

Supporting Information

Widespread FRA1-dependent control of mesenchymal transdifferentiation programs in colorectal cancer cells

Jeannine Diesch^{1,2}, Elaine Sanij^{1,3,4}, Omer Gilan^{1,2}, Christopher Love⁵, Hoanh Tran⁶, Nicholas I. Fleming⁵, Jason Ellul¹, Marcia Amalia^{1,2}, Izhak Haviv⁷, Richard B. Pearson^{1,2,3}, Eugene Tulchinsky⁸, John M. Mariadason⁶, Oliver M. Sieber^{5,11}, Ross D. Hannan^{1,2,3,9,10,11} and Amardeep S. Dhillon^{1,3,4,11*}

*To whom correspondence should be addressed: Amardeep.Dhillon@petermac.org;

Ph: + 61 3 9656 1279; Fax: + 61 3 9656 1411

Table S1. Relative changes in expression of FRA1 bound EMT-related genes upon FRA1 knockdown in BE CRC cells. Data represent means from 3 independent RNA-Seq experiments.

Gene symbol	shFRA1-A1 vs shNS (log2)	shFRA1-A2 vs shNS (log2)
ADHESION		
CLDN4	6.295790479	6.876151546
TPM2	2.525388332	2.760680361
CDH1	8.257600651	8.188627939
CLDN7	4.947907433	5.025261684
EPCAM	6.06897627	6.209767802
OLCN	1.844890865	1.752921708
TJP3	5.393108929	5.440078454
LPXN	-5.179435147	-5.195820698
PCDHB9	-5.53027117	-4.851388807
CDH4	-8.974351387	-8.314814613
TPM1	-2.721804346	-2.577430334
TJP2	-2.077037931	-1.952244558
SIGNALING		
WNT16	9.836522059	10.77369936
FZD3	1.476620222	1.321437611
WNT10B	4.657953714	4.71506399
PDGFB	3.786449239	3.422630213
RAC3	3.131805551	3.219393614
NRP1	-7.666989679	-6.204335866
ROBO1	-9.19985079	-11.81316047
EGFR	-1.888197577	-2.98739624
RND3	-2.607296099	-3.120533259
RAC2	-2.390926409	-2.282730659
WNT5A	-10.05601808	-8.883612275
AXL	-4.98352569	-4.78509022
TRANSCRIPTION		
SNAI2	-8.317520305	-11.02624484
LEF1	-9.326497653	-10.33717393
STAT3	-1.404080032	-1.451621599
JUN	-3.749516015	-2.9990092
STAT5B	-3.752912711	-3.503903836
ZEB1	-4.853994015	-4.823022834
ETS1	-2.727966164	-2.870310427

ECM

RAB25	9.9954161	9.952912414
TNC	-10.84675053	-13.72765288
FBN1	-6.340193087	-6.597707995
LAMA3	-2.866431027	-2.790325669
ITGA6	-1.790897657	-1.917338348
ITGAV	-1.455695175	-1.142714962
ITGA3	-2.007918425	-1.889281641
LAMC1	-2.080575652	-1.692933554
SERPINE1	-4.230554369	-4.214337837
LAMC2	-3.314121432	-3.218130073
LAMB3	-3.285678298	-4.263050812
PLAU	-4.46943822	-3.577735794
MMP14	-3.473348296	-4.282728087
MMP16	-7.137263075	-10.52306725
LAMA4	-6.075175744	-5.049612234
ITGA2	-2.676398874	-3.165680981
ITGBL1	-4.787614888	-4.861324474
ITGA5	-1.549570822	-1.747777255
LAMB1	-3.004725793	-1.897362424
ITGB2	-5.290391571	-4.958685772
PLAUR	-3.170031299	-2.302493668
FN1	-7.845234765	-7.691191505
VIM	-10.00237061	-12.93717126

TGF β PATHWAY

CD109	9.034302717	8.57297631
BMP4	3.794933632	1.032242403
BMP7	9.010137623	8.831907176
TGFBI	6.67	6.71
SMAD3	-2.683074478	-2.324191377
TGFB2	-6.969617857	-6.847828316
TGFBR2	-4.189646407	-3.90078682
NOG	-4.53457067	-5.873693216

Table S2. ChIP-Seq reads identified near FRA1^{EMT} genes.

Chr	Start	End	Strand	Ensembl geneid	Gene symbol
7	73199513	73200397	+	ENSG00000189143	CLDN4
7	73205611	73206569	+	ENSG00000189143	CLDN4
7	73208087	73208769	+	ENSG00000189143	CLDN4
7	73211362	73212733	+	ENSG00000189143	CLDN4
7	73217903	73218582	+	ENSG00000189143	CLDN4
7	73222154	73223061	+	ENSG00000189143	CLDN4
7	73223264	73224294	+	ENSG00000189143	CLDN4
7	73224388	73225999	+	ENSG00000189143	CLDN4
7	73226088	73227210	+	ENSG00000189143	CLDN4
7	73231297	73232276	+	ENSG00000189143	CLDN4
7	73236162	73237197	+	ENSG00000189143	CLDN4
7	73239033	73241022	+	ENSG00000189143	CLDN4
7	73242759	73243464	+	ENSG00000189143	CLDN4
7	73245065	73246980	+	ENSG00000189143	CLDN4
6	74405521	74406286	+	ENSG00000156535	CD109
6	74413466	74414095	+	ENSG00000156535	CD109
6	74417743	74419203	+	ENSG00000156535	CD109
6	74427171	74428022	+	ENSG00000156535	CD109
6	74449184	74449818	+	ENSG00000156535	CD109
6	74469465	74470402	+	ENSG00000156535	CD109
6	74486009	74487080	+	ENSG00000156535	CD109
6	74488850	74489457	+	ENSG00000156535	CD109
6	74490567	74490972	+	ENSG00000156535	CD109
6	74495439	74495992	+	ENSG00000156535	CD109
6	74499024	74499852	+	ENSG00000156535	CD109
6	74545048	74546981	+	ENSG00000156535	CD109
6	74550211	74551188	+	ENSG00000156535	CD109
1	92133752	92134186	-	ENSG00000069702	TGFBR3
1	92142225	92143099	-	ENSG00000069702	TGFBR3
1	92149135	92149504	-	ENSG00000069702	TGFBR3
1	92194414	92195021	-	ENSG00000069702	TGFBR3
1	92205408	92206340	-	ENSG00000069702	TGFBR3
1	92233330	92233826	-	ENSG00000069702	TGFBR3
1	92245979	92246499	-	ENSG00000069702	TGFBR3
1	92267817	92268246	-	ENSG00000069702	TGFBR3
1	92321509	92322036	-	ENSG00000069702	TGFBR3

1	92323715	92324787	-	ENSG00000069702	TGFBR3
1	92338535	92339168	-	ENSG00000069702	TGFBR3
1	92339944	92340424	-	ENSG00000069702	TGFBR3
1	92347620	92348280	-	ENSG00000069702	TGFBR3
1	92350812	92352145	-	ENSG00000069702	TGFBR3
1	92363764	92364526	-	ENSG00000069702	TGFBR3
1	92370852	92371334	-	ENSG00000069702	TGFBR3
1	92376114	92376799	-	ENSG00000069702	TGFBR3
1	92383747	92384874	-	ENSG00000069702	TGFBR3
1	92385983	92387061	-	ENSG00000069702	TGFBR3
1	92388857	92389527	-	ENSG00000069702	TGFBR3
14	54403726	54404224	-	ENSG00000125378	BMP4
14	54412738	54413979	-	ENSG00000125378	BMP4
14	54416685	54417394	-	ENSG00000125378	BMP4
14	54420021	54421089	-	ENSG00000125378	BMP4
14	54422342	54423934	-	ENSG00000125378	BMP4
14	54429842	54430902	-	ENSG00000125378	BMP4
14	54433802	54434482	-	ENSG00000125378	BMP4
14	54436525	54437369	-	ENSG00000125378	BMP4
20	55731983	55732560	-	ENSG00000101144	BMP7
20	55732663	55733560	-	ENSG00000101144	BMP7
20	55735919	55737743	-	ENSG00000101144	BMP7
20	55739679	55740454	-	ENSG00000101144	BMP7
20	55740514	55742416	-	ENSG00000101144	BMP7
20	55748074	55748803	-	ENSG00000101144	BMP7
20	55752237	55754932	-	ENSG00000101144	BMP7
20	55755019	55755892	-	ENSG00000101144	BMP7
20	55756919	55757769	-	ENSG00000101144	BMP7
20	55764495	55766140	-	ENSG00000101144	BMP7
20	55769714	55771078	-	ENSG00000101144	BMP7
20	55772818	55775359	-	ENSG00000101144	BMP7
20	55778301	55778955	-	ENSG00000101144	BMP7
20	55782592	55783294	-	ENSG00000101144	BMP7
20	55798627	55800471	-	ENSG00000101144	BMP7
20	55800724	55802179	-	ENSG00000101144	BMP7
20	55818380	55819272	-	ENSG00000101144	BMP7
20	55825835	55826432	-	ENSG00000101144	BMP7
20	55839181	55843214	-	ENSG00000101144	BMP7
15	67357104	67359319	+	ENSG00000166949	SMAD3

15	67361934	67362493	+	ENSG00000166949	SMAD3
15	67365880	67366477	+	ENSG00000166949	SMAD3
15	67413343	67413932	+	ENSG00000166949	SMAD3
15	67442889	67444164	+	ENSG00000166949	SMAD3
15	67456949	67458256	+	ENSG00000166949	SMAD3
15	67459962	67460914	+	ENSG00000166949	SMAD3
15	67472098	67473284	+	ENSG00000166949	SMAD3
15	67473383	67474480	+	ENSG00000166949	SMAD3
15	67481507	67482193	+	ENSG00000166949	SMAD3
10	123205221	123205790	-	ENSG00000066468	FGFR2
2	47594236	47595256	+	ENSG00000119888	EPCAM
2	47595426	47598092	+	ENSG00000119888	EPCAM
2	47599316	47600400	+	ENSG00000119888	EPCAM
2	47609917	47611160	+	ENSG00000119888	EPCAM
2	47611175	47612227	+	ENSG00000119888	EPCAM
2	47614041	47615170	+	ENSG00000119888	EPCAM
2	47617276	47618060	+	ENSG00000119888	EPCAM
19	41720206	41721304	+	ENSG00000167601	AXL
19	41724438	41726773	+	ENSG00000167601	AXL
19	41727514	41728773	+	ENSG00000167601	AXL
19	41729222	41730350	+	ENSG00000167601	AXL
19	41731457	41733185	+	ENSG00000167601	AXL
19	41742898	41747468	+	ENSG00000167601	AXL
19	41754998	41755842	+	ENSG00000167601	AXL
19	41756000	41757682	+	ENSG00000167601	AXL
19	41759711	41760622	+	ENSG00000167601	AXL
19	41761094	41761950	+	ENSG00000167601	AXL
19	41765359	41766591	+	ENSG00000167601	AXL
5	135339438	135339942	+	ENSG00000120708	TGFBI
5	135364095	135365544	+	ENSG00000120708	TGFBI
5	135381904	135382275	+	ENSG00000120708	TGFBI
5	135402462	135402939	+	ENSG00000120708	TGFBI
11	58299067	58300192	-	ENSG00000110031	LPXN
11	58321364	58321992	-	ENSG00000110031	LPXN
15	48817164	48817746	-	ENSG00000166147	FBN1
15	48870559	48871200	-	ENSG00000166147	FBN1
15	48897682	48898177	-	ENSG00000166147	FBN1
15	48903305	48903908	-	ENSG00000166147	FBN1
15	48905689	48906249	-	ENSG00000166147	FBN1

15	48936795	48938624	-	ENSG00000166147	FBN1
1	183144103	183144720	+	ENSG00000058085	LAMC2
1	183150523	183151322	+	ENSG00000058085	LAMC2
1	183154874	183155698	+	ENSG00000058085	LAMC2
9	117839117	117839894	-	ENSG00000041982	TNC
9	117847910	117849615	-	ENSG00000041982	TNC
9	117852669	117853490	-	ENSG00000041982	TNC
1	209790660	209792394	-	ENSG00000196878	LAMB3
1	209795578	209797515	-	ENSG00000196878	LAMB3
1	209798755	209799499	-	ENSG00000196878	LAMB3
1	209799815	209801939	-	ENSG00000196878	LAMB3
1	209803805	209804687	-	ENSG00000196878	LAMB3
1	209807401	209808621	-	ENSG00000196878	LAMB3
10	75654955	75656684	+	ENSG00000122861	PLAU
10	75670520	75671907	+	ENSG00000122861	PLAU
19	44148760	44150146	-	ENSG00000011422	PLAUR
19	44150851	44151252	-	ENSG00000011422	PLAUR
19	44154162	44154771	-	ENSG00000011422	PLAUR
19	44155007	44156198	-	ENSG00000011422	PLAUR
19	44158351	44159434	-	ENSG00000011422	PLAUR
19	44159851	44161729	-	ENSG00000011422	PLAUR
19	44169018	44170360	-	ENSG00000011422	PLAUR
19	44171528	44172282	-	ENSG00000011422	PLAUR
19	44172654	44174633	-	ENSG00000011422	PLAUR
19	44179710	44180671	-	ENSG00000011422	PLAUR
19	44181667	44182392	-	ENSG00000011422	PLAUR
19	44184971	44185664	-	ENSG00000011422	PLAUR
19	44186555	44187139	-	ENSG00000011422	PLAUR
19	44191484	44192232	-	ENSG00000011422	PLAUR
3	30629847	30630379	+	ENSG00000163513	TGFBR2
3	30632693	30633410	+	ENSG00000163513	TGFBR2
3	30647769	30649022	+	ENSG00000163513	TGFBR2
3	30649347	30649833	+	ENSG00000163513	TGFBR2
3	30659570	30660143	+	ENSG00000163513	TGFBR2
3	30678073	30678673	+	ENSG00000163513	TGFBR2
3	30694580	30695177	+	ENSG00000163513	TGFBR2
3	30719570	30720120	+	ENSG00000163513	TGFBR2
6	112445804	112446321	-	ENSG00000112769	LAMA4
6	112457500	112457989	-	ENSG00000112769	LAMA4

6	112502859	112503323	-	ENSG00000112769	LAMA4
6	112511904	112512554	-	ENSG00000112769	LAMA4
6	112532951	112533767	-	ENSG00000112769	LAMA4
11	127845612	127846709	-	ENSG00000134954	ETS1
11	127868765	127869322	-	ENSG00000134954	ETS1
11	127902786	127903385	-	ENSG00000134954	ETS1
11	128009832	128010536	-	ENSG00000134954	ETS1
11	128084686	128085854	-	ENSG00000134954	ETS1
11	128092781	128093738	-	ENSG00000134954	ETS1
11	128106707	128107738	-	ENSG00000134954	ETS1
11	128111614	128112048	-	ENSG00000134954	ETS1
11	128189066	128189513	-	ENSG00000134954	ETS1
11	128210432	128210950	-	ENSG00000134954	ETS1
11	128292414	128292968	-	ENSG00000134954	ETS1
11	128295389	128296054	-	ENSG00000134954	ETS1
11	128345300	128345785	-	ENSG00000134954	ETS1
11	128428073	128428600	-	ENSG00000134954	ETS1
11	128489281	128489839	-	ENSG00000134954	ETS1
11	128502289	128502751	-	ENSG00000134954	ETS1
17	40351455	40352115	-	ENSG00000173757	STAT5B
17	40353736	40354783	-	ENSG00000173757	STAT5B
17	40357754	40359166	-	ENSG00000173757	STAT5B
17	40359624	40361287	-	ENSG00000173757	STAT5B
17	40365169	40366160	-	ENSG00000173757	STAT5B
17	40367532	40368244	-	ENSG00000173757	STAT5B
17	40369478	40372404	-	ENSG00000173757	STAT5B
17	40372472	40373402	-	ENSG00000173757	STAT5B
17	40373470	40374411	-	ENSG00000173757	STAT5B
17	40378377	40379405	-	ENSG00000173757	STAT5B
17	40380238	40381016	-	ENSG00000173757	STAT5B
17	40385393	40385817	-	ENSG00000173757	STAT5B
17	40387330	40387887	-	ENSG00000173757	STAT5B
17	40388406	40388913	-	ENSG00000173757	STAT5B
17	40389652	40390744	-	ENSG00000173757	STAT5B
17	40396980	40398123	-	ENSG00000173757	STAT5B
17	40427479	40429191	-	ENSG00000173757	STAT5B
7	107581975	107582783	-	ENSG00000091136	LAMB1
7	107592031	107592683	-	ENSG00000091136	LAMB1
7	107594676	107595260	-	ENSG00000091136	LAMB1

7	107596039	107596760	-	ENSG00000091136	LAMB1
7	107597434	107598040	-	ENSG00000091136	LAMB1
7	107606310	107606955	-	ENSG00000091136	LAMB1
7	107617187	107617741	-	ENSG00000091136	LAMB1
7	107621316	107621880	-	ENSG00000091136	LAMB1
7	107625760	107626461	-	ENSG00000091136	LAMB1
7	107633466	107634008	-	ENSG00000091136	LAMB1
7	107641691	107642777	-	ENSG00000091136	LAMB1
7	107643656	107644061	-	ENSG00000091136	LAMB1
7	107651702	107652205	-	ENSG00000091136	LAMB1
12	54798618	54799559	-	ENSG00000161638	ITGA5
12	54801822	54804196	-	ENSG00000161638	ITGA5
12	54808188	54808933	-	ENSG00000161638	ITGA5
12	54809419	54810150	-	ENSG00000161638	ITGA5
12	54812076	54813318	-	ENSG00000161638	ITGA5
12	54827481	54828315	-	ENSG00000161638	ITGA5
12	54828391	54828844	-	ENSG00000161638	ITGA5
17	48137179	48137953	+	ENSG00000005884	ITGA3
17	48138240	48140311	+	ENSG00000005884	ITGA3
17	48141023	48142621	+	ENSG00000005884	ITGA3
17	48145081	48146768	+	ENSG00000005884	ITGA3
17	48149389	48150257	+	ENSG00000005884	ITGA3
17	48150674	48152312	+	ENSG00000005884	ITGA3
17	48152600	48153407	+	ENSG00000005884	ITGA3
17	48153412	48155158	+	ENSG00000005884	ITGA3
17	48156049	48158040	+	ENSG00000005884	ITGA3
17	48159160	48160096	+	ENSG00000005884	ITGA3
17	48163658	48164472	+	ENSG00000005884	ITGA3
17	48164650	48165987	+	ENSG00000005884	ITGA3
17	48166030	48168371	+	ENSG00000005884	ITGA3
1	182985051	182985788	+	ENSG00000135862	LAMC1
1	182986464	182986852	+	ENSG00000135862	LAMC1
1	182989367	182990281	+	ENSG00000135862	LAMC1
1	182991803	182993820	+	ENSG00000135862	LAMC1
1	183003256	183003794	+	ENSG00000135862	LAMC1
1	183005245	183006209	+	ENSG00000135862	LAMC1
1	183019261	183020089	+	ENSG00000135862	LAMC1
1	183022728	183023166	+	ENSG00000135862	LAMC1
1	183047286	183047709	+	ENSG00000135862	LAMC1

1	183056793	183057350	+	ENSG00000135862	LAMC1
1	183080066	183080591	+	ENSG00000135862	LAMC1
1	183084831	183085760	+	ENSG00000135862	LAMC1
1	183087429	183088369	+	ENSG00000135862	LAMC1
1	183118338	183119585	+	ENSG00000135862	LAMC1
9	71751987	71752723	+	ENSG00000119139	TJP2
9	71764918	71765624	+	ENSG00000119139	TJP2
9	71788712	71789592	+	ENSG00000119139	TJP2
9	71794262	71794728	+	ENSG00000119139	TJP2
9	71806504	71807228	+	ENSG00000119139	TJP2
9	71821207	71821946	+	ENSG00000119139	TJP2
9	71823971	71824692	+	ENSG00000119139	TJP2
9	71827932	71828360	+	ENSG00000119139	TJP2
9	71833698	71834274	+	ENSG00000119139	TJP2
9	71835705	71837562	+	ENSG00000119139	TJP2
9	71837577	71838598	+	ENSG00000119139	TJP2
9	71850060	71850655	+	ENSG00000119139	TJP2
9	71868864	71869563	+	ENSG00000119139	TJP2
9	71873651	71874377	+	ENSG00000119139	TJP2
9	71878681	71879334	+	ENSG00000119139	TJP2
9	71879888	71880386	+	ENSG00000119139	TJP2
9	71883765	71884266	+	ENSG00000119139	TJP2
9	71889784	71890312	+	ENSG00000119139	TJP2
9	71891993	71893460	+	ENSG00000119139	TJP2
9	71896680	71897503	+	ENSG00000119139	TJP2
2	187431364	187431949	+	ENSG00000138448	ITGAV
2	187436040	187436560	+	ENSG00000138448	ITGAV
2	187438843	187439403	+	ENSG00000138448	ITGAV
2	187451700	187452409	+	ENSG00000138448	ITGAV
2	187452895	187453551	+	ENSG00000138448	ITGAV
2	187454340	187455426	+	ENSG00000138448	ITGAV
2	187467172	187467696	+	ENSG00000138448	ITGAV
2	187480872	187481435	+	ENSG00000138448	ITGAV
2	187510051	187510888	+	ENSG00000138448	ITGAV
2	187513122	187513541	+	ENSG00000138448	ITGAV
2	187517493	187518103	+	ENSG00000138448	ITGAV
2	187536509	187537024	+	ENSG00000138448	ITGAV
2	187538272	187538977	+	ENSG00000138448	ITGAV
17	40466779	40467320	-	ENSG00000168610	STAT3

17	40481987	40483006	-	ENSG00000168610	STAT3
17	40483616	40484599	-	ENSG00000168610	STAT3
17	40490877	40491340	-	ENSG00000168610	STAT3
17	40491846	40492494	-	ENSG00000168610	STAT3
17	40496005	40497413	-	ENSG00000168610	STAT3
17	40506054	40506789	-	ENSG00000168610	STAT3
17	40518830	40519709	-	ENSG00000168610	STAT3
17	40521610	40522899	-	ENSG00000168610	STAT3
17	40523254	40524055	-	ENSG00000168610	STAT3
17	40529876	40530655	-	ENSG00000168610	STAT3
17	40531922	40533007	-	ENSG00000168610	STAT3
17	40534533	40535675	-	ENSG00000168610	STAT3
17	40535849	40536979	-	ENSG00000168610	STAT3
17	40539563	40540999	-	ENSG00000168610	STAT3
18	21269174	21270329	+	ENSG00000053747	LAMA3
18	21278018	21278587	+	ENSG00000053747	LAMA3
18	21320688	21321167	+	ENSG00000053747	LAMA3
18	21321682	21322210	+	ENSG00000053747	LAMA3
18	21341937	21343157	+	ENSG00000053747	LAMA3
18	21356583	21357112	+	ENSG00000053747	LAMA3
18	21370705	21371399	+	ENSG00000053747	LAMA3
18	21391423	21392299	+	ENSG00000053747	LAMA3
18	21422285	21422642	+	ENSG00000053747	LAMA3
18	21474670	21475138	+	ENSG00000053747	LAMA3
18	21499497	21499927	+	ENSG00000053747	LAMA3
18	21504067	21504794	+	ENSG00000053747	LAMA3
18	21520555	21521414	+	ENSG00000053747	LAMA3
18	21524768	21525481	+	ENSG00000053747	LAMA3
3	78631839	78633556	-	ENSG00000169855	ROBO1
3	78729316	78730529	-	ENSG00000169855	ROBO1
3	78760266	78760907	-	ENSG00000169855	ROBO1
3	78764608	78765138	-	ENSG00000169855	ROBO1
3	78988344	78988804	-	ENSG00000169855	ROBO1
3	79012384	79012965	-	ENSG00000169855	ROBO1
3	79067788	79068952	-	ENSG00000169855	ROBO1
3	79070668	79071269	-	ENSG00000169855	ROBO1
3	79138988	79139485	-	ENSG00000169855	ROBO1
3	79168844	79169338	-	ENSG00000169855	ROBO1
3	79179795	79180596	-	ENSG00000169855	ROBO1

3	79182129	79182751	-	ENSG00000169855	ROBO1
3	79215594	79216056	-	ENSG00000169855	ROBO1
3	79222223	79223224	-	ENSG00000169855	ROBO1
3	79246120	79247008	-	ENSG00000169855	ROBO1
3	79257679	79258131	-	ENSG00000169855	ROBO1
3	79286212	79286725	-	ENSG00000169855	ROBO1
3	79332690	79333315	-	ENSG00000169855	ROBO1
3	79339110	79339540	-	ENSG00000169855	ROBO1
3	79349075	79350113	-	ENSG00000169855	ROBO1
3	79372070	79372562	-	ENSG00000169855	ROBO1
3	79412990	79413411	-	ENSG00000169855	ROBO1
3	79416927	79417412	-	ENSG00000169855	ROBO1
3	79421243	79421787	-	ENSG00000169855	ROBO1
3	79430020	79430683	-	ENSG00000169855	ROBO1
3	79494505	79495333	-	ENSG00000169855	ROBO1
3	79545241	79545946	-	ENSG00000169855	ROBO1
3	79549912	79550283	-	ENSG00000169855	ROBO1
3	79551136	79552160	-	ENSG00000169855	ROBO1
3	79555455	79555964	-	ENSG00000169855	ROBO1
3	79568340	79568853	-	ENSG00000169855	ROBO1
3	79660461	79661927	-	ENSG00000169855	ROBO1
3	79733728	79734153	-	ENSG00000169855	ROBO1
3	79769839	79770485	-	ENSG00000169855	ROBO1
3	79774222	79774780	-	ENSG00000169855	ROBO1
3	79815450	79816720	-	ENSG00000169855	ROBO1
3	79834126	79834656	-	ENSG00000169855	ROBO1
3	79863606	79864372	-	ENSG00000169855	ROBO1
3	79873165	79873836	-	ENSG00000169855	ROBO1
10	33460696	33461147	-	ENSG00000099250	NRP1
10	33477323	33477830	-	ENSG00000099250	NRP1
10	33492500	33492925	-	ENSG00000099250	NRP1
10	33493529	33493994	-	ENSG00000099250	NRP1
10	33497676	33498114	-	ENSG00000099250	NRP1
10	33504877	33505709	-	ENSG00000099250	NRP1
10	33559098	33559672	-	ENSG00000099250	NRP1
10	33566249	33566607	-	ENSG00000099250	NRP1
10	33623035	33626337	-	ENSG00000099250	NRP1
10	33675991	33676937	-	ENSG00000099250	NRP1
10	33705638	33706045	-	ENSG00000099250	NRP1

10	33707507	33708112	-	ENSG00000099250	NRP1
10	33709071	33709652	-	ENSG00000099250	NRP1
10	33727722	33728371	-	ENSG00000099250	NRP1
10	33730971	33731871	-	ENSG00000099250	NRP1
14	23305534	23307093	+	ENSG00000157227	MMP14
14	23309441	23310355	+	ENSG00000157227	MMP14
14	23311258	23312029	+	ENSG00000157227	MMP14
14	23314892	23315623	+	ENSG00000157227	MMP14
14	23315741	23316679	+	ENSG00000157227	MMP14
14	23317640	23318273	+	ENSG00000157227	MMP14
8	89092501	89092972	-	ENSG00000156103	MMP16
8	89161038	89162177	-	ENSG00000156103	MMP16
8	89163070	89163968	-	ENSG00000156103	MMP16
8	89169878	89171040	-	ENSG00000156103	MMP16
8	89339501	89340541	-	ENSG00000156103	MMP16
10	17270013	17272890	+	ENSG00000026025	VIM
10	17275993	17276623	+	ENSG00000026025	VIM
10	17314436	17315186	+	ENSG00000026025	VIM
2	216250354	216251240	-	ENSG00000115414	FN1
2	216276303	216276803	-	ENSG00000115414	FN1
2	216289932	216291190	-	ENSG00000115414	FN1
2	216291471	216291940	-	ENSG00000115414	FN1
2	216300198	216300946	-	ENSG00000115414	FN1
8	49835794	49836343	-	ENSG00000019549	SNAI2
8	49880992	49881640	-	ENSG00000019549	SNAI2
8	49889581	49890269	-	ENSG00000019549	SNAI2
1	218541048	218541884	+	ENSG00000092969	TGFB2
1	218551228	218552131	+	ENSG00000092969	TGFB2
1	218568619	218569323	+	ENSG00000092969	TGFB2
1	218586285	218586829	+	ENSG00000092969	TGFB2
1	218600533	218602516	+	ENSG00000092969	TGFB2
1	218628539	218629602	+	ENSG00000092969	TGFB2
4	108977908	108978404	-	ENSG00000138795	LEF1
4	108978982	108979370	-	ENSG00000138795	LEF1
4	108998099	108999116	-	ENSG00000138795	LEF1
4	109001926	109002908	-	ENSG00000138795	LEF1
4	109045040	109045877	-	ENSG00000138795	LEF1
4	109053708	109054406	-	ENSG00000138795	LEF1
4	109087613	109090536	-	ENSG00000138795	LEF1

5	52284656	52285880	+	ENSG00000164171	ITGA2
10	31619909	31620397	+	ENSG00000148516	ZEB1
10	31628289	31628797	+	ENSG00000148516	ZEB1
10	31694566	31695307	+	ENSG00000148516	ZEB1
10	31695899	31697118	+	ENSG00000148516	ZEB1
10	31730493	31731220	+	ENSG00000148516	ZEB1
10	31732421	31733742	+	ENSG00000148516	ZEB1
10	31737435	31738398	+	ENSG00000148516	ZEB1
10	31796881	31797956	+	ENSG00000148516	ZEB1
10	31828312	31828727	+	ENSG00000148516	ZEB1
17	45320806	45322021	+	ENSG00000056345	ITGB3
17	45327484	45328259	+	ENSG00000056345	ITGB3
17	45330706	45333349	+	ENSG00000056345	ITGB3
17	45352577	45353465	+	ENSG00000056345	ITGB3
17	45357550	45358415	+	ENSG00000056345	ITGB3
17	45369368	45370040	+	ENSG00000056345	ITGB3
17	45376182	45377219	+	ENSG00000056345	ITGB3
17	45390242	45391095	+	ENSG00000056345	ITGB3
17	45391127	45391768	+	ENSG00000056345	ITGB3
13	102104875	102105369	+	ENSG00000198542	ITGBL1
13	102105808	102106847	+	ENSG00000198542	ITGBL1
13	102121617	102122072	+	ENSG00000198542	ITGBL1
13	102184013	102184449	+	ENSG00000198542	ITGBL1
13	102191242	102193168	+	ENSG00000198542	ITGBL1
13	102208540	102208995	+	ENSG00000198542	ITGBL1
13	102330723	102331675	+	ENSG00000198542	ITGBL1
13	102333868	102334395	+	ENSG00000198542	ITGBL1
13	102361268	102361836	+	ENSG00000198542	ITGBL1
22	37621548	37624023	-	ENSG00000128340	RAC2
22	37624414	37626185	-	ENSG00000128340	RAC2
22	37626978	37628247	-	ENSG00000128340	RAC2
22	37629185	37630949	-	ENSG00000128340	RAC2
22	37631303	37631783	-	ENSG00000128340	RAC2
22	37632777	37634892	-	ENSG00000128340	RAC2
22	37636800	37638057	-	ENSG00000128340	RAC2
22	37638708	37639672	-	ENSG00000128340	RAC2
22	37639711	37641290	-	ENSG00000128340	RAC2
22	37643506	37644035	-	ENSG00000128340	RAC2
22	37646961	37647431	-	ENSG00000128340	RAC2

22	37649476	37650603	-	ENSG00000128340	RAC2
22	37651513	37652930	-	ENSG00000128340	RAC2
2	151278081	151278520	-	ENSG00000115963	RND3
2	151341645	151343563	-	ENSG00000115963	RND3
2	151349839	151350277	-	ENSG00000115963	RND3
2	151357787	151358335	-	ENSG00000115963	RND3
2	151369097	151369739	-	ENSG00000115963	RND3
2	151372747	151373253	-	ENSG00000115963	RND3
2	151386938	151387527	-	ENSG00000115963	RND3
2	151390320	151390802	-	ENSG00000115963	RND3
2	151399130	151399743	-	ENSG00000115963	RND3
2	151399787	151400290	-	ENSG00000115963	RND3
15	63309435	63310044	+	ENSG00000140416	TPM1
15	63325084	63325678	+	ENSG00000140416	TPM1
15	63333918	63336377	+	ENSG00000140416	TPM1
15	63340144	63341436	+	ENSG00000140416	TPM1
15	63345735	63346259	+	ENSG00000140416	TPM1
15	63376065	63376939	+	ENSG00000140416	TPM1
15	63379337	63380213	+	ENSG00000140416	TPM1
20	59823031	59823842	+	ENSG00000179242	CDH4
20	59826752	59829928	+	ENSG00000179242	CDH4
20	59831471	59832061	+	ENSG00000179242	CDH4
20	59854615	59857168	+	ENSG00000179242	CDH4
20	59857426	59859217	+	ENSG00000179242	CDH4
20	59862223	59863039	+	ENSG00000179242	CDH4
20	59863276	59864817	+	ENSG00000179242	CDH4
20	59867282	59870225	+	ENSG00000179242	CDH4
20	60318398	60320287	+	ENSG00000179242	CDH4
20	60320566	60322646	+	ENSG00000179242	CDH4
20	60338989	60343417	+	ENSG00000179242	CDH4
20	60345057	60346661	+	ENSG00000179242	CDH4
20	60347849	60348848	+	ENSG00000179242	CDH4
20	60359531	60360980	+	ENSG00000179242	CDH4
20	60364244	60366220	+	ENSG00000179242	CDH4
20	60366547	60369235	+	ENSG00000179242	CDH4
20	60370707	60371828	+	ENSG00000179242	CDH4
20	60371850	60374148	+	ENSG00000179242	CDH4
20	60374406	60377225	+	ENSG00000179242	CDH4
20	60377464	60379886	+	ENSG00000179242	CDH4

20	60380236	60383421	+	ENSG00000179242	CDH4
20	60383569	60384557	+	ENSG00000179242	CDH4
20	60384612	60386312	+	ENSG00000179242	CDH4
20	60386528	60387633	+	ENSG00000179242	CDH4
20	60387667	60390691	+	ENSG00000179242	CDH4
20	60391509	60392046	+	ENSG00000179242	CDH4
20	60392146	60393315	+	ENSG00000179242	CDH4
20	60393494	60394819	+	ENSG00000179242	CDH4
20	60394884	60396750	+	ENSG00000179242	CDH4
20	60403717	60406308	+	ENSG00000179242	CDH4
20	60408994	60410220	+	ENSG00000179242	CDH4
20	60410257	60411320	+	ENSG00000179242	CDH4
20	60411930	60413795	+	ENSG00000179242	CDH4
20	60419594	60423976	+	ENSG00000179242	CDH4
20	60424237	60425318	+	ENSG00000179242	CDH4
20	60425579	60429039	+	ENSG00000179242	CDH4
20	60429048	60431247	+	ENSG00000179242	CDH4
20	60434695	60435266	+	ENSG00000179242	CDH4
20	60435456	60437813	+	ENSG00000179242	CDH4
20	60438163	60440489	+	ENSG00000179242	CDH4
20	60442888	60445884	+	ENSG00000179242	CDH4
20	60446981	60451872	+	ENSG00000179242	CDH4
20	60451918	60455136	+	ENSG00000179242	CDH4
20	60455165	60460578	+	ENSG00000179242	CDH4
20	60460596	60462406	+	ENSG00000179242	CDH4
20	60462775	60467065	+	ENSG00000179242	CDH4
20	60467513	60469287	+	ENSG00000179242	CDH4
20	60469644	60472112	+	ENSG00000179242	CDH4
20	60472209	60476157	+	ENSG00000179242	CDH4
20	60476195	60477758	+	ENSG00000179242	CDH4
20	60478568	60480227	+	ENSG00000179242	CDH4
20	60480370	60480825	+	ENSG00000179242	CDH4
20	60480892	60483282	+	ENSG00000179242	CDH4
20	60483314	60484792	+	ENSG00000179242	CDH4
20	60484869	60486039	+	ENSG00000179242	CDH4
20	60487821	60489420	+	ENSG00000179242	CDH4
20	60489754	60490894	+	ENSG00000179242	CDH4
20	60497491	60503886	+	ENSG00000179242	CDH4
20	60504280	60510622	+	ENSG00000179242	CDH4

20	60510661	60512351	+	ENSG00000179242	CDH4
20	60512552	60514751	+	ENSG00000179242	CDH4
2	173248534	173249024	+	ENSG00000091409	ITGA6
2	173282086	173282689	+	ENSG00000091409	ITGA6
2	173288260	173288735	+	ENSG00000091409	ITGA6
2	173291898	173293161	+	ENSG00000091409	ITGA6
5	140568055	140569190	+	ENSG00000177839	PCDHB9
9	101866553	101868409	+	ENSG00000106799	TGFBR1
9	101921480	101922177	+	ENSG00000106799	TGFBR1
9	101923985	101924597	+	ENSG00000106799	TGFBR1
1	156029632	156031210	+	ENSG00000132698	RAB25
1	156035595	156036227	+	ENSG00000132698	RAB25
1	156036288	156037009	+	ENSG00000132698	RAB25
1	156037319	156039431	+	ENSG00000132698	RAB25
1	156039558	156041079	+	ENSG00000132698	RAB25
17	7163994	7166613	-	ENSG00000181885	CLDN7
17	7166712	7167376	-	ENSG00000181885	CLDN7
16	68757400	68758228	+	ENSG00000039068	CDH1
16	68759099	68759837	+	ENSG00000039068	CDH1
16	68761789	68762608	+	ENSG00000039068	CDH1
16	68763352	68764449	+	ENSG00000039068	CDH1
16	68769167	68772534	+	ENSG00000039068	CDH1
16	68811246	68812334	+	ENSG00000039068	CDH1
16	68821275	68822112	+	ENSG00000039068	CDH1
16	68828377	68828990	+	ENSG00000039068	CDH1
16	68829110	68830152	+	ENSG00000039068	CDH1
16	68838640	68840457	+	ENSG00000039068	CDH1
16	68847351	68848424	+	ENSG00000039068	CDH1
16	68852138	68853193	+	ENSG00000039068	CDH1
16	68857741	68858359	+	ENSG00000039068	CDH1
16	68870690	68871962	+	ENSG00000039068	CDH1
9	35682527	35683372	-	ENSG00000198467	TPM2
9	35684500	35685649	-	ENSG00000198467	TPM2
9	35689139	35691700	-	ENSG00000198467	TPM2
9	35692696	35693749	-	ENSG00000198467	TPM2
17	79989492	79992990	+	ENSG00000169750	RAC3
19	3717741	3718343	+	ENSG00000105289	TJP3
19	3720647	3721396	+	ENSG00000105289	TJP3
19	3721398	3722269	+	ENSG00000105289	TJP3

19	3724064	3724847	+	ENSG00000105289	TJP3
19	3727657	3729180	+	ENSG00000105289	TJP3
19	3729312	3731188	+	ENSG00000105289	TJP3
19	3732526	3733418	+	ENSG00000105289	TJP3
19	3733751	3735498	+	ENSG00000105289	TJP3
19	3735838	3737244	+	ENSG00000105289	TJP3
19	3738325	3739585	+	ENSG00000105289	TJP3
19	3741008	3741827	+	ENSG00000105289	TJP3
19	3742478	3743240	+	ENSG00000105289	TJP3
19	3744275	3745462	+	ENSG00000105289	TJP3
19	3746076	3748545	+	ENSG00000105289	TJP3
19	3750537	3755032	+	ENSG00000105289	TJP3
7	55047639	55048090	+	ENSG00000146648	EGFR
7	55071433	55073479	+	ENSG00000146648	EGFR
7	55086020	55088310	+	ENSG00000146648	EGFR
7	55123241	55123682	+	ENSG00000146648	EGFR
7	55145508	55147231	+	ENSG00000146648	EGFR
7	55163191	55163806	+	ENSG00000146648	EGFR
7	55189887	55190448	+	ENSG00000146648	EGFR
7	55198346	55198822	+	ENSG00000146648	EGFR
7	55201158	55202229	+	ENSG00000146648	EGFR
7	55211997	55213112	+	ENSG00000146648	EGFR
7	55219028	55219762	+	ENSG00000146648	EGFR
7	55220726	55221155	+	ENSG00000146648	EGFR
7	55221543	55222285	+	ENSG00000146648	EGFR
7	55228582	55229392	+	ENSG00000146648	EGFR
7	55234129	55235562	+	ENSG00000146648	EGFR
7	55236691	55237133	+	ENSG00000146648	EGFR
7	55245005	55246565	+	ENSG00000146648	EGFR
7	55259820	55260450	+	ENSG00000146648	EGFR
7	55270639	55271618	+	ENSG00000146648	EGFR
7	55271739	55273106	+	ENSG00000146648	EGFR
7	55287001	55289015	+	ENSG00000146648	EGFR
7	55290850	55291591	+	ENSG00000146648	EGFR
7	55318364	55318910	+	ENSG00000146648	EGFR
7	55321971	55323179	+	ENSG00000146648	EGFR
7	55325216	55325889	+	ENSG00000146648	EGFR
8	28351140	28352474	+	ENSG00000104290	FZD3
8	28358172	28358624	+	ENSG00000104290	FZD3

8	28400745	28401309	+	ENSG00000104290	FZD3
8	28405277	28405766	+	ENSG00000104290	FZD3
8	28418454	28418874	+	ENSG00000104290	FZD3
1	59242032	59242625	-	ENSG00000177606	JUN
1	59247591	59251299	-	ENSG00000177606	JUN
5	68788039	68790332	+	ENSG00000197822	OCLN
5	68803812	68804585	+	ENSG00000197822	OCLN
5	68810501	68812531	+	ENSG00000197822	OCLN
5	68812939	68813458	+	ENSG00000197822	OCLN
5	68829365	68829844	+	ENSG00000197822	OCLN
5	68832094	68833204	+	ENSG00000197822	OCLN
5	68844010	68844794	+	ENSG00000197822	OCLN
5	68847722	68848463	+	ENSG00000197822	OCLN
5	68850668	68851406	+	ENSG00000197822	OCLN
22	39594848	39595349	-	ENSG00000100311	PDGFB
22	39596317	39597020	-	ENSG00000100311	PDGFB
22	39600659	39601842	-	ENSG00000100311	PDGFB
22	39602988	39604612	-	ENSG00000100311	PDGFB
22	39605505	39606985	-	ENSG00000100311	PDGFB
22	39609142	39609900	-	ENSG00000100311	PDGFB
22	39615898	39616989	-	ENSG00000100311	PDGFB
22	39619070	39619731	-	ENSG00000100311	PDGFB
22	39620393	39621094	-	ENSG00000100311	PDGFB
22	39621379	39622188	-	ENSG00000100311	PDGFB
22	39622646	39623516	-	ENSG00000100311	PDGFB
22	39625971	39627127	-	ENSG00000100311	PDGFB
22	39627269	39628192	-	ENSG00000100311	PDGFB
22	39629335	39629979	-	ENSG00000100311	PDGFB
22	39631026	39632094	-	ENSG00000100311	PDGFB
22	39633554	39634410	-	ENSG00000100311	PDGFB
22	39636973	39642244	-	ENSG00000100311	PDGFB
22	39645643	39646742	-	ENSG00000100311	PDGFB
22	39648764	39649292	-	ENSG00000100311	PDGFB
22	39649354	39651455	-	ENSG00000100311	PDGFB
22	39651990	39654451	-	ENSG00000100311	PDGFB
22	39654638	39655737	-	ENSG00000100311	PDGFB
22	39656395	39657251	-	ENSG00000100311	PDGFB
22	39658149	39658879	-	ENSG00000100311	PDGFB
22	39659967	39660963	-	ENSG00000100311	PDGFB

22	39661258	39662312	-	ENSG00000100311	PDGFB
22	39663034	39663721	-	ENSG00000100311	PDGFB
7	100753566	100754201	+	ENSG00000106366	SERPINE1
7	100757870	100758882	+	ENSG00000106366	SERPINE1
7	100760328	100761451	+	ENSG00000106366	SERPINE1
7	100765313	100765878	+	ENSG00000106366	SERPINE1
7	100768299	100768843	+	ENSG00000106366	SERPINE1
7	100779045	100779643	+	ENSG00000106366	SERPINE1
7	100785682	100786435	+	ENSG00000106366	SERPINE1
12	49359736	49360430	-	ENSG00000169884	WNT10B
12	49360648	49361505	-	ENSG00000169884	WNT10B
12	49361683	49362161	-	ENSG00000169884	WNT10B
12	49363500	49364708	-	ENSG00000169884	WNT10B
12	49365192	49366224	-	ENSG00000169884	WNT10B
12	49366228	49366869	-	ENSG00000169884	WNT10B
7	120968721	120969948	+	ENSG00000002745	WNT16
3	55504013	55504634	-	ENSG00000114251	WNT5A
3	55507986	55508964	-	ENSG00000114251	WNT5A
3	55516480	55517392	-	ENSG00000114251	WNT5A
3	55518269	55518844	-	ENSG00000114251	WNT5A
3	55520094	55522160	-	ENSG00000114251	WNT5A
3	55522369	55523836	-	ENSG00000114251	WNT5A

Table S3. AP-1 consensus motifs identified in FRA1^{EMT} genes.

Sequence name	Start	Stop	Score	P-value	Matched sequence
CD109	599	590	16.7038	9.09E-07	ATGAGTCACC
EPCAM	926	917	16.7038	9.09E-07	ATGAGTCACC
LEF1	764	773	16.7038	9.09E-07	ATGAGTCACC
FZD3	433	442	16.7038	9.09E-07	ATGAGTCACC
CLDN4	886	895	15.5695	2.56E-06	CTGAGTCACC
BMP7	894	885	15.5695	2.56E-06	CTGAGTCACC
SMAD3	195	204	15.5695	2.56E-06	CTGAGTCACC
ITGA3	135	144	15.5695	2.56E-06	CTGAGTCACC
RAC2	1373	1382	15.5695	2.56E-06	CTGAGTCACC
SERPINE1	437	428	15.5695	2.56E-06	CTGAGTCACC
CLDN4	815	824	15.4277	4.42E-06	GTGAGTCACC
BMP4	572	581	15.4277	4.42E-06	GTGAGTCACC
BMP7	840	831	15.4277	4.42E-06	GTGAGTCACC
AXL	647	638	15.4277	4.42E-06	GTGAGTCACC
TJP2	462	453	15.4277	4.42E-06	GTGAGTCACC
STAT3	679	670	15.4277	4.42E-06	GTGAGTCACC
VIM	511	520	15.4277	4.42E-06	GTGAGTCACC
PDGFB	838	829	15.4277	4.42E-06	GTGAGTCACC
CLDN4	970	961	15.1441	6.07E-06	ATGAGTCAGC
AXL	217	208	15.1441	6.07E-06	CTGACTCACC
AXL	440	449	15.1441	6.07E-06	ATGAGTCAGC
ZEB1	495	486	15.1441	6.07E-06	CTGACTCACC
WNT10B	192	201	15.1441	6.07E-06	CTGACTCACC
BMP4	580	571	15.0023	7.92E-06	GTGACTCACC
BMP7	2508	2517	15.0023	7.92E-06	GTGACTCACC
LAMC2	440	431	15.0023	7.92E-06	GTGACTCACC
PLAUR	50	59	15.0023	7.92E-06	GTGACTCACC
VIM	519	510	15.0023	7.92E-06	GTGACTCACC
TJP3	310	319	15.0023	7.92E-06	GTGACTCACC
TNC	619	610	14.7188	9.94E-06	ATGACTCAGC
EGFR	258	249	14.4352	1.22E-05	ATGACTCACA
PDGFB	1152	1143	14.4352	1.22E-05	ATGAGTCACT
LAMB3	1329	1320	14.0098	1.58E-05	CTGAGTCAGC
STAT5B	1496	1505	14.0098	1.58E-05	ATGACTCACT
ITGAV	70	79	14.0098	1.58E-05	ATGACTCACT

MMP14	48	57	14.0098	1.58E-05	CTGAGTCAGC
MMP16	273	282	14.0098	1.58E-05	CTGAGTCAGC
LAMB3	1247	1238	13.8681	1.75E-05	GTGAGTCAGC
ITGA3	1170	1179	13.8681	1.75E-05	CTGACTCATC
CDH1	876	867	13.8681	1.75E-05	GTGAGTCAGC
EPCAM	918	927	13.7263	1.93E-05	GTGACTCATC
RAC2	477	486	13.7263	1.93E-05	CTGAGTCACA
LAMC2	432	441	13.5845	2.23E-05	GTGAGTCACA
STAT5B	555	546	13.5845	2.23E-05	CTGACTCAGC
ITGA3	1071	1062	13.5845	2.23E-05	CTGACTCAGC
MMP14	56	47	13.5845	2.23E-05	CTGACTCAGC
TJP3	1150	1159	13.5845	2.23E-05	CTGACTCAGC
OCLN	241	250	13.5845	2.23E-05	CTGACTCAGC
PDGFB	818	827	13.5845	2.23E-05	GTGAGTCACA
PDGFB	194	203	13.5845	2.23E-05	CTGACTCAGC
SMAD3	203	194	13.4427	2.30E-05	GTGACTCAGC
ITGA3	143	134	13.4427	2.30E-05	GTGACTCAGC
CLDN4	107	98	13.3009	2.60E-05	CTGAGTCACT
BMP7	637	628	13.3009	2.60E-05	CTGAGTCACT
AXL	392	383	13.3009	2.60E-05	CTGAGTCACT
FBN1	91	100	13.3009	2.60E-05	ATGAGTCAGA
LAMB3	1239	1248	13.3009	2.60E-05	CTGACTCACA
ITGA3	1178	1169	13.3009	2.60E-05	ATGAGTCAGA
EGFR	81	90	13.3009	2.60E-05	CTGACTCACA
CLDN4	911	902	13.1591	3.05E-05	GTGAGTCACT
CLDN4	903	912	13.1591	3.05E-05	GTGACTCACA
BMP7	2516	2507	13.1591	3.05E-05	GTGAGTCACT
BMP7	832	841	13.1591	3.05E-05	GTGACTCACA
AXL	158	149	13.1591	3.05E-05	GTGACTCACA
TGFBR2	317	326	13.1591	3.05E-05	GTGAGTCACT
STAT5B	396	387	13.1591	3.05E-05	GTGACTCACA
STAT5B	388	397	13.1591	3.05E-05	GTGAGTCACT
STAT3	671	680	13.1591	3.05E-05	GTGACTCACA
ROBO1	723	732	13.1591	3.05E-05	GTGAGTCACT
ROBO1	418	427	13.1591	3.05E-05	GTGAGTCACT
TJP3	318	309	13.1591	3.05E-05	GTGAGTCACT
TJP3	1131	1122	13.1591	3.05E-05	GTGAGTCACT
TJP3	1123	1132	13.1591	3.05E-05	GTGACTCACA
PDGFB	826	817	13.1591	3.05E-05	GTGACTCACA

PDGFB	830	839	13.1591	3.05E-05	GTGACTCACA
CD109	335	326	12.8756	3.47E-05	CTGACTCACT
TGFBR2	29	38	12.8756	3.47E-05	ATGAGTCAGT
CDH1	868	877	12.8756	3.47E-05	CTGACTCACT
PDGFB	55	46	12.8756	3.47E-05	CTGACTCACT
CLDN4	823	814	12.7338	3.70E-05	GTGACTCACT
TGFBR2	325	316	12.7338	3.70E-05	GTGACTCACT
BMP4	414	423	12.592	3.79E-05	TTGAGTCACC
CDH1	35	26	12.4502	4.01E-05	ATGACTCAGT
TJP3	1256	1247	12.4502	4.01E-05	ATGACTCAGT
BMP7	572	563	12.1666	4.30E-05	CTGAGTCAGA
AXL	357	348	12.1666	4.30E-05	CTGAGTCAGA
LAMB3	1851	1860	12.1666	4.30E-05	CTGAGTCAGA
STAT5B	547	556	12.1666	4.30E-05	CTGAGTCAGA
PDGFB	1121	1112	12.1666	4.30E-05	CTGAGTCAGA
SERPINE1	163	172	12.1666	4.30E-05	CTGAGTCAGA
LAMB3	116	125	12.0249	4.70E-05	ATGAGTCACG
SNAI2	356	365	12.0249	4.70E-05	GTGAGTCAGA
CDH1	27	36	12.0249	4.70E-05	CTGAGTCATT
PDGFB	47	56	12.0249	4.70E-05	GTGAGTCAGA
EGFR	250	259	11.8831	4.92E-05	GTGAGTCATT
BMP7	564	573	11.7413	5.20E-05	CTGACTCAGA
SMAD3	914	923	11.7413	5.20E-05	CTGACTCAGA
NRP1	255	264	11.7413	5.20E-05	CTGAATCACC
PDGFB	202	193	11.7413	5.20E-05	CTGAGTCAGT
CLDN4	414	405	11.5995	5.81E-05	GTGAATCACC
CLDN4	894	885	11.5995	5.81E-05	GTGACTCAGA
CD109	610	601	11.5995	5.81E-05	ATGAATCATC
BMP7	886	895	11.5995	5.81E-05	GTGACTCAGA
TGFBR2	37	28	11.5995	5.81E-05	CTGACTCATT
ETS1	240	249	11.5995	5.81E-05	GTGAATCACC
STAT5B	222	231	11.5995	5.81E-05	GTGAATCACC
LAMB1	312	321	11.5995	5.81E-05	GTGAATCACC
TJP2	497	506	11.5995	5.81E-05	GTGAATCACC
ZEB1	487	496	11.5995	5.81E-05	GTGAGTCAGT
RAC2	485	476	11.5995	5.81E-05	GTGACTCAGA
RAC2	1381	1372	11.5995	5.81E-05	GTGACTCAGA
TJP3	1611	1602	11.5995	5.81E-05	GTGAATCACC
EGFR	89	80	11.5995	5.81E-05	GTGAGTCAGT

SERPINE1	429	438	11.5995	5.81E-05	GTGACTCAGA
LAMB3	124	115	11.4577	5.92E-05	GTGACTCATT
CD109	122	113	11.3159	6.23E-05	ATGAATCAGC
LAMC2	481	472	11.3159	6.23E-05	CTGACTCAGT
LAMB3	1859	1850	11.3159	6.23E-05	CTGACTCAGT
LAMB3	1321	1330	11.3159	6.23E-05	CTGACTCAGT
PLAUR	625	634	11.3159	6.23E-05	CTGACTCAGT
STAT5B	144	135	11.3159	6.23E-05	CTGACTCAGT
PDGFB	744	753	11.3159	6.23E-05	CTGACTCAGT
SERPINE1	171	162	11.3159	6.23E-05	CTGACTCAGT
AXL	277	268	11.0324	6.66E-05	ATGAATCACA
ROBO1	386	377	11.0324	6.66E-05	ATGAATCACA
AXL	150	159	10.7488	7.36E-05	GTGAGTCACG
LAMB3	162	153	10.7488	7.36E-05	ATTACTCACC
PLAUR	58	49	10.7488	7.36E-05	GTGAGTCACG
PDGFB	282	291	10.7488	7.36E-05	ATGAGTCATG
PDGFB	40	49	10.7488	7.36E-05	GTGAGTCACG
ROBO1	72	63	10.607	7.58E-05	ATGAATCACT
ROBO1	444	453	10.607	7.58E-05	ATGAATCACT
CLDN4	342	351	10.4652	7.97E-05	CTGACTCACG
PLAUR	1854	1845	10.4652	7.97E-05	ATGAGTCAGG
ITGA5	973	982	10.4652	7.97E-05	ATGACTCAAC
SNAI2	364	355	10.4652	7.97E-05	CTGACTCACG
AXL	639	648	10.3234	8.49E-05	GTGACTCACG
TJP2	454	463	10.3234	8.49E-05	GTGACTCACG
TJP2	341	332	10.3234	8.49E-05	GTGAATCATC
ROBO1	731	722	10.3234	8.49E-05	GTGACTCACG
ROBO1	426	417	10.3234	8.49E-05	GTGACTCACG
ITGB3	461	452	10.3234	8.49E-05	ATGACTCATG
PDGFB	290	281	10.3234	8.49E-05	ATGACTCATG
PDGFB	48	39	10.3234	8.49E-05	GTGACTCACG
VIM	533	524	10.0399	8.85E-05	CTTAGTCACC
OCLN	1071	1080	10.0399	8.85E-05	CTTAGTCACC
CLDN4	26	17	9.89808	9.30E-05	CTGAATCACA
PLAU	658	667	9.89808	9.30E-05	TTGACTCACT
ITGAV	414	423	9.89808	9.30E-05	CTGAATCACA
NRP1	226	235	9.89808	9.30E-05	TTGACTCACT
NRP1	360	351	9.89808	9.30E-05	TTGACTCACT
ITGBL1	138	147	9.89808	9.30E-05	TTGACTCACT

TGFBR2	4	13	9.7563	9.66E-05	ATGAATCATA
STAT3	57	66	9.7563	9.66E-05	ATGAATCATA
CDH4	3633	3642	14.7188	9.94E-06	ATGACTCAGC
CDH4	3641	3632	14.2934	1.31E-05	CTGAGTCATC
CDH4	2613	2622	14.1516	1.40E-05	GTGAGTCATC
CDH4	2621	2612	14.0098	1.58E-05	ATGACTCACT
CDH4	941	932	13.8681	1.75E-05	CTGACTCATC
CDH4	2527	2536	13.3009	2.60E-05	CTGAGTCACT
CDH4	933	942	13.3009	2.60E-05	ATGAGTCAGA
CDH4	27	18	12.7338	3.70E-05	ATGACTCATT
CDH4	393	402	12.4502	4.01E-05	ATGACTCAGT
CDH4	819	828	12.1666	4.30E-05	TTGACTCACC
CDH4	19	28	10.7488	7.36E-05	ATGAGTCATG
CDH4	3693	3684	10.4652	7.97E-05	CTGAATCATC
CDH4	441	450	9.89808	9.30E-05	CTGAATCACA
CDH4	1501	1510	9.89808	9.30E-05	CTGAATCACA
CDH4	2879	2870	9.7563	9.66E-05	ATGAATCATA

Table S4. Mean gene expression levels (log₂) for the two main groups resulting from unsupervised clustering of stage B and C colorectal cancers using FRA1^{EMT} genes. P-values are for t-tests and adjusted for multiple testing using the Benjamini and Hochberg multiple testing correction.

Gene name	Affymetrix probe ID	Mean log ₂ expression in the right branch	Mean log ₂ expression in the left branch	P-value	Right vs left branch	shFRA1 vs shNS
VIM	1555938_x_at	4.8	5.3	3.26X10 ⁰⁶	down	down
VIM	201426_s_at	11.4	12.4	1.08X10 ²⁵	down	down
TGFB1	201506_at	12.0	12.2	1.89X10 ⁰¹	down	down
FN1	1558199_at	5.6	6.1	2.31X10 ¹⁴	down	down
FN1	210495_x_at	11.5	12.9	1.26X10 ²⁴	down	down
FN1	211719_x_at	11.6	12.9	2.64X10 ²³	down	down
FN1	212464_s_at	11.2	12.6	8.71X10 ²⁵	down	down
FN1	214701_s_at	7.6	8.6	5.23X10 ¹⁴	down	down
FN1	214702_at	5.0	5.5	2.38X10 ¹¹	down	down
FN1	216442_x_at	11.5	13.0	3.52X10 ²⁵	down	down
LPXN	216250_s_at	8.2	8.5	1.47X10 ⁰⁵	down	down
LPXN	242778_at	5.7	5.7	8.95X10 ⁰²	down	down
NRP1	1561365_at	4.0	4.1	1.16X10 ⁰³	down	down
NRP1	210510_s_at	6.6	6.9	6.53X10 ⁰⁶	down	down
NRP1	210615_at	5.2	5.2	4.17X10 ⁰¹	down	down
NRP1	212298_at	7.4	8.5	2.14X10 ¹⁹	down	down
SNAI2	213139_at	7.4	8.6	1.45X10 ²⁶	down	down
FBN1	202765_s_at	7.8	9.2	1.40X10 ²⁸	down	down
FBN1	202766_s_at	8.5	9.9	1.40X10 ²⁹	down	down
FBN1	235318_at	5.6	6.8	1.08X10 ²⁵	down	down
ROBO1	213194_at	8.2	8.8	8.23X10 ⁰⁶	down	down
TNC	201645_at	8.2	9.5	1.38X10 ¹⁵	down	down
TNC	216005_at	5.1	5.8	2.40X10 ¹⁰	down	down
LEF1	210948_s_at	5.7	6.0	8.79X10 ⁰³	down	down
LEF1	221557_s_at	5.9	5.8	3.25X10 ⁰³	up	down
LEF1	221558_s_at	8.1	8.5	7.52X10 ⁰³	down	down
LAMC2	202267_at	8.6	8.9	3.25X10 ⁰³	down	down
LAMC2	207517_at	6.3	6.5	7.94X10 ⁰⁴	down	down
TGFB2	209908_s_at	4.5	4.6	3.69X10 ⁰²	down	down
TGFB2	209909_s_at	4.4	4.6	2.63X10 ⁰²	down	down
TGFB2	220406_at	6.6	6.6	6.96X10 ⁰¹	down	down
TGFB2	220407_s_at	6.4	6.5	1.89X10 ⁰²	down	down
TGFB2	228121_at	6.9	7.5	4.45X10 ¹¹	down	down
SERPINE1	1568765_at	5.8	6.1	1.72X10 ⁰⁷	down	down
SERPINE1	202627_s_at	7.6	8.7	2.64X10 ²¹	down	down

SERPINE1	202628_s_at	7.4	8.6	4.68X10 ²⁰	down	down
AXL	202685_s_at	7.7	7.8	3.48X10 ⁰²	down	down
AXL	202686_s_at	7.7	8.5	3.47X10 ¹⁶	down	down
MMP14	160020_at	8.7	9.1	1.66X10 ¹⁰	down	down
MMP14	202827_s_at	7.9	8.3	1.30X10 ⁰⁶	down	down
MMP14	202828_s_at	8.0	8.4	9.90X10 ⁰⁹	down	down
MMP14	217279_x_at	8.0	8.2	2.20X10 ⁰⁹	down	down
PLAU	205479_s_at	8.5	9.4	3.32X10 ¹⁶	down	down
PLAU	211668_s_at	8.0	8.8	3.47X10 ¹⁶	down	down
TGFBR2	207334_s_at	6.9	7.1	1.00X10 ⁰²	down	down
TGFBR2	208944_at	9.9	10.1	1.76X10 ⁰²	down	down
LAMB3	209270_at	9.0	9.0	4.71X10 ⁰¹	down	down
JUN	201464_x_at	11.3	11.5	1.25X10 ⁰²	down	down
JUN	201465_s_at	8.7	8.3	4.71X10 ⁰³	up	down
JUN	201466_s_at	10.1	10.0	4.23X10 ⁰¹	up	down
ITGA2	205032_at	8.9	8.9	8.24X10 ⁰¹	up	down
ITGA2	227314_at	10.0	9.9	5.58X10 ⁰¹	up	down
LAMA4	202202_s_at	8.4	9.2	8.00X10 ²²	down	down
LAMA4	210089_s_at	6.7	7.1	1.11X10 ¹⁰	down	down
LAMA4	210989_at	4.6	4.7	1.00X10 ⁰²	down	down
LAMA4	210990_s_at	6.3	6.5	3.56X10 ⁰⁷	down	down
LAMA4	216081_at	6.6	6.4	1.03X10 ⁰²	up	down
ZEB1	210875_s_at	5.9	7.0	2.19X10 ¹⁹	down	down
ZEB1	212758_s_at	7.2	7.6	8.62X10 ⁰⁸	down	down
ZEB1	212764_at	8.0	9.1	4.77X10 ¹⁸	down	down
ZEB1	239952_at	6.1	6.3	3.02X10 ⁰⁷	down	down
PLAUR	210845_s_at	9.5	10.0	1.71X10 ⁰⁸	down	down
PLAUR	211924_s_at	8.9	9.4	1.10X10 ⁰⁷	down	down
PLAUR	214866_at	7.9	8.1	2.81X10 ⁰²	down	down
MMP16	207012_at	4.6	4.8	2.69X10 ⁰⁵	down	down
MMP16	207013_s_at	7.0	7.1	2.03X10 ⁰²	down	down
MMP16	208166_at	4.2	4.3	4.49X10 ⁰¹	down	down
MMP16	208167_s_at	5.0	5.0	1.89X10 ⁰¹	down	down
MMP16	223614_at	5.3	5.8	8.95X10 ¹²	down	down
ITGB3	204625_s_at	5.5	5.4	1.54X10 ⁰²	up	down
ITGB3	204626_s_at	6.5	6.6	2.88X10 ⁰¹	down	down
ITGB3	204627_s_at	5.4	5.8	8.75X10 ¹⁴	down	down
ITGB3	204628_s_at	7.1	7.0	6.21X10 ⁰²	up	down
ITGB3	211579_at	5.5	5.5	9.06X10 ⁰¹	up	down
ITGB3	215240_at	3.8	3.8	1.22X10 ⁰¹	down	down
ITGB3	216261_at	6.4	6.5	7.94X10 ⁰⁴	down	down
ETS1	1555355_a_at	7.1	7.7	4.62X10 ¹⁰	down	down
ETS1	214447_at	7.2	7.4	1.98X10 ⁰³	down	down
ETS1	224833_at	9.5	10.1	2.03X10 ¹⁸	down	down
STAT5B	1555086_at	8.2	8.2	2.11X10 ⁰¹	down	down
STAT5B	1555088_x_at	8.4	8.4	2.27X10 ⁰¹	down	down
STAT5B	205026_at	6.5	6.6	2.59X10 ⁰¹	down	down

STAT5B	212549_at	8.3	8.5	8.38X10^05	down	down
STAT5B	212550_at	7.5	7.5	6.61X10^01	down	down
ITGBL1	1557079_at	3.6	3.7	1.45X10^03	down	down
ITGBL1	1557080_s_at	5.3	6.2	4.42X10^08	down	down
ITGBL1	205422_s_at	5.8	7.1	2.77X10^12	down	down
ITGBL1	214927_at	6.4	7.1	1.12X10^08	down	down
ITGBL1	231993_at	4.9	5.6	2.85X10^08	down	down
LAMB1	201505_at	9.3	9.5	2.74X10^03	down	down
LAMB1	211651_s_at	9.0	9.3	2.45X10^03	down	down
ITGA5	201389_at	8.1	8.7	2.34X10^16	down	down
RAC2	207419_s_at	7.5	7.7	3.26X10^02	down	down
RAC2	213603_s_at	9.2	9.5	2.18X10^04	down	down
ITGA3	201474_s_at	8.1	8.1	8.26X10^01	down	down
LAMC1	200770_s_at	9.1	9.4	1.72X10^07	down	down
LAMC1	200771_at	9.8	10.4	1.85X10^19	down	down
WNT5A	205990_s_at	9.1	9.5	4.71X10^03	down	down
WNT5A	213425_at	8.1	8.4	1.46X10^02	down	down
WNT5A	231227_at	6.4	6.6	6.76X10^02	down	down
SMAD3	205396_at	6.7	6.8	1.54X10^01	down	down
SMAD3	205397_x_at	7.3	7.3	6.61X10^01	up	down
SMAD3	205398_s_at	7.3	7.4	1.54X10^02	down	down
SMAD3	218284_at	8.6	8.7	4.64X10^01	down	down
RND3	212724_at	10.5	10.6	4.98X10^02	down	down
TJP2	202085_at	10.5	10.4	3.06X10^02	up	down
TJP2	232017_at	7.8	7.8	8.43X10^01	up	down
TJP2	237132_at	5.3	5.3	7.75X10^01	down	down
TJP2	242991_at	5.1	5.1	1.62X10^02	up	down
TPM1	1558532_at	5.7	5.8	2.15X10^01	down	down
TPM1	206116_s_at	10.0	10.6	1.22X10^10	down	down
TPM1	206117_at	6.8	7.3	2.27X10^11	down	down
TPM1	210986_s_at	11.7	12.1	2.69X10^10	down	down
TPM1	210987_x_at	11.0	11.5	3.54X10^14	down	down
TPM1	238688_at	8.0	8.1	3.42X10^02	down	down
CDH4	1563587_at	5.9	5.8	3.11X10^04	up	down
CDH4	206866_at	5.7	5.5	8.42X10^04	up	down
CDH4	220227_at	6.4	6.3	9.55X10^02	up	down
CDH4	239485_at	6.2	6.1	6.10X10^02	up	down
ITGAV	202351_at	10.7	11.2	5.67X10^14	down	down
ITGA6	201656_at	10.9	10.8	1.24X10^01	up	down
ITGA6	215177_s_at	10.3	10.2	4.64X10^01	up	down
PCDHB9	223927_at	7.1	7.2	1.76X10^02	down	down
PCDH18	225975_at	8.7	9.1	2.01X10^04	down	down
PCDH18	225977_at	7.1	7.2	1.03X10^01	down	down
STAT3	208991_at	11.1	11.1	2.25X10^01	down	down
STAT3	208992_s_at	10.2	10.3	2.27X10^01	down	down
STAT3	225289_at	9.3	9.4	1.22X10^01	down	down
STAT3	243213_at	6.8	6.9	4.01X10^03	down	down

EGFR	1565483_at	9.5	9.9	2.17X10 ⁰²	down	down
EGFR	1565484_x_at	9.2	9.7	1.34X10 ⁰²	down	down
EGFR	201983_s_at	9.0	8.6	7.06X10 ⁰⁵	up	down
EGFR	201984_s_at	8.5	8.3	3.54X10 ⁰²	up	down
EGFR	210984_x_at	8.2	7.9	7.00X10 ⁰⁸	up	down
EGFR	211550_at	6.2	6.1	2.45X10 ⁰²	up	down
EGFR	211551_at	6.5	6.4	4.42X10 ⁰²	up	down
EGFR	211607_x_at	7.8	7.6	3.13X10 ⁰⁶	up	down
LAMA3	1560078_at	6.3	6.4	6.76X10 ⁰²	down	down
LAMA3	1563772_a_at	6.5	6.4	6.39X10 ⁰³	up	down
LAMA3	1568879_a_at	7.2	7.2	3.88X10 ⁰¹	down	down
LAMA3	203726_s_at	8.8	9.0	2.87X10 ⁰¹	down	down
LAMA3	234608_at	5.8	5.9	2.75X10 ⁰¹	down	down
LAMA3	234719_at	5.9	5.8	3.57X10 ⁰³	up	down
OCN	209925_at	8.1	7.9	1.11X10 ⁰¹	up	up
OCN	227492_at	10.3	10.0	1.06X10 ⁰⁴	up	up
OCN	231022_at	8.5	8.2	2.69X10 ⁰⁵	up	up
FZD3	219683_at	6.9	7.0	4.03X10 ⁰¹	down	up
FZD3	227499_at	5.7	5.7	6.42X10 ⁰¹	up	up
FZD3	227524_at	7.5	7.3	7.94X10 ⁰⁴	up	up
FZD3	239082_at	8.6	8.6	7.75X10 ⁰¹	down	up
TJP3	213412_at	7.8	7.4	3.35X10 ⁰⁹	up	up
TJP3	35148_at	8.3	8.0	6.47X10 ⁰⁷	up	up
PDGFB	204200_s_at	6.5	6.7	2.19X10 ⁰⁸	down	up
PDGFB	216055_at	5.4	5.4	7.61X10 ⁰¹	down	up
PDGFB	216061_x_at	7.4	7.5	9.96X10 ⁰⁴	down	up
PDGFB	217112_at	5.7	5.5	3.35X10 ⁰⁷	up	up
RAC3	206103_at	6.2	6.2	8.82X10 ⁰¹	up	up
BMP7	209590_at	7.4	7.4	8.19X10 ⁰¹	up	up
BMP7	209591_s_at	6.4	6.4	9.64X10 ⁰¹	down	up
BMP7	211259_s_at	6.2	6.0	3.43X10 ⁰²	up	up
BMP7	211260_at	7.1	6.8	5.16X10 ⁰⁸	up	up
BMP4	211518_s_at	9.4	9.3	6.69X10 ⁰¹	up	up
TPM2	204083_s_at	9.3	10.4	2.03X10 ¹⁸	down	up
TPM2	212654_at	6.4	6.7	8.08X10 ⁰⁶	down	up
TPM2	227397_at	6.4	6.3	5.82X10 ⁰³	up	up
TPM2	229911_at	6.4	6.3	5.62X10 ⁰³	up	up
CLDN4	1569421_at	7.2	7.2	4.93X10 ⁰¹	down	up
CLDN4	201428_at	10.2	10.0	9.87X10 ⁰³	up	up
WNT16	221113_s_at	6.6	6.6	3.81X10 ⁰¹	down	up
WNT16	224022_x_at	3.7	3.8	1.11X10 ⁰¹	down	up
CDH1	201130_s_at	9.0	8.8	1.20X10 ⁰¹	up	up
CDH1	201131_s_at	12.0	11.7	1.98X10 ⁰³	up	up
CLDN7	202790_at	11.0	10.8	1.34X10 ⁰²	up	up
RAB25	218186_at	10.6	10.4	8.53X10 ⁰⁴	up	up
CD109	226545_at	6.8	8.1	6.95X10 ¹⁴	down	up
CD109	229900_at	6.0	6.4	9.69X10 ⁰⁸	down	up

CD109	239719_at	6.7	6.7	3.82X10 ⁰¹	down	up
EPCAM	201839_s_at	12.9	12.7	6.38X10 ⁰³	up	up

Table S5. Clinicopathological and molecular associations for *FOSL1* expression levels in stage B and C CRC patients. P-values are for the χ^2 test for categorical variables and the Wilcoxon rank-sum test for continuous variables.

Characteristic	All cases N	<i>FOSL1</i> ^{low} N (%)	<i>FOSL1</i> ^{high} N (%)	P-value
Total	185	146 (80.2)	36 (19.8)	
FRA1 ^{EMT} signature				
Epithelial	149	81 (85.3)	14 (14.7)	
Mesenchymal	36	68 (74.7)	22(25.3)	0.11
Age				
Median (range)	67, 26-92	67 (26-92)	69 (30-90)	0.679
Gender				
Male	98	83 (84.7)	15 (15.3)	0.169
Female	87	66 (75.9)	21 (24.1)	
Tumour location				
Colon	163	129 (79.1)	34 (20.9)	0.307
Rectum	22	20 (90.9)	2 (9.1)	
Tumor stage				
B	91	70 (76.9)	21 (23.1)	0.3
C	94	79 (84.0)	15 (16.0)	
T stage				
2	9	9 (100)	0 (0)	
3	163	133 (81.6)	30 (18.4)	
4	13	7 (53.8)	6 (46.2)	0.017*
N stage				
0	91	76 (83.5)	15 (16.5)	
1	66	51 (77.3)	15 (22.7)	
2	25	19 (76.0)	6 (24.0)	0.531
Unknown	3	-	-	

Table S6. Clinicopathological and molecular associations for FRA1^{EMT} signature in stage B and C CRC patients. P-values are for the χ^2 test for categorical variables and the Wilcoxon rank-sum test for continuous variables.

Characteristic	All cases N	Epithelial signature N (%)	Mesenchymal signature N (%)	P-value
Total	185	95 (51.3)	90 (48.6)	
FRA1 ^{EMT} signature				
Epithelial	149	81 (54.4)	68 (45.6)	
Mesenchymal	36	14 (38.9)	22 (61.1)	0.139
Age				
Median (range)	67 (26-92)	70 (26-92)	64 (26-92)	0.005*
Gender				
Male	98	82 (54.1)	45 (45.9)	0.521
Female	87	42 (48.3)	21 (51.7)	
Tumour location				
Colon	163	82 (50.3)	81 (49.7)	0.585
Rectum	22	13 (59.1)	9 (40.9)	
Tumor stage				
B	94	52 (55.3)	42 (44.7)	0.342
C	91	43 (47.3)	48 (52.7)	
T stage				
2	9	6 (66.7)	3 (33.3)	0.622
3	163	82 (50.3)	81 (49.7)	
4	13	7 (53.8)	6 (46.2)	
N stage				
0	91	52 (57.1)	39 (42.9)	
1	66	37 (56.1)	29 (43.9)	
2	25	6 (24.0)	19 (76.0)	0.0098*
Unknown	3	-	-	

Table S7. Univariate and multivariate Cox proportional-hazards analysis of survival for stage B and C colorectal cancer patients according to *FOSL1* expression and the concordant *FRA1*^{EMT} gene expression patterns. P-values are for the Wald test.

Molecular Feature	N	Events/ years obs.	Univariate model		Multivariate model	
			HR (95% CI)	P-value	HR (95% CI)	P-value
Total	182	47/640.2				
Classifier						
<i>FOSL1</i> ^{low} /epithelial	81	10/300.0	1 (Referent)		1 (Referent)	
<i>FOSL1</i> ^{high} /epithelial	14	5/45.95	3.26 (1.11-9.53)	0.03	3.38 (1.10-10.46)	0.03
<i>FOSL1</i> ^{low} /mesenchymal	65	14/44.22	2.12 (0.97-4.64)	0.06	1.70 (0.75-1.17)	0.21
<i>FOSL1</i> ^{high} /mesenchymal	22	18/250.1	8.16 (3.60-18.49)	<0.001	7.06 (3.03-16.48)	<0.01
Age						
Age in decades			0.90 (0.73-1.11)	0.322	0.94 (0.75-1.17)	0.56
Gender						
Male	97	27/347.7	1 (Referent)		1 (Referent)	
Female	85	20/292.5	0.87 (0.49-1.55)	0.635	0.91 (0.48-1.71)	0.76
Tumor location						
Colon	160	41/556.1	1 (Referent)		1 (Referent)	
Rectum	22	6/84.0	1.01 (0.43-2.39)	0.975	1.32 (0.52-3.33)	0.55
Tumor stage						
B	91	13/336.4	1 (Referent)		1 (Referent)	
C, N1	66	20/227.2	2.37 (1.18-4.76)	0.016	2.32 (1.07-5.05)	0.03*
C, N2	25	14/76.5	4.56 (2.14-9.71)	<0.001	3.06 (1.76-9.37)	0.001*
Adjuvant treatment						
No	98	20/269.8	1 (Referent)		1 (Referent)	
Yes	84	27/298.2	1.5 (0.84-2.68)	0.17	0.84 (0.42-1.67)	0.62

Table S8. List of qRT-PCR and ChIP primers used in this study.

Primers used for ChIP

Gene	Forward primer	Reverse primer	Product size
<i>AXL</i>	AGGAGGCAGGGGTGCTGAGA	ACGCCATGGGTGCCAAACTT	193bp
<i>BMP4</i>	TCTGCCTGTCTCCCCTCACC	TGGGATTCCCGTCCAAGCTA	164bp
<i>BMP7</i>	GGCCCTGGGTACTGAAGACG	GAGATGCAGCGCGAGATCCT	190bp
<i>FN1</i>	TGGGGCTGAACCATTTGCTG	TTTTCCCGCAGGTTGCGAAG	200bp
<i>FOSL1</i>	GCCTTCGACGTACCCCTGGA	TCCACCTGGTGCCAAGCATC	183bp
<i>LEF1</i>	TGGCCGGGATGATTTGAGAC	CCACAGCGGAGCGGAGATTA	232bp
<i>SNAI2</i>	TAATCCAGCCCAGCCCCATC	CGTCTGACTCACGCCATCAGC	223bp
<i>TGFB2</i>	TGGAGTAACCAAGCGGGTCA	GCGTGCGTGTGTGTGTGTGT	219bp
<i>VIM</i>	CCGCTAGGAGCCCTCAATCGG	TTCGGACGGCGGGAGTTGCG	126bp
<i>ZEB1</i>	CCTGGTCTCTCTCCGCCTAGC	AGAAGCAACAGCCGCTCCAC	151bp

Primers used for RT-PCR

Gene	Forward primer	Reverse primer	Product size
<i>AXL</i>	GAGAACATTAGTGCTACGCGGAA	CCTTAGCCCTATGTCCATTAGCA	124bp
<i>BMP4</i>	GCATTCGGTTACCAGGAATC	TGAGCCTTTCCAGCAAGTTT	106bp
<i>BMP7</i>	CTTCCCCTTCTGGGATCTTG	GATAGCCATTTCTCACCAG	136bp
<i>CDLN7</i>	CACCAGGGAGACCACCATTA	ATGTACAAGGGGCTGTGGAT	132bp
<i>EPCAM</i>	AGAACCTACTGGATCATCATTGAACTAA	CGCGTTGTGATCTCCTTCTG	100bp
<i>FN1</i>	CCATCAAGCCAGATGTCAGAAGCT	GGATGGTGCATCAATGGCA	139bp
<i>FOSL1</i>	CACCGACCCATCTGCAAA	CACTGGTACTGCCTGTGT	60bp
<i>LAMC2</i>	CAGCGGAATCCATTACCAGT	TGCTTCTCGCTCCTCCTG	128bp
<i>SNAI2</i>	CATGAGGAATCTGGCTGCTGTGTA	GCACAGGAGAAAATGCCTTTGGAC	123bp
<i>TGFB2</i>	CTCCATTGCTGAGACGTCAA	CGACGAAGAGTACTACGCCA	133bp
<i>TGFBI</i>	TTGAGAGTGGTAGGGCTGCT	CCAAAGGAAAATCTGTGGCA	107bp
<i>VIM</i>	CGCCAGATGCGTGAAATGG	ACCAGAGGGAGTGAATCCAGA	278bp
<i>ZEB1</i>	GCACCTGAAGAGGACCAGAG	TGGTGATGCTGAAAGAGACG	537bp
<i>ZEB2</i>	CAAGAGGCGCAAACAAGC	GGTTGGCAATACCGTCATCC	127bp