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Supplemental Information

circFN1 Mediates Sorafenib Resistance of Hepatocellular Carcinoma Cells by Sponging miR-1205 and Regulating E2F1 Expression

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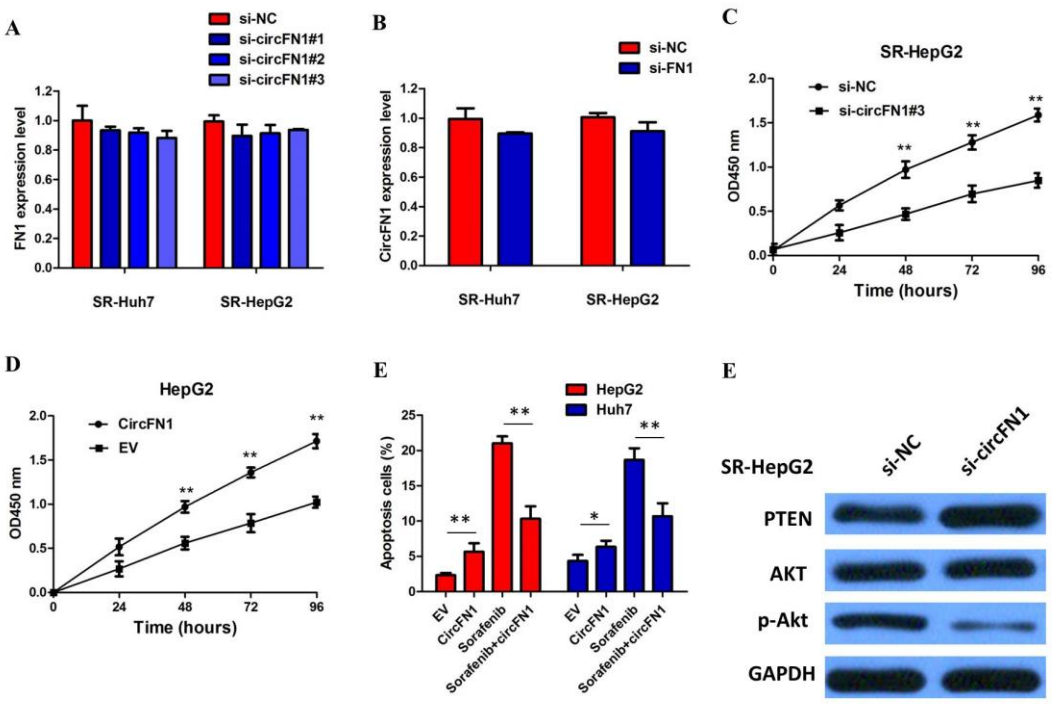

Figure S1. A-B. siRNA directed against the backsplice sequence knocked down only the circular transcript and did not affect the expression of linear species, and siRNA targeting the sequence in the linear transcript knocked down only the linear transcript and did not affect the expression of the circular transcript in SR-HepG2 and SR-Huh7 cells; C. The results of CCK8 assay showed that circFN1 silencing suppressed the proliferation of SR-HepG2 and SR-Huh7 cells after exposure to sorafenib (3 μM); D. The results of CCK8 assay showed that the growth rate of HepG2 and Huh7 cells were significantly increased compared to the control group after overexpression of circFN1; E. Cell apoptosis assays revealed that overexpression of circFN1 significantly decreased the apoptosis of HepG2 and Huh7 cells after exposure to sorafenib (3 μM) compared to the control group; F. Inhibition of circFN1 significantly

increased the expression of PTEN protein and decreased the activation of Akt in sorafenib-resistant HCC cells; All tests were at least performed three times. Data were expressed as mean ± SD. *$P < 0.05$. **$P < 0.01$.

TargetScan miRNA predictions												
CircRNA Mirbase ID	CircRNA (Top) - miRNA (Bottom) pairing	Site Type	CircRNA Start	CircRNA End	3' pairing	local AU	position	TA	SPS	context+ score	context+ score percentile
hsa_circ_0058124 (5' ... 3') hsa-miR-1205 (3' ... 5')	GCCCUCUCCCAGGGACCUGCAGU GAGUUUCGUUUGGGACGUCU	7mer-m8	614	620	0.003	0.003	-0.027	0.028	-0.064	-0.177	91
hsa_circ_0058124 (5' ... 3') hsa-miR-1231 (3' ... 5')	CCUCUGACUGCUCAA-CAGACAAC CGUCGACAGGCGGGUCUGUG	7mer-1a	855	861	-0.006	0.041	-0.05	-0.001	-0.015	-0.105	79
hsa_circ_0058124 (5' ... 3') hsa-miR-1245 (3' ... 5')	GGUGUUCAGUAUAACAUCACUAU UACAUCCGGAAAUCUAGUGAA	7mer-1a	510	516	0.004	-0.02	-0.012	-0.013	0.018	-0.097	88
hsa_circ_0058124 (5' ... 3') hsa-miR-1279 (3' ... 5')	CGGGAUUCCGGGUGGAAUAUGAG UCUUUCUUCGUUAUACU	7mer-1a	136	142	0.004	0.06	-0.035	0.004	0.084	0.043	71
hsa_circ_0058124 (5' ... 3') hsa-miR-187 (3' ... 5')	CCUGAUGCCCCUCCUGACACGAC GGCCGACGUUGUGUUCUGUGCU	7mer-1a	324	330	-0.002	0.05	-0.015	-0.077	-0.035	-0.153	67
hsa_circ_0058124 (5' ... 3') hsa-miR-224 (3' ... 5')	ACUCCGUCACCCUCAGUGACUUG UUGCCUUGGUGAUCACUGAAC	7mer-m8	481	487	-0.016	0.023	-0.008	0.004	0.014	-0.103	89
hsa_circ_0058124 (5' ... 3') hsa-miR-370 (3' ... 5')	GCAGAGGCUGCCCAUCAGCAGGA UGGUCCAAGGUGGGGUCGUCCG	8mer-1a	746	753	-0.008	0.041	-0.086	0.033	-0.112	-0.379	98
hsa_circ_0058124 (5' ... 3') hsa-miR-411 (3' ... 5')	GCAGAGUUUGAUCCUGUCUACUU GCAUGCGAUAUGCCAGAUGAU	7mer-m8	287	293	0.012	-0.002	-0.021	-0.009	0.006	-0.134	95
hsa_circ_0058124 (5' ... 3') hsa-miR-512-5p (3' ... 5')	CCGGGUGGAAUAUGAGCUGAGUG CUUUCACGGGAGUUCCGACUCAC	7mer-m8	143	149	0.012	0.015	-0.042	0	-0.037	-0.172	93
hsa_circ_0058124 (5' ... 3') hsa-miR-513a-5p (3' ... 5')	CAAGCACAGCCACUUCUGUGAAC UACUGUGGAGG--GACACUU	7mer-1a	199	205	-0.006	0.032	-0.028	0.022	-0.015	-0.069	76
hsa_circ_0058124 (5' ... 3') hsa-miR-518a-5p (3' ... 5')	CAUCAGCAGGAACACCUUUGCAG CUUUCCCGAAGGGAAACGUC	7mer-m8	758	764	-0.007	0.067	-0.048	0.022	0.023	-0.063	87
hsa_circ_0058124 (5' ... 3') hsa-miR-527 (3' ... 5')	CAUCAGCAGGAACACCUUUGCAG CUUUCCCGAAGGGAAACGUC	7mer-m8	758	764	-0.007	0.067	-0.048	0.022	0.023	-0.063	87
hsa_circ_0058124 (5' ... 3') hsa-miR-518a-5p (3' ... 5')	CUAUUACUUCAAAGUCUUUGCAG CUUUCCCGAAGGGAAACGUC	7mer-m8	809	815	0.012	0.006	-0.055	0.022	0.023	-0.112	93
hsa_circ_0058124 (5' ... 3') hsa-miR-527 (3' ... 5')	CUAUUACUUCAAAGUCUUUGCAG CUUUCCCGAAGGGAAACGUC	7mer-m8	809	815	0.012	0.006	-0.055	0.022	0.023	-0.112	93
hsa_circ_0058124 (5' ... 3') hsa-miR-526b (3' ... 5')	UGCUGUGGAAGAAAAUCAAGAAA UGUCUUUCACGAAGGG--AGUUCUC	7mer-1a	536	542	-0.006	-0.014	-0.015	0.004	0.019	-0.086	83
hsa_circ_0058124 (5' ... 3') hsa-miR-549 (3' ... 5')	CAAGAAAGUACACCUGUUGUCAU UCUCGAGUAGGUAUCAACAGU	7mer-1a	552	558	0.004	0.008	-0.016	-0.016	-0.002	-0.096	80
hsa_circ_0058124 (5' ... 3') hsa-miR-578 (3' ... 5')	GCUGUGGAAGAAAAUCAAGAAAG UGUUAGGAUCUCGUGUUCUUC	7mer-1a	537	543	0.001	-0.008	-0.015	0.017	0.042	-0.037	79
hsa_circ_0058124 (5' ... 3') hsa-miR-578 (3' ... 5')	ACCUGUUGUCAUUCAACAAGAAA UGUUAGGAUCUCGUGUUCUUC	8mer-1a	563	570	0.013	0.032	-0.04	0.028	0.081	-0.133	94
hsa_circ_0058124 (5' ... 3') hsa-miR-615-5p (3' ... 5')	UUGUUCGCUGGAGCA-----GACCCCAG CUAGGCUCGUGGCCCCUGGGGG	7mer-1a	376	382	-0.006	0.055	-0.009	-0.002	-0.105	-0.141	62
hsa_circ_0058124 (5' ... 3') hsa-miR-636 (3' ... 5')	AGUACCUGGAUCUUCCAAGCACA ACGCCCGCCCUGCUC-GUUCGUGU	8mer-1a	184	191	-0.018	0.076	-0.068	0.002	-0.033	-0.288	97
hsa_circ_0058124 (5' ... 3') hsa-miR-653 (3' ... 5')	GUACACCUGUUGUCAUUCAACAA GUCAUCUCUAACAAAGUUGUG	8mer-1a	559	566	0.003	0.013	-0.039	-0.006	0.08	-0.196	97
hsa_circ_0058124 (5' ... 3') hsa-miR-657 (3' ... 5')	UGCCCUCUCCCAGGGACCUGCAG GGAUCUCUCCCACUCUUGGACGG	7mer-1a	613	619	-0.002	0.043	-0.023	-0.004	-0.066	-0.126	77
hsa_circ_0058124 (5' ... 3') hsa-miR-657 (3' ... 5')	GAUGUGAUCCCCGUCAACCUGCC GGAUCUCUCCCACUCUUGGACGG	7mer-m8	711	717	0.012	0.103	-0.041	-0.004	-0.032	-0.082	65
hsa_circ_0058124 (5' ... 3') hsa-miR-661 (3' ... 5')	UUCGCUGGAGCAGAC-CCCAGGCU UGCGCGUCCGGUCUCUGGGUCCGU	7mer-m8	379	385	-0.016	0.049	-0.008	0.039	-0.115	-0.171	92
hsa_circ_0058124 (5' ... 3') hsa-miR-665 (3' ... 5')	CAGUAGCUUUGUGGUCUCCUGGG UCCCCGGAGUCGGAGGACCA	7mer-m8	92	98	0.003	0.022	-0.049	0.033	-0.066	-0.177	93
hsa_circ_0058124 (5' ... 3') hsa-miR-668 (3' ... 5')	CCUGCAGUUUGUGGAAGUGACAG CAUCACCCGGCUCGGCUCACUGU	7mer-1a	629	635	0.004	0.048	-0.025	-0.009	-0.018	-0.074	71
hsa_circ_0058124 (5' ... 3') hsa-miR-758 (3' ... 5')	UUGAUCCUGUCUACUUCACAAAC CCAAUCACCUGGUCCAGUGUUU	7mer-1a	294	300	0.001	0.036	-0.018	-0.002	0.021	-0.036	74
hsa_circ_0058124 (5' ... 3') hsa-miR-766 (3' ... 5')	CCUCAAUUGUUGUUCGCUGGAGC CGACUCCGACACCCCGACCUCA	7mer-m8	367	373	-0.007	0.041	-0.01	0.031	-0.069	-0.134	86
hsa_circ_0058124 (5' ... 3') hsa-miR-767-3p (3' ... 5')	AUAUCUGAGGAUGGG----GAGCAGAG UCUUUGGUACCCCAUACUCGUCU	7mer-1a	270	276	-0.009	0.016	-0.021	0.011	-0.052	-0.129	82
hsa_circ_0058124 (5' ... 3') hsa-miR-767-3p (3' ... 5')	AAUUGUUGUUCGCUGGAGCAGAC UCUUUGGUACCCCAUACUCGUCU	7mer-1a	371	377	0.001	0.042	-0.009	0.011	-0.052	-0.081	70
hsa_circ_0058124 (5' ... 3') hsa-miR-769-5p (3' ... 5')	CUUUGUGGUCUCCUGGGUCUCAG UCGAGUCUUGGGUCUCCAGAGU	7mer-1a	98	104	0.004	0.041	-0.039	-0.004	-0.058	-0.13	89
hsa_circ_0058124 (5' ... 3') hsa-miR-7 (3' ... 5')	GCCACAGUACCUGGAUCUUCCAA UGUUGUUUUAGUGAUCAGAAGGU	7mer-1a	179	185	0.004	0.041	-0.031	0.014	-0.017	-0.063	75
hsa_circ_0058124 (5' ... 3') hsa-miR-873 (3' ... 5')	GCACAGAACUCAACC-UUCCUGAA UCCUCUGAGUGUUCAAGGACG	7mer-1a	451	457	-0.016	0.011	-0.005	0.02	-0.012	-0.076	80
hsa_circ_0058124 (5' ... 3') hsa-miR-892a (3' ... 5')	AGGAGGGAGAUGAGCCACAGUAC GAUGCGUCUUUCCUGUGUCAC	7mer-1a	166	172	-0.006	0.041	-0.032	0.001	-0.013	-0.083	81
hsa_circ_0058124 (5' ... 3') hsa-miR-892b (3' ... 5')	UGUGACCGAAAUCACAGCCAGUA AGAUGGGUCUUUCC--UCGGUCAC	8mer-1a	74	81	-0.018	0.069	-0.096	-0.011	-0.084	-0.387	98
hsa_circ_0058124 (5' ... 3') hsa-miR-940 (3' ... 5')	UGUGAUCCCCGUCAACCUGCCUG CCCCUCGCCCCCGGGACGGAA	7mer-m8	713	719	0.003	0.063	-0.041	0.037	-0.079	-0.137	92