SUPPLEMENTARY DATA

Supplementary Experimental Procedures

Cytoplasmic/nuclear fractionation –Cells were washed and harvested in PBS by scraping. The cell pellet was resuspended in hypotonic buffer A (MgCl2 1.5mM, KCl 10mM, Tris pH 7.9 10mM). After adding 2% NP40, cells were allowed to lyse for 10 minutes on ice by additional mixing. After centrifugation for 15 minutes at 2,500x g, the cytoplasmic supernatant was collected and the pellet was resuspended in hypotonic buffer B (Glycerol 20%, MgCl2 1.5mM, KCl 10mM, Tris pH 7.9 20mM). Afterwards, the homogenate was mixed with hypertonic buffer C (Glycerol 20%, MgCl2 1.5mM, KCl 1.2M, Tris pH 7.9 20mM) and incubated for 45 minutes at 4°C with occasional mixing. Finally, the protein lysate was centrifuged at 20,000x g for 45 minutes at 4°C and the supernatant (nuclear fraction) was collected.

Western Blot – To analyze the expression and subcellular location of the importin alpha 7-mycHis fusion protein in NIH3T3 cells, transfected and mock transfected cells were harvested after 24 hours of transfection by scrapping. Nuclear and cytoplasmic levels of Ash2l, Chd3, Mcm3, Mcm5, and Smarcc1 were analyzed using wildtype and importin alpha 7-/- MEFs. Cytoplasmic and nuclear cell fractions were mixed with 1x Laemmli buffer and incubated at 95°C for five minutes. 10 µl of cytoplasmic or nuclear samples were loaded on a 10% SDS gel. After the transfer of proteins, the PVDF membrane was blocked by Odyssey blocking solution (LiCor, Bad Homburg, Germany) and subsequently incubated with primary antibodies at 4°C overnight. Importin alpha 7-mycHis labeling via its myc-tag was done using a rabbit anti-C-myc antibody (1:500 diluted; Sigma-Aldrich). To label the recombinant and the endogenous importin alpha 7 protein, a rabbit anti-importin alpha 7 antibody was used (1:1000 diluted; (1)). The following antibodies were used to detect importin alpha 7 cargo candidates in MEFs: rabbit anti-Ash2l (Cell Signalling, 1:2000 diluted), rabbit anti-Chd3 (abcam, 1:1000 diluted), rabbit anti-Mcm3 (Cell Signalling, 1:1000 diluted), rabbit anti-Mcm5 (abcam, 1:5000 diluted) and rabbit anti-Smarcc1 (abcam, 1:1000 diluted). On the next day, the membrane was incubated with an IRDye coupled secondary anti-rabbit antibody (1:10,000 diluted; LiCor, Bad Homburg, Germany) for 1 hour at room temperature and detection was performed using the Odyssey Infrared Scanner (LiCor, Bad Homburg, Germany). Signals

were quantified using the Odyssey Infrared Scanner software (LiCor, Bad Homburg, Germany) and unpaired t-test was performed using GraphPad Prism version 6.00 for Windows, GraphPad Software, La Jolla California USA, www.graphpad.com.

Importin alpha 7 MEF Genotyping PCR – To genotype murine embryonic fibroblasts (MEFs), genomic MEF DNA was prepared and importin alpha 7 wildtype as well as – Knockout (KO) alleles were amplified by common PCR techniques. In order to detect the wildtype allele, a DNA fragment spanning the insertion site of the importin alpha 7 KO gene trap cassette was amplified using the following primer pair: 5'-GACAAACATGCAGGCAAATCAC-3' and 5'-ATGAACCAGTATGCCCATCAAAT-3'. For the detection of the importin alpha 7 KO allele, a DNA fragment spanning an intronic part of the importin alpha 7 gene and the inserted KO cassette was amplified. For this purpose, the primer pair 5'-GACGTCTCGTTGCTGCATAAAC-3' and 5'-CAGCAGCAGCAGACCATTTTCAA-3' was used.

Quantitative Realtime PCR – Total RNA was extracted from wildtype and importin alpha 7 KO MEFs using TRIzol reagent (Invitrogen, Darmstadt, Germany). After DNase I (Roche, Mannheim, Germany) treatment, first-strand DNA synthesis was performed using M-MLV Reverse Transcriptase (Invitrogen, Darmstadt, Germany) and random primers according to the manufacturer's instructions. Quantitative PCR was performed using Go Taq (Promega, Mannheim, Germany) on an IQ 5 Multicolour Realtime PCR Detection System (Bio-Rad laboratories, München,Germany). Relative gene expression was calculated using the ΔCt method with GAPDH as normalizing gene. Primer sequences were as follows (F, forward primer; R, reverse primer):

GAPDH: (F) CTTTGTCAAGCTCATTTCCTGG, (R) TCTTGCTCAGTGTCCTTGC

ash2lF: (F) TCGAGCTCCCCAGTTAAAGA, (R) GAACTTGGTGCCTTTCTTGC

anp32e: (F) TGCAGCAGATCACCTACCTG, (R) CCAGCTTCATCTTCGTCCTC

chd3: (F) CGGGAGAAGTCAGAGAGTGG, (R) ACATCCTCTAAGCCCCAGGT

mcm3: (F) TGACCTGCTCTTCATCATGC, (R) CTGTGGCCAGGATATCCACT

mcm5: (F) CCTTCCCAGGAAGTGCAATA, (R) GCATCTCACCATGAGGGACT

smarcc1: (F) TGGTGGTGCAGCTTCTACAG, (R) CCAGCCCTGTTCATTTTTGT

Supplementary Figure Legends

Supplementary Figure 1: Expression and localization of importin alpha 7-mycHis in NIH3T3 cells. Cytoplasmic (c) and nuclear (n) fractions were prepared of NIH3T3 cells. Cells were treated with the transfection mix without vector (mock) or including the importin alpha 7-mycHis construct (transf.). The nuclear protein p84 served as nuclear marker, GAPDH served as cytoplasmic marker. The anti-importin alpha 7 antibody detects endogenous importin alpha 7 as well as overexpressed importin alpha 7-mycHis. The anti-C-myc antibody detects only the mycHis tagged version of importin alpha 7. *: cross reactivity with importin alpha 5.

Supplementary Figure 2: Genotyping PCR of importin alpha 7 KO MEFs. MEFs were genotyped by PCR amplification of a DNA fragment spanning the insertion site of the importin alpha 7 KO (imp a7 -/-) gene trap cassette for detection of the wild type allele (upper panel). To detect the importin alpha 7 KO allele, a DNA fragment was amplified spanning an intronic part of the importin alpha 7 gene and the inserted KO cassette (lower panel). Wildtype (+/+ control) and importin alpha 7 KO (-/- control) tissue DNA served as controls. Water (H2O) was used to ensure the absence of DNA contaminations in the PCR mix.

Supplementary Figure 3: mRNA levels of Ash2l, Chd3, Mcm3, Mcm5, and Smarcc1 in wildtype and importin alpha 7-/- MEFs. The cDNA was reverse transcribed from three independent RNA samples of wildtype (wt) and importin alpha 7-/- (a7KO) MEFs. Relative gene expression was calculated using the ΔCt method with GAPDH as normalizing gene.

Supplementary Tables

Overview Supplementary Tables:

Supplementary Table 1– attached

Supplementary Table 2– attached

Supplementary Table 3– included (see below)

Supplementary Table 4– included (see below)

Supplementary Table 5– attached

Supplementary Table 6– attached

Supplementary Table 7– included (see below)

Attached Supllementary Table Legends:

Supplementary Table 1: Importin alpha 7 binding partners identified by GST pull-down from ovary lysate. 1-757: proteins bound to importin alpha 7 and not to the GST-control. 758-807: Top 5% of importin alpha 7 binding partners found to bind also very weakly to the GST-control. Proteins were ranked according to their relative LFQ intensity compared to the GST-control.

Supplementary Table 2: Importin alpha 7 binding partners identified by co-immunoprecipitation from fibroblast cells. 1-266: proteins bound to importin alpha7 and not to the mycHis-control. 267-299: Top 5% of importin alpha 7 binding partners found to bind also very weakly to the mycHis-control peptide. Proteins were ranked according to their relative LFQ intensity compared to the mycHis control.

Supplementary Table 3: Importin alpha 2 binding partners identified by co-immunoprecipitation from fibroblast cells. 1-254: proteins bound to importin alpha 2 and not to the mycHis-control. 255-266: Top 5% of importin alpha 2 binding partners found to bind also very weakly to the mycHis-control peptide. Proteins were ranked according to their relative LFQ intensity compared to the mycHis control.

Supplementary Table 6: Importin alpha 3 binding partners identified by co-immunoprecipitation from fibroblast cells. 1-231: proteins bound to importin alpha 3 and not to the mycHis-control. 232-276: Top 5% of importin alpha 3 binding partners found to bind also very weakly to the mycHis-control peptide. Proteins were ranked according to their relative LFQ intensity compared to the mycHis control.

Supplementary Table 4: Top 5 enriched GO-terms among importin alpha 7-mycHis binding partners identified by co-immunoprecipitation from NIH3T3 cells. 296 proteins were analyzed using the ToppFun analysis software from the ToppGene Suite. List entries are ranked according to p-value;p<0.01

A) Biological Process

	ID	Name	P-value	Term in Query	Term in Genome
1	GO:0006396	RNA processing	1.35E-24	59	680
2	GO:0051276	chromosome organization	6.77E-20	56	751
3	GO:0006397	mRNA processing	3.42E-17	40	418
4	GO:0016568	chromatin modification	3.95E-17	42	468
5	GO:0006325	chromatin organization	2.65E-16	45	571

B) Cellular Component

	ID	Name	P-value	Term in Query	Term in Genome
1	GO:0016585	chromatin remodeling complex	1.96E-31	35	133
2	GO:0044451	nucleoplasm part	5.48E-22	62	906
3	GO:0030529	ribonucleoprotein complex	2.15E-15	43	594
4	GO:0016581	NuRD complex	2.79E-14	11	17
5	GO:0016514	SWI/SNF complex	4.79E-13	10	15

Supplementary Table 5: Overlay of importin alpha7 binding partners from ovary and fibroblast cells. Comparison of 807 importin alpha 7 binding partners identified by GST pull-down from ovary lysate and 299 proteins identified by co-immunoprecipitation from fibroblast cells. Candidate genes were ranked according to their LFQ intensity from the importin alpha7-GST pull-down experiment using ovary lysate. Protein information about cellular localization (Cell. Loc.) and association to certain protein complexes was extracted using the UniProt webpage (http://www.uniprot.org/); Nuc: nucleus, Cyt: cytoplasm, secr.Ves: secretory vesicle. Proteins with NLS are marked by an asterisk, information taken from *The Nuclear Protein Database* (http://npd.hgu.mrc.ac.uk/user/). Listed biological information is not experimentally proven in all cases.

	Gene name (Protein name)	**Function**
1	Lmnb1 (Lamin B1) *	scaffolding, interaction with chromatin
2	Chd4 (Chromodomain-helicase-DNA-binding protein 4) *	remodeling of chromatin
3	Lmn1 (lamin 1) *	scaffolding
4	Kiaa0398 (mRNA cap guanine-N7 methyltransferase)	mRNA-capping
5	Mta1l1 (Metastasis-associated protein MTA2)*	modification of chromatin
6	Mcm3 (DNA replication licensing factor MCM3) *	replicative helicase essential for 'once per cell cycle' DNA replication
7	Taf2s (Transcription elongation regulator 1) *	Transcription factor that binds RNA polymerase II and inhibits elongation of transcripts
8	Cdc46 (DNA replication licensing factor MCM5) *	replicative helicase essential for 'once per cell cycle' DNA replication
9	Ars2 (Serrate RNA effector molecule homolog) *	mediator between cap-binding complex and primary microRNAs processing machinery during cell proliferation
10	Baf170 (SWI/SNF complex subunit SMARCC2) *	remodeling of chromatin
11	Npap60 (Nuclear pore complex protein Nup50)	facilitates disassembly of importin-alpha:beta-cargo complex
12	Hdac2 (Histone deacetylase 2)	modification of chromatin
13	Nup153 (Nuclear pore complex protein Nup153) *	Possible DNA-binding subunit of the NPC
14	Gatad2b (Transcriptional repressor p66-beta)	transcriptional repressor activity, targets MBD3 to discrete loci in nucleus
15	Ddx21 (Nucleolar RNA helicase 2) *	rRNA processing
16	Dhm1 (5'-3' exoribonuclease 2) *	termination of transcription by RNA polymerase II
17	Baf190a (Transcription activator BRG1) *	remodeling of chromatin
18	Rbap48 (Histone-binding protein RBBP4)	remodeling of chromatin

19	Rbap46 (Histone-binding protein RBBP7)	remodeling of chromatin
20	Hnrnpc (Heterogeneous nuclear ribonucleoproteins C1/C2) *	Binds pre-mRNA and nucleates assembly of 40S hnRNP particles
21	Tceb3 (Transcription elongation factor B polypeptide 3)	increases RNA polymerase II transcription elongation
22	Mta1 (Metastasis-associated protein MTA1) *	modification of chromatin
23	Ctnnbl1 (Beta-catenin-like protein 1)	Induces apoptosis in CHO cells
24	Smarca5 (SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5) *	Helicase, remodeling of chromatin
25	Kiaa1113 (E3 ubiquitin-protein ligase TRIM33) *	Promotes SMAD4 ubiquitination, nuclear exclusion and degradation via ubiquitin proteasome pathway
26	Edd1 (E3 ubiquitin-protein ligase UBR5)	ubiquitination and subsequent degradation
27	Anp32e (Acidic leucine-rich nuclear phosphoprotein 32 family member E)	Inhibits activity of protein phosphatase 2A (PP2A)
28	Adnp (ADNP homeobox protein 2)	transcriptional regulation
29	Aprin (Sister chromatid cohesion protein PDS5 homolog B)	Regulator of sister chromatid cohesion in mitosis which may stabilize cohesin complex association with chromatin
30	Hdac1 (Histone deacetylase 1)	modification of chromatin
31	Baf60b (SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2) *	remodeling of chromatin
32	Abh5 (Probable alpha-ketoglutarate-dependent dioxygenase ABH5)	dioxygenase, may repair alkylated DNA and RNA by oxidative demethylation
33	Ase1 (DNA-directed RNA polymerase I subunit RPA34) *	transcription of DNA into RNA
34	Baf47 (SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1)	remodeling of chromatin
35	Nol5 (Nucleolar protein 58) *	Required for 60S ribosomal subunit biogenesis
36	Gatad2a (Transcriptional repressor p66-alpha)	Transcriptional repressor
37	Nol5a (Nucleolar protein 56)	early to middle stages of 60S ribosomal subunit biogenesis
38	Arid1a (AT-rich interactive domain-containing protein 1A) *	remodeling of chromatin
39	Myo1c (Unconventional myosin-Ic)	intracellular movements, regulation of transcription
40	Fbl (rRNA 2'-O-methyltransferase fibrillarin)	pre-rRNA processing
41	Bod1l (Biorientation of chromosomes in cell division protein 1-like 1)	?
42	Alpha-CP2 (Poly(rC)-binding protein 2)	Major cellular poly(rC)-binding protein. Negatively regulates cellular antiviral responses mediated by MAVS signaling.
43	Arid1b (AT-rich interactive domain-containing protein 1B)	remodeling of chromatin

44	Mbd3 (Methyl-CpG-binding domain protein 3) *	Recruits histone deacetylases and DNA methyltransferases. Acts as transcriptional repressor and plays a role in gene silencing.
45	Tex10 (Testis-expressed sequence 10 protein)	?
46	Mbd2 (Methyl-CpG-binding domain protein 2) *	Demethylase, binds CpG islands in promoters where the DNA is methylated, recruits histone deacetylases and DNA methyltransferases
47	Mta3 (Metastasis-associated protein MTA3)	maintenance of normal epithelial architecture through the repression of SNAI1 transcription in a histone deacetylase-dependent manner, and thus the regulation of E-cadherin levels
48	Paf53 (DNA-directed RNA polymerase I subunit RPA49) *	DNA-dependent RNA polymerase
49	Pcif1 (Phosphorylated CTD-interacting factor 1)	transcription elongation or in coupling transcription to pre-mRNA processing
50	Carf (CDKN2A-interacting protein) *	Activates p53/TP53 by CDKN2A-dependent and CDKN2A-independent pathways
51	Nolc1 (Nucleolar and coiled-body phosphoprotein 1) *	maintenance of fundamental structure of fibrillar center and dense fibrillar component in the nucleolus, transcription catalyzed by RNA polymerase I
52	Nup121 (Nuclear envelope pore membrane protein POM 121) *	anchoring components of the pore complex to the pore membrane
53	Hnrnpu (Heterogeneous nuclear ribonucleoprotein U) *	promotes MYC mRNA stabilization
54	Nipbl (Nipped-B-like protein) *	structural role in chromatin, sister chromatid cohesion
55	Baf45d (Zinc finger protein ubi-d4)	transcription factor required for apoptosis response following survival factor withdrawal from myeloid cells, role in the development and maturation of lymphoid cells
56	Cspg6 (Structural maintenance of chromosomes protein 3) *	chromosome cohesion during the cell cycle
57	Baf155 (SWI/SNF complex subunit SMARCC1) *	remodeling of chromatin
58	Mnar (Proline-, glutamic acid- and leucine-rich protein 1) *	Plays a role in estrogen receptor (ER) genomic activity
59	Cwc15 (Pre-mRNA-splicing factor CWC15)	Involved in pre-mRNA splicing
60	Maged1 (Melanoma-associated antigen D1)	apoptotic response after nerve growth factor (NGF) binding in neuronal cells, regulator of the function of DLX family members
61	Hnrnpl (Heterogeneous nuclear ribonucleoprotein L) *	pre-mRNAs processing
62	Gnl3 (Guanine nucleotide-binding protein-like 3) *	regulating cellular proliferation
63	Smc1a (Structural maintenance of chromosomes protein 1A) *	chromosome cohesion during cell cycle and in DNA repair
64	Baf60a (SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1) *	remodeling of chromatin
65	Metap1 (Methionine aminopeptidase 1)	Removes the N-terminal methionine from nascent proteins. Required for normal progression through

		the cell cycle.
66	Ppil1 (Peptidyl-prolyl cis-trans isomerase-like 1)	PPIases accelerate the folding of proteins
67	Chd3 (Chromodomain-helicase-DNA-binding protein 3) *	remodeling of chromatin
68	Wdr18 (WD repeat-containing protein 18)	May play a role during development
69	Ash2l (Set1/Ash2 histone methyltransferase complex subunit ASH2) *	modification of chromatin
70	Baf60c (SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 3) *	remodeling of chromatin
71	Kiaa0425 (Zinc finger MYM-type protein 4)	regulation of cell morphology and cytoskeletal organization
72	Rps27l (40S ribosomal protein S27-like)	?
73	Clk2 (Dual specificity protein kinase CLK2) *	Dual specificity kinase acting on both serine/threonine and tyrosine-containing substrates
74	RAM (RNMT-activating mini protein)	mRNA cap methylation
75	Baf180 (Protein polybromo-1) *	remodeling of chromatin
76	Trrap (Transformation/transcription domain-associated protein) *	adapter protein, remodeling and modification of chromatin
77	Dhx16 (Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16) *	RNA helicase involved in pre-mRNA splicing
78	Dinb1 (DNA polymerase kappa)	DNA repair
79	Abra1 (BRCA1-A complex subunit Abraxas)	DNA repair
80	Nhp2l1 (NHP2-like protein 1)	late stage of spliceosome assembly
81	Brcc3 (Lys-63-specific deubiquitinase BRCC36)	Metalloprotease, DANN repair
82	Rbbp5 (Retinoblastoma-binding protein 5) *	modification of chromatin
83	Aimp1 (Aminoacyl tRNA synthase complex-interacting multifunctional protein 1)	Stimulates the catalytic activity of cytoplasmic arginyl-tRNA synthase, …
84	Anp32b (Acidic leucine-rich nuclear phosphoprotein 32 family member B) *	Multifunctional protein working as cell cycle progression factor, cell survival factor, histone chaperone, stimulating core histones to assemble into nucleosome
85	Bptf (Nucleosome-remodeling factor subunit BPTF) *	remodeling of chromatin
86	Csnk1d (Casein kinase I isoform delta)	Essential serine/threonine-protein kinase that regulates diverse cellular growth and survival processes including Wnt signaling, DNA repair and circadian rhythms
87	Dsp (High mobility group protein DSP1) *	Binds preferentially single-stranded DNA and unwinds double stranded DNA
88	Tada1 (Transcriptional adapter 1)	transcriptional regulation
89	Carp1 (Cell division cycle and apoptosis regulator protein 1)	transduces regulatory signals from upstream transcriptional activator proteins to basal

		transcription machinery at the core promoter, p53 coactivator, cell cycle progression and/or cell proliferation
90	Rsbn1l (Round spermatid basic protein 1-like protein)	?
91	Kifc1 (Kinesin-like protein KIFC1)	spindle formation, May contribute to movement of early endocytic vesicles
92	Emp2 (Epithelial membrane protein 2)	?
93	Ylpm1 (YLP motif-containing protein 1) *	reduction of telomerase activity during differentiation of embryonic stem cells by binding to core promoter of TERT and controlling its down-regulation
94	Baf57 (SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1) *	remodeling of chromatin
95	Nvl (Putative ribosome biogenesis ATPase nvl) *	ribosome biogenesis
96	H1f3 (Histone H1.3) *	forms chromatin fiber, remodeling of chromatin
97	Spty2d1 (Protein SPT2 homolog)	?
98	Polr2e (DNA-directed RNA polymerases I, II, and III subunit RPABC1) *	synthesize ribosomal RNA precursors, mRNA precursors and many functional non-coding RNAs, and small RNAs
99	Paf65b (TAF5-like RNA polymerase II p300/CBP-associated factor-associated factor 65 kDa subunit 5L)	modification of chromatin
100	Gtf2h4 (General transcription factor IIH subunit 4) *	involved in nucleotide excision repair of DNA and, when complexed to CAK, in RNA transcription by RNA polymerase II
101	Paf65a (TAF6-like RNA polymerase II p300/CBP-associated factor-associated factor 65 kDa subunit 6L)	modification of chromatin
102	Lyar (Cell growth-regulating nucleolar protein)	?
103	Qk (Protein quaking)	RNA-binding protein that plays a central role in myelinization, regulating pre-mRNA splicing, mRNA export, mRNA stability and protein translation
104	Atxn2l (Ataxin-2-like protein)	?

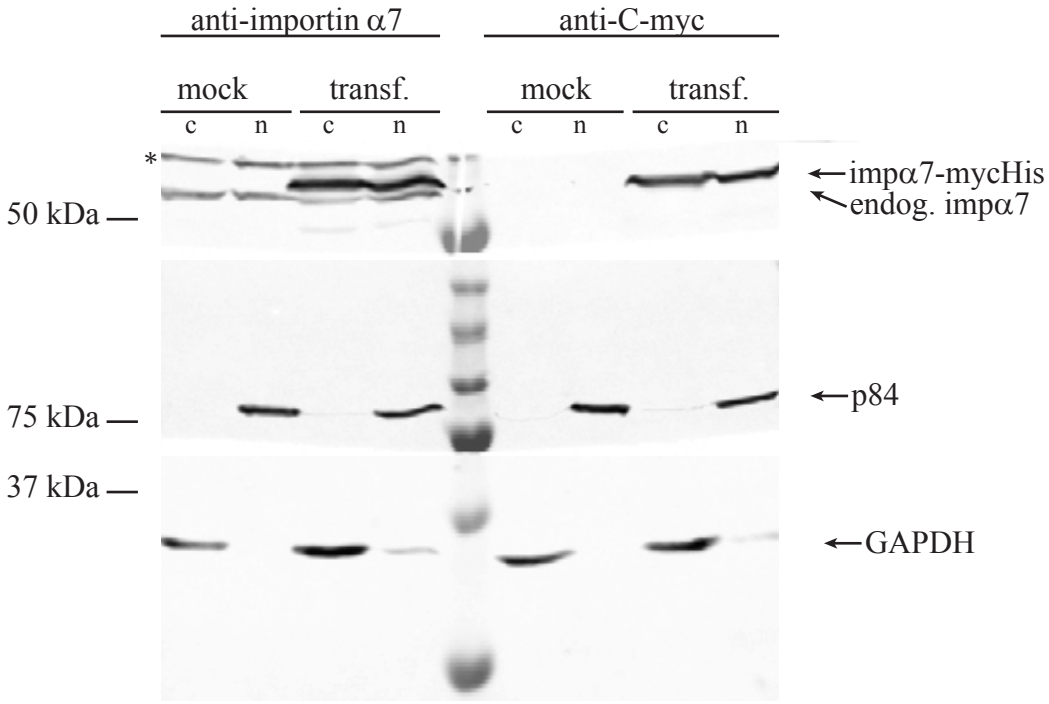
Supplementary Table 7: Proteins that bound importin alpha 7 preferentially and overlap with importin alpha 7 binding partners from ovary. Importin alpha 7, -alpha 2 and -alpha 3 binding partners were identified from fibroblast cells by co-immunoprecipitation. Importin -alpha 2 or -alpha 3 binding binders having a higher LFQ intensity compared to importin alpha 7 were excluded. Remaining importin alpha 7 binding partners were ranked according to their relative LFQ intensity from the ovary pull-down experiment.

	Gene name	LFQ-intensity		Gene name	LFQ-intensity		Gene name	LFQ-intensity		Gene name	LFQ-intensity
1	Hnrnpu	3.76E+10	**21**	Abh5	8.54E+08	**41**	Smc1a	1.1E+08	**61**	Dsp	36318000
2	Lmnb1	3.29E+10	**22**	Ase1	8.48E+08	**42**	Smarcd1	1.08E+08	**62**	Tada1	32645000
3	Hnrnpl	9.71E+09	**23**	Nol5	5.97E+08	**43**	Ppil1	97006000	**63**	Emp2	26632000
4	Mcm3	6.73E+09	**24**	Nol5a	5.97E+08	**44**	Chd3	96858000	**64**	Qka1	21759000
5	Anp32b	6.58E+09	**25**	Smarce1	5.79E+08	**45**	Wdr18	96488000	**65**	Ylpm1	20613000
6	Taf2s	5.1E+09	**26**	Arid1a	5.29E+08	**46**	Ash2l	94731000	**66**	Smarcb	18988000
7	Cdc46	3.8E+09	**27**	Bod1l	4.5E+08	**47**	Smarcd3	94429000	**67**	Nvl	17584000
8	Dhm1	3.73E+09	**28**	Arid1b	4.07E+08	**48**	Clk2	77581000	**68**	Spty2d1	15244000
9	Smarcc2	3.45E+09	**29**	Tex10	3.79E+08	**49**	Fam103a1	76178000	**69**	Paf65b	10681000
10	smarca4	2.21E+09	**30**	Mta3	3.41E+08	**50**	Pb1	75851000	**70**	Gtf2h4	9828500
11	Rbap48	2E+09	**31**	Paf53	3.37E+08	**51**	Trrap	69640000	**71**	Adnp	9524200
12	Hnrnpc	1.92E+09	**32**	Pcif1	2.84E+08	**52**	Dhx16	68796000	**72**	Set1b	8308700
13	Tceb3	1.76E+09	**33**	Nolc1	2.39E+08	**53**	Dinb1	60927000	**73**	Paf65a	7735300
14	Ctnnbl1	1.37E+09	**34**	Cbp	1.8E+08	**54**	Abra1	58297000	**74**	Atxn2l	2188200
15	Smarca5	1.28E+09	**35**	Nipbl	1.68E+08	**55**	Nhp2l1	56352000			
16	Trim33	1.22E+09	**36**	Dpf2	1.67E+08	**56**	Brcc3	56226000			
17	Edd1	1.19E+09	**37**	Smc3	1.55E+08	**57**	Rbbp5	54128000			
18	Anp32e	1.14E+09	**38**	Smarcc1	1.51E+08	**58**	Aimp1	54077000			
19	Aprin	1.08E+09	**39**	Mnar	1.45E+08	**59**	Bptf	40443000			
20	Smarcd2	8.74E+08	**40**	Gnl3	1.13E+08	**60**	Csnk1d	39791000			

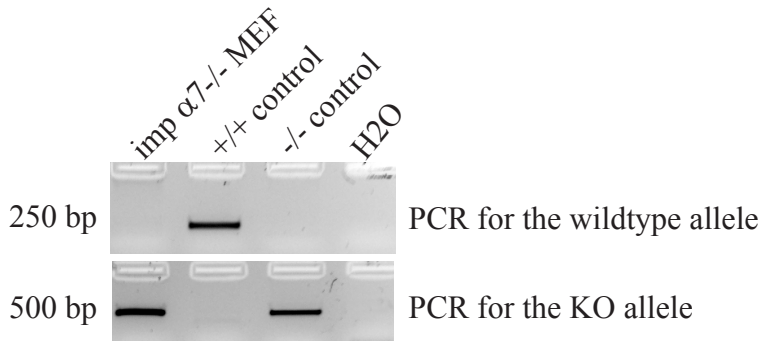
Supplementary References

1. Kohler, M., Ansieau, S., Prehn, S., Leutz, A., Haller, H., and Hartmann, E. (1997) Cloning of two novel human importin-alpha subunits and analysis of the expression pattern of the importin-alpha protein family. *FEBS Lett* **417**, 104-108

Supplementary Figure 1



Supplementary Figure 2



Supplementary Figure 3