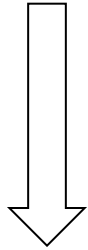


1. Expression values for each mRNA were obtained by the Robust Multi-array Analysis (RMA) method.

54,675 probe sets



Loaded data (14 arrays at 4 conditions)

1. DMSO (Control) treatment
2. Pitavastatin treatment
3. siControl with pitavastatin treatment
4. siKLF4 with pitavastatin treatment

5 samples

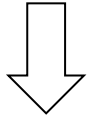
5 samples

2 samples

2 samples

2. Excluding the probes which have low expression.

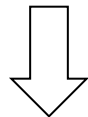
49,463 probe sets



The probe sets, which were expressed lower than 20 percentile in all the fourteen arrays were eliminated from the analyses.

3. Integrating the multiple probe sets which represent the same transcript into one, as more than one probe set is designed for the same transcript.

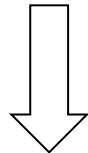
30,344 probe sets



To analyze expression data based on the gene-level, the intensity signal values were summarized using Entrez Gene ID and averaged.

4. Excluding the probe sets which do not have an annotated gene symbol.

20,756 genes



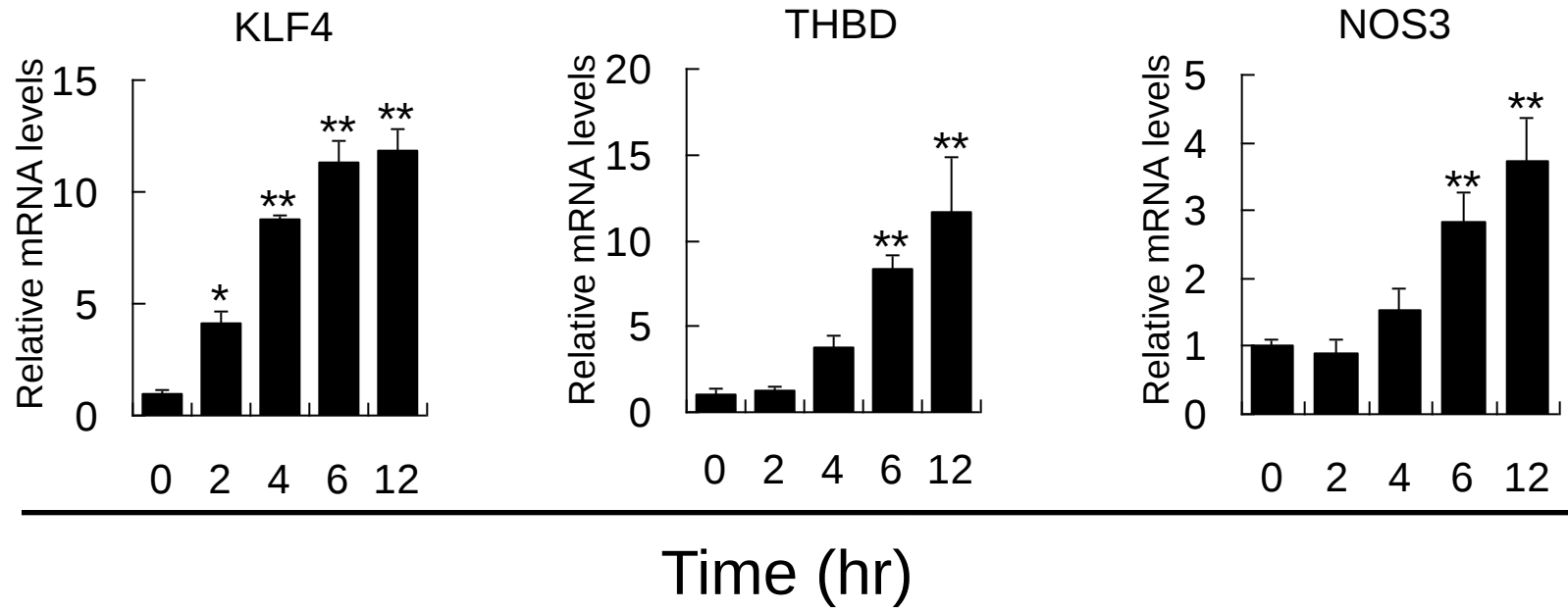
Only the probe sets which have Gene Symbols were used for further analysis. At this stage, five or two independent data sets were summarized and averaged into one data set (14 arrays into 4 conditions).

5. Selecting the genes, which had significant changes (fold change ≥ 2.0 or ≤ 0.5) in expression compared to control treatment.

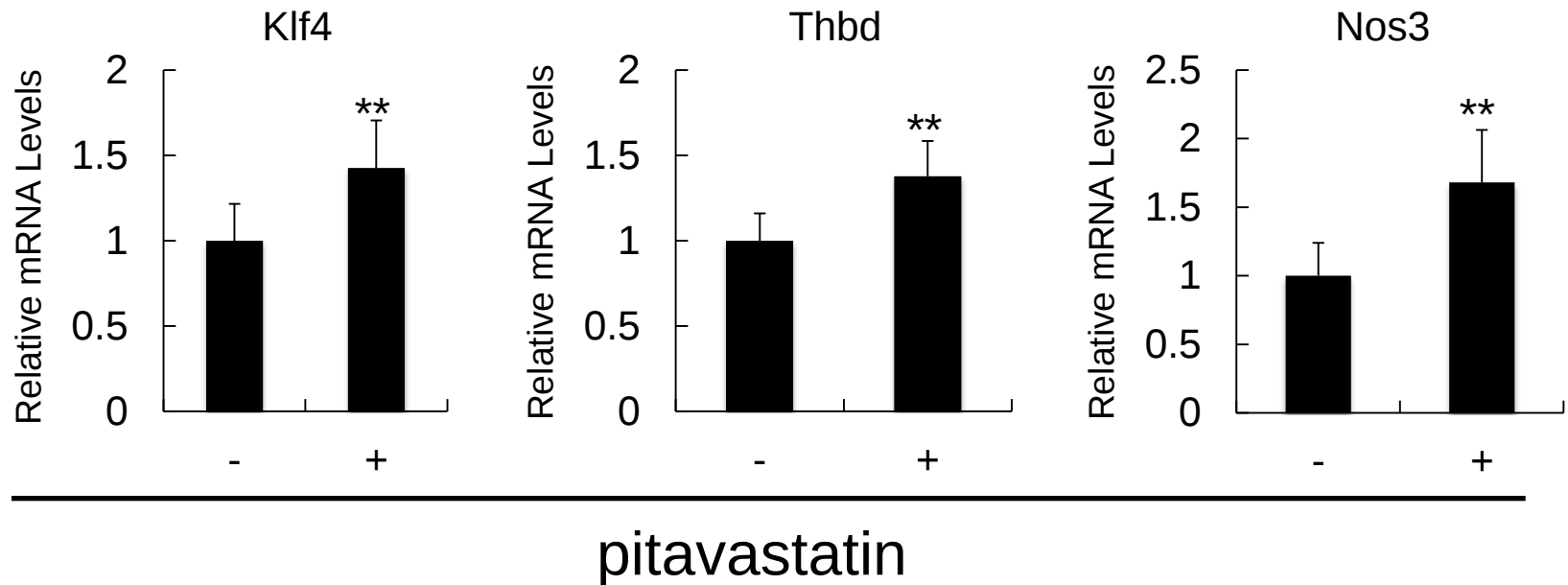
384 genes

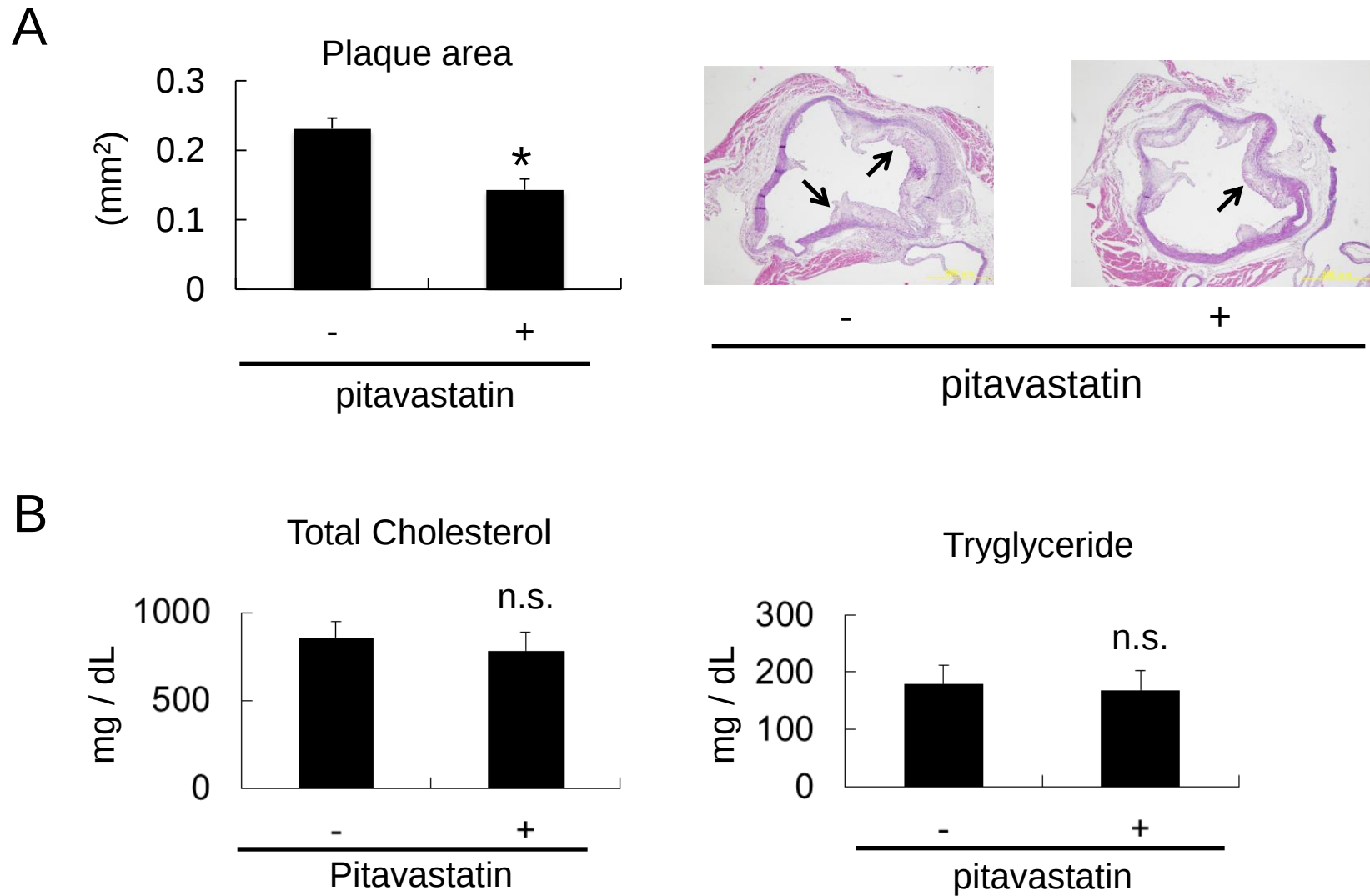
The gene expression changes in pitavastatin treatment/DMSO treatment and siKLF4/siControl under pitavastatin were calculated. Then the genes which had significant changes (fold change ≥ 2.0 or ≤ 0.5) under either condition were selected for hierarchical clustering analysis in Figure 1.

A



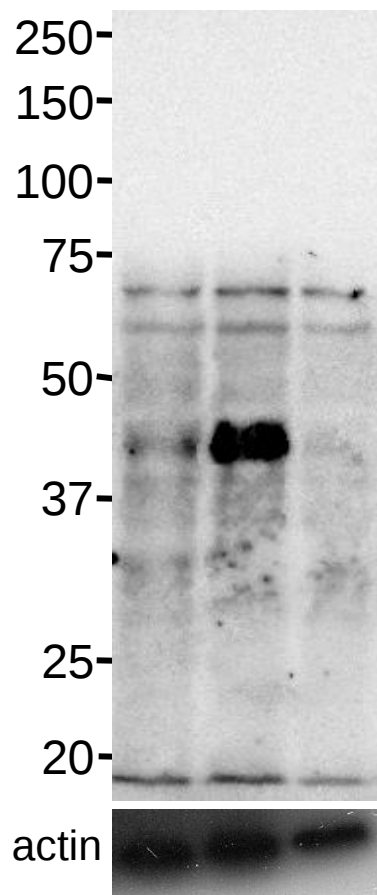
B





A

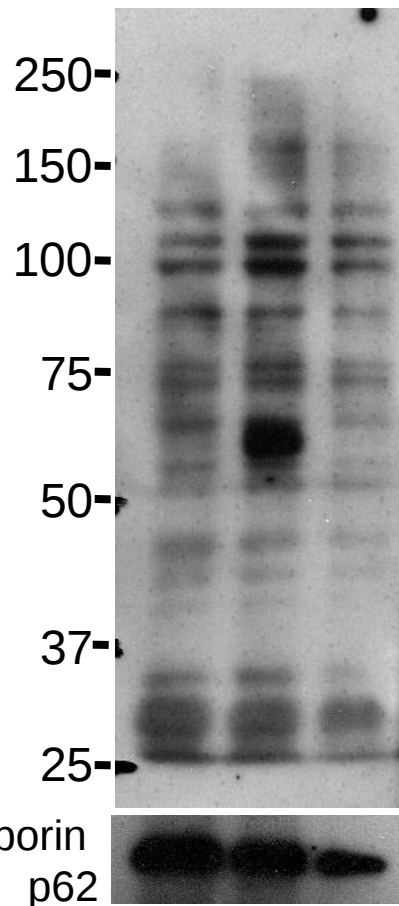
α -KLF2
(N2212)



siRNA	NS	NS	KLF2
pitavastatin	-	+	+

B

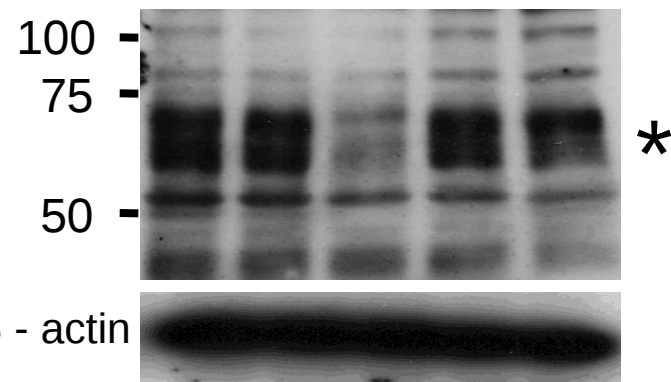
α -KLF4
(Y6929)



siRNA	NS	NS	KLF4
pitavastatin	-	+	+

C

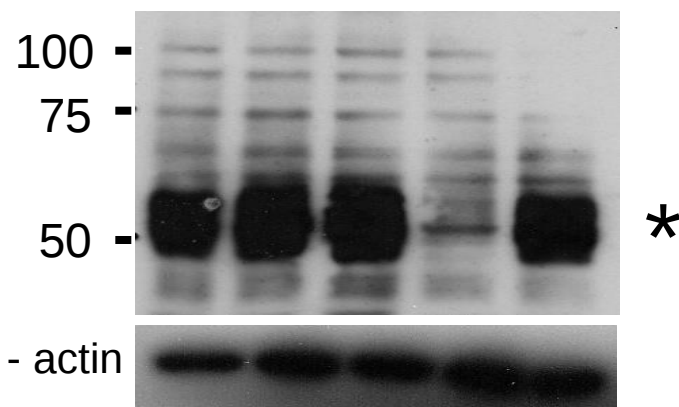
α -MEF2A (Y0841)



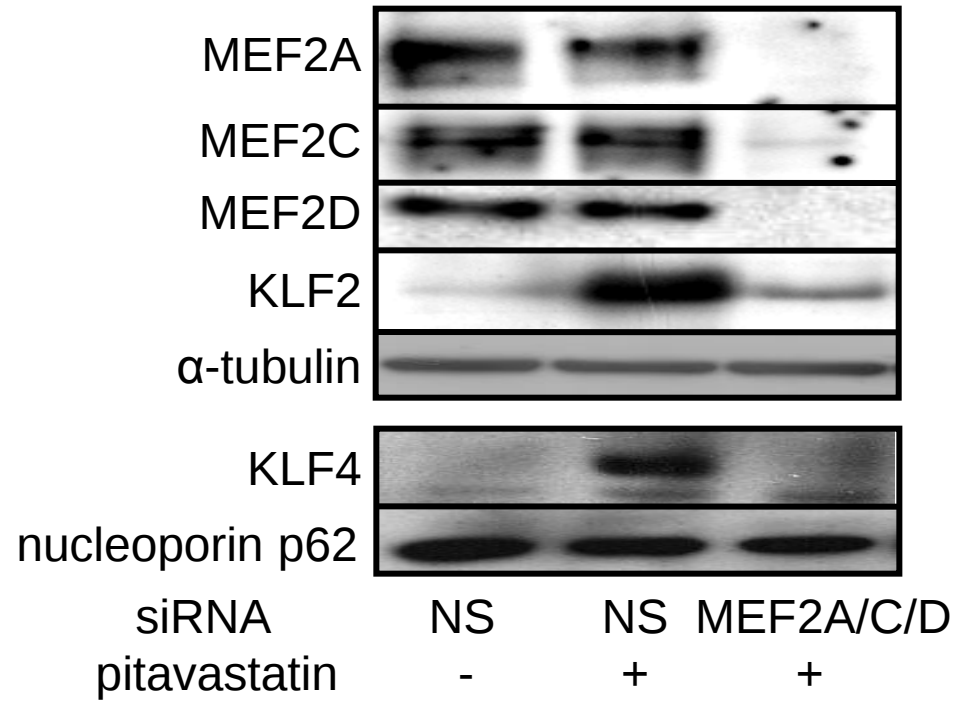
siRNA	NS	NS	MEF 2A	MEF 2C	MEF 2D
pitavastatin	-	+	+	+	+

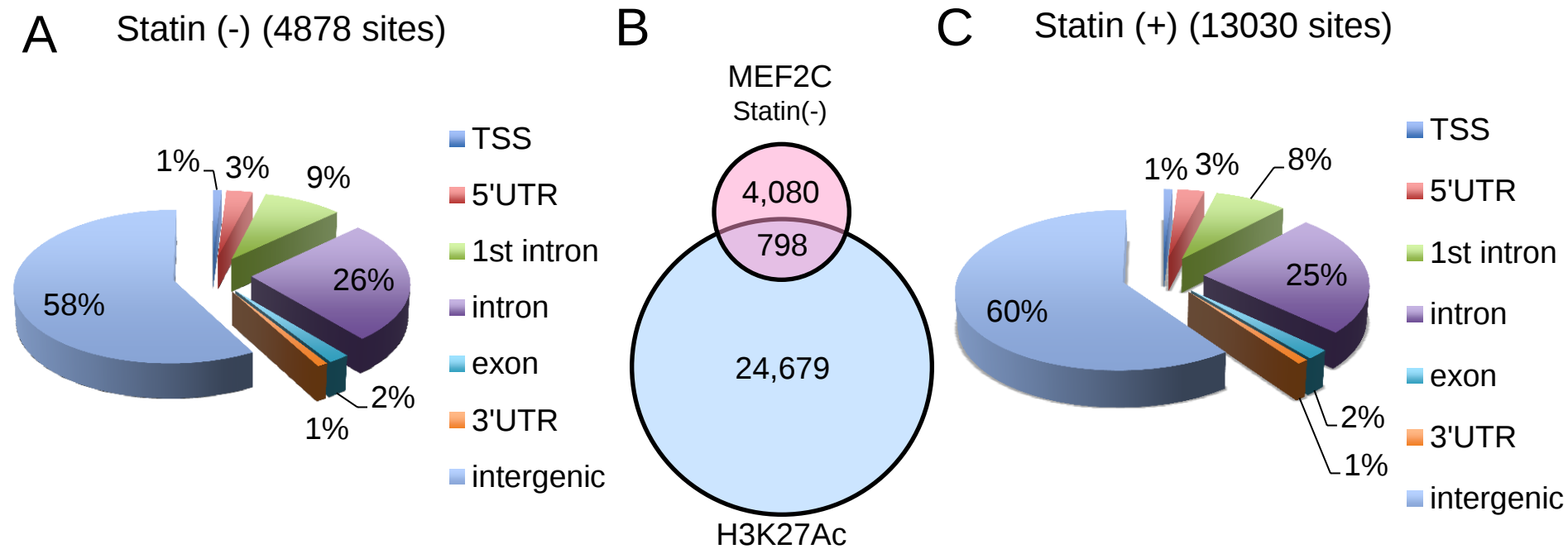
D

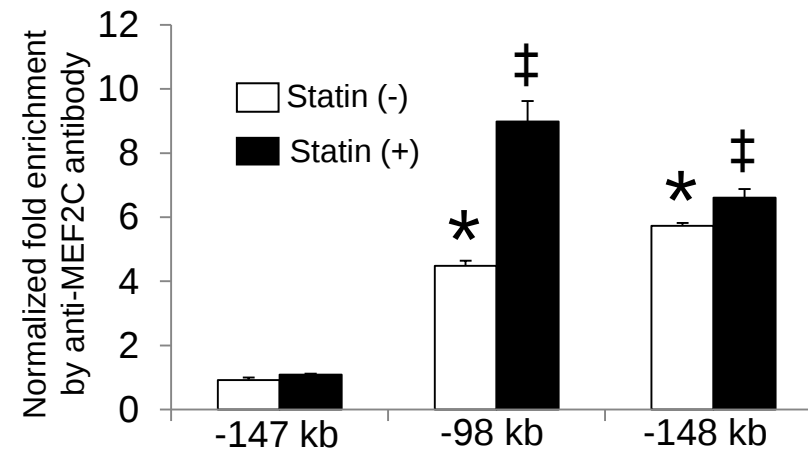
α -MEF2C (Y1740)



siRNA	NS	NS	MEF 2A	MEF 2C	MEF 2D
pitavastatin	-	+	+	+	+



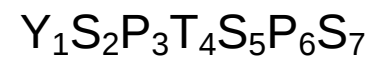




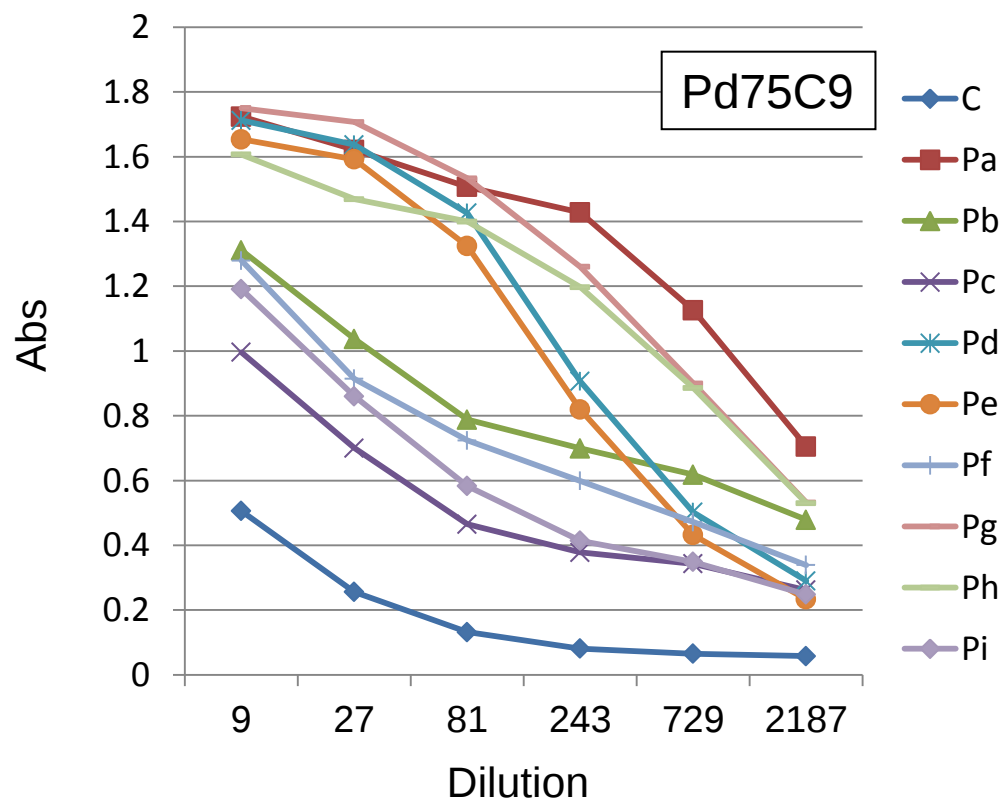
A

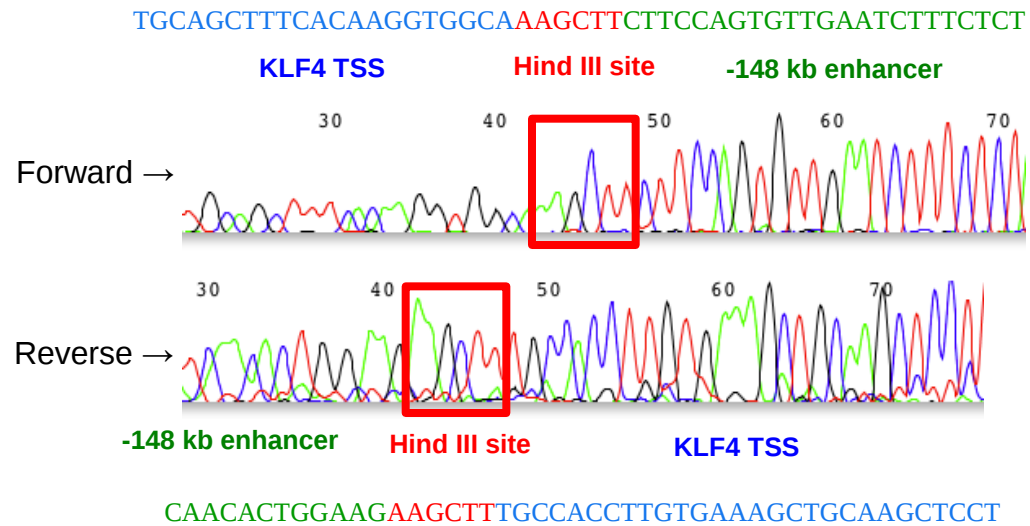
peptide	phosphorylation	
C	none	SYSPTSPSYSPTSPSYSPC
Pa	S5	SYSPTSPSYSPTSPSYSPC
Pb	S7	SYSPTSPSYSPTSPSYSPC
Pc	S2	SYSPTSPSYSPSYSPC
Pd	S5, S7	SYSPTSPSYSPTSPSYSPC
Pe	S5, S2	SYSPTSPSYSPSYSPC
Pf	S7, S2	SYSPTSPSYSPSYSPC
Pg	S7, S5	SYSPTSPSYSPSYSPC
Ph	S2, S5	SYSPTSPSYSPSYSPC
Pi	S2, S7	SYSPTSPSYSPSYSPC

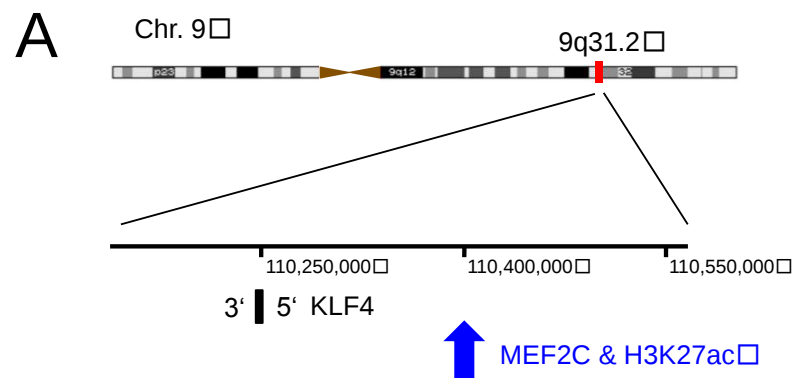
Maejima&Inoue_Fig. S8



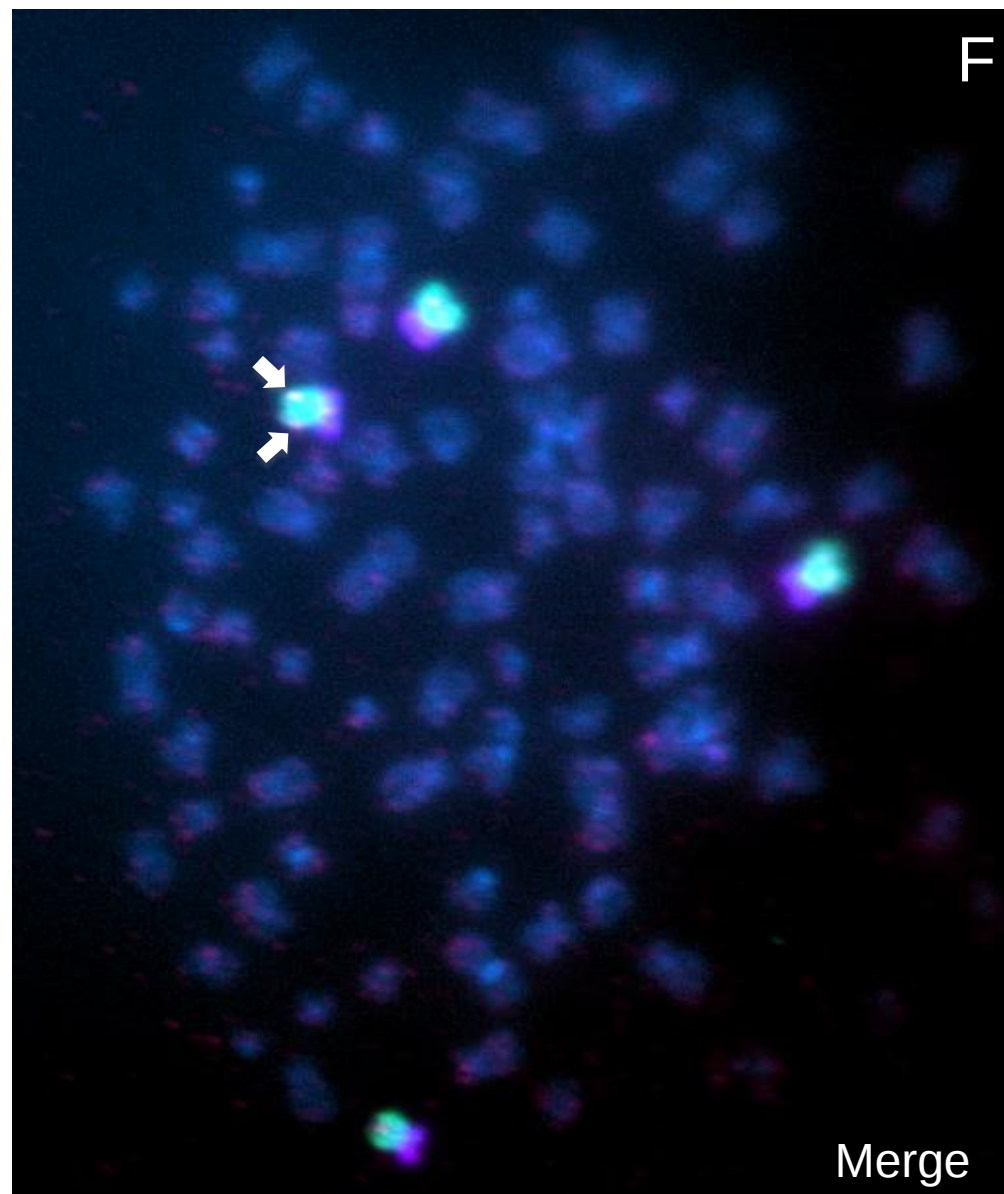
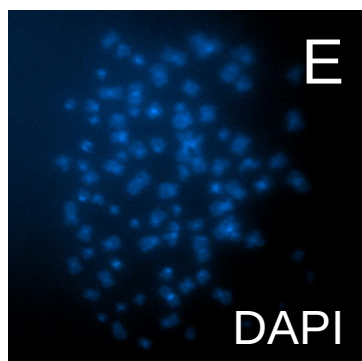
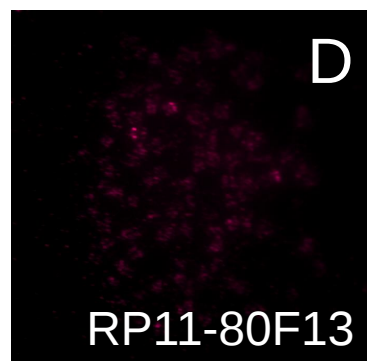
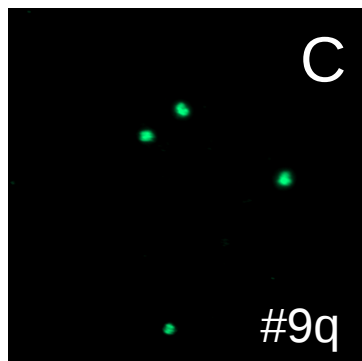
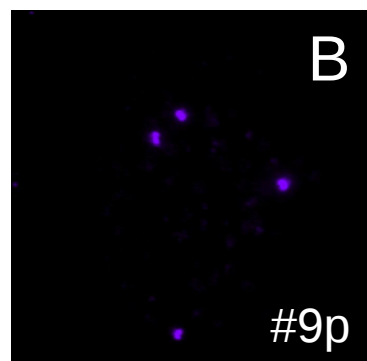
B

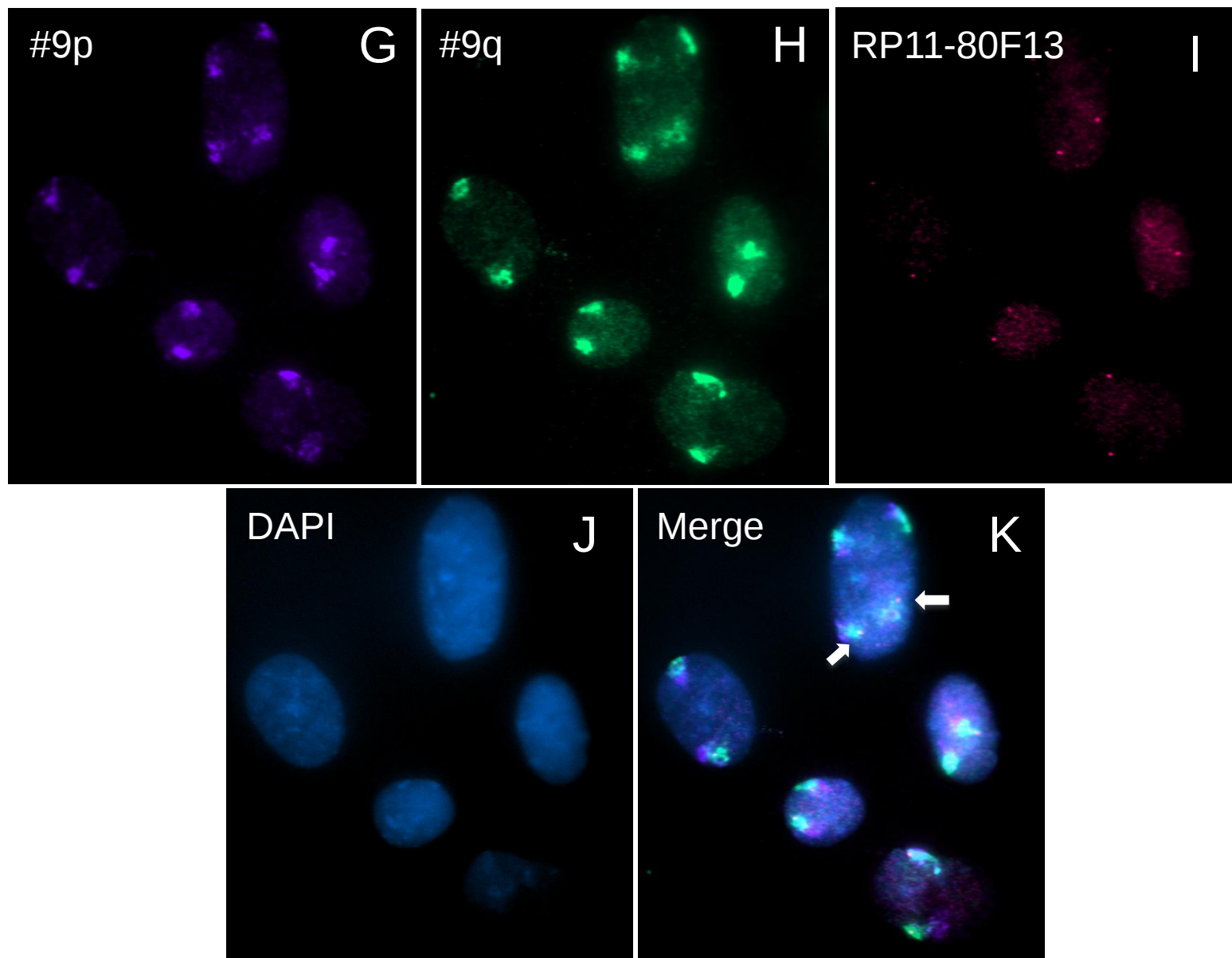


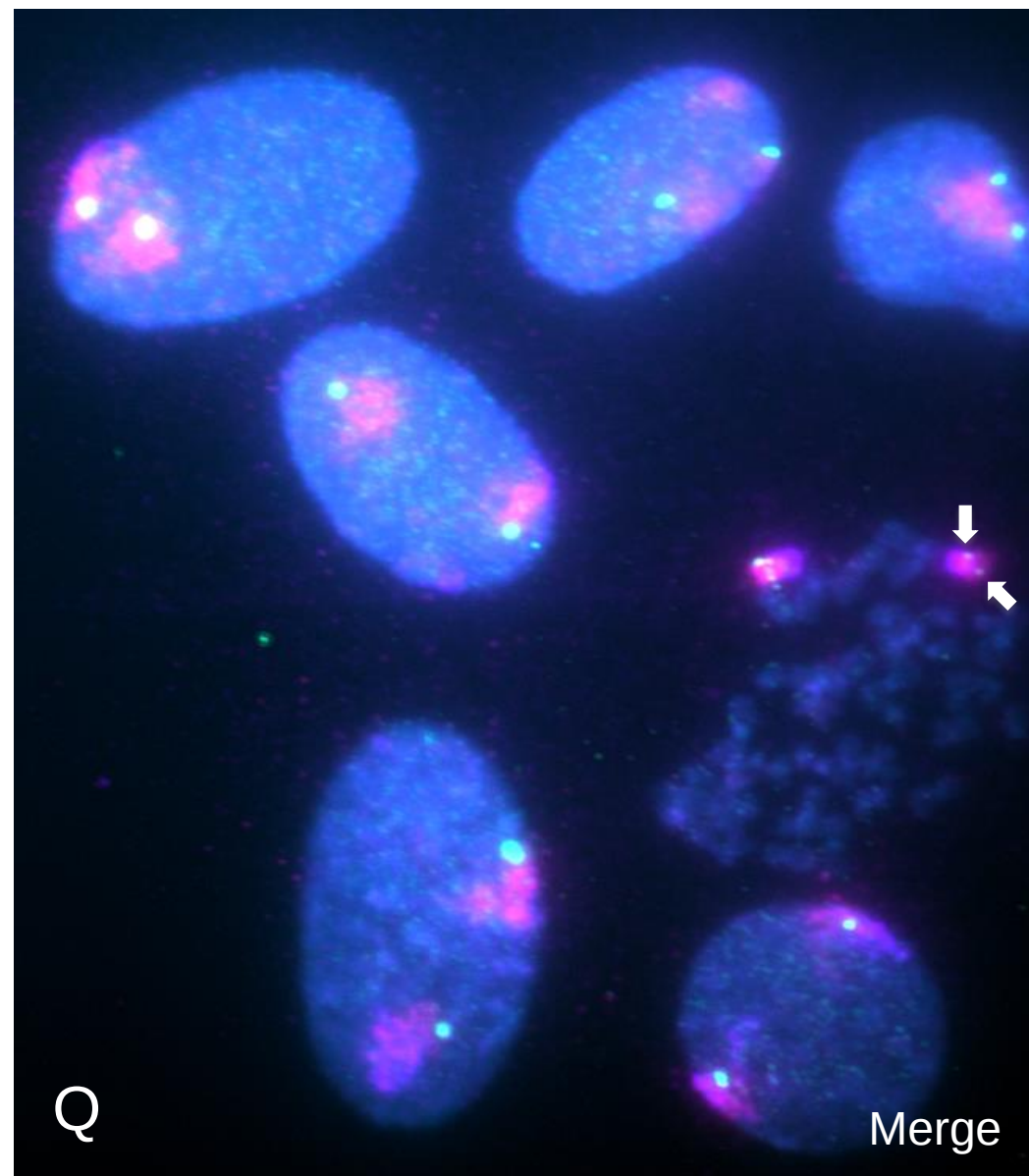
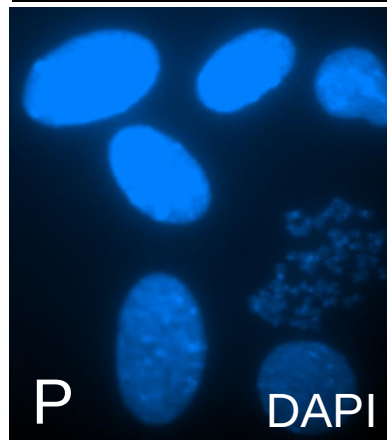
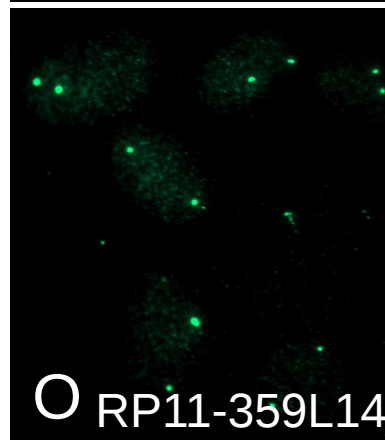
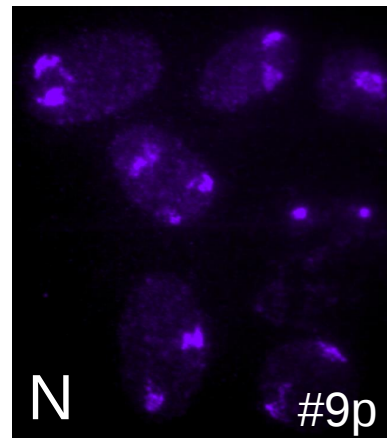
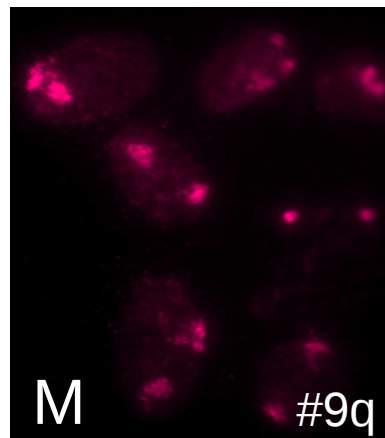
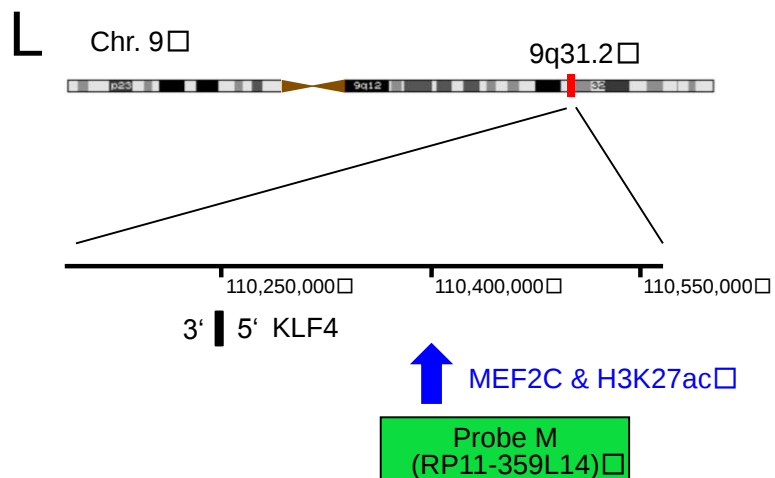




Probe K
(RP11-80F13)







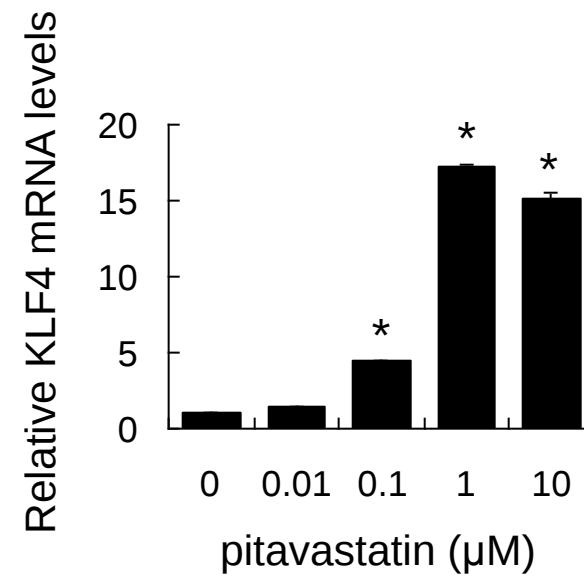


Table S1. List of genes induced by pitavastatin (top 20 genes)

Probe ID	Entrez Gene	Gene Symbol	Microarray analysis (Fold change compared to DMSO)
220266_s_at, 221841_s_at	9314	KLF4	13.03
219371_s_at, 226645_at, 226646_at	10365	KLF2	3.95
222162_s_at, 222486_s_at	9510	ADAMTS1	3.86
203887_s_at, 203888_at, 237252_at	7056	THBD	3.72
205749_at	1543	CYP1A1	3.09
230746_s_at	100288985	LOC100288985	2.58
208937_s_at	3397	ID1	2.34
203665_at	3162	HMOX1	2.31
206049_at	6403	SELP	2.24
229873_at	283219	KCTD21	2.21
207001_x_at, 208763_s_at, 235364_at	1831	TSC22D3	2.19
204284_at, 240187_at	5507	PPP1R3C	2.16
202393_s_at	7071	KLF10	2.12
214218_s_at, 221728_x_at, 224588_at, 224589_at, 224590_at, 227671_at, 235446_at, 243712_at	7503	XIST	2.11
215506_s_at	9077	DIRAS3	2.08
221087_s_at	80833	APOL3	2.00
206320_s_at, 227719_at	4093	SMAD9	1.99
225954_s_at, 231072_at	90007	MIDN	1.98
205581_s_at	4846	NOS3	1.98
229172_at, 234610_at	116835	HSPA12B	1.96

Table S2A. si RNA

MEF2A	AAUAAUCAGUGUUGUAGGCAGUCGG
MEF2C	UAAACCCAGACAGAGAUGACAGGUC
MEF2D	ACUAAAGGCUGGUAAGGAGGAGAGC
KLF4	AUUGGAGAGAAUAAAGUCCAGGUCC

Table S2B. Primer pairs for real Time PCR

Cyclophilin	Fw	TTCGTGCTCTGAGCACTGGAGA
	Rv	GGACCCGTATGCTTTAGGATGAAG
KLF4	Fw	GACGGCTGTGGATGGAAATTC
	Rv	CGGTGCCCCGTGTGTTTAC
NOS3	Fw	CCCTTCAGTGGCTGGTACAT
	Rv	TATCCAGGTCCATGCAGACA
Thrombomodulin	Fw	TTGCGAGAAGAGACAAACACCTC
	Rv	CAAGCTCCCAATTCCACAAGAC

Table S2C. Primer pairs for ChIP-PCR

KLF4 (-98 kb)	Fw	TTACCCAGCAAATCGGGAAGG
	Rv	AGCCGGGCTTCTGTGTGTAT
KLF4 (-148 kb)	Fw	GCTGCCTGACGTAGGGAGATA
	Rv	GGCCTCGGGAAGTACCA
KLF4 (-147 kb)	Fw	CAGGCAGTGCTAGGGCGTA
	Rv	GGGAATCTGGGAGGCTCAG

Table S2D. Primer pairs for reporter assay

For cloning gene		
KLF4 promoter	Fw	CAGGAGGCGGAGGTTGCACTGAG
	Rv	TAATGTGGGGGCCCAGAA
KLF4 enhancer (-98 kb)	Fw	TACCCAGCAAATCGGGAAGGAACTG
	Rv	GTTCTTTGGCGAACAACTGCTCCG
KLF4 enhancer (-148 kb)	Fw	TGCGCTTCCCTCCGACGCGCGGAG
	Rv	TGCCTCGGGCCGGTCTTGCTCGG

Table S2E. Primers and TaqMan probes for 3C assay

KLF4 Fw	ACCCGAATTGCTTTGAAATGAA
KLF4 TaqMan probe	(6-FAM)TCCCTGCTAATAAATAAC(MGB)
KLF4 (-1kb) Rv	TCCAACCTGGGCAATAGAATG
KLF4 (-45 kb) Rv	TCTGTGACTCCAGCACCCAAG
KLF4 (-98 kb) Rv	TGCAACCCTGGCCAAGA
KLF4 (-120 kb) Rv	TTGTACTGGTTCATCACGGATTG
KLF4 (-148 kb) Rv	TGCGCACATACACACCATACTC
KLF4 (-180 kb) Rv	AGAAATACATCTCTCCTCAGACTAACTCTGA