

Supplemental Table 4. Mammary tumor transcripts differentially regulated by virulent sectional metastasis at $Q < 0.05$, $n = 66$ microarrays). The gene expression data from individual mammary tumor samples were ordered such that 25% (33 samples) of the total samples came from mice with no surface- or section- metastatic lesions and the longest tumor onset. Gene expression data from these 33 samples served as the reference group when paired with the gene expression data of 33 mammary tumor samples from mice that had the most sectional metastatic lesions detected (AMD66). Annotation was performed with Ingenuity Pathway Analysis Knowledge Base.

*Positive fold change is significant fold change increase in gene expression from mammary tumors with virulent sectional metastasis relative to mammary tumors with no metastasis. Negative fold change is significant fold change increase in gene expression from mammary tumors with no metastasis relative to mammary tumors with virulent sectional metastasis.

†Identification of transcript by RefSeq or Illumina probe ID where RefSeq was not available.

‡Highlights significant transcripts that appear in duplicate due to the redundancy of transcript representation on Illumina Bead Chips.

§Official symbolic name of transcript

||Official descriptive name of transcript

	A	B	C	D	E	F
1	Fold Change*	False Discovery Rate (q-value)	ID†	Notes‡	Molecules§	Description
2	-0.793	1.239	NM_007382		ACADM	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain
3	-0.82	2.422	NM_007393.1		ACTB	actin, beta
4	-0.768	0	NM_175643.1	D	ADAMTS2	ADAM metalloproteinase with thrombospondin type 1 motif, 2
5	-0.812	2.144	NM_175643.1	D	ADAMTS2	ADAM metalloproteinase with thrombospondin type 1 motif, 2
6	-0.56	4.592	NM_009605.3		ADIPOQ	adiponectin, C1Q and collagen domain containing
7	-0.821	2.422	NM_009636.1		AEBP1	AE binding protein 1
8	-0.838	4.864	NM_025337.2		AKR7A2	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)
9	1.246	0	NM_024204		ANKRD22	ankyrin repeat domain 22
10	-0.887	4.864	NM_011784.2		APLNR	apelin receptor
11	-0.81	0	NM_007470.1		APOD	apolipoprotein D
12	1.255	1.845	NM_173743.2		APOL9B	apolipoprotein L 9b
13	1.535	1.845	NM_007482		ARG1	arginase, liver
14	1.268	0	NM_009705.1		ARG2	arginase, type II
15	-0.877	2.144	NM_008488.1		ARHGEF1	Rho guanine nucleotide exchange factor (GEF) 1
16	-0.828	3.131	NM_026369.1		ARPC5	actin related protein 2/3 complex, subunit 5, 16kDa
17	1.453	0	NM_012055.1		ASNS	asparagine synthetase
18	1.149	3.131	NM_022305.2		B4GALT1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1
19	-0.791	0	NM_007542.3		BGN	biglycan
20	1.257	1.845	NM_010800.2	D	BHLHB8	basic helix-loop-helix domain containing, class B, 8
21	1.243	0.967	NM_010800.2	D	BHLHB8	basic helix-loop-helix domain containing, class B, 8
22	-0.8	0	NM_031397.1		BICC1	bicaudal C homolog 1 (Drosophila)
23	1.183	4.592	NM_008528.3		BLNK	B-cell linker
24	1.246	0	NM_009761.2		BNIP3L	BCL2/adenovirus E1B 19kDa interacting protein 3-like
25	-0.85	2.422	NM_023336.2		BRD3	bromodomain containing 3
26	-0.76	4.864	NM_013483.1		BTN1A1	butyrophilin, subfamily 1, member A1
27	1.145	4.592	AK049325	D	C12ORF30	chromosome 12 open reading frame 30
28	1.092	4.592	NM_172722	D	C12ORF30	chromosome 12 open reading frame 30
29	-0.86	4.864	NM_198609		C15ORF15	chromosome 15 open reading frame 15
30	1.12	3.406	NM_175287.2		C1ORF174	chromosome 1 open reading frame 174
31	-0.793	0	NM_198860.1		C22ORF36	chromosome 22 open reading frame 36
32	1.114	4.592	NM_024495.2		CA13	carbonic anhydrase XIII
33	-0.757	0	NM_026439.1		CCDC80	coiled-coil domain containing 80
34	-0.764	0	NM_010545.2		CD74	CD74 molecule, major histocompatibility complex, class II invariant chain
35	1.216	4.592	NM_007669.2		CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
36	1.128	4.864	NM_173370.3		CDS1	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1
37	-0.774	2.422	NM_009885.1		CEL	carboxyl ester lipase (bile salt-stimulated lipase)
38	-0.676	3.668	NM_017392		CELSR2	cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)
39	-0.56	1.239	NM_013459.1		CFD	complement factor D (adipsin)
40	1.45	0	NM_026929.2		CHAC1	ChaC, cation transport regulator homolog 1 (E. coli)

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1	Fold Change*	False Discovery Rate (q-value)	ID†	Notes‡	Molecules§	Description
41	-0.876	3.406	NM_145979.1		CHD4	chromodomain helicase DNA binding protein 4
42	1.179	3.406	NM_023543.1		CHN2	chimerin (chimaerin) 2
43	-0.827	3.131	NM_007714.2		CLK4	CDC-like kinase 4
44	-0.91	3.406	NM_029738.1		CLUAP1	clusterin associated protein 1
45	-0.709	2.144	NM_007742.2		COL1A1	collagen, type I, alpha 1
46	-0.815	2.144	NM_015734.1		COL5A1	collagen, type V, alpha 1
47	-0.755	0	NM_009933.1	D	COL6A1	collagen, type VI, alpha 1
48	-0.771	2.422	NM_009933.1	D	COL6A1	collagen, type VI, alpha 1
49	-0.839	4.864	NM_134002.1		CSNK1G2	casein kinase 1, gamma 2
50	1.311	4.592	NM_033616.2		CSPRS	component of Sp100-rs
51	-0.8	0	NM_007802.2		CTSK	cathepsin K
52	1.235	2.144	NM_022325.3		CTSZ	cathepsin Z
53	-0.876	3.131	NM_009987.2		CX3CR1	chemokine (C-X3-C motif) receptor 1
54	-0.711	2.422	NM_007833.1		DCN	decorin
55	1.327	1.845	NM_029083.1		DDIT4	DNA-damage-inducible transcript 4
56	-0.864	2.422	NM_022563.2		DDR2	discoidin domain receptor tyrosine kinase 2
57	-0.849	1.845	NM_015814.2		DKK3	dickkopf homolog 3 (<i>Xenopus laevis</i>)
58	1.18	2.144	NM_007904.2		EDNRB	endothelin receptor type B
59	-0.829	1.845	NM_028889.1		EFHD1	EF-hand domain family, member D1
60	1.143	3.131	NM_010107.2		EFNA1	ephrin-A1
61	1.704	0	NM_028133.1		EGLN3	egl nine homolog 3 (<i>C. elegans</i>)
62	-0.866	3.668	NM_146200		EIF3C	eukaryotic translation initiation factor 3, subunit C
63	-0.725	0	NM_007925.2		ELN	elastin (supravalvular aortic stenosis, Williams-Beuren syndrome)
64	-0.819	3.131	NM_080595.1		EMID1	EMI domain containing 1
65	-0.874	3.131	NM_010129.1		EMP3	epithelial membrane protein 3
66	1.255	2.144	NM_023119		ENO1	enolase 1, (alpha)
67	-0.808	0	NM_010169.2		F2R	coagulation factor II (thrombin) receptor
68	-0.886	4.592	NM_024170		FAM127C	family with sequence similarity 127, member C
69	-0.865	3.406	NM_023605.1		FBXO9	F-box protein 9
70	-0.795	2.144	NM_010189		FCGRT	Fc fragment of IgG, receptor, transporter, alpha
71	1.169	4.592	NM_146054.1		FERMT2	fermitin family homolog 2 (<i>Drosophila</i>)
72	-0.86	2.422	NM_153573.1		FKBP14	FK506 binding protein 14, 22 kDa
73	1.197	0	NM_010220.2		FKBP5	FK506 binding protein 5
74	-0.831	4.592	NM_008028.1		FLOT2	flotillin 2
75	-0.855	3.131	XM_129845.3		FN1	fibronectin 1
76	-0.789	1.845	NM_008047.2		FSTL1	follicle-stimulating-like 1
77	1.263	2.144	NM_008084.1	D	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
78	1.225	0	NM_008084.2	D	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
79	1.373	0	NM_010288.2		GJA1	gap junction protein, alpha 1, 43kDa
80	1.173	0.967	NM_015828		GNE	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase
81	-0.864	4.864	NM_175193.2		GOLIM4	golgi integral membrane protein 4

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82	-0.835	4.592	NM_016696.1		GPC1	glypican 1
83	1.174	0	NM_173866.1		GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2
84	-0.884	3.131	NM_027127.1		GPX8	glutathione peroxidase 8
85	-0.806	0	NM_145558		HADHB	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit
86	1.192	0	NM_178192.1		HIST1H4F	histone cluster 1, H4f
87	1.202	4.592	NM_175655.1		HIST1H4I	histone cluster 1, H4i
88	1.173	0	NM_178211.1	D	HIST4H4	histone cluster 4, H4
89	1.165	4.592	NM_178210.1	D	HIST4H4	histone cluster 4, H4
90	1.329	0	NM_013820.1		HK2	hexokinase 2
91	-0.736	1.239	NM_207105.1	D	HLA-DQB2	major histocompatibility complex, class II, DQ beta 2
92	-0.74	1.239	NM_010379.2	D	HLA-DQB2	major histocompatibility complex, class II, DQ beta 2
93	-0.711	0	NM_182650.2		HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1
94	1.186	0.967	NM_152134.1	D	HOMER1	homer homolog 1 (Drosophila)
95	1.171	0.967	NM_152134.1	D	HOMER1	homer homolog 1 (Drosophila)
96	-0.806	1.239	NM_017370.1		HPR	haptoglobin-related protein
97	-0.808	1.845	NM_008288		HSD11B1	hydroxysteroid (11-beta) dehydrogenase 1
98	-0.749	3.131	NM_008302.2	D	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1
99	-0.824	3.406	NM_008302.2	D	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1
100	-0.829	3.406	NM_008305.2		HSPG2	heparan sulfate proteoglycan 2
101	1.48	0	NM_025378.1	D	IFITM3	interferon induced transmembrane protein 3 (1-8U)
102	1.448	0.967	NM_025378.1	D	IFITM3	interferon induced transmembrane protein 3 (1-8U)
103	-0.641	3.668	XM_132633.4		IGK	immunoglobulin kappa chain complex
104	-0.844	2.422	XM_194109.2		IGSF3	immunoglobulin superfamily, member 3
105	-0.751	2.144	NM_010549.1		IL11RA	interleukin 11 receptor, alpha
106	-0.8	1.239	NM_008361		IL1B	interleukin 1, beta
107	-0.881	4.592	NM_182784.1		IQSEC1	IQ motif and Sec7 domain 1
108	1.253	0	XM_194279		JMJD1A	jumonji domain containing 1A
109	-0.839	4.592	NM_008416.1		JUNB	jun B proto-oncogene
110	-0.905	3.131	NM_145611		KANK2	KN motif and ankyrin repeat domains 2
111	-0.855	2.422	NM_172872.2		KANK4	KN motif and ankyrin repeat domains 4
112	-0.838	4.864	XM_133614.4		KCTD14	potassium channel tetramerisation domain containing 14
113	1.158	1.845	NM_028791.3		KIAA0082	KIAA0082
114	-0.707	1.239	NM_020568.1		KIAA1881	KIAA1881
115	-0.853	0	XM_358544.1		KIF1A	kinesin family member 1A
116	-0.878	2.422	NM_007905.1		LOC653441	similar to polyhomeotic 1-like
117	-0.78	0	NM_010729.2		LOXL1	lysyl oxidase-like 1
118	-0.704	1.239	NM_029796.2		LRG1	leucine-rich alpha-2-glycoprotein 1
119	-0.873	2.144	NM_177152.4		LRIG3	leucine-rich repeats and immunoglobulin-like domains 3
120	-0.746	0	XM_358823.1		LRRC15	leucine rich repeat containing 15
121	1.174	3.406	NM_025948.1		LSM14A	LSM14A, SCD6 homolog A (S. cerevisiae)

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1	Fold Change*	False Discovery Rate (q-value)	ID†	Notes‡	Molecules§	Description
122	-0.788	3.131	NM_010741		LY6C1	lymphocyte antigen 6 complex, locus C1
123	-0.869	4.864	NM_008567.1		MCM6	minichromosome maintenance complex component 6
124	-0.843	1.239	NM_015776		MFAP5	microfibrillar associated protein 5
125	-0.76	0	NM_012022.1		MGI:1349458	per-pentamer repeat gene
126	-0.701	1.239	NM_008597.2		MGP	matrix Gla protein
127	-0.761	2.144	NM_026178.2		MMD	monocyte to macrophage differentiation-associated
128	-0.73	0	NM_008610.1		MMP2	matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)
129	-0.83	3.406	NM_028722.1		MSL-1	male-specific lethal-1 homolog
130	-0.83	1.239	NM_010833.1		MSN	moesin
131	-0.833	4.592	NM_013827.1		MTF2	metal response element binding transcription factor 2
132	1.168	0	NM_172308.2		MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like
133	1.378	0	NM_008638		MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase
134	1.265	2.144	NM_013606		MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)
135	1.185	0.967	NM_021524.1		NAMPT	nicotinamide phosphoribosyltransferase
136	-0.849	3.131	NM_010882.2		NDN	necdin homolog (mouse)
137	1.361	0.967	NM_008681		NDRG1	N-myc downstream regulated gene 1
138	-0.784	1.239	NM_010906.1		NFIX	nuclear factor I/X (CCAAT-binding transcription factor)
139	-0.847	2.144	NM_010917.1		NID1	nidogen 1
140	-0.855	3.131	NM_008737.1	D	NRP1	neuropilin 1
141	-0.883	3.406	NM_008737.1	D	NRP1	neuropilin 1
142	-0.865	2.144	NM_008740.2		NSF	N-ethylmaleimide-sensitive factor
143	-0.831	0	NM_008788.1		PCOLCE	procollagen C-endopeptidase enhancer
144	-0.836	0	AK011999		PDE4B	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)
145	-0.803	0	NM_011058.1		PDGFRA	platelet-derived growth factor receptor, alpha polypeptide
146	1.174	0.967	NM_008827.2		PGF	placental growth factor
147	1.429	0	NM_008828		PGK1	phosphoglycerate kinase 1
148	1.694	0	NM_008843.1		PIP	prolactin-induced protein
149	-0.844	3.668	NM_011962.2		PLOD3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3
150	-0.785	0	NM_011101.3		PRKCA	protein kinase C, alpha
151	-0.883	3.131	XM_131444.4		PRPF4	PRP4 pre-mRNA processing factor 4 homolog (yeast)
152	-0.809	2.422	NM_028195		PSCD4	pleckstrin homology, Sec7 and coiled-coil domains 4
153	-0.846	4.864	XM_355811		PTMS	parathyrosin
154	-0.81	0	NM_008997.1		RAB11B	RAB11B, member RAS oncogene family
155	-0.821	1.239	NM_178045.3	D	RASSF4	Ras association (RalGDS/AF-6) domain family member 4
156	-0.838	2.144	NM_178045.3	D	RASSF4	Ras association (RalGDS/AF-6) domain family member 4
157	-0.816	2.422	NM_009031.2		RBBP7	retinoblastoma binding protein 7
158	1.171	0	NM_178608.2		REEP1	receptor accessory protein 1

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1	Fold Change*	False Discovery Rate (q-value)	ID†	Notes‡	Molecules§	Description
159	-0.828	0	NM_007874.2		REEP5	receptor accessory protein 5
160	1.187	0.967	NM_139292.1		REEP6	receptor accessory protein 6
161	1.143	4.592	XM_128488.3		RGS11	regulator of G-protein signaling 11
162	1.511	2.144	NR_003278.1		RN18S	18S RNA
163	-0.859	3.668	NM_013876.2		RNF11	ring finger protein 11
164	-0.853	1.239	NM_022891.1		RPL23	ribosomal protein L23
165	1.16	4.864	NM_011297.2		RPS24	ribosomal protein S24
166	1.406	3.131	NM_021384.2		RSAD2	radical S-adenosyl methionine domain containing 2
167	-0.847	3.131	NM_153790.1		SCARF2	scavenger receptor class F, member 2
168	-0.725	0	NM_011325.1		SCNN1B	sodium channel, nonvoltage-gated 1, beta (Liddle syndrome)
169	-0.67	0	NM_011340.2		SERPINF1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1
170	-0.838	2.144	NM_030261		SESN3	sestrin 3
171	-0.808	3.131	NM_009186		SFRS10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)
172	-0.804	1.845	NM_172755.2		SFRS14	splicing factor, arginine/serine-rich 14
173	-0.88	3.406	NM_024480.2		SH3BP5L	SH3-binding domain protein 5-like
174	1.321	0	NM_018861.2		SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4
175	-0.836	4.592	NM_153150.1		SLC25A1	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1
176	1.383	0	NM_011400.1		SLC2A1	solute carrier family 2 (facilitated glucose transporter), member 1
177	-0.902	4.592	NM_021435.1		SLC35B4	solute carrier family 35, member B4
178	-0.871	4.592	AK019479		SLIT3	slit homolog 3 (Drosophila)
179	-0.838	3.668	NM_022315.1		SMOC2	SPARC related modular calcium binding 2
180	1.196	3.406	NM_011451.1		SPHK1	sphingosine kinase 1
181	-0.883	3.406	NM_029035.2		SPSB1	splA/ryanodine receptor domain and SOCS box containing 1
182	1.16	0	NM_153091.2		ST7L	suppression of tumorigenicity 7 like
183	-0.805	3.406	NM_009368.1		TGFB3	transforming growth factor, beta 3
184	-0.88	3.668	XM_129857.4		TGFBRAP1	transforming growth factor, beta receptor associated protein 1
185	-0.8	1.845	NM_009382.2		THY1	Thy-1 cell surface antigen
186	-0.783	0	NM_011593		TIMP1	TIMP metalloproteinase inhibitor 1
187	-0.767	1.845	NM_009388.2		TKT	transketolase (Wernicke-Korsakoff syndrome)
188	-0.855	1.239	NM_133804.1		TMEM132A	transmembrane protein 132A
189	1.196	2.144	NM_009415.1		TPI1	triosephosphate isomerase 1
190	-0.63	2.422	NM_022314		TPM3	tropomyosin 3
191	1.321	0	NM_144554.1		TRIB3	tribbles homolog 3 (Drosophila)
192	-0.859	3.668	NM_030706.1		TRIM2	tripartite motif-containing 2
193	1.289	3.131	NM_011909.1		USP18	ubiquitin specific peptidase 18
194	-0.83	1.239	NM_144826.2		UTP6	UTP6, small subunit (SSU) processome component, homolog (yeast)
195	1.592	0	NM_009505.2		VEGFA	vascular endothelial growth factor A

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196	1.251	0	NM_013703.1	D	VLDLR	very low density lipoprotein receptor
197	1.185	0	NM_013703	D	VLDLR	very low density lipoprotein receptor
198	-0.563	4.864	NM_011709.2		WAP	whey acidic protein
199	-0.823	2.144	NM_009525.2		WNT5B	wingless-type MMTV integration site family, member 5B
200	-0.838	4.592	NM_007496.1		ZFH3	zinc finger homeobox 3
201	1.497	0	2610528A11Rik			This ID not mapped to the IPAKB
202	1.347	0.967	XM_147335.2			This ID not mapped to the IPAKB
203	1.303	3.131	XM_356224.1			This ID not mapped to the IPAKB
204	1.118	2.144	XM_284356.2			This ID not mapped to the IPAKB
205	-0.518	0	XM_354700			This ID not mapped to the IPAKB
206	-0.682	0	XM_354700			This ID not mapped to the IPAKB
207	-0.808	4.864	NM_012059.2			This ID not mapped to the IPAKB
208	-0.815	2.144	XM_484355			This ID not mapped to the IPAKB
209	-0.83	3.668	1110003O08Rik			This ID not mapped to the IPAKB
210	-0.836	2.422	XM_358661.1			This ID not mapped to the IPAKB
211	-0.851	2.144	9530083O12Rik			This ID not mapped to the IPAKB
212	-0.869	2.144	XM_134183.4			This ID not mapped to the IPAKB
213	-0.871	3.406	XM_489155			This ID not mapped to the IPAKB
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