microRNA-9 targets the long non-coding RNA *MALAT1* for degradation in the nucleus

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Running Title: miR-9 targets MALAT1 in the nucleus

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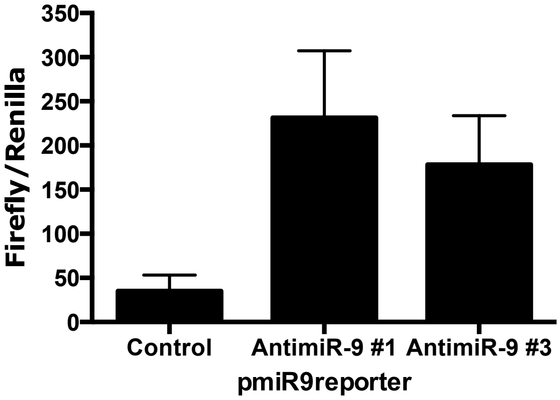
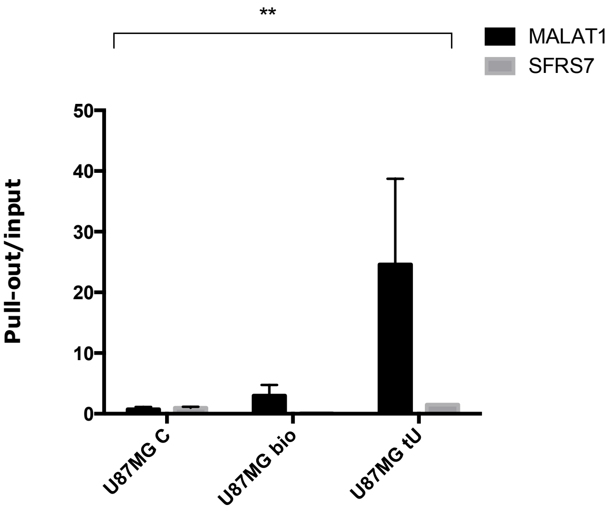
Supplementary figures:



a



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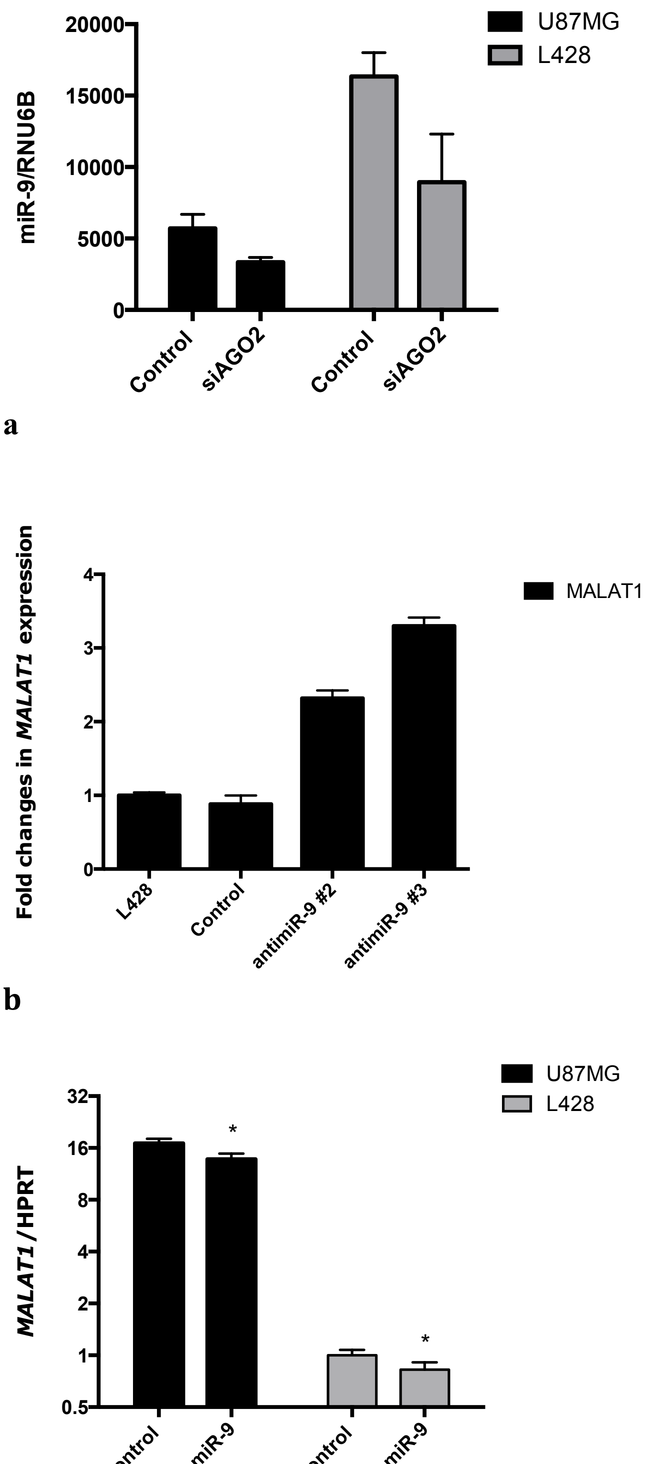
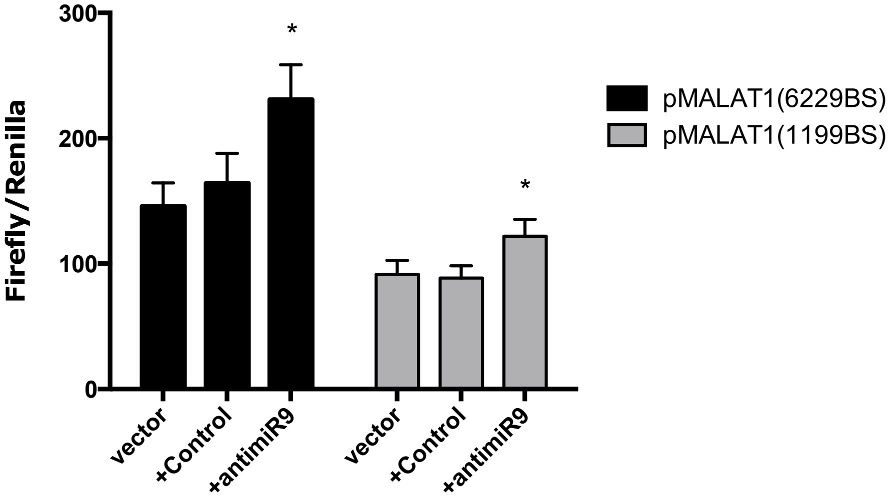
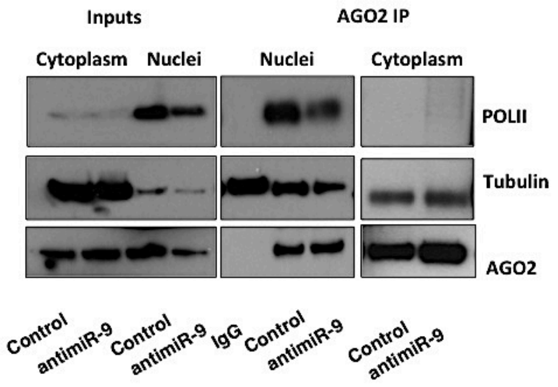
Supplementary Fig.1a-b:



Supplementary Fig.2a-c:



Supplementary Fig.3:



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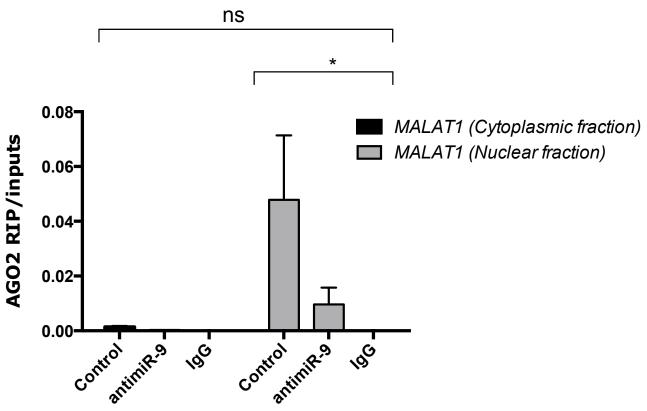

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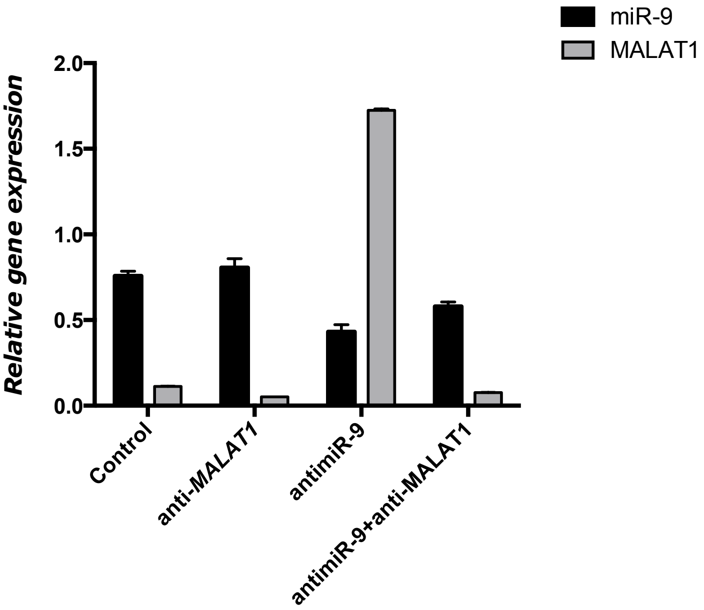
Supplementary Fig. 4a-b



Supplementary figure 5

Supplementary figure legends:

Supplementary Table 1:

Differentially expressed genes were identified by RNA-seq, sequencing was carried on in biological duplicates and hits filtered for FDR < 0.05, yielding 8,295,863 and 106,747,280 reads for the scramble transfected control, and 8,177,967 and 21,921,280 for the antimiR-9 transfected cells. 72% and 51% reads mapped to the scrambled treated duplicates, and 73% and 60% mapped to the antimiR-9 treated duplicates.

Supplementary Fig.1a-b:

a) The efficiency and specificity of miR-9 inhibition antimiR-9 #1 and #3 (an 8-mer and a full-length antimiR-9) was checked by co-transfection of a luciferase reporter containing 2X perfect match miR-9 binding sites.

b) U87MG were transfected with a miR-9 mimic, a miR-9 mimic labeled with biotin or a miR-9 mimic labeled with biotin and containing thiouridin. qPCR was used to measure *MALAT1* enrichment in the pull-out samples over the inputs. The p value was calculated by ANOVA

Supplementary Fig.2a-c:

a) qPCR shows down-regulation of miR-9 following AGO2 down-regulation in two different cell lines. Bars show mean +/- SEM (n=3).

b) qPCR shows that up-regulation of *MALAT1* following miR-9 inhibition in L428, can still be detected by using a full length (antimiR-9 #3) or a 15-mer (antimiR-9 #2) antimiR-9. Bars show mean +/- SD.

b) qPCR shows down-regulation of *MALAT1* following miR-9 overexpression in two different cell lines. p-values were calculated by t-test. Bars show mean +/- SEM (n=3).

Supplementary Fig.3:

Cells were transfected with two different constructs encoding luciferase activity under control of miR-9 binding sites (position 6229 and position 1199 respectively) in *MALAT1* sequence, alone, in presence of a antimiR-9 or a scrambled control oligonucleotide. antimiR-9 induces an increase in luciferase activity. p-values were calculated by two-ways ANOVA. Bars show mean +/- SEM (n=3)

Supplementary Fig. 4a-b:

a) Nuclear and cytoplasmic fractions were isolated from L428 transfected with a scramble control or an antimiR-9, and immunoprecipitated using AGO2 antibody. The western blot shows the purity of the extracts and the efficiency of AGO2 immunoprecipitation. The signal for tubulin in the nuclei is the result of a cross-reaction of the antibody with the Immunoglobulin.

b) The amount of *MALAT1* bound to AGO2 was measured by qPCR in nuclear and cytoplasmic fractions in presence of a scrambled control or an antimiR-9. Bars show mean +/- SEM (n=3). p-values were calculated by two-ways ANOVA.

Supplementary figure 5:

MALAT1 inhibition did not affect miR-9 expression. Levels of *MALAT1* (relative to HPRT) and miR-9 (relative to RNU6B) were measured by qPCR in L428 upon inhibition of miR-9 only, *MALAT1* only or a combination of the two. Error bars represent standard deviations.

Symbol	Locus	FPKM_KO	FPKM_WT	[fold change KO/WT]	pvalue	FDR
MTRNR2L9	chr6:62284007-62284534	71.7536	0.599774	-6.9025	2.65E-08	1.15E-05
LOC91948	chr15:98285845-98417659	9.01638	0.232217	-5.2790	2.19E-06	4.61E-04
-	chr1:42965490-42966014	25.2106	1.11367	-4.5006	7.63E-05	7.85E-03
EIF4A3	chr17:78109012-78121038	32.2404	1.4874	-4.4380	0.000773	4.42E-02
GSTA4	chr6:52842745-52860751	151.195	7.21972	-4.3883	0	0.00E+00
-	chr3:96336458-96337011	67.8731	3.48933	-4.2818	1.44E-05	2.12E-03
MALAT1	chr11:65265232-65273939	20.332	1.23015	-4.0469	0.000271	2.04E-02
-	chr5:14637426-14653547	5.94365	0.436944	-3.7658	8.80E-06	1.44E-03
RPS17	chr15:82821160-82824865	27.2284	2.05439	-3.7283	1.15E-05	1.79E-03
MRPL2	chr6:43021766-43027242	27.392	2.52882	-3.4372	8.81E-05	8.76E-03
MIR3648	chr21:9825439-9827602	938.919	108.103	-3.1186	1.18E-09	8.18E-07
AGPAT3	chr21:45285115-45407475	16.059	2.0597	-2.9629	0.000412	2.78E-02
RMRP	chr9:35657747-35658015	83.8952	11.3264	-2.8889	0.000152	1.31E-02
CCDC117	chr22:29168661-29185283	9.51769	1.86075	-2.3547	0.000399	2.72E-02
NEAT1	chr11:65183915-65212973	3.53397	0.760942	-2.2154	8.12E-05	8.24E-03
NOMO3	chr16:16326388-16388668	1.91484	0.421409	-2.1839	0.000575	3.54E-02
RPS17L	chr15:83205503-83209208	38.6027	8.91287	-2.1147	0.000291	2.14E-02
BMS1	chr10:43277953-43330385	11.3499	2.84696	-1.9952	0.000212	1.70E-02
RPL23A	chr17:27046999-27053949	1472.66	416.216	-1.8230	5.87E-05	6.40E-03
CKS2	chr9:91926112-91931618	81.494	26.2233	-1.6359	0.000857	4.73E-02
H3F3B	chr17:73772514-73775860	65.243	159.663	1.2911	0.000799	4.53E-02
BTF3	chr5:72794243-72801448	184.665	469.695	1.3468	0.000919	4.99E-02
PSMA6	chr14:35761554-35786682	59.5217	156.212	1.3920	0.000809	4.57E-02
RPL22	chr1:6245079-6260600	71.2372	188.57	1.4044	0.000339	2.40E-02
FABP5	chr8:82192717-82197012	86.7022	230.273	1.4092	0.000421	2.83E-02
RPS3	chr11:75110561-75116733	316.626	852.598	1.4291	0.00036	2.51E-02
CALM2	chr2:47387220-47403740	137.881	373.881	1.4392	0.000172	1.45E-02
RPS8	chr1:45241245-45244412	662.411	1800.56	1.4426	0.000423	2.84E-02
PSMB6	chr17:4699456-4701790	43.8906	122.281	1.4782	0.000585	3.60E-02
RPL18	chr19:49118587-49122433	481.601	1355.85	1.4933	0.000259	1.98E-02
RPL35	chr9:127615754-127624240	543.074	1546.29	1.5096	0.000373	2.58E-02
RPL17	chr18:47007547-47018935	538.927	1544.42	1.5189	0.000538	3.37E-02
CD81	chr11:2398546-2418649	18.673	53.5429	1.5197	0.000705	4.12E-02
LSM3	chr3:14220227-14239869	58.0316	169.315	1.5448	0.0002	1.63E-02
TSSC1	chr2:3192740-3381653	7.31716	21.4274	1.5501	0.000777	4.43E-02
RPS9	chr19:54704707-54711515	163.522	481.268	1.5574	0.00054	3.38E-02
RPL32	chr3:12838170-12883081	938.831	2767.71	1.5598	0.000282	2.10E-02
GSTP1	chr11:67351065-67354124	27.654	82.5213	1.5773	0.000539	3.37E-02
RPL7	chr8:74202873-74205869	272.91	831.848	1.6079	3.58E-05	4.35E-03
PSMD13	chr11:236807-252984	17.5476	55.3819	1.6582	0.000136	1.21E-02
GADD45GIP	chr19:13064971-13068050	15.7883	50.0452	1.6644	0.000818	4.60E-02
PSMD14	chr2:162164785-162268227	23.0729	74.1381	1.6840	0.000134	1.20E-02
C17orf79	chr17:30178883-30186326	10.8375	35.8992	1.7279	0.000397	2.71E-02
RPS27L	chr15:63437219-63450051	10.9062	36.4737	1.7417	0.000482	3.11E-02
RPLP2	chr11:809935-812876	384.629	1331.66	1.7917	2.91E-05	3.66E-03

RPL23	chr17:37004268-37010053	584.03	2049.45	1.8111	0.00014	1.24E-02
ISG15	chr1:948846-949919	10.6179	38.8108	1.8700	0.000335	2.39E-02
RPL15	chr3:23933571-23962332	134.495	500.714	1.8964	0.000615	3.73E-02
VDAC1	chr5:133307563-133340824	57.7159	217.341	1.9129	0.000464	3.03E-02
TSPAN8	chr12:71518871-71552560	9.54896	36.6865	1.9418	0.000809	4.57E-02
SEC61G	chr7:54819939-54826939	18.6801	72.4305	1.9551	0.000263	2.00E-02
RGS16	chr1:182567757-182573548	0.888233	3.4927	1.9753	0.000502	3.21E-02
RPL41	chr12:56510373-56511616	1863.37	7356.38	1.9811	9.40E-06	1.52E-03
FAM162A	chr3:122103022-122128961	8.92841	36.1602	2.0179	0.000121	1.13E-02
PRDX5	chr11:64085559-64089295	16.9015	70.1162	2.0526	0.000134	1.20E-02
ISG20	chr15:89182038-89198879	2.61343	12.3345	2.2387	0.000455	2.99E-02
HLA-DRB1	chr6:32485153-32557610	51.2171	262.416	2.3572	8.86E-08	3.17E-05
BNIP3	chr10:133780749-13379585	4.12045	23.3322	2.5015	0.00012	1.12E-02
DDIT4	chr10:74033676-74035797	2.00027	12.1298	2.6003	9.29E-07	2.25E-04
S100A10	chr1:151955385-151966714	29.078	186.627	2.6822	3.09E-06	6.15E-04
CRIP1	chr14:105952350-10595512	48.9306	326.008	2.7361	2.33E-05	3.05E-03
BATF3	chr1:212859758-212897575	28.4778	279.329	3.2941	0.000757	4.34E-02
RPL13AP20	chr12:13028385-13029261	0.746306	8.44167	3.4997	0.000822	4.62E-02
GLUD2	chrX:120181461-120183796	0.124602	1.77807	3.8349	4.40E-05	5.09E-03
ANXA2P2	chr9:33624222-33625532	0.435799	6.33699	3.8621	1.95E-06	4.20E-04
IRF1	chr5:131746464-131827446	2.5931	37.9666	3.8720	0.000865	4.77E-02
LOC653566	chr1:28421445-28423069	0.154899	2.47363	3.9972	5.85E-05	6.38E-03
FAM45B	chrX:129628914-129631421	0.155573	3.52287	4.5011	1.53E-07	5.06E-05
-	chr14:95267731-95267848	117.904	5592.31	5.5678	0.000134	1.20E-02
-	chr7:45291571-45291711	262.817	16680.2	5.9879	0	0.00E+00
-	chr7:57634331-57634470	24.1537	2191.63	6.5036	1.79E-05	2.48E-03
-	chr20:26145800-26145943	21.6398	2303.17	6.7338	9.74E-05	9.47E-03
-	chr4:33840812-33840965	36.9155	5558.16	7.2342	3.41E-09	2.00E-06
-	chr20:32788393-32788552	15.454	2854.63	7.5292	1.68E-08	7.90E-06
-	chr7:57634082-57634206	15.7394	3933.74	7.9654	9.20E-05	9.05E-03
-	chr4:33843590-33843715	14.0018	4915.52	8.4556	0.000704	4.11E-02
-	chr17:21544415-21544526	68.0117	29228.6	8.7474	5.79E-10	4.36E-07
-	chr7:57608150-57608312	2.75867	2310.98	9.7103	6.36E-09	3.39E-06
-	chr20:26141552-26141700	13.4318	13953.6	10.0208	0	0.00E+00
HSP90AA1	chr14:102547074-10260608	500.565	0	Inf	0.00038	2.62E-02
PDIA6	chr2:10861774-10952960	107.662	0	Inf	0.000188	1.56E-02
KLF7	chr2:207940082-208031639	1.024	0	Inf	0.000911	4.96E-02
EIF3D	chr22:36906874-36925277	56.5165	0	Inf	0.000575	3.55E-02
RER1	chr1:2323213-2345488	0	11.7973	-Inf	2.17E-06	4.59E-04
PHF13	chr1:6673755-6684093	0	2.43253	-Inf	1.07E-06	2.56E-04
MFN2	chr1:12040237-12073702	0	27.6929	-Inf	6.26E-06	1.09E-03
TMEM39B	chr1:32537999-32568529	0	3.94927	-Inf	0.000504	3.21E-02
LMO4	chr1:87794118-87814607	0	4.0075	-Inf	8.25E-06	1.37E-03
RNF11	chr1:51701563-51739252	0	13.194	-Inf	0.000639	3.83E-02
RPL5	chr1:93297593-93307481	0	2163.74	-Inf	7.89E-08	2.88E-05
LRRC8B	chr1:89989286-90185096	0	1.61027	-Inf	0.000474	3.07E-02

ATP5F1	chr1:111982511-112004525	0	71.1217	-Inf	1.69E-08	7.90E-06
TARS2	chr1:150459808-150486265	0	6.07803	-Inf	1.09E-05	1.72E-03
ATF3	chr1:212738696-212794116	0	27.9198	-Inf	5.21E-11	5.42E-08
SETDB1	chr1:150898814-150937220	0	2.03008	-Inf	0.00042	2.83E-02
DEPDC1	chr1:68939834-68962799	0	11.3227	-Inf	2.03E-10	1.76E-07
CASP9	chr1:15818759-15851377	0	2.37474	-Inf	0.000337	2.40E-02
POGZ	chr1:151375011-151431941	0	2.45075	-Inf	5.00E-05	5.64E-03
NRD1	chr1:52082545-52344609	0	13.9573	-Inf	0.000471	3.06E-02
MRPL9	chr1:151732122-151743806	0	28.5022	-Inf	6.73E-05	7.09E-03
DCAF8	chr1:160175124-160234231	0	12.7709	-Inf	1.42E-06	3.21E-04
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EIF4EBP2	chr10:72163860-72188374	0	3.40582	-Inf	5.99E-06	1.05E-03
PDCD4	chr10:112631552-11267912	0	4.39896	-Inf	1.47E-05	2.15E-03
DLG5	chr10:79550546-79689583	0	2.5075	-Inf	2.32E-13	5.14E-10
SMNDC1	chr10:112052797-11206500	0	7.31461	-Inf	2.92E-05	3.68E-03
-	chr10:98510319-98510670	0	69.58	-Inf	2.15E-10	1.84E-07
NOLC1	chr10:103892786-10392362	0	21.2027	-Inf	0.000142	1.25E-02
MRPL23	chr11:1968501-1977839	0	30.0062	-Inf	1.39E-06	3.15E-04
C10orf137	chr10:127408083-12745271	0	1.92688	-Inf	0.000343	2.43E-02
CCDC88B	chr11:64104494-64125006	0	3.61562	-Inf	7.55E-08	2.78E-05
POLL	chr10:103338518-10334802	0	2.61614	-Inf	0.000131	1.19E-02
NDUFS8	chr11:67798083-67804114	0	35.3347	-Inf	2.27E-06	4.74E-04
CTTN	chr11:70244026-70282690	0	16.0494	-Inf	6.03E-07	1.61E-04
C11orf1	chr11:111744779-11175479	0	12.5173	-Inf	1.41E-05	2.09E-03
PAK1	chr11:77032591-77185108	0	4.07502	-Inf	3.70E-05	4.47E-03
MARK2	chr11:63606396-63678492	0	1.60391	-Inf	0.000355	2.49E-02
DDX6	chr11:118618469-11866197	0	5.47037	-Inf	2.46E-09	1.51E-06
DERA	chr12:16064185-16190315	0	28.1275	-Inf	3.89E-14	1.10E-10
SFSWAP	chr12:132195616-13228428	0	6.05825	-Inf	9.13E-06	1.48E-03
DNAJC14	chr12:56211805-56236735	0	13.1304	-Inf	1.78E-07	5.74E-05
NACA	chr12:57106204-57146175	0	364.436	-Inf	2.69E-07	8.14E-05
NAA16	chr13:41885340-41951166	0	1.4618	-Inf	1.97E-05	2.68E-03
BUD13	chr11:116618885-11664381	0	2.64185	-Inf	0.000359	2.50E-02
LIG4	chr13:108859791-10887071	0	1.70593	-Inf	5.60E-05	6.18E-03
C11orf61	chr11:124636393-12467946	0	2.56952	-Inf	0.000915	4.98E-02
SOCS4	chr14:55493843-55516206	0	2.83591	-Inf	1.35E-05	2.02E-03
LRMP	chr12:25189575-25348094	0	8.05643	-Inf	0.000503	3.21E-02
TARBP2	chr12:53893594-53900215	0	4.93973	-Inf	0.00043	2.87E-02
MTHFD1	chr14:64854758-64926725	0	24.1528	-Inf	2.90E-06	5.81E-04
CNOT2	chr12:70636773-70748773	0	7.4114	-Inf	0.000314	2.27E-02
KNTC1	chr12:122987943-12311099	0	6.45815	-Inf	0.000481	3.10E-02
ACIN1	chr14:23527771-23569665	0	20.6801	-Inf	7.05E-05	7.34E-03
ABCD2	chr12:39940914-40013975	0	2.28595	-Inf	0.000842	4.68E-02
CFL2	chr14:35179587-35184330	0	5.23177	-Inf	1.90E-11	2.31E-08
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RAGE	chr14:102691361-10277153	0	4.26016	-Inf	8.31E-05	8.37E-03

ITM2B	chr13:48807273-48836232	0	5.84056	-Inf	0.000829	4.64E-02
CDCA4	chr14:105475909-10548742	0	13.9895	-Inf	3.40E-09	2.00E-06
BAHD1	chr15:40733102-40760441	0	2.41344	-Inf	3.56E-06	6.92E-04
PIAS1	chr15:68346571-68498448	0	4.99079	-Inf	5.25E-06	9.52E-04
FAH	chr15:80445135-80478924	0	8.87236	-Inf	5.56E-06	9.94E-04
RAB27A	chr15:55495163-55582088	0	4.0446	-Inf	5.95E-06	1.05E-03
AAGAB	chr15:67493366-67547074	0	11.5917	-Inf	2.28E-11	2.72E-08
FLYWCH2	chr16:2933195-2949383	0	10.099	-Inf	1.47E-05	2.14E-03
BFAR	chr16:14726667-14763093	0	13.1617	-Inf	9.82E-12	1.36E-08
BCKDK	chr16:31119661-31124112	0	7.23094	-Inf	1.44E-05	2.12E-03
PHKB	chr16:47188904-47735434	0	2.97904	-Inf	2.45E-05	3.18E-03
MT2A	chr16:56642477-56643409	0	95.8869	-Inf	8.64E-07	2.13E-04
TRAPPC2L	chr16:88880141-88929204	0	5.80755	-Inf	2.09E-06	4.46E-04
AKAP13	chr15:85923811-86292586	0	2.47305	-Inf	0.000191	1.58E-02
GOLGA8A	chr15:34671267-34875771	0	2.19794	-Inf	0.000475	3.08E-02
RAD51C	chr17:56769962-56811692	0	10.9474	-Inf	3.02E-05	3.77E-03
MRPL12	chr17:79670399-79674556	0	22.7748	-Inf	1.68E-06	3.68E-04
PFN1	chr17:4848946-4852383	0	2016.98	-Inf	2.11E-08	9.51E-06
VAMP2	chr17:8061893-8066323	0	4.2356	-Inf	4.49E-06	8.39E-04
DDX5	chr17:62473901-62534062	0	56.254	-Inf	8.57E-09	4.34E-06
SNX29	chr16:12070584-12668146	0	2.85352	-Inf	0.000541	3.38E-02
CBX4	chr17:77806953-77813213	0	3.46777	-Inf	5.63E-05	6.20E-03
PYCR1	chr17:79890266-79895195	0	18.501	-Inf	3.78E-10	2.98E-07
ATP5A1	chr18:43664109-43684199	0	119.346	-Inf	6.05E-12	9.00E-09
GPI	chr19:34850753-34893318	0	93.2597	-Inf	3.74E-11	4.04E-08
XRCC1	chr19:44047463-44086256	0	7.08449	-Inf	3.90E-05	4.65E-03
ZNF598	chr16:2047651-2059763	0	4.77443	-Inf	0.000188	1.56E-02
ZNF434	chr16:3432082-3451075	0	2.16353	-Inf	0.000115	1.08E-02
RRN3	chr16:15012052-15475278	0	8.2762	-Inf	0.000275	2.06E-02
CHMP2A	chr19:59062932-59066486	0	24.7512	-Inf	8.99E-06	1.47E-03
ZNF638	chr2:71503689-71662189	0	7.72398	-Inf	6.28E-10	4.67E-07
RPE	chr2:210867304-211036051	0	6.67795	-Inf	3.66E-05	4.43E-03
TRPV1	chr17:3468739-3539616	0	1.64728	-Inf	0.000652	3.89E-02
WDSUB1	chr2:160092303-160143236	0	7.06243	-Inf	6.40E-11	6.37E-08
C20orf4	chr20:34824368-34844853	0	8.62204	-Inf	9.36E-14	2.23E-10
BLCAP	chr20:36145818-36156333	0	6.2178	-Inf	4.00E-06	7.63E-04
CHD6	chr20:40030749-40247216	0	1.64967	-Inf	7.65E-06	1.29E-03
ATP5O	chr21:35275756-35288158	0	102.589	-Inf	2.70E-11	3.05E-08
C17orf62	chr17:80347085-80408707	0	11.1274	-Inf	0.000457	3.00E-02
MRPL40	chr22:19419618-19423596	0	27.5322	-Inf	8.44E-07	2.10E-04
EIF3D	chr22:36906874-36925277	0	97.4004	-Inf	6.58E-17	2.93E-13
KIF15	chr3:44803182-44915459	0	3.70414	-Inf	1.39E-05	2.07E-03
FCGRT	chr19:50010110-50029723	0	3.04165	-Inf	0.000213	1.71E-02
KLF16	chr19:1852397-1876160	0	2.01837	-Inf	0.000773	4.42E-02
EPHB1	chr3:134514098-134979307	0	16.1644	-Inf	1.24E-07	4.23E-05
NOSIP	chr19:50058231-50083844	0	6.34014	-Inf	0.000151	1.30E-02

SELT	chr3:150320788-150348234	0	28.0473	-Inf	5.46E-09	2.95E-06
-	chr2:7913872-7928740	0	2.26791	-Inf	0.00047	3.06E-02
GPN1	chr2:27848505-27917847	0	16.1367	-Inf	0.000576	3.55E-02
TBC1D5	chr3:17198608-17784240	0	3.37185	-Inf	5.70E-07	1.54E-04
IFT57	chr3:107879658-107943673	0	6.06757	-Inf	5.35E-06	9.66E-04
SLC41A3	chr3:125725170-125820391	0	4.1081	-Inf	8.00E-06	1.34E-03
PIK3CB	chr3:138372036-138553781	0	2.16904	-Inf	4.30E-05	5.00E-03
TNK2	chr3:195590095-195636094	0	2.2565	-Inf	8.68E-05	8.66E-03
WHSC1	chr4:1873122-2010962	0	5.79231	-Inf	5.51E-05	6.10E-03
DCK	chr4:71859264-71896629	0	6.91794	-Inf	2.31E-05	3.04E-03
SCOC	chr4:141178439-141303710	0	5.75409	-Inf	6.54E-08	2.50E-05
UBE2D3	chr4:103717132-103790032	0	36.7881	-Inf	1.72E-07	5.64E-05
POLR3G	chr5:89754019-89810370	0	7.56898	-Inf	4.76E-07	1.32E-04
MX1	chr21:42792519-42831141	0	3.44889	-Inf	0.000108	1.03E-02
GCFC1	chr21:34100424-34144249	0	4.94089	-Inf	0.000302	2.21E-02
C5orf27	chr5:95187727-95195849	0	3.98666	-Inf	6.88E-06	1.18E-03
DMXL1	chr5:118406714-118584822	0	4.78624	-Inf	5.00E-05	5.64E-03
TOM1	chr22:35695267-35743987	0	2.88768	-Inf	0.000383	2.64E-02
LMNB1	chr5:126112314-126172712	0	32.1904	-Inf	1.68E-09	1.10E-06
REEP2	chr5:137774773-137782852	0	1.75049	-Inf	4.03E-05	4.79E-03
PARP14	chr3:122399383-122449765	0	2.65912	-Inf	0.000147	1.28E-02
HARS2	chr5:140071017-140078890	0	4.62844	-Inf	7.06E-06	1.20E-03
ARMC8	chr3:137906126-138048728	0	5.55877	-Inf	0.000708	4.13E-02
SKP1	chr5:133491731-133512724	0	66.4989	-Inf	3.91E-13	7.98E-10
ATOX1	chr5:151122382-151138210	0	49.3501	-Inf	3.01E-07	8.95E-05
ERC2	chr3:55542335-56502526	0	1.6281	-Inf	0.000607	3.70E-02
SLU7	chr5:159828647-159846168	0	9.38768	-Inf	7.53E-10	5.45E-07
DUSP1	chr5:172189940-172205684	0	4.10551	-Inf	7.45E-05	7.70E-03
FBXO9	chr6:52929740-52965670	0	4.49831	-Inf	1.59E-06	3.51E-04
CD109	chr6:74405507-74538041	0	1.5744	-Inf	7.24E-05	7.51E-03
TNIK	chr3:170779028-171178262	0	1.66377	-Inf	0.000635	3.82E-02
NRN1	chr6:5998059-6008208	0	5.10868	-Inf	8.14E-07	2.06E-04
DLG1	chr3:196769430-197030621	0	3.49459	-Inf	0.00047	3.06E-02
COX7A2	chr6:75947390-75953644	0	142.382	-Inf	2.08E-14	6.54E-11
EXOC1	chr4:56719815-56771244	0	2.86141	-Inf	0.000232	1.82E-02
EXOC1	chr4:56719815-56771244	0	2.72366	-Inf	0.000436	2.90E-02
LYRM2	chr6:90142896-90348474	0	4.53024	-Inf	3.95E-05	4.70E-03
LARP1B	chr4:128981412-129132935	0	3.81394	-Inf	0.000257	1.97E-02
BZW2	chr7:16685646-16824161	0	36.8867	-Inf	2.58E-11	2.97E-08
GRSF1	chr4:71681498-71709089	0	3.29974	-Inf	0.000106	1.01E-02
MDH2	chr7:75677392-75695930	0	49.4065	-Inf	5.78E-05	6.33E-03
ZKSCAN1	chr7:99613216-99639741	0	2.11349	-Inf	4.24E-05	4.97E-03
PIK3CG	chr7:106505611-106549427	0	10.2501	-Inf	1.42E-05	2.09E-03
TNRC18	chr7:5346420-5463177	0	2.67833	-Inf	2.18E-07	6.81E-05
C7orf70	chr7:6369039-6388590	0	4.7983	-Inf	1.90E-05	2.61E-03
SBDS	chr7:66452689-66460588	0	12.0417	-Inf	3.63E-05	4.40E-03

YWHAG	chr7:75956084-75988342	0	25.5515	-Inf	6.89E-09	3.62E-06
COPG2	chr7:130126045-130371406	0	7.04319	-Inf	4.86E-05	5.51E-03
FDFT1	chr8:11660189-11725646	0	32.203	-Inf	3.98E-05	4.73E-03
DECR1	chr8:91013579-91064227	0	14.6529	-Inf	3.75E-07	1.08E-04
MFHAS1	chr8:8640860-8751179	0	12.8497	-Inf	2.15E-09	1.35E-06
GGH	chr8:63927638-63951683	0	24.9475	-Inf	4.16E-09	2.36E-06
EYA1	chr8:72109600-72274488	0	1.5611	-Inf	5.36E-05	5.97E-03
NQO2	chr6:3000064-3025547	0	17.7734	-Inf	0.000165	1.41E-02
PGBD1	chr6:28249277-28271079	0	1.53192	-Inf	0.000694	4.07E-02
ABCF1	chr6:30539169-30559309	0	7.21045	-Inf	0.000386	2.65E-02
COX6C	chr8:100890222-100906242	0	53.7245	-Inf	1.00E-08	4.99E-06
RNF20	chr9:104296132-104500862	0	4.11365	-Inf	3.78E-06	7.32E-04
PHF3	chr6:64344491-64424463	0	3.64649	-Inf	0.00017	1.44E-02
CA5BP1	chrX:15692888-15721814	0	2.06357	-Inf	6.02E-05	6.53E-03
GNL3L	chrX:54556643-54593720	0	2.63714	-Inf	3.88E-09	2.26E-06
PGK1	chrX:77320672-77382324	0	212.766	-Inf	1.79E-10	1.57E-07
HPRT1	chrX:133507141-133648069	0	30.9591	-Inf	5.94E-05	6.45E-03
ATP6AP1	chrX:153656977-153664862	0	14.1113	-Inf	8.58E-07	2.12E-04
SNX14	chr6:86214961-86353107	0	20.7651	-Inf	0.000356	2.49E-02
POP7	chr7:100303675-100305123	0	10.7324	-Inf	0.000737	4.25E-02
PDLIM2	chr8:22436253-22455538	0	5.2254	-Inf	0.00014	1.24E-02
INTS9	chr8:28625174-28747698	0	3.37628	-Inf	0.000212	1.70E-02
KLF10	chr8:103661004-103667983	0	3.23787	-Inf	0.000738	4.26E-02
NDOR1	chr9:140098534-140113815	0	2.3363	-Inf	0.000197	1.61E-02
TCEAL3	chrX:102862833-102866289	0	1.88523	-Inf	0.000405	2.75E-02
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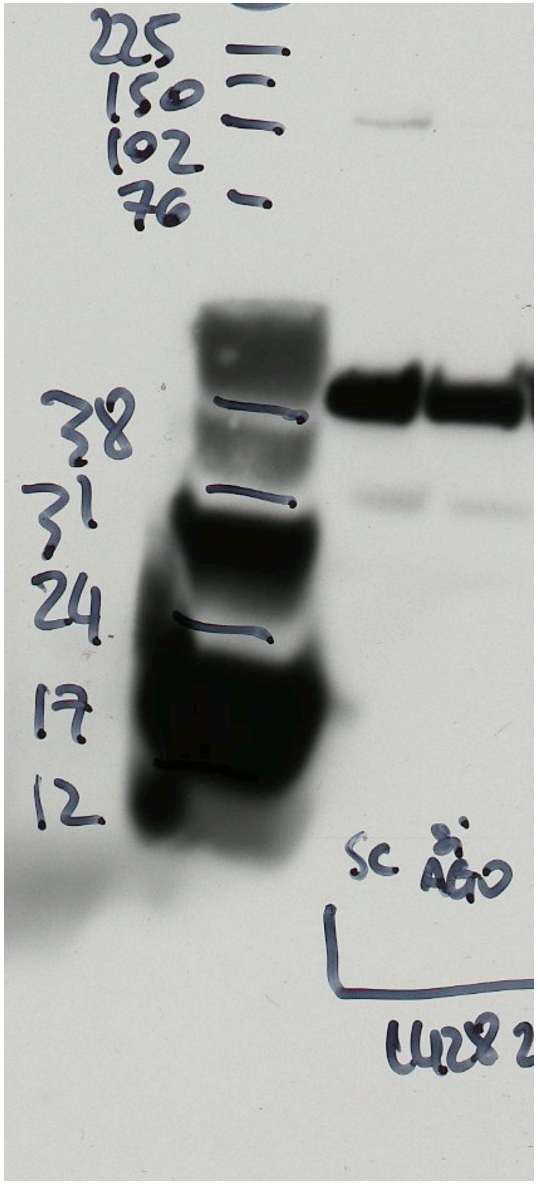
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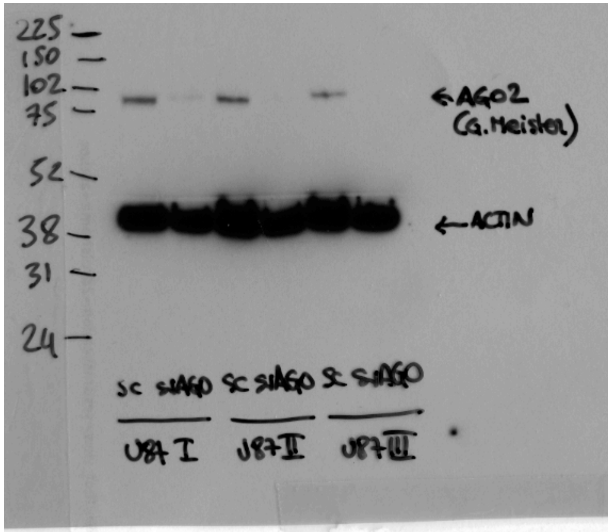
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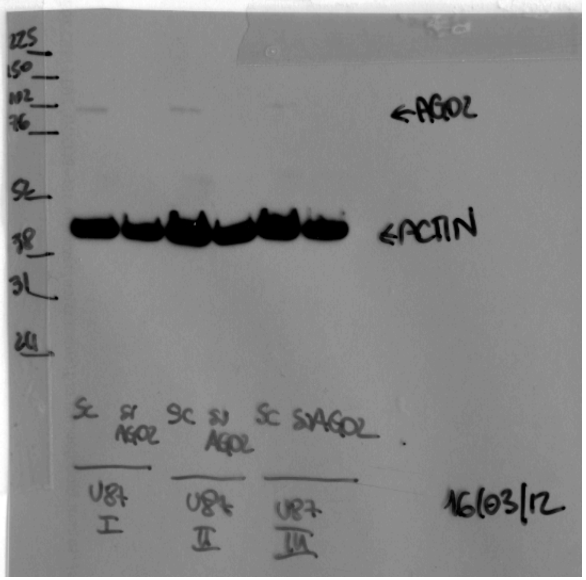
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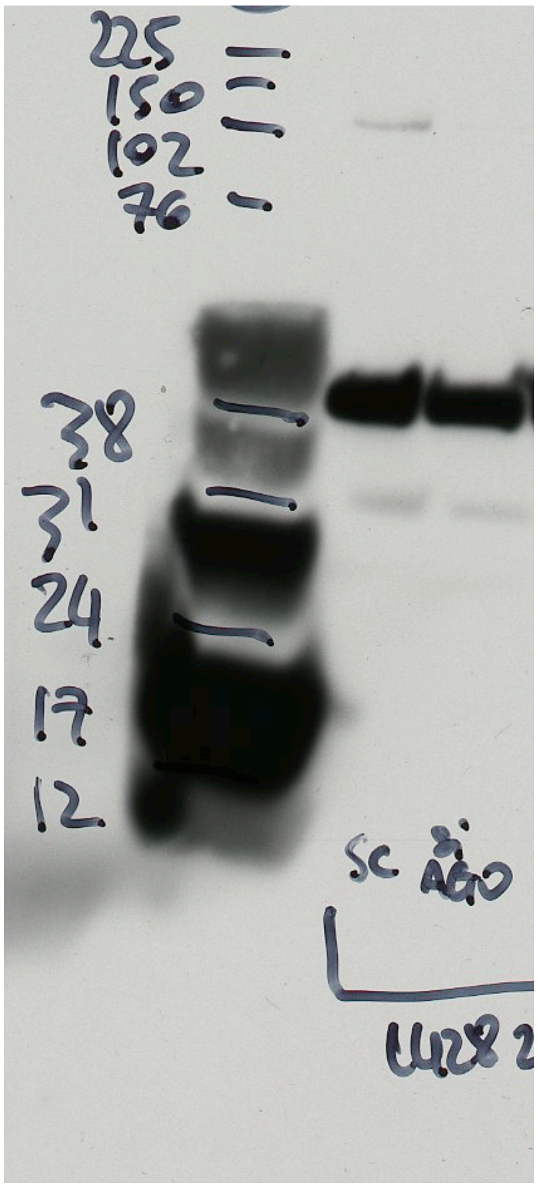

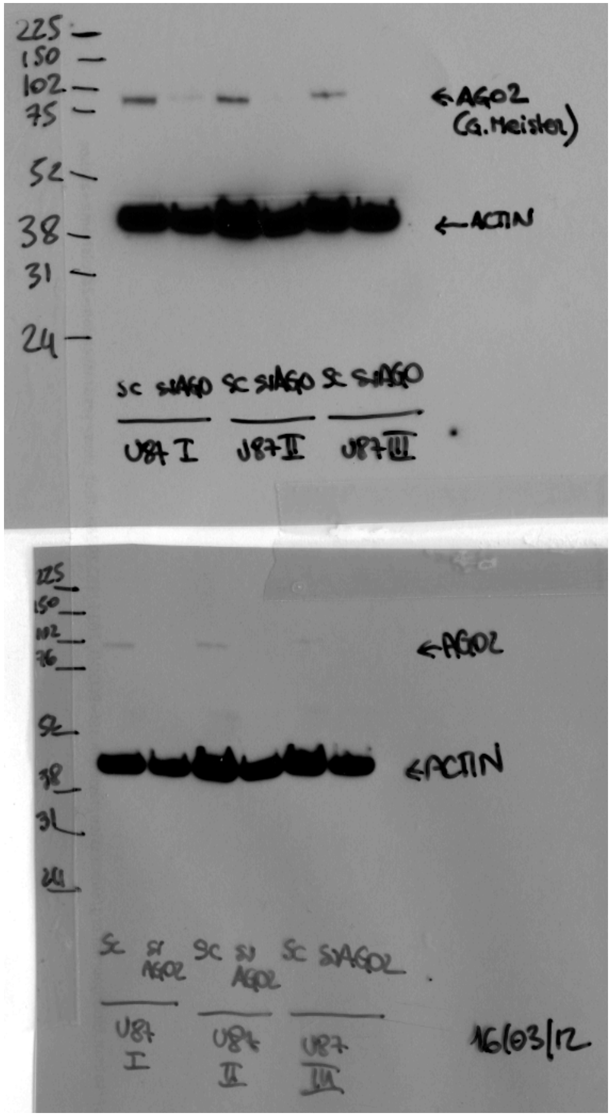

Figure 2a full gel

Figure 4c full gel