



Correction to: Secretomes reveal several novel proteins as well as TGF- β 1 as the top upstream regulator of metastatic process in breast cancer

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Correction to: Breast Cancer Research and Treatment
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In the original publication of the article, Acknowledgement section was missed out and Table 1 was published

incompletely. The Acknowledgment and complete Table 1 are given in this correction. The original article has been corrected.

The original article can be found online at <https://doi.org/10.1007/s10549-018-4752-8>.

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Table 1 Proteins secreted into the conditioned medium by highly metastatic breast cancer cells 4TBM, 4TLM and 4THM as compared to the non-metastatic 67NR breast cancer cell line

No	Protein name	Symbol	Protein access no	Peptide sequence detected	Anova <i>p</i> -value	Average fold change		
						4TBM	4TLM	4THM
1	Collagen, type V, alpha 1	COL5A1	O88207	FGFEVGPACFLG	0.0062	8.2	1.3	7.7
				SSSEPDVAYR	0.0469	15.6	2.8	11.3
				DLQLCHPDFPDGEYWVDP-NQGCSR	0.0021	7.1	0.93	6.4
2	Complement component 3	C3	P01027	LITQGENCEIK	0.0072	3.4	38.3	20.1
				DTWVEHWPEAEECQDQK	0.0034	1.6	19.9	12
				QIFSAEFEVK	0.0043	5.4	45.1	28.3
3	Laminin, beta 1	LAMB1	P02469	AELLLEEAK	0.0117	14.6	17.0	12.1
				NSDIQALDSITK	0.0018	7.1	11.3	6.9
				EGFYDLSAEDPYGCK	0.0032	7.8	7.0	5.6
				QNAQDVLLK	0.0141	5.8	8.9	5.0
				LHTLGDNLLDSR	0.005	11.5	8.0	8.4
				CVCNYLGTVK	0.0093	5.9	7.8	4.3
4	Transforming growth factor, beta 1	TGFB1	P04202	AAQNSGEAEYIEK	0.0074	9.2	10.6	8.3
				VAGESADPEPEADYYAK	0.0055	23.4	30.6	41.3
				QWLNQGDGIQGFR	0.0021	10.5	19.0	20.4
5	Heat shock protein 90 kDa beta (Grp94), member 1	HSP90B1	P08113	DISTNYASQK	0.0152	15.8	14.4	10.0
				GLFDEYGSK	0.0134	11.6	9.8	5.2
				EAESSPFVER	0.0077	12.7	11.2	7.6
				FAFQAEVNR	0.0115	7.9	7.2	4.4
				SILFVPTSAPR	0.0044	14.5	13.9	8.0
				EESDDEAAVEEEEEEEK	0.0104	43.6	39.2	26.9
				TETVEEPLEDEAAK	0.0094	12.4	12.5	7.7
				TFEINPR	0.0047	13.4	13.8	8.3
6	Fibronectin 1	FN1	P11276	YLNFBVK	0.0131	12.5	13.8	7.7
				ISCTIANR	0.0113	2.9	22.6	12.7
				IGDQWDK	0.0309	0.55	4.7	2.3
				DSMIWDCTCIGAGR	0.022	0.79	10.2	3.6
				TYLGNALVCTCYGGSR	0.0381	1.1	10.6	4.1
				YSFCTDHAVLVQTR	0.026	0.82	10.8	3.7
				GVTYNIIVEALQNQR	0.0287	1.2	9.7	4.5
				WCGTTQNYDADQK	0.0396	0.6	6.5	2.5
				GLAFTDVIDVDSIK	0.0326	1.2	6.9	3.4
				TASPDQTEMTIEGLQPT-VEYVVSVYAQNR	0.0224	0.8	6.7	3.8
				LTCQCLGFGSGHFR	0.0498	0.8	11.0	3.9
				RPGAAEPSPDGTTGHTYN-QYTQR	0.0456	0.79	6.8	3.5
				TYHVGEQWQK	0.0161	0.71	7.8	2.9
				IAWESPQGQVSR	0.0324	0.93	6.0	2.8
				HYQINQWER	0.0181	0.72	6.8	2.4
CFDHAAGTSYVVGETWEK	0.0375	0.91	8.7	3.5				
PVSINYK	0.018	0.80	11.5	3.9				
TEIDKPSQMQVTDVQDN-SISVR	0.0423	3.8	41.7	17.7				

Table 1 (continued)

No	Protein name	Symbol	Protein access no	Peptide sequence detected	Anova <i>p</i> -value	Average fold change		
						4TBM	4TLM	4THM
7	Heat shock 706 kDa protein 5 {glucose- regulated protein, 78 kDa}	HSPA5	P20029	ETA EAYLGK	0.0004	6.9	8.1	8.4
				VYEGERPLTK	0.0011	25.6	27.4	24.6
				ITITNDQNR	0.0005	48.8	38.7	76.1
				IEWLESHQDADIEDFK	0.0009	38.9	32.7	32.5
				SQIFSTASDNQPTVTIK	0.0023	18.1	18.0	15.5
8	Milk fat globule-EGF factor 8 protein	MFGE8	P21956	NQLTSNPENTVFDK	0.0012	8.7	8.9	12.2
				QVTGIITQGAR	0.018	2.4	1.2	2.0
				EWLQVDLGTQR	0.0242	2.4	1.4	2.3
				VAHSDDGVQWTVY-EEQGSSK	0.0264	3.0	1.5	2.9
				WGPELAR	0.0168	2.1	1.1	1.9
9	Peptidylprolyl isomerase B (cyclophilin B.)	PIIB	P24369	TVDNFVALATGEK	0.003	5.3	9.6	5.4
				VVFGLFGK	0.0178	18.0	26.5	15.8
				DTNGSQFFITTVK	0.0008	7.2	15.2	8.2
				DFMIQGGDFTR	0.0293	19.8	29.1	18.3
				VYFDLQIGDESVGR	0.035	11.3	14.3	9.8
10	Protein disulfide-isomerase family A, member 3	PDIA3	P27773	TADGIVSHLK	0.0271	9.4	9.2	8.1
				DASVVGFFR	0.0241	48.4	45.3	22.6
				YGVSGYPTLK	0.0212	5.4	6.1	4.4
				SEPIPESNEGPVK	0.0049	9.0	9.1	6.7
				FAHTNIESLVK	0.0043	8.6	9.5	7.3
11	Granulin	GRN	P28798	TFSHELSDFGLESTT-GEVPPVAIR	0.0044	7.1	6.9	5.6
				VVVAENFDDIVNEEDK	0.0024	10.1	10.0	9.3
				EATNPPIIQEEK	0.005	9.5	9.8	8.0
				LNSGDWGCCPIEAVCCS-DNQHCCPQGFTCLAQGY-CQK	0.0483	58.3	5.6	23.8
				QTTPLQIG-DIGCDQHTSCPVGQTC-CPSLK	0.0263	24.5	4.9	10.2
12	Matrix metalloproteinase 3	MMP3	P28862	CGVPDVGGFSTFPGSPK	0.0006	9.3	25.4	8.7
				YLENYYGLAK	0.0007	17.8	68.0	21.0
				TYFFVEDK	< 0.0001	19.0	65.9	21.3
13	Thrombospondin 1	THBS1	P35441	IMADSGPIYDK	0.0379	7.4	18.0	10.7
				GDVNDNFQGV LQNVR	0.02	11.7	25.8	21.5
				DNCPNLPNSGQEDYDK	0.0361	10.3	19.4	18.4
				AQGYSGLSVK	0.042	6.2	15.7	11.1
14	Protein tyrosine phosphatase, receptor type, K	PTPRK	P35822	IFLNWK	0.0113	25.4	7.4	19.5
				VLLTRPGE GGTGLPGP-PLITR	0.0118	8.0	4.4	7.1
15	Matrix metalloproteinase 9	MMP9	P41245	VSFQNEV NK	0.0112	0.30	2.3	2.5
				ALLFSK	0.0018	0.22	3.6	2.9.
				LGLGPEVTHVSGLLPR	0.012	0.12	3.2	2.9
				QLSLPQTGELDSQTLK	0.0079	0.33	2.4	2.6
				GSPLQGPFLTR	0.0062	0.35	2.4	2.6
				WCATTANYDQDK	0.0032	0.13	2.1	2.6
				QPTFVVFPK	0.0159	0.29	2.9	2.9
				AFAVWGEVAPLTFTR	0.0018	0.23	2.0	2.4
				TWPALPATLDSAFEDPQTK	0.0021	0.28	2.2	3.1

Table 1 (continued)

No	Protein name	Symbol	Protein access no	Peptide sequence detected	Anova <i>p</i> -value	Average fold change		
						4TBM	4TLM	4THM
16	Bone morphogenetic protein 1	BMP1	P98063	LPEIVSTDSR	0.0001	12.3	12.6	11.1
				GFQASHSTECGGQVR	< 0.0001	18.1	15.6	17.3
				VTSTSGTITSPNWPDK	0.0001	76.9	87.2	71.6
				ENIQPGQEYNFLK	0.0001	24.6	21.2	24.0
				FVSDGSINK	< 0.0001	21.7	22.8	20.3
				FYSDNSVQR	0.0002	26.8	23.4	21.9
				CSCDPGYELAPDK	0.002	8.4	8.6	6.9
				YDFVEVR	< 0.0001	61.4	57.3	54.9
				NCIWQLVAPTQYR	< 0.0001	34.8	33.8	31.7
17	Carboxypeptidase E	CPE	Q00493	GGGPQAISIGK	0.0002	29.6	22.9	23.0
				IHIMPSLNPDGFEK	0.0133	3.7	10.2	5.5
				SNAQGIDLNR	0.0311	4.1	7.7	5.3
				LTASAPGYLAITK	0.0243	3.6	9.8	5.2
				LLAPGNYK	0.036	3.3	7.8	3.8
				SGTAHEYSSCPD-DAIFQLAR	0.0266	3.1	5.4	3.8
				DGDYWR	0.0456	6.0	13.6	8.7
				EALVSVWLQCTAISR	0.0241	4.5	7.7	6.6
				18	Heparan sulfate proteoglycan 2	HSPG2	Q05793	DIYIGGAPDVATLTR
TSTADGLLLWQGVVR	0.0268	6.4	3.3					5.5
CLCLPGFSGPR	0.0489	4.0	2.1					3.0
19	Amyloid beta (A4) precursor-like protein 2	APLP2	Q06335	LNMHVNIQTGK	0.0123	40.5	10.6	30.8
				QQLVETHLAR	0.0003	5.0	14.5	9.2
20	Serpine peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1)	SERPINE2	Q07235	GMIDNLLSPNLIDGALTR	0.0137	7.9	9.8	16.5
				SRPHENVVVSPHGIASIL-GMLQLGADGK	0.0412	6.4	7.6	11.0
21	Fibulin 1	FBLN1	Q08879	TCVDINECQR	0.0398	5.6	3.1	3.2
				CVDVDECSPPAEPCGK	0.0178	56.4	32.2	25.5
				DIDECETGIHNCPPDFIC-QNTLGSFR	0.0007	13.4	7.7	7.0
				AGFYFDGISR	0.0015	9.4	7.5	5.9
				CLSFECPENYRR	0.0405	3.7	2.9	2.1
				ARENSDFVQNGADLQD-PAK	0.0011	4.1	2.9	2.4
				DSSCGTYELTEDNNCK	0.0011	17.8	8.2	8.7
22	Laminin, alpha 5	LAMAS	Q61001	APDQPLDSPHVCPCDCES-DFTDGTCEDLTGR	0.014	22.1	24.6	21.7
				STDFGHTYQPWQFFASSK	0.0432	8.8	13.1	9.5
				FANSPRPDLWVLER	0.0197	6.9	12.1	7.8
				AHPVSNADGTER	0.0007	17.6	28.7	20.9

Table 1 (continued)

No	Protein name	Symbol	Protein access no	Peptide sequence detected	Anova <i>p</i> -value	Average fold change		
						4TBM	4TLM	4THM
23	Ceruloplasmin (ferroxidase)	CP	Q61147	MYYSGVDPTK	0.0478	35.5	23.3	27.5
				TYTWQIPER	0.0327	17.4	7.4	10.7
				SLTLLMNPDTK	0.0218	49.5	20.0	30.0
				ALYFEYTDGTFISK	0.0083	47.2	17.6	29.6
				DIFTGLIGPMK	0.0493	11.0	4.0	7.1
				DIASGLIGPLILCK	0.0097	69.6	25.8	39.6
				VLPGQQYVYVLHANEP- SPGEGDSNCVTR	0.0161	17.1	7.9	11.4
				VFFEQGATR	0.0036	105.6	26.7	58.5
				EYTDGSFTNRK	0.0109	65.0	25.6	43.4
24	Insulin-like growth factor binding protein 7	IGFBP7	Q61581	GPDEEHLGILGPVIWAEVGD- DTIK	0.0191	18.8	3.8	10.5
				DACGCCPVCAR	0.0273	0.84	8.8	13.4
				VFLSCEVIGIPTPVWVK	0.0291	0.79	9.6	13.9
				ITVVDALHEIPLK	0.0484	1.0	10.1	13.5
				TELLPGDRENLAIQTR	0.0414	0.68	10.7	13.2
25	Glucosidase, alpha: neutral AB	GANAB	Q88HN3	EDAGEYECHASN- SQGASAAAK	0.0405	0.61	8.5	10.9
				NPEPELLVR	0.015	8.6	8.4	10.7
26	Quiescin Q6 sulfhydryl oxidase 1	QSOX1	Q8BND5	DPAEGNGAQPEATPGDGD- KPEETQEK	0.0201	10.2	5.5	13.3
				EFNIAGFPTVR	0.0111	50.7	37.3	40.7
27	Latent transforming growth factor beta binding protein 1	LTBP1	Q8CG19	VLNTESDLVVK	0.0044	26.0	22.1	20.6
				LSGALSEDPHFPK	0.0151	13.4	14.9	9.7
				AHFSPANIVIDSSASR	0.0008	30.8	28.8	24.5
				SFYTSYLR	0.0008	58.8	50.1	47.9
				FFQAFTK	0.0014	19.8	17.7	15.0
				ELCSACHNELNGQVPL- WDLGATLNFLK	0.0106	26.2	15.6	22.3
28	Latent transforming growth factor beta binding protein 4	LTBP4	Q8K4G1	FLNSFEELQAEECGILNG- CENGR	0.0114	11.4	5.0	7.2
				EAQPGQSQVSYQGLPVQK	0.049	4.2	4.1	3.9
29	OAF homolog (Drosophila)	OAF	Q8CQZR4	GGYTVCVCPDGFLLDSSR	0.0366	4.7	4.6	4.7
				CVPRPSGYTCACDPGFR	0.0451	4.3	6.2	4.8
				GSFPEPEESSER	0.0037	58.0	21.2	27.7
				CVCAPGFR	0.0138	5.8	6.6	6.2
				GSYTGALSEPYEGLEAEEC- GILDGCPHGR	0.0005	31.4	17.1	17.3
30	Protein disulfide isomerase family A, member 6	PDIA6	Q922R8	ALEQAELPR	0.0062	2.5	6.4	4.5
				GQSQFQALCFVTR	0.0166	2.3	5.2	4.2
				SYTFDFYVPQK	0.0068	2.8	5.3	4.9
				ALILGELEK	0.0024	2.6	7.0	5.2
31	Tubulointerstitial nephritis antigen-like 1	TINAGL1	Q99JR5	GVDSSVFEALPK	0.0024	3.0	6.5	5.7
				GSFSEQGINEFLR	0.0119	25.9	16.2	12.6
32	Thymic stromal lymphopoietin	TSLP	Q9JIE6	NLEPEWAAAATEVK	0.0381	14.1	12.1	7.5
				ITGWGEETLPDGR	< 0.0001	25.6	6.9	30.0
				IYPVFGTYWDNCNR	0.0014	11.9	2.8	11.8
33	Thymic stromal lymphopoietin	TSLP	Q9JIE6	YWTAANSWGPWWGER	0.0003	19	1.8	5.1
				FEQIEDCESK	0.011	58.4	25.3	29.3
34	Thymic stromal lymphopoietin	TSLP	Q9JIE6	IYCNIIFHDLTGDLK	0.0281	51.9	24.9	25.8

Table 1 (continued)

No	Protein name	Symbol	Protein access no	Peptide sequence detected	Anova <i>p</i> -value	Average fold change		
						4TBM	4TLM	4THM
33	Procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	PLOD1	Q9ROE2	SEDYVDIVQGR	0.0132	6.0	0.60	2.7
				VGWVWNPYISNIYLIK	0.0306	8.5	0.23	2.5
34	Cathepsin Z	CTSZ	Q9WUU7	NSWGEPWGEK	0.0138	7.6	6.7	5.0
				FNQCGTCTEFK	0.0208	7.0	6.0	53
				VGDYGSLSGR	0.0178	10.0	6.4	6.6
				HGIPDETCNNYQAK	0.01	11.2	10.1	8.0
35	EGF containing fibulin-like extracellular matrix protein 2	EFEMP2	Q9WVJ9	SCVDVNECDMGAPCEQR	0.0054	44.6	5.6	29.7
				FSCHCPQGYQLLATR	0.0007	29.9	93	21.8
				SVPADVVFQIQATSVYP-GAYNAFQIR	0.0101	26.0	7.1	18.9

Proteins were detected by label-free nLC-MS/MS. Proteins with at least 2 or more peptides detected were presented. The statistical significance was determined by one-way ANOVA at $p < 0.05$ ($n = 3$)

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