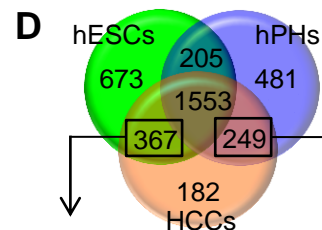
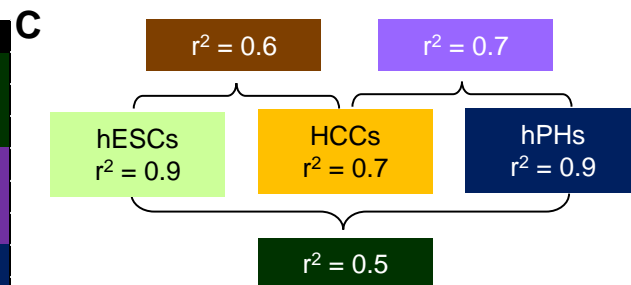
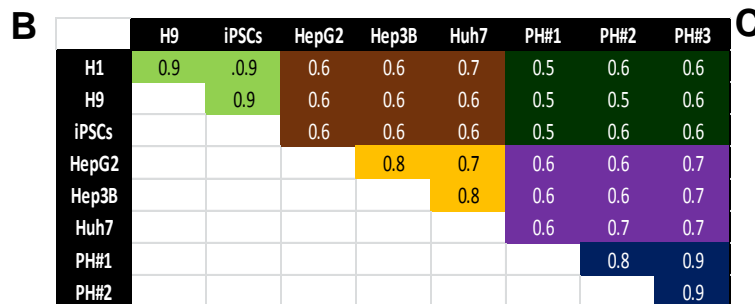
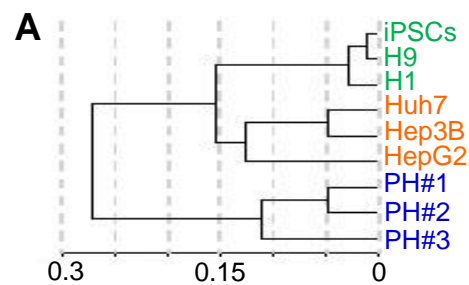


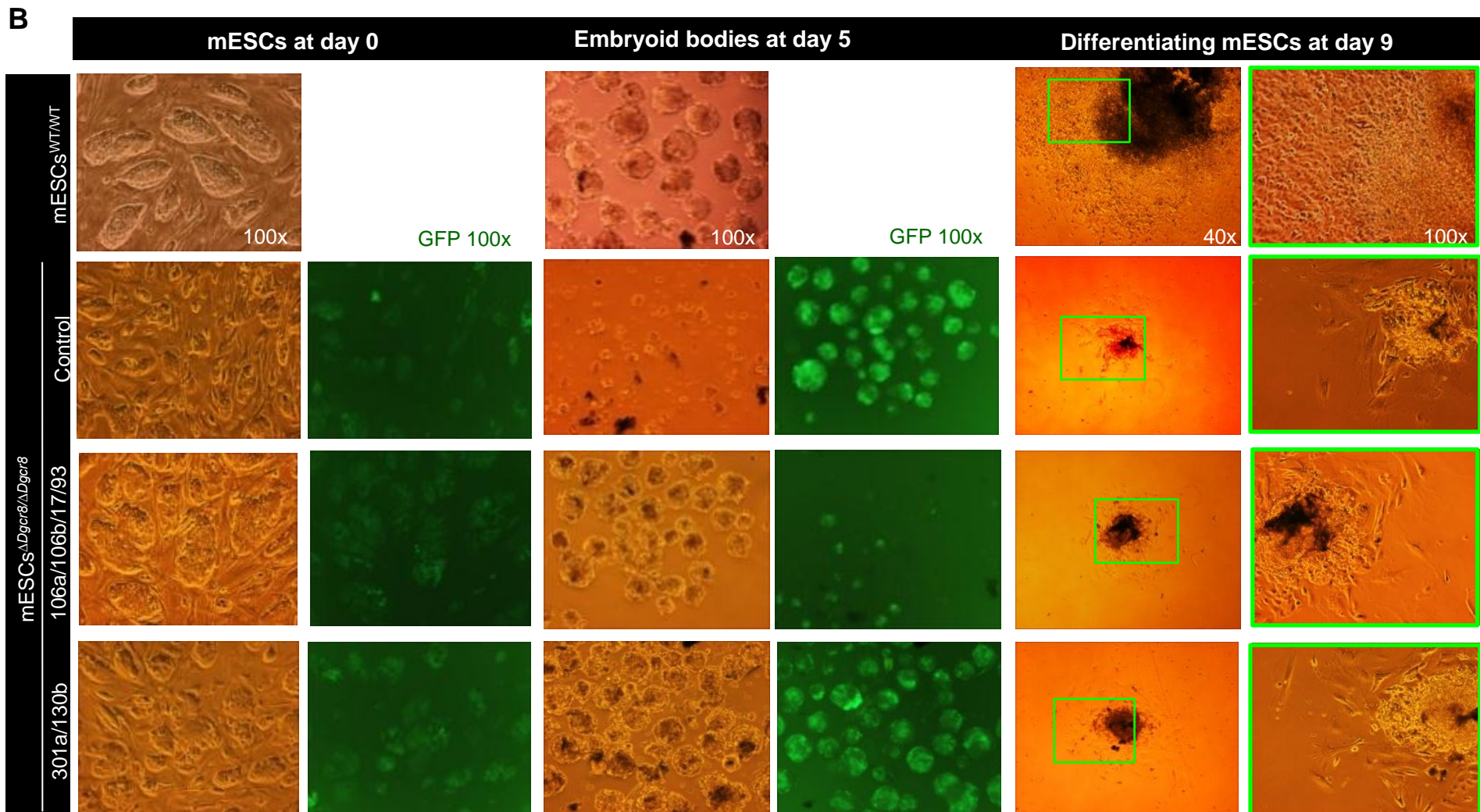
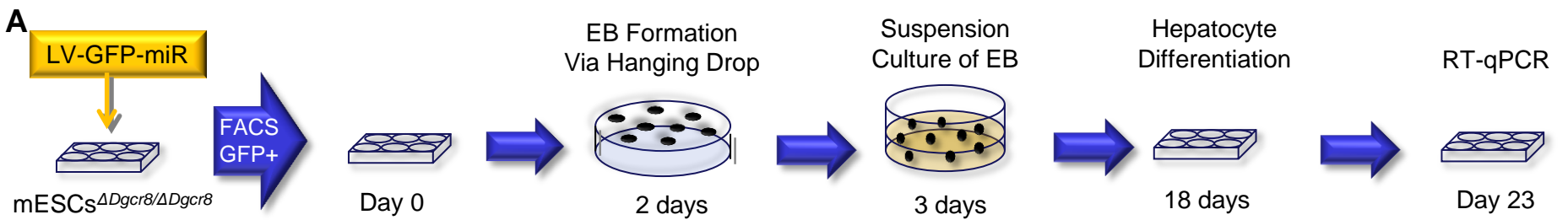
Supplementary Figure S1



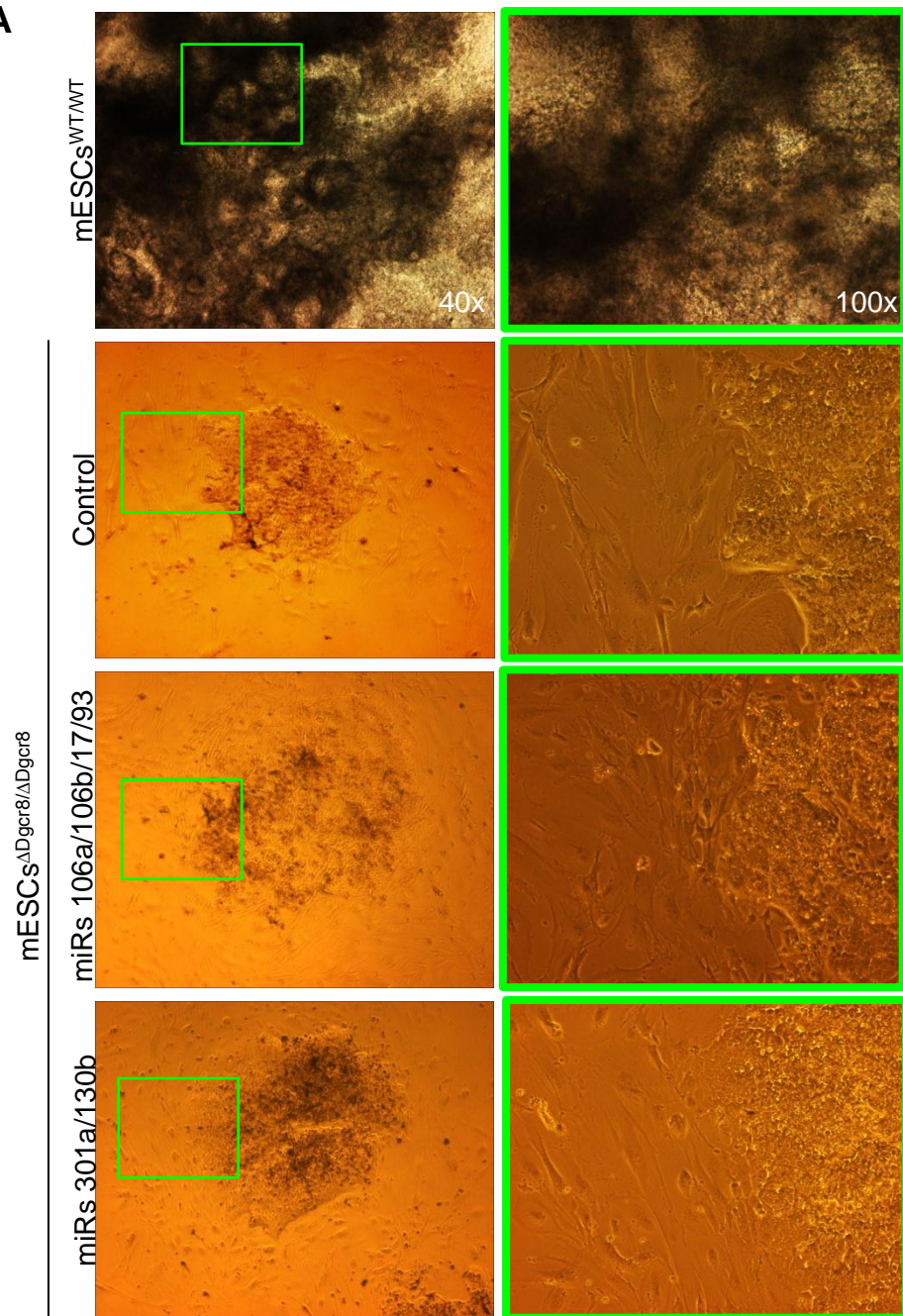
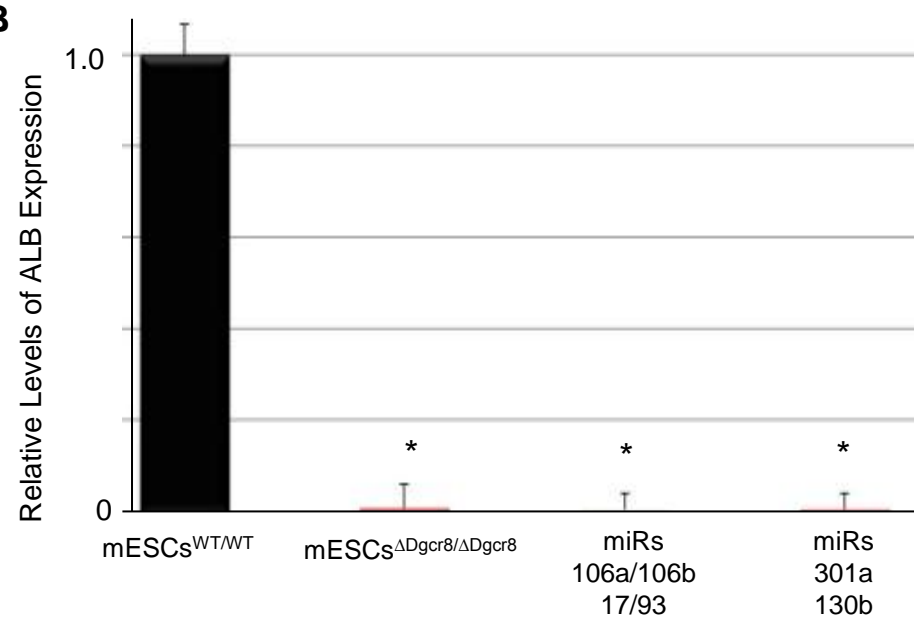
Cluster	Enrichment Score	GO Term	P-Value	Fold Enrichment	FDR
1	7.943	GO:0000279~M phase	0.000	4.013	0.000
2	4.849	GO:0016070~RNA metabolic process	0.000	2.544	0.000
3	4.802	GO:0051276~chromosome organization	0.000	3.141	0.000
4	4.671	GO:0006260~DNA replication	0.000	4.543	0.002
5	3.402	GO:0006259~DNA metabolic process	0.000	2.910	0.001
6	3.381	GO:0006807~nitrogen compound metabolic process	0.000	1.693	0.000
7	3.296	GO:0050657~nucleic acid transport	0.000	6.282	0.005
8	3.170	GO:0006270~DNA replication initiation	0.038	9.521	48.197
9	2.595	GO:0010605~macromolecule metabolic process	0.000	2.283	0.032
10	1.963	GO:0051726~regulation of cell cycle	0.000	2.915	0.162
11	1.950	GO:0051188~cofactor biosynthetic process	0.003	4.188	4.869
12	1.930	GO:0007059~chromosome segregation	0.001	5.015	1.744
13	1.729	GO:0009116~nucleoside metabolic process	0.008	4.760	13.112
14	1.525	GO:0034621~macromolecular complex subunit organization	0.011	2.133	17.014
15	1.521	GO:0009127~nucleoside monophosphate biosynthetic process	0.005	11.284	7.921
16	1.401	GO:0034660~ncRNA metabolic process	0.002	2.870	3.286
17	1.389	GO:0006268~DNA unwinding during replication	0.030	10.881	39.919
18	1.317	GO:0051329~interphase of mitotic cell cycle	0.016	3.451	23.550
19	1.306	GO:0034470~ncRNA processing	0.012	2.715	17.770
20	1.249	GO:0000226~microtubule cytoskeleton organization	0.026	2.763	35.687

Cluster	Enrichment Score	GO Term	P-Value	Fold Enrichment	FDR
1	7.382	GO:0009605~response to external stimulus	0.000	3.105	0.000
2	6.562	GO:0009611~response to wounding	0.000	4.119	0.000
3	4.026	GO:0002526~acute inflammatory response	0.000	8.167	0.002
4	3.394	GO:0034381~lipoprotein particle clearance	0.000	36.381	0.000
5	3.343	GO:0042060~wound healing	0.000	5.333	0.004
6	2.823	GO:0070482~response to oxygen levels	0.000	5.160	0.233
7	2.736	GO:0006519~amino acid and derivative metabolic process	0.000	3.307	0.172
8	2.695	GO:0043691~reverse cholesterol transport	0.000	36.381	0.000
9	2.353	GO:0008219~cell death	0.000	2.328	0.573
10	2.339	GO:0016044~membrane organization	0.001	2.865	1.288
11	2.204	GO:0006810~transport	0.003	1.467	4.506
12	2.076	GO:0051704~multi-organism process	0.006	2.030	9.242
13	1.947	GO:0002526~acute inflammatory response	0.000	7.870	0.001
14	1.927	GO:0002237~response to molecule of bacterial origin	0.001	5.923	1.930
15	1.728	GO:0030100~regulation of endocytosis	0.001	7.157	2.435
16	1.713	GO:0006082~organic acid metabolic process	0.002	2.339	2.967
17	1.632	GO:0006518~peptide metabolic process	0.006	6.864	9.528
18	1.592	GO:0042445~hormone metabolic process	0.003	4.805	5.499
19	1.550	GO:0019216~regulation of lipid metabolic process	0.001	5.197	1.459
20	1.523	GO:0043933~macromolecular complex subunit organization	0.002	2.152	2.909

Supplementary Figure S2

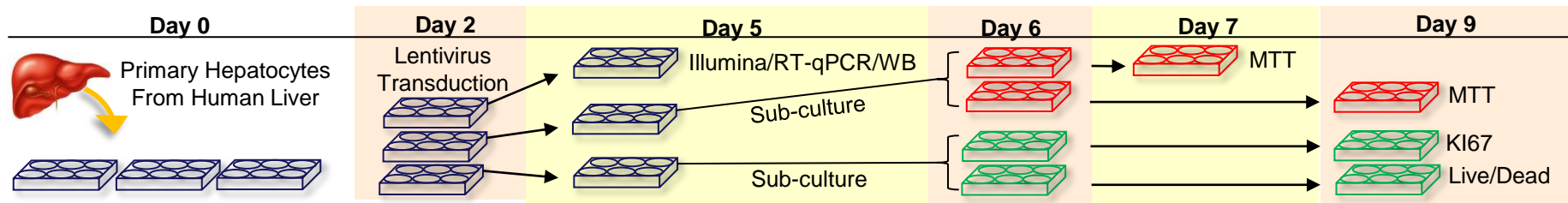


Supplementary Figure S3

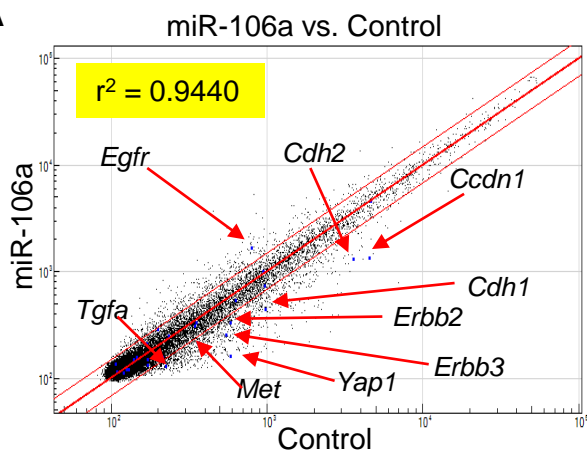
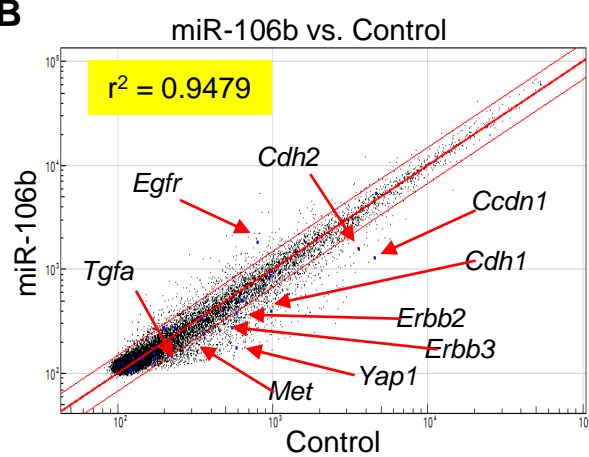
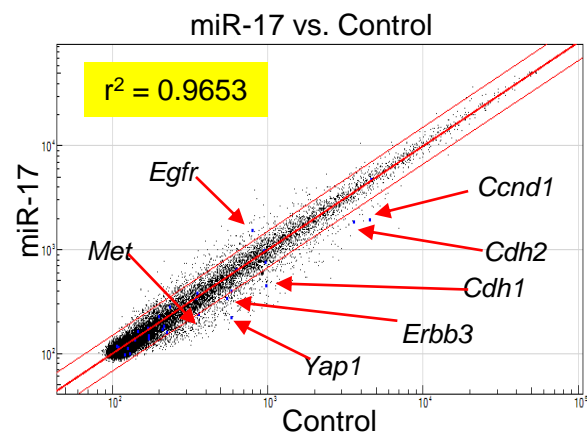
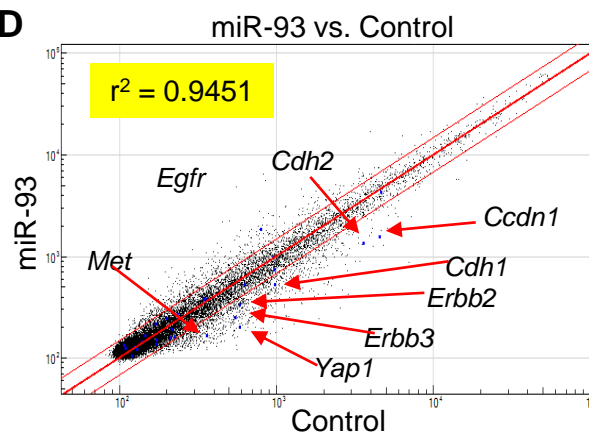
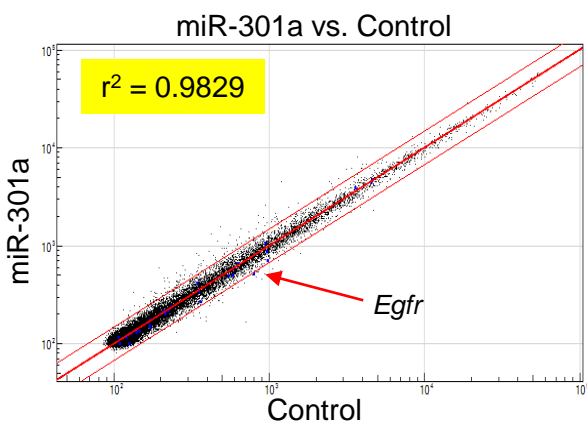
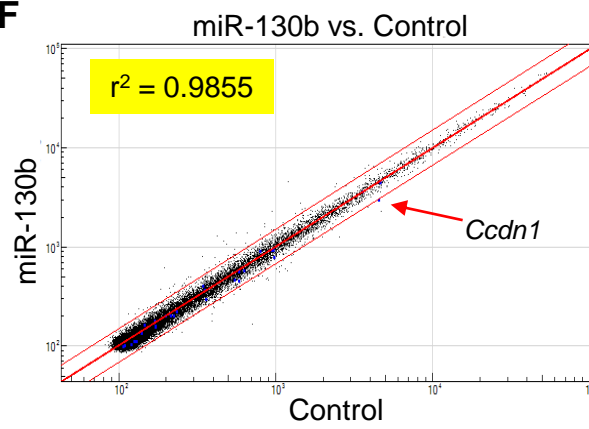
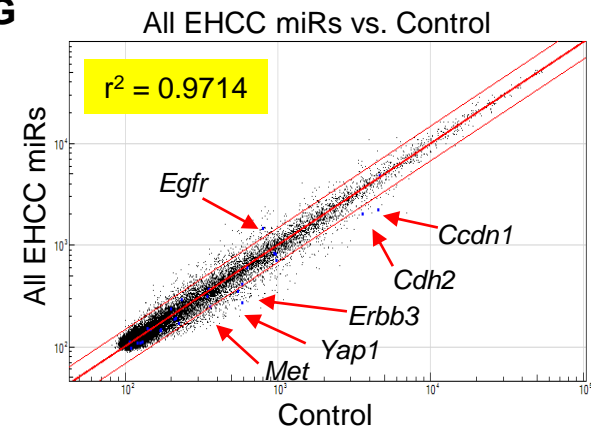
A**B**

Supplementary Figure S4

A



Supplementary Figure S5

A**B****C****D****E****F****G**

Supplementary Figure S6

	miR-106a			miR-106b			miR-17			miR-93			miR-301a			miR-130b			All EHCC miRs			
	P-Value	Diff. Score	Fold Δ > 1.5	P-Value	Diff. Score	Fold Δ > 1.5	P-Value	Diff. Score	Fold Δ > 1.5	P-Value	Diff. Score	Fold Δ > 1.5	P-Value	Diff. Score	Fold Δ > 1.5	P-Value	Diff. Score	Fold Δ > 1.5	P-Value	Diff. Score	Fold Δ > 1.5	
HCC Associated Genes	APC	0.340	1.153		0.679	0.515		0.116	1.390		0.071	3.340		0.798	-0.805		0.671	-0.779		0.963	-1.667	
	AXIN1	0.001	-1.690		0.001	0.043		0.001	0.575		0.001	3.856		0.001	6.312		0.001	6.837		0.001	-2.031	
	BRCA2	0.012	5.435		0.140	3.599		0.073	2.566		0.010	6.451		0.166	2.263		0.746	-0.763		0.388	1.167	
	CCND1	0.001	-80.559	+	0.001	-80.939	+	0.001	-53.896	+	0.001	-73.194	+	0.001	0.392		0.001	-18.704		0.001	-40.078	
	CDH1	0.001	-31.367	+	0.001	-36.464	+	0.001	-32.093	+	0.001	-23.165	+	0.001	-9.536		0.001	-5.400	+	0.001	-8.814	+
	CDH2	0.001	-53.729	+	0.001	-40.863	+	0.001	-33.552	+	0.001	-55.542	+	0.001	3.277		0.001	0.921		0.001	-26.485	+
	CDK4	0.001	-3.013		0.001	-4.100		0.001	0.859		0.001	-4.286		0.001	1.597		0.001	-1.572		0.001	-0.430	
	CIAPIN1	0.001	-7.915		0.001	-7.959		0.001	-4.437		0.001	-6.635		0.001	1.296		0.001	0.602		0.001	-1.827	
	CTTN	0.001	1.824		0.001	-0.240		0.001	3.905		0.001	4.166		0.001	-0.890		0.001	3.896		0.001	0.883	
	CTNNB1	0.001	-0.334		0.001	-0.262		0.001	3.038		0.001	3.908		0.001	0.389		0.001	1.940		0.001	1.918	
	EGFR	0.001	28.308	+	0.001	31.781	+	0.001	45.222	+	0.001	55.095	+	0.001	-18.741	+	0.001	5.469		0.001	42.202	+
	ERBB2	0.001	-22.093	+	0.001	-13.341	+	0.001	-13.734		0.001	-24.421	+	0.001	-2.621		0.001	0.076		0.001	-12.212	
	ERBB3	0.001	-25.840	+	0.001	-22.728	+	0.001	-14.740	+	0.001	-29.395	+	0.001	-1.505		0.001	-2.998		0.001	-12.742	+
	ERBB4	0.001	2.112		0.005	0.355		0.001	0.068		0.001	1.593		0.003	-0.696		0.001	-0.257		0.001	2.770	
	FLRT2	0.196	-0.925		0.463	-1.720		0.680	-5.918		0.087	-0.425		0.017	0.244		0.177	-2.336		0.354	-2.656	
	HBXIP	0.001	0.479		0.001	3.795		0.001	1.129		0.001	-0.778		0.001	1.542		0.001	-0.285		0.001	1.742	
	HDGF	0.001	-7.342		0.001	-1.152		0.001	-7.610		0.001	-7.791		0.001	-1.646		0.001	-0.508		0.001	-4.529	
	HGF	0.524	-0.884		0.813	-1.425		0.788	-4.358		0.859	-2.063		0.146	-0.043		0.550	-2.765		0.495	-1.538	
	MET	0.001	-17.478	+	0.001	-10.428	+	0.001	-14.886	+	0.001	-37.058	+	0.001	-7.188		0.001	-4.555		0.001	-12.133	+
	MMP7	0.001	4.804		0.001	1.158		0.001	1.140		0.001	7.882		0.001	-1.161		0.001	1.844		0.001	-2.742	
MYC	0.001	2.057		0.001	0.893		0.001	1.225		0.001	0.863		0.001	4.131		0.001	0.322		0.001	-2.345		
NAP1L5	0.001	-7.072		0.001	-6.888		0.001	-2.835		0.001	-1.483		0.001	-0.645		0.001	-0.791		0.001	-1.636		
PIM1	0.001	2.151		0.001	5.002		0.001	6.970		0.001	5.573		0.001	1.229		0.001	-0.285		0.001	9.889		
PTGS2	0.015	-4.890		0.035	-4.702		0.001	-2.761		0.001	-4.584		0.001	1.222		0.001	-1.354		0.001	-2.806		
RB1	0.001	12.645		0.001	6.518		0.001	3.970		0.001	6.574		0.001	1.012		0.001	0.612		0.001	5.804		
TERT	0.164	-0.245		0.001	2.737		0.176	-1.982		0.032	0.930		0.790	-4.623		0.205	-2.170		0.536	-2.817		
TGFA	0.036	-18.905	+	0.001	-13.194	+	0.001	-11.334		0.001	-9.333		0.001	0.119		0.001	-1.868		0.001	-7.280		
TP53	0.001	-1.967		0.001	-1.055		0.001	-4.413		0.001	-1.804		0.001	-2.795		0.001	-1.039		0.001	-3.796		
YAP1	0.001	-75.685	+	0.001	-68.028	+	0.001	-48.582	+	0.001	-61.779	+	0.001	0.601		0.001	-6.138		0.001	-40.038	+	
ESC and/or Hepatic Progenitor Associated Genes	ABCG2	0.995	-3.045		0.150	2.070		0.502	-1.081		0.803	-0.325		0.070	2.029		0.932	-3.653		0.397	0.111	
	AFP	0.001	-1.332		0.001	-0.547		0.001	-1.163		0.001	0.121		0.001	-2.317		0.001	-2.172		0.001	1.218	
	ALB	0.001	4.721		0.001	2.568		0.001	-0.787		0.001	3.229		0.001	-0.183		0.001	1.054		0.001	-0.619	
	CD34	0.001	4.187		0.001	2.514		0.001	2.118		0.001	2.790		0.001	2.125		0.001	1.113		0.001	0.622	
	CD44	0.001	-150.803	+	0.001	-125.990	+	0.001	-102.627	+	0.001	-124.661	+	0.001	15.382		0.001	-1.667		0.001	-83.179	+
	KIT	0.020	3.464		0.014	4.029		0.080	0.584		0.038	2.706		0.185	0.421		0.253	-0.597		0.001	6.347	
	KRT7	0.001	-11.648		0.001	-2.952		0.001	-8.628		0.001	-31.681	+	0.001	2.146		0.001	2.108		0.001	-29.864	+
	KRT8	0.001	-8.812		0.001	-3.040		0.001	-5.895		0.001	-13.597		0.001	-2.452		0.001	-0.513		0.001	-17.793	
	KRT14	0.688	-0.319		0.901	-0.801		0.770	-2.480		0.708	-0.012		0.248	0.519		0.854	-2.869		0.810	-1.527	
	KRT18	0.001	2.860		0.001	2.022		0.001	1.741		0.001	0.174		0.001	-0.568		0.001	-1.735		0.001	0.596	
	KRT19	0.001	-32.144		0.001	-13.425		0.001	-19.040		0.001	-37.138		0.001	6.623		0.001	3.224		0.001	-28.068	
	NANOG	0.731	1.705		0.506	3.209		0.301	2.336		0.211	5.609		0.491	2.083		0.586	1.101		0.676	1.651	
	NOTCH1	0.014	-9.995		0.001	-3.211		0.001	-7.797		0.001	-6.567		0.001	-2.137		0.001	-1.749		0.001	-2.202	
	PCGF4	0.001	-20.768		0.001	-11.670		0.001	-7.377		0.001	-26.773		0.001	4.084		0.001	0.588		0.001	-2.201	
	POU5F1	0.502	-0.005		0.420	0.557		0.915	-3.971		0.390	0.544		0.377	-0.372		0.891	-3.716		0.570	-0.781	
	PROM1	0.104	-1.166		0.151	-1.153		0.025	-1.342		0.001	1.991		0.001	3.722		0.001	2.444		0.019	-0.157	
	SMAD4	0.001	-2.131		0.001	-2.923		0.001	-0.955		0.001	-3.902		0.001	2.708		0.001	2.846		0.001	-1.572	
	SOX2	0.657	-1.370		0.619	-0.748		0.487	-2.536		0.414	-0.325		0.967	-4.737		0.242	-1.214		0.508	-1.482	
	SPTBN1	0.001	-2.426		0.001	-0.791		0.001	1.280		0.001	-1.185		0.001	0.516		0.001	1.280		0.001	-0.755	
	STAT3	0.001	-34.160	+	0.001	-22.218		0.001	-20.809		0.001	-26.955		0.001	5.949		0.001	-2.164		0.001	-14.665	
TACSTD1	0.001	3.725		0.003	0.356		0.001	-0.015		0.035	-1.095		0.043	-1.910		0.001	-0.216		0.001	1.697		
THY1	0.954	-3.437		0.273	-0.103		0.539	-3.395		0.971	-3.909		0.253	-1.159		0.434	-2.676		0.653	-2.674		
WNT3A	0.164	4.817		0.080	6.502		0.159	3.054		0.971	0.776		0.759	1.096		0.994	-1.416		0.405	2.880		