Figure S1

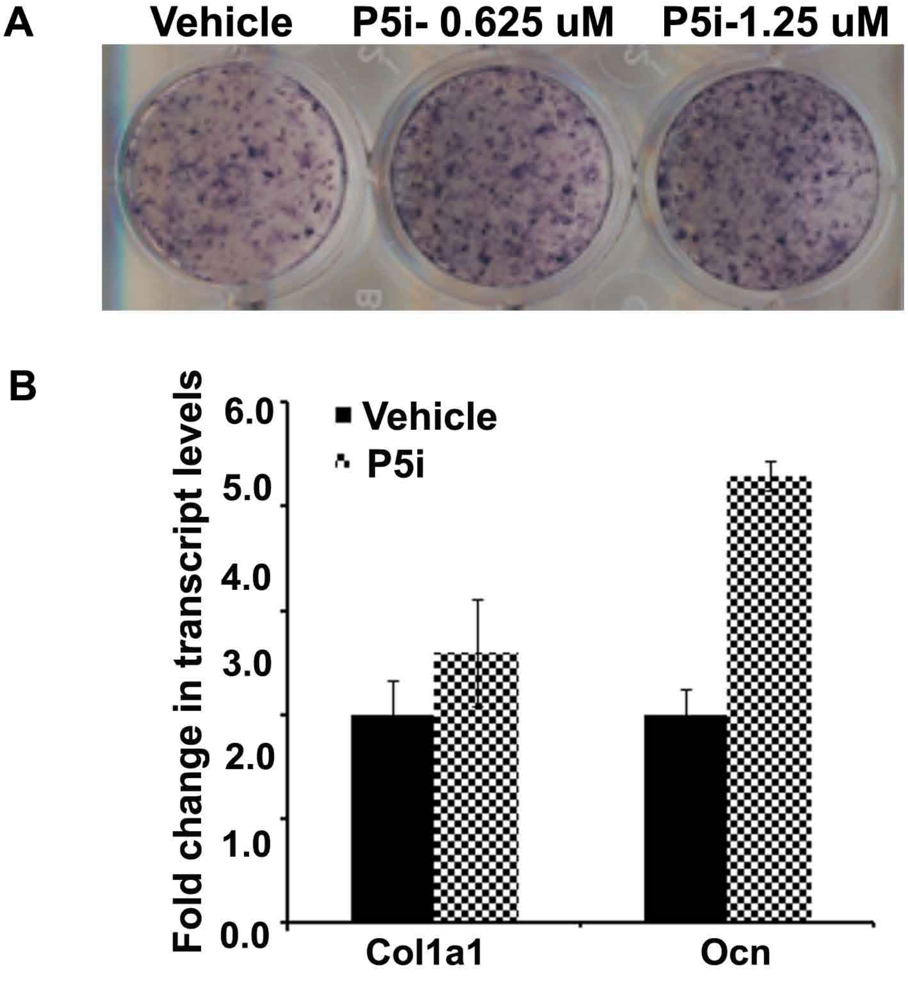

A
Vehicle
P5i- 0.625 uM
P5i-1.25 uM
B
Fold change in transcript levels
0.0
1.0
2.0
3.0
4.0
5.0
6.0
■ Vehicle
▨ P5i
Col1a1
Ocn

Figure S2

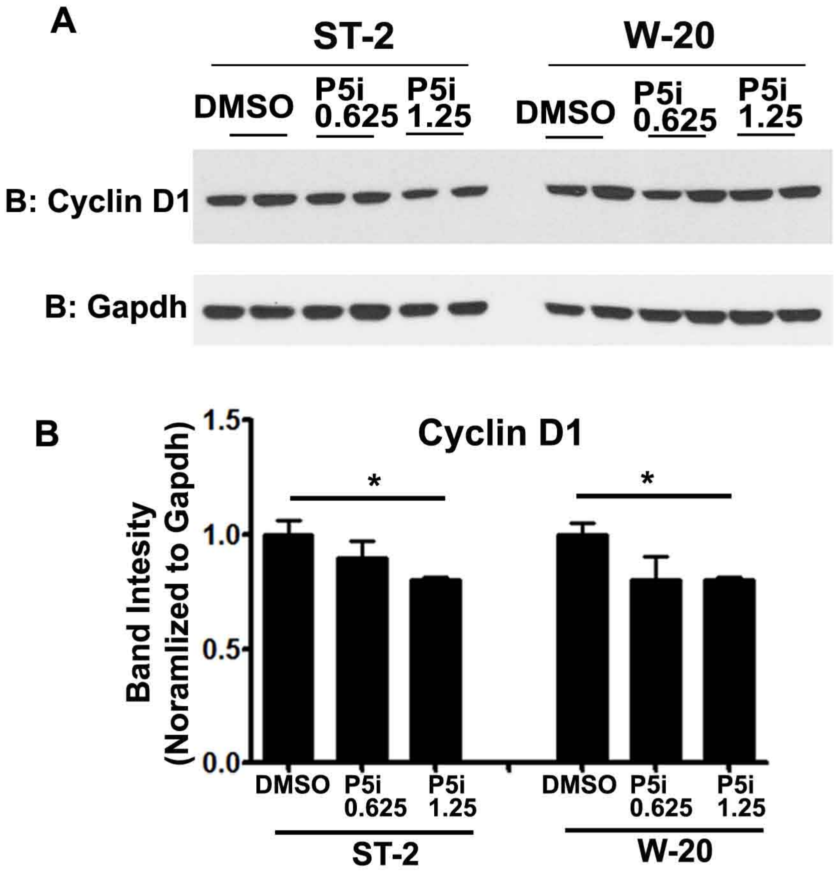

A
ST-2
W-20
DMSO
P5i 0.625
P5i 1.25
DMSO
P5i 0.625
P5i 1.25
B: Cyclin D1
B: Gapdh
B
Cyclin D1
Band Intesity (Noramlized to Gapdh)
1.5
1.0
0.5
0.0
*
*
DMSO
P5i 0.625
P5i 1.25
DMSO
P5i 0.625
P5i 1.25
ST-2
W-20

Figure S3

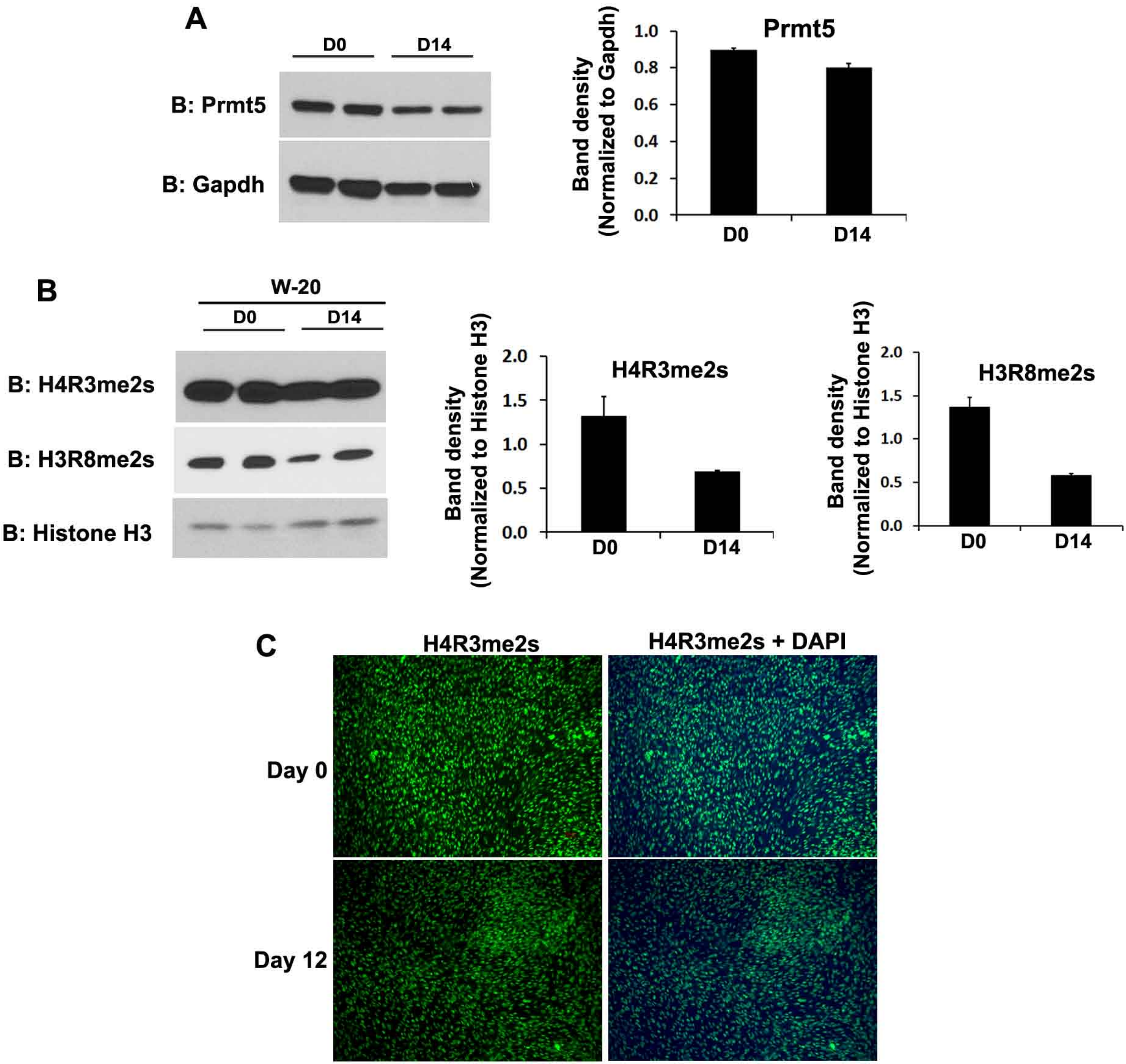
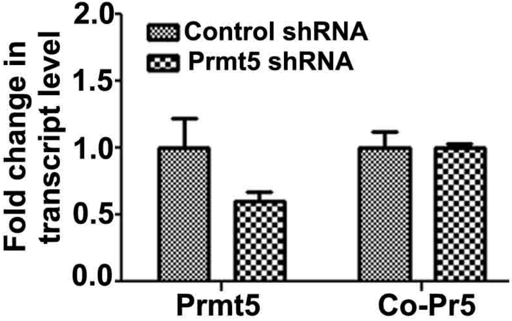
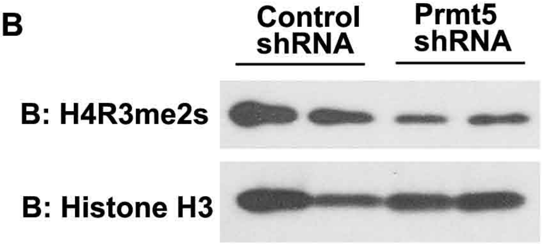

A
D0
D14
B: Prmt5
B: Gapdh
Prmt5
Band density (Normalized to Gapdh)
1.0
0.8
0.6
0.4
0.2
0.0
D0
D14
B
W-20
D0
D14
B: H4R3me2s
B: H3R8me2s
B: Histone H3
H4R3me2s
Band density (Normalized to Histone H3)
2.0
1.5
1.0
0.5
0.0
D0
D14
H3R8me2s
Band density (Normalized to Histone H3)
2.0
1.5
1.0
0.5
0.0
D0
D14
C
H4R3me2s
H4R3me2s + DAPI
Day 0
Day 12

Figure S4

A



B



C

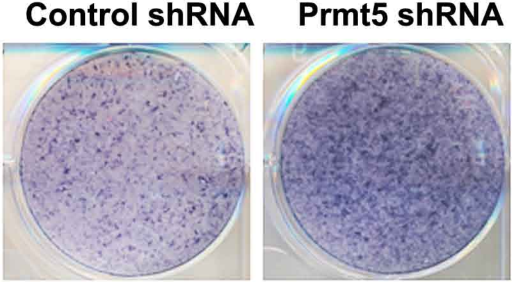


Figure S5

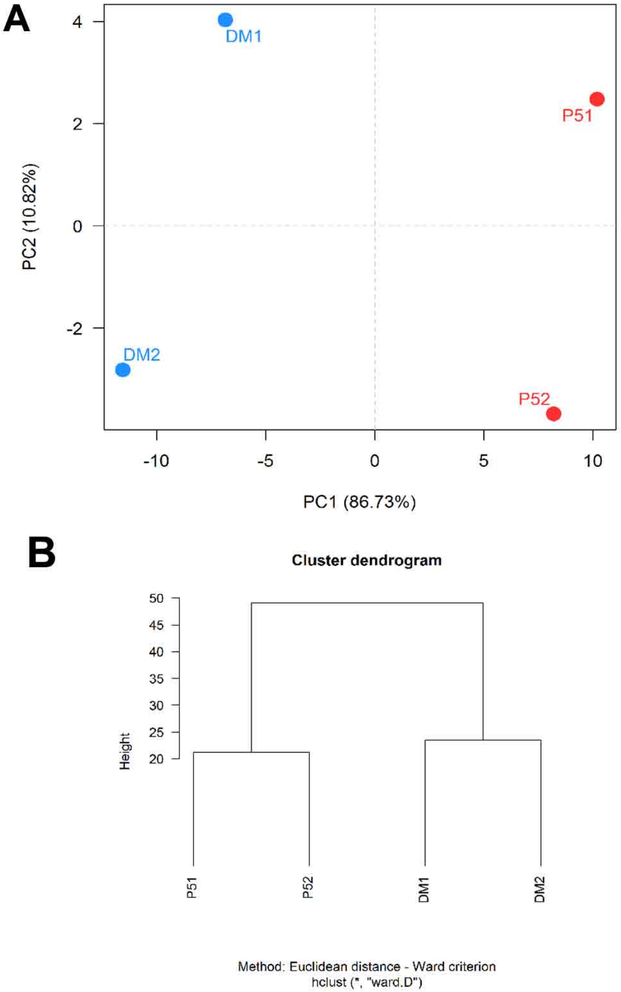

A
DM1
P51
DM2
P52
4
2
0
-2
PC2 (10.82%)
-10
-5
0
5
10
PC1 (86.73%)
B
Cluster dendrogram
50
45
40
35
30
25
20
Height
P51
P52
DM1
DM2
Method: Euclidean distance - Ward criterion
hclust (*, "ward.D")

Figure S6

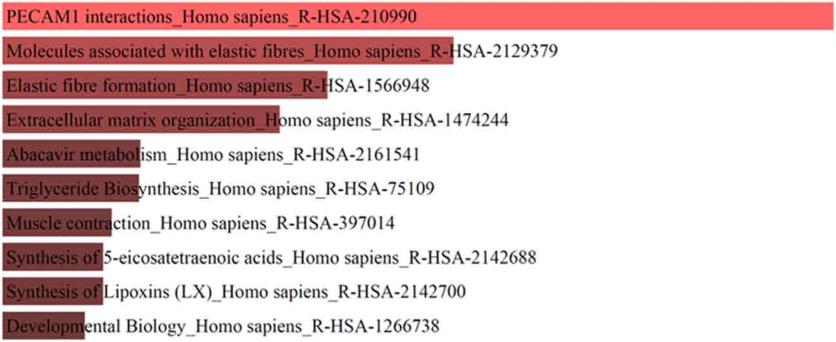

PECAM1 interactions_Homo sapiens_R-HSA-210990
Molecules associated with elastic fibres_Homo sapiens_R-HSA-2129379
Elastic fibre formation_Homo sapiens_R-HSA-1566948
Extracellular matrix organization_Homo sapiens_R-HSA-1474244
Abacavir metabolism_Homo sapiens_R-HSA-2161541
Triglyceride Biosynthesis_Homo sapiens_R-HSA-75109
Muscle contraction_Homo sapiens_R-HSA-397014
Synthesis of 5-eicosatetraenoic acids_Homo sapiens_R-HSA-2142688
Synthesis of Lipoxins (LX)_Homo sapiens_R-HSA-2142700
Developmental Biology_Homo sapiens_R-HSA-1266738

Figure S7

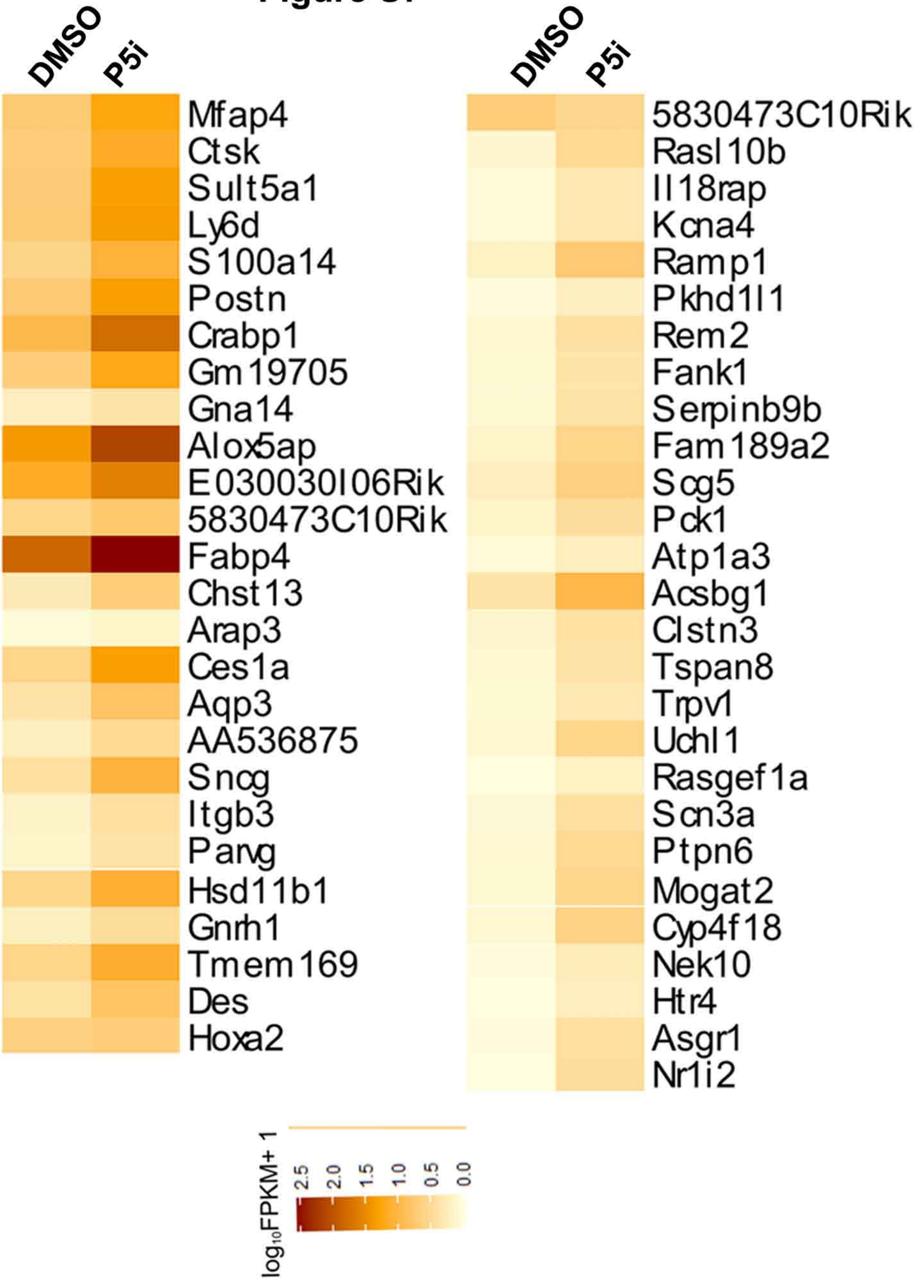

DMSO
P5i
Mfap4
Ctsk
Sult5a1
Ly6d
S100a14
Postn
Crabp1
Gm19705
Gna14
Alox5ap
E030030I06Rik
5830473C10Rik
Fabp4
Chst13
Arap3
Ces1a
Aqp3
AA536875
Sncg
Itgb3
Parvg
Hsd11b1
Gnrh1
Tmem169
Des
Hoxa2
DMSO
P5i
5830473C10Rik
Rasl10b
Il18rap
Kcna4
Ramp1
Pkhd1l1
Rem2
Fank1
Serpinb9b
Fam189a2
Scg5
Pck1
Atp1a3
Acsbg1
Clstn3
Tspan8
Trpv1
Uchl1
Rasgef1a
Scn3a
Ptpn6
Mogat2
Cyp4f18
Nek10
Htr4
Asgr1
Nr1i2
log10FPKM+ 1
2.5
2.0
1.5
1.0
0.5
0.0

Figure S8

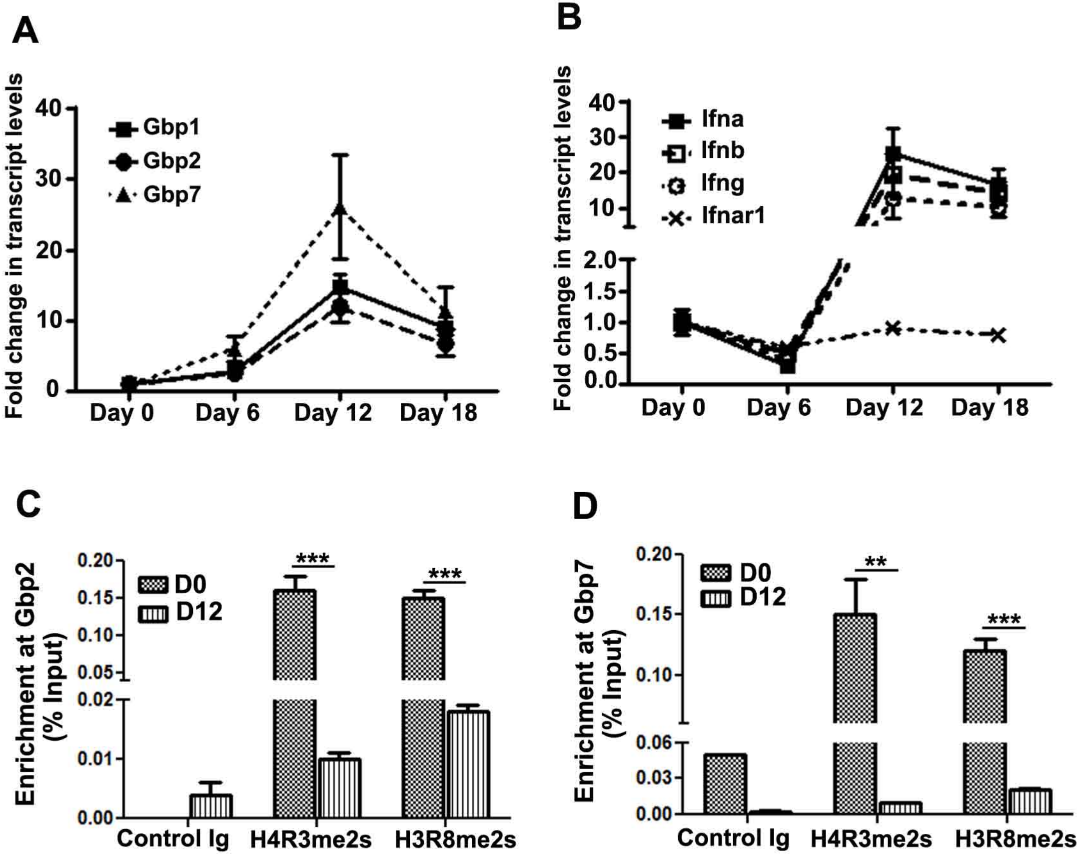

A
Fold change in transcript levels
40
30
20
10
0
Gbp1
Gbp2
Gbp7
Day 0
Day 6
Day 12
Day 18
B
Fold change in transcript levels
40
30
20
10
2.0
1.5
1.0
0.5
0.0
Ifna
Ifnb
Ifng
Ifnar1
Day 0
Day 6
Day 12
Day 18
C
Enrichment at Gbp2 (% Input)
0.20
0.15
0.10
0.05
0.02
0.01
0.00
D0
D12
***
***
Control Ig
H4R3me2s
H3R8me2s
D
Enrichment at Gbp7 (% Input)
0.20
0.15
0.10
0.06
0.03
0.00
D0
D12
**
***
Control Ig
H4R3me2s
H3R8me2s

Figure S9

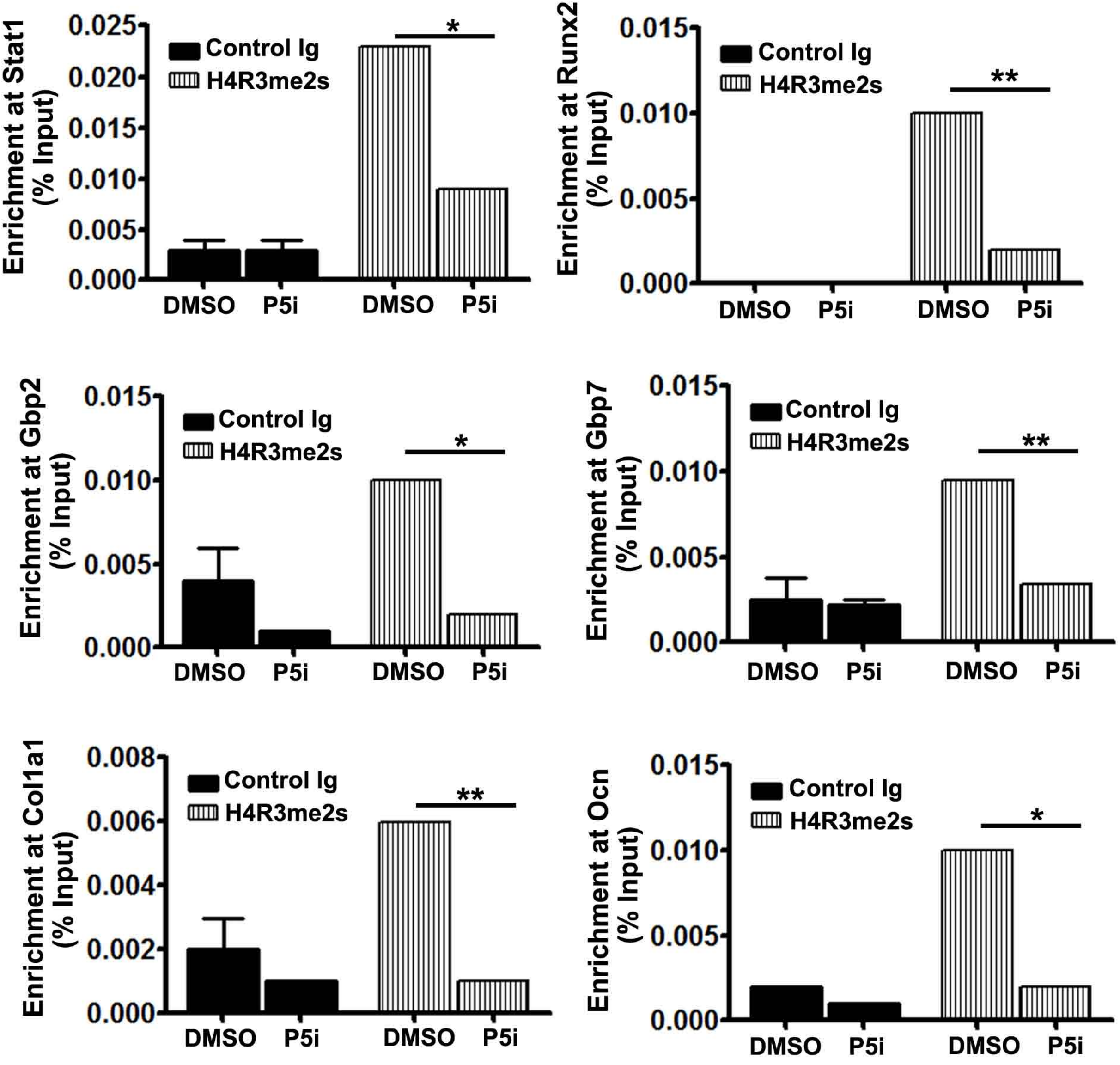

Enrichment at Stat1 (% Input)
0.025
0.020
0.015
0.010
0.005
0.000
Control Ig
H4R3me2s
*
DMSO
P5i
DMSO
P5i
Enrichment at Runx2 (% Input)
0.015
0.010
0.005
0.000
Control Ig
H4R3me2s
**
DMSO
P5i
DMSO
P5i
Enrichment at Gbp2 (% Input)
0.015
0.010
0.005
0.000
Control Ig
H4R3me2s
*
DMSO
P5i
DMSO
P5i
Enrichment at Gbp7 (% Input)
0.015
0.010
0.005
0.000
Control Ig
H4R3me2s
**
DMSO
P5i
DMSO
P5i
Enrichment at Col1a1 (% Input)
0.008
0.006
0.004
0.002
0.000
Control Ig
H4R3me2s
**
DMSO
P5i
DMSO
P5i
Enrichment at Ocn (% Input)
0.015
0.010
0.005
0.000
Control Ig
H4R3me2s
*
DMSO
P5i
DMSO
P5i

Figure S10

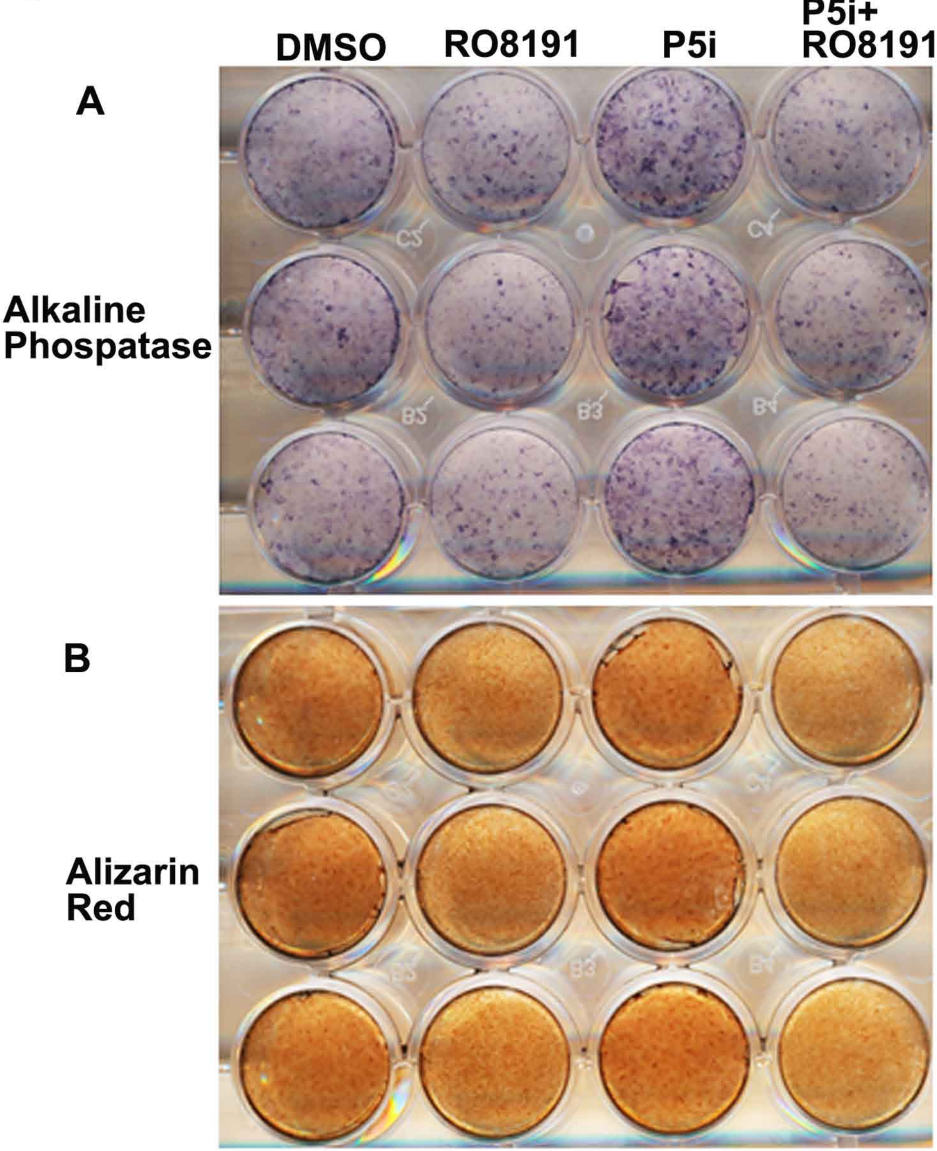
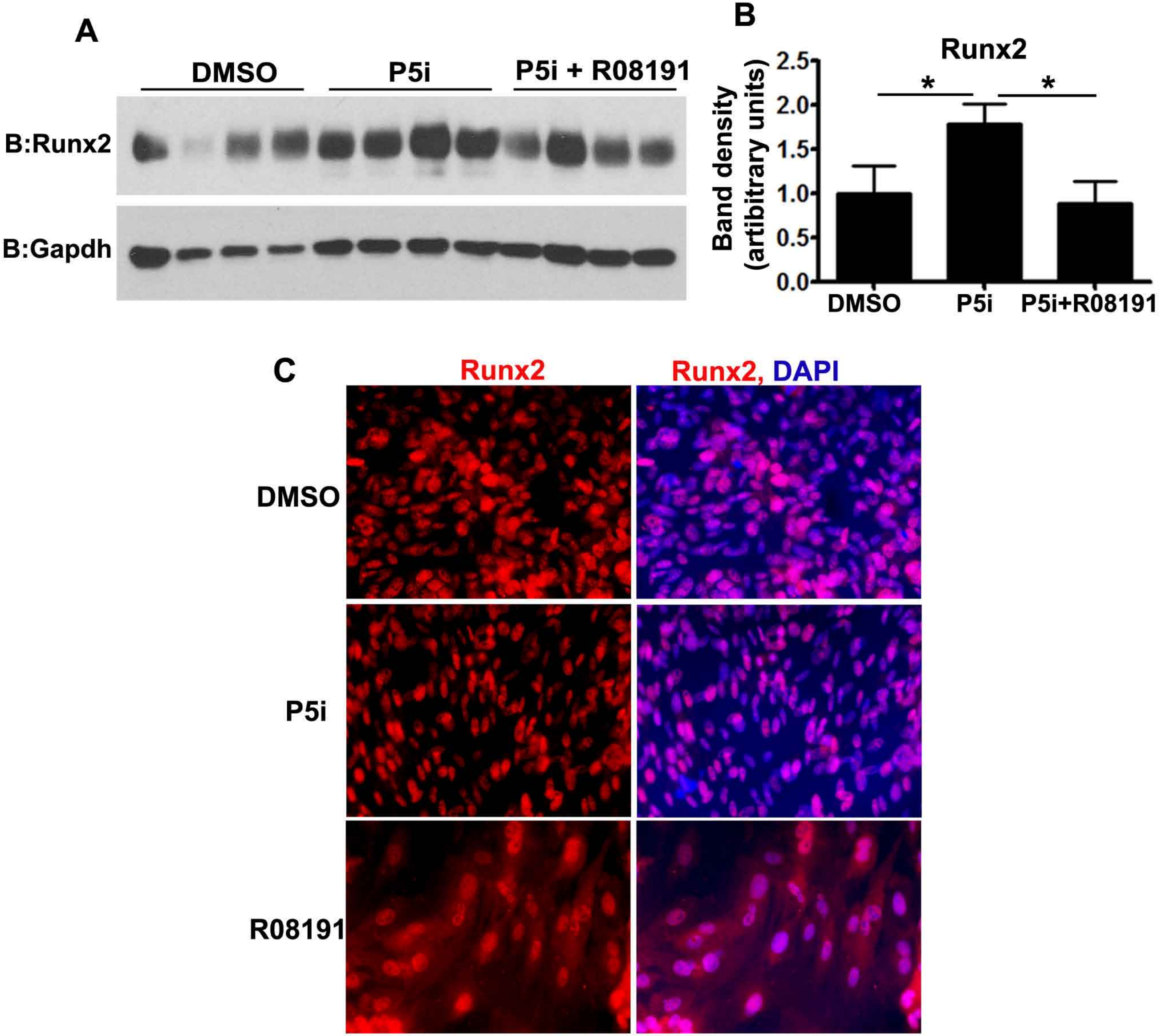

DMSO
RO8191
P5i
P5i+ RO8191
A
Alkaline Phospatase
B
Alizarin Red

Figure S11


A
DMSO
P5i
P5i + R08191
B:Runx2
B:Gapdh
B
Runx2
Band density
(arbitrary units)
2.5
2.0
1.5
1.0
0.5
0.0
*
*
DMSO
P5i
P5i+R08191
C
Runx2
Runx2, DAPI
DMSO
P5i
R08191

Supplementary Table-1

gene_id	locus	log2(fold_change)	q_value
XLOC_004934	chr11:48865185-48872556	-1.50041	0.00354515
XLOC_010675	chr15:84324719-84342978	1.50534	0.00354515
XLOC_020415	chr3:95499285-95509412	1.5063	0.00354515
XLOC_023763	chr4:156199423-156200818	-1.50703	0.00354515
XLOC_002744	chr10:22113049-22149270	1.515	0.00354515
XLOC_009407	chr14:67745228-67749569	1.52804	0.0214093
XLOC_023084	chr4:41092723-41108859	1.54695	0.00354515
XLOC_031787	chr8:61921910-62038234	-1.54852	0.00354515
XLOC_015369	chr18:37972622-37998969	1.5509	0.0291337
XLOC_020639	chr3:142594846-142638008	-1.55192	0.00354515
XLOC_028225	chr6:41073529-41074798	1.55306	0.0306172
XLOC_030129	chr7:24978156-25005895	1.5561	0.0161319
XLOC_027710	chr6:90308350-90325185	1.55764	0.00652959
XLOC_031584	chr8:9140053-9153598	1.55811	0.00354515
XLOC_000434	chr1:136683377-136690806	1.55824	0.0266625
XLOC_004139	chr11:61485443-61494230	1.56832	0.0412234
XLOC_004636	chr11:104607999-104670471	1.57126	0.00354515
XLOC_001427	chr1:193207699-193264046	1.57131	0.00354515
XLOC_026886	chr6:52158403-52166355	1.57189	0.00354515
XLOC_020352	chr3:90526848-90528835	1.5789	0.00354515
XLOC_020700	chr3:10204342-10208576	1.57983	0.00354515
XLOC_016813	chr19:12002228-12002647	-1.58143	0.00354515
XLOC_013388	chr17:35342332-35384674	-1.58423	0.00354515
XLOC_020196	chr3:54361106-54391041	1.58439	0.00354515
XLOC_004087	chr11:58199555-58222783	-1.5981	0.00354515
XLOC_011700	chr15:85663116-85664907	-1.59815	0.00354515
XLOC_009523	chr14:123168502-123254035	1.6101	0.0278683
XLOC_028306	chr6:65150940-65151254	1.61217	0.0115819
XLOC_035181	chr9:41610229-41611677	-1.61857	0.0178458
XLOC_013993	chr17:35994503-36038174	-1.61896	0.00354515
XLOC_000217	chr1:75360343-75367970	1.62319	0.00354515
XLOC_034549	chr9:48537708-48539257	-1.62567	0.00354515
XLOC_005508	chr11:100690712-100704455	-1.62648	0.00354515
XLOC_014676	chr17:44593390-44595400	-1.64398	0.0318953
XLOC_006439	chr12:26469214-26479837	-1.64583	0.00354515
XLOC_000187	chr1:72284372-72303091	1.65824	0.00354515
XLOC_032756	chr8:123141652-123158414	1.67887	0.00354515
XLOC_006580	chr12:78224728-78684769	-1.68645	0.00354515
XLOC_011002	chr15:74762055-74763567	1.68963	0.00354515
XLOC_013932	chr17:33996011-34000421	-1.69319	0.00354515
XLOC_025177	chr5:149264703-149288142	1.69629	0.00354515
XLOC_004936	chr11:48903580-49135387	-1.6964	0.00354515
XLOC_007797	chr13:32450366-32453157	1.70673	0.00354515
XLOC_006223	chr11:98056525-98057909	1.71393	0.00354515

XLOC_012464	chr16:35832877-35871539	-1.7196	0.00354515
XLOC_024941	chr5:120812631-120824773	-1.72221	0.00354515
XLOC_018062	chr2:173153072-173159253	1.73901	0.00354515
XLOC_027840	chr6:124430755-124464784	1.74274	0.00354515
XLOC_029531	chr7:104244456-104262236	-1.74872	0.00354515
XLOC_032983	chr8:44934522-44935141	1.75899	0.00354515
XLOC_004441	chr11:88066398-88068183	1.76027	0.00354515
XLOC_025627	chr5:114896833-114912245	-1.77493	0.0178458
XLOC_018412	chr2:65457117-65567541	1.78853	0.00354515
XLOC_002562	chr10:115817283-115849893	1.80115	0.0291337
XLOC_013390	chr17:35424876-35428361	-1.81219	0.00354515
XLOC_020438	chr3:96497777-96498179	-1.82455	0.00354515
XLOC_014612	chr17:36215586-36215649	-1.8504	0.00354515
XLOC_024741	chr5:90518948-90598209	1.85875	0.0090981
XLOC_025666	chr5:120876141-120907525	-1.90894	0.00354515
XLOC_010487	chr15:44457552-44597135	1.91615	0.00354515
XLOC_003760	chr10:115269945-115270317	-1.92324	0.00354515
XLOC_005338	chr11:88063166-88066135	1.93513	0.00354515
XLOC_033862	chr9:54764807-54773109	1.94478	0.00354515
XLOC_018745	chr2:113776312-113829091	1.95872	0.0139716
XLOC_007801	chr13:33027413-33040558	1.97117	0.0196514
XLOC_021287	chr3:151730843-151749959	-1.99198	0.00354515
XLOC_019136	chr2:173206611-173218922	-2.01213	0.00354515
XLOC_013385	chr17:35263093-35267497	-2.02333	0.00354515
XLOC_012249	chr16:97535329-97561195	-2.03498	0.00354515
XLOC_017607	chr2:107290588-107298504	2.07354	0.00354515
XLOC_027144	chr6:118066384-118091546	2.09008	0.0306172
XLOC_016151	chr19:34640888-34651845	-2.09203	0.00354515
XLOC_000093	chr1:40515361-40549529	2.1094	0.00652959
XLOC_004253	chr11:72301628-72313813	-2.1107	0.00354515
XLOC_012031	chr16:23601529-23614297	-2.11852	0.00354515
XLOC_016532	chr19:23972672-24031019	2.12874	0.00354515
XLOC_026518	chr5:125408781-125409095	-2.13392	0.0090981
XLOC_029761	chr7:133776890-133881532	2.13633	0.0139716
XLOC_009307	chr14:54476099-54480434	2.13908	0.0231011
XLOC_009643	chr14:34370273-34374670	2.16334	0.00354515
XLOC_032575	chr8:93020214-93048382	2.17724	0.00354515
XLOC_034592	chr9:54604996-54661885	2.18205	0.00354515
XLOC_024899	chr5:114896833-114912245	-2.19171	0.00354515
XLOC_022173	chr3:144624501-144626202	-2.19459	0.00354515
XLOC_019361	chr2:36219180-36220412	2.20454	0.0365657
XLOC_036958	chrY:90739145-90739258	2.21354	0.0278683
XLOC_015132	chr18:60439244-60443858	-2.26006	0.00354515
XLOC_025663	chr5:120753097-120777659	-2.26103	0.0090981
XLOC_000286	chr1:91179821-91225196	2.38091	0.00354515
XLOC_026109	chr5:38563201-38563830	-2.3827	0.0487371
XLOC_004393	chr11:83410071-83421038	2.39092	0.00354515

XLOC_009129	chr14:14820814-15006693	2.39419	0.0214093
XLOC_027845	chr6:124720717-124738709	2.39821	0.00354515
XLOC_020637	chr3:142530337-142550083	-2.4064	0.00354515
XLOC_016083	chr19:16435666-16611353	2.46176	0.00354515
XLOC_004267	chr11:73232767-73260507	2.46378	0.00354515
XLOC_024663	chr5:66676120-66687234	2.52507	0.0291337
XLOC_034180	chr9:108953744-108984875	2.54276	0.00652959
XLOC_019360	chr2:36217144-36218504	2.54534	0.0178458
XLOC_020638	chr3:142560051-142573212	-2.78903	0.00354515
XLOC_032499	chr8:71988481-72009626	2.80618	0.00354515
XLOC_015157	chr18:62324203-62467802	2.81133	0.00354515
XLOC_026605	chr5:147408853-147409579	2.8149	0.00354515
XLOC_030571	chr7:99219083-99238611	2.85136	0.00652959
XLOC_004223	chr11:70054368-70057894	2.98046	0.0306172
XLOC_025662	chr5:120730295-120749848	-3.35716	0.00354515
XLOC_012500	chr16:38248327-38294873	3.47898	0.00354515

Supplementary table 2

Gene	***ChIP-PCR***	***Sequence***
Gbp7	Forward	5'-CGA CTT GTT TTC ATC CGC CG-3'
	Reverse	5'-ACC GGA TAT TGC CTG CAC TT-3'
Gbp2	Forward	5'-AGT GCC TGT GAG AGA GGA CA-3'
	Reverse	5'-TCT GTG CTG GTT TCA GCC TC-3'
	qRT-PCR	
Oas3	Forward	5'-CCT CCC TTG GCA ATC CTT A-3'
	Reverse	5'-CTG AGT TCA CAG CAG CCG TA-3'
Adar	Forward	5'-CTT GCC CTG TTT CTT GCT GT-3'
	Reverse	5'-ATG GCT TTG CTG CTG AGT TC-3'
Gbp2	Forward	5'-CCA CTC TGG TCA GGT GAT GA-3'
	Reverse	5'-GAT CTT TGC TTT GGC AGT CC-3'
Nat1	Forward	5'-ATT CTT CGT TGT CAA GCC GCC AAA GTG GAG-3'
	Reverse	5'-AGT TGT TTG CTG CGG AGT TGT CAT CTC GTC-3'
Gbp7	Forward	5'-TTG CTT TGG AGT TCA CCC TC-3'
	Reverse	5'-TCC AGG TAG CAG AGA ATC CG-3'
Gbp1	Forward	5'-AGA TGC CCT TGG TGT GAG AC-3'
	Reverse	5'-CTC TAC CGC ACA GGC AAA TC-3'
Prmt5	Forward	5'-CTG AAT TGC GTC CCC GAA ATA-3'
	Reverse	5'-AGG TTC CTG AAT GAA CTC CCT-3'
Prmt7	Forward	5'-GCC AGG TCA TCC TAT GCC G-3'
	Reverse	5'-GCC AAT GTC AAG AAC CAA GGC-3'
Co-Pr5	Forward	5'-GCT CTG AGC TCC ACT GGC T-3'
	Reverse	5'-GAG CGG AGT TCG CAG GAG-3'
Col1a1	Forward	CCT GGA ATG AAG GGA CAC CG
	Reverse	CCA TCG TTA CCG CGA GCA CC
Runx2	Forward	GAG AGG TAC CAG ATG GGA CT
	Reverse	CAC TTG GGG AGG ATT TGT GA
Osx	Forward	AGG CAC AAA GAA GCC ATA C
	Reverse	AAT GAG TGA GGG AAG GGT
Ocn	Forward	CGC TCT GTC TCT CTG ACC TC
	Reverse	GAC TGA GGC TCC AAG GTA GC