

TABLE S1. DETs in MCF7_{HG->LG} vs MCF7_{HG}

Gene symbol	Description	mRNA transcripts	log2 FC	p-val
IFI6	Interferon alpha inducible protein 6	NM_002038	0.97	4.03E-02
		NM_022873	0.97	4.03E-02
		NM_022872	0.97	4.03E-02
ITGA11	Integrin subunit alpha 11	NM_001004439	0.93	3.24E-02
SPARC	Secreted protein acidic and cysteine rich	NM_001309443	0.88	1.85E-02
		NM_001309444	0.88	1.92E-02
		NM_003118	0.88	1.92E-02
KHDRBS3	KH RNA binding domain containing, signal transduction associated 3	NM_006558	0.79	4.13E-02
SLC30A4	Solute carrier family 30 member 4	NM_013309	0.61	4.38E-02
C3orf18	Chromosome 3 open reading frame 18	NM_001171741	0.50	4.34E-02
TCF4	Transcription factor 4	NM_001330605	0.37	2.98E-02
		NM_001243236	0.36	4.11E-02
		NM_001243231	0.36	2.67E-02
		NM_001243234	0.36	4.15E-02
		NM_001243232	0.36	4.13E-02
		NM_001243235	0.36	4.29E-02
		NM_001243233	0.35	4.14E-02
		NM_001306208	0.35	4.26E-02
		NM_001243230	0.34	3.46E-02
		NM_001330604	0.34	3.79E-02
		NM_001083962	0.34	3.79E-02
		NM_001243227	0.34	3.54E-02
		NM_001243228	0.34	3.68E-02
		NM_001306207	0.34	3.62E-02
		NM_003199	0.34	3.92E-02
		NM_001243226	0.33	4.41E-02
CALML4	Calmodulin like 4	NM_001286695	0.24	3.75E-02
		NM_001031733	0.24	3.90E-02
		NM_001286694NM	0.23	4.35E-02
		_033429	0.23	4.51E-02
CDK2AP2	Cyclin dependent kinase 2 associated protein 2	NM_001271849	0.22	4.82E-02
PLD3	Phospholipase D family member 3	NM_001291311	0.14	4.59E-02
GART *	Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	NM_001136005	0.12	3.32E-02
		NM_001136006	0.11	3.51E-02
		NM_000819	0.11	4.03E-02
CAST	Calpastatin	NM_001042440NM	-0.11	4.47E-02
		_001330627	-0.11	4.35E-02
		NM_001284213	-0.12	3.83E-02
GNS	Glucosamine (N-acetyl)-6-sulfatase	NM_002076	-0.11	4.07E-02
TRA2A	Transformer 2 alpha homolog	NM_001282758	-0.12	3.22E-02
		NM_013293	-0.12	3.03E-02
MUS81	MUS81 structure-specific endonuclease subunit	NM_025128	-0.15	3.45E-02
ZNF181	Zinc finger protein 181	NM_001029997	-0.18	3.37E-02
		NM_001145665	-0.18	3.36E-02
KLHL5	Kelch like family member 5	NM_015990	-0.19	4.83E-02
		NM_199039	-0.23	1.61E-02
CDKN2D	Cyclin dependent kinase inhibitor 2D	NM_001800	-0.45	4.86E-02
DRAM1 **	DNA damage regulated autophagy modulator 1	NM_018370	-0.46	4.40E-02
RPS6KA6	Ribosomal protein S6 kinase A6	NM_001330512	-0.48	2.47E-02
		NM_014496	-0.50	2.02E-02
LURAP1L **	Leucine rich adaptor protein 1 like	NM_203403	-0.58	7.74E-03
CSPG4	Chondroitin sulfate proteoglycan 4	NM_001897	-0.64	4.32E-02
FAM188B	Family with sequence similarity 188 member B	NM_032222	-0.64	4.99E-02
GLRB	Glycine receptor beta	NM_001166061	-0.71	4.88E-03
		NM_000824	-0.78	3.65E-03
		NM_001166060	-0.82	3.76E-03
ZNF549	Zinc finger protein 549	NM_153263	-0.76	2.06E-02
		NM_001199295	-0.77	1.79E-02
PDE1A	Phosphodiesterase 1A	NM_001258314	-0.86	4.72E-02

* UP-regulated in Co-cultured MCF7_{HG->LG} vs Co-cultured MCF7_{HG}** DW-regulated in Co-cultured MCF7_{HG->LG} vs Co-cultured MCF7_{HG}

TABLE S2. DETs in Co-Cultured MCF7 MCF7 (both HG and HG->LG)

Gene symbol	Description	mRNA transcripts	log2 FC Co-culture LG	p-val	adjusted p-val	log2 FC Co-culture HG	p-val	adjusted p-val
INHBE	Inhibin beta E subunit	NM_031479	2.96	1.04E-13	6.87E-11	2.40	3.12E-10	1.02E-07
ANXA1	Annexin A1	NM_000700	2.67	2.02E-07	4.40E-05	3.15	1.59E-08	3.79E-06
MID1	Midline 1	NM_001193278	2.65	8.55E-13	5.38E-10	1.65	6.20E-06	5.97E-04
		NM_001193279	2.61	1.70E-12	1.05E-09	1.64	7.20E-06	6.68E-04
		NM_001098624	2.59	5.74E-14	4.18E-11	1.76	3.12E-07	5.60E-05
		NM_001193277	2.58	6.75E-14	4.68E-11	1.77	2.89E-07	5.24E-05
		NM_000381	2.58	5.56E-14	4.16E-11	1.77	2.64E-07	4.80E-05
		NM_033290	2.58	5.44E-14	4.16E-11	1.75	3.22E-07	5.72E-05
		NM_033289	2.55	8.06E-14	5.44E-11	1.79	1.64E-07	3.25E-05
		NM_001193280	2.52	2.15E-11	1.17E-08	1.68	7.25E-06	6.70E-04
PTGS1	Prostaglandin-endoperoxide synthase 1	NM_001271164	2.65	2.35E-17	2.41E-14	2.15	2.80E-12	1.33E-09
		NM_000962	2.59	3.09E-17	2.87E-14	2.13	1.92E-12	9.80E-10
		NM_001271368	2.58	3.13E-17	2.87E-14	2.10	2.85E-12	1.33E-09
		NM_001271367	2.57	4.41E-17	3.59E-14	2.08	4.39E-12	1.77E-09
		NM_080591	2.57	3.25E-17	2.87E-14	2.09	3.23E-12	1.39E-09
		NM_001271166	2.57	3.31E-17	2.87E-14	2.09	2.95E-12	1.36E-09
		NM_001271165	2.55	3.57E-17	3.00E-14	2.12	1.10E-12	6.38E-10
ACOX2	Acyl-CoA oxidase 2	NM_003500	2.02	1.47E-08	4.57E-06	2.25	5.52E-10	1.72E-07
GDF15	Growth differentiation factor 15	NM_004864	1.84	3.78E-12	2.27E-09	1.66	3.85E-10	1.25E-07
JPH2	Junctophilin 2	NM_020433	1.61	2.59E-06	3.51E-04	2.09	1.11E-09	3.30E-07
HOXB2	Homeobox B2	NM_002145	1.54	1.29E-05	1.25E-03	1.28	1.53E-04	8.03E-03
BGN	Biglycan	NM_001711	1.49	4.67E-06	5.77E-04	1.18	8.22E-05	5.04E-03
SPATS2L *	Spermatogenesis associated serine rich 2 like	NM_001100423	1.49	1.64E-20	3.24E-17	1.11	3.68E-12	1.56E-09
		NM_001282735	1.48	7.05E-20	1.12E-16	1.13	3.08E-12	1.39E-09
		NM_001282743	1.48	3.76E-20	6.94E-17	1.12	3.15E-12	1.39E-09
		NM_015535	1.48	1.20E-19	1.69E-16	1.13	4.43E-12	1.77E-09
		NM_001282744	1.47	7.25E-20	1.12E-16	1.13	3.22E-12	1.39E-09
		NM_001100422	1.47	6.23E-20	1.08E-16	1.13	2.77E-12	1.33E-09
		NM_001100424	1.46	1.22E-19	1.69E-16	1.13	2.05E-12	1.01E-09
GSTM3	Glutathione S-transferase mu 4	NM_000850	-0.93	1.42E-07	3.19E-05	-0.78	8.52E-06	7.56E-04
		NM_147148	-0.98	1.58E-06	2.43E-04	-0.87	1.89E-05	1.55E-03
		NM_000849	-1.32	6.52E-14	4.63E-11	-1.20	1.10E-11	4.20E-09
ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	NM_001042437	-1.20	4.71E-12	2.72E-09	-1.18	1.20E-11	4.48E-09
		NM_003896	-1.20	4.27E-12	2.52E-09	-1.17	1.54E-11	5.35E-09
PLEKHF1	Pleckstrin homology and FYVE domain containing 1	NM_024310	-1.33	3.84E-10	1.71E-07	-1.10	1.60E-07	3.22E-05
EFEMP1	EGF containing fibulin like extracellular matrix protein 1	NM_001039349	-1.33	3.51E-10	1.61E-07	-1.50	1.31E-12	7.28E-10
		NM_001039348	-1.33	3.01E-10	1.46E-07	-1.51	1.16E-12	6.56E-10
ID4	Inhibitor of DNA binding 4, HLH protein	NM_001546	-1.44	1.32E-06	2.08E-04	-1.70	1.23E-08	3.03E-06
LIN7A	lin-7 homolog A, crumbs cell polarity complex component	NM_004664	-1.54	2.99E-07	5.79E-05	-1.71	1.34E-08	3.27E-06
		NM_001324423	-1.56	1.37E-07	3.19E-05	-1.72	5.57E-09	1.44E-06
IL1R1 *	Interleukin 1 receptor type 1	NM_001320986	-1.67	3.94E-11	2.10E-08	-2.68	5.25E-23	1.19E-19
		NM_001320985	-1.94	4.09E-23	8.70E-20	-2.64	1.43E-40	4.87E-37
		NM_001320980	-1.97	3.42E-24	3.71E-20	-2.63	7.82E-41	3.04E-37
		NM_001320981	-1.95	7.79E-24	2.16E-20	-2.63	2.32E-41	1.55E-37
		NM_001320978	-1.95	6.24E-24	2.10E-20	-2.63	1.95E-41	1.55E-37
		NM_001320982	-1.95	6.84E-24	2.10E-20	-2.63	2.86E-41	1.55E-37
		NM_000877	-1.95	1.61E-23	3.71E-20	-2.62	2.97E-40	8.97E-37
		NM_001320984	-1.95	2.86E-24	1.58E-20	-2.63	8.45E-42	1.55E-37
		NM_001288706	-1.96	4.58E-24	1.81E-20	-2.63	2.60E-41	1.55E-37
		NM_001320983	-1.95	1.49E-23	1.58E-20	-2.63	6.85E-41	3.04E-37
PREX1	Phosphatidylinositol-3,4,5-trisphosphate dependent Rac exchange factor 1	NM_020820	-2.11	1.12E-05	1.10E-03	2.08	1.56E-05	1.30E-03
SLC7A8	Solute carrier family 7 member 8	NM_012244	-2.29	2.11E-05	1.80E-03	-2.48	4.10E-06	4.44E-04
		NM_001267036	-2.37	1.57E-05	1.44E-03	-2.47	6.89E-06	6.46E-04
		NM_182728	-2.38	1.32E-05	1.26E-03	-2.43	8.73E-06	7.67E-04
		NM_001267037	-2.39	1.34E-05	1.27E-03	-2.46	7.47E-06	6.81E-04
KCNMA1	Potassium calcium-activated channel subfamily M alpha 1	NM_001161352	-5.90	2.77E-07	5.59E-05	-5.10	8.09E-06	7.25E-04
		NM_002247	-5.94	2.22E-07	4.59E-05	-5.17	5.85E-06	5.70E-04
		NM_001322836	-5.94	2.22E-07	4.59E-05	-5.17	5.85E-06	5.70E-04
		NM_001161353	-5.94	2.22E-07	4.59E-05	-5.17	5.84E-06	5.70E-04
		NM_001271519	-5.94	2.22E-07	4.59E-05	-5.17	5.85E-06	5.70E-04
		NM_001322837	-5.94	2.22E-07	4.59E-05	-5.17	5.84E-06	5.70E-04
		NM_001322838	-5.95	1.34E-07	3.19E-05	-5.24	3.04E-06	3.56E-04
		NM_001271518	-6.02	1.61E-07	3.57E-05	-5.24	4.42E-06	4.60E-04
		NM_001322832	-6.06	1.41E-07	3.19E-05	-5.25	4.34E-06	4.56E-04
		NM_001322829	-6.06	1.41E-07	3.19E-05	-5.25	4.35E-06	4.56E-04
		NM_001014797	-6.06	1.41E-07	3.19E-05	-5.25	4.34E-06	4.56E-04
		NM_001322835	-6.06	1.41E-07	3.19E-05	-5.25	4.33E-06	4.56E-04
		NM_001322830	-6.06	1.40E-07	3.19E-05	-5.25	4.34E-06	4.56E-04

* UP-regulated in Co-cultured MCF7 HG->LG vs Co-cultured MCF7 HG

TABLE S3. DETs in Co-Cultured Adipo_{HG→LG} vs Adipo_{HG}

Gene symbol	Description	mRNA transcripts	log2 FC	p-val
HIST1H3A	Histone cluster 1 H3 family member a	NM_003529	1.15	7.37E-04
KRT8	Keratin 8	NM_001256282	0.84	4.52E-04
		NM_002273	0.84	4.39E-04
		NM_001256293	0.83	5.54E-04
AGAP9	ArfGAP with GTPase domain. ankyrin repeat and PH domain 9	NM_001190810	0.81	5.79E-03
CDC20	Cell division cycle 20	NM_001255	0.79	7.51E-05
ZNF326	Zinc finger protein 326	NM_182975	0.74	7.62E-03
		NM_181781	0.51	8.09E-03
YPEL1	Yippee like 1	NM_013313	0.70	1.73E-03
ATAD5	ATPase family. AAA domain containing 5	NM_024857	0.69	1.05E-03
KIF20B	Kinesin family member 20B	NM_016195	0.68	9.32E-03
CDCA5	Cell division cycle associated 5	NM_080668	0.67	1.01E-03
L2HGDH	L-2-hydroxyglutarate dehydrogenase	NM_001291311	0.62	1.87E-03
KDM4D	Lysine demethylase 4D	NM_018039	-2.14	1.27E-04
CFAP206	Cilia and flagella associated protein 206	NM_001031743	-2.20	6.93E-04
TACSTD2	Tumor-associated calcium signal transducer 2	NM_002353	-2.33	3.54E-04
DNM3	dynammin 3	NM_001278252	-2.41	1.68E-04
ENTPD3	Ectonucleoside triphosphate diphosphohydrolase 3	NM_001291960	-2.44	2.16E-03
		NM_001248	-2.44	2.28E-03
HPSE	Heparanase	NM_006665	-2.38	1.03E-04
		NM_001098540	-2.38	1.04E-04
		NM_001166498	-2.51	6.18E-05
		NM_001199830	-2.51	9.17E-05
KCTD4	Potassium channel tetramerization domain containing 4	NM_198404	-2.49	2.42E-04
RASL10B	RAS like family 10 member B	NM_033315	-2.56	1.73E-05
EFNB3	Ephrin B3	NM_018370	-2.94	9.28E-06
CD274	CD274 molecule	NM_001314029	-3.06	5.85E-04

TABLE S4. DETs in Co-Cultured Adipo vs Adipo (both Hg and HG->LG)

Gene symbol	Description	mRNA transcripts	log2 FC Co-culture LG	p-val	adjusted p-val	log2 FC Co-culture HG	p-val	adjusted p-val
MX1	MX dynamin like GTPase 1	NM_001178046	5.65	3.78E-26	2.84E-22	5.86	4.79E-28	4.42E-24
		NM_002462	5.63	4.11E-26	2.84E-22	5.84	4.62E-28	4.42E-24
		NM_001282920	5.61	2.58E-26	2.84E-22	5.75	9.31E-28	6.44E-24
		NM_001144925	5.58	3.30E-26	2.84E-22	5.79	3.32E-28	4.42E-24
IFI6	Interferon alpha inducible protein 6	NM_002038	2.89	2.38E-11	2.99E-08	3.05	1.63E-12	2.05E-09
		NM_022872	2.89	2.38E-11	2.99E-08	3.05	1.63E-12	2.05E-09
		NM_022873	2.89	2.38E-11	2.99E-08	3.05	1.63E-12	2.05E-09
ISG15	ISG15 ubiquitin-like modifier	NM_005101	2.84	9.52E-17	5.27E-13	3.07	2.42E-19	1.34E-15
IFI44	Interferon induced protein 44	NM_006417	2.58	1.64E-14	6.49E-11	2.50	6.29E-14	1.02E-10
IFIT3	Interferon induced protein with tetratricopeptide repeats 3	NM_001031683	2.53	8.15E-14	2.05E-10	2.64	6.66E-15	1.32E-11
		NM_001289759	2.53	8.15E-14	2.05E-10	2.64	6.66E-15	1.32E-11
		NM_001289758	2.46	7.94E-14	2.05E-10	2.70	2.39E-16	6.61E-13
		NM_001549	2.46	7.94E-14	2.05E-10	2.70	2.39E-16	6.61E-13
IFIT1	Interferon induced protein with tetratricopeptide repeats 1	NM_001270928	2.36	2.02E-06	7.65E-04	3.06	7.03E-10	5.57E-07
		NM_001270929	2.36	2.02E-06	7.65E-04	3.06	7.03E-10	5.57E-07
		NM_001548	2.36	2.02E-06	7.65E-04	3.06	7.03E-10	5.57E-07
		NM_001270927	2.36	2.07E-06	7.65E-04	3.06	7.29E-10	5.61E-07
		NM_001270930	2.35	1.89E-06	7.65E-04	3.06	6.06E-10	5.41E-07
PFKFB4	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	NM_001317135	2.07	1.60E-06	7.53E-04	2.21	3.07E-07	1.35E-04
		NM_001317136	2.06	1.93E-06	7.65E-04	2.21	3.66E-07	1.51E-04
		NM_001317134	2.06	1.80E-06	7.65E-04	2.21	3.03E-07	1.35E-04
		NM_001317138	2.05	1.88E-06	7.65E-04	2.21	2.99E-07	1.35E-04
		NM_004567	2.05	1.88E-06	7.65E-04	2.21	2.99E-07	1.35E-04
		NM_001317137	2.05	1.85E-06	7.65E-04	2.19	3.44E-07	1.48E-04
IFITM1	Interferon induced transmembrane protein 1	NM_003641	2.01	7.40E-10	7.32E-07	2.25	6.34E-12	7.64E-09
IFI27	Interferon alpha inducible protein 27	NM_001288958	1.75	8.49E-09	7.84E-06	1.74	9.58E-09	6.32E-06
DDX58	DExD/H-box helicase 58	NM_014314	1.74	2.81E-12	4.87E-09	1.90	2.62E-14	4.53E-11
IFI27	Interferon alpha inducible protein 27	NM_001288957	1.73	1.32E-08	1.11E-05	1.76	7.52E-09	5.08E-06
		NM_001288956	1.73	3.61E-08	2.78E-05	1.71	5.17E-08	2.87E-05
		NM_001288995	1.73	4.05E-08	3.03E-05	1.70	6.39E-08	3.40E-05
		NM_001288959	1.73	1.07E-08	9.55E-06	1.72	1.32E-08	8.49E-06
		NM_001288960	1.73	1.27E-08	1.10E-05	1.71	1.77E-08	1.12E-05
		NM_001288952	1.73	7.60E-08	5.26E-05	1.72	8.65E-08	4.35E-05
		NM_001288954	1.73	8.34E-08	5.63E-05	1.71	1.04E-07	5.14E-05
		NM_001130080	1.72	6.06E-08	4.41E-05	1.72	6.85E-08	3.58E-05
		NM_005532	1.72	6.68E-08	4.74E-05	1.71	8.29E-08	4.25E-05
ATP5A1	ATP synthase. H+ transporting. mitochondrial F1 complex. alpha subunit 1. cardiac muscle	NM_001257335	-0.15	3.07E-03	2.16E-01	-0.13	1.28E-02	1.58E-01
		NM_001001937	-0.15	3.14E-03	2.19E-01	-0.13	1.21E-02	1.55E-01
		NM_004046	-0.15	3.14E-03	2.19E-01	-0.13	1.21E-02	1.55E-01
		NM_001001935	-0.15	3.18E-03	2.20E-01	-0.13	1.23E-02	1.55E-01
SMG5 **	SMG5. nonsense mediated mRNA decay factor	NM_001323617	-0.19	1.36E-04	2.39E-02	-0.18	3.15E-04	2.83E-02
		NM_015327	-0.19	6.87E-05	1.37E-02	-0.18	2.08E-04	2.21E-02
		NM_001323616	-0.19	6.83E-05	1.37E-02	-0.18	2.23E-04	2.30E-02
CACYBP	Calcyclin binding protein	NM_014412	-0.25	4.45E-05	9.94E-03	0.14	1.70E-02	1.81E-01
NADK	NAD kinase	NM_001198995	-0.27	3.00E-04	4.42E-02	0.24	1.04E-03	5.16E-02
PLSCR4	Phospholipid scramblase 4	NM_001128305	-0.33	1.58E-06	7.53E-04	-0.22	1.73E-03	6.78E-02
		NM_020353	-0.33	8.14E-07	4.10E-04	-0.23	7.17E-04	4.36E-02
		NM_001128304	-0.33	8.75E-07	4.25E-04	-0.23	7.50E-04	4.50E-02
		NM_001177304	-0.34	2.21E-06	7.95E-04	-0.25	3.92E-04	3.06E-02
		NM_001128306	-0.34	2.47E-06	8.76E-04	-0.26	2.94E-04	2.75E-02
		NM_020422	-0.35	1.96E-04	3.23E-02	-0.24	9.16E-03	1.40E-01
TMEM159	Transmembrane protein 159							
ENPP4	Ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative)	NM_014936	-0.45	3.00E-04	4.42E-02	0.40	9.12E-04	4.89E-02

** DW-regulated in Co-Cultured Adipo HG->LG vs Co-Cultured Adipo HG

TABLE S5. Primer Pairs

Gene	Sense Primer (5'-3')	Tm	Antisense Primer (5'-3')	Tm	Size (bp)
<i>cPPARG</i>	GAGAAGGAGAAGCTGTTGGC	62	ATGGCCACCTCTTTGCTCT	58	272
<i>PLIN2</i>	GGGCTAGACAGGATTGAGGA	62	TCACTGCCCCCTTTGGTCTTG	62	181
<i>FABP4</i>	TGTGTGATGCTTTTGTAGGTAC	62	CTTCGTCAAATTCCTGGCCC	62	215
<i>LPIN2</i>	AGGAGGGAAAAATCTGAGGCA	60	GATCTGGTCTGAGGAGAGGC	64	215
<i>KLF6</i>	AGCCAGGTGACAAGGGAAAT	60	CACTCACACCCTTCCCATGA	62	172
<i>INSR</i>	CCCGTACTACCACTTCCAGG	64	CGATGGTCTTCTCGCCTTCT	62	236
<i>CEBPB</i>	TGCCATTTACAGACGGGAA	60	GCACCTTCTATGTACCAGGC	62	164
<i>EPAS1</i>	AAGGACCAATGCAGTACCCA	60	TGCTGCTGAAACTTGTCCAG	60	239
<i>WNT5B</i>	ACGCATCTGTCTTTGGGAGA	60	TACTCCACGTTGTCCCCAC	60	205
<i>CEBPD</i>	CCCCGCCATGTACGACGA	60	AGCAGGCGGGGAGCGGCA	64	210
<i>PPIA</i>	TACGGGTCCTGGCATCTTGT	62	GGTGATCTTCTTGCTGGTCT	60	196
<i>OCT4</i>	TCAGCCACATCGCCCAGCA	62	AGGGAAAGGGACCGAGGAG	62	242
<i>SOX2</i>	CAACCAGAAAAACAGCCCG	58	CAGCCGCTTAGCCTCGTC	60	196
<i>NANOG</i>	CCTGAAGAAAACTATCCATCC	60	GTTCTGGTCTTCTGTTTCTTG	60	209
<i>AXIN2</i>	GGTTCTGGCTATGTCTTTGCA	62	GCGATGCATTTCTCTCTGGA	60	162
<i>RPS23</i>	TCGTGGACTTCGTACTGCT	58	GCTGTGATTTTCTTGCCATTC	60	237
<i>CDKN1A</i>	AGGCCCGTGAGCGATGGAA	62	CGGCGTTTGGAGTGGTAGAA	62	337
<i>FAS</i>	GTGTTAATGCCCAAGTGA CTG	62	TCTGTGTACTCCTTCCCTTCT	62	214
<i>FABP3</i>	ACACTGGATGGAGGGAAACT	60	GGCAGAGTAGTAGTCAGCAA	60	180
<i>CEBPA</i>	GGCGGCGGCGACTTTGAC	62	GGCGGCTGGTAAGGGAAGA	62	248

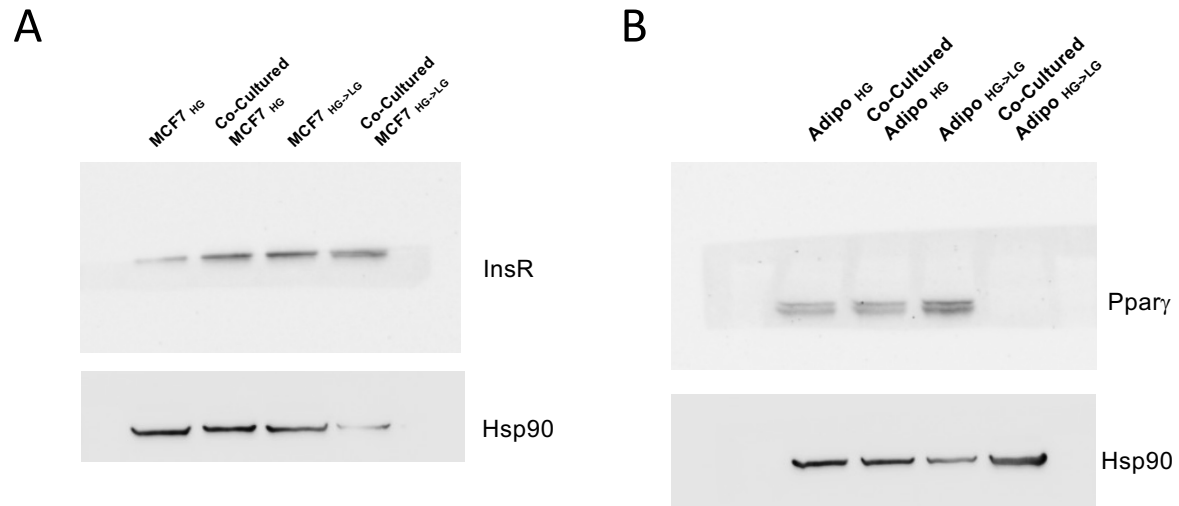
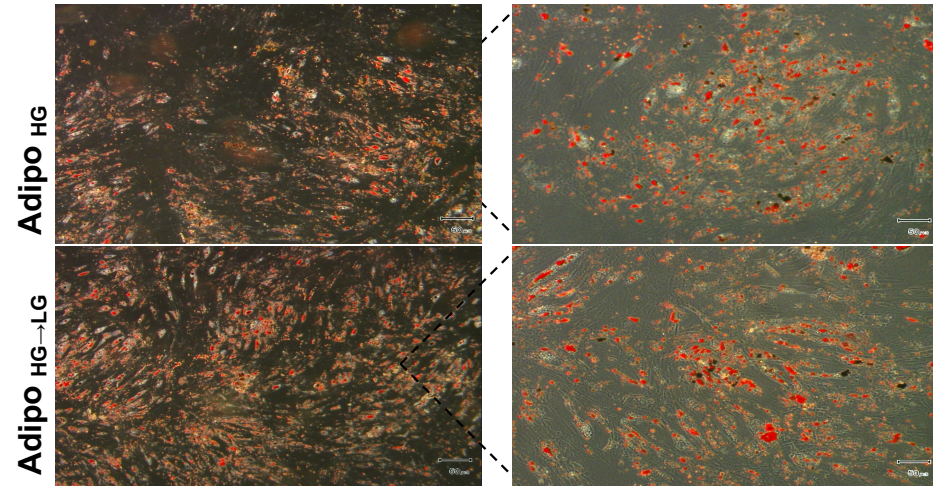


Figure S1. Additional images of original blots showing InsR (A) and PPAR γ (B) protein levels in Co-Cultured or mono-cultured MCF7 (A) and Adipo (B) while exposed to HG or HG->LG. Hsp90 was used as loading control. Immunoreactive bands were detected by using the ChemiDoc Imaging System (BioRad), with instantaneous exposure for Hsp90, exposure times of 3 minutes for PPAR γ and 5 minutes for InsR. The images were vertically cropped to display only samples relevant to this specific research. For HSP90, low-contrast images were shown.

A



B

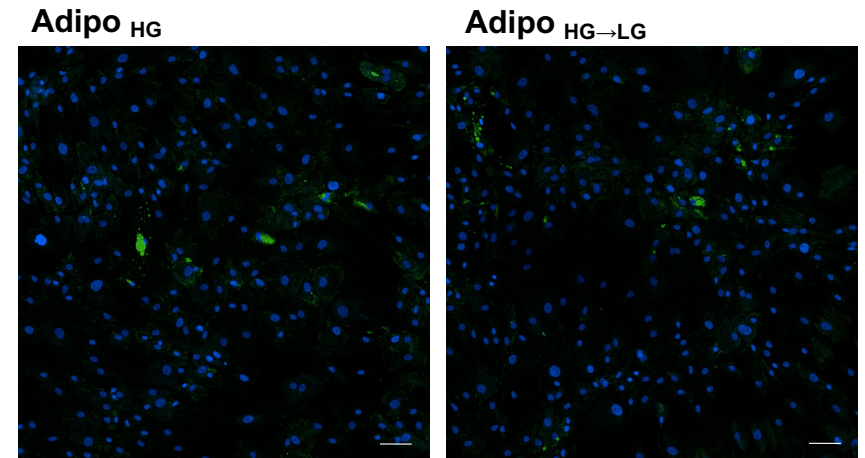


Figure S2. Effect of glucose onto adipocyte differentiation of MAd-MSC. MAd-MSCs were differentiated into mature adipocytes while exposed to basal 25mM glucose (High Glucose; HG). At the 15th days of the adipogenic process, cells were shifted to 5.5mM glucose (Low Glucose; LG). Representative images show lipid droplets accumulation evaluated by (a) Oil Red O Staining (4X and 10X magnification; scale bars 50 μm) and (b) confocal microscopy (10X air objective; scale bars 100 μm).