

Supplementary Material

Supplementary Table S1. GEO accession number, tumor stage, location and previous treatment details for the colorectal cancer samples from the Expression Project for Oncology (expO) for which microarray data were retrieved.

GEO accession	Stage	Location	Prior therapy
GSM38075	A	Colon	None
GSM53055	A	Colon	None
GSM53087	A	Rectosigmoid	None
GSM76530	A	Colon	None
GSM76576	A	Colon	None
GSM76629	A	Colon	None
GSM88982	A	Rectum	None
GSM89044	A	Colon	None
GSM89074	A	Rectum	None
GSM89095	A	Rectum	None
GSM102479	A	Rectosigmoid	None
GSM102517	A	Rectosigmoid	None
GSM102549	A	Colon	None
GSM102561	A	Colon	None
GSM102572	A	Colon	None
GSM102579	A	Colon	None
GSM117577	A	Rectum	None
GSM117652	A	Rectosigmoid	None
GSM117656	A	Colon	None
GSM117672	A	Colon	None
GSM117676	A	Colon	None
GSM117681	A	Colon	None
GSM117699	A	Rectosigmoid	None
GSM117707	A	Rectum	None
GSM117720	A	Colon	None
GSM137922	A	Colon	None
GSM138022	A	Colon	None
GSM152602	A	Colon	None

GSM152632	A	Colon	None
GSM152666	A	Colon	None
GSM152684	A	Colon	None
GSM152725	A	Colon	None
GSM179820	A	Colon	None
GSM179838	A	Colon	None
GSM179844	A	Colon	None
GSM179859	A	Colon	None
GSM179889	A	Colon	None
GSM179894	A	Rectosigmoid	None
GSM203625	A	Colon	None
GSM203673	A	Colon	None
GSM203687	A	Colon	None
GSM203788	A	Rectum	None
GSM38077	B	Rectosigmoid	None
GSM38098	B	Rectosigmoid Junction	None
GSM46878	B	Colon	None
GSM46895	B	Colon	None
GSM46930	B	Colon	None
GSM53106	B	Colon	None
GSM53113	B	Colon	None
GSM53178	B	Colon	None
GSM76520	B	Colon	None
GSM76522	B	Colon	None
GSM76555	B	Colon	None
GSM76573	B	Colon	None
GSM76583	B	Colon	None
GSM76607	B	Colon	None
GSM76608	B	Colon	None
GSM76617	B	Colon	None
GSM76618	B	Colon	None
GSM88945	B	Colon	None
GSM88963	B	Colon	None
GSM88999	B	Colon	None
GSM89004	B	Colon	None

GSM89007	B	Colon	None
GSM89026	B	Colon	None
GSM89047	B	Colon	None
GSM89049	B	Colon	None
GSM89052	B	Colon	None
GSM89061	B	Colon	None
GSM89062	B	Colon	None
GSM102429	B	Colon	None
GSM102460	B	Colon	None
GSM102462	B	Rectosigmoid	None
GSM102485	B	Colon	None
GSM102486	B	Rectum	None
GSM102516	B	Colon	None
GSM102519	B	Colon	None
GSM102539	B	Rectosigmoid	None
GSM102551	B	Colon	None
GSM102559	B	Colon	None
GSM102577	B	Colon	None
GSM102581	B	Colon	None
GSM117635	B	Colon	None
GSM117649	B	Colon	None
GSM117662	B	Colon	None
GSM117709	B	Colon	None
GSM117728	B	Colon	None
GSM117742	B	Colon	None
GSM137947	B	Colon	None
GSM137949	B	Colon	None
GSM137967	B	Colon	None
GSM138015	B	Colon	None
GSM138021	B	Rectosigmoid	None
GSM138044	B	Colon	None
GSM138048	B	Colon	None
GSM138050	B	Colon	None
GSM138052	B	Colon	None
GSM152573	B	Colon	None

GSM152591	B	Colon	None
GSM152604	B	Hepatic Flexure	None
GSM152610	B	Colon	None
GSM152614	B	Colon	None
GSM152630	B	Rectum	None
GSM152658	B	Colon	None
GSM152762	B	Colon	None
GSM152780	B	Colon	None
GSM152799	B	Colon	None
GSM179803	B	Colon	None
GSM179804	B	Colon	None
GSM179839	B	Colon	None
GSM179856	B	Cecum	None
GSM179860	B	Colon	None
GSM179887	B	Colon	None
GSM179897	B	Colon	None
GSM179899	B	Colon	None
GSM203642	B	Colon	None
GSM203667	B	Colon	None
GSM203700	B	Colon	None
GSM203755	B	Colon	None
GSM203782	B	Colon	None
GSM231879	B	Colon	None
GSM231905	B	Colon	None
GSM231908	B	Colon	None
GSM231956	B	Colon	None
GSM231988	B	Colon	None
GSM38055	C	Colon	None
GSM38074	C	Colon	None
GSM38105	C	Colon	None
GSM38107	C	Colon	None
GSM46841	C	Colon	None
GSM46861	C	Colon	None
GSM46887	C	Colon	None
GSM46921	C	Colon	None

GSM46931	C	Colon	None
GSM46972	C	Rectosigmoid	None
GSM76501	C	Colon	None
GSM76519	C	Colon	None
GSM76526	C	Colon	None
GSM76546	C	Rectosigmoid	None
GSM76548	C	Colon	None
GSM76575	C	Rectum	None
GSM76639	C	Colon	None
GSM88968	C	Colon	None
GSM89037	C	Colon	None
GSM89040	C	Colon	None
GSM89053	C	Colon	None
GSM89069	C	Colon	None
GSM89075	C	Rectosigmoid Colon	None
GSM89090	C	Colon	None
GSM89098	C	Colon	None
GSM102431	C	Colon	None
GSM102436	C	Colon	None
GSM102524	C	Colon	None
GSM102540	C	Colon	None
GSM117642	C	Colon	None
GSM117673	C	Colon	None
GSM117702	C	Rectosigmoid	None
GSM117738	C	Colon	None
GSM117746	C	Colon	None
GSM138007	C	Colon	None
GSM138018	C	Colon	None
GSM152572	C	Rectosigmoid	None
GSM152613	C	Colon	None
GSM152664	C	Colon	None
GSM152695	C	Colon	None
GSM152703	C	Rectosigmoid	None
GSM152712	C	Rectum	None
GSM152714	C	Colon	None

GSM152730	C	Colon	None
GSM179793	C	Colon	None
GSM179795	C	Colon	None
GSM179831	C	Colon	None
GSM179845	C	Rectum	None
GSM179858	C	Rectum	None
GSM179880	C	Colon	None
GSM179882	C	Colon	None
GSM179908	C	Colon	None
GSM179920	C	Rectum	None
GSM179930	C	Colon	None
GSM179937	C	Colon	None
GSM203627	C	Colon	None
GSM203640	C	Colon	None
GSM203645	C	Colon	None
GSM203653	C	Colon	None
GSM203674	C	Colon	None
GSM203684	C	Colon	None
GSM203702	C	Colon	None
GSM203705	C	Colon	None
GSM203728	C	Colon	None
GSM203733	C	Colon	None
GSM203780	C	Rectosigmoid	None
GSM231875	C	Colon	None
GSM231915	C	Colon	None
GSM231928	C	Colon	None
GSM231936	C	Colon	None
GSM231958	C	Colon	None
GSM231961	C	Colon	None
GSM231987	C	Rectum	None
GSM38061	D	Colon	None
GSM38089	D	Colon	None
GSM53132	D	Rectosigmoid	None
GSM76529	D	Colon	None
GSM76571	D	Rectum	None

GSM76605	D	Colon	None
GSM88994	D	Colon	None
GSM89103	D	Colon	None
GSM102472	D	Colon	None
GSM102513	D	Colon	None
GSM102533	D	Colon	None
GSM102535	D	Rectosigmoid	None
GSM117760	D	Colon	None
GSM137985	D	Rectosigmoid	None
GSM137998	D	Colon	None
GSM152692	D	Colon	None
GSM152710	D	Rectosigmoid	None
GSM152750	D	Rectosigmoid	None
GSM179778	D	Colon	None
GSM179805	D	Colon	None
GSM179867	D	Colon	None
GSM179925	D	Colon	None
GSM179928	D	Colon	None
GSM179948	D	Colon	None
GSM203657	D	Colon	None
GSM203688	D	Colon	None
GSM203691	D	Rectosigmoid	None
GSM203743	D	Colon	None
GSM203763	D	Colon	None
GSM231904	D	Colon	None
GSM231959	D	Colon	None
GSM231964	D	Colon	None
GSM38078	Deposit	Liver (primary: colon)	None
GSM46828	Deposit	Liver or Omentum (primary: colon)	Chemotherapy
GSM46946	Deposit	Adrenal gland (primary: colon)	None
GSM46970	Deposit	Liver (primary: rectosigmoid)	Chemotherapy
GSM46971	Deposit	Liver (primary: colon)	None
GSM76540	Deposit	Omentum (primary: colon)	None
GSM76625	Deposit	Abdominal wall mass (primary: rectum)	Chemotherapy
GSM88946	Deposit	Liver (primary: colon)	Chemotherapy

GSM89001	Deposit	Ovary (primary: rectosigmoid)	None
GSM89030	Deposit	Liver (primary: colon)	Chemotherapy
GSM89036	Deposit	Ovary (primary: colon)	Chemotherapy
GSM102484	Deposit	Small intestine (primary: colon)	Chemotherapy
GSM137897	Deposit	Liver (primary: rectosigmoid)	None
GSM137933	Deposit	Liver (primary: colon)	Chemotherapy
GSM137935	Deposit	Liver (primary: rectum)	None
GSM137976	Deposit	Bladder (primary: colon)	None
GSM138043	Deposit	Liver (primary: colon)	Chemotherapy
GSM138047	Deposit	Lung (primary: colon)	Chemotherapy
GSM152592	Deposit	Lung (primary: colon)	Chemotherapy
GSM152612	Deposit	Liver (primary: colon)	None
GSM152619	Deposit	Small bowel (primary: colon)	Chemotherapy
GSM152626	Deposit	Liver (primary: colon)	None
GSM152708	Deposit	Liver (primary: colon)	Chemotherapy
GSM152709	Deposit	Ovary (primary: colon)	None
GSM152760	Deposit	Liver (primary: colon)	Chemotherapy
GSM152765	Deposit	Liver (primary: colon)	None
GSM179840	Deposit	Liver (primary: colon)	Chemotherapy
GSM179865	Deposit	Liver (primary: colon)	Chemotherapy
GSM203775	Deposit	Liver (primary: colon)	None
GSM231883	Deposit	Liver (primary: rectum)	Chemotherapy

Supplementary Table S2. Details of the 128 reproducible metastasis-associated genes (163 probe sets) identified across three cohorts of early-stage and metastatic colorectal cancers.

¹ Cohort 1 consists of 44 stage A and 61 stage D colorectal cancers from this study

² Cohort 2 consists of 42 stage A and 32 primary stage D colorectal cancers from expO

³ Cohort 3 consists of 42 stage A colorectal cancers and 30 metastectomy specimens from expO

⁴ q-values from Significance Analysis of Microarrays (SAM) with a false-discovery rate (FDR) of 10%

⁵ Fold change (on log2 scale) = the median log2 value of the metastatic cancer samples subtracted the median log2 value of the early-stage cancer samples

Affymetrix ID	Gene symbol	Accession number	Cohort 1 ¹		Cohort 2 ²		Cohort 3 ³	
			q-value (%) ⁴	Fold change ⁵	q-value (%)	Fold change	q-value (%)	Fold change
209875_s_at	SPP1	M83248	0.00	1.80	0.00	2.46	0.00	3.32
219054_at	C5orf23	NM_024563	0.00	1.14	0.00	1.37	0.00	1.80
235944_at	HMCN1	BF446673	0.00	1.17	3.54	0.85	0.00	1.44
219087_at	ASPN	NM_017680	1.10	1.11	3.54	1.33	0.05	1.87
202436_s_at	CYP1B1	AU144855	3.59	0.46	0.00	1.48	0.00	2.32
229479_at	LOC646324	AI739132	3.59	1.40	0.00	1.01	0.00	1.42
230175_s_at	DCBLD2	AA805633	3.59	0.41	0.00	0.89	0.00	0.81
201125_s_at	ITGB5	NM_002213	2.74	0.29	1.57	0.38	0.26	0.38
228176_at	C9orf47	AA534817	2.74	0.41	2.69	0.72	0.00	0.94
228224_at	PRELP	AA573140	1.10	0.87	5.98	1.88	0.00	2.86

224396_s_at	ASPN	AF316824	1.10	1.22	5.98	1.16	0.26	1.50
229669_at	LOC339260	AA166965	3.59	0.54	1.57	0.59	0.16	0.56
228335_at	CLDN11	AW264204	3.59	0.51	1.94	0.98	0.00	1.68
218718_at	PDGFC	NM_016205	3.59	0.60	1.94	0.75	0.00	0.96
203640_at	MBNL2	BE328496	1.10	0.33	8.38	0.35	0.26	0.44
205422_s_at	ITGBL1	NM_004791	5.65	1.19	0.00	1.56	0.00	2.11
213352_at	TMCC1	AB018322	5.65	0.29	0.00	0.56	0.00	0.54
214927_at	ITGBL1	AL359052	5.65	0.57	0.00	1.00	0.00	1.38
217949_s_at	VKORC1	NM_024006	2.74	0.31	5.98	0.25	0.00	0.85
205713_s_at	COMP	NM_000095	5.65	0.95	0.00	1.89	0.88	1.37
231317_at	TSNARE1	AI741779	2.74	0.75	2.69	0.40	4.32	0.35
227112_at	TMCC1	AW270037	5.65	0.31	1.57	0.35	0.00	0.55
204619_s_at	VCAN	BF590263	5.65	0.57	1.57	1.17	0.16	0.90
203083_at	THBS2	NM_003247	5.65	1.07	1.94	1.44	0.00	1.79
235408_x_at	ZNF117	AW058673	5.65	0.52	1.57	0.55	0.53	0.57
222379_at	KCNE4	AI002715	5.65	0.35	2.69	0.89	0.00	0.90
227566_at	HNT	AW085558	5.65	1.04	1.94	1.30	0.88	0.76
226930_at	FNDC1	AI345957	5.65	1.10	2.69	1.16	0.26	1.16
228850_s_at	SLIT2	AI963304	5.65	0.81	2.69	0.61	0.26	0.58
209581_at	HRASLS3	BC001387	3.59	0.52	5.98	0.60	1.36	0.72
226237_at	COL8A1	AL359062	3.59	1.43	1.57	1.40	5.83	0.75

217428_s_at	COL10A1	X98568	3.59	1.81	0.00	2.61	7.49	1.51
212464_s_at	FN1	X02761	5.65	0.94	3.54	1.43	0.00	2.22
226137_at	ZFHX3	AI288759	5.65	0.34	2.69	0.34	0.88	0.24
205941_s_at	COL10A1	AI376003	3.59	1.45	1.94	1.91	5.83	1.26
1557080_s_at	ITGBL1	AI753143	7.72	0.70	0.00	0.81	0.00	1.19
202435_s_at	CYP1B1	AU154504	7.72	0.62	0.00	0.99	0.00	1.61
213351_s_at	TMCC1	AB018322	7.72	0.25	0.00	0.41	0.00	0.65
208626_s_at	VAT1	BC001913	1.10	0.51	5.98	0.49	7.49	0.46
210511_s_at	INHBA	M13436	7.72	0.96	0.00	1.43	0.53	1.27
201162_at	IGFBP7	NM_001553	7.72	0.49	1.57	0.59	0.00	0.71
211709_s_at	CLEC11A	BC005810	5.65	0.62	1.57	0.76	4.32	0.67
200665_s_at	SPARC	NM_003118	7.72	0.41	1.57	0.95	0.26	0.57
205381_at	LRRC17	NM_005824	5.65	0.48	5.98	0.39	0.00	0.73
211597_s_at	HOP	AB059408	5.65	1.08	5.98	0.73	0.05	1.14
204468_s_at	TIE1	NM_005424	7.72	0.68	1.94	0.86	0.05	1.28
37022_at	PRELP	U41344	7.72	0.40	1.94	0.45	0.05	0.76
227121_at	N/A	BF476076	5.65	0.33	5.98	0.33	0.16	0.64
211071_s_at	MLLT11	BC006471	3.59	0.35	5.98	0.32	4.32	0.30
226497_s_at	FLT1	AA149648	7.72	0.45	1.94	0.49	0.16	0.54
210517_s_at	AKAP12	AB003476	2.74	1.13	8.38	0.77	4.32	0.54
201150_s_at	TIMP3	NM_000362	2.74	0.97	8.38	0.93	4.32	0.69

212667_at	SPARC	AL575922	7.72	0.52	2.69	0.99	0.05	1.15
224911_s_at	DCBLD2	AA722799	7.72	0.30	1.94	0.58	0.88	0.69
236297_at	N/A	AI420817	5.65	0.55	4.55	0.64	3.12	0.49
211719_x_at	FN1	BC005858	7.72	0.89	3.54	1.37	0.00	2.06
216442_x_at	FN1	AK026737	7.72	0.91	3.54	1.14	0.00	1.97
210004_at	OLR1	AF035776	7.72	0.81	3.54	0.88	0.00	1.32
209894_at	LEPR	U50748	7.72	0.51	3.54	0.66	0.00	0.97
223279_s_at	UACA	AF322916	7.72	0.24	3.54	0.26	0.05	0.44
1553530_a_at	ITGB1	NM_033669	5.65	0.40	5.98	0.44	2.08	0.45
210495_x_at	FN1	AF130095	7.72	0.89	4.55	1.20	0.00	1.99
225566_at	NRP2	AI819729	7.72	1.12	4.55	0.55	0.00	1.08
204589_at	NUAK1	NM_014840	5.65	0.65	8.38	0.52	0.53	0.56
210809_s_at	POSTN	D13665	7.72	1.10	3.54	1.16	1.36	0.95
202133_at	WWTR1	BF674349	7.72	0.53	3.54	0.90	1.36	0.91
219179_at	DACT1	NM_016651	5.65	0.46	5.98	0.79	3.12	0.53
213413_at	STON1	BG434174	3.59	0.40	4.55	0.82	9.75	0.29
219922_s_at	LTBP3	NM_021070	7.72	0.37	5.98	0.54	0.26	0.78
204223_at	PRELP	NM_002725	7.72	0.63	5.98	0.68	0.26	0.99
225450_at	AMOTL1	AI433831	7.72	0.49	5.98	0.57	0.26	0.94
201560_at	CLIC4	NM_013943	5.65	0.66	4.55	0.55	5.83	0.51
210078_s_at	KCNAB1	L39833	5.65	0.47	8.38	0.94	2.08	0.81

1555778_a_at	POSTN	AY140646	7.72	1.11	5.98	1.04	0.88	1.09
213125_at	OLFML2B	AW007573	7.72	0.40	2.69	0.77	4.32	0.52
213656_s_at	KLC1	BF593594	7.72	0.28	5.98	0.25	1.36	0.23
227529_s_at	AKAP12	BF511276	2.74	0.98	8.38	0.65	9.75	0.45
225021_at	ZNF532	AA861416	5.65	0.33	2.69	0.36	9.75	0.47
214770_at	MSR1	AI299239	7.72	0.59	8.38	0.62	0.00	1.52
209747_at	TGFB3	J03241	7.72	0.40	8.38	0.41	0.26	0.59
212488_at	COL5A1	N30339	7.72	0.54	8.38	0.49	1.36	0.69
225381_at	LOC399959	AW162210	3.59	0.76	8.38	0.78	9.75	0.57
202766_s_at	FBN1	NM_000138	7.72	0.72	5.98	0.91	4.32	0.52
203238_s_at	NOTCH3	NM_000435	5.65	0.38	5.98	0.59	9.75	0.61
226364_at	HIP1	AU145049	7.72	0.39	1.94	0.70	9.75	0.46
226997_at	ADAMTS12	W74476	7.72	0.51	3.54	0.63	9.75	0.46
227530_at	AKAP12	BF511276	5.65	0.59	8.38	0.71	9.75	0.53
225946_at	RASSF8	BG484552	7.72	0.47	8.38	0.63	7.49	0.58
1558027_s_at	PRKAB2	AL552001	7.72	0.37	8.38	0.31	7.49	0.20
207076_s_at	ASS1	NM_000050	1.41	-0.39	1.57	-0.95	1.36	-0.37
224240_s_at	CCL28	AF266504	1.41	-0.91	3.54	-0.71	0.00	-0.85
211367_s_at	CASP1	U13699	0.00	-1.12	5.98	-0.70	1.36	-0.48
209374_s_at	IGHM	BC001872	1.41	-1.65	4.55	-2.07	0.00	-2.31
205267_at	POU2AF1	NM_006235	1.41	-0.97	4.55	-1.20	0.05	-1.69

205891_at	ADORA2B	NM_000676	1.41	-0.38	4.55	-0.73	0.16	-0.72
217378_x_at	IGKV1OR 2-108	X51887	1.41	-1.33	4.55	-1.46	0.16	-2.11
214836_x_at	IGKC	BG536224	1.41	-1.18	4.55	-1.13	0.16	-1.46
218096_at	AGPAT5	NM_018361	1.41	-0.50	5.98	-0.40	0.05	-0.81
215949_x_at	IGHM	BF002659	2.74	-1.19	3.54	-1.52	0.00	-2.00
226147_s_at	PIGR	AA838075	2.74	-0.85	3.54	-1.37	0.00	-4.32
202659_at	PSMB10	NM_002801	1.41	-0.47	3.54	-0.57	3.12	-0.40
214916_x_at	IL8	BG340548	2.74	-1.07	4.55	-1.60	0.00	-1.78
211881_x_at	IGLJ3	AB014341	2.74	-0.85	4.55	-1.18	0.05	-1.33
216576_x_at	NTN2L	AF103529	2.74	-1.24	4.55	-1.85	0.16	-1.84
209970_x_at	CASP1	M87507	0.00	-0.68	8.38	-0.62	2.08	-0.51
216207_x_at	IGKV1D-13	AW408194	1.41	-0.95	8.38	-1.26	0.16	-1.56
205049_s_at	CD79A	NM_001783	2.74	-0.59	5.98	-0.81	0.00	-1.47
211645_x_at	N/A	M85256	2.74	-1.07	5.98	-1.26	0.16	-2.21
234366_x_at	IGL@	AF103591	2.74	-0.77	5.98	-0.76	0.26	-1.15
217480_x_at	HLA-C	M20812	2.74	-1.08	5.98	-0.82	0.26	-1.33
238750_at	N/A	AW083576	3.59	-0.79	4.55	-0.99	0.00	-1.91
217157_x_at	N/A	AF103530	3.59	-0.89	4.55	-0.86	0.16	-1.49
209208_at	MPDU1	AF059752	1.41	-0.29	8.38	-0.47	0.88	-0.56
211368_s_at	CASP1	U13700	0.00	-0.86	8.38	-0.46	4.32	-0.37
214440_at	NAT1	NM_000662	3.59	-0.54	5.98	-0.72	0.00	-0.96

211366_x_at	CASP1	U13698	1.41	-0.77	8.38	-0.58	2.08	-0.53
238725_at	IRF1	AW392551	1.41	-0.80	3.54	-0.68	7.49	-0.45
234884_x_at	N/A	L21961	2.74	-0.84	8.38	-0.92	0.05	-1.12
221286_s_at	MGC29506	NM_016459	2.74	-1.17	8.38	-1.03	0.05	-1.48
205476_at	CCL20	NM_004591	2.74	-0.90	8.38	-1.14	0.16	-1.48
212592_at	IGJ	AV733266	5.65	-0.79	3.54	-1.99	0.00	-3.28
204213_at	PIGR	NM_002644	5.65	-1.03	3.54	-2.03	0.00	-2.28
226499_at	NRARP	W72331	5.65	-0.30	3.54	-0.53	0.00	-1.09
214214_s_at	C1QBP	AU151801	5.65	-0.29	3.54	-0.49	0.16	-0.61
211798_x_at	IGLJ3	AB001733	3.59	-0.96	8.38	-0.98	0.00	-1.45
215176_x_at	NTN2L	AW404894	3.59	-0.65	8.38	-1.08	0.16	-2.15
209397_at	ME2	BC000147	2.74	-0.30	4.55	-0.50	5.83	-0.25
206641_at	TNFRSF17	NM_001192	5.65	-1.03	4.55	-1.00	0.00	-1.50
216557_x_at	IFI6	U92706	5.65	-1.10	4.55	-1.52	0.00	-1.41
221651_x_at	IGKC	BC005332	5.65	-0.34	4.55	-0.60	0.26	-1.23
229568_at	MOBKL2B	AI692878	7.72	-0.24	1.57	-0.59	0.00	-0.73
219727_at	DUOX2	NM_014080	5.65	-1.47	5.98	-2.35	0.00	-2.92
217281_x_at	IL8	AJ239383	5.65	-1.10	5.98	-1.47	0.00	-2.13
221671_x_at	IGKC	M63438	5.65	-0.34	5.98	-0.66	0.16	-1.28
215946_x_at	CTA-246H3.1	AL022324	5.65	-0.74	5.98	-0.88	0.26	-1.12
214777_at	N/A	BG482805	5.65	-1.55	5.98	-1.95	0.53	-1.72

209040_s_at	PSMB8	U17496	5.65	-0.39	4.55	-0.31	3.12	-0.27
216542_x_at	IGHA1	AJ275355	7.72	-0.72	3.54	-1.34	0.00	-1.50
224027_at	CCL28	AF110384	5.65	-0.70	8.38	-1.04	0.00	-1.42
229070_at	C6orf105	AA470369	5.65	-1.07	8.38	-1.83	0.05	-2.09
211641_x_at	N/A	L06101	7.72	-0.67	4.55	-0.93	0.00	-1.30
204301_at	KBTBD11	NM_014867	7.72	-0.46	4.55	-0.68	0.00	-0.99
221841_s_at	KLF4	BF514079	7.72	-0.42	4.55	-0.72	0.05	-0.80
211647_x_at	IGHG1	L14454	7.72	-0.30	4.55	-0.72	0.53	-0.64
235350_at	C4orf19	AI935586	7.72	-0.53	4.55	-0.73	0.53	-0.66
216829_at	NTN2L	X72475	5.65	-1.03	8.38	-0.79	0.88	-1.27
203110_at	PTK2B	U43522	7.72	-0.53	3.54	-0.39	2.08	-0.35
214433_s_at	SELENBP1	NM_003944	7.72	-1.04	5.98	-0.86	0.00	-1.49
226319_s_at	THOC4	AF047002	7.72	-0.35	5.98	-0.47	0.16	-0.65
227014_at	ASPHD2	BE550881	5.65	-0.43	5.98	-0.49	4.32	-0.34
209569_x_at	D4S234E	NM_014392	5.65	-0.34	5.98	-0.39	4.32	-0.50
225667_s_at	FAM84A	AI601101	7.72	-0.41	5.98	-0.81	0.26	-1.16
211635_x_at	IGHV1-69	M24670	7.72	-0.96	5.98	-1.38	0.53	-1.12
205242_at	CXCL13	NM_006419	5.65	-1.55	3.54	-1.17	7.49	-0.82
219148_at	PBK	NM_018492	7.72	-0.66	8.38	-0.82	0.05	-1.26
219450_at	C4orf19	NM_018302	7.72	-0.28	8.38	-0.71	0.16	-0.71
209138_x_at	IGL@	M87790	7.72	-0.61	8.38	-1.20	0.26	-1.35

214677_ x_at	IGLJ3	X57812	7.72	-0.44	8.38	-0.89	0.26	-1.12
1555779 _a_at	CD79A	M74721	7.72	-0.48	8.38	-0.59	0.26	-0.49
210885_ s_at	TRIM15	AF220133	7.72	-0.55	8.38	-0.52	0.53	-0.59
216430_ x_at	IGL@	AF043586	7.72	-1.69	8.38	-1.58	2.08	-0.83
225053_ at	CNOT7	W94952	7.72	-0.38	8.38	-0.23	5.83	-0.19
204279_ at	PSMB9	NM_002800	7.72	-0.42	8.38	-0.50	7.49	-0.55

Supplementary Table S3. Comparison of gene expression changes between the two main groups of stage B or stage C colorectal cancers resulting from unsupervised clustering using our set of 128 metastasis-associated genes (163 probe sets) with those observed between early-stage and metastatic colorectal cancers.

Clustering was performed separately for 95 stage B and 93 stage C colorectal cancers from this study, and 83 stage B and 73 stage C colorectal cancers from expO. Up- or down-regulation in median gene expression between the two main resulting groups was compared to that observed between early-stage and metastatic colorectal cancers using Pearson's chi-squared test.

	Metastatic vs. early-stage		
	Up-regulated	Down-regulated	P value
Stage B – this study: Group 2 vs. 1			
Up-regulated	89 (54.6%)	2 (1.2%)	< 0.001
Down-regulated	0 (0.0%)	72 (44.2%)	
Stage C – this study: Group 1 vs. 2			
Up-regulated	88 (54.0%)	2 (1.2%)	< 0.001
Down-regulated	1 (0.6%)	72 (44.2%)	
Stage B – expO: Group 2 vs. 1			
Up-regulated	89 (54.6%)	4 (2.5%)	< 0.001
Down-regulated	0 (0.0%)	70 (42.9%)	
Stage C – expO: Group 1 vs. 2			
Up-regulated	89 (54.6%)	0 (0.0%)	< 0.001
Down-regulated	0 (0.0%)	74 (45.4%)	

Supplementary Table S4. Cox proportional-hazard analysis of the risk of recurrence as a first event in 95 stage B and 93 stage C colorectal cancer patients for individual probe sets of our 128 metastasis-associated genes.

¹Hazard ratios are adjusted for adjuvant treatment.

²P values are adjusted using the Benjamini-Hochberg False Discovery Rate multiple testing correction.

P values less than 0.05 are shown in bold. Genes with unadjusted P<0.05 in both stage B and C patients are shown in bold.

Affymetri x ID	Gene symbol	Accessi on number	Stage B				Stage C				Metastatic vs. early- stage
			Hazard ratio ¹ (95% CI)		P val ue	P val ue ²	Hazard ratio ¹ (95% CI)		P val ue	P val ue ²	
209875_s_at	SPP1	M83248	1.21	(0.82-1.77)	0.340	0.440	1.17	(0.93-1.46)	0.180	0.362	upregulated
219054_at	C5orf23	NM_024563	1.56	(1.00-2.43)	0.051	0.163	1.28	(1.00-1.63)	0.054	0.313	upregulated
235944_at	HMCN1	BF446673	1.16	(0.76-1.78)	0.490	0.579	1.13	(0.84-1.51)	0.420	0.552	upregulated
219087_at	ASPN	NM_017680	1.23	(0.78-1.94)	0.380	0.480	1.23	(0.95-1.59)	0.120	0.315	upregulated
202436_s_at	CYP1B1	AU144855	1.66	(1.02-2.68)	0.041	0.163	1.21	(0.96-1.52)	0.100	0.313	upregulated
229479_at	LOC646324	AI739132	1.43	(0.95-2.15)	0.085	0.201	1.22	(0.97-1.53)	0.088	0.313	upregulated
230175_s_at	DCBLD2	AA805633	2.30	(1.22-4.32)	0.010	0.120	1.31	(0.90-1.91)	0.160	0.339	upregulated
201125_s_at	ITGB5	NM_002213	2.41	(0.83-7.04)	0.110	0.216	1.63	(0.85-3.11)	0.140	0.331	upregulated
228176_at	C9orf47	AA534817	1.17	(0.51-2.69)	0.720	0.757	1.73	(0.94-3.19)	0.079	0.313	upregulated
228224_at	PRELP	AA573140	1.20	(0.81-1.77)	0.370	0.471	1.13	(0.92-1.39)	0.230	0.383	upregulated
224396_s_at	ASPN	AF316824	1.10	(0.78-1.54)	0.600	0.670	1.11	(0.93-1.33)	0.250	0.392	upregulated
229669_at	LOC339260	AA166965	1.69	(0.68-4.21)	0.260	0.362	0.97	(0.66-1.42)	0.870	0.909	upregulated

228335_at	CLDN11	AW264204	1.34	(0.79-2.25)	0.280	0.384	0.97	(0.74-1.26)	0.810	0.869	upregulated
218718_at	PDGFC	NM_016205	1.48	(0.67-3.28)	0.330	0.430	0.99	(0.67-1.47)	0.970	0.992	upregulated
203640_at	MBNL2	BE328496	4.30	(1.44-12.80)	0.009	0.120	1.77	(0.83-3.77)	0.140	0.331	upregulated
205422_s_at	ITGBL1	NM_004791	1.24	(0.83-1.85)	0.290	0.387	1.08	(0.90-1.31)	0.400	0.534	upregulated
213352_at	TMCC1	AB018322	9.00	(2.15-37.72)	0.003	0.120	0.99	(0.39-2.49)	0.980	0.992	upregulated
214927_at	ITGBL1	AL359052	1.71	(0.92-3.17)	0.087	0.203	1.15	(0.85-1.58)	0.370	0.503	upregulated
217949_s_at	VKORC1	NM_024006	3.39	(0.74-15.48)	0.110	0.216	1.55	(0.81-2.95)	0.180	0.362	upregulated
205713_s_at	COMP	NM_000095	1.21	(0.87-1.67)	0.250	0.357	1.13	(0.93-1.36)	0.210	0.372	upregulated
231317_at	TSNARE1	AI741779	1.36	(0.82-2.25)	0.230	0.347	1.04	(0.78-1.39)	0.780	0.859	upregulated
227112_at	TMCC1	AW270037	5.54	(1.69-18.21)	0.005	0.120	0.75	(0.26-2.15)	0.590	0.692	upregulated
204619_s_at	VCAN	BF590263	1.53	(0.83-2.80)	0.170	0.280	1.22	(0.88-1.67)	0.230	0.383	upregulated
203083_at	THBS2	NM_003247	1.42	(0.86-2.36)	0.170	0.280	1.26	(0.95-1.66)	0.110	0.315	upregulated
235408_x_at	ZNF117	AW058673	1.27	(0.46-3.48)	0.640	0.706	1.26	(0.74-2.12)	0.390	0.525	upregulated
222379_at	KCNE4	AI002715	2.07	(0.88-4.89)	0.095	0.212	1.48	(1.05-2.09)	0.025	0.278	upregulated
227566_at	HNT	AW085558	1.62	(0.93-2.81)	0.089	0.204	1.22	(0.91-1.65)	0.180	0.362	upregulated
226930_at	FNDC1	AI345957	1.06	(0.67-1.67)	0.800	0.836	1.18	(0.92-1.52)	0.200	0.372	upregulated
228850_s_at	SLIT2	AI963304	0.79	(0.54-1.16)	0.240	0.356	1.10	(0.75-1.60)	0.630	0.728	upregulated
209581_at	HRASLS3	BC001387	2.55	(1.25-5.19)	0.010	0.120	1.16	(0.86-1.56)	0.340	0.482	upregulated
226237_at	COL8A1	AL359062	1.30	(0.80-2.13)	0.290	0.387	1.21	(0.91-1.61)	0.200	0.372	upregulated
217428_s_at	COL10A1	X98568	1.41	(0.93-2.13)	0.110	0.216	1.20	(0.95-1.51)	0.130	0.331	upregulated
212464_s_at	FN1	X02761	1.47	(0.84-2.59)	0.180	0.293	1.52	(1.04-2.22)	0.031	0.281	upregulated
226137_at	ZFH3	AI288759	1.61	(0.38-6.79)	0.520	0.601	1.24	(0.57-2.70)	0.590	0.692	upregulated

205941_s_at	COL10A1	AI376003	1.61	(1.01-2.54)	0.043	0.163	1.20	(0.95-1.52)	0.120	0.315	upregulated
1557080_s_at	ITGBL1	AI753143	1.11	(0.64-1.95)	0.710	0.751	1.08	(0.84-1.41)	0.550	0.664	upregulated
202435_s_at	CYP1B1	AU154504	1.59	(0.87-2.91)	0.130	0.241	1.25	(0.96-1.62)	0.100	0.313	upregulated
213351_s_at	TMCC1	AB018322	3.66	(0.98-13.69)	0.054	0.163	0.90	(0.40-1.99)	0.790	0.864	upregulated
208626_s_at	VAT1	BC001913	2.52	(1.09-5.86)	0.031	0.158	1.77	(1.03-3.02)	0.038	0.283	upregulated
210511_s_at	INHBA	M13436	1.51	(0.91-2.51)	0.110	0.216	1.26	(0.97-1.63)	0.081	0.313	upregulated
201162_at	IGFBP7	NM_001553	1.28	(0.59-2.80)	0.530	0.604	1.28	(0.86-1.91)	0.220	0.383	upregulated
211709_s_at	CLEC11A	BC005810	1.32	(0.65-2.71)	0.440	0.539	1.23	(0.84-1.81)	0.290	0.426	upregulated
200665_s_at	SPARC	NM_003118	1.85	(0.74-4.65)	0.190	0.298	1.69	(0.98-2.91)	0.059	0.313	upregulated
205381_at	LRRC17	NM_005824	1.76	(0.82-3.81)	0.150	0.263	1.19	(0.77-1.83)	0.440	0.560	upregulated
211597_s_at	HOP	AB059408	1.93	(1.00-3.72)	0.051	0.163	1.20	(0.86-1.68)	0.290	0.426	upregulated
204468_s_at	TIE1	NM_005424	0.80	(0.54-1.17)	0.250	0.357	1.37	(0.97-1.94)	0.073	0.313	upregulated
37022_at	PRELP	U41344	1.34	(0.57-3.10)	0.500	0.586	1.13	(0.77-1.67)	0.540	0.657	upregulated
227121_at	N/A	BF476076	1.77	(0.67-4.68)	0.250	0.357	1.43	(0.75-2.74)	0.280	0.419	upregulated
211071_s_at	MLLT11	BC006471	2.31	(0.90-5.91)	0.082	0.197	1.29	(0.69-2.41)	0.430	0.552	upregulated
226497_s_at	FLT1	AA149648	2.42	(0.73-8.06)	0.150	0.263	1.86	(1.17-2.96)	0.009	0.278	upregulated
210517_s_at	AKAP12	AB003476	1.63	(1.04-2.56)	0.032	0.158	1.53	(1.10-2.14)	0.013	0.278	upregulated
201150_s_at	TIMP3	NM_000362	1.47	(0.78-2.76)	0.230	0.347	1.26	(0.86-1.85)	0.240	0.391	upregulated
212667_at	SPARC	AL575922	1.27	(0.65-2.48)	0.480	0.571	1.32	(0.90-1.93)	0.160	0.339	upregulated
224911_s_at	DCBLD2	AA722799	2.66	(1.69-4.18)	0.000	0.004	1.55	(1.11-2.16)	0.010	0.278	upregulated
236297_at	N/A	AI420817	0.96	(0.43-2.14)	0.910	0.927	1.13	(0.73-1.75)	0.580	0.690	upregulated
211719_x_at	FN1	BC005858	1.53	(0.82-2.87)	0.190	0.298	1.51	(0.99-2.31)	0.057	0.313	upregulated

216442_x_at	FN1	AK026737	1.56	(0.85-2.88)	0.150	0.263	1.58	(1.02-2.44)	0.039	0.283	upregulated
210004_at	OLR1	AF035776	1.13	(0.72-1.76)	0.600	0.670	1.23	(0.95-1.58)	0.120	0.315	upregulated
209894_at	LEPR	U50748	0.77	(0.33-1.81)	0.550	0.623	1.33	(0.84-2.10)	0.230	0.383	upregulated
223279_s_at	UACA	AF322916	2.93	(0.99-8.66)	0.052	0.163	1.74	(0.95-3.19)	0.075	0.313	upregulated
1553530_a_at	ITGB1	NM_033669	1.63	(0.48-5.58)	0.440	0.539	2.64	(1.22-5.71)	0.013	0.278	upregulated
210495_x_at	FN1	AF130095	1.61	(0.84-3.09)	0.150	0.263	1.62	(1.03-2.56)	0.038	0.283	upregulated
225566_at	NRP2	AI819729	1.21	(0.75-1.95)	0.430	0.535	1.34	(0.97-1.85)	0.080	0.313	upregulated
204589_at	NUAK1	NM_014840	1.83	(0.69-4.88)	0.220	0.338	1.22	(0.81-1.86)	0.340	0.482	upregulated
210809_s_at	POSTN	D13665	1.45	(0.83-2.55)	0.190	0.298	1.33	(0.93-1.90)	0.120	0.315	upregulated
202133_at	WWTR1	BF674349	2.08	(1.05-4.14)	0.037	0.159	1.65	(1.06-2.56)	0.027	0.278	upregulated
219179_at	DACT1	NM_016651	0.82	(0.47-1.42)	0.470	0.563	0.82	(0.49-1.35)	0.430	0.552	upregulated
213413_at	STON1	BG434174	1.07	(0.56-2.05)	0.840	0.872	1.28	(0.85-1.92)	0.230	0.383	upregulated
219922_s_at	LTBP3	NM_021070	1.84	(0.77-4.38)	0.170	0.280	1.37	(0.85-2.21)	0.200	0.372	upregulated
204223_at	PRELP	NM_002725	0.99	(0.57-1.71)	0.960	0.966	1.12	(0.83-1.50)	0.460	0.572	upregulated
225450_at	AMOTL1	AI433831	1.29	(0.67-2.47)	0.450	0.543	1.26	(0.78-2.05)	0.350	0.488	upregulated
201560_at	CLIC4	NM_013943	2.21	(0.87-5.64)	0.097	0.212	1.61	(0.94-2.73)	0.080	0.313	upregulated
210078_s_at	KCNAB1	L39833	0.85	(0.56-1.29)	0.450	0.543	1.05	(0.71-1.54)	0.810	0.869	upregulated
1555778_a_at	POSTN	AY140646	1.28	(0.82-2.01)	0.280	0.384	1.26	(0.95-1.66)	0.110	0.315	upregulated
213125_at	OLFML2B	AW007573	1.55	(0.79-3.03)	0.200	0.310	1.37	(0.97-1.95)	0.076	0.313	upregulated
213656_s_at	KLC1	BF593594	0.75	(0.22-2.62)	0.650	0.706	2.66	(1.13-6.27)	0.025	0.278	upregulated
227529_s_at	AKAP12	BF511276	1.38	(0.98-1.95)	0.065	0.163	1.41	(1.07-1.85)	0.015	0.278	upregulated
225021_at	ZNF532	AA861416	2.29	(1.05-4.97)	0.037	0.159	1.89	(1.11-3.24)	0.020	0.278	upregulated

214770_at	MSR1	AI299239	1.67	(0.81-3.47)	0.170	0.280	1.04	(0.77-1.41)	0.780	0.859	upregulated
209747_at	TGFB3	J03241	1.69	(0.68-4.23)	0.260	0.362	1.42	(0.90-2.25)	0.140	0.331	upregulated
212488_at	COL5A1	N30339	1.36	(0.76-2.44)	0.290	0.387	1.37	(0.96-1.97)	0.083	0.313	upregulated
225381_at	LOC399959	AW162210	1.28	(0.79-2.06)	0.320	0.421	1.29	(0.90-1.85)	0.160	0.339	upregulated
202766_s_at	FBN1	NM_000138	1.27	(0.72-2.25)	0.410	0.514	1.23	(0.89-1.71)	0.210	0.372	upregulated
203238_s_at	NOTCH3	NM_000435	1.79	(0.85-3.80)	0.130	0.241	1.85	(1.16-2.96)	0.010	0.278	upregulated
226364_at	HIP1	AU145049	2.06	(0.87-4.92)	0.100	0.212	1.58	(0.84-2.96)	0.150	0.339	upregulated
226997_at	ADAMTS12	W74476	1.16	(0.61-2.24)	0.650	0.706	1.26	(0.83-1.92)	0.280	0.419	upregulated
227530_at	AKAP12	BF511276	1.43	(0.93-2.20)	0.100	0.212	1.52	(1.08-2.13)	0.016	0.278	upregulated
225946_at	RASSF8	BG484552	1.86	(0.97-3.60)	0.064	0.163	1.30	(0.82-2.06)	0.260	0.400	upregulated
1558027_s_at	PRKAB2	AL552001	1.09	(0.39-3.07)	0.870	0.892	2.91	(1.31-6.43)	0.008	0.278	upregulated
207076_s_at	ASS1	NM_000050	0.34	(0.15-0.78)	0.011	0.120	1.34	(0.86-2.09)	0.200	0.372	downregulated
224240_s_at	CCL28	AF266504	0.49	(0.24-0.99)	0.048	0.163	0.74	(0.49-1.13)	0.160	0.339	downregulated
211367_s_at	CASP1	U13699	0.56	(0.34-0.94)	0.027	0.157	0.72	(0.50-1.05)	0.084	0.313	downregulated
209374_s_at	IGHM	BC001872	0.72	(0.55-0.94)	0.015	0.129	0.90	(0.75-1.08)	0.240	0.391	downregulated
205267_at	POU2AF1	NM_006235	0.55	(0.33-0.89)	0.016	0.130	0.80	(0.57-1.13)	0.210	0.372	downregulated
205891_at	ADORA2B	NM_000676	1.20	(0.49-2.93)	0.690	0.740	0.88	(0.54-1.44)	0.610	0.710	downregulated
217378_x_at	IGKV1OR2-108	X51887	0.82	(0.66-1.02)	0.080	0.197	0.91	(0.79-1.05)	0.210	0.372	downregulated
214836_x_at	IGKC	BG536224	0.68	(0.46-0.99)	0.045	0.163	0.79	(0.58-1.08)	0.140	0.331	downregulated
218096_at	AGPAT5	NM_018361	0.74	(0.28-1.93)	0.530	0.604	0.75	(0.47-1.22)	0.250	0.392	downregulated
215949_x_at	IGHM	BF002659	0.74	(0.55-1.01)	0.057	0.163	0.92	(0.74-1.13)	0.420	0.552	downregulated
226147_s_at	PIGR	AA838075	0.80	(0.67-0.95)	0.013	0.129	0.99	(0.85-1.14)	0.840	0.883	downregulated

202659_a t	PSMB10	NM_002 801	0.39	(0.16-0.9 9)	0.0 49	0.16 3	1.07	(0.55-2.0 9)	0.8 40	0.88 3	downregulat ed
214916_x _at	IL8	BG3405 48	0.72	(0.57-0.9 1)	0.0 06	0.12 0	0.86	(0.72-1.0 3)	0.1 00	0.31 3	downregulat ed
211881_x _at	IGLJ3	AB0143 41	0.65	(0.39-1.0 8)	0.0 93	0.21 1	0.80	(0.60-1.0 6)	0.1 30	0.33 1	downregulat ed
216576_x _at	NTN2L	AF1035 29	0.74	(0.58-0.9 4)	0.0 15	0.12 9	0.88	(0.75-1.0 4)	0.1 50	0.33 9	downregulat ed
209970_x _at	CASP1	M87507	0.50	(0.28-0.9 1)	0.0 22	0.14 9	0.64	(0.40-1.0 4)	0.0 73	0.31 3	downregulat ed
216207_x _at	IGKV1D-1 3	AW4081 94	0.70	(0.48-1.0 2)	0.0 61	0.16 3	0.83	(0.65-1.0 7)	0.1 50	0.33 9	downregulat ed
205049_s _at	CD79A	NM_001 783	0.59	(0.35-0.9 7)	0.0 38	0.15 9	0.73	(0.50-1.0 8)	0.1 20	0.31 5	downregulat ed
211645_x _at	N/A	M85256	0.78	(0.62-0.9 8)	0.0 30	0.15 8	0.88	(0.74-1.0 4)	0.1 40	0.33 1	downregulat ed
234366_x _at	IGL@	AF1035 91	0.66	(0.41-1.0 8)	0.0 99	0.21 2	0.77	(0.56-1.0 4)	0.0 93	0.31 3	downregulat ed
217480_x _at	HLA-C	M20812	0.69	(0.48-0.9 9)	0.0 47	0.16 3	0.82	(0.65-1.0 3)	0.0 95	0.31 3	downregulat ed
238750_a t	N/A	AW0835 76	0.73	(0.53-1.0 1)	0.0 61	0.16 3	0.88	(0.67-1.1 6)	0.3 70	0.50 3	downregulat ed
217157_x _at	N/A	AF1035 30	0.69	(0.47-1.0 2)	0.0 60	0.16 3	0.76	(0.58-1.0 0)	0.0 50	0.31 3	downregulat ed
209208_a t	MPDU1	AF0597 52	0.82	(0.30-2.2 2)	0.7 00	0.74 6	0.80	(0.42-1.5 2)	0.4 90	0.60 5	downregulat ed
211368_s _at	CASP1	U13700	0.61	(0.36-1.0 3)	0.0 64	0.16 3	0.66	(0.43-1.0 0)	0.0 50	0.31 3	downregulat ed
214440_a t	NAT1	NM_000 662	0.44	(0.19-1.0 5)	0.0 65	0.16 3	0.63	(0.38-1.0 6)	0.0 82	0.31 3	downregulat ed
211366_x _at	CASP1	U13698	0.41	(0.21-0.8 1)	0.0 10	0.12 0	0.71	(0.44-1.1 5)	0.1 60	0.33 9	downregulat ed
238725_a t	IRF1	AW3925 51	0.64	(0.40-1.0 2)	0.0 61	0.16 3	1.20	(0.75-1.9 4)	0.4 50	0.56 9	downregulat ed
234884_x _at	N/A	L21961	0.73	(0.52-1.0 2)	0.0 65	0.16 3	0.79	(0.58-1.0 6)	0.11 0	0.31 5	downregulat ed
221286_s _at	MGC2950 6	NM_016 459	0.78	(0.57-1.0 7)	0.1 30	0.24 1	0.82	(0.66-1.0 2)	0.0 70	0.31 3	downregulat ed
205476_a t	CCL20	NM_004 591	0.95	(0.75-1.2 1)	0.6 80	0.73 4	0.91	(0.70-1.1 9)	0.5 00	0.61 3	downregulat ed
212592_a t	IGJ	AV7332 66	0.72	(0.57-0.9 2)	0.0 07	0.12 0	0.84	(0.71-0.9 9)	0.0 40	0.28 3	downregulat ed
204213_a t	PIGR	NM_002 644	0.69	(0.49-0.9 6)	0.0 28	0.15 7	0.97	(0.79-1.1 7)	0.7 20	0.81 5	downregulat ed

226499_at	NRARP	W72331	0.59	(0.30-1.17)	0.130	0.241	0.86	(0.51-1.44)	0.560	0.671	downregulated
214214_s_at	C1QBP	AU151801	1.30	(0.42-4.04)	0.650	0.706	0.63	(0.30-1.33)	0.230	0.383	downregulated
211798_x_at	IGLJ3	AB001733	0.74	(0.49-1.13)	0.160	0.277	0.81	(0.62-1.04)	0.100	0.313	downregulated
215176_x_at	NTN2L	AW404894	0.81	(0.65-1.01)	0.056	0.163	0.86	(0.72-1.03)	0.110	0.315	downregulated
209397_at	ME2	BC000147	0.60	(0.28-1.29)	0.190	0.298	0.74	(0.33-1.64)	0.460	0.572	downregulated
206641_at	TNFRSF17	NM_001192	0.72	(0.54-0.95)	0.022	0.149	0.89	(0.74-1.07)	0.210	0.372	downregulated
216557_x_at	IFI6	U92706	0.69	(0.45-1.05)	0.081	0.197	0.86	(0.66-1.12)	0.270	0.411	downregulated
221651_x_at	IGKC	BC005332	0.70	(0.48-1.01)	0.055	0.163	0.78	(0.59-1.03)	0.085	0.313	downregulated
229568_at	MOBK2L2B	AI692878	0.29	(0.10-0.91)	0.034	0.158	0.65	(0.31-1.36)	0.250	0.392	downregulated
219727_at	DUOX2	NM_014080	0.89	(0.69-1.14)	0.350	0.449	0.89	(0.74-1.08)	0.250	0.392	downregulated
217281_x_at	IL8	AJ239383	0.76	(0.62-0.94)	0.011	0.120	0.90	(0.78-1.05)	0.190	0.372	downregulated
221671_x_at	IGKC	M63438	0.72	(0.51-1.01)	0.056	0.163	0.79	(0.63-0.98)	0.034	0.283	downregulated
215946_x_at	CTA-246H 3.1	AL022324	0.60	(0.38-0.95)	0.028	0.157	0.74	(0.57-0.97)	0.029	0.278	downregulated
214777_at	N/A	BG482805	0.76	(0.63-0.92)	0.004	0.120	0.89	(0.76-1.03)	0.100	0.313	downregulated
209040_s_at	PSMB8	U17496	0.59	(0.25-1.42)	0.240	0.356	0.89	(0.47-1.69)	0.730	0.821	downregulated
216542_x_at	IGHA1	AJ275355	0.66	(0.36-1.20)	0.170	0.280	0.74	(0.50-1.08)	0.120	0.315	downregulated
224027_at	CCL28	AF110384	0.65	(0.49-0.86)	0.003	0.120	1.06	(0.81-1.37)	0.680	0.775	downregulated
229070_at	C6orf105	AA470369	0.75	(0.59-0.97)	0.030	0.158	0.91	(0.76-1.09)	0.320	0.462	downregulated
211641_x_at	N/A	L06101	0.59	(0.37-0.93)	0.023	0.150	0.69	(0.49-0.99)	0.043	0.292	downregulated
204301_at	KBTBD11	NM_014867	1.03	(0.55-1.92)	0.930	0.942	0.96	(0.55-1.68)	0.890	0.918	downregulated
221841_s_at	KLF4	BF514079	0.55	(0.32-0.96)	0.036	0.159	1.27	(0.84-1.92)	0.260	0.400	downregulated
211647_x_at	IGHG1	L14454	0.79	(0.53-1.18)	0.250	0.357	0.78	(0.58-1.05)	0.096	0.313	downregulated

235350_a t	C4orf19	AI93558 6	0.43	(0.23-0.7 8)	0.0 06	0.12 0	1.09	(0.64-1.8 5)	0.7 50	0.83 7	downregulat ed
216829_a t	NTN2L	X72475	0.73	(0.58-0.9 3)	0.01 1	0.12 0	0.92	(0.78-1.0 9)	0.3 50	0.48 8	downregulat ed
203110_a t	PTK2B	U43522	0.73	(0.47-1.1 2)	0.1 50	0.26 3	1.07	(0.81-1.4 1)	0.6 50	0.74 6	downregulat ed
214433_s _at	SELENBP 1	NM_003 944	0.68	(0.45-1.0 2)	0.0 61	0.16 3	0.72	(0.54-0.9 6)	0.0 23	0.27 8	downregulat ed
226319_s _at	THOC4	AF0470 02	1.68	(0.63-4.5 2)	0.3 00	0.39 8	1.07	(0.60-1.9 1)	0.8 10	0.86 9	downregulat ed
227014_a t	ASPHD2	BE5508 81	0.53	(0.25-1.1 4)	0.11 0	0.21 6	1.56	(0.99-2.4 6)	0.0 55	0.31 3	downregulat ed
209569_x _at	D4S234E	NM_014 392	0.39	(0.17-0.8 8)	0.0 24	0.15 0	0.66	(0.36-1.2 3)	0.1 90	0.37 2	downregulat ed
225667_s _at	FAM84A	AI60110 1	0.69	(0.44-1.0 8)	0.11 0	0.21 6	0.68	(0.52-0.8 8)	0.0 03	0.27 8	downregulat ed
211635_x _at	IGHV1-69	M24670	0.75	(0.58-0.9 9)	0.0 40	0.16 3	0.94	(0.79-1.1 0)	0.4 30	0.55 2	downregulat ed
205242_a t	CXCL13	NM_006 419	0.84	(0.67-1.0 4)	0.1 20	0.23 3	1.00	(0.85-1.1 8)	1.0 00	1.00 0	downregulat ed
219148_a t	PBK	NM_018 492	1.01	(0.48-2.1 3)	0.9 70	0.97 0	0.96	(0.65-1.4 1)	0.8 20	0.87 4	downregulat ed
219450_a t	C4orf19	NM_018 302	0.57	(0.34-0.9 5)	0.0 33	0.15 8	1.05	(0.59-1.8 6)	0.8 80	0.91 4	downregulat ed
209138_x _at	IGL@	M87790	0.72	(0.54-0.9 5)	0.0 18	0.13 3	0.81	(0.67-0.9 8)	0.0 29	0.27 8	downregulat ed
214677_x _at	IGLJ3	X57812	0.71	(0.53-0.9 4)	0.0 18	0.13 3	0.78	(0.64-0.9 6)	0.0 20	0.27 8	downregulat ed
1555779_ a_at	CD79A	M74721	0.93	(0.43-1.9 9)	0.8 50	0.87 7	0.73	(0.45-1.1 6)	0.1 80	0.36 2	downregulat ed
210885_s _at	TRIM15	AF2201 33	0.70	(0.48-1.0 1)	0.0 57	0.16 3	1.15	(0.86-1.5 3)	0.3 60	0.49 7	downregulat ed
216430_x _at	IGL@	AF0435 86	0.68	(0.50-0.9 3)	0.0 15	0.12 9	0.90	(0.75-1.0 9)	0.3 00	0.43 7	downregulat ed
225053_a t	CNOT7	W94952	1.61	(0.38-6.9 2)	0.5 20	0.60 1	1.00	(0.45-2.2 3)	0.9 90	0.99 6	downregulat ed
204279_a t	PSMB9	NM_002 800	0.75	(0.45-1.2 4)	0.2 60	0.36 2	1.01	(0.66-1.5 4)	0.9 80	0.99 2	downregulat ed

Supplementary Table S5. Three significant gene ontology (GO) annotation clusters and two significant KEGG pathways identified for the 128 metastasis-associated genes (163 probe sets) identified in colorectal cancer.

Analysis was performed using the Functional Annotation Clustering tool on the Database for Annotation, Visualization and Integrated Discovery (DAVID). GO annotation levels one to three were considered. *P*-values were adjusted using the Benjamini-Hochberg False Discovery Rate multiple testing correction.

*GenBank accession number

A. Genes up-regulated in metastatic cancers as compared to early-stage cancers

GO Annotation Cluster 1	GO Annotation	Enrichment Score: 5.81	Count	P value
C9orf47, CLDN11, CLIC4, COL10A1, COL8A1, COMP, CYP1B1, DACT1, DCBLD2, FBN1, FLT1, HIP1, HMCN1, HOP, IGFBP7, INHBA, ITGB1, ITGB5, LEPR, LTBP3, NOTCH3, NRP2, OLR1, PDGFC, POSTN, PRELP, SLIT2, SPARC, SPP1, TGFB3, TIE1, TIMP3, UACA, VAT1, VCAN, WWTR1	GOTERM_BP_1	developmental process	33	5.40E-08
	GOTERM_BP_2	multicellular organismal development	25	4.90E-05
	GOTERM_BP_2	anatomical structure development	23	1.30E-04
	GOTERM_BP_3	organ development	17	6.00E-03
	GOTERM_BP_1	multicellular organismal process	29	1.40E-04
	GOTERM_BP_3	system development	19	1.10E-02
GO Annotation Cluster 2	GO Annotation	Enrichment Score: 5.79	Count	P value
CLDN11, CLEC11A, COL10A1, COL5A1, COL8A1, COMP, FBN1, FLT1, FN1, HIP1, HMCN1, IGFBP7, INHBA, LTBP3, PDGFC, POSTN, PRELP, SLIT2, SPARC, SPP1, THBS2, TIMP3, UACA, VCAN	GOTERM_CC_3	proteinaceous extracellular matrix	14	1.20E-07
	GOTERM_CC_2	proteinaceous extracellular matrix	14	3.10E-08
	GOTERM_CC_1	extracellular matrix	14	9.60E-09
	GOTERM_CC_1	extracellular region	22	1.00E-07
	GOTERM_CC_2	extracellular region part	17	1.50E-06

	GOTERM_CC_1	extracellular region part	17	2.70E-07
	GOTERM_CC_2	extracellular matrix part	7	1.10E-04
	GOTERM_CC_1	extracellular matrix part	7	1.90E-05
	GOTERM_CC_3	basement membrane	5	2.80E-02
	GOTERM_CC_2	basement membrane	5	3.20E-03
	GOTERM_MF_1	structural molecule activity	10	3.00E-02
	GOTERM_CC_3	collagen	3	7.30E-01
	GOTERM_CC_2	collagen	3	1.50E-01
KEGG Pathway Cluster 1	KEGG Pathway		Count	P value
COL5A1, FN1, FNDC1, ITGB1, ITGB5, SPP1, THBS2	ECM-receptor interaction		7	1.80E-03
KEGG Pathway Cluster 2	KEGG Pathway		Count	P value
COL5A1, COMP, FLT1, FN1, ITGB1, ITGB5, PDGFC, SPP1, THBS2	Focal adhesion		9	1.20E-03

B. Genes down-regulated in metastatic cancers as compared to early-stage cancers

GO Annotation Cluster 1	GO Annotation	Enrichment Score: 13.97	Count	P value
	GOTERM_BP_2	immune response	24	6.20E-16
ADORA2B, C1QBP, CCL20, CCL28, CD79A, CTA-246H3.1, CXCL13, DUOX2, IFI6, IGHA1, IGHG1, IGHM, IGH@, IGJ, IGKC, IGK@, IGL@, IGLJ3, IL8, POU2AF1, PSMB10, PSMB8, PSMB9, PTK2B, TNFRSF17, AW083576*, AW392551*	GOTERM_BP_1	immune system process	24	1.40E-14
	GOTERM_MF_2	antigen binding	13	3.40E-13
	GOTERM_BP_1	response to stimulus	27	1.60E-08

Supplementary Fig S1. Overall and class-specific misclassification errors for ten-fold cross-validation PAM with increasing values of centroid shrinkage for 86 stage A and 93 stage D colorectal cancers from this study and expO classified using our set of 128 metastasis-associated genes (163 probe sets).

Increasing values of centroid shrinkage are designed to progressively eliminate noisy genes. For our samples, classification accuracy for cross-validation did not improve with increasing shrinkage thresholds. Misclassification errors remained consistently low at approximately 25% for threshold values between zero and two, and rose with further increases in centroid shrinkage. Our initial 163 probe set therefore appeared to be a robust PAM classifier for our primary stage A and stage D cancers with some redundancy in information content. Redundancy is a feature desired for robust microarray-based classification.

Supplementary Fig S2. Prediction probabilities for the classification of (A) 95 stage B and (B) 93 stage C colorectal cancers into stage A- and stage D-like types using Prediction Analysis of Microarrays (PAM).

Predictions for single samples were made against a common reference set of stage A and stage D CRCs. Prior (expected) five-year recurrence probabilities were set as 20% for stage B and 40% for stage C patients based on relapse rates observed in clinical practice. The dashed line shows the prediction probability cut-off set at 90%.

Supplementary Fig S3. PAM-based prognosis prediction for stage B and C colorectal cancer patients based on metastasis-associated genes.

Disease-free survival curves generated using our 128-gene PAM classifier show a significant difference in outcome. For single-sample PAM classification, prior (expected) six-year recurrence probabilities were set as 20% for stage B and 40% for stage C patients based on relapse rates observed in clinical practice (21). Class predictions with a >90% were scored.

Supplementary Fig S4. Representative examples of haematoxylin & eosin stained tissue sections from colorectal cancers showing low, moderate and high average density of mononuclear chronic inflammatory cells.

The average density of mononuclear chronic inflammatory cells was scored within tumor areas comprising more than 60% of neoplastic cells as outlined; areas of adenoma, ulceration and necrosis were excluded from the analysis.