

Supplementary table2:

Downregulated genes in CTSB⁺⁰ versus wild-type co-cultures of primary tumor cells and BMDM

Genes were filtered according to the criteria: BH q-value ≤ 0.05 (unpaired Bayes t-test) and an effect size > 2 .
Probe ID: Affymetrix Identifier; FDR: False discovery rate.

Probe ID	Gene Description	Gene Symbol	Effect Size	FDR
10551293	cytochrome P450, family 2, subfamily f, polypeptide 2	Cyp2f2	7.42	3.68E-07
10403420	isopentenyl-diphosphate delta isomerase 2	Idi2	6.61	3.83E-03
10457707	desmocollin 1	Dsc1	6.58	5.49E-03
10407537	isopentenyl-diphosphate delta isomerase 2	Idi2	6.36	3.89E-04
10455446	serine peptidase inhibitor, Kazal type 11	Spink12	5.45	4.85E-02
10469786	interleukin 1 family, member 9	Il1f9	4.48	5.44E-02
10499891	small proline-rich protein 1B	Sprr1b	4.33	5.73E-02
10552462	kallikrein related-peptidase 14	Klk14	4.32	9.53E-02
10454113	desmoglein 1 alpha : desmoglein 1 beta : desmoglein 1 gamma	Dsg1c : Dsg1a : Dsg1b	3.86	7.53E-02
10432897	keratin 79	Krt79	3.83	4.16E-02
10511353	short chain dehydrogenase/reductase family 16C, member 6	Sdr16c6	3.73	4.47E-02
10469774	interleukin 1 family, member 8	Il1f8	3.69	5.55E-02
10494016	thioesterase superfamily member 5	Them5	3.45	4.58E-02
10522827	casein alpha s1	Csn1s1	3.40	2.03E-04
10467206	protein phosphatase 1, regulatory (inhibitor) subunit 3C	Ppp1r3c	3.13	4.93E-03
10539449	ATPase, H ⁺ transporting, lysosomal V1 subunit B1	Atp6v1b1	3.04	6.29E-02
10530960	transmembrane protease, serine 11d	Tmprss11d	3.03	9.55E-02
10443854	cytochrome P450, family 4, subfamily f, polypeptide 39	Cyp4f39	2.92	4.32E-02
10366546	carboxypeptidase M	Cpm	2.83	1.28E-02
10581605	haptoglobin	Hp	2.82	4.54E-04
10431962	endonuclease, polyU-specific	Endou	2.71	8.69E-02
10419261	bone morphogenetic protein 4	Bmp4	2.67	1.96E-03
10428376	angiopoietin 1	Angpt1	2.64	3.39E-03
10359689	ATPase, Na ⁺ /K ⁺ transporting, beta 1 polypeptide	Atp1b1	2.58	8.94E-03
10421853	leukocyte cell derived chemotaxin 1	Lect1	2.57	5.57E-02
10545096	melanoma antigen family B, 16, pseudogene 1 : melanoma antigen family B, 16	Mageb16 : Mageb16-ps1	2.51	7.28E-02
10569344	insulin-like growth factor 2	Igf2	2.51	3.99E-06
10493856	small proline-rich protein 2A1 : small proline-rich protein 2A3	Sprr2a1 : Sprr2a3	2.49	5.54E-02
10493858	small proline-rich protein 2A1 : small proline-rich protein 2A3	Sprr2a1 : Sprr2a3	2.49	5.54E-02
10440647	claudin 8	Cldn8	2.46	1.48E-03
10462313	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system	Slc1a1	2.44	2.13E-03

	Xag), member 1			
10390860	keratin 23	Krt23	2.40	2.42E-02
10493850	small proline-rich protein 2A1 : small proline-rich protein 2A2 : small proline-rich protein 2A3	Sprr2a1 : Sprr2a2 : Sprr2a3	2.34	4.85E-02
10380398	chondroadherin	Chad	2.32	6.16E-03
10434719	kininogen 1	Kng1	2.31	1.07E-04
10497203	hairy/enhancer-of-split related with YRPW motif 1	Hey1	2.30	2.42E-02
10444883	corneodesmosin	Cdsn	2.25	2.84E-02
10485700	butyrobetaine (gamma), 2-oxoglutarate dioxygenase 1 (gamma-butyrobetaine hydroxylase)	Bbox1	2.22	5.44E-02
10387821	arachidonate 12-lipoxygenase	Alox12	2.19	6.20E-02
10439282	cystatin A	Csta	2.18	5.23E-02
10514576	KN motif and ankyrin repeat domains 4	Kank4	2.18	4.30E-02
10406461	microRNA 9-2	Mir9-2	2.18	3.26E-02
10503502	tocopherol (alpha) transfer protein	Ttpa	2.17	7.44E-02
10579442	solute carrier family 5 (sodium iodide symporter), member 5	Slc5a5	2.16	7.02E-05
10407416	calmodulin-like 3	Calml3	2.16	5.44E-02
10416023	scavenger receptor class A, member 5 (putative)	Scara5	2.14	2.77E-02
10521892	solute carrier family 34 (sodium phosphate), member 2	Slc34a2	2.13	1.98E-02
10445061	ring finger protein 39	Rnf39	2.12	4.58E-02
10599008	solute carrier family 6 (neurotransmitter transporter), member 14	Slc6a14	2.09	2.46E-02
10394954	grainyhead-like 1 (Drosophila)	Grhl1	2.08	9.43E-02
10382321	potassium inwardly-rectifying channel, subfamily J, member 2	Kcnj2	2.02	1.81E-02
10472757	cytochrome b reductase 1	Cybrd1	2.01	3.26E-02
10390897	keratin associated protein 1-5	Krtap1-5	2.01	3.86E-02
10399470	tribbles homolog 2 (Drosophila)	Trib2	2.00	9.00E-03