Supplementary Table 1. LogFC of candidate DEGs in choriocarcinoma.

ID	logFC	Gene.symbol	ID	logFC	Gene.symbol
Upregulated DEGs			**Downregulated DEGs**		
201131_s_at	6.9625187	CDH1	201110_s_at	-2.3859976	THBS1
209242_at	6.559966	PEG3	202484_s_at	-2.3902142	MBD2
221690_s_at	6.4585211	NLRP2	212993_at	-2.3931943	NACC2
204637_at	6.0593847	CGA	203102_s_at	-2.3948523	MGAT2
219529_at	5.9037535	CLIC3	212530_at	-2.4076347	NEK7
201650_at	5.6965555	KRT19	212771_at	-2.4116616	FAM171A1
219823_at	5.6128078	LIN28A	203243_s_at	-2.4120027	PDLIM5
209757_s_at	5.0380612	MYCN	209909_s_at	-2.4124992	TGFB2
214612_x_at	5.0379065	MAGEA6	206382_s_at	-2.4207037	BDNF
201839_s_at	4.9950881	EPCAM	205596_s_at	-2.422273	SMURF2
204724_s_at	4.9442599	COL9A3	212295_s_at	-2.4266278	SLC7A1
205081_at	4.9310658	CRIP1	216442_x_at	-2.4364651	FN1
204351_at	4.9251753	S100P	203987_at	-2.4427915	FZD6
209942_x_at	4.8877608	MAGEA6///MAGEA3	209040_s_at	-2.4459169	PSMB8
202525_at	4.8813919	PRSS8	202946_s_at	-2.4547014	BTBD3
204437_s_at	4.8796714	FOLR1	45297_at	-2.4584934	EHD2
204836_at	4.7940932	GLDC	201474_s_at	-2.4719752	ITGA3
202499_s_at	4.7138591	SLC2A3	202794_at	-2.482235	INPP1
218035_s_at	4.6423814	RBM47	207714_s_at	-2.4822967	SERPINH1
210074_at	4.4322237	CTSV	200794_x_at	-2.4908886	DAZAP2
210467_x_at	4.3976936	MAGEA12	212614_at	-2.4921641	ARID5B
202546_at	4.3849334	VAMP8	218651_s_at	-2.5126333	LARP6
205555_s_at	4.3691432	MSX2	219148_at	-2.5184369	PBK
209735_at	4.284078	ABCG2	215313_x_at	-2.5216421	HLA-A
202409_at	4.2454308	INS-IGF2///IGF2	204115_at	-2.5302393	GNG11
212964_at	4.2286195	HIC2	204141_at	-2.531647	TUBB2A
213523_at	4.2246408	CCNE1	205573_s_at	-2.5341625	SNX7
208146_s_at	4.2127124	CPVL	210139_s_at	-2.5371745	PMP22
204588_s_at	4.2068905	SLC7A7	218718_at	-2.54679	PDGFC

200606_at	4.1466021	DSP	204285_s_at	-2.5472628	PMAIP1
218186_at	3.9942991	RAB25	214500_at	-2.5525395	H2AFY
221245_s_at	3.9729582	FZD5	216438_s_at	-2.5553122	TMSB4X
215729_s_at	3.9466441	VGLL1	204135_at	-2.584004	FILIP1L
209604_s_at	3.9117233	GATA3	212203_x_at	-2.5871735	IFITM3
220139_at	3.8888106	DNMT3L	214104_at	-2.594476	GPR161
219228_at	3.8482337	ZNF331	202519_at	-2.601936	MLXIP
219814_at	3.8265668	MBNL3	212453_at	-2.6030536	KIF1BP
222088_s_at	3.8082437	SLC2A14///SLC2A3	201578_at	-2.6043031	PODXL
201909_at	3.7770245	RPS4Y1	221211_s_at	-2.6093691	MAP3K7CL
209324_s_at	3.7613025	RGS16	221728_x_at	-2.6230205	XIST
205286_at	3.7567236	TFAP2C	218782_s_at	-2.6354862	ATAD2
204039_at	3.7331461	CEBPA	221748_s_at	-2.6384718	TNS1
206269_at	3.6776311	GCM1	220014_at	-2.6446729	PRR16
202345_s_at	3.6642185	FABP5	208818_s_at	-2.6737521	COMT
209652_s_at	3.6626521	PGF	201825_s_at	-2.6837305	SCCPDH
210715_s_at	3.6318393	SPINT2	209210_s_at	-2.6851955	FERMT2
205030_at	3.6225526	FABP7	212887_at	-2.7080788	SEC23A
37117_at	3.6056698	PRR5-ARHGAP8///ARHGAP8	211671_s_at	-2.7101071	NR3C1
205387_s_at	3.5891815	CGB1///CGB8///CGB7///CGB5///CGB3	212314_at	-2.7383566	SEL1L3
202965_s_at	3.5857235	CAPN6	203510_at	-2.7492264	MET
211737_x_at	3.5531314	PTN	205904_at	-2.7607491	MICA
209301_at	3.5147479	CA2	204159_at	-2.7638653	CDKN2C
214603_at	3.4820017	MAGEA2B///MAGEA2	202760_s_at	-2.7666903	PALM2-AKAP2///AKAP2
212737_at	3.4715262	GM2A	212739_s_at	-2.7892787	NME4
219010_at	3.469412	C1orf106	221011_s_at	-2.7898937	LBH
208885_at	3.4633421	LCP1	209946_at	-2.7931387	VEGFC
209031_at	3.454259	CADM1	209524_at	-2.7983664	HDGFRP3
204364_s_at	3.4507996	REEP1	213428_s_at	-2.8009271	COL6A1
220668_s_at	3.4164807	DNMT3B	217826_s_at	-2.8023462	UBE2J1
218764_at	3.4114633	PRKCH	218005_at	-2.8079056	ZNF22
203126_at	3.3975533	IMPA2	204521_at	-2.8087672	FAM216A

215440_s_at	3.3707005	BEX4	203939_at	-2.8149911	NT5E
212057_at	3.3477748	GSE1	211564_s_at	-2.8262103	PDLIM4
212070_at	3.3112588	ADGRG1	201152_s_at	-2.8270052	MBNL1
203638_s_at	3.2860893	FGFR2	202628_s_at	-2.8338719	SERPINE1
219121_s_at	3.2846767	ESRP1	212012_at	-2.8381513	PXDN
219932_at	3.2727223	SLC27A6	213093_at	-2.841262	PRKCA
208096_s_at	3.1970703	COL21A1	212185_x_at	-2.8537095	MT2A
218454_at	3.1786126	PLBD1	218888_s_at	-2.8571782	NETO2
217744_s_at	3.1622768	PERP	211458_s_at	-2.8581717	GABARAPL3///GABARAPL1
202826_at	3.1569022	SPINT1	203789_s_at	-2.8717846	SEMA3C
220225_at	3.1075835	IRX4	202983_at	-2.8734781	HLTF
220136_s_at	3.1036574	CRYBA2	203148_s_at	-2.8756434	TRIM14
218404_at	3.0842759	SNX10	212154_at	-2.8913341	SDC2
202790_at	2.9999624	CLDN7	203417_at	-2.9103402	MFAP2
210367_s_at	2.9823138	PTGES	202845_s_at	-2.9170707	RALBP1
209723_at	2.981811	SERPINB9	204421_s_at	-2.9199539	FGF2
204416_x_at	2.9512144	APOC1	211071_s_at	-2.9329121	MLLT11
209448_at	2.9497027	HTATIP2	201631_s_at	-2.9411407	IER3
202688_at	2.9291537	TNFSF10	200974_at	-2.9747922	ACTA2
210274_at	2.9188173	MAGEA8	201462_at	-2.9964636	SCRN1
208510_s_at	2.9095517	PPARG	221773_at	-3.0152618	ELK3
212611_at	2.9070617	DTX4	209356_x_at	-3.0188241	EFEMP2
205865_at	2.8639192	ARID3A	208966_x_at	-3.0216697	IFI16
204731_at	2.8582289	TGFBR3	204073_s_at	-3.0323551	MYRF
205829_at	2.8475361	HSD17B1	215016_x_at	-3.0337409	DST
201428_at	2.8413697	CLDN4	209156_s_at	-3.0338115	COL6A2
202286_s_at	2.825582	TACSTD2	201315_x_at	-3.0394173	IFITM2
206683_at	2.8217647	ZNF165	213455_at	-3.0518443	FAM114A1
218967_s_at	2.7862674	PTER	205967_at	-3.0538278	HIST2H4B///HIST4H4///HIST2H4A///HIST1H4L///HIST1H4E///HIST1H4B///HIST1H4H///HIST1H4C///HIST1H4J///HIST1H4K///HIST1H4F///HIST1H4D///HIST1H4A///HIST1H4I

203767_s_at	2.7549178	STS	204992_s_at	-3.0594099	PFN2
205710_at	2.7517133	LRP2	200985_s_at	-3.0759796	CD59
209758_s_at	2.7429191	MFAP5	201850_at	-3.0805146	CAPG
202800_at	2.7296546	SLC1A3	219778_at	-3.1355202	ZFPM2
204672_s_at	2.7150961	ANKRD6	203851_at	-3.1371783	IGFBP6
207085_x_at	2.697452	CSF2RA	201579_at	-3.1475539	FAT1
219461_at	2.6883962	PAK6	206825_at	-3.1605738	OXTR
209016_s_at	2.6812301	KRT7	213094_at	-3.1661372	ADGRG6
209822_s_at	2.6430367	VLDLR	201464_x_at	-3.1837305	JUN
208650_s_at	2.6308021	CD24	219654_at	-3.1851474	HACD1
38918_at	2.6167875	SOX13	215446_s_at	-3.1989765	LOX
202454_s_at	2.5935931	ERBB3	210302_s_at	-3.1990127	MAB21L2
219142_at	2.5696987	RASL11B	218380_at	-3.2054539	LOC728392
204309_at	2.5589676	CYP11A1	219117_s_at	-3.2139169	FKBP11
221766_s_at	2.5219122	FAM46A	202718_at	-3.2173525	IGFBP2
203185_at	2.5092865	RASSF2	208998_at	-3.2231454	UCP2
213030_s_at	2.4916299	PLXNA2	209581_at	-3.2287246	PLA2G16
220161_s_at	2.4742882	EPB41L4B	201841_s_at	-3.2317488	HSPB1
213050_at	2.4706436	COBL	210095_s_at	-3.2444609	IGFBP3
204087_s_at	2.4702059	SLC5A6	201842_s_at	-3.2589811	EFEMP1
213133_s_at	2.4476246	LOC101060817///GCSH	201150_s_at	-3.2654929	TIMP3
203786_s_at	2.4441059	TPD52L1	201041_s_at	-3.2659027	DUSP1
218963_s_at	2.4330877	KRT23	200762_at	-3.2722633	DPYSL2
212762_s_at	2.4143047	TCF7L2	210764_s_at	-3.2849993	CYR61
207076_s_at	2.4085244	ASS1	201324_at	-3.2892799	EMP1
46665_at	2.345595	SEMA4C	209803_s_at	-3.2910508	PHLDA2
202712_s_at	2.3338626	CKMT1A///CKMT1B	201522_x_at	-3.2921739	SNURF///SNRPN
203381_s_at	2.3327772	APOE	210105_s_at	-3.316063	FYN
203074_at	2.3301863	ANXA8L1///ANXA8	214085_x_at	-3.3254088	GLIPR1
213707_s_at	2.3276717	DLX5	205990_s_at	-3.3452337	WNT5A
201849_at	2.3233637	BNIP3	204881_s_at	-3.3508429	UGCG
202113_s_at	2.3085771	SNX2	208850_s_at	-3.3597248	THY1
202263_at	2.3058001	CYB5R1	203108_at	-3.4053548	GPRC5A

212415_at	2.3005972	septin 6
221802_s_at	2.2994673	SHTN1
218170_at	2.2863485	ISOC1
220138_at	2.2779845	HAND1
209806_at	2.2690863	HIST1H2BK
210827_s_at	2.2687129	ELF3
205632_s_at	2.2514636	PIP5K1B
221664_s_at	2.2480754	F11R
201272_at	2.2322946	AKR1B1
215177_s_at	2.2267281	ITGA6
210859_x_at	2.2265339	CLN3
205000_at	2.2177618	DDX3Y
218499_at	2.2166675	STK26
203124_s_at	2.2166299	SLC11A2
209710_at	2.2154082	GATA2
204044_at	2.2114613	QPRT
217707_x_at	2.2020828	SMARCA2
35148_at	2.191809	TJP3
201236_s_at	2.1877629	BTG2
47069_at	2.1763575	PRR5
214369_s_at	2.1515952	RASGRP2
221841_s_at	2.1439636	KLF4
216092_s_at	2.1428528	SLC7A8
206117_at	2.1221184	TPM1
204484_at	2.088286	PIK3C2B
221609_s_at	2.0784872	WNT6
201801_s_at	2.0778809	SLC29A1
219761_at	2.0662018	CLEC1A
204400_at	2.0615216	EFS
206385_s_at	2.0608787	ANK3
218731_s_at	2.0601132	VWA1
218507_at	2.0556559	HILPDA
219147_s_at	2.0455625	NMRK1
201811_x_at	2.0454916	SH3BP5

212646_at	-3.4343153	RFTN1
212386_at	-3.4347254	TCF4
203083_at	-3.4452165	THBS2
204017_at	-3.4490302	KDELR3
202998_s_at	-3.4534356	LOXL2
221269_s_at	-3.4677147	SH3BGRL3
209094_at	-3.4734053	DDAH1
201860_s_at	-3.4782946	PLAT
201995_at	-3.4925526	EXT1
201300_s_at	-3.4953301	PRNP
204475_at	-3.4999821	MMP1
202096_s_at	-3.5054547	TSPO
213069_at	-3.5102396	HEG1
204337_at	-3.5129535	RGS4
202732_at	-3.5926168	PKIG
201136_at	-3.6063411	PLP2
206414_s_at	-3.6613716	ASAP2
207480_s_at	-3.6771302	MEIS2
213906_at	-3.7004299	MYBL1
201540_at	-3.7533218	FHL1
202350_s_at	-3.7913589	LOC100506558///MATN2
209386_at	-3.8089674	TM4SF1
204602_at	-3.8090388	DKK1
202458_at	-3.8100343	PRSS23
218025_s_at	-3.8435326	ECI2
212724_at	-3.8612036	RND3
201431_s_at	-3.8790028	DPYSL3
201470_at	-3.9044204	GSTO1
202555_s_at	-3.9495746	MYLK
207039_at	-3.9548912	CDKN2A
202363_at	-3.9622499	SPOCK1
217728_at	-4.0059936	S100A6
204083_s_at	-4.0247761	TPM2
209290_s_at	-4.0489231	NFIB

201998_at	2.0285112	ST6GAL1	202766_s_at	-4.0746809	FBN1
201015_s_at	2.0156519	JUP	213258_at	-4.1939966	TFPI
204717_s_at	2.0072799	SLC29A2	201744_s_at	-4.2151951	LUM
211795_s_at	2.0044933	FYB	211959_at	-4.2248976	IGFBP5
204984_at	1.9947143	GPC4	201666_at	-4.2618106	TIMP1
218346_s_at	1.9855101	SESN1	201508_at	-4.3243196	IGFBP4
202449_s_at	1.982758	RXRA	212190_at	-4.3623718	SERPINE2
201403_s_at	1.9818084	MGST3	218468_s_at	-4.3635211	GREM1
201417_at	1.9797076	SOX4	209651_at	-4.3866402	TGFB1I1
202890_at	1.9780349	MAP7	201058_s_at	-4.3904809	MYL9
205864_at	1.9744383	SLC7A4	209278_s_at	-4.4279892	TFPI2
204515_at	1.9721103	HSD3B1	201669_s_at	-4.4639047	MARCKS
203775_at	1.9642719	SLC25A13	201667_at	-4.5339402	GJA1
215017_s_at	1.9600482	FNBP1L	203060_s_at	-4.5618747	PAPSS2
33323_r_at	1.956688	SFN	214247_s_at	-4.6229345	DKK3
212136_at	1.9456735	ATP2B4	201952_at	-4.6557027	ALCAM
202023_at	1.9436104	EFNA1	210220_at	-4.668718	FZD2
44783_s_at	1.9405923	HEY1	208789_at	-4.6915474	PTRF
208474_at	1.9332574	CLDN6	203570_at	-4.714006	LOXL1
202085_at	1.9233907	TJP2	203729_at	-4.7857216	EMP3
205180_s_at	1.9148941	ADAM8	201506_at	-4.8173403	TGFBI
219763_at	1.9143253	DENND1A	212233_at	-4.8881178	MAP1B
208579_x_at	1.9128455	H2BFS	210809_s_at	-4.8989316	POSTN
202295_s_at	1.901602	CTSH	212667_at	-4.9114664	SPARC
209122_at	1.8952234	PLIN2	221729_at	-4.9244534	COL5A2
219316_s_at	1.8903365	FLVCR2	206157_at	-4.9822934	PTX3
213624_at	1.8878642	SMPDL3A	201105_at	-4.9882452	LGALS1
204217_s_at	1.8768499	RTN2	201859_at	-5.1533652	SRGN
202625_at	1.8473937	LYN	202976_s_at	-5.2559531	RHOBTB3
212919_at	1.8392118	DCP2	212063_at	-5.2644583	CD44
220289_s_at	1.8370174	AIM1L	209101_at	-5.3922257	CTGF
209848_s_at	1.8369636	PMEL	201163_s_at	-5.4451343	IGFBP7
204224_s_at	1.8252385	GCH1	200600_at	-5.4679768	MSN
215785_s_at	1.8245996	CYFIP2	205547_s_at	-5.625041	TAGLN

201549_x_at	1.8178212	KDM5B	202016_at	-5.7484468	MEST
222035_s_at	1.8175067	PAPOLA	201387_s_at	-5.76438	UCHL1
219863_at	1.8169089	HERC5	202686_s_at	-5.8124314	AXL
216929_x_at	1.8077177	ABO	202237_at	-5.8740511	LOC101928916///NNMT
219355_at	1.8050843	CXorf57	202310_s_at	-5.9427998	COL1A1
222240_s_at	1.8042456	ISYNA1	209118_s_at	-5.969484	TUBA1A
212841_s_at	1.7980905	PPFIBP2	215076_s_at	-6.4522917	COL3A1
208296_x_at	1.7942368	TNFAIP8	201426_s_at	-6.6674864	VIM
203225_s_at	1.7939803	RFK	208782_at	-6.906946	FSTL1

Supplementary Table 2. LogFC of 140 candidate DEMs from GSE32346 and GSE130489 in choriocarcinoma.

DEMs	LogFC (GSE130489)	logFC （GSE32346）	DEMs	logFC （GSE130489）	logFC （GSE32346）
Upregulated DEMs			**Downregulated DEMs**		
hsa-miR-331-3p	3.97	3.83988	hsa-miR-522	-12.1	-13.43924
hsa-miR-433	11.3	13.90422	hsa-miR-517c	-17.4	-16.0155
hsa-let-7e	6.43	6.78341	hsa-miR-518d-5p	-14.1	-13.738
hsa-miR-574-3p	4.82	5.15491	hsa-miR-516a-5p	-11.6	-11.42127
hsa-let-7f	13.1	15.07193	hsa-miR-519c-3p	-14.2	-14.686
hsa-miR-126	4.88	5.37099	hsa-miR-520f	-13.2	-12.70239
hsa-miR-145	2.84	3.38113	hsa-miR-520a-5p	-12.3	-12.43449
hsa-miR-132	3.72	4.13704	hsa-miR-520g	-13.6	-12.32072
hsa-miR-340	4.71	5.39538	hsa-miR-483-5p	-4.89	-5.10129
hsa-miR-410	10.9	12.38457	hsa-miR-517a	-15	-16.07375
hsa-miR-369-3p	6.61	7.49074	hsa-miR-375	-11.1	-10.74841
hsa-miR-935	17.1	12.36823	hsa-miR-515-3p	-14.4	-13.72839
hsa-miR-147	4.24	5.97349	hsa-miR-520e	-6.73	-6.89354
hsa-miR-125b	8.39	9.04702	hsa-miR-519d	-12.7	-14.00106
hsa-miR-411	13.7	15.58015	hsa-miR-516b	-11.8	-10.98254
hsa-let-7c	8.9	10.94958	hsa-miR-518c	-13.4	-13.55799
hsa-miR-301a	5.74	6.20744	hsa-miR-526b	-14.4	-13.92791
hsa-miR-15b	3.79	4.39013	hsa-miR-518f	-13	-12.68424
hsa-miR-100	9	9.66957	hsa-miR-515-5p	-15.7	-15.02586
hsa-miR-148b	3.18	3.75634	hsa-miR-519e	-13	-12.65281
hsa-let-7b	16.9	18.43336	hsa-miR-934	-6.98	-18.84203
hsa-miR-642	5.44	6.12036	hsa-miR-520a-3p	-13.6	-12.97076
hsa-miR-218	8.36	8.48809	hsa-miR-517	-12.4	-15.95335
hsa-miR-758	12.3	13.20144	hsa-miR-372	-16.2	-15.84692
hsa-let-7d	7.81	8.49914	hsa-miR-518e	-15.9	-17.05001
hsa-miR-127-3p	13.4	16.25119	hsa-miR-512-5p	-15.6	-15.28283
hsa-miR-337-5p	11.3	12.68994	hsa-miR-521	-10	-9.80591
hsa-miR-183	2.56	3.29083	hsa-miR-524-5p	-6.38	-6.2933
hsa-miR-876-5p	5.38	7.47904	hsa-miR-519a	-14.2	-15.12709

hsa-miR-99a	8.94	8.9486
hsa-miR-125a-5p	3.28	3.3682
hsa-miR-338-3p	10.6	11.10964
hsa-miR-133b	8.48	7.96669
hsa-miR-330-3p	2.87	3.54234
hsa-miR-598	13.3	13.88619
hsa-miR-329	8.71	13.32066
hsa-miR-744	2.7	3.80686
hsa-miR-361-5p	2.51	2.98871
hsa-miR-301b	3.77	4.49966
hsa-miR-345	3.3	3.86239
hsa-miR-146b-5p	4.01	4.15219
hsa-miR-324-5p	6.19	7.26626
hsa-miR-370	15.6	16.56394
hsa-miR-873	7.49	8.98087
hsa-miR-485-3p	12.2	13.75477
hsa-miR-194	3.59	5.14564
hsa-miR-886-5p	8.54	9.05811
hsa-miR-487a	9.64	10.68054
hsa-miR-138	8.39	8.06464
hsa-miR-296-5p	4.66	4.89705
hsa-miR-222	4.92	5.24896
hsa-miR-539	15.4	17.06524
hsa-miR-369-5p	7.94	8.81589
hsa-miR-99b	4.2	4.95951
hsa-miR-544	4.61	6.49099
hsa-miR-376a	11.3	12.00286
hsa-let-7g-4395393	8.54	10.53196
hsa-miR-143	9.03	11.04966
hsa-miR-495	13.6	14.24634
hsa-miR-134	15.5	16.13129
hsa-miR-140-5p	3.18	3.37244
hsa-miR-10a	15.1	16.23664
hsa-miR-654-5p	12.7	13.26434

hsa-miR-517b	-17.4	-17.65231
hsa-miR-520b	-13.4	-13.2038
hsa-miR-373	-10.7	-10.5139
hsa-miR-371-3p	-13.2	-12.81666
hsa-miR-525-3p	-15.7	-15.25869
hsa-miR-523	-11	-10.30649
hsa-miR-525-5p	-11.6	-11.09259
hsa-miR-512-3p	-18	-20.48689
hsa-miR-518b	-13.1	-14.76404

hsa-miR-487b	12.1	13.57731
hsa-miR-889	12.6	13.64579
hsa-miR-21	4.2	4.72501
hsa-miR-376b	5.61	7.99429
hsa-miR-221	5.04	6.10226
hsa-miR-541	11.7	11.87434
hsa-miR-615-3p	14.8	15.45659
hsa-miR-196b	13.3	12.87756
hsa-miR-10b	16.5	16.86834
hsa-miR-133a	3.36	4.96634
has-miR-155	15.8	17.46989
hsa-miR-128	2.8	3.83271
hsa-miR-24	4.23	4.20163
hsa-miR-137	14	15.11784
hsa-miR-328	5.47	6.41962
hsa-miR-146a	5.61	7.64234
hsa-miR-655	11.7	14.35806
hsa-miR-30b	2.09	2.64874
hsa-miR-409-5p	10.6	11.78454
hsa-miR-382	15.6	16.72119
hsa-miR-493	8.53	8.49749
hsa-miR-29a	5.41	5.46323
hsa-miR-876-3p	5.31	7.48709
hsa-miR-192	3.41	4.16486
hsa-miR-376c	14.5	17.31459
hsa-miR-153	3.58	4.97439
hsa-miR-28-5p	3.31	3.81311
hsa-miR-496	5.14	6.98404
hsa-miR-379	14.1	15.13389
hsa-miR-152	13.4	16.4739
hsa-miR-98	11.9	10.03796
hsa-miR-299-5p	11.1	13.19404
hsa-miR-29b-3p	5.83	6.60099
hsa-miR-323-3p	7.96	10.27258

hsa-miR-423-5p	2.81	4.06328
hsa-miR-103	3.77	4.40215
hsa-miR-589	3.12	4.68261
hsa-miR-324-3p	5.21	5.93032

Abbreviations: DEMs,differentially expressed miRNAs.

Supplementary Table 3. GO analysis of candidate DEGs in choriocarcinoma.

Term	Description	Count	P-Value	Corrected P-value
GO Biological Processes				
GO:0000902	cell morphogenesis	65	7.75E-14	3.41E-12
GO:0000904	cell morphogenesis involved in differentiation	49	2.36E-11	7.09E-10
GO:0001568	blood vessel development	53	3.53E-15	1.70E-13
GO:0001932	regulation of protein phosphorylation	63	3.22E-07	2.26E-06
GO:0004672	protein kinase activity	56	2.79E-07	2.23E-06
GO:0008233	peptidase activity	45	3.06E-05	6.11E-05
GO:0008284	positive regulation of cell population proliferation	47	1.10E-07	1.21E-06
GO:0008285	negative regulation of cell population proliferation	47	1.82E-11	5.64E-10
GO:0009790	embryo development	62	2.71E-12	1.03E-10
GO:0009887	animal organ morphogenesis	75	9.90E-19	5.84E-17
GO:0009968	negative regulation of signal transduction	63	1.99E-09	4.38E-08
GO:0010648	negative regulation of cell communication	66	9.23E-09	1.66E-07
GO:0016301	kinase activity	65	7.73E-08	9.27E-07
GO:0016477	cell migration	96	1.62E-21	1.02E-19
GO:0023014	signal transduction by protein phosphorylation	44	3.02E-06	1.51E-05
GO:0023057	negative regulation of signaling	66	9.77E-09	1.66E-07
GO:0030198	extracellular matrix organization	42	5.07E-18	2.84E-16
GO:0030334	regulation of cell migration	64	1.94E-17	1.05E-15
GO:0030855	epithelial cell differentiation	49	2.69E-11	7.81E-10
GO:0035239	tube morphogenesis	63	3.32E-17	1.76E-15
GO:0035295	tube development	77	1.31E-20	8.14E-19
GO:0042127	regulation of cell population proliferation	85	1.26E-13	5.43E-12
GO:0043067	regulation of programmed cell death	68	6.32E-08	8.85E-07
GO:0043069	negative regulation of programmed cell death	45	6.97E-07	4.18E-06
GO:0043549	regulation of kinase activity	52	4.32E-10	1.12E-08
GO:0045595	regulation of cell differentiation	93	4.02E-14	1.81E-12
GO:0045597	positive regulation of cell differentiation	59	4.99E-12	1.79E-10
GO:0045859	regulation of protein kinase activity	47	1.66E-09	3.82E-08

GO:0048468	cell development	109	5.69E-17	2.90E-15
GO:0048513	animal organ development	166	2.61E-23	1.67E-21
GO:0048514	blood vessel morphogenesis	48	2.73E-14	1.26E-12
GO:0048585	negative regulation of response to stimulus	80	1.39E-11	4.59E-10
GO:0048598	embryonic morphogenesis	44	5.59E-12	1.96E-10
GO:0048729	tissue morphogenesis	57	2.97E-18	1.72E-16
GO:0051093	negative regulation of developmental process	57	4.05E-11	1.13E-09
GO:0051094	positive regulation of developmental process	80	1.49E-15	7.29E-14
GO:0051248	negative regulation of protein metabolic process	54	6.35E-08	8.26E-07
GO:0051270	regulation of cellular component movement	71	4.34E-18	2.47E-16
GO:0051338	regulation of transferase activity	56	4.55E-10	1.14E-08
GO:0060284	regulation of cell development	51	1.33E-08	2.12E-07
GO:0060429	epithelium development	81	7.92E-18	4.36E-16
GO:0060548	negative regulation of cell death	49	2.44E-07	2.20E-06
GO:0070848	response to growth factor	51	1.96E-13	8.21E-12
GO:0071363	cellular response to growth factor stimulus	49	5.53E-13	2.21E-11
GO:0072359	circulatory system development	72	5.59E-17	2.91E-15
GO:2000026	regulation of multicellular organismal development	113	3.66E-20	2.23E-18
GO:2000145	regulation of cell motility	69	5.77E-19	3.46E-17
GO:2000147	positive regulation of cell motility	41	9.86E-12	3.35E-10
GO Cellular Components				
GO:0005604	basement membrane	14	1.57E-08	1.57E-08
GO:0005615	extracellular space	149	8.71E-21	8.71E-21
GO:0005911	cell-cell junction	25	8.92E-05	8.92E-05
GO:0005925	focal adhesion	23	3.28E-05	3.28E-05
GO:0009897	external side of plasma membrane	18	0.005134072	0.005134072
GO:0016323	basolateral plasma membrane	25	3.90E-11	3.90E-11
GO:0016324	apical plasma membrane	22	4.86E-06	4.86E-06
GO:0030017	sarcomere	12	0.001656909	0.001656909
GO:0030141	secretory granule	38	2.88E-05	2.88E-05
GO:0031012	extracellular matrix	52	9.92E-20	9.92E-20
GO:0031091	platelet alpha granule	13	6.88E-08	6.88E-08

GO:0031093	platelet alpha granule lumen	10	1.63E-06	1.63E-06
GO:0031253	cell projection membrane	17	0.001844487	0.001844487
GO:0031674	I band	10	0.001095986	0.001095986
GO:0034774	secretory granule lumen	19	1.32E-04	1.32E-04
GO:0043292	contractile fiber	13	0.001839951	0.001839951
GO:0043296	apical junction complex	13	1.59E-05	1.59E-05
GO:0045121	membrane raft	23	1.39E-06	1.39E-06
GO:0062023	collagen-containing extracellular matrix	46	6.93E-20	6.93E-20
GO:0070062	extracellular exosome	103	6.40E-16	6.40E-16
GO:0070160	tight junction	12	2.36E-05	2.36E-05
GO:0070161	anchoring junction	44	4.10E-08	4.10E-08
GO:0098552	side of membrane	27	5.64E-04	5.64E-04
GO:0098590	plasma membrane region	62	1.88E-10	1.88E-10
GO:1903561	extracellular vesicle	105	1.19E-16	1.19E-16
GO Molecular Functions				
GO:0001228	DNA-binding transcription activator activity, RNA polymerase II-specific	22	0.001037712	0.001037712
GO:0004175	endopeptidase activity	40	5.64E-06	6.20E-05
GO:0004672	protein kinase activity	56	3.20E-07	4.80E-06
GO:0004674	protein serine/threonine kinase activity	38	7.44E-05	3.72E-04
GO:0004857	enzyme inhibitor activity	23	2.77E-05	2.21E-04
GO:0008233	peptidase activity	45	3.31E-05	2.32E-04
GO:0008234	cysteine-type peptidase activity	22	5.31E-04	0.001593772
GO:0016301	kinase activity	65	9.44E-08	1.60E-06
GO:0016773	phosphotransferase activity, alcohol group as acceptor	61	1.30E-07	2.08E-06
GO:0033674	positive regulation of kinase activity	35	1.27E-06	1.66E-05
GO:0043085	positive regulation of catalytic activity	71	9.91E-10	2.18E-08
GO:0043086	negative regulation of catalytic activity	41	2.72E-06	3.27E-05
GO:0043549	regulation of kinase activity	52	5.83E-10	1.40E-08
GO:0045859	regulation of protein kinase activity	47	2.19E-09	4.37E-08
GO:0045860	positive regulation of protein kinase activity	30	1.17E-05	1.06E-04
GO:0051336	regulation of hydrolase activity	60	6.87E-08	1.24E-06
GO:0051338	regulation of transferase activity	56	5.99E-10	1.38E-08

GO:0051345	positive regulation of hydrolase activity	34	1.41E-04	5.66E-04
GO:0051346	negative regulation of hydrolase activity	23	6.50E-04	0.001300171
GO:0051347	positive regulation of transferase activity	39	3.33E-07	4.66E-06
GO:0052547	regulation of peptidase activity	34	1.06E-09	2.23E-08
GO:0052548	regulation of endopeptidase activity	32	2.67E-09	5.07E-08
GO:0070011	peptidase activity, acting on L-amino acid peptides	43	6.26E-05	3.75E-04
GO:0071900	regulation of protein serine/threonine kinase activity	29	6.92E-06	6.92E-05

Supplementary Table 4. KEGG Pathway analysis of candidate DEGs in choriocarcinoma.

Pathway	ID	Database	Gene count	P-value	Corrected P-value	Genes
MAPK signaling pathway	KEGG:04010	KEGG pathway	15	0.013728734	0.041186203	BDNF, DUSP1, EFNA1, ERBB3, FGF2, FGFR2, HSPB1, JUN, MET, PDGFC, PGF, PRKCA, RASGRP2, TGFB2, VEGFC
Ras signaling pathway	KEGG:04014	KEGG pathway	14	0.005046425	0.045417827	BDNF, EFNA1, FGF2, FGFR2, GNG11, MET, PAK6, PDGFC, PGF, PLAAT3, PRKCA, RALBP1, RASGRP2, VEGFC
Rap1 signaling pathway	KEGG:04015	KEGG pathway	13	0.00354277	0.046056015	CDH1, EFNA1, FGF2, FGFR2, FYB1, MET, PDGFC, PFN2, PGF, PRKCA, RASGRP2, THBS1, VEGFC
PI3K-Akt signaling pathway	KEGG:04151	KEGG pathway	22	2.11E-04	0.0035847	BDNF, CCNE1, COL1A1, COL6A1, COL6A2, COL9A3, EFNA1, ERBB3, FGF2, FGFR2, FN1, GNG11, ITGA3, ITGA6, MET, PDGFC, PGF, PRKCA, RXRA, THBS1, THBS2, VEGFC
Wnt signaling pathway	KEGG:04310	KEGG pathway	10	0.009450501	0.037802002	DKK1, FZD2, FZD5, FZD6, GPC4, JUN, PRKCA, TCF7L2, WNT5A, WNT6
Axon guidance	KEGG:04360	KEGG pathway	11	0.008116756	0.048700534	DPYSL2, EFNA1, FYN, MET, MYL9, PAK6, PLXNA2, PRKCA, SEMA3C, SEMA4C, WNT5A
Hippo signaling pathway	KEGG:04390	KEGG pathway	10	0.008321645	0.041608225	CCN2, CDH1, FZD2, FZD5, FZD6, SERPINE1, TCF7L2, TGFB2, WNT5A, WNT6
Focal adhesion	KEGG:04510	KEGG pathway	19	1.05E-06	2.31E-05	COL1A1, COL6A1, COL6A2, COL9A3, FN1, FYN, ITGA3, ITGA6, JUN, MET, MYL9, MYLK, PAK6, PDGFC, PGF, PRKCA, THBS1, THBS2, VEGFC
ECM-receptor interaction	KEGG:04512	KEGG pathway	10	9.63E-05	0.001733155	CD44, COL1A1, COL6A1, COL6A2, COL9A3, FN1, ITGA3, ITGA6, THBS1, THBS2
Cell adhesion molecules	KEGG:04514	KEGG pathway	10	0.005549083	0.03884358	ALCAM, CADM1, CDH1, CLDN4, CLDN6, CLDN7, F11R, HLA-A, ITGA6, SDC2

Tight junction	KEGG:04530	KEGG pathway	11	0.004901865	0.049018649	CLDN4, CLDN6, CLDN7, EPB41L4B, F11R, JUN, MSN, MYL9, TJP2, TJP3, TUBA1A
Signaling pathways regulating pluripotency of stem cells	KEGG:04550	KEGG pathway	10	0.004357765	0.047935413	DLX5, FGF2, FGFR2, FZD2, FZD5, FZD6, HAND1, KLF4, WNT5A, WNT6
Regulation of actin cytoskeleton	KEGG:04810	KEGG pathway	14	0.001428897	0.021433459	CYFIP2, FGF2, FGFR2, FN1, ITGA3, ITGA6, MSN, MYL9, MYLK, PAK6, PDGFC, PFN2, PIP5K1B, TMSB4X
Cushing syndrome	KEGG:04934	KEGG pathway	11	0.002525991	0.035363878	CCNE1, CDKN2A, CDKN2C, CYP11A1, FZD2, FZD5, FZD6, HSD3B1, TCF7L2, WNT5A, WNT6
Pathogenic Escherichia coli infection	KEGG:05130	KEGG pathway	10	0.044562328	0.044562328	CLDN4, CLDN6, CLDN7, CYFIP2, FYN, JUN, LYN, TNFSF10, TUBA1A, TUBB2A
Human papillomavirus infection	KEGG:05165	KEGG pathway	18	0.00391393	0.046967161	CCNE1, COL1A1, COL6A1, COL6A2, COL9A3, FN1, FZD2, FZD5, FZD6, HEY1, HLA-A, ITGA3, ITGA6, TCF7L2, THBS1, THBS2, WNT5A, WNT6
Pathways in cancer	KEGG:05200	KEGG pathway	33	3.20E-06	6.39E-05	CCNE1, CDH1, CDKN2A, CEBPA, CSF2RA, FGF2, FGFR2, FN1, FZD2, FZD5, FZD6, GNG11, GSTO1, HEY1, ITGA3, ITGA6, JUN, JUP, MET, MGST3, MMP1, PGF, PMAIP1, PPARG, PRKCA, RALBP1, RASGRP2, RXRA, TCF7L2, TGFB2, VEGFC, WNT5A, WNT6
Proteoglycans in cancer	KEGG:05205	KEGG pathway	19	1.65E-06	3.47E-05	ANK3, CD44, COL1A1, ERBB3, FGF2, FN1, FZD2, FZD5, FZD6, LUM, MET, MSN, PRKCA, SDC2, TGFB2, THBS1, TIMP3, WNT5A, WNT6
MicroRNAs in cancer	KEGG:05206	KEGG pathway	17	0.005371163	0.042969303	CCNE1, CD44, CDKN2A, DNMT3B, EFNA1, ERBB3, MARCKS, MET, PRKCA, SLC7A1, SOX4, TGFB2, THBS1, TIMP3, TPM1, VIM, ZFPM2
Hepatocellular carcinoma	KEGG:05225	KEGG pathway	13	4.65E-04	0.007436564	CDKN2A, FZD2, FZD5, FZD6, GSTO1, MET, MGST3, PRKCA, SMARCA2,

						TCF7L2, TGFB2, WNT5A, WNT6
Gastric cancer	KEGG:05226	KEGG pathway	14	3.48E-05	6.61E-04	CCNE1, CDH1, FGF2, FGFR2, FZD2, FZD5, FZD6, JUP, MET, RXRA, TCF7L2, TGFB2, WNT5A, WNT6

Supplementary Table 5. GO terms and KEGG pathway analysis of 29 hub genes in choriocarinoma.

Term	Description	Count	LogP
GO Biological Processes			
GO:0030198	extracellular matrix organization	18	-26.046
GO:0043687	post-translational protein modification	12	-15.141
GO:0002576	platelet degranulation	8	-12.238
GO:0030336	negative regulation of cell migration	8	-8.946
GO:0071363	cellular response to growth factor stimulus	10	-8.915
GO:0043408	regulation of MAPK cascade	10	-8.886
GO:0031589	cell-substrate adhesion	8	-8.65
GO:0001501	skeletal system development	8	-7.635
GO:0001503	ossification	7	-6.865
GO:0016049	cell growth	7	-6.388
GO:0034284	response to monosaccharide	5	-5.783
GO:0051043	regulation of membrane protein ectodomain proteolysis	3	-5.766
GO:0007229	integrin-mediated signaling pathway	4	-5.346
GO:0035987	endodermal cell differentiation	3	-4.898
GO:0048545	response to steroid hormone	5	-4.695
GO:0030199	collagen fibril organization	3	-4.629
GO:0034330	cell junction organization	6	-4.169
GO:0022617	extracellular matrix disassembly	3	-4.069
GO:0022604	regulation of cell morphogenesis	4	-3.587
GO Cellular Components			
GO:0062023	collagen-containing extracellular matrix	20	-29.694
GO:0005788	endoplasmic reticulum lumen	17	-25.917
GO:0031091	platelet alpha granule	8	-13.453
GO:0005581	collagen trimer	4	-5.721
GO:0098978	glutamatergic synapse	3	-2.416
GO Molecular Functions			
GO:0005201	extracellular matrix structural constituent	12	-19.125
GO:0005539	glycosaminoglycan binding	10	-13.722
GO:0005518	collagen binding	6	-10.143

GO:0019838	growth factor binding	7	-10.081
GO:0002020	protease binding	5	-6.66
GO:0008083	growth factor activity	5	-6.201
GO:0050840	extracellular matrix binding	3	-4.605
KEGG Pathway			
hsa04512	ECM-receptor interaction	6	-9.643
ko05205	Proteoglycans in cancer	7	-8.905
ko04933	AGE-RAGE signaling pathway in diabetic complications	5	-7.269
ko04974	Protein digestion and absorption	4	-5.662
hsa05200	Pathways in cancer	6	-5.577
ko04390	Hippo signaling pathway	4	-4.736
hsa04115	p53 signaling pathway	3	-4.309

Supplementary Table 6. The interaction between drugs and hub genes.

Gene	Drug	Sources	PMIDs	Query Score	Interaction Score
COL6A1	COLLAGENASE CLOSTRIDIUM HISTOLYTICUM	ChemblInteractions	None found	0.78	1.01
COL6A1	OCRIPLASMIN	ChemblInteractions	None found	0.56	0.73
COL5A2	COLLAGENASE CLOSTRIDIUM HISTOLYTICUM	ChemblInteractions	None found	0.78	1.01
COL5A2	OCRIPLASMIN	ChemblInteractions	None found	0.56	0.73
CTGF	PAMREVLUMAB	TdgClinicalTrial ChemblInteractions	None found	8.71	5.98
CTGF	ACRIDINE	NCI	16950763	8.71	5.98
CTGF	RAMIPRIL	NCI	15128880	1.74	1.2
CTGF	INOSITOL	NCI	15560785	0.62	0.43
CTGF	2-METHOXYESTRADIOL	NCI	18292194	0.58	0.4
CTGF	PROPRANOLOL	NCI	12691286	0.46	0.31
CTGF	ENALAPRIL	NCI	18812665	0.44	0.3
CTGF	VITAMIN E	NCI	12023009	0.41	0.28
CTGF	ANDROSTANOLONE	NCI	11181522	0.38	0.26
CTGF	PRASTERONE	NCI	15675949	0.34	0.23
TGFB2	LERDELIMUMAB	TdgClinicalTrial ChemblInteractions	None found	8.71	28.4
TGFB2	TRABEDERSEN	TdgClinicalTrial	None found	4.36	14.2
TGFB2	BELAGENPUMATUCEL-L	TdgClinicalTrial	None found	4.36	14.2
TGFB2	FRESOLIMUMAB	TALC ChemblInteractions	None found	2.9	9.47
COL6A2	COLLAGENASE CLOSTRIDIUM HISTOLYTICUM	ChemblInteractions	None found	0.78	1.01
COL6A2	OCRIPLASMIN	ChemblInteractions	None found	0.56	0.73

THBS1	METHYLCELLULOSE	NCI	9016860	4.36	7.1
THBS1	ABT-510	TTD	None found	1.24	1.01
THBS1	VESNARINONE	NCI	15356428	1.24	2.03
THBS1	CORTICOTROPIN	NCI	8698834	0.62	1.01
THBS1	PIOGLITAZONE	NCI	17063547	0.51	0.84
THBS1	SIMVASTATIN	NCI	10543307	0.31	0.25
THBS1	CAMPTOTHECIN	NCI	16962673	0.24	0.39
THBS1	LOVASTATIN	NCI	10543307	0.19	0.32
SPARC	CALCIUM PHOSPHATE, TRIBASIC	DrugBank	None found	0.13	0.86
SPARC	CALCIUM CITRATE	DrugBank	None found	0.13	0.86
COL3A1	COLLAGENASE CLOSTRIDIUM HISTOLYTICUM	ChemblInteractions TEND	None found	1.56	2.03
COL3A1	OCRIPLASMIN	ChemblInteractions	None found	0.56	0.73
IGFBP3	MECASERMIN	DrugBank	15777106 19627167 18363546	4.36	11.36
IGFBP3	LONAFARNIB	DrugBank	15494604	1.24	3.25
IGFBP3	ALITRETINOIN	DrugBank	16760641	0.73	1.89
IGFBP3	CELECOXIB	PharmGKB	22336956	0.13	0.34
IGFBP3	FLUOROURACIL	PharmGKB	20860465	0.08	0.22
SDC2	SARGRAMOSTIM	DrugBank	17139284 17016423 10734053	3.48	45.44
SERPINE1	TIPLASININ	DTC	17276980	8.71	4.21
SERPINE1	ALEPLASININ	ChemblInteractions	None found	4.36	2.1
SERPINE1	PREMARIN	NCI	8888658	4.36	2.1
SERPINE1	DIAPLASININ	TTD	None found	4.36	2.1
SERPINE1	UROKINASE	DrugBank TdgClinicalTrial	12709915 12785198 12745435 12642587	3.05	1.47

			12579271		
SERPINE1	RETEPLASE	DrugBank	17963464	2.9	1.4
SERPINE1	ANISTREPLASE	DrugBank	17963464	2.9	1.4
SERPINE1	CETRORELIX	NCI	16391860	2.18	1.05
SERPINE1	DEFIBROTIDE	NCI	12745658	1.74	0.84
SERPINE1	TROGLITAZONE	DrugBank	10871202 10418858 10770198 10831180 10768100	1.54	0.37
THBS2	BEVACIZUMAB	NCI	16365183	0.42	2.77
CD44	BIVATUZUMAB	DrugBank	14530488	8.71	22.72
CD44	HYALURONAN	TdgClinicalTrial	None found	1.45	3.79
CD44	GENTAMICIN	NCI	14967965	0.38	0.99
CD44	HYALURONATE SODIUM	DrugBank	None found	0.29	0.76
CD44	PROGESTERONE	NCI	11605071	0.11	0.3
CDH1	VOLASERTIB	JAX-CKB	26597303	2.18	4.73
CDH1	BICALUTAMIDE	CGI	None found	0.54	1.18
CDH1	LAPATINIB	JAX-CKB	26487584	0.31	0.68
CDH1	SELUMETINIB	JAX-CKB	26251290	0.25	0.54
CDH1	CAPECITABINE	JAX-CKB	26487584	0.24	0.53
CDH1	ERLOTINIB	JAX-CKB	26251290	0.16	0.36
TIMP3	PIMAGEDINE	DrugBank	None found	1.09	14.2
LGALS1	THIODIGALACTOSIDE	DrugBank	10592235 17139284 17016423	8.71	28.4
LGALS1	DITHIOTHREITOL	DrugBank	10592235 17139284 17016423	1.74	5.68
LGALS1	2-MERCAPTOETHANOL	DrugBank	10592235	1.74	5.68
LGALS1	ARTENIMOL	DrugBank	26340163	0.11	0.35
FGF2	SUCRALFATE	DrugBank	7948825	6.1	3.61

		TTD	8578218 1957124 1970337 8578198		
FGF2	ABT-510	DrugBank NCI	16051960	3.73	1.11
FGF2	REBAMIPIDE	NCI	8774986	2.9	1.72
FGF2	FAMOTIDINE	NCI	11943947	2.18	1.29
FGF2	THYROTROPIN	NCI	7519916	1.74	1.03
FGF2	PYRAZOLE	NCI	9730230	1.24	0.74
FGF2	TRIAMCINOLONE	NCI	15923512	1.14	0.22
FGF2	LENALIDOMIDE	PharmGKB	28373444	1.09	0.32
FGF2	SQUALAMINE	TTD	None found	1.09	0.65
FGF2	QUIZARTINIB	CIViC	27671675	0.97	0.57
VEGFC	VGX-100	TTD	None found	4.36	9.47
VEGFC	AFLIBERCEPT	PharmGKB	20124951	1.74	3.79
VEGFC	CONBERCEPT	ChemblInteractions	None found	1.09	2.37
VEGFC	BEVACIZUMAB	ClearityFoundationClinicalTrial PharmGKB	20124951	0.64	0.69
VEGFC	LENALIDOMIDE	ClearityFoundationClinicalTrial	None found	0.54	0.59
VEGFC	SUNITINIB	CIViC	21787417	0.2	0.44
APOE	LUTEIN	NCI	11413081	4.36	2.84
APOE	GANCICLOVIR	NCI	16322528	2.18	1.42
APOE	SOYBEAN OIL	NCI	3021887	1.74	1.14
APOE	ACENOCOUMAROL	PharmGKB	29432897	1.45	0.95
APOE	TRIAMCINOLONE	NCI	9150415	1.14	0.25
APOE	IRBESARTAN	NCI	12827021	0.73	0.47
APOE	ATORVASTATIN	PharmGKB	16103896 19667110 20031582 17289397	0.68	0.22
APOE	RITONAVIR	PharmGKB	17700364	0.65	0.43

APOE	FLUVASTATIN	PharmGKB	15809899 17289397 30363031	0.59	0.39
APOE	TROGLITAZONE	NCI	15057551	0.51	0.17
MMP1	CHEMBL1235735	DrugBank	10592235	8.71	4.54
MMP1	CHEMBL92608	DrugBank	10592235	8.71	4.54
MMP1	CHEMBL45483	DrugBank	10592235	8.71	4.54
MMP1	CIPEMASTAT	GuideToPharmacology TTD	None found	4.36	2.27
MMP1	LEUPROLIDE ACETATE	NCI	9433928	4.36	2.27
MMP1	CHEMBL267178	DrugBank	10592235	4.36	2.27
MMP1	CHEMBL11306	DrugBank	10592235	4.36	2.27
MMP1	PENTOSAN POLYSULFATE SODIUM	NCI	1384503	4.36	2.27
MMP1	APRATASTAT	GuideToPharmacology TTD	None found	2.9	1.51
MMP1	TRIAMCINOLONE	NCI	12123742	1.14	0.2
FN1	L19IL2	ChemblInteractions	None found	4.36	8.12
FN1	L19TNFA	ChemblInteractions	None found	4.36	8.12
FN1	L19SIP 131I	ChemblInteractions	None found	4.36	8.12
FN1	OCRIPLASMIN	DrugBank ChemblInteractions TTD	23193358	2.23	0.83
FN1	ZINC CHLORIDE	DrugBank	23896426 20541508	0.27	0.25
FN1	LANOTEPLASE	DrugBank	None found	0.26	0.48
FN1	METHYLDOPA	DrugBank	23896426	0.11	0.1
POSTN	-				
FBN1	-				
PRSS23	-				
FSTL1	-				
TIMP1	-				

VWA1	-
IGFBP7	-
IGFBP4	-

Supplementary Table 7. Screening DETGs in choriocarcinoma by integrated microarray.

DETGs	Gene names
Upregulated	BTG2 EPB41L4B FNBP1L KLF4 CAPN6 MAP7 IMPA2 MBD2 DTX4 KDM5B PGF SESN1 FZD5 RASL11B MYCN ATP2B4 PEG3 SLC1A3 TGFBR3 PRKCH LIN28A FLVCR2 SOX13 SOX4 RGS16 SLC2A3 COL21A1 PLXNA2 ERBB3 HAND1 TFAP2C DCP2 CEBPA PRSS8
Downregulated	ITGA3 PRR16 ALCAM PXDN OXTR ZFPM2 COL5A2 WNT5A IGFBP5 MYBL1 DAZAP2 LOX SLC7A1 LBH CYR61 RALBP1 MLXIP NETO2 GJA1 TIMP3 ARID5B EMP1 PFN2 DUSP1 FBN1 COL3A1 MARCKS ATAD2 SERPINE1 MAP1B SPARC TMSB4X TGFBI PRKCA SEMA3C SPOCK1

Abbreviations:DETGs, differentially expressed target genes

Supplementary Table 8. GO terms and KEGG pathway analysis of 70 DETGs in choriocarinoma.

Term	Description	Count	LogP
GO Biological Processes			
GO:0007507	heart development	16	-12.39
GO:0001568	blood vessel development	16	-10.4
GO:0030155	regulation of cell adhesion	15	-9.54
GO:0009611	response to wounding	14	-9.137
GO:0001667	ameboidal-type cell migration	12	-8.683
GO:0001704	formation of primary germ layer	7	-7.816
GO:0071363	cellular response to growth factor stimulus	13	-7.746
GO:0001501	skeletal system development	11	-7.505
GO:0009791	post-embryonic development	6	-7.442
GO:0030198	extracellular matrix organization	10	-7.307
GO:0006935	chemotaxis	12	-7.232
GO:0030324	lung development	7	-6.773
GO:0060174	limb bud formation	3	-5.621
GO:0010232	vascular transport	5	-5.562
GO:1901652	response to peptide	9	-5.214
GO:0007162	negative regulation of cell adhesion	7	-5.056
GO:0032355	response to estradiol	5	-4.816
GO:0070371	ERK1 and ERK2 cascade	7	-4.767
GO:0051098	regulation of binding	7	-4.516
GO:0090066	regulation of anatomical structure size	8	-4.511
GO Cellular Components			
GO:0031012	extracellular matrix	13	-8.897
GO:0009925	basal plasma membrane	6	-4.504
GO:0031093	platelet alpha granule lumen	3	-3.202
GO:0005604	basement membrane	3	-2.776
GO:0048471	perinuclear region of cytoplasm	7	-2.686
GO:0070160	tight junction	3	-2.434
GO:0098797	plasma membrane protein complex	6	-2.081
GO Molecular Functions			
GO:0005201	extracellular matrix structural constituent	8	-7.989

GO:0019838	growth factor binding	7	-7.268
GO:0005178	integrin binding	6	-5.828
GO:0001228	DNA-binding transcription activator activity, RNA polymerase II-specific	8	-4.849
GO:0061980	regulatory RNA binding	3	-3.685
GO:0002020	protease binding	4	-3.49
GO:0008201	heparin binding	4	-3.123
GO:0030165	PDZ domain binding	3	-2.916
GO:0019900	kinase binding	7	-2.619
GO:0008509	anion transmembrane transporter activity	5	-2.231
GO:0001227	DNA-binding transcription repressor activity, RNA polymerase II-specific	4	-2.141
KEGG Pathway			
hsa05205	Proteoglycans in cancer	7	-5.921
ko05206	MicroRNAs in cancer	7	-5.018
hsa04020	Calcium signaling pathway	4	-2.955
ko04974	Protein digestion and absorption	3	-2.83
ko04933	AGE-RAGE signaling pathway in diabetic complications	3	-2.711

Supplementary Table 9. DEMs ranked with the number of screened DETGs in choriocarcinoma.

miRNA	Gene1	Gene2	Gene3	Gene4	Gene5	Gene6	Gene7	Gene8	Gene9	Gene10	Gene11	The number of reverseregulated genes
Upregulated miRNA												
hsa-miR-29b-3p	LOX	PXDN	OXTR	EMP1	FBN1	COL3A1	SPARC	COL21A1	TFAP2C	BTG2	KDM5B	7
hsa-let-7b-5p	PXDN	COL5A2	LBH	RGS16	DUSP1	COL3A1	HAND1	BTG2	DTX4	MYCN	LIN28A	5
hsa-let-7c-5p	PXDN	COL5A2	LBH	RGS16	DUSP1	COL3A1	HAND1	BTG2	DTX4	MYCN	LIN28A	5
hsa-miR-133a-3p	ITGA3	WNT5A	MLXIP	FBN1	CEBPA	SOX4						4
hsa-miR-133b	ITGA3	WNT5A	MLXIP	FBN1	CEBPA	SOX4						4
hsa-let-7f-5p	LBH	PXDN	COL3A1	RGS16	HAND1	DTX4	MYCN	LIN28A	BTG2			3
hsa-let-7e-5p	PXDN	LBH	DUSP1	HAND1	DTX4	MYCN	LIN28A	BTG2				3
hsa-miR-98-5p	PXDN	COL5A2	LBH	HAND1	BTG2	MYCN	LIN28A					3
hsa-miR-29a-3p	PXDN	OXTR	FBN1	TFAP2C	ATP2B4	COL21A1						3
hsa-miR-30b-5p	LOX	GJA1	MARCKS	LIN28A	FLVCR2							3
hsa-miR-301a-3p	ZFPM2	MYBL1	RALBP1	LIN28A								3
hsa-miR-301b	ZFPM2	MYBL1	RALBP1	LIN28A								3
hsa-miR-221-3p	ZFPM2	MYBL1	TIMP3									3
hsa-miR-24-3p	IGFBP5	LOX	ARID5B	PRSS8								3
hsa-let-7g-5p	LBH	PXDN	RGS16	HAND1	BTG2	DTX4	MYCN	LIN28A				2
hsa-miR-143-3p	IGFBP5	RALBP1	COL21A1	ERBB3								2
hsa-miR-103a-3p	ZFPM2	MYBL1	TGFBR3	BTG2								2
hsa-let-7b-3p	TIMP3	MARCKS	DCP2	TGFBR3								2
hsa-miR-495-3p	RALBP1	GJA1	TGFBR3	SOX13								2
hsa-miR-132-3p	DAZAP2	ARID5B	BTG2	SOX4								2
hsa-miR-125b-5p	SLC7A1	LBH	DTX4									2
hsa-miR-140-5p	IGFBP5	FBN1	FNBP1L									2
hsa-miR-152-3p	DUSP1	SERPINE1	ERBB3									2
hsa-miR-183-5p	TMSB4X	PRKCA	LIN28A									2
hsa-miR-539-5p	NETO2	PRKCA	SOX4									2
hsa-miR-21-5p	TIMP3	TGFBI										2
hsa-let-7g-3p	MARCKS	MAP1B										2
hsa-miR-340-5p	WNT5A	PRKCA										2

hsa-miR-433-3p	MAP1B	SPARC						2
hsa-miR-323a-3p	GJA1	TIMP3						2
hsa-miR-15b-5p	MYBL1	SESN1	TGFBR3	SLC2A3	BTG2	EPB41L4B	CAPN6	1
hsa-miR-128-3p	LBH	COL21A1	DCP2	BTG2	DTX4			1
hsa-let-7d-5p	PXDN	DTX4	SOX13	RGS16				1
hsa-miR-137	PRR16	IMPA2	KDM5B	HAND1				1
hsa-miR-145-5p	SLC7A1	PLXNA2	MYCN					1
hsa-miR-299-5p	ALCAM	SOX4						1
hsa-miR-876-3p	MYBL1	CEBPA						1
hsa-miR-125a-5p	LBH							1
hsa-miR-148b-3p	DUSP1							1
hsa-miR-654-5p	ITGA3							1
hsa-miR-758-3p	ZFPM2							1
hsa-miR-541-3p	ITGA3							1
hsa-miR-487a-3p	SEMA3C							1
hsa-miR-222-3p	ZFPM2							1
hsa-miR-196b-5p	MYBL1							1
hsa-miR-873-5p	FNBP1L	TGFBR3	SOX4					0
hsa-miR-330-3p	TGFBR3	PLXNA2						0
hsa-miR-10a-5p	KLF4	TFAP2C						0
hsa-miR-10b-5p	KLF4	TFAP2C						0
hsa-miR-138-5p	DTX4	SOX4						0
hsa-miR-134-5p	MYCN							0
hsa-miR-155-5p	PEG3							0
hsa-miR-194-5p	FZD5							0
hsa-miR-329-3p	SOX4							0
hsa-miR-338-3p	SOX4							0
hsa-miR-361-5p	SLC1A3							0
hsa-miR-369-3p	DCP2							0
hsa-miR-376c-3p	KDM5B							0
hsa-miR-493-3p	PRKCH							0
hsa-miR-496	PLXNA2							0
hsa-miR-544a	DCP2							0
hsa-miR-589-5p	LIN28A							0

hsa-miR-598-3p	LIN28A							0
hsa-miR-889-3p	FLVCR2							0
Downregulated miRNA								
hsa-miR-519c-3p	MAP7	RASL11B	SOX4	ZFPM2	MYBL1	DAZAP2	NETO2	3
hsa-miR-520a-5p	DTX4	PGF	FZD5					3
hsa-miR-519a-3p	RASL11B	SOX4	MAP1B	ZFPM2	DAZAP2			2
hsa-miR-515-5p	BTG2	LIN28A	CYR61	MLXIP				2
hsa-miR-520a-3p	MYCN	MAP1B	ZFPM2	DAZAP2				1
hsa-miR-373-3p	MYCN	ATAD2	MAP1B	DAZAP2				1
hsa-miR-372-3p	MYCN	ZFPM2	DAZAP2					1
hsa-miR-520f-3p	MBD2	ATAD2	WNT5A					1
hsa-miR-512-5p	FNBP1L	SPOCK1						1
hsa-miR-525-5p	PGF							1
hsa-miR-512-3p	WNT5A	DAZAP2	PFN2					0
hsa-miR-520e	DAZAP2	MAP1B						0
hsa-miR-520b	DAZAP2							0
hsa-miR-519e-3p	DAZAP2							0
hsa-miR-375	WNT5A							0

The downregulated miRNA and genes are labeled in red.