCACUGUUAAUACGGg AAUCUUCUUAAUACGAGCCag UGUGCGAUAGUGACGCa
NM_021174 NM_004992 NM_004992 NM_004739 NM_004739 NM_004739 NM_004739 NM_002479 NM_002479 NM_020967 NM_020967 NM_020967 NM_020967 NM_020967 NM_01223 NM_014223 NM_014223 NM_014223 NM_02592	MECP2 MECP2 MECP2 MTA2 MTA2 MTA2 MTA2 MTA2 MYOG MYOG MYOG NCOA5 NCOA5 NCOA5 NCOA5 NCOA5 NCOA5 NCOA5 NFYC NFYC PCNA	methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) metastasia sasociated 1 family, member 2 metastasis associated 1 family, member 2 metastasis associated 1 family, member 2 myogenin (myogenic factor 4) myogenin (myogenic factor 4) myogenin (myogenic factor 4) muclear receptor coactivator 5 nuclear resciption factor Y, gamma nuclear transcription factor Y, gamma	s8645 s8646 s17629 s17630 s17631 s9232 s9233 s9234 s33688 s33689 s9535 s9535 s10133 s10134	Not Determined Not Determined 13 10 10 3 3 4 3 Not Determined Not Determined Not Determined Not Determined	GACAUUGUUUCAUCCUCCAII GCUUCCCGAUUAACUGAAAI GCUUCCCGAUUAACUGAAAI GCAUCACUGAACAAGUAII GCAUCACUGAACAAGUUIA GCAUCACUGAGUUUAUUAUAII CCACACGGUAUAUUCAII CCACACGGUAUAUUCAII CAAGGUCCUGUGCUGAAII CCUCAUCCAUGUAGUUAII CCGUACACACAAGUUACUUUII CAAGGUCCUGUGCUGAAII CCGUUACAGAACACUGGAAI GGAUCUUCAGUGAGGAAI GGAUUUUCAGGAUCAGCGAII GGCUCGUAUUAACAGUGAAGAII GGCUCGUAUUAACAGAUGAAGAII GGCUCGUAUUAACAGAUUAUUACUCACACII GGAUUGUUCAUCACACGAAII GGCUCGUAUUAACAGAUUUACUCAAII GGAUUGAUCUCAAUCUCAAII	UGGAGGAUGAAACAAUGUCtt UUUCAGUUAAUCGGGAAGGtt UACUUCUUCCAGUAGUCCaa UAAUAAACUGGACUAUGCtg UGAAUAUACCGGUCUGUGGtt AAAGGAAUCCAAUAAGUa UUCAGCACAGGAGACCUUGgt UAACCUUACAUGGAUGAGGaa UCUCUCUGUCUGUGUCCCg AAAGCUAUCUCUGUAACGGtc UCUUUCACUGUUAAUGCCt UCUUUCACUGUUAAUGCCg AAUCUUCUUAAUACGAGCCag UGUGGAUGAUGAUCUCCGg UGGAGAUCUCGGCAUAUACGtg UUGCAGAAAUUUCACUCCgt
NM_021174 NM_004992 NM_004992 NM_004739 NM_004739 NM_002479 NM_002479 NM_002479 NM_020967 NM_020967 NM_020967 NM_014223 NM_014223 NM_015292	MECP2 MECP2 MECP2 MTA2 MTA2 MTA2 MTA2 MTA2 MYOG MYOG NCOA5 NCOA5 NCOA5 NCOA5 NCOA5 NCOA5 NCOA5 NFYC PCNA	methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) methyl CpG binding protein 2 (Rett syndrome) metastasis associated 1 family, member 2 metastasis associated 1 family, member 2 metastasis associated 1 family, member 2 metastasis associated 1 family, member 2 myogenin (myogenic factor 4) myogenin (myogenic factor 4) myogenin (myogenic factor 4) myogenin (myogenic factor 4) muclear receptor coactivator 5 nuclear receptor coactivator 5 nuclear receptor coactivator 5 nuclear receptor coactivator 5 nuclear transcription factor Y, gamma nuclear transcription factor Y, gamma proliferating cell nuclear antigen	s8645 s8646 s17629 s17630 s17631 s9232 s9233 s9234 s33688 s33689 s33690 s9535 s9536 s10133	Not Determined Not Determined 13 10 10 3 3 3 3 4 3 Not Determined Not Determined 5.4	GACAUUGUUUCAUCCUCCAH GCUUCCCGAUUAACUGAAAt GGAUCUACUGAAGAAGAAGAA CGAUACUCCAGUUUUAUUAt CCACAGACCGGUAUAUUCAt ACUUUUUGAUUUCCUUUH CAAGGUCUCCUGUGCUGAAt CCUCAUCCAUGUAAGGUUAH GGAUUUCCAGAUAGCUUH GGAUUUCAGAAUAGCUUH GGAUUUCAGAAUACGCGAt GGAUUUAACAAGGAU GGCAUCUCAUCACACA	UGGAGGAUGAAACAAUGUCtt UUUCAGUUAAUCGGGAAGCtt UACUUCUUCCAGUAGAUCCaa UAAUAAACUGGACUAUGCtg UGAAUAACUGGACUAUGCtg UGAAUAACUGGACUAUGGtt UUCAGCACAGGACACUUGt UUCAGCACAGGACACUUGt UAACCUUACUGGAUGAGGaa UCUACUUCUGUAACGGtc UCCUGGUAUCUCGAAAAUCCct UCCUUGUUCACUGUAACGGtc UCCUGUAUCCGAAAUCCct UCUUUCACUGUUAAUCCgg AAUCUUCUUAAUACGAGCCag UGUGCGAUAGUGCCCa

NM_013374 NM 001009552				1		1
	PDCD6IP	programmed cell death 6 interacting protein	s19467	Not Determined	GAAUUACUGCAACGAAAUAtt	UAUUUCGUUGCAGUAAUUCag
-	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	member / Swi/Swr related, matrix associated, actin dependent redulator of chromatin, subramity a.	s13139	Not Determined	GGAAUACCUCAAUAGCAUUtt	AAUGCUAUUGAGGUAUUCCtg
NM_003072	SMARCA4					
		member / related, mainx associated, actin dependent regulator or chromatin, subramily a,	s13140	Not Determined	GGCUUGAUGGAACCACGAAtt	UUCGUGGUUCCAUCAAGCCtg
NM_003072	SMARCA4	SWINK/related, mainx associated, actin dependent regulator or chromatin, subrannity a, SWINK/related, mainx associated, actin dependent regulator or chromatin, subrannity a,	s13141	Not Determined	GUAGCUCCGAGGUCUGAUAtt	UAUCAGACCUCGGAGCUACtt
NM_003601	SMARCA5		s13141 s16081		GUAGCUCCGAGGUCUGAUAtt GGAGAUACUUAGUAAUAGAtt	UAUCAGACCUCGGAGCUACtt UCUAUUACUAAGUAUCUCCaa
NM_003601 NM_003601	SMARCA5 SMARCA5	SWISSN-4related, matrix associated, actin dependent regulator or chromatin, subramily a,	s13141 s16081 s16082	Not Determined 7 3	GUAGCUCCGAGGUCUGAUAtt GGAGAUACUUAGUAAUAGAtt GGGCAAAUAGAUUCGAGUAtt	UAUCAGACCUCGGAGCUACtt UCUAUUACUAAGUAUCUCCaa UACUCGAAUCUAUUUGCCCgg
NM_003601 NM_003601 NM_003601	SMARCA5 SMARCA5 SMARCA5	SWISSN-4related, matrix associated, actin dependent regulator or chromatin, subramily a,	s13141 s16081 s16082 s16083	Not Determined 7 3 16	GUAGCUCCGAGGUCUGAUAtt GGAGAUACUUAGUAAUAGAtt GGGCAAAUAGAUUCGAGUAtt GGGCGAAAGUUCACUUAGAtt	UAUCAGACCUCGGAGCUACtt UCUAUUACUAAGUAUCUCCaa UACUCGAAUCUAUUUGCCCgg UCUAAGUGAACUUUCGCCCat
NM_003601 NM_003601 NM_003601 NM_003074	SMARCA5 SMARCA5 SMARCA5 SMARCC1	SWISSN-4related, matrix associated, actin dependent regulator or chromatin, subramily a,	s13141 s16081 s16082 s16083 s13145	Not Determined 7 3 16 Not Determined	GUAGCUCCGAGGUCUGAUAtt GGAGAUACUUAGUAAUAGAtt GGGCAAAUAGAUUCGAGUAtt GGGCGAAAGUUCACUUAGAtt CCAACACCUGUACCCAAUAtt	UAUCAGACCUCGGAGCUACtt UCUAUUACUAAGUAUCUCCaa UACUCGAAUCUAUUUGCCCgg UCUAAGUGAACUUUGCCCgg UAUUGGGUACAGGUGUUGGgt
NM_003601 NM_003601 NM_003601 NM_003074 NM_003074	SMARCA5 SMARCA5 SMARCA5 SMARCC1 SMARCC1	сонтубли- ⁴ енакои, тнатих associateu, асып оерепоетстедианог ог сполтанл, subnaminy a, SMMSMR-Tenakov, тнатих associateu, асып оерепоетстедианог ог сполтанл, subnaminy a, SMMSMR-Tenakov, тнатих associateu, асып оерепоетстедианог ог сполтанл, subnaminy a, SMMSMR-Tenakov, тнатих associateu, асып оерепоется годианого ог сполтанл, subnaminy a,	s13141 s16081 s16082 s16083 s13145 s13146	Not Determined 7 3 16 Not Determined Not Determined	GUAGCUCCGAGGUCUGAUAtt GGAGAUACUUAGUAAUAGAtt GGCGAAAUAGAUUCGAGUAtt GGCGAAAGUUCACUUAGAtt CCAACACCUGUACCCAAUAtt CAAGAGUAUUUAACUAGCAtt	UAUCAGACCUCGGAGCUACtt UCUAUUACUAAGUAUCUCCaa UACUCGAAUCUAUUGCCCgg UCUAAGUGAACUUUCGCCCat UAUUGGGUACAGGUGUUGGgt UGCUAGUUAAAUACUCUUGgg
NM_003601 NM_003601 NM_003601 NM_003074 NM_003074 NM_003074	SMARCA5 SMARCA5 SMARCA5 SMARCC1 SMARCC1 SMARCC1	SYMPSN- ⁴ etated, mainx associated, acuin dependent regulator or chromaun, subnamny a, SYMPSN- ⁴ etated, mainx associated, acuin dependent regulator or chromaun, subnamny a, SYMPSN- ⁶ related, mainx associated, acuin dependent regulator or chromaun, subnamny a, SYMPSN- ⁶ related, mainx associated, acuin dependent regulator or chromaun, subnamny c, SYMPSN- ⁶ related, mainx associated, acuin dependent regulator or chromaun, subnamny c,	s13141 s16081 s16082 s16083 s13145 s13146 s13147	Not Determined 7 3 16 Not Determined	GUAGCUCCGAGGUCUGAUAtt GGAGAUACUUAGUAAUAGAtt GGGCGAAAGUUCACUUAGUAtt GGGCGAAAGUUCACUUAGAtt CCAACACUGUACCCAAUAtt CAAGAGUAUUAACUAGGAtt CCAUCUCGAAUGGAUCGUAtt	UAUCAGACCUCGGAGCUACI UCUAUUACUAAGUAUCUCCas UACUCGAUCUAUUGCCCgg UCUAAGUGAACUUUCGCCCgt UAUUGGGUACAGGUGGUUGGgt UACGAUCCAUUCGAGAUGGgt UACGAUCCAUUCGAGAUGGgt
NM_003601 NM_003601 NM_003074 NM_003074 NM_003074 NM_003074 NM_003079	SMARCA5 SMARCA5 SMARCA5 SMARCC1 SMARCC1 SMARCC1 SMARCC1	SWMSNF4 related, man x associated, acun dependent regulator or chromatin, subnamny a, SWMSNF4 related, man x associated, acun dependent regulator or chromatin, subnamny a, SWMSNF4 related, man x associated, acun dependent regulator or chromatin, subnamny a, SWMSNF4 related, man x associated, acun dependent regulator or chromatin, subnamny c, SWMSNF4 related, man x associated, acun dependent regulator or chromatin, subnamny c, SWMSNF4 related, man x associated, acun dependent regulator or chromatin, subnamny c, SWMSNF4 related, man x associated, acun dependent regulator or chromatin, subnamny c,	s13141 s16081 s16082 s16083 s13145 s13146 s13147 s13160	Not Determined 7 3 16 Not Determined Not Determined	GUAGCUCCGAGGUCUGAUAtt GGAGAUACUUAGUAAUAGAtt GGCGAAAGUUCACUAGAUtt GGCGAAAGUUCACUUAGAtt CCAACACCUGUACCCAAUAtt CCAACACCUGUACCCAAUAtt CCAACACAAUGAUCGUACCAtt GCAGAAAGAUAGAUGAUCGUAtt	UAUCAGACCUCGGAGCUACIt UCUAUUACUAAGUAUCUCCaa UACUCGAAUUAUUACUCCag UUCUAAGUGAACUUUCGCCCgt UAUUGGGUACAGUUCGUUCGgt UGCUAGUGAACUUUCGGAUGgt UGCAUCCUUUGGAGUGGgt UGUACUCUAUCUUUUCUGCt
NM_003601 NM_003601 NM_003601 NM_003074 NM_003074 NM_003074 NM_003079 NM_003079	SMARCA5 SMARCA5 SMARCC1 SMARCC1 SMARCC1 SMARCC1 SMARCE1 SMARCE1	сумлови 4 челаее, тианти засоснатео, асши обрегоени гединатог от сплотналит, зорлатну а, SMMSMA Fenareo, тианти засоснатео, асши обрегоени гединатог от сплотналит, зорлатну а, SMMSMA Fenareo, тианти засоснатео, асши обрегоени гединато от сплотналит, зорлатну а, SMMSMA Fenareo, тианти засоснатео, асши обрегоени гединато от сплотналит, зорлатну с, SMMSMA fenareo, тианти засоснатео, асши обрегоени гединато от сплотнали, зорлатну с, SMMSMA fenareo, тианти засоснатео, асши обрегоени гединато от сплотнали, зорлатну с, SMMSMA fenareo, тианти засоснатео, асши обрегоени гединато от сплотнали, зорлатну с, SMMSMA fenareo, тианти засоснатео, асши обрегоени гединато от сплотнали, зорлатну с, SMMSMA fenareo, тианти засоснатео, асши обрегоени гединато от сплотнали, зорлатну с, SMMSMA fenareo, тианти засоснатео, асши обрегоени гединато от сплотнали, sopranny с, SMMSMA fenareo, тианти засоснатео, асши обрегоени гединато от сплотнали, sopranny с,	s13141 s16081 s16082 s16083 s13145 s13146 s13147 s13160 s13161	Not Determined 7 3 16 Not Determined Not Determined	GUAGCUCCGAGGUCUGAUAtt GGAGAUACUUAGUAAUAGAtt GGGCAAAUAGUUCGAGUAtt GGGCGAAGUUCACUUAGAtt CCAACACCUGUACCCAAUAtt CCAACACUGUACCUAGCAtt CCAUCUCGAUGAUCGAUCGAItt GCAGAAAGAUAGAUACAtt GUACCUUGCUUACAUAAAUtt	UAUCAGACCUCGGAGCUACI UCUAUUACUAAGUAUCUCCaa UACUCGAAUCUAUUUGCCCgg UCUAAGUGACUUUCGCCCat UAUUGGGUACAGGUGUUGGgt UGCUAGUUAAUACUCUUGgg UACGAUCCAUUCGGGAUGGgt UGUACUCUAUCUUUCUCCtt AUUUAUGUAAGCAAGGUACgc
NM_003601 NM_003601 NM_003601 NM_003074 NM_003074 NM_003074 NM_003079 NM_003079 NM_003079	SMARCA5 SMARCA5 SMARCA5 SMARCC1 SMARCC1 SMARCC1 SMARCE1 SMARCE1 SMARCE1	symbolin ⁴ fetaleo, mainx associateo, acun oppendent regulator or chromatin, subranny a, SYMBolin ⁴ fetaleo, mainx associateo, acun oppendent regulator or chromatin, subranny a, SYMBolin ⁴ fetaleo, mainx associateo, acun oppendent regulator or chromatin, subranny a, SYMBolin ⁴ fetaleo, mainx associateo, acun oppendent regulator or chromatin, subranny a, SYMBolin ⁴ fetaleo, mainx associateo, acun oppendent regulator or chromatin, subranny a, SYMBolin ⁴ fetaleo, mainx associateo, acun oppendent regulator or chromatin, subranny c, SYMBolin ⁴ fetaleo, mainx associateo, acun oppendent regulator or chromatin, subranny c, SYMBolin ⁴ fetaleo, mainx associateo, acun oppendent regulator or chromatin, subranny c, SYMBolin ⁴ fetaleo, mainx associateo, acun oppendent regulator or chromatin, subranny c, SYMBolin ⁴ fetaleo, mainx associateo, acun oppendent regulator or chromatin, subranny c, SYMBolin ⁴ fetaleo, mainx associateo, acun oppendent regulator or chromatin, subranny c, SYMBolin ⁴ fetaleo, mainx associateo, acun oppendent regulator or chromatin, subranny c, SYMBolin ⁴ fetaleo, mainx associateo, acun oppendent regulator or chromatin, subranny c, SYMBolin ⁴ fetaleo, mainx associateo, acun oppendent regulator or chromatin, subranny e, SYMBolin ⁴ fetaleo, mainx associateo, acun oppendent regulator or chromatin, subranny e, SYMBolin ⁴ fetaleo, mainx associateo, acun oppendent regulator or chromatin, subranny e, SYMBolin ⁴ fetaleo, mainx associateo, acun oppendent regulator or chromatin, subranny e, SYMBolin ⁴ fetaleo, mainx associateo, acun oppendent regulator or chromatin, subranny e, SYMBolin ⁴ fetaleo, mainx associateo, acun oppendent regulator or chromatin, subranny e, SYMBolin ⁴ fetaleo, mainx associateo, acun oppendent regulator or chromatin, subranny e, SYMBolin ⁴ fetaleo, mainx associateo, acun oppendent regulator or chromatin, subranny e, SYMBolin ⁴ fetaleo, mainx associateo, acun oppendent regulator or	s13141 s16081 s16082 s16083 s13145 s13145 s13146 s13147 s13160 s13161 s13162	Not Determined 7 3 16 Not Determined Not Determined 6 7 6	GUAGCUCCGAGGUCUGAUAtt GGAGAUACUUAGUAAUAGAtt GGGCGAAAGUUCACUUAGAtt GGGCGAAAGUUCACUUAGAtt CCAACACUGUACCCAAUAtt CCAAGAGUUUAACUAGGAtt CCAUCUCGAAUGGAUCGUAtt GCAGAAAGAGUAGAGUACAtt GUACCUUACAUAAAUtt GACCUAAAGUUGUGGGAGAtt	UAUCAGACCUCGGAGCUACI UCUAUUACUAAGUAUCUCCas UACUGAAUCUAUUGCCCgg UCUAAGUGAACUUUCGCCCg UAUGGGUACAGGUGUUGGg UACGAUCAAUUCGGUUGGg UACGAUCCAUUCGAGAUGGg UGUACUUAAUACUCUUCGG AUUUAUGUAAGCAAGGUACgc UCUCCCACACUUUAGGUCgg
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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	403	1.312698364	0.14543843	Yes
12	Pleiomorphic adenoma gene-like 1	PLAGL1	474	1.258885026	0.15156297	Yes
12		FAIM	474 497			Yes
	Fas apoptotic inhibitory molecule			1.244239688	0.15913047	
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	22130	0.694423258	0.287643	Yes
42	Membrane metallo-endopeptidase	MME	2223	0.693363011	0.29218966	Yes
43	Ankyrin 2, neuronal	ANK2	2223	0.681526303	0.2935673	Yes
44 45	Adrenergic, beta-1-, receptor	ADRB1	2297	0.67876333	0.2933673	Yes
		RSU1				
46 47	Ras supressor 1		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 CaPO₄ 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 CaPO₄. 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.

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

Supplementary Table S4: shRNA hairpin sequences

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.

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

Supplementary Table S5: TaqMan Gene Expression Assays

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.

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 4x10⁶ 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[™] 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[™] 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.

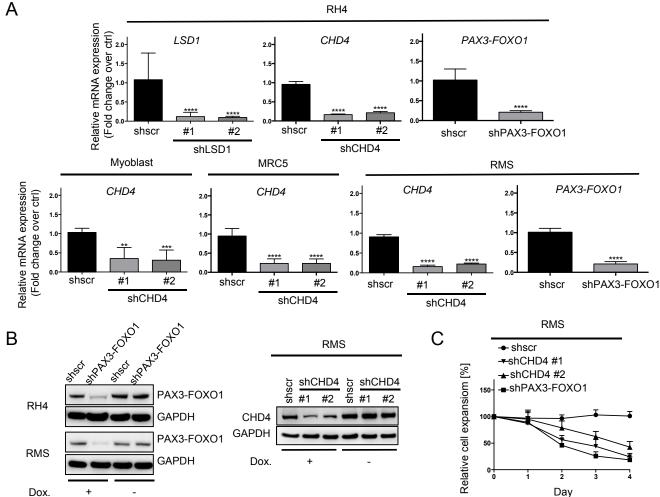
³ Wachtel M, Runge T, Leuschner I, et al. Subtype and prognostic classification of rhabdomyosarcoma by immunohistochemistry. Journal of clinical oncology : official journal of the American Society of Clinical Oncology. 2006 Feb 10;**24**(5):816-22.

А							В					
			G-PAX				51	MTTLAGAVPR LPNHIRHKIV IGGSKPKQVT	EMAHHGIRPC	VISRQLRVSH	GCVSKILCRY	QETGSIRPGA
	pCMV	-	+	-	-		10000000	VSSISRILRS SDEGSDIDSE				
	pBABE	-	-	+	+			ELAQRAKLTE				
		J	1			FLAG-PAX3-FOXO1 PAX3-FOXO1 wt		TLPTYQLSET SSAYCLPSTR				
		1	I		1	β-Actin		HSKFIRVQNE AAKKKASLQS				
		R	MS13		RH4		501	NASTISGRLS NMENLLDNLN	PIMTEQDDLG	EGDVHSMVYP	PSAAK MASTL	PSLSEISNPE
							601	NYQKYTYGQS SPPHNDIMTP	SMSPLPQMPI	QTLQDNKSSY	GGMSQYNCAP	GLLKELLTSD
							701 751	SSHTHPGHAQ MQMSALGGYS	QTSAVNGRPL SVSSCNGYGR	PHTVSTMPHT MGLLHQEKLP	SGMNRLTQVK SDLDGMFIER	TPVQVPLPHP
							801	NDLMDGDTLD	FNFDNVLPNQ	SFPHSVKTTT	HSWVSG	

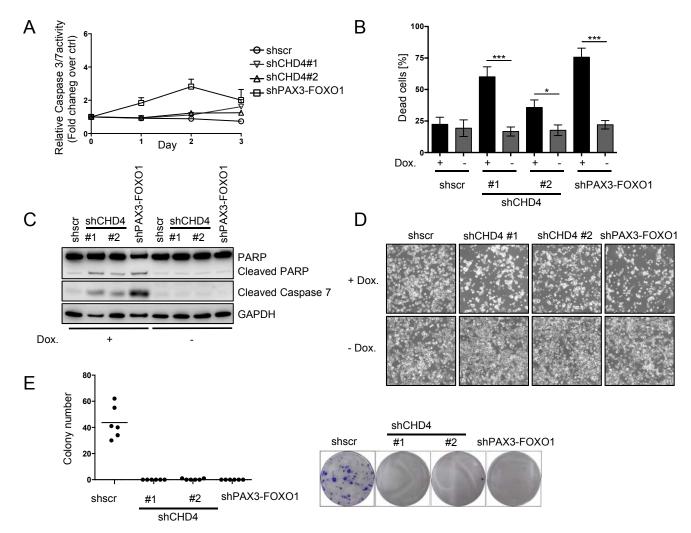
Supplementary Figure 1. Immunoprecipitation of FLAG-PAX3-FOXO1. (A) Qualitative comparison of different FLAG-PAX3-FOXO1 expression systems in RH4 and RMS13 cells. pCMV expression system for high over expression and pBABE for expression levels comparable to endogenous PAX3-FOXO1 expression level (wt). (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)

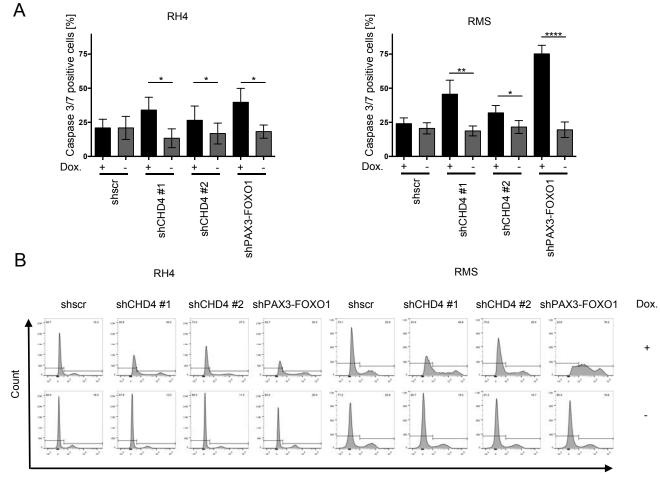
Supplementary Figure 2. Biological role of candidate interactors from siRNA screen



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 gRT-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.

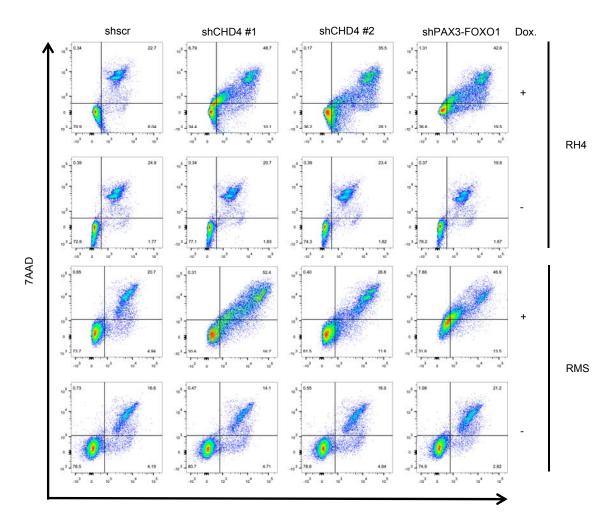


Supplementary Figure 4. CHD4 knockdown induces cell death of FP-RMS cell line RMS in vitro. (A) Caspase 3/7 activity in RMS cells 72hrs after induction of CHD4 silencing. Fold change of Caspase 3/7 activity was normalized to the uninduced control cells (ctrl). Shscr treated cells served as negative and PAX3-FOXO1 knockdown cells as positive control. Values are means \pm 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 \pm SD of four independent experiments ($\star \star \pm p < 0.001$; $\pm p < 0.05$; 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.



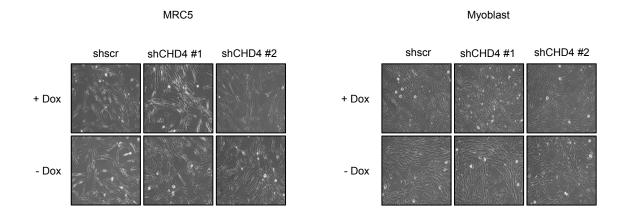
Nucview 405 Caspase 3

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 \pm SD of four independent experiments ($\star \star \star \pm p < 0.0001$; $\star p < 0.01$; $\star p < 0.05$; 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.

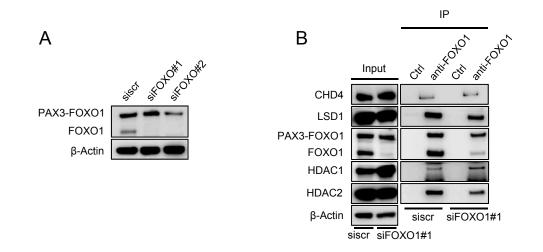


Nucview 405 Caspase 3

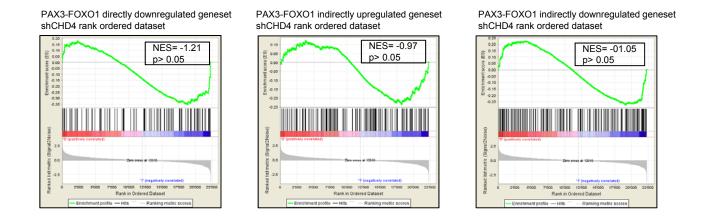
Supplementary Figure 6. Percentage of Caspase 3/7 and/or 7AAD positive FP-RMS cells. FACS histogram analysis of indicated cells 96hrs after induction of CHD4 silencing with doxycycline and uninduced controls stained with Nucview 405 Caspase 3 substrate and 7AAD. Plots show live and dead cells after exclusion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



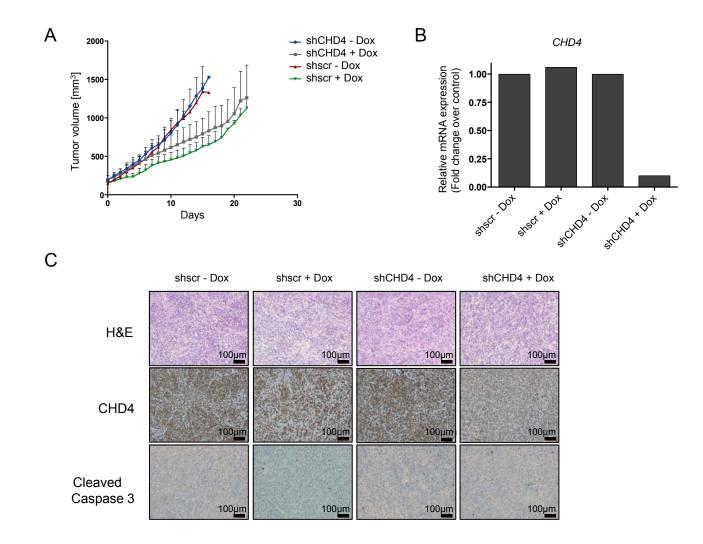
Supplementary Figure 7. CHD4 silencing does not affect normal human MRC5 or myoblast cells. Representative bright-field images of MRC5 and myoblast cells 72hrs after induction of CHD4 silencing with doxycycline (Dox) in indicated cell lines and uninduced control cells, magnification 100x.

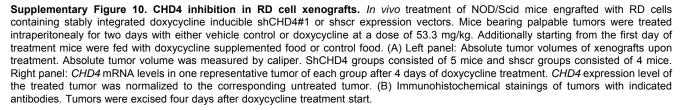


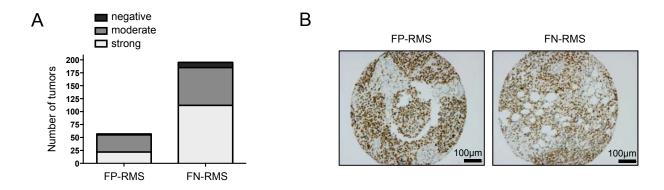
Supplementary Figure 8. Interaction of PAX3-FOXO1 with NuRD complex components persists after FOXO1 silencing. (A) Western blots showing FOXO1 silencing efficiency and effect on PAX3-FOXO1 expression level after treatment of RH4 cells with indicated siRNAs. SiFOXO1#1, not affecting PAX3-FOXO1 expression 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).



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 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 : \geq 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.