

Supplemental Table 1

Supplemental Table 1. List of the genes with upregulated expression comparing liver metastatic colon cancer L-1 and L-2 cells with non-metastatic SW480 and SW620 cells.

UniGene	Gene Symbol	Descriptions	Fold Change	P Value
Hs.654472	LIPC	Hepatic lipase	8.3	0.000225
Hs.614734	CD133	prominin-like 1 (PROML1)	7.6	0.000044
Hs.660143	APOBEC3G	phorbol-in-like protein (MDS019)	7.4	0.00007
Hs.65425	CALB1	calbindin 1	6.8	0.000052
Hs.374650	IFITM3	interferon induced transmembrane protein 3	5.5	0.000581
Hs.149239	EFNB2	Human LERK-5 (EPLG5)	5.1	0.001796
Hs.438102	IGFBP2	insulin-like growth factor binding protein 2	4.3	0.018281
Hs.2962	S100P	S100 calcium-binding protein P	4.2	0.000109
Hs.524910	FTH1	ferritin, heavy polypeptide 1	4.1	0.000169
Hs.291196	ATP1B1	ATPase, Na+K+ transporting, beta 1 polypeptide	4.1	0.000081
Hs.3416	ADFP	adipose differentiation-related protein	3.8	0.000132
Hs.458414	IFITM1	interferon induced transmembrane protein 1	3.8	0.000258
Hs.720143	FAAH	fatty acid hydroxylase	3.7	0.00006
Hs.461086	CDH1	cadherin 1, type 1, E-cadherin (epithelial)	3.7	0.000244
Hs.474783	TST	Thiosulfate sulfurtransferase (rhodanese)	3.7	0.00293
Hs.647116	HCA112	hepatocellular carcinoma-associated antigen 112	3.6	0.000732
Hs.507798	LHFP	lipoma HMGIC fusion partner	3.6	0.005565
Hs.508480	RAP2A	RAP2A, member of RAS oncogene family	3.6	0.000081
Hs.647090	LRS	Transmembrane protein 176B	3.5	0.023929
Hs.461086	Uvo	Human uvomorulin (E-cadherin)	3.5	0.003212
Hs.278658	KRT86	type II intermediate filament of hair keratin	3.5	0.000468
Hs.486470	EPB41L2	erythrocyte membrane protein band 4.1-like 2	3.5	0.001892
Hs.523847	G1P3	interferon induced 6-16 protein, isoform c	3.5	0.007543
Hs.90232	ProSAP1	proSAP-interacting protein 1	3.4	0.006532
Hs.486548	MAP7	microtubule-associated protein 7	3.3	0.011447
Hs.592095	SLC16A5	solute carrier family 16, member 5	3.3	0.000266
Hs.67397	HOXA1	Homeobox A1 {alternatively spliced}	3.3	0.021866
Hs.729392	RAB20	member RAS oncogene family	3.2	0.000468
Hs.525529	KCNMB4	potassium large conductance calcium-activated channel	3.2	0.031336
Hs.280932	PEX7	peroxisomal biogenesis factor 7	3.1	0.002617
Hs.148641	CTSH	Homo sapiens cathepsin H	3.1	0.000232
Hs.284141	TSPYL4	TSPYL-like 4	3.1	0.023926
Hs.258429	ERCC5	excision repair cross-complementing repair deficiency	3.1	0.001953
Hs.7277	PEX3	peroxisomal biogenesis factor 3	2.9	0.00415
Hs.439440	INTS6	integrator complex subunit 6	2.9	0.018555
Hs.562227	HSPG2	Human heparan sulfate proteoglycan	2.9	0.001221
Hs.153563	LY75	lymphocyte antigen 75	2.9	0.01416
Hs.47099	GaNAc-T12	polypeptide N-acetylgalactosaminyltransferase 12	2.9	0.008057
Hs.445981	CTNNA1	cadherin-associated protein	2.7	0.015525
Hs.279908	TFB1M	transcription factor B1, mitochondrial isoform	2.7	0.046143
Hs.166091	LIG4	DNA ligase IV	2.7	0.033505
Hs.709952	TOB1	transducer of ERBB2	2.7	0.001953
Hs.279257	PCMT1	protein-L-isoaspartate (D-aspartate) O-methyltransferase	2.7	0.001267
Hs.418367	NMU	neuromedin U	2.7	0.008057
Hs.659681	BCOR	BCL6 corepressor	2.6	0.005859
Hs.495250	CCBL1	cysteine conjugate-beta lyase, cytoplasmic	2.6	0.000805
Hs.78771	FGK1	phosphoglycerate kinase 1	2.6	0.011836
Hs.367900	PDCD2	programmed cell death 2	2.6	0.000322
Hs.643544	GW128	tyrosine 5-monooxygenase activation protein	2.5	0.00418
Hs.486835	RMND1	required for meiotic nuclear division 1 homolog	2.5	0.004863
Hs.520414	IFNGR1	interferon gamma receptor 1	2.5	0.014937
Hs.3352	HDAC2	histone deacetylase 2	2.5	0.003067
Hs.726226	SUCLA2	succinate-CoA ligase, ADP-forming, beta subunit	2.5	0.048995
Hs.12969	LOC54103	Homo sapiens cDNA: FLJ23094 fis, clone LNG07379	2.4	0.000266
Hs.507498	MIPEP	mitochondrial intermediate peptidase	2.4	0.013092
Hs.487046	SOD2	superoxide dismutase 2	2.3	0.024711
Hs.513617	MMP2	metalloproteinase 2	2.3	0.000219
Hs.306123	MAGEF1	Melanoma antigen family F, 1	2.3	0.003067
Hs.499725	ANK3	ankyrin 3, isoform 1	2.3	0.00023
Hs.249441	WEE1	wee1+ (S. pombe) homolog	2.3	0.001602
Hs.458358	TSPYL1	hypothetical protein	2.2	0.002617
Hs.445999	TCTEL1	t-complex-associated-testis-expressed 1-like 1	2.1	0.013092
Hs.655055	HSMNP1	uncharacterized hypothalamus protein	2.1	0.008689
Hs.530291	ANXA11	annexin XI	2.1	0.000339
Hs.448588	TNFRSF16	growth factor receptor associated protein	2.1	0.000805
Hs.643683	ITM2B	integral membrane protein 2B	2.1	0.000388
Hs.105940	JRKL	jerky (mouse) homolog-like	2	0.017001
Hs.654539	KIAA1253	Diff33 protein homolog	2	0.000762

Supplemental Table 2

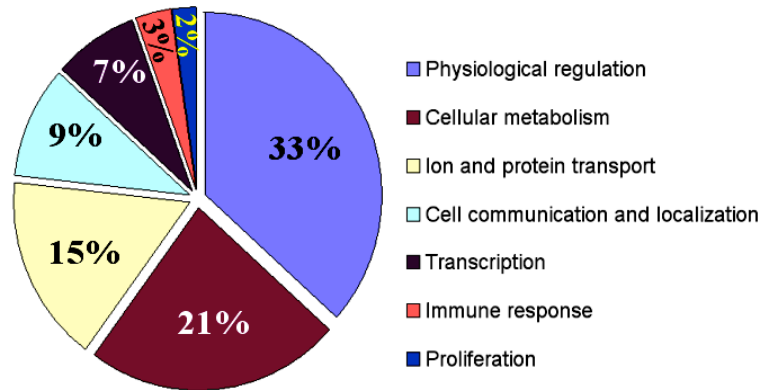
Supplemental Table 2. List of the genes with downregulated expression comparing liver metastatic colon cancer L-1 and L-2 cells with non-metastatic SW480 and SW620 cells.

UniGene	Gene Symbol	Descriptions	Fold Change	P Value
Hs_80296	PCP4	Purkinje cell protein 4	-7.8	0.00102
Hs_13397	ITGA6	integrin, alpha 6	-6.7	0.000052
Hs_645227	TGF-beta	Human transforming growth factor-beta	-6.5	0.00007
Hs_193557	PTPN14	s protein tyrosine phosphatase, non-receptor type 14	-5.6	0.002559
Hs_326801	ZNF6	zinc finger protein 6 (CMPX1)	-5.5	0.000509
Hs_170355	MEOX2	mesenchyme homeo box 2 (growth arrest-specific homeo box)	-5.2	0.000044
Hs_436803	VBP1	von Hippel-Lindau binding protein 1	-4.9	0.00039
Hs129452	DACH	dachshund (Drosophila) homolog	-4.8	0.004017
Hs_727516	DDAH1	dimethylarginine dimethylaminohydrolase 1	-4.6	0.00006
Hs_558396	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	-4.3	0.00011
Hs_522819	IRAK1	interleukin-1 receptor-associated kinase 1	-4.2	0.000662
Hs_522826	SLC10A3	Solute carrier family 10, member 3	-4.1	0.00007
Hs_701324	ARHGAP4	Rho GTPase activating protein 4	-4.1	0.000169
Hs_655087	MCTP1	multiple C2 domains, transmembrane 1	-3.8	0.00011
Hs_432822	MAN2A1	mannosidase, alpha, class 2A, member 1	-3.8	0.001953
Hs_380138	CHN1	chimerin (chimaerin) 1	-3.7	0.00293
Hs_517216	PEA15	phosphoprotein enriched in astrocytes 15	-3.7	0.000244
Hs_4747	DKC1	dyskeratosis congenita 1, dyskerin	-3.7	0.000754
Hs_57698	H105E3	NAD(P) dependent steroid dehydrogenase-like	-3.6	0.001102
Hs_558499	LOC51293	Homo sapiens 8D6 antigen	-3.5	0.00006
Hs_118400	SNL	sea urchin fascin homolog like	-3.5	0.000095
Hs_534404	RPL10	ribosomal protein L10	-3.4	0.013811
Hs_401929	DNASE1L1	Homo sapiens deoxyribonuclease I-like 1	-3.4	0.030976
Hs_606320	MYB	v-myb avian myeloblastosis viral oncogene homolog	-3.1	0.001796
Hs_6917	MTCP1	mature T-cell proliferation 1, clone MGC:2069	-3.1	0.000266
Hs_81874	MGST2	microsomal glutathione S-transferase 2	-3.1	0.000398
Hs_103183	FMR1	fragile X mental retardation 1	-3	0.039365
Hs_291904	DXS1357E	accessory proteins BAP31BAP29	-2.9	0.001892
Hs_58974	CCNA2	cyclin A2	-2.9	0.003585
Hs_354056	POR	NADPH-cytochrome P450 reductase mRNA	-2.8	0.000328
Hs_619593	MGC4175	Homo sapiens hypothetical protein MGC4175	-2.8	0.017001
Hs_24167	SYBL1	synaptobrevin-like 1	-2.8	0.001238
Hs_199695	MAC30	hypothetical protein	-2.7	0.035163
Hs_433291	ARD1	N-acetyltransferase, homolog of S. cerevisiae ARD1	-2.6	0.000562
Hs_303808	C2ORF3	Similar to chromosome 2 open reading frame 3	-2.6	0.000244
Hs_435512	PPP3CA	protein phosphatase 3, catalytic subunit, alpha isoform	-2.5	0.001221
Hs_472101	PLCB4	phospholipase C, beta 4	-2.5	0.00293
Hs_6838	ARHE	ras homolog gene family, member E	-2.5	0.010742
Hs_377010	CAD	carbamoyl-phosphate synthetase 2	-2.4	0.00293
Hs_303649	CCL2	Chemokine (C-C motif) ligand 2	-2.4	0.00415
Hs_410197	IDH3G	isocitrate dehydrogenase 3 (NAD+) gamma	-2.4	0.010742
Hs458336	POP3	popeye protein 3	-2.3	0.00415
Hs_98967	ATP6N1B	ATPase, H(+)-transporting noncatalytic accessory protein 1B	-2.3	0.001584
Hs_477352	PDIA5	protein disulfide isomerase-related protein	-2.2	0.00392
Hs_288193	KPNA4	importin alpha 3	-2.2	0.000268
Hs_195464	FLNA	filamin A, alpha (actin-binding protein-280)	-2.2	0.01024
Hs_54277	FAM50A	XAP-5 protein	-2.2	0.03011
Hs_727540	ADCY3	type III adenylyl cyclase	-2.2	0.000244
Hs_30174	SNAPC5	small nuclear RNA activating complex, polypeptide 5	-2.1	0.02032
Hs_278569	SNX17	Sorting nexin 17	-2.1	0.000419
Hs_15591	COPS6	COP9 subunit 6	-2	0.005232
Hs_203952	TRRAP	transformation/transcription domain-associated protein	-2	0.021984

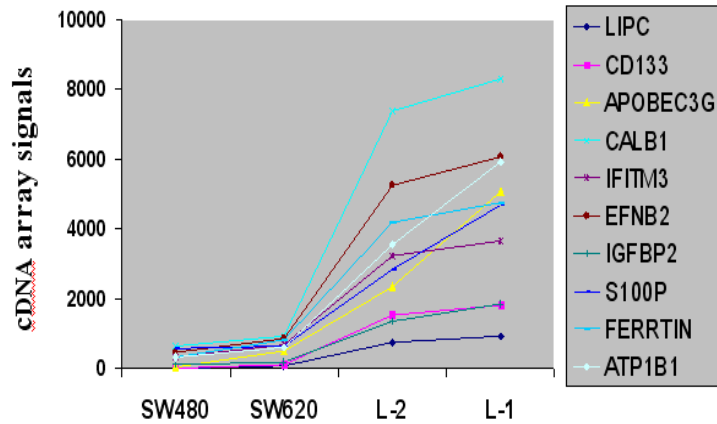
Supplemental Figure 1

Supplemental Figure 1. Selection of the genes that may mediate colorectal cancer hepatic metastasis. A, Functional-clustering analysis of the 68 genes upregulated in L-1 and L-2 cells compared with SW480 and SW620 cells. **B,** 10 genes with at least a 4-fold increase in their expression levels (according to cDNA microarray signals) in L-1 and L-2 cells were selected.

A

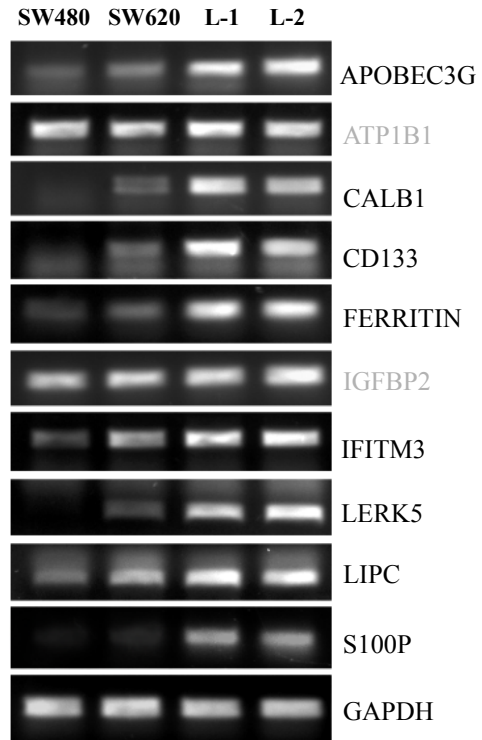


B



Supplemental Figure 2

Supplemental Figure 2. 10 gene expression levels in the SW480, SW620, L-1 and L-2 cells using RT-PCR analysis.



Supplemental Figure 3

Supplemental Figure 3. List of siRNA sequences for constructing specific shRNAs.

APOBEC3G

5'GATCCCCGTAAGATTGTGCTCAATTCAAGAGATTGAGCACAATCTTAGTACTTTTTA3'
5'AGCTTAAAAAGTACTAAGATTGTGCTCAATCTCTTGAATTGAGCACAATCTTAGTACGGG3'

CALB1

5'GATCCCCAGAAGAAAGTCTATGCTTATCAAGAGATAAGCATAGACTTTCTTCTTTTTTA3'
5'AGCTTAAAAAAGAAGAAAGTCTATGCTTATCTCTTGAATAAGCATAGACTTTCTTCTGGG3'

CD133

5'GATCCCCCATGAAAGCACAAGGTAATTCAAGAGATTACCTTGTGCTTTCATGTTTTTA3'
5'AGCTTAAAAACATGAAAGCACAAGGTAATCTCTTGAATTTACCTTGTGCTTTCATGGGG3'

FERRITIN

5'GATCCCCGGTACAAATCAAAGAACTTTTCAAGAGAAAAGTTCTTTGATTTGTACCTTTTTTA3'
5'AGCTTAAAAAGGTACAAATCAAAGAACTTTCTCTTGA AAAAGTTCTTTGATTTGTACCGGG3'

IFITM3

5'GATCCCCCAATAAAGTGCACGTGTTTTTCAAGAGAAAACACGTGCACTTTATTGTTTTTA3'
5'AGCTTAAAAACAATAAAGTGCACGTGTTTTCTCTTGA AAAACACGTGCACTTTATTGGGG3'

LERK5

5'GATCCCCGCAAAGATCTCTAGAGTTTTTCAAGAGAAAACCTCTAGAGATCTTTGCTTTTTTA3'
5'AGCTTAAAAAGCAAAGATCTCTAGAGTTTAGAGAACTTAAACTCTAGAGATCTTTGCGGG3'

LIPC

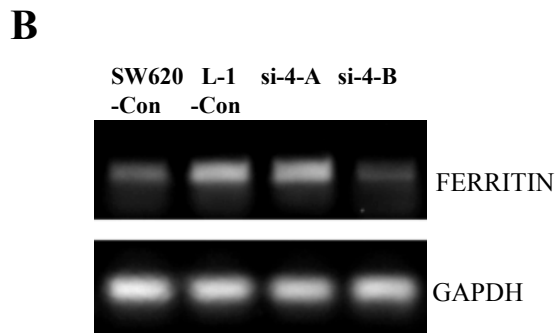
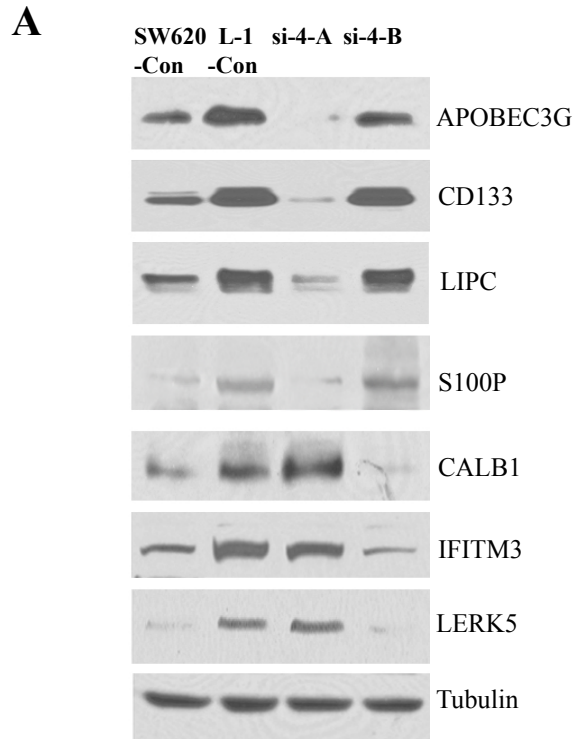
5'GATCCCCTAATGAAGACCCAGTGTAATTCAAGAGATTACACTGGGTCTTCATTATTTTTTA3'
5'AGCTTAAAAATAATGAAGACCCAGTGTAATCTCTTGAATTACACTGGGTCTTCATTAGGG3'

S100P

5'GATCCCCGCTCATGTACCTCTGATTATTCAAGAGATAATCAGAGGTACATGAGCTTTTTTA3'
5'AGCTTAAAAAGCTCATGTACCTCTGATTATCTCTTGAATAATCAGAGGTACATGAGCGGG3'

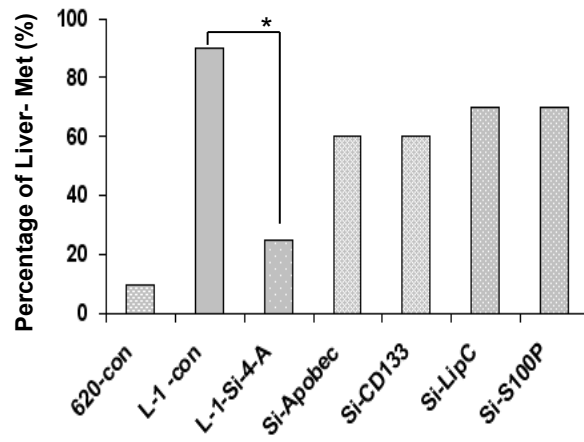
Supplemental Figure 4

Supplemental Figure 4. Validation of retroviral shRNAs in L-1 cells. **A**, shRNAs targeting Group A genes (APOBEC3G, CD133, LIPC, and S100P), and group B genes (CALB1, IFITM3, LERK5, and FERRITIN). The effectiveness of shRNAs (si-4A, si-4B) was validated by immunoblotting. **B**, Because of the unavailability of an antibody for FERRITIN, FERRITIN expression was detected by RT-PCR.

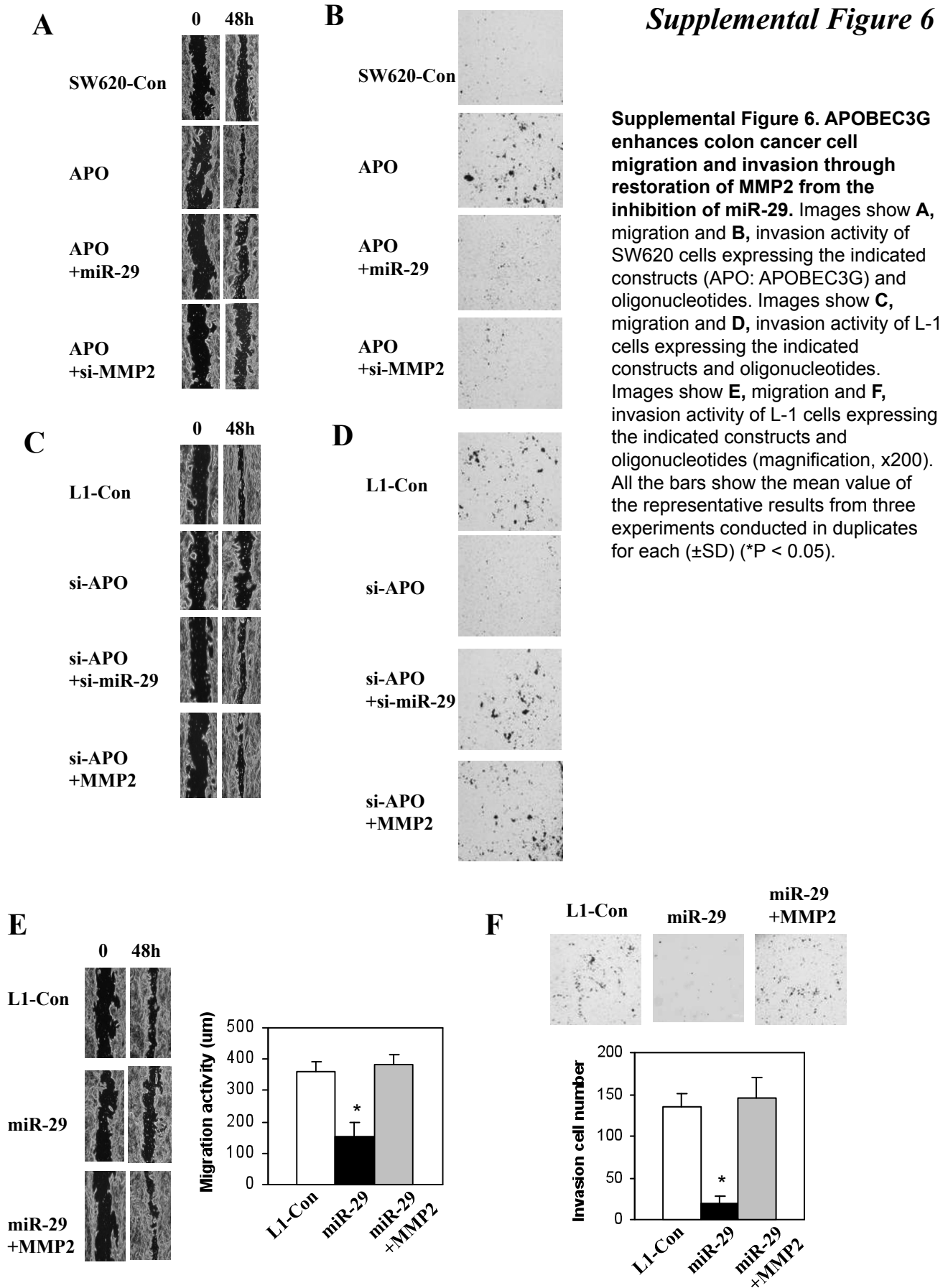


Supplemental Figure 5

Supplemental Figure 5. Knocking-down either one of the four Group A genes was not sufficient to decrease the liver metastasis rate in orthotopic animal model, compared with knocking-down all four genes (*P<0.05).



Supplemental Figure 6



Supplemental Figure 7

Supplemental Figure 7. Knocking-down APOBEC3G does not affect cell apoptosis and viability. L-1 cells knocked-down Apobec3G (APO) alone or knocked-down APOBEC3G and miR-29 together were measure for **A**, sub-G1 population detected by propidium iodide- flow cytometry analysis (n.s. non-significant); **B**, cell viability detected by MTT assay. Bars show the mean value of the representative results from three experiments conducted in duplicates for each (\pm SD).

