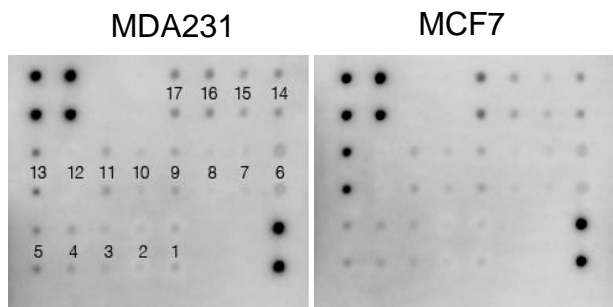
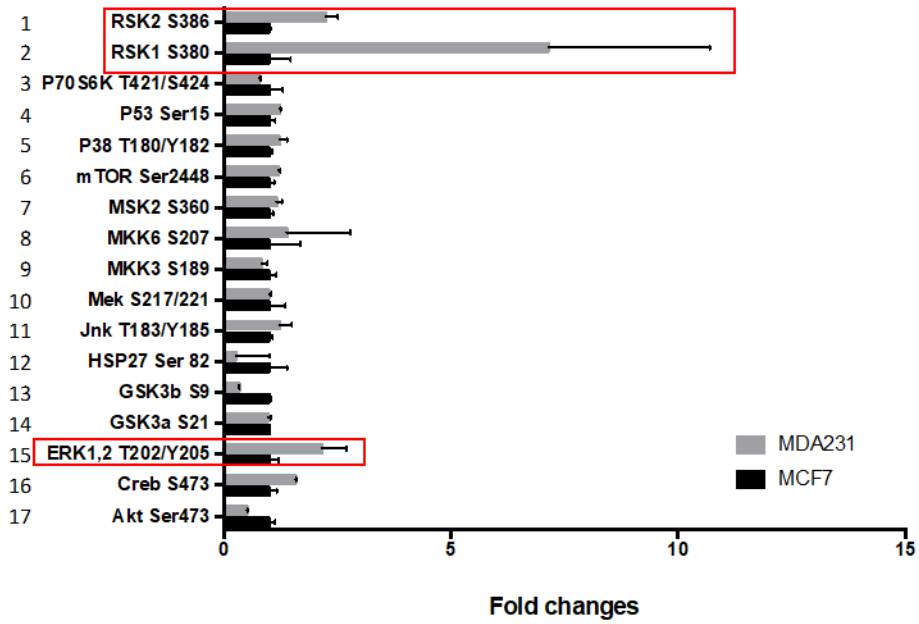
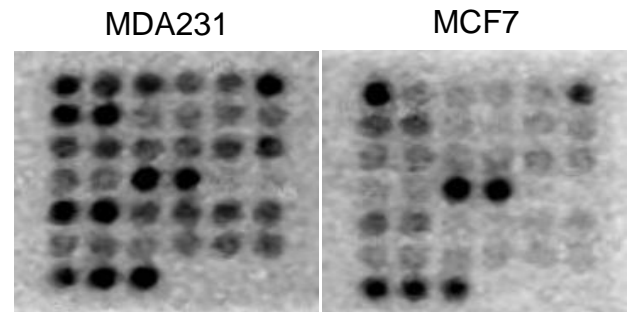
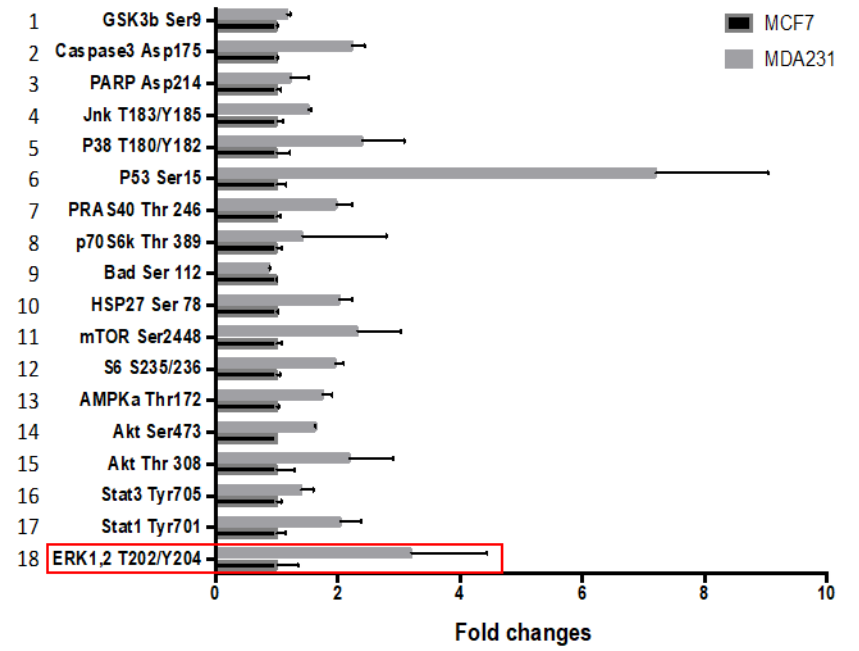
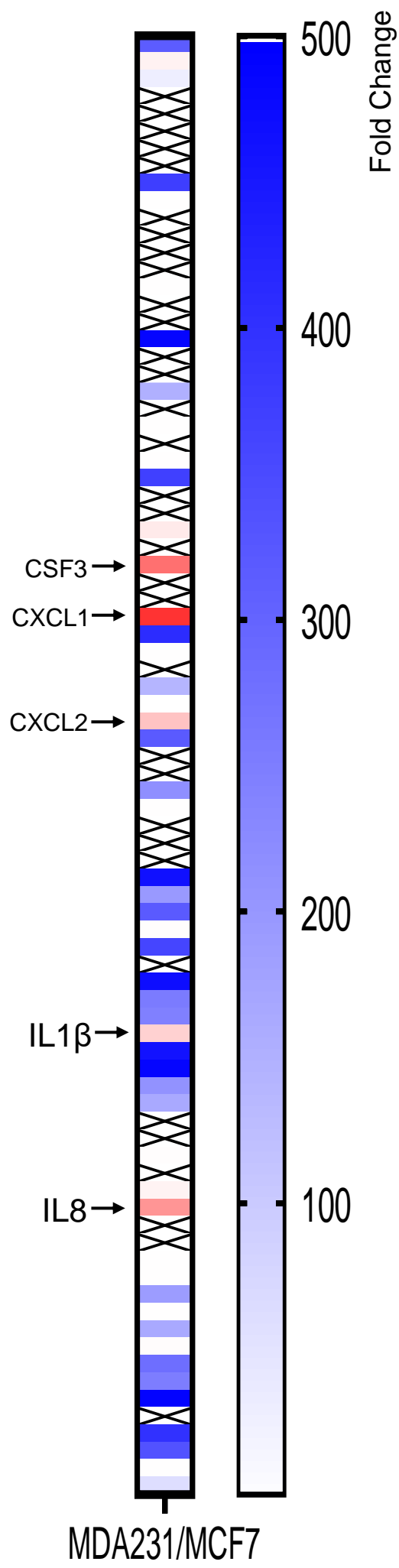
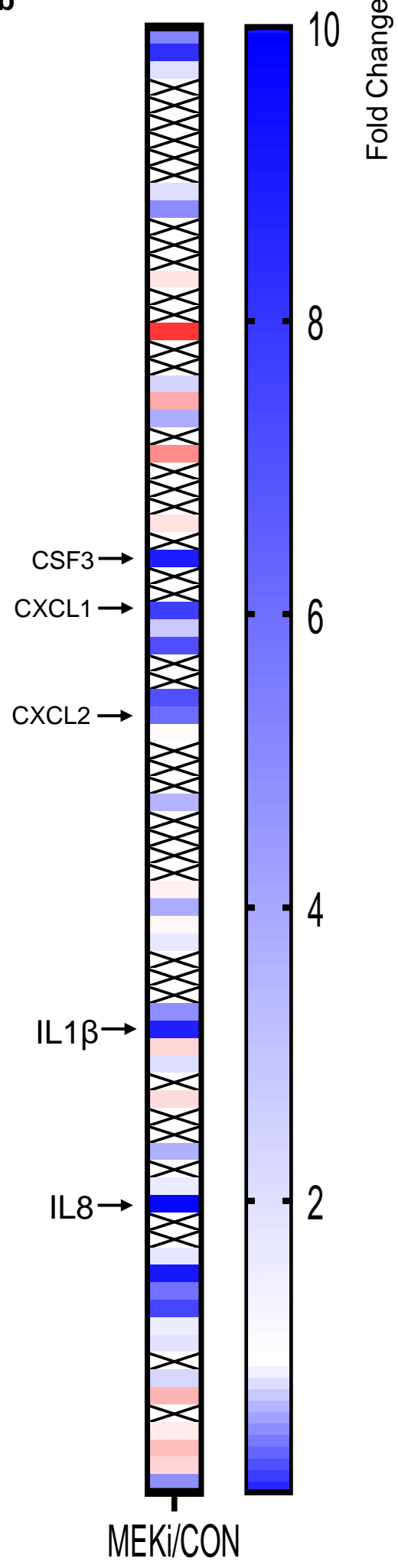


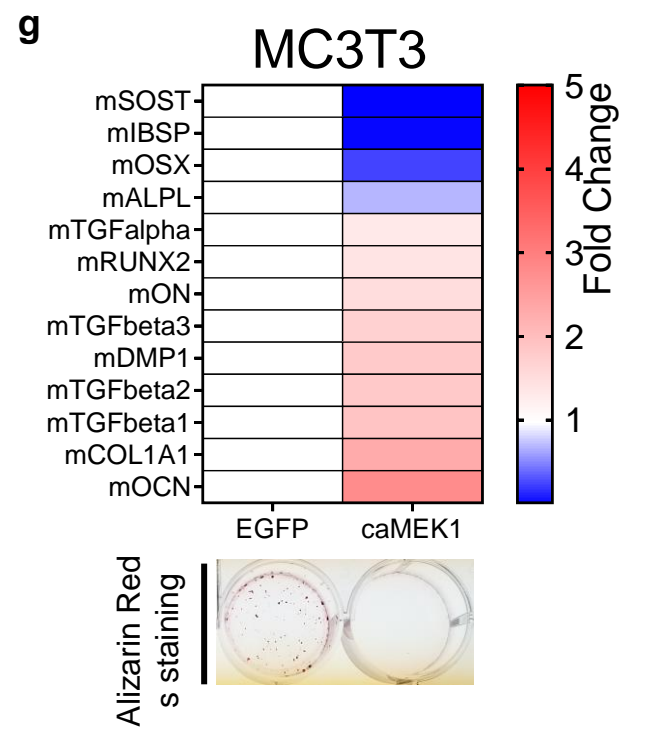
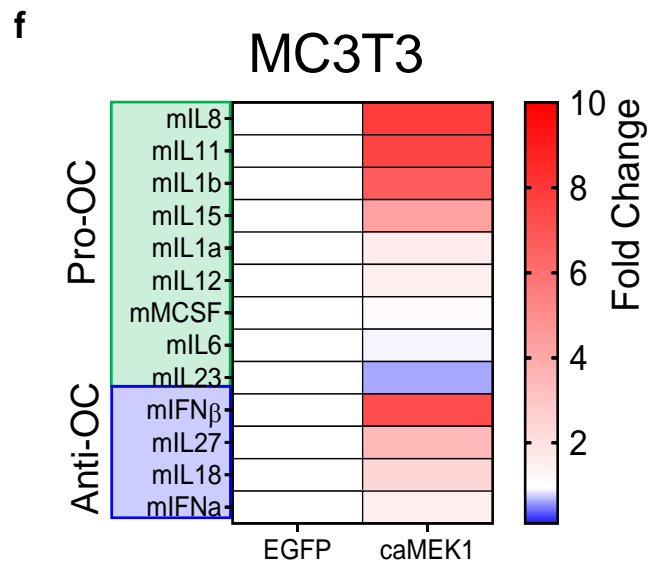
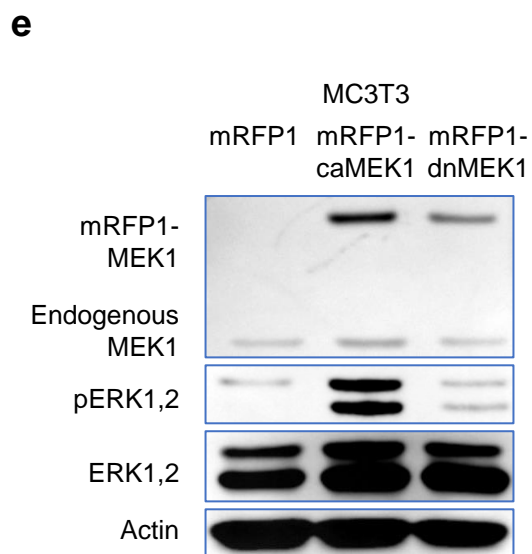
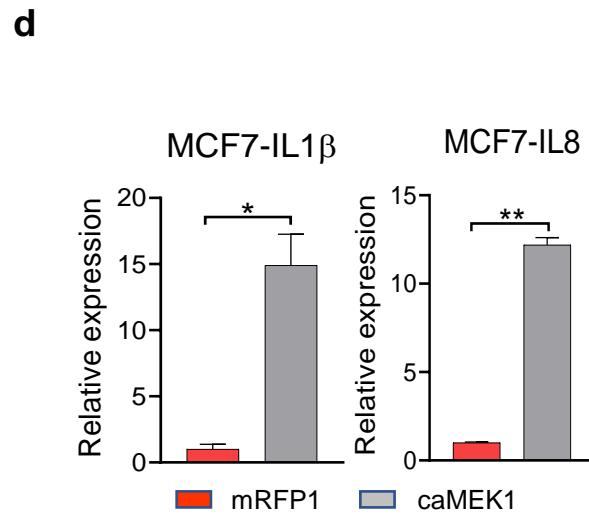
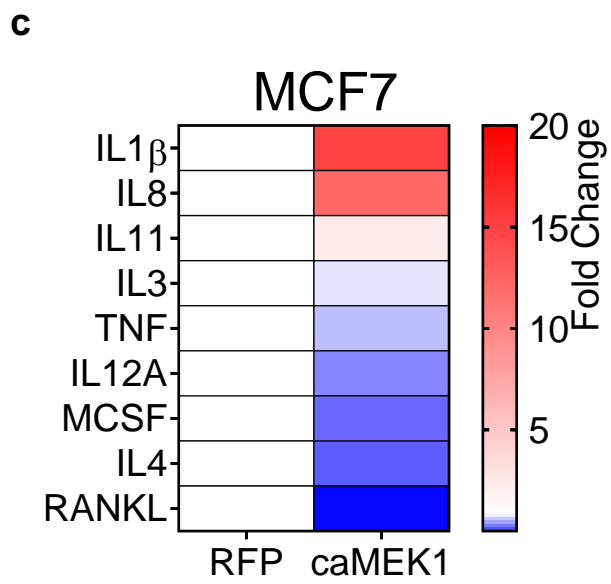
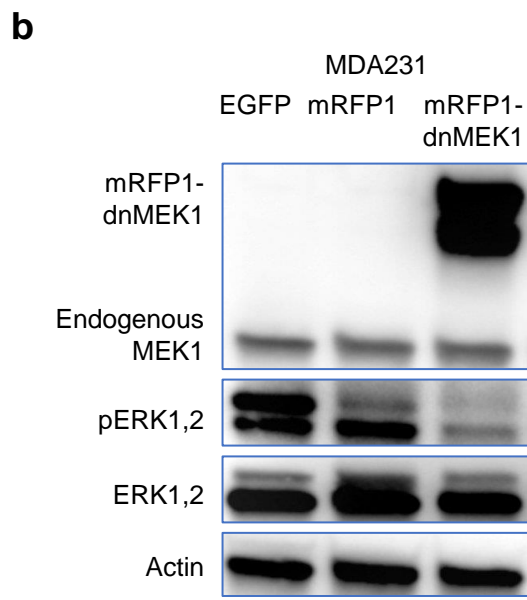
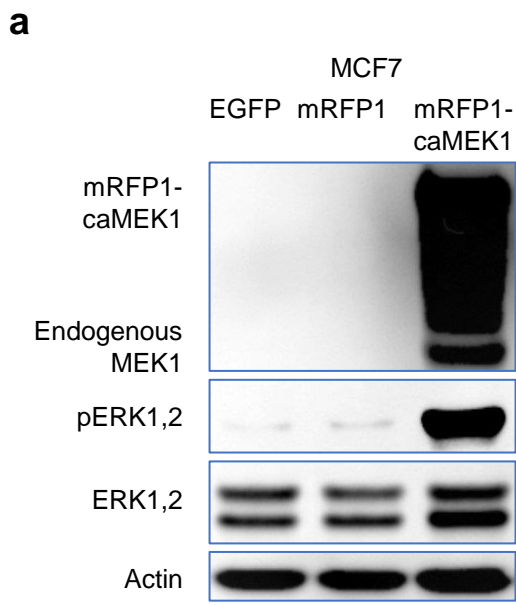
a**Raybiotech****b****Cell signaling-columbia**

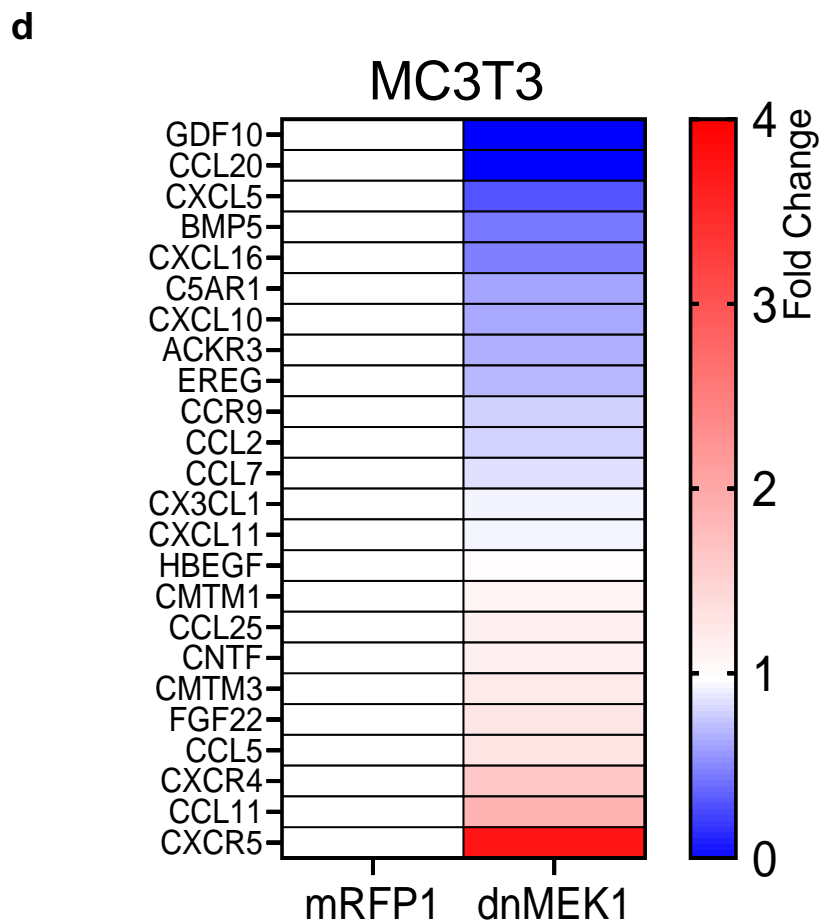
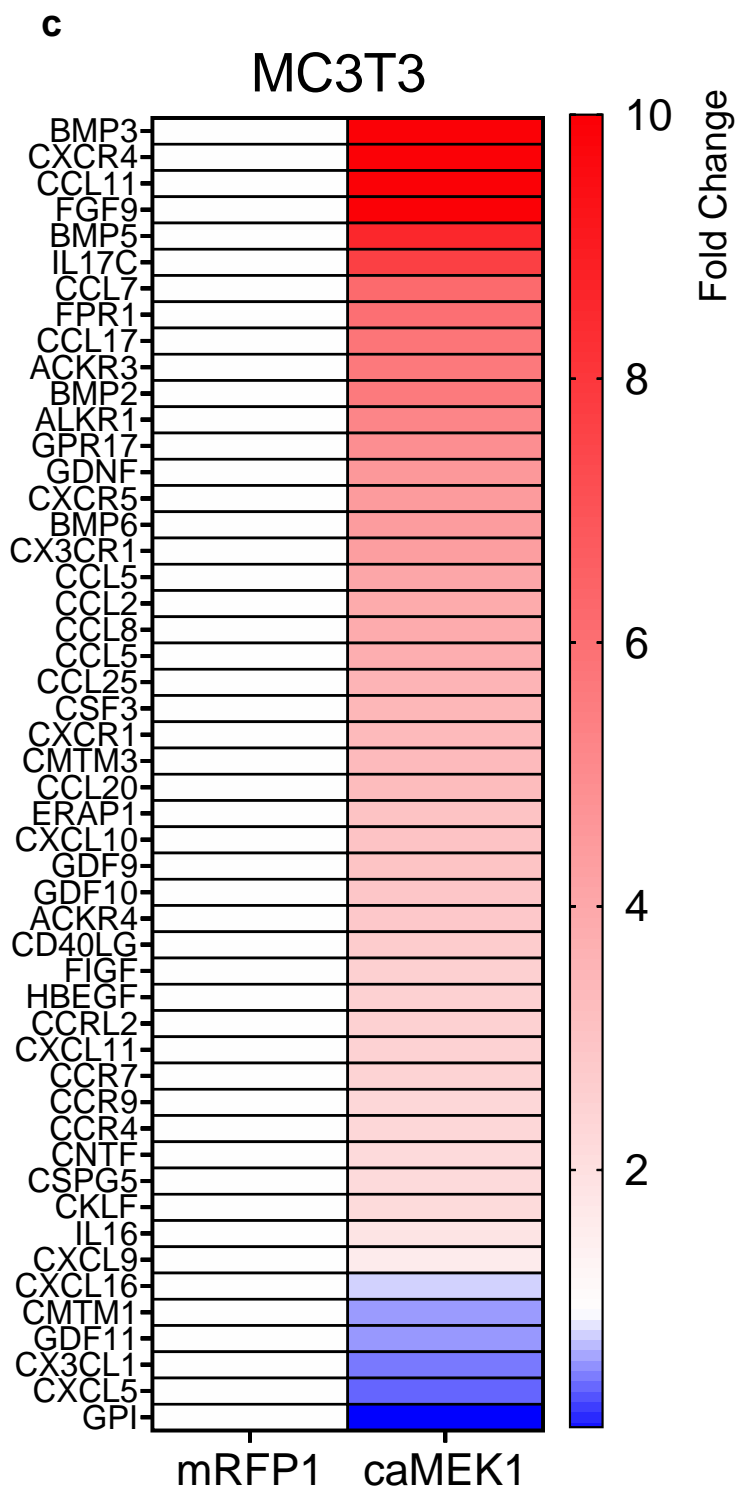
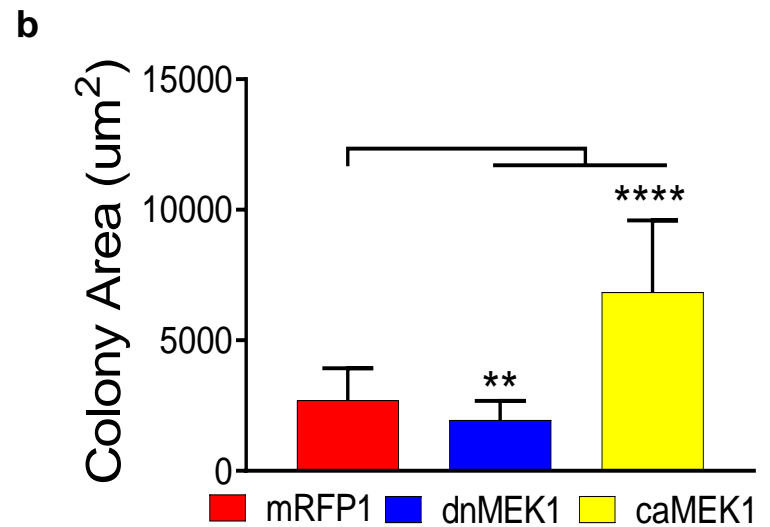
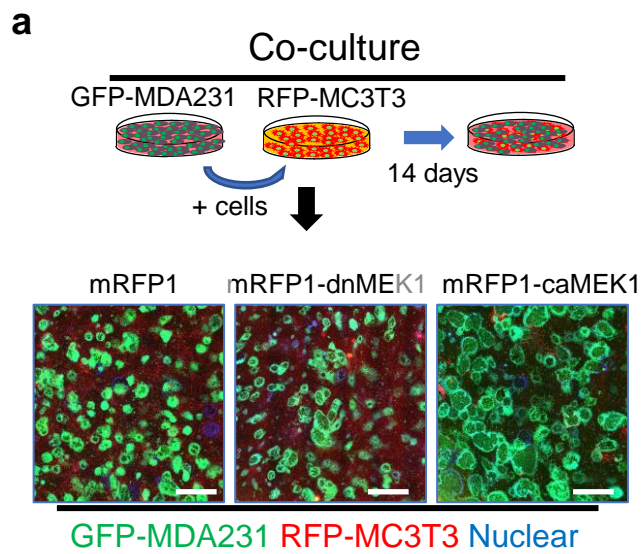
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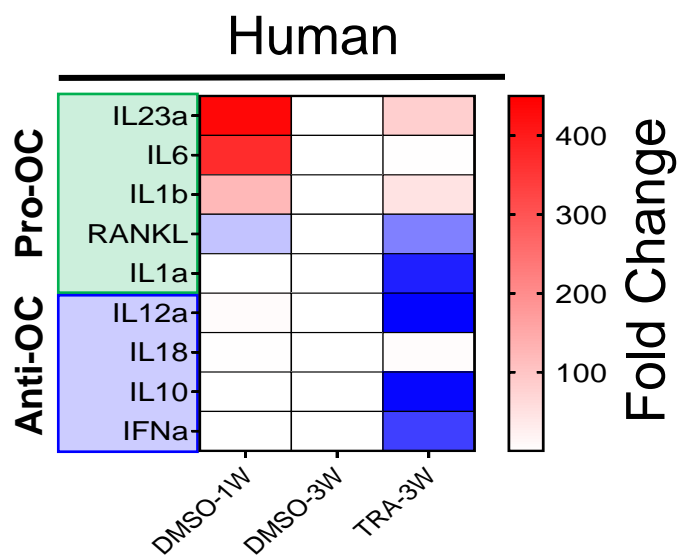
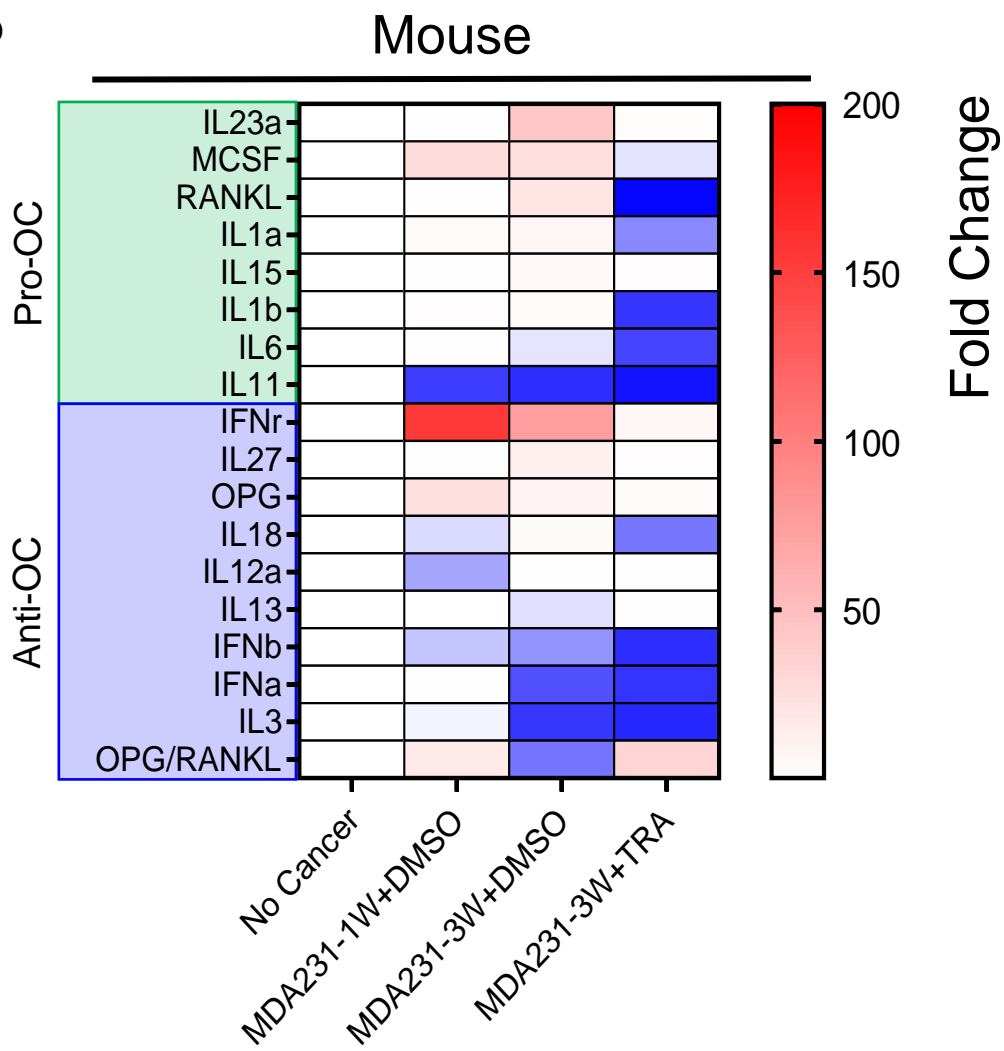


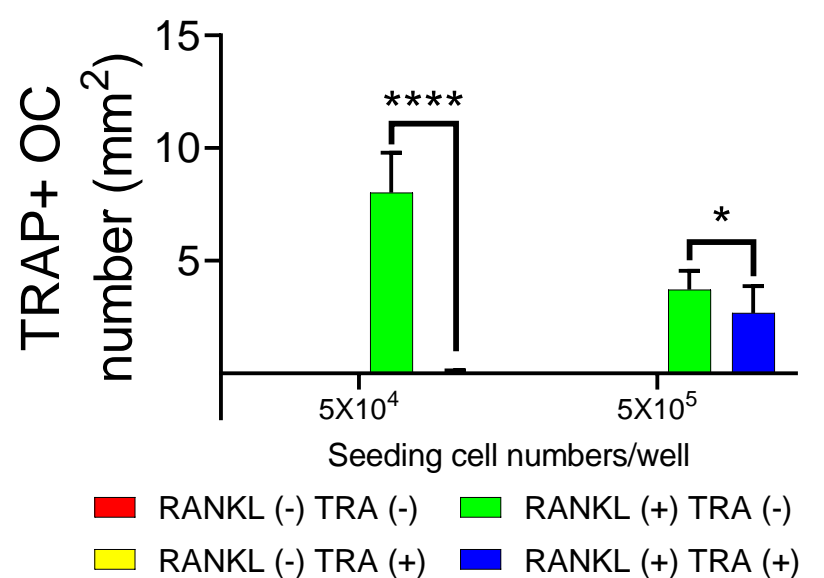
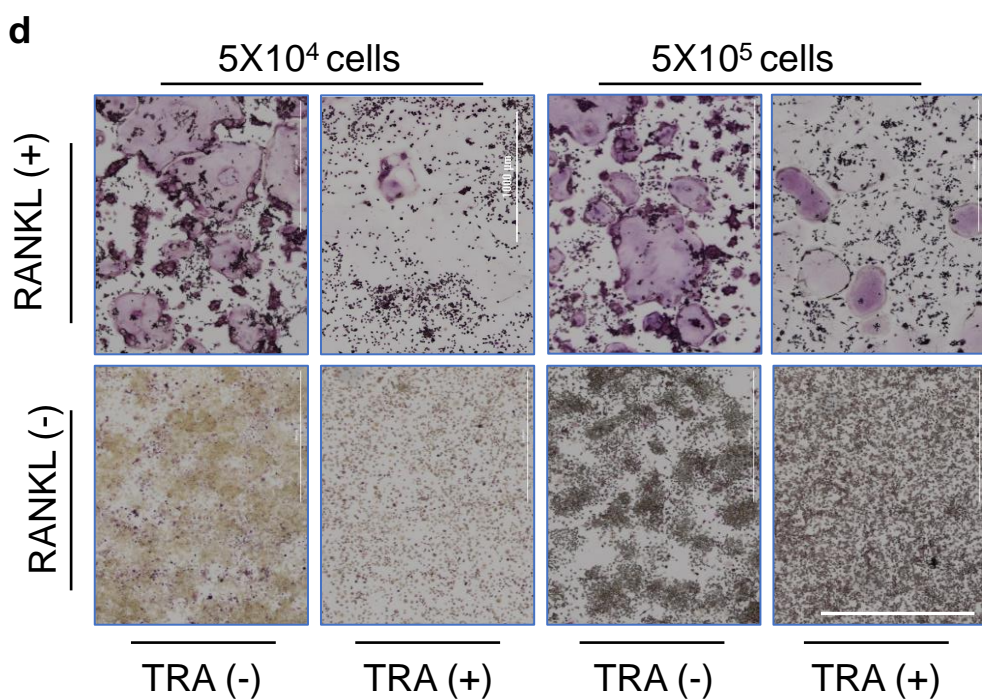
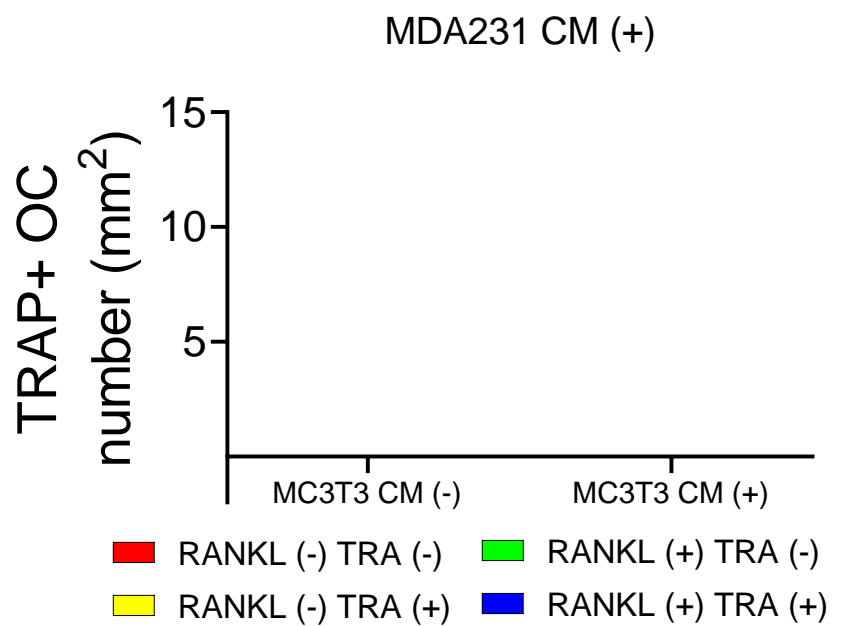
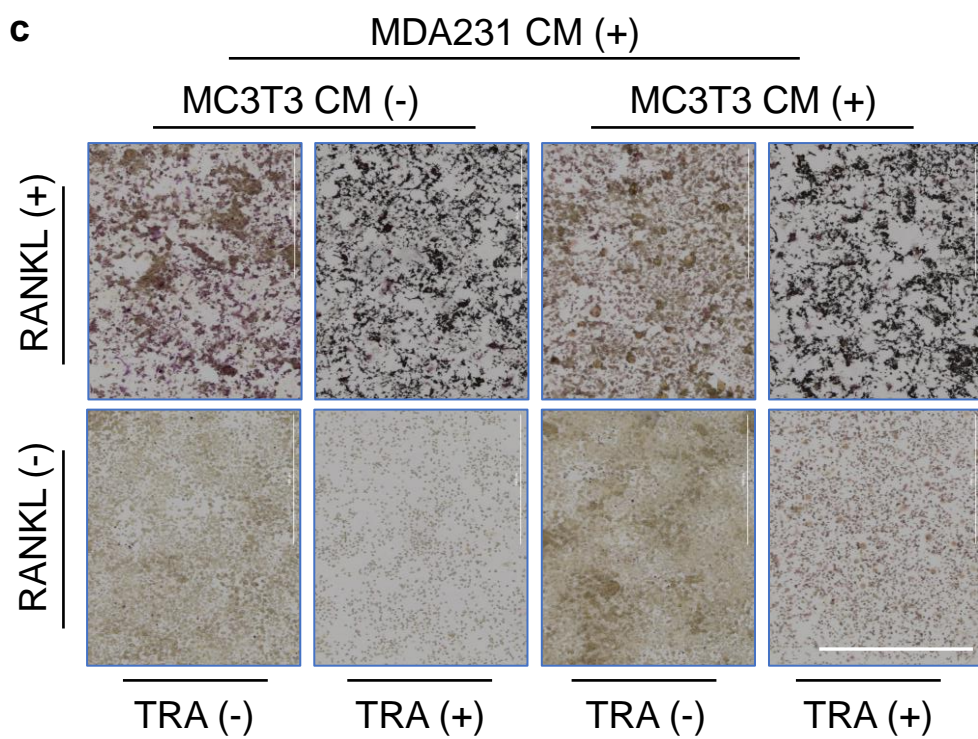
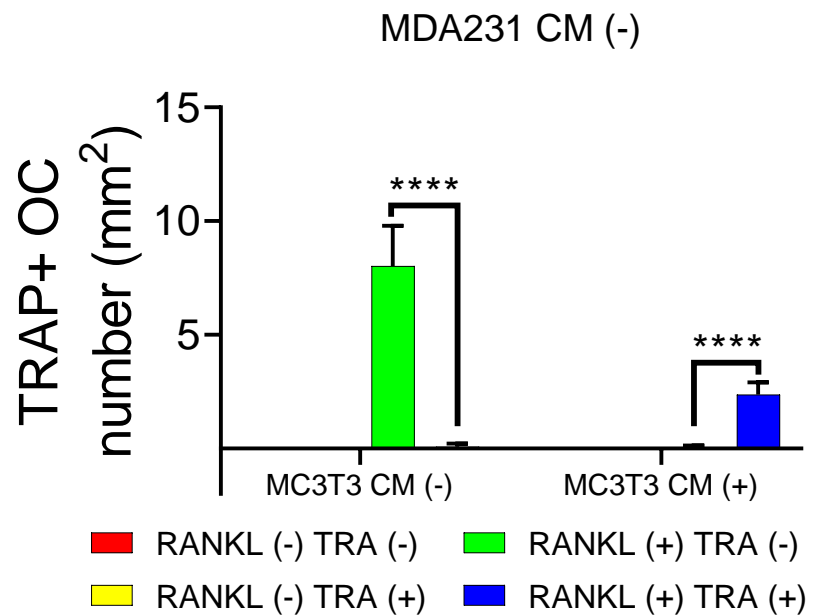
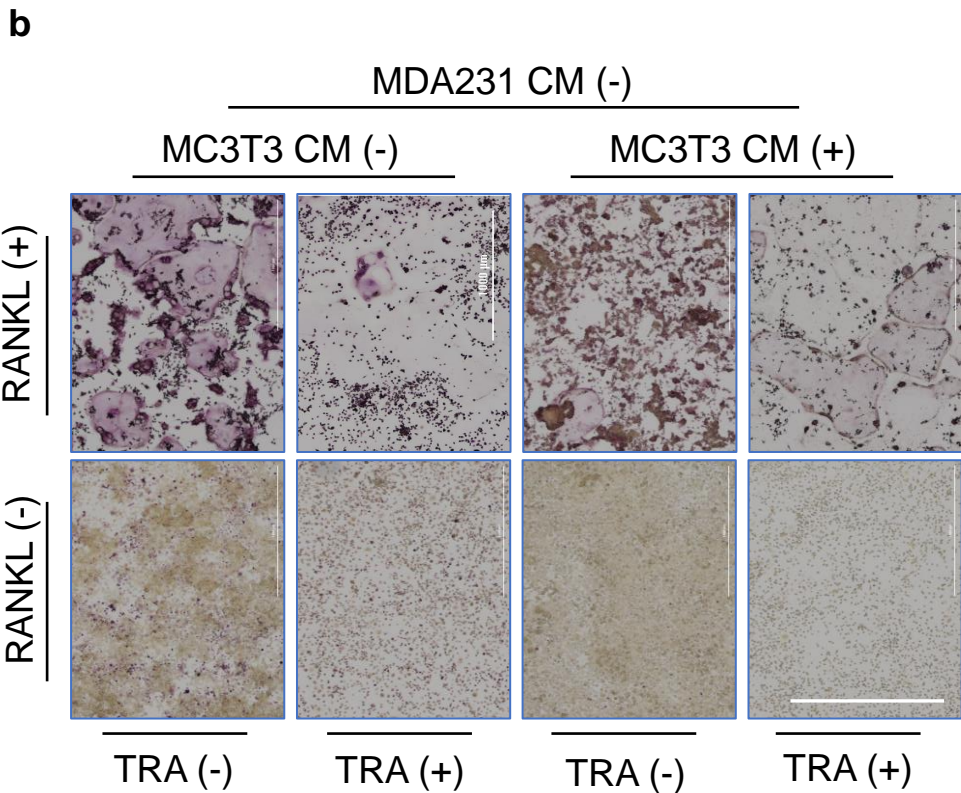
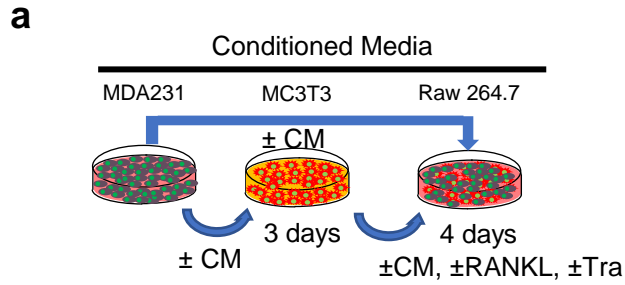
b







a**b**



Breast cancer cell lines (ATCC)

Name	ER	Histology	Tumor Source	Mutant Gene	Morphology
MCF7	ER positive	Adenocarcinoma	metastasis, pleural effusion	CDKN2A (c.1_471del471), PIK3CA (p.E545K)	Epithelial
HCC1806	TRIPLE NEGATIVE	Primary acantholytic squamous cell carcinoma	primary	CDKN2A (c.1_471del471), KDM6A (c.444_564del121), STK11 (c.1109_1302del194), TP53 (p.T256fs*90)	Basal-Like Morphology
MDA-MB-231	TRIPLE NEGATIVE	Adenocarcinoma	metastasis, pleural effusion	BRAF (p.G464V), CDKN2A(c.1_471del471), KRAS (p.G13D), NF2 (p.E231*), TP53 (p.R280K)	Mesenchymal- Like Morphology
MDA-MB-436	TRIPLE NEGATIVE	Adenocarcinoma	metastasis, pleural effusion	BRCA1(c.5277+1G>A), RB1 (p.G203fs*9)	Mesenchymal- Like Morphology
MDA-MB-157	TRIPLE NEGATIVE	Medullary carcinoma	metastasis, pleural effusion	NF1(p.S2751fs*27), TP53 (p.A88fs*52)	Mesenchymal- Like Morphology
Hs 578T	TRIPLE NEGATIVE	Carcinoma	primary	CDKN2(c.1_471del471), HRAS (p.G12D) , PIK3R1(p.N453_T454insN), TP53 (p.V157F)	Mesenchymal- Like Morphology

Well	Gene Symbol	Fold Difference		Well	Gene Symbol	Fold Difference	
		MDA231 /MCF7	MDA231- /MEKi/Con			MDA231 /MCF7	MDA231- /MEKi/Con
A01	AIMP1	0.36	0.52	D07	CXCL9	N.D	N.D
A02	BMP2	25.07	0.19	D08	CXCR1	0.56	N.D
A03	C5	0.93	0.88	D09	CXCR2	1.40	0.71
A04	CCL1	N.D	N.D	D10	FASLG	N.D	N.D
A05	CCL11	N.D	N.D	D11	IFNA2	N.D	N.D
A06	CCL13	N.D	N.D	D12	IFNG	N.D	N.D
A07	CCL15	N.D	N.D	E01	IL10RA	0.06	N.D
A08	CCL16	N.D	N.D	E02	IL10RB	0.60	1.46
A09	CCL17	0.24	N.D	E03	IL13	0.35	0.67
A10	CCL2	1.02	0.87	E04	IL15	3.12	1.28
A11	CCL20	N.D	0.55	E05	IL16	0.27	0.91
A12	CCL22	N.D	N.D	E06	IL17A	N.D	N.D
B01	CCL23	N.D	N.D	E07	IL17C	0.05	N.D
B02	CCL24	N.D	N.D	E08	IL17F	0.48	N.D
B03	CCL26	1.04	1.95	E09	IL1A	0.50	0.56
B04	CCL3	N.D	N.D	E10	IL1B	89.20	0.13
B05	CCL4	N.D	N.D	E11	IL1R1	0.07	2.43
B06	CCL5	0.02	8.05	E12	IL1RN	0.02	0.87
B07	CCL7	N.D	N.D	F01	IL21	0.57	N.D
B08	CCL8	N.D	N.D	F02	IL27	0.66	2.21
B09	CCR1	0.69	0.83	F03	IL3	N.D	N.D
B10	CCR2	N.D	4.01	F04	IL33	N.D	N.D
B11	CCR3	2.11	0.68	F05	IL5	3.25	0.69
B12	CCR4	N.D	N.D	F06	IL5RA	N.D	N.D
C01	CCR5	1.33	5.07	F07	IL7	24.39	0.92
C02	CCR6	0.25	N.D	F08	IL8	207.36	0.03
C03	CCR8	N.D	N.D	F09	IL9	N.D	N.D
C04	CD40LG	N.D	N.D	F10	IL9R	N.D	N.D
C05	CSF1	41.21	2.00	F11	LTA	1.31	0.90
C06	CSF2	N.D	N.D	F12	LTB	2.54	0.10
C07	CSF3	278.98	0.12	G01	MIF	0.61	0.45
C08	CX3CL1	N.D	N.D	G02	NAMPT	1.78	0.28
C09	CX3CR1	N.D	N.D	G03	OSM	0.66	0.93
C10	CXCL1	398.38	0.25	G04	SPP1	5.88	0.89
C11	CXCL10	0.17	0.79	G05	TNF	0.43	N.D
C12	CXCL11	2.88	0.31	G06	OPG	0.49	0.84
D01	CXCL12	N.D	N.D	G07	TNFSF10	0.01	3.62
D02	CXCL13	0.71	N.D	G08	RANKL	N.D	N.D
D03	CXCL2	654.39	0.32	G09	TNFSF13	0.19	1.68
D04	CXCL3	116.89	0.43	G10	TNFSF13B	0.32	3.25
D05	CXCL5	0.35	1.13	G11	TNFSF4	1.03	2.51
D06	CXCL6	N.D	N.D	G12	VEGFA	0.87	0.56

Sample ID	Phenotype	Location	pERK1/2 ⁺	p-CaMKII ⁺	pAKT1 ⁺	P-PKA ⁺	pCREB ⁺	P-NF-kB ⁺	P-cMyc ⁺	RANKL ⁺
BCBM011316b	Osteolytic	Femur	++/30%	+++/50%	-	+/10%	++/30%	+/40%	+++/90%	++/90%
BCBM012815b	Mixed	Femur	++/60%	+++/100%	-	++/100%	++/80%	-	+++/90%	++/100%
BCBM012815S	Mixed	Femur	++/25%	+/80%	-	++/40%	+/10%	++/40%	++/60%	++/90%
BCBM020516	Mixed	Femur	+++/70%	+/90%	+/-50%	+/70%	++/60%	+/30%	+/20%	+++/100%
BCBM022015B1	Osteolytic	Femur	++/10%	++/100%	-	++/100%	+/25%	+/60%	+/-70%	+++/100%
BCBM41316-A	Osteoblastic	Femur	++/70%	++/10%	-	+++/80%	++/50%	-	++/80%	+++/100%
BCBM072215T+	Mixed	Femur	++/60%	+/100%	-	++/100%	+/-40%	-	++/100%	+/80%
BCBM111314-2	Mixed	Femur	-	++/20%	-	++/80%	+++/40%			++/90%
Breastmet1	Osteolytic	Femur	++80%	++/70%	-	++/70%	++/90%	+++/50%	++/50%	++/90%
Breastmet2	Osteolytic	Femur	+++/60%	+++/60%	-	++/60%	+++/10%	+++/70%	++/50%	++/80%
157283	Osteoblastic	Femur	-	ND	ND	ND	-	ND	ND	ND
157288	Mixed	Femur	+++/50%	ND	ND	ND	++/40%	ND	ND	ND
157291	Mixed	Femur	+++/80%	ND	ND	ND	+++/70%	ND	ND	ND
157293	Osteoblastic	Femur	+/10%	ND	ND	ND	-	ND	ND	ND
157289	Osteolytic	Femur	+/10%	ND	ND	ND	+++/10%	ND	ND	ND
157297	Mixed	Femur	++/80%	ND	ND	ND	+/30%	ND	ND	ND
157300	Osteoblastic	Femur	+++/100%	ND	ND	ND	ND	ND	ND	ND
157284	Mixed	Femur	++/30%	ND	ND	ND	-	ND	ND	ND
157286	Osteolytic	Femur	++/80%	ND	ND	ND	+++/50%	ND	ND	ND

Human		Mouse	
Primer Name	Sequence (5' to 3')	Primer Name	Sequence (5' to 3')
hACKR1-F624	GCAGGCCACACACTGTAG	mACKR1-F678	CAAGGGGCTGAAGATAGCAC
hACKR1-R824	AACAGCAACAGCTTGGACCT	mACKR1-R867	GGCTTCTGTCCATTTCAGCA
hACKR2-F344	TCTTGTGCAAGATGGTGAGC	mACKR2-F177	CTCCGTAGTTGTGGCGATTT
hACKR2-R541	CCATATCAGGGATGGAGACG	mACKR2-F630	CTCCAGCTGAACCTTCTGG
hACKR3-F277	GTTGTCTCACCATCCCAGT	mACKR2-R324	GCCTAGAATCCATCCGTGAA
hACKR3-R416	CTCATGCACGTGAGGAAGAA	mACKR2-R823	GCAACGAGTGCAGAAACAAG
hACKR4-F153	TTTCGTCATTGGACTTGCAG	mACKR3-F633	CATGGAGCTGGTCTCTGTCA
hACKR4-R302	GCATTAACAGCCAAAAAGG	mACKR3-R796	GCCAACATACCAGGAAGACC
hADIPOQ-F47	ATGACCAGGAAACCAAGACT	mADIPOQ-F9	GTGCAAGCTCTCCTGTTCC
hADIPOQ-R244	CACCGATGTCTCCCTTAGGA	mADIPOQ-R202	TCTCTCCAGGAGTGCCATCT
hAMH-F576	CACCCGCTACCTGGTGTAG	mAMH-F544	CAGAACCTCTGCCCTACTCG
hAMH-R738	GGTCATCCGTGTGAAGCAG	mAMH-R710	CGGGAATCAGAGCCAAATAG
hBDNF-F164	GCTTGACATCATTGGCTGAC	mBDNF-F79	GCGCCCATGAAAGAAGTAAA
hBDNF-R320	AGAAGAGGAGGCTCCAAAGG	mBDNF-R234	TTCCGATGACGTGCTCAAAG
hBMP10-F546	CATGCTGGTCTTGGTGTCTG	mBMP10-F1047	CCGGGGTGTGTGTAAGTACC
hBMP10-R747	ATGCTTATTCTGGGCACTGG	mBMP10-R1248	AGACACAGCCATCCCTTCAT
hBMP1-F702	TTCCATCGTTCTGTGAGAACA	mBMP1-F828	CTATGCCCGGAACACATTCT
hBMP1-R885	CACCCCGTTCCACTCATACT	mBMP1-R1004	GTGCTGTCTTGGAGGGTCTC
hBMP2-F413	CTATCCCCACGGAGGATTT	mBMP2-F619	GCTCCACAAACGAGAAAAGC
hBMP2-R590	ACCAACCTGGTGTCCAAAAG	mBMP2-R996	AGCAAGGGGAAAAGGACACT
hBMP3-F1137	TGCAGATATTGGCTGGAGTG	mBMP3-F500	TCCTCAAATCCAACCAAAGC
hBMP3-R1317	TGGTACACAGCAAGGCTCAG	mBMP3-R682	TCCTCTTGGGTAGCTCGTGT
hBMP4-F296	TCCACAGCACTGGTCTTGAG	mBMP4-F716	TGACTCACCTCCACCAGACA
hBMP4-R443	GGGATGCTGTGTGAGGTTAAA	mBMP4-R888	ATGCTTGGGACTACGTTTGG
hBMP5-F255	CAATGCCATGACCAATGAAG	mBMP5-F1193	ACCATGCCATAGTCCAGACC
hBMP5-R425	AGAGGAGGACTCTGGGTGGT	mBMP5-R1359	GCAGCCACACGAACGTACTA
hBMP6-F1300	AAGGGCTATGCTGCCAATTA	mBMP6-F534	CTCCTTGAACCGCAAGAGTC
hBMP6-R1465	GAACCGAGATGGCATTAGC	mBMP6-R683	TGTGGGAGAACTCCTTGTG
hBMP7-F416	TCGTGGAACATGACAAGGAA	mBMP7-F726	GGGCTTACAGCTCTCTGTGG
hBMP7-R578	CTGATCCGGAACGTCTCATT	mBMP7-R873	CCGGATACTACGGAGATGGA
hBMP8B-F853	CTCCAGGGATCTTTGATGA	mBMP8B-F1037	CTATGCAGGCCCTGGTACAT
hBMP8B-R1003	AGCACTCCCCCTCACAGTAA	mBMP8B-R1186	AGGCCTGGACTACCATGTTG
hC5AR1-F840	GCTGGACTCCCTGTGTGTCT	mC5AR1-F499	CTCACCATTCCATCCTTCGT
hC5AR1-R991	CCCTAACCCAGGACTTTCA	mC5AR1-R653	GTGACAGAGGCAACACAAA
hC5-F1087	CTGAAGCCTGGGATTCCATA	mC5-F681	TGTCTTGCCACGATTCTCTG
hC5-R1287	CGTCACTCCAGATGGGAGAT	mC5-R877	GTGTGGCTTTGTGCATCATC
hCCL1-F72	GAGCATGCAGGTACCCTTCT	mCCL1-F74	GCATGCTTACGGTCTCCAAT
hCCL1-R217	AGGCCTCTTTGCCTCTCTTC	mCCL1-R232	TAGTTGAGGCGCAGCTTTCT
hCCL2-F89	TCAGCCAGATGCAATCAATG	mCCL2-F129	CCAATGAGTAGGCTGGAGA
hCCL2-R223	AGATCTCCTTGGCCACAATG	mCCL2-R284	ATTTGGTTCCGATCCAGGTT
hCCL3-F53	GCAACCAGTTCTCTGCATCA	mCCL3-F98	CCTGCTGCTTCTCTACAGC
hCCL3-R207	GCTTCGCTTGGTTAGGAAGA	mCCL3-R247	CTTGGACCCAGGTCTCTTTG
hCCL4-F10	TGCGTGACTGTCTGTCTCT	mCCL4-F89	CTCCACTTCTGCTGTTTC
hCCL4-R146	ACCACAAAGTTGCGAGGAAG	mCCL4-R237	CTCACTGGGTTAGCACAGA
hCCL5-F24	CGCTGTCATCCTATTGCTA	mCCL5-F20	CCCTCACCATCATCCTCACT
hCCL5-R173	GAGCACTTGCCACTGGTGTA	mCCL5-R171	GCATTGCTGCTGGTGTAGA
hCCL7-F1	ATGAAAGCCTCTGCAGCACT	mCCL7-F85	AATGCATCCACATGCTGCTA
hCCL7-R150	GCTCTCCAGCCTCTGCTTAG	mCCL7-R254	ATAGCCTCCTCGACCCACTT
hCCL8-F84	TTCCATTCCAATCACCTGCT	mCCL8-F50	TCAGCCAGAGAAGCTGACT
hCCL8-R232	GGTCAGCACAGACCTCCTTG	mCCL8-R196	TCTGGAACACACAGCTTCC
hCCL11-F75	AGCTTCTGTCCCAACCACCT	mCCL11-F36	CAGGGTCACTTCTTCACT
hCCL11-R214	TATCCTTGGCCAGTTTGGTC	mCCL11-R187	CTATGGCTTTCAGGGTGCAT
hCCL13-F86	CTTACCACCCCTCAGAGTGC		
hCCL13-F87	CGTCCATCTACTTGTGCT		
hCCL13-R233	GGGTTGGTACAGACGGAATG		
hCCL13-R240	CTTCTCCTTTGGTCAAGC		
hCCL15-F141	TCACTTTGCTGCTGACTGCT		
hCCL15-R291	ACTGGGTTTGGCACAGACTT		
hCCL16-F162	CAGAAAGGCCCTCAACTGTC		
hCCL16-R307	TGGACAAGTTCCTGGTAGGC		
hCCL17-F47	CTTCTCTGCAGCACATCCAC	mCCL17-F65	TGCTTCTGGGGACTTTTCTG
hCCL17-R209	CTGCCCTGCACAGTTACAAA	mCCL17-R211	CATCCCTGGAACACTCCACT
hCCL18-F83	AGCTCTGCTGCCTCGTCTAT		
hCCL18-R232	CCCACTTCTTATTGGGGTCA		
hCCL19-F95	CTGTGACCCAGAAACCCATC	mCCL19-F141	GAAAGCCTTCCGCTACCTTC
hCCL19-R252	CTGGATGATGCGTTTACCC	mCCL19-R304	TGCTGTTGCCTTTGTTCTTG
hCCL20-F79	GCAAGCAACTTTGACTGCTG	mCCL20-F249	CACCCAGTTCTGCTTTGGAT
hCCL20-R228	ATTTGCGCACACAGACAAT	mCCL20-F93	CGACTGTTGCCTCTCGTACA
hCCL21-F30	TATCCTGGTTCTGGCCTTTG	mCCL21-F222	ATGTGCAACCCCTGAGGAAG
hCCL21-R170	CAGCCTAAGCTTGGTTCTCTG	mCCL21-F399	TCCTCTTGGGGCTGTGTCT
hCCL22-F16	ACTGCACTCCTGGTTGTCT	mCCL22-F40	CTTCTTGTGTGGCAATTCA
hCCL22-R180	GCAGGAGTCTGAGGTCCAGT	mCCL22-R219	TCGGTTCTTGACGGTTATCA
hCCL23-F202	AGTGCTGACTGCTGCATCTC		
hCCL23-R382	GCTTCAGCACTTCTCATGCAA		
hCCL24-F75	CTCTGTGGTCAATCCCTCTC	mCCL24-F77	CTGTGACCATCCCTCATCT
hCCL24-R254	TACCTCTGGACCCACTCCTG	mCCL24-R258	TATGTGCTCTGAACCCACA
hCCL25-F212	ACAGGAAGGTGTGTGGGAAC	mCCL25-F173	GCAACCTACGTGCTGTGAGA
hCCL25-R409	TACTGCTGCTGATGGGATTG	mCCL25-R359	GGGTTCTCCACCTTGGACTT
hCCL26-F42	CCTCCTGAGTCTCCACTTTG	mCCL26-F23	TTGTTCTCTGGCCATCTTC
hCCL26-R176	TGGGAGCAGCTGTACTGGT	mCCL26-R176	TCACTGGTGCAGCTCTTGTC
hCCL27-F55	CCAGACCCTACAGCAGCATT		
hCCL27-R201	GAAAGCCTGGAGGTGACAGT		
hCCL28-F160	GCTGATGGGAAATGTGACTT	mCCL28-F226	CCGCACAATCGTACTTTGAA
hCCL28-R324	CCTGTGGCAACATTTCTT	mCCL28-R375	CCTGTGTGTTCCAGTGTTC
hCCR1-F571	AGCCTGAAGCAGTGAAGAG	mCCR1-F521	CCAATGGGAATTCCTCAC
hCCR1-R771	CAGATTGTAGGGGTCCAGA	mCCR1-R720	CAAACGGACAGCTTTGGATT
hCCR2-F681	AAGGTTTCAGGGAGCAGAGGT	mCCR2-F539	TGGCTGTGTTTGCCTCTTA
hCCR2-F806	AGGAATTCTTCGGCCTGAGT	mCCR2-F680	TGAGGAGAAGGCAGAGCTTC
hCCR2-R1004	GGACCTCCACACACTGGTTT	mCCR2-R738	CCTACAGCAAAACAGGGTGT
hCCR2-R818	TTGCAGTCACTCAGGGAGAA	mCCR2-R828	CTCATCCTGCAGGGACAAGT
hCCR3-F445	TTGGTGTCACTACCAGCAT	mCCR3-F295	CTGTGGAATGAGTGGGGTTT
hCCR3-R638	AGCAGAGGGAGAACCAGACA	mCCR3-R493	CAAGGCCCCAGGTAATGATA
hCCR4-F874	CTGGCTTTTGTTCAGTCTG	mCCR4-F778	GTGGTGTCTTCTCTGGAGAC
hCCR4-R1040	TAAGATGAGCTGGGGTGTCT	mCCR4-R949	GGGTGATGTACTTGGGGAAT
hCCR5-F409	TTAAAAGCCAGGACGGTAC	mCCR5-F875	GCTGCCTAAACCCTGTCATC
hCCR5-R612	GACCAGCCCAAGATGACTA	mCCR5-R1042	GTTCTCCTGTGGATCGGGTA
hCCR6-F929	GCCTGAACCCTGTGCTCTAC	mCCR6-F270	CCTACCGTTCTGGGCAGTTA
hCCR6-R1095	ATCTGCGGTCTCACTGGTCT	mCCR6-R438	GAAAGATTTGGTTGCCTGGA
hCCR7-F230	GGCTGGTCTGTGTTGACTAT	mCCR7-F226	AACGGGCTGGTGATACTGAC
hCCR7-R432	CATGCCACTGAAGAAGCTCA	mCCR7-R430	TCCCGCTGAAGAAGCTTAAC
hCCR8-F163	CTGGTCACTCTGGTCTTGT	mCCR8-F529	GGCATGCTACAATGTTCCA

Primer Name	Sequence (5 to 3)
Dominant Negative MEK1 mutant	
DNMEK1-Gibson-up	TCTGGCCTGGTCATGGCCAGAATGCTAATTCATCTGGAGATCAA
DNMEK1-Gibson-down	TTTGATCTCCAGATGAATTAGCATTCTGGCCATGACCAGGCCAGA
Constitutively Active MEK1 mutant	
ActMEK1-Gibson-up	GGGCAGCTCATCGACGAGATGGCCAACGATTCGTGGGCACAAGGTCC
ActMEK1-Gibson-down	GGACCTTGTGCCACGAAATCGTTGGCCATCTCGTCGATGAGCTGCC
pLJM1-RFP-MEK1	
EGFP-DsRED2_fwd2	tagcgctaccggctgccaccATGGCCTCCTCCGAGGACGT
hMEK1-DsRED2_rev2	gtcggcttcttcttgggcatGGCGCCGGTGGAGTGGCGGC
pLJM1-hMEK1_rev	gctcgagatctgagtccggaTTAGACGCCAGCAGCATGGG
DsRED2-hMEK1_fwd2	gcccactccaccggcgccATGCCAAGAAGAAGCCGAC
pLJM1-DsRED2-hMEK1-1095F	cccatgctgctggcgtctaaTCCGGACTCAGATCTCGAGCTCAAG
pLJM1-EGFP-DsRED2-377R2	acgtcctcgaggaggccatGGTGGCGACCGGTAGCGCTA