

SUPPLEMENTAL FIGURE LEGENDS

Supplemental Figure S1. Overexpression of miR-194 reduces proliferation in HepaRG cells.

(A): Relative expression levels of *Ki-67* at day 14 and day 28 of hepatocytic differentiation process in HepaRG-miR-194 compared to HepaRG-empty cell lines. The results were presented as means \pm SEM from two independent experiments ($P < 0.05$). **(B):** Proliferation of HepaRG-empty and HepaRG-miR-194 cell lines assessed by Ki-67 immunofluorescence staining at day 28 of hepatocytic differentiation process. Nuclei are stained with DAPI blue. Scale bar, 100 μ m.

Supplemental Figure S2. Deactivation of *YAP1* upon directed hepatocytic differentiation of

HepaRG cells and hESCs. **(A):** *YAP1* mRNA expression upon hepatocytic differentiation of liver progenitor HepaRG cells measured by quantitative PCR and shown as fold-changes and SEM, at day 28 relative to day 2, in two independent experiments. **(B):** Phospho-YAP1 and YAP1 protein expression levels upon hepatocytic differentiation of HepaRG cells determined respectively by western blot analysis. Expression of α -tubulin was used to control protein loading. **(C):** *YAP1* mRNA expression during the hepatocyte differentiation process of hESCs. The graphs show fold-changes and SEM relative to day 0 in two independent experiments. **(D):** Phospho-YAP1 and YAP1 protein expression levels upon hepatocytic differentiation of hESCs determined respectively by western blot analysis. Expression of α -tubulin was used to control protein loading.

Supplemental Tables

Supplemental Table S1. Primers information for qRT-PCR analysis

Gene Symbol (Human)	Forward Primer (5'-3')	Reverse Primer (5'-3')	Size
ALB	gtcaactccaactctgtaga	ttggtgactctgtcacttact	171
ALDOB	agtgcattctatgaacagtc	gttgaagaccttactgttga	198
BICD2	ctccttgttacacatgttctt	agtctaaagctacacgctatg	215
CENPF	aactcacatcagtaaagcaac	agtgactcttaaggagggtgt	162
CYP3A4	aagtcgctcgaagatacaca	aaggagagaacctgctcgtg	174
ECT2	agtagagcatcaagagcaata	acgactcattacatgcttacc	162
ELOVL6	caggggtatatactagaacga	atgcagtgaagatgaagttag	156
FGFR3	gtccttttcaggagaattag	ttgcgtaagaagtgttaagtc	261
GALNT7	aaaggagtcttccaactagag	ataaggcctaatacacaagg	211
HAND1	gacgcactgagagcatta	atccgccttcttgagttc	197
HDAC2	aagaccagataacatgtctga	ctgatgcttctgatttcttag	209
HNF4A	gaatgcgactctccaaaacc	ggcactggttcctcttctgtct	339
IGF1R	tcattatccacagttctagc	gatcaagttcaacagtgctc	260
Ki-67	ctgaggtctttgtattagcag	tgactttgtctctaggtatgg	132
NANOG	ccgaagaatagcaatgggtgacg	aggagaattggctggaactgc	303
NOTCH2	agttatacttgcttgtgtgct	agtattcactccatccataca	231
OCT4	acatcaaagctctgcagaaagaact	ctgaataacctcccaatagacct	127
PRC1	atgagtgttacagttgaaagc	cagcaagtagaattatgtggt	145
RACGAP1	ctattgagactgtgcatatt	gtctcgacacttcagagataa	251
RAP2B	tgagagaaattaggaacctg	cccttatctcttcacacacta	112
REV3L	cagtaagcaaagaagtgttc	ttagattgtgaaggagagcta	256
RHEB	ttcctcagacatactccatag	cagtctgattttcttagcag	258
THBS1	tctgtgaaagttgtaaactcc	ccagcataggtttatcatag	251
YAP1	ctctcgagatgagagtacaga	taaggatgtcagaactcaaag	275

Supplemental Table S2. MiRNAs that are significantly (P value < 0.05) downregulated during hepatocytic differentiation of HepaRG cells by at least 2 fold (FC HepaRG D/P). ~ indicates estimated changes from limit of detection.

miRNA	FC (HepaRG D/P)	P value
hsa-miR-122	~506.7	0.005
hsa-miR-194	~459.8	0.008
hsa-miR-135a	~166.0	0.006
hsa-miR-1975	54.4	0.02
hsa-miR-455-5p	50.9	0.05
hsa-miR-210	46.7	0.008
hsa-miR-146b-5p	44.2	0.006
hsa-miR-509-3p	41.5	0.05
hsa-miR-218	33.2	0.05
hsa-miR-98	32.8	0.03
hsa-miR-296-5p	26.2	0.02
hsa-miR-190b	26.2	0.008
hsa-miR-769-5p	24.1	0.006
hsa-miR-767-5p	21.9	<0.001
hsa-miR-520b	20.6	0.006
hsa-miR-1263	19.1	0.05
hsa-miR-363	19.3	0.01
hsa-miR-493	19.3	0.01
hsa-miR-590-3p	18.9	0.05
hsa-miR-532-3p	18.8	0.02
hsa-miR-1275	18.4	0.01
hsa-miR-147	18.4	0.01
hsa-miR-500+hsa-miR-501-5p	18.0	0.02
hsa-miR-326	18.0	0.007
hsa-miR-570	17.9	0.03
hsa-miR-656	17.2	0.006
hsa-miR-1255a	17.1	0.04
hsa-miR-184	16.5	0.05
hsa-miR-1266	15.8	0.03
hsa-miR-1183	15.7	0.05
hsa-miR-330-3p	15.7	0.05
hsa-miR-30b	4.7	0.04
hsa-miR-30d	4.6	0.01
hsa-miR-30a	4.1	0.05
hsa-miR-26b	4.1	0.05
hsa-miR-148a	3.8	0.04

hsa-miR-30e	3.8	0.05
hsa-miR-26a	3.3	0.05
hsa-miR-101	2.9	0.02
hsa-miR-23b	2.5	0.02
hsa-miR-128	-2.0	0.05
hsa-miR-223	-2.6	0.05
hsa-miR-92b	-2.7	0.05
hsa-miR-10a	-2.8	0.03
hsa-miR-221	-2.9	0.05
hsa-miR-421	-3.0	0.02
hsa-miR-18a	-3.6	0.05
hsa-miR-34c-5p	-3.8	0.05
hsa-miR-145	-42.7	0.05
hsa-miR-1825	-43.3	0.05
hsa-miR-1181	-44.6	0.04
hsa-miR-1231	-44.6	0.04

Supplemental Table S3. Genes that are significantly (P value <0.05) downregulated during hepatocytic differentiation of HepaRG cells by at least 2 fold (FC HepaRG D/P) and that are predicted to be targets of miR-194 by at least two programs in miRwalk (Sum).

Gene symbol	FC (HepaRG D/P)	P value	Sum
ACTB	-2.64	0.007	6
ACTG1	-2.62	<0.001	6
ACVR2B	-2.23	<0.001	6
ADAM10	-2.98	0.015	6
AIM1	-2.26	0.003	4
AP1G1	-4.95	0.013	4
AP2B1	-3.15	0.007	4
APC	-2.71	0.005	4
ARF3	-2.02	0.018	3
ARF4	-2.13	0.003	7
ARF6	-2.16	0.002	4
ASB1	-3.46	0.008	6
ASB6	-2.63	0.001	5
ASPH	-2.27	<0.001	4
ATM	-3.06	0.002	5
ATP10D	-4.79	0.027	5
ATP6V0A2	-2.59	0.001	6
ATP6V1C1	-4.20	<0.001	5
ATP6V1H	-2.16	0.025	6
B4GALT1	-2.05	0.005	3
B4GALT4	-2.03	<0.001	5
BICD2	-14.24	0.006	6
BIRC5	-16.11	0.001	6
BLM	-3.12	0.014	3
BNIP2	-3.01	0.001	6
C9orf40	-3.20	0.002	5
CAMK2G	-2.57	0.007	7
CAMSAP1	-2.78	0.006	5
CARD8	-2.43	0.011	5
CASK	-2.03	0.019	4
CBFB	-2.37	0.04	5
CBLL1	-2.18	<0.001	3
CBX5	-4.71	0.002	3
CCNT2	-4.92	<0.001	5
CCT5	-2.08	0.045	5
CCT6A	-2.56	0.032	3

CD2AP	-3.87	0.011	6
CD44	-3.44	0.049	3
CD47	-2.27	0.007	5
CDC25A	-14.81	<0.001	3
CDC42BPA	-2.69	0.001	5
CDKN1B	-2.04	0.001	6
CELSR1	-2.02	0.01	5
CENPF	-3.09	0.004	5
CHORDC1	-4.23	<0.001	3
CHSY1	-3.66	0.012	5
CIT	-5.43	<0.001	4
CLASP2	-2.08	0.001	5
CLCN4	-4.10	0.009	4
CLN5	-2.48	0.008	3
CNTNAP2	-3.46	0.002	6
COIL	-9.92	0.015	3
COPS7B	-2.07	0.002	5
CORO1C	-9.70	0.004	5
CPSF6	-3.20	0.001	4
CREBBP	-2.16	0.001	5
CSE1L	-4.90	0.014	8
CSTF3	-2.02	0.027	5
CTDSPL	-2.82	0.004	5
CTPS	-6.65	<0.001	3
CUL3	-2.05	<0.001	5
CUL4A	-2.18	0.018	4
CXCL10	-3.40	<0.001	6
CYR61	-7.03	0.005	3
DCK	-4.49	<0.001	5
DCP2	-5.06	<0.001	6
DDEF1	-6.91	0.039	8
DDX10	-3.82	0.001	3
DDX11	-6.55	0.001	3
DDX18	-2.82	0.011	5
DDX46	-3.63	<0.001	5
DENR	-2.98	0.008	3
DFNA5	-7.62	0.03	4
DHX15	-2.33	<0.001	7
DISC1	-2.26	0.015	6
DIXDC1	-4.69	0.035	4
DNAJC6	-6.66	0.024	4
DPYSL3	-8.64	0.001	6
DR1	-2.36	0.003	7

DUSP1	-2.94	0.012	5
DYRK2	-2.14	<0.001	5
E2F3	-7.09	0.021	6
ECT2	-22.46	<0.001	6
EDN1	-10.91	0.002	6
EIF2S2	-2.01	0.009	5
ELF2	-2.11	0.024	6
ELOVL6	-3.63	0.027	3
ENAH	-4.89	0.007	5
EPB41L2	-6.90	<0.001	3
EPB41L4B	-2.50	0.026	5
EXTL2	-2.24	0.004	3
FAM20B	-2.74	0.007	5
FCGR2B	-2.60	<0.001	5
FECH	-3.56	0.003	3
FEN1	-9.14	0.001	5
FGFR1	-2.48	0.004	5
FGFR3	-2.83	0.021	5
FMR1	-3.53	0.009	6
FTSJ1	-4.26	<0.001	4
FUBP3	-2.54	0.001	3
FUS	-2.49	<0.001	3
FUT4	-6.83	<0.001	3
GAD1	-2.05	0.039	7
GALNT7	-5.96	<0.001	5
GBF1	-4.07	0.026	3
GCC1	-2.76	0.003	5
GGA1	-2.09	0.031	3
GGA2	-3.55	0.002	5
GGA3	-2.71	0.017	6
GGCX	-2.03	0.005	3
GMDS	-2.42	0.003	5
GMEB2	-2.65	0.033	5
GMFB	-2.48	0.005	6
GNAI3	-3.21	<0.001	3
GORASP2	-2.60	0.006	5
GPD2	-3.91	0.009	4
GRSF1	-2.23	0.001	3
GSPT1	-2.43	0.008	4
GTF2A2	-2.41	0.006	3
GTF2E2	-2.00	0.002	5
GTF2H1	-2.03	0.004	6
HBS1L	-3.29	<0.001	4

HDAC2	-3.07	0.006	5
HIF1A	-2.79	0.043	5
HIVEP2	-3.05	0.034	3
HMGB1	-2.89	0.002	5
HOXB5	-2.49	<0.001	3
HS2ST1	-2.58	0.007	4
HSPA12A	-2.68	0.027	3
IDS	-2.31	<0.001	3
IGF1R	-2.16	0.019	4
IGSF3	-2.44	0.001	5
IL2RB	-2.79	<0.001	4
IPO4	-2.95	<0.001	6
ITGB3	-2.40	<0.001	5
KARS	-2.41	0.003	3
KCTD15	-3.26	<0.001	5
KCTD7	-4.83	0.002	3
KIAA0226	-4.90	0.048	5
KIAA0241	-2.72	0.003	6
KIAA0317	-2.98	0.045	5
KIAA0888	-2.05	<0.001	5
KIAA1128	-4.50	0.017	5
KIAA1219	-4.41	0.011	5
KLHL4	-3.89	0.008	4
KPNA1	-2.45	<0.001	5
KPNB1	-2.77	0.004	5
LIN7C	-2.58	<0.001	6
LPHN2	-5.24	<0.001	7
LPP	-3.49	0.044	3
MAN1A2	-2.08	0.006	5
MAP1B	-4.39	0.006	4
MAP4K5	-2.35	0.022	5
MAPRE1	-2.06	0.008	5
MARCKS	-5.04	0.002	3
MBP	-2.10	<0.001	3
MCL1	-3.59	0.001	5
MCM10	-12.04	0.019	3
MKLN1	-3.01	0.007	6
MLL	-2.21	0.003	3
MLLT3	-5.14	0.001	6
MMP24	-6.19	0.043	3
MPHOSPH1	-11.00	<0.001	3
MPHOSPH6	-5.19	0.001	5
MPP5	-2.75	0.002	5

MRE11A	-4.24	<0.001	4
MRP63	-2.34	0.004	5
MTF1	-2.85	0.004	5
MTMR2	-6.16	<0.001	3
MTMR6	-3.30	0.003	5
MYO1C	-2.47	0.01	4
MYO5A	-2.52	0.023	6
NAP1L1	-2.04	0.001	4
NCL	-2.47	0.005	6
NFATC1	-3.88	<0.001	4
NOLC1	-2.01	0.018	4
NOTCH2	-2.26	0.031	3
NPAT	-3.97	<0.001	5
NR2F2	-2.16	0.004	7
NRCAM	-3.03	0.001	4
NSD1	-2.73	<0.001	3
NUDT4	-2.49	0.003	5
NUFIP1	-2.22	0.013	5
NUP50	-3.12	<0.001	6
NVL	-7.34	<0.001	7
OCRL	-2.39	0.011	4
OSBPL3	-4.59	0.016	5
PAFAH1B1	-2.01	0.014	7
PCM1	-2.67	<0.001	4
PCNX	-4.80	0.005	4
PDE4D	-3.50	0.001	5
PDXK	-2.04	0.013	3
PEA15	-3.38	0.041	5
PEX3	-2.85	0.001	5
PFDN4	-2.91	0.002	5
PHLDA1	-3.11	<0.001	5
PIGA	-2.48	0.018	4
PKNOX1	-2.17	0.025	3
PLAA	-2.57	0.001	4
PLAGL2	-3.91	0.001	3
PLEK2	-3.62	0.005	5
POLD3	-4.43	<0.001	5
POLI	-2.16	0.002	4
PPAT	-2.38	0.021	5
PPP2R1B	-3.26	0.013	4
PRC1	-42.38	0.001	5
PRDM10	-3.62	0.001	5
PRMT3	-3.41	0.019	5

PRPF4	-2.65	0.016	3
PRPF4B	-2.51	0.009	5
PSME3	-2.34	0.049	4
PSME4	-3.30	0.001	6
PTBP1	-2.57	<0.001	5
PTPN2	-2.73	0.001	6
QRSL1	-2.29	0.027	5
RACGAP1	-14.43	<0.001	3
RAD1	-2.82	<0.001	3
RAD21	-3.21	<0.001	5
RAD51	-6.21	<0.001	5
RANBP2	-2.21	0.01	4
RAP2B	-3.81	0.006	5
RB1	-6.76	0.011	3
RELB	-2.83	0.001	5
REV3L	-2.60	0.027	7
RFC5	-3.06	0.002	4
RHEB	-2.27	0.001	5
RHOBTB1	-4.76	0.044	5
RIF1	-2.94	0.001	3
RNF111	-2.53	0.009	5
RNGTT	-2.49	<0.001	5
RPA2	-2.48	0.001	5
RPIA	-5.88	<0.001	5
RRAS2	-4.12	0.035	5
RUNX1	-3.64	0.008	4
SAV1	-2.46	<0.001	5
SCHIP1	-15.08	0.021	5
SEC23B	-2.14	0.006	5
SEPHS1	-2.19	0.002	8
SERPINE2	-5.04	0.016	6
SF3B4	-2.02	0.003	5
SFRS1	-2.37	0.028	3
SFRS10	-2.22	<0.001	6
SFRS11	-2.17	<0.001	5
SFRS7	-4.14	0.029	4
SLBP	-3.64	0.011	6
SLC16A1	-2.64	<0.001	5
SLC25A14	-2.05	0.002	5
SLC26A2	-5.82	0.012	5
SLC30A1	-2.03	0.02	5
SLC31A1	-2.00	0.006	5
SLC35C1	-2.62	0.012	4

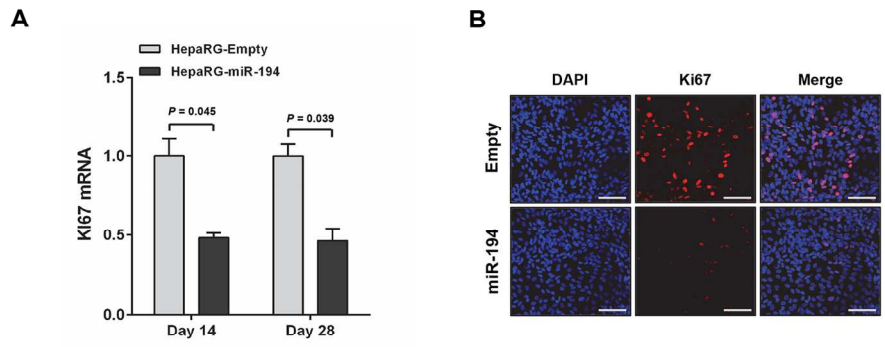
SLC39A6	-6.07	0.011	5
SLC7A1	-4.30	<0.001	3
SLC7A11	-11.36	0.017	4
SLC7A6	-3.46	0.009	4
SLC9A3R1	-2.91	0.013	5
SMARCC1	-6.39	0.011	5
SMURF1	-2.00	0.001	4
SNAPC1	-8.50	0.023	3
SNRPE	-2.84	0.011	3
SNX11	-3.32	0.002	4
SNX5	-2.31	0.004	4
SOCS2	-3.34	0.033	6
SP3	-4.34	0.007	6
SPATS2	-3.77	<0.001	5
SPTLC2	-2.44	<0.001	5
U2SURP	-4.55	0.001	3
SRI	-2.42	0.019	6
SRM	-2.92	0.008	5
SRP72	-2.31	0.004	6
SRR	-2.19	0.022	4
SS18	-2.02	<0.001	7
STAC	-2.48	0.037	4
STAT5B	-2.04	<0.001	6
STK24	-2.19	0.014	5
STK38L	-6.83	0.019	5
STMN1	-2.67	<0.001	4
STX6	-2.49	0.005	6
SWAP70	-4.13	0.007	3
SYNJ2	-3.27	0.004	5
TAF5L	-4.27	<0.001	3
TBL2	-2.48	0.001	5
TFAM	-4.15	0.001	5
THAP10	-4.39	0.008	8
THBS1	-4.19	0.037	6
TJP1	-6.40	0.009	7
TPD52L2	-2.16	0.005	6
TRAF1	-3.62	<0.001	5
TRAM2	-5.40	<0.001	4
TRPA1	-3.29	0.021	3
TTC4	-5.45	<0.001	4
TULP4	-2.92	0.03	5
UBA2	-2.18	0.008	7
UBE2B	-2.01	0.011	5

UBE2V2	-5.18	<0.001	7
UBE3A	-2.48	0.002	4
UBE4A	-2.41	0.018	4
UFD1L	-3.55	<0.001	6
USP46	-2.37	0.005	4
VAPB	-2.32	<0.001	3
WEE1	-4.40	0.002	4
WRN	-2.36	<0.001	6
WTAP	-2.79	0.001	3
XPO7	-2.10	0.043	4
YAP1	-2.55	<0.001	4
YES1	-2.82	0.019	5
YWHAB	-4.87	0.002	3
ZAK	-2.38	0.001	3
ZC3HAV1	-2.08	0.001	6
ZCCHC2	-3.27	0.04	5
ZFX	-3.15	0.009	4
ZFYVE16	-3.35	0.023	3
ZNF180	-2.18	0.004	6
ZNF202	-3.23	<0.001	6
ZNF22	-2.30	<0.001	5
ZNF330	-2.74	0.015	5
ZNF337	-2.54	<0.001	4
ZNF473	-2.81	0.024	4
ZWINT	-12.56	0.003	5

Supplemental Table S4. Expression changes (fold change and p value) of 16 predicted miR-194 target genes upon miR-194 overexpression in HepaRG cells (HepaRG-miR-194 cell lines vs HepaRG-empty cell lines) and in hESCs (hESC-miR-194 cell lines vs hESC-empty cell lines).

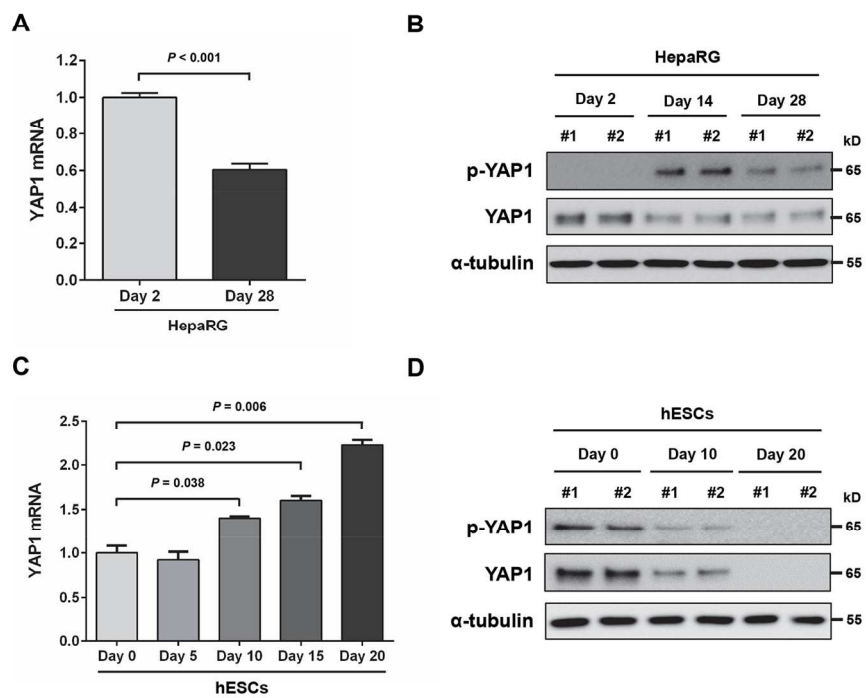
Gene Symbol	Gene description	FC HepaRG	P value	FC hESC	P value
BICD2	bicaudal D homolog 2 (Drosophila)	-3.6	0.010	-1.3	0.011
CENPF	centromere protein F, 350/400ka (mitosin)	-3.3	0.005	-1.6	0.004
ECT2	epithelial cell transforming sequence 2 oncogene	-2.0	0.012	-1.6	<0.001
ELOVL6	ELOVL family member 6, elongation of long chain fatty acids	-2.5	0.008	-1.6	0.023
FGFR3	fibroblast growth factor receptor 3	-2.3	0.048	-1.5	0.040
GALNT7	polypeptide N-acetylgalacto-saminyltransferase 7	-2.6	0.004	-1.8	0.004
HDAC2	histone deacetylase 2	-1.8	0.005	-1.7	0.001
IGF1R	insulin-like growth factor 1 receptor	-2.0	0.025	-1.6	<0.001
NOTCH2	Notch homolog 2 (Drosophila)	-1.9	0.001	-1.5	<0.001
PRC1	protein regulator of cytokinesis 1	-3.9	< 0.001	-1.3	0.002
RACGAP1	Rac GTPase activating protein 1	-3.2	0.002	-1.5	0.000
RAP2B	RAP2B, member of RAS oncogene family	-3.0	0.030	-1.5	0.003
REV3L	REV3-like, polymerase zeta, catalytic subunit	-2.6	0.001	-1.2	0.028
RHEB	Ras homolog enriched in brain	-2.7	0.009	-2.0	<0.001
THBS1	thrombospondin 1	-8.8	0.026	-2.3	0.000
YAP1	Yes-associated protein 1	-1.8	0.029	-1.7	0.003

Supplementary Figure S1



147x76mm (300 x 300 DPI)

Supplementary Figure S2



147x119mm (300 x 300 DPI)