

Table S1. Complete list of genes with the fold change in expression compared with control HepG2 pre-fusion

			Pre Fusion		C2 +HepG2 MyoD prePEG		Day6 Heterokaryons		C2 +HepG2 TSA Day6		C2 + HepG2 MyoD Day6	
Acc_Num	name	category	FoldChange	P.value	Fold Change	P.value	FoldChange	P.value	Fold Change	P.value	Fold Change	P.value
NM_000069	CACNA1S: cal	contraction/excitation	0.8619	0.7742	0.938	0.6264	1.1593	0.3299	0.7509	0.9691	1.1102	0.6783
NM_000079	CHRNA1: choli	contraction/excitation	0.8594	0.8457	1.1036	0.3786	1.464	0.1608	1.4707	0.2377	4.0237	0.0026
NM_000257	MYH7: myosin	contraction/excitation	0.8182	0.8477	0.9535	0.5966	0.9969	0.6441	1.3506	0.3091	1.4363	0.4114
NM_000334	SCN4A: sodiur	contraction/excitation	0.8439	0.7964	1.0076	0.5227	0.9228	0.7493	1.1117	0.5722	0.8686	0.8478
NM_000727	CACNG1: calci	contraction/excitation	0.6406	0.9662	0.8954	0.5747	0.8695	0.7409	0.881	0.7855	1.534	0.2087
NM_001100.3	actin, alpha 1,	contraction/excitation	1.385	0.0718	1.082	0.3137	1.9102	0.077	2.9504	0.0043	4.6586	2.00E-04
NM_002465	MYBPC1: myo:	contraction/excitation	0.9474	0.6742	0.7379	0.9596	1.555	0.1084	1.9449	0.0624	3.8649	0.003
NM_003279	TNNC2: tropor	contraction/excitation	0.493	0.9784	0.6436	0.9434	3.31	8.00E-04	2.3265	0.0257	15.9675	0
NM_003280	TNNC1: tropor	contraction/excitation	0.8669	0.4876	0.9613	0.1539	2.1734	0.0067	3.2609	0.0014	10.8374	0
NM_003281	TNNI1: tropon	contraction/excitation	0.9449	0.7782	1.1796	0.2585	1.0357	0.6638	0.9635	0.8324	1.1199	0.6399
NM_003282	TNNI2: tropon	contraction/excitation	1.527	0.0212	0.6185	0.9957	1.446	0.0278	3.9885	3.00E-04	4.0792	0.0057
NM_003283	TNNT1: tropor	contraction/excitation	1.255	0.0425	0.7688	0.3444	1.9558	0.0053	3.771	1.00E-04	11.0939	0
NM_004320	ATP2A1: ATPa	contraction/excitation	0.8948	0.7738	0.661	0.9886	1.5394	0.0599	3.5177	1.00E-04	2.63	0.0666
NM_006757	TNNT3: tropor	contraction/excitation	1.0112	0.0335	1.0112	0.3479	1.9139	0.0177	3.8166	3.00E-04	6.1866	0
NM_013292	MYLPF: fast sk	contraction/excitation	1.5957	0.0177	0.5502	0.9232	1.241	0.3198	2.666	0.0087	3.7812	0.005
NM_017534	MYH2: myosin	contraction/excitation	1.249	0.1799	0.7656	0.833	1.2644	0.2741	0.8291	0.9274	0.8535	0.8595
NM_079420	MYL1: myosin,	contraction/excitation	1.0593	0.5051	0.9401	0.7294	2.9158	0.0104	2.6122	0.0243	6.9207	0
NM_000290	PGAM2: phosp	metabolism	1.476	0.0095	1.5183	0.012	1.4157	0.0706	2.8819	0.0033	1.9172	0.0957
NM_000766.3	Homo sapiens	metabolism	0.8879	0.7903	0.5491	0.999	0.7682	0.9377	0.9032	0.8175	0.9802	0.7424
NM_00100197	ATP5D: ATP s _y	metabolism	0.904	0.5603	0.6976	0.8087	0.362	0.9996	0.8372	0.7634	0.5827	0.8493
NM_001824	CKM: creatine	metabolism	1.0257	0.2893	1.1134	0.322	1.8535	0.0736	1.6178	0.1907	4.6498	0.0022
NM_002103.3	glycogen synt _t	metabolism	1.1589	0.3113	1.1526	0.163	0.9884	0.6453	1.0012	0.7855	1.1331	0.5986
NM_002625	PFKFB1: 6-ph _t	metabolism	0.9921	0.5411	0.9766	0.5878	0.8484	0.8684	0.7626	0.9587	0.7436	0.9607
NM_003837	FBP2: fructose	metabolism	0.8756	0.6637	1.1853	0.2126	1.1366	0.3311	0.877	0.8176	1.1884	0.4966
NM_004102	FABP3: fatty a	metabolism	0.8458	0.913	0.676	0.9949	1.0372	0.6239	0.9894	0.8206	0.9011	0.9226
NM_004776	B4GALT5: UDF	metabolism	1.4472	0.0384	0.9298	0.5996	1.3497	0.2326	1.8493	0.0852	1.4077	0.1559
NM_021245.2	myozenin 1	metabolism	1.07	0.5232	1.2307	0.3046	1.6976	0.1621	1.2937	0.3926	1.2675	0.3962
NM_133371.2	myozenin 3	metabolism	1.0317	0.6205	1.1225	0.3649	0.9809	0.7928	0.809	0.9711	1.021	0.7828
NM_00100281	PDE4DIP: pho:	Misc	0.9654	0.632	0.6714	0.9759	0.9016	0.678	0.7743	0.9541	0.6561	0.9759
NM_001234	CAV3: caveolin	Misc	1.0096	0.6461	1.1517	0.3435	1.1424	0.5362	1.0752	0.6885	1.0732	0.6184
NM_001835	CLTCL1: clath _r	Misc	1.0383	0.4075	1.0113	0.5083	1.0113	0.5083	1.2439	0.3284	0.9912	0.779
NM_002152	HRC: histidine	Misc	0.9373	0.7349	0.5851	0.9607	0.7277	0.7989	1.5014	0.2344	1.6063	0.407
NM_002422.3	Homo sapiens	Misc	1.1771	0.3055	1.0746	0.4219	0.8932	0.913	1.0223	0.7592	0.7624	0.9564
NM_003356	UCP3: uncoup	Misc	0.9178	0.801	0.7241	0.8617	0.8284	0.9272	0.806	0.9393	0.9473	0.7324
NM_003673	TCAP: titin-ca _r	Misc	0.7586	0.898	0.5816	0.9916	1.4212	0.1462	3.9784	0	5.1229	6.00E-04
NM_006308	HSPB3: heat s	Misc	0.7967	0.7944	0.8007	0.7657	1.0677	0.5312	1.0449	0.6227	1.3686	0.3053
NM_007078	LDB3: LIM dor	Misc	0.9387	0.7562	0.8057	0.9068	0.916	0.8561	0.7886	0.9578	0.7282	0.9649
NM_015206	KIAA1024: KI/	Misc	0.9034	0.7886	1.1365	0.3529	1.1592	0.3147	1.1803	0.4707	0.8979	0.8649
NM_000540	RYR1: ryanodi	sarcoplasmic reticulum	0.6473	0.9362	1.0011	0.2326	0.9854	0.6038	1.965	0.0624	2.0742	0.1425
NM_001231.2	calsequestrin	sarcoplasmic reticulum	1.0608	0.5329	0.6675	0.9736	1.2553	0.2551	1.1552	0.4497	1.1325	0.6271
NM_001232	CASQ2: calsec	sarcoplasmic reticulum	1.0608	0.2487	0.6563	0.9502	1.0908	0.3134	1.5677	0.0638	1.1989	0.4389
NM_004274.3	A kinase (PRK,	sarcoplasmic reticulum	1.0738	0.4072	1.1452	0.261	1.0244	0.5735	0.9854	0.7848	1.1682	0.4692
NM_006073.1	triadin	sarcoplasmic reticulum	1.2387	0.2423	1.4644	0.0791	1.1913	0.3374	1.2423	0.3957	1.0243	0.7981
NM_020647.2	junctophilin 1	sarcoplasmic reticulum	1.2364	0.2141	0.6472	0.9907	1.6824	0.0683	1.3255	0.3162	0.9645	0.6824
NM_000109.2	dystrophin (m	surface/structure	1.5284	0.0307	0.9091	0.5422	1.2772	0.2905	1.1493	0.5824	1.1877	0.3532
NM_000117.1	emerin (Emery	surface/structure	0.6802	0.9914	1.2276	0.2628	0.8752	0.8188	0.9013	0.847	0.9413	0.8907
NM_000231	SGCG: sarcogl	surface/structure	1.2055	0.2652	1.0582	0.4526	1.176	0.4262	1.0951	0.6536	1.0935	0.7405
NM_000337	SGCD: sarcogl	surface/structure	1.0506	0.5864	1.0017	0.6245	0.964	0.7976	1.0036	0.7833	0.895	0.8684
NM_001104	ACTN3: actinir	surface/structure	1.4479	0.0274	0.9626	0.397	1.5427	0.1084	3.0884	0.0025	3.1087	0.0261
NM_001782	CD72: CD72 a	surface/structure	0.6817	0.9909	0.9591	0.6575	0.904	0.7846	1.1063	0.3734	0.8344	0.9399
NM_003637	ITGA10: integri	surface/structure	0.9721	0.7091	0.6803	0.9699	0.8524	0.8391	0.8619	0.8516	0.874	0.8886
NM_004393.1	dystroglycan 1	surface/structure	1.1926	0.2547	1.2026	0.1574	1.0127	0.6359	1.0564	0.5936	1.0643	0.6408
NM_004933.2	cadherin 15, I	surface/structure	1.0205	0.5655	1.0797	0.446	0.9062	0.7812	1.2212	0.4266	1.23	0.4172
NM_005055	RAPSN: recept	surface/structure	1.097	0.5302	1.3449	0.1495	0.8962	0.8751	1.2155	0.4966	1.2707	0.5259
NM_000325	PITX2: paired-	transcription factors	1.1476	0.3426	1.1204	0.4086	1.0368	0.533	1.0835	0.6736	1.1427	0.6421
NM_00100141	SMAD5: SMAD	transcription factors	0.8066	0.9675	1.0555	0.5482	0.9046	0.9051	0.7453	0.9937	0.812	0.9472
NM_002165.2	inhibitor of DN	transcription factors	1.1002	0.2997	0.7448	0.9268	0.5188	0.9868	0.5165	0.9977	0.7705	0.9012
NM_002478	MYOD1: Myo _c	transcription factors	0.6438	0.8273	1.1613	0.0906	0.7625	0.3787	0.5802	0.7591	0.6984	0.9013
NM_002479	MYOG: myoge	transcription factors	0.8473	0.2214	0.6608	0.5226	0.3355	0.9203	0.4548	0.741	0.3207	0.9988
NM_003199.1	transcription fi	transcription factors	1.1036	0.4257	0.7415	0.9749	1.1059	0.5422	1.2442	0.3186	0.8862	0.8771
NM_003200.1	transcription fi	transcription factors	1.0284	0.6016	1.1082	0.3981	0.9129	0.8457	0.8316	0.9654	0.7281	0.9861
NM_003205.3	transcription fi	transcription factors	1.2646	0.133	0.9732	0.5262	1.2931	0.308	1.032	0.6457	0.8697	0.8599
NM_005098.2	musculin (acti	transcription factors	1.0818	0.4093	1.0392	0.5466	1.0131	0.6613	1.1247	0.5748	0.8736	0.9406
NM_005587.1	MADS box trar	transcription factors	1.0704	0.3061	0.9244	0.6004	0.9191	0.7219	0.9102	0.8418	0.9234	0.6926
NM_005593	MYF5: myoge	transcription factors	1.0989	0.4249	0.9942	0.5189	1.0844	0.5247	1.0167	0.7697	0.7086	0.983
NM_005919.1	MADS box trar	transcription factors	0.7883	0.9724	0.9039	0.8193	1.0566	0.6175	0.9996	0.7845	1.0646	0.677