#	#	#	#	#	#	ASTRO	ASTRO + TGFɑ	IRRADIATED ASTRO + TGFα ADHERENT CELLS	IRRADIATED ASTRO + TGFɑ FLOATING CELLS	TUMORS FROM IRRADIATED ASTRO + TGFɑ ADHERENT CELLS	TUMORS FROM IRRADIATED ASTRO + TGFɑ FLOATING CELLS
n	**chrxx**	**chr**	**arm**	**band**	**band2**						
1	chr1:0-8912711	1	1q	1qA1	1qA1	0	0	0	0	0	0
2	chr1:8912711-12378766	1	1q	1qA2	1qA2	0	0	0	0	0	0
3	chr1:12378766-20301176	1	1q	1qA3	1qA3	0	0	0	0	0	0
4	chr1:20301176-22281779	1	1q	1qA4	1qA4	0	0	0	0	0	0
5	chr1:22281779-31194491	1	1q	1qA5	1qA5	0	0	0	0	0	0
6	chr1:31194491-43573257	1	1q	1qB	1qB	0	0	0	0	0	0
7	chr1:43573257-54961723	1	1q	1qC1	1qC1.1	0	0	0	0	0	0
8	chr1:54961723-	1	1q	1qC1	1qC1.2	0	0	0	0	0	0

	56447175										
9	chr1:56447175-59913229	1	1q	1qC1	1qC1.3	0	0	0	0	0	0
10	chr1:59913229-65855037	1	1q	1qC2	1qC2	0	0	0	0	0	0
11	chr1:65855037-75262900	1	1q	1qC3	1qC3	0	0	0	0	0	0
12	chr1:75262900-80709557	1	1q	1qC4	1qC4	0	0	0	0	0	0
13	chr1:80709557-88136817	1	1q	1qC5	1qC5	0	0	0	0	0	0
14	chr1:88136817-100515583	1	1q	1qD	1qD	0	0	0	0	0	0
15	chr1:100515583-103486487	1	1q	1qE1	1qE1.1	0	0	0	0	0	0
16	chr1:103486487-104476788	1	1q	1qE1	1qE1.2	0	0	0	0	0	0
17	chr1:104476788-113389500	1	1q	1qE2	1qE2.1	0	0	0	0	0	0
18	chr1:113389500-114874952	1	1q	1qE2	1qE2.2	0	0	0	0	0	0
19	chr1:114874952-126758568	1	1q	1qE2	1qE2.3	0	0	0	0	0	0
20	chr1:126758568-129729472	1	1q	1qE3	1qE3	0	0	0	0	0	0

21	chr1:129729472-140622786	1	1q	1qE4	1qE4	0	0	0	0	0	0
22	chr1:140622786-148545197	1	1q	1qF	1qF	0	1.2800	0	0	0	0
23	chr1:148545197-153001553	1	1q	1qG1	1qG1	0	0	0	0	0	0
24	chr1:153001553-153991854	1	1q	1qG2	1qG2	0	0	0	0	0	0
25	chr1:153991854-158448210	1	1q	1qG3	1qG3	0	0	0	0	0	0
26	chr1:158448210-161419114	1	1q	1qH1	1qH1	0	0	0	0	0	0
27	chr1:161419114-165380319	1	1q	1qH2	1qH2.1	0	0	0	0	0	0
28	chr1:165380319-166865771	1	1q	1qH2	1qH2.2	0	0	0	0	0	0
29	chr1:166865771-171322127	1	1q	1qH2	1qH2.3	0	0	0	0	0	0
30	chr1:171322127-177263935	1	1q	1qH3	1qH3	-1.5200	-1.5500	-1.5700	-1.6200	0.6200	-1.0700
31	chr1:177263935-183205743	1	1q	1qH4	1qH4	0	0	0	0	0	0
32	chr1:183205743-189642702	1	1q	1qH5	1qH5	0	0	0	-1.1000	-1.0500	-1.0100
33	chr1:189642702	1	1q	1qH6	1qH6	0	0	0	0	0	0

	-197069962										
34	chr2:0-14070368	2	2q	2qA1	2qA1	0	0	0	0	0	0
35	chr2:14070368-16415429	2	2q	2qA2	2qA2	0	0	0	0	0	0
36	chr2:16415429-29078760	2	2q	2qA3	2qA3	0	0	0	0	0	0
37	chr2:29078760-48308264	2	2q	2qB	2qB	0	0	0	0	-0.4200	0
38	chr2:48308264-60502583	2	2q	2qC1	2qC1.1	0	0	0	0	0	0
39	chr2:60502583-60971595	2	2q	2qC1	2qC1.2	0	0	0	0	0	0
40	chr2:60971595-68475791	2	2q	2qC1	2qC1.3	0	0	0	0	0	0
41	chr2:68475791-71758877	2	2q	2qC2	2qC2	0	0	0	0	0	0
42	chr2:71758877-81139123	2	2q	2qC3	2qC3	-2.4700	-2.5300	-2.5700	-2.6100	-2.5500	-2.5500
43	chr2:81139123-88643319	2	2q	2qD	2qD	0	0	-0.2800	0	0	0
44	chr2:88643319-101306651	2	2q	2qE1	2qE1	0	0	-0.2800	0	0	0
45	chr2:101306651-105058749	2	2q	2qE2	2qE2	0	0	0	0	0	0

46	chr2:105058749-113031957	2	2q	2qE3	2qE3	0	0	0	0	0	0
47	chr2:113031957-115846031	2	2q	2qE4	2qE4	0	0	0	0	0	0
48	chr2:115846031-123819240	2	2q	2qE5	2qE5	0.8400	0.8600	1.0400	0.9200	0.8200	0.7700
49	chr2:123819240-131792448	2	2q	2qF1	2qF1	0	0	0	0	0	0
50	chr2:131792448-134606522	2	2q	2qF2	2qF2	0	0	0	0	0	0
51	chr2:134606522-141172694	2	2q	2qF3	2qF3	0	0	0	0	0	0
52	chr2:141172694-146800841	2	2q	2qG1	2qG1	0	0	0	0	0	0
53	chr2:146800841-147738866	2	2q	2qG2	2qG2	0	0	0	0	0	0
54	chr2:147738866-152428988	2	2q	2qG3	2qG3	0	0	0	0	0	0
55	chr2:152428988-158995160	2	2q	2qH1	2qH1	0	0	0	0	0	0
56	chr2:158995160-163216271	2	2q	2qH2	2qH2	0	0	0	0	0	0
57	chr2:163216271-173534541	2	2q	2qH3	2qH3	0	0	0	0	0	0
58	chr2:173534541	2	2q	2qH4	2qH4	0	0	0	0	0	0

	-181976762										
59	chr3:0-18521769	3	3q	3qA1	3qA1	0	0	0	0	0	0
60	chr3:18521769-20471428	3	3q	3qA2	3qA2	0	0	0	0	0	0
61	chr3:20471428-35581293	3	3q	3qA3	3qA3	0	0	0	0	0	0
62	chr3:35581293-46791837	3	3q	3qB	3qB	0	0	0	0	0	0
63	chr3:46791837-56540137	3	3q	3qC	3qC	0	0	0.9000	0	0	0
64	chr3:56540137-60926871	3	3q	3qD	3qD	0	0	0	0	0	0
65	chr3:60926871-69700341	3	3q	3qE1	3qE1	0	0	0	0	0	0
66	chr3:69700341-72624831	3	3q	3qE2	3qE2	0	0	0	0	0	0
67	chr3:72624831-83835375	3	3q	3qE3	3qE3	0	0	0	0	0	0
68	chr3:83835375-93096260	3	3q	3qF1	3qF1	0	0	0	0.3000	0	0
69	chr3:93096260-97482995	3	3q	3qF2	3qF2.1	0	0	0	0	0	0
70	chr3:97482995-106256464	3	3q	3qF2	3qF2.2	0	0	0	0	0	0

71	chr3:106256464-108206124	3	3q	3qF2	3qF2.3	0	0	0	0	0	0
72	chr3:108206124-115029934	3	3q	3qF3	3qF3	0	0	0	0	0	0
73	chr3:115029934-126727893	3	3q	3qG1	3qG1	0	0	0	0	0	0
74	chr3:126727893-128677553	3	3q	3qG2	3qG2	0	0	0	0	0	0
75	chr3:128677553-138425853	3	3q	3qG3	3qG3	0	0	0	0	0	0
76	chr3:138425853-143787417	3	3q	3qH1	3qH1	0	0	0	0	0	0
77	chr3:143787417-148174152	3	3q	3qH2	3qH2	0	0	0	0	0	0
78	chr3:148174152-154023132	3	3q	3qH3	3qH3	0	0	0	0	0	0
79	chr3:154023132-159872112	3	3q	3qH4	3qH4	0	0	0	0	0	0
80	chr4:0-14742088	4	4q	4qA1	4qA1	0	0	0	0	0	0
81	chr4:14742088-17595395	4	4q	4qA2	4qA2	0	0	0	0	0	0
82	chr4:17595395-28057522	4	4q	4qA3	4qA3	0	0	0	0	0	0
83	chr4:28057522-	4	4q	4qA4	4qA4	0	0	0	0	0	0

	29959727										
84	chr4:29959727-43275161	4	4q	4qA5	4qA5	0	0	0	0	0	0
85	chr4:43275161-51359532	4	4q	4qB1	4qB1	0	0	0	0	0	0
86	chr4:51359532-54688391	4	4q	4qB2	4qB2	0	0	0	0	0	0
87	chr4:54688391-62772762	4	4q	4qB3	4qB3	-1.2200	-1.1700	-1.1700	-1.2100	-0.9900	-0.9400
88	chr4:62772762-68954928	4	4q	4qC1	4qC1	0	0	0	0	0	0
89	chr4:68954928-71332684	4	4q	4qC2	4qC2	0	0	0	0	0	0
90	chr4:71332684-83221465	4	4q	4qC3	4qC3	0	0	0	0	0	0
91	chr4:83221465-88928080	4	4q	4qC4	4qC4	0	0	-0.9100	-0.9700	-0.7100	0
92	chr4:88928080-96536899	4	4q	4qC5	4qC5	0	0	0	0	0	0
93	chr4:96536899-104621270	4	4q	4qC6	4qC6	0	0	0	0	0	0
94	chr4:104621270-109852334	4	4q	4qC7	4qC7	0	0	0	0	0	0
95	chr4:109852334-116510051	4	4q	4qD1	4qD1	2.6500	2.6300	2.3800	2.4200	3.8300	4.1700

96	chr4:116510051-119363358	4	4q	4qD2	4qD2.1	0	0	0	0	0	0
97	chr4:119363358-129825485	4	4q	4qD2	4qD2.2	0	0	0	0	0	0
98	chr4:129825485-132678793	4	4q	4qD2	4qD2.3	0	0	0	0	0	0
99	chr4:132678793-140287612	4	4q	4qD3	4qD3	0	0	-0.8400	-1.0600	-0.7500	-0.4900
100	chr4:140287612-146469778	4	4q	4qE1	4qE1	0	0	0	0.4800	0	0
101	chr4:146469778-155029701	4	4q	4qE2	4qE2	0	0.0800	0	0	0	0
102	chr5:0-14911692	5	5q	5qA1	5qA1	0	0	0	0	0	0
103	chr5:14911692-16354759	5	5q	5qA2	5qA2	0	0	0	0	0	0
104	chr5:16354759-25494184	5	5q	5qA3	5qA3	0	0	0	0	0	0
105	chr5:25494184-33671564	5	5q	5qB1	5qB1	0	0	0	1.2000	0	0
106	chr5:33671564-35595653	5	5q	5qB2	5qB2	0	0	0	0	0	0
107	chr5:35595653-50507346	5	5q	5qB3	5qB3	0	0	0	0	0	0
108	chr5:50507346-	5	5q	5qC1	5qC1	0	0	0	0	0	0

	58684726										
109	chr5:58684726-61089838	5	5q	5qC2	5qC2	0	0	0	0	0	0
110	chr5:61089838-71672330	5	5q	5qC3	5qC3.1	0	0	0	0	0	0
111	chr5:71672330-73596419	5	5q	5qC3	5qC3.2	0	0	0	0	0	0
112	chr5:73596419-77925620	5	5q	5qC3	5qC3.3	0	0	0	0	0	0
113	chr5:77925620-81773799	5	5q	5qD	5qD	0	0	0	0	0	0
114	chr5:81773799-91394246	5	5q	5qE1	5qE1	0	0	-0.2600	0	-0.2500	0
115	chr5:91394246-93799358	5	5q	5qE2	5qE2	0	0	0	0	0	0
116	chr5:93799358-99571626	5	5q	5qE3	5qE3	0	0	0	0	0	0
117	chr5:99571626-101976738	5	5q	5qE4	5qE4	0	0	0	0	0	0
118	chr5:101976738-107749006	5	5q	5qE5	5qE5	0	0	0	0	0	0
119	chr5:107749006-125065811	5	5q	5qF	5qF	0	0	0	0	0	0
120	chr5:125065811-126989900	5	5q	5qG1	5qG1.1	0	0	0	0	0	0

121	chr5:126989900-127951945	5	5q	5qG1	5qG1.2	0	0	0	0	0	0
122	chr5:127951945-130838079	5	5q	5qG1	5qG1.3	0	0	0	0	0	0
123	chr5:130838079-146230794	5	5q	5qG2	5qG2	0	0	0	0	0	0
124	chr5:146230794-152003063	5	5q	5qG3	5qG3	0	0	0	0	0	0
125	chr6:0-16613965	6	6q	6qA1	6qA1	0	0	-1.0200	-1.0300	-0.8300	-0.7500
126	chr6:16613965-21500425	6	6q	6qA2	6qA2	0	0	0.2900	0.4300	0.3600	0.3500
127	chr6:21500425-27364177	6	6q	6qA3	6qA3.1	0	0	0.2900	0.4300	0.3600	0.3500
128	chr6:27364177-28341469	6	6q	6qA3	6qA3.2	0	0	0.2900	0.4300	0.3600	0.3500
129	chr6:28341469-34205222	6	6q	6qA3	6qA3.3	0	0	0.2900	0.4300	0.3600	0.3500
130	chr6:34205222-41534912	6	6q	6qB1	6qB1	0	0	0.2900	0.4300	0.3600	0.3500
131	chr6:41534912-44466788	6	6q	6qB2	6qB2.1	0	0	0.2900	0.4300	0.3600	0.3500
132	chr6:44466788-45932726	6	6q	6qB2	6qB2.2	0	0	0.2900	0.4300	0.3600	0.3500
133	chr6:45932726-	6	6q	6qB2	6qB2.3			0.2900	0.4300	0.3600	0.3500

	50819187					0.9400	1.0000				
134	chr6:50819187-62546691	6	6q	6qB3	6qB3	0	0	0.2900	0.4300	0.3600	0.3500
135	chr6:62546691-74274196	6	6q	6qC1	6qC1	0	0	0.2900	0.4300	0.3600	0.3500
136	chr6:74274196-76717426	6	6q	6qC2	6qC2	0	0	0.2900	0.4300	0	0.3500
137	chr6:76717426-86001701	6	6q	6qC3	6qC3	0	0	0.2900	0.4300	0.3600	0.3500
138	chr6:86001701-94308683	6	6q	6qD1	6qD1	0	0	0.2900	0.4300	0.3600	0.3500
139	chr6:94308683-95774621	6	6q	6qD2	6qD2	0	0	0.2900	0.4300	0.3600	0.3500
140	chr6:95774621-103104312	6	6q	6qD3	6qD3	0	0	0.2900	0.4300	0.3600	0.3500
141	chr6:103104312-108479418	6	6q	6qE1	6qE1	0	0	0.2900	0.4300	0.3600	0.3500
142	chr6:108479418-109456710	6	6q	6qE2	6qE2	0	0	0.2900	0.4300	0.3600	0.3500
143	chr6:109456710-116786401	6	6q	6qE3	6qE3	0	0	0.2900	0.4300	0.3600	0.3500
144	chr6:116786401-122650153	6	6q	6qF1	6qF1	0	0	0	0	0	0
145	chr6:122650153-125093383	6	6q	6qF2	6qF2	0	0	0	0	0	0

146	chr6:125093383-131934427	6	6q	6qF3	6qF3	0.9500	1.0500	-0.2700	-0.2700	0.6400	0.8400
147	chr6:131934427-139264118	6	6q	6qG1	6qG1	0	0	-0.2700	-0.2700	-0.2600	0
148	chr6:139264118-142684640	6	6q	6qG2	6qG2	0	0	0	0	0	0
149	chr6:142684640-149525685	6	6q	6qG3	6qG3	0	0	0	0	0	0
150	chr7:0-15170811	7	7q	7qA1	7qA1	0	0	0.3000	0.3000	0.2900	0
151	chr7:15170811-18204973	7	7q	7qA2	7qA2	0	0	0.3600	0.4500	0.2900	0
152	chr7:18204973-28318847	7	7q	7qA3	7qA3	0	0	0.3600	0.4500	0.3600	0
153	chr7:28318847-34387172	7	7q	7qB1	7qB1	0	0	0.3600	0.4500	0.3600	0
154	chr7:34387172-37421334	7	7q	7qB2	7qB2	0	0	0.3600	0.4500	0.3600	0
155	chr7:37421334-47535208	7	7q	7qB3	7qB3	0.8900	0.9000	0.4300	0.4500	0.2900	0.2600
156	chr7:47535208-54109226	7	7q	7qB4	7qB4	0	0	0.3000	0.3000	0.2900	0
157	chr7:54109226-60683244	7	7q	7qB5	7qB5	0	0	0.3000	0.3000	0	0
158	chr7:60683244-	7	7q	7qC	7qC	-	-	0.3000	-0.4000	0.2900	-0.5500

	71302812					0.7200	0.6800				
159	chr7:71302812-76865443	7	7q	7qD1	7qD1	0	0	0.3000	0.2200	0.2900	0
160	chr7:76865443-80405299	7	7q	7qD2	7qD2	0	0	0.3000	0.2200	0.2900	0
161	chr7:80405299-90013479	7	7q	7qD3	7qD3	0	0	0.3000	0.2200	0.2900	0
162	chr7:90013479-99621660	7	7q	7qE1	7qE1	0	0	0.3000	0.2200	0.2900	0
163	chr7:99621660-102150128	7	7q	7qE2	7qE2	0	0	0.3000	0.2200	0.2900	0
164	chr7:102150128-111252615	7	7q	7qE3	7qE3	1.9800	2.0000	0.3000	0.2200	0.2900	1.7300
165	chr7:111252615-118332327	7	7q	7qF1	7qF1	0	0	0.3000	0	0.2900	0
166	chr7:118332327-122883570	7	7q	7qF2	7qF2	0	0	0.3000	0	0.2900	0
167	chr7:122883570-137042994	7	7q	7qF3	7qF3	0	0	0.3000	0	0.2900	0.9500
168	chr7:137042994-140582850	7	7q	7qF4	7qF4	0	0	0.3000	0	0.2900	0
169	chr7:140582850-145134094	7	7q	7qF5	7qF5	0	0	0.3000	0.3000	0.2900	0
170	chr8:0-16271352	8	8q	8qA1	8qA1.1	0	0	0	0	0	0

171	chr8:16271352-17228491	8	8q	8qA1	8qA1.2	0	0	0	0	0	0
172	chr8:17228491-20578475	8	8q	8qA1	8qA1.3	0	0	0	0	0	0
173	chr8:20578475-30149859	8	8q	8qA2	8qA2	0	0	0	0	0	0
174	chr8:30149859-34456982	8	8q	8qA3	8qA3	1.0500	0.7800	0	0	0.7900	0
175	chr8:34456982-44985504	8	8q	8qA4	8qA4	0	0	0	0	-0.3200	0
176	chr8:44985504-49292627	8	8q	8qB1	8qB1.1	0	0	0	0	-0.3200	0
177	chr8:49292627-51206903	8	8q	8qB1	8qB1.2	0	0	0	0	0	0
178	chr8:51206903-56949734	8	8q	8qB1	8qB1.3	0	0	0	0	0	0
179	chr8:56949734-60778287	8	8q	8qB2	8qB2	0	0	0	0	0	0
180	chr8:60778287-68435394	8	8q	8qB3	8qB3.1	0	0	0	0	0	0
181	chr8:68435394-69392533	8	8q	8qB3	8qB3.2	0	0	0	0	0	0
182	chr8:69392533-76092502	8	8q	8qB3	8qB3.3	0	0	0	0	0	0
183	chr8:76092502-	8	8q	8qC1	8qC1	0	0	0	0	0	0

	81835332										
184	chr8:81835332-86621024	8	8q	8qC2	8qC2	0	0	1.9500	0	0	0
185	chr8:86621024-91885285	8	8q	8qC3	8qC3	0	0	0	0	0	0
186	chr8:91885285-93320993	8	8q	8qC4	8qC4	0	0	0	0	0	0
187	chr8:93320993-97628115	8	8q	8qC5	8qC5	0	0	0	0	0	0
188	chr8:97628115-105285223	8	8q	8qD1	8qD1	0	0	0	0	0	0
189	chr8:105285223-106242361	8	8q	8qD2	8qD2	0	0	0	0	0	0
190	chr8:106242361-112942330	8	8q	8qD3	8qD3	0	0	0	0	0	0
191	chr8:112942330-126342267	8	8q	8qE1	8qE1	0	0	0	0.9900	0	0
192	chr8:126342267-132085098	8	8q	8qE2	8qE2	0	0	0	0	0	0
193	chr9:0-14343360	9	9q	9qA1	9qA1	0	0	0	0	0	0
194	chr9:14343360-19432940	9	9q	9qA2	9qA2	0	0	0	0	-0.3100	0
195	chr9:19432940-24059831	9	9q	9qA3	9qA3	0	0	0	0	-0.3100	0

196	chr9:24059831-37940503	9	9q	9qA4	9qA4	0	0	0	0	0	0
197	chr9:37940503-43955461	9	9q	9qA5	9qA5.1	0	0	0	0	0	0
198	chr9:43955461-46268906	9	9q	9qA5	9qA5.2	0	0	0	0	0	0
199	chr9:46268906-54597309	9	9q	9qA5	9qA5.3	0	0	0	0	0	0
200	chr9:54597309-62925712	9	9q	9qB	9qB	0	0	0	0	0	0
201	chr9:62925712-69403359	9	9q	9qC	9qC	0	0	0	0	0	0
202	chr9:69403359-77269073	9	9q	9qD	9qD	0	0	0	0	0	0
203	chr9:77269073-82358653	9	9q	9qE1	9qE1	0	0	0	0	0	0
204	chr9:82358653-84209409	9	9q	9qE2	9qE2	0	0	0	0	0	0
205	chr9:84209409-90687056	9	9q	9qE3	9qE3.1	0	0	0	0	0	0
206	chr9:90687056-91149745	9	9q	9qE3	9qE3.2	0	0	0	0	0	0
207	chr9:91149745-100403526	9	9q	9qE3	9qE3.3	0	0	0	0	0	0
208	chr9:100403526	9	9q	9qE4	9qE4	0	0	0	0	0	0

	-101328904										
209	chr9:101328904-107806551	9	9q	9qF1	9qF1	0	0	0	0	0	0
210	chr9:107806551-110582686	9	9q	9qF2	9qF2	0	0	0	0	0	0
211	chr9:110582686-119373778	9	9q	9qF3	9qF3	0	0	0	0	0	0
212	chr9:119373778-124000669	9	9q	9qF4	9qF4	0	0	0	0.9400	0	0
213	chr10:0-12750708	10	10q	10qA1	10qA1	0	0	0	0	0	0
214	chr10:12750708-17654827	10	10q	10qA2	10qA2	0	0	0	0	0	0
215	chr10:17654827-23539770	10	10q	10qA3	10qA3	0	0	0	0	0	0
216	chr10:23539770-33348007	10	10q	10qA4	10qA4	0	0	0	0	-0.2500	-0.2600
217	chr10:33348007-41194597	10	10q	10qB1	10qB1	0	0	0	0	-0.2500	-0.2600
218	chr10:41194597-48060364	10	10q	10qB2	10qB2	0	0	-0.3000	0	0	0
219	chr10:48060364-55906954	10	10q	10qB3	10qB3	0	0	-0.3000	0	0	0
220	chr10:55906954-63753544	10	10q	10qB4	10qB4	0	0	-0.3000	0	0	0

221	chr10:63753544-67676839	10	10q	10qB5	10qB5.1	0	0	0	0	0	0
222	chr10:67676839-68167251	10	10q	10qB5	10qB5.2	0	0	0	0	0	0
223	chr10:68167251-74542605	10	10q	10qB5	10qB5.3	0	0	0	0	0	0
224	chr10:74542605-88764550	10	10q	10qC1	10qC1	0	0	0	0	0	0
225	chr10:88764550-95630316	10	10q	10qC2	10qC2	0	1.3300	1.2100	1.2400	0	0
226	chr10:95630316-98572787	10	10q	10qC3	10qC3	0	0	-0.2800	0	0	0
227	chr10:98572787-111323496	10	10q	10qD1	10qD1	0	0	-0.2800	0	0	0
228	chr10:111323496-124074205	10	10q	10qD2	10qD2	0	0	0	0	0	0
229	chr10:124074205-129959148	10	10q	10qD3	10qD3	0	0	0	0	0	0
230	chr11:0-13016647	11	11q	11qA1	11qA1	0	0	0	0	0	0
231	chr11:13016647-17200570	11	11q	11qA2	11qA2	0	0	0	0	0	0
232	chr11:17200570-21849372	11	11q	11qA3	11qA3.1	0	0	0	0	0	0
233	chr11:21849372	11	11q	11qA	11qA3.	0	0	0	0	0	0

	-25568415			3	2						
234	chr11:25568415-30217217	11	11q	11qA3	11qA3.3	0	0	0	0	0	0
235	chr11:30217217-36260661	11	11q	11qA4	11qA4	0	0	1.5300	1.2400	0	0
236	chr11:36260661-43233865	11	11q	11qA5	11qA5	0	0	0	0	0	0
237	chr11:43233865-47882668	11	11q	11qB1	11qB1.1	0	1.2900	0	1.2000	0	0
238	chr11:47882668-49742189	11	11q	11qB1	11qB1.2	0	0	0	0	0	0
239	chr11:49742189-59969555	11	11q	11qB1	11qB1.3	0	0	0	0	0	0
240	chr11:59969555-62758837	11	11q	11qB2	11qB2	0	0	0	0	0	0
241	chr11:62758837-70661801	11	11q	11qB3	11qB3	0	0	0.5200	0.5000	0.4400	0.4200
242	chr11:70661801-73915963	11	11q	11qB4	11qB4	0	0	0.5200	0.5000	0.4400	0.4200
243	chr11:73915963-81818928	11	11q	11qB5	11qB5	0	0	0.5200	0.5000	0.2600	0.4200
244	chr11:81818928-90186773	11	11q	11qC	11qC	0	0	0.5200	0.5000	0.4400	0.4200
245	chr11:90186773-102273660	11	11q	11qD	11qD	0	0	0.5200	0.5000	0.4400	0.4200

246	chr11:102273660-110176625	11	11q	11qE1	11qE1	0	0	0.5200	0.5000	0.4400	0.4200
247	chr11:110176625-121798632	11	11q	11qE2	11qE2	0	0	0.5200	0.5000	0.4400	0.4200
248	chr12:0-17650279	12	12q	12qA1	12qA1.1	0	0	0	0	0	0
249	chr12:17650279-21180335	12	12q	12qA1	12qA1.2	0	0	0	0	0	0
250	chr12:21180335-26034162	12	12q	12qA1	12qA1.3	0	0	0	0	0	0
251	chr12:26034162-31770503	12	12q	12qA2	12qA2	2.4000	2.2000	2.0700	2.4200	0	0
252	chr12:31770503-39271872	12	12q	12qA3	12qA3	1.1800	1.2200	1.0500	1.1200	0.9700	1.0400
253	chr12:39271872-44125699	12	12q	12qB1	12qB1	0	0	0	0	0	0
254	chr12:44125699-45008213	12	12q	12qB2	12qB2	0	0	0	0	0	0
255	chr12:45008213-52068325	12	12q	12qB3	12qB3	0	0	0	0	0	0
256	chr12:52068325-66188548	12	12q	12qC1	12qC1	0	0	0	0	0	0
257	chr12:66188548-71483632	12	12q	12qC2	12qC2	0	0	0	0	0	0
258	chr12:71483632	12	12q	12qC	12qC3	0	0	0	0	0	0

	-81191286			3							
259	chr12:81191286-85603856	12	12q	12qD1	12qD1	0	0	0	0	0	0
260	chr12:85603856-88692655	12	12q	12qD2	12qD2	0	0	0	0	0	0
261	chr12:88692655-95752767	12	12q	12qD3	12qD3	0	0	0	0	0	0
262	chr12:95752767-106342935	12	12q	12qE	12qE	0	0	0	0	0	0
263	chr12:106342935-114726818	12	12q	12qF1	12qF1	0	0	0	0	0	0
264	chr12:114726818-120463159	12	12q	12qF2	12qF2	0	0	0	0	0	0
265	chr13:0-16312600	13	13q	13qA1	13qA1	0	0	0	0	0	0
266	chr13:16312600-21255812	13	13q	13qA2	13qA2	0	0	0	0	-0.3700	0
267	chr13:21255812-29659273	13	13q	13qA3	13qA3.1	0	0	0	0	0	0
268	chr13:29659273-33119521	13	13q	13qA3	13qA3.2	0	0	0	0	0	0
269	chr13:33119521-41522982	13	13q	13qA3	13qA3.3	0	0	0	0	0	0
270	chr13:41522982-44488909	13	13q	13qA4	13qA4	0	0	0	0	0	0

271	chr13:44488909-52892370	13	13q	13qA5	13qA5	0	0	0	0	0	0
272	chr13:52892370-59318546	13	13q	13qB1	13qB1	0	0	0	0	0	0
273	chr13:59318546-61790152	13	13q	13qB2	13qB2	0	0	0	0	0	0
274	chr13:61790152-69699292	13	13q	13qB3	13qB3	0	0	0	0	0	0
275	chr13:69699292-78597074	13	13q	13qC1	13qC1	0	0	0	0	0	0
276	chr13:78597074-81068680	13	13q	13qC2	13qC2	0	0	0	0	0	0
277	chr13:81068680-94909674	13	13q	13qC3	13qC3	0	0	0	0	0	0
278	chr13:94909674-106773383	13	13q	13qD1	13qD1	0	0	0	0	0.8100	0.8700
279	chr13:106773383-110727953	13	13q	13qD2	13qD2.1	0	0	0	0	0	0
280	chr13:110727953-116659808	13	13q	13qD2	13qD2.2	0	0	0	0	0	0
281	chr13:116659808-120614378	13	13q	13qD2	13qD2.3	0	0	0	0	0	0
282	chr14:0-14877464	14	14q	14qA1	14qA1	0	0	0	0	0	0
283	chr14:14877464	14	14q	14qA	14qA2	0	0	0	0	0	0

	-19340703			2							
284	chr14:19340703-29754928	14	14q	14qA3	14qA3	0	0	0	0	0	0
285	chr14:29754928-43144646	14	14q	14qB	14qB	0	0	0	0	0	0
286	chr14:43144646-51575209	14	14q	14qC1	14qC1	0	0	-0.2400	0	-0.3000	0
287	chr14:51575209-54550702	14	14q	14qC2	14qC2	0.6200	0.6300	0.5600	0.5500	0.5500	0.5600
288	chr14:54550702-59509857	14	14q	14qC3	14qC3	0	0	0	0	0	0
289	chr14:59509857-68436336	14	14q	14qD1	14qD1	0	0.8300	0.3600	0.4400	0.3000	0
290	chr14:68436336-72403660	14	14q	14qD2	14qD2	0	0	0	0	0	0
291	chr14:72403660-84305631	14	14q	14qD3	14qD3	0	0	0	0	0	0
292	chr14:84305631-88272955	14	14q	14qE1	14qE1	0	0	0	0	0	0
293	chr14:88272955-98191265	14	14q	14qE2	14qE2.1	0	0	0	0	0	0
294	chr14:98191265-99183096	14	14q	14qE2	14qE2.2	0	0	0	0	0	0
295	chr14:99183096-106621828	14	14q	14qE2	14qE2.3	0	0	0	0	0	0

296	chr14:106621828-110093236	14	14q	14qE3	14qE3	0	0	0	0	0	0
297	chr14:110093236-120011546	14	14q	14qE4	14qE4	0	0	0	0	0	0
298	chr14:120011546-123978870	14	14q	14qE5	14qE5	0	0	0	0	0	0
299	chr15:0-16412919	15	15q	15qA1	15qA1	0	0	0.3500	0	0.3400	0.4200
300	chr15:16412919-24163465	15	15q	15qA2	15qA2	0	0	0.3500	0	0.3400	0.4200
301	chr15:24163465-29634438	15	15q	15qB1	15qB1	0	0	0.3500	0	0.3400	0.4200
302	chr15:29634438-31914010	15	15q	15qB2	15qB2	0	0	0.3500	0	0.3400	0.4200
303	chr15:31914010-42855956	15	15q	15qB3	15qB3.1	0	0	0.3500	0	0.3400	0.4200
304	chr15:42855956-44679614	15	15q	15qB3	15qB3.2	0	0	0.3500	0	0.3400	0.4200
305	chr15:44679614-49694673	15	15q	15qB3	15qB3.3	0	0	0.3500	0	0.3400	0.4200
306	chr15:49694673-53341989	15	15q	15qC	15qC	0	0	0.3500	0	0.3400	0.4200
307	chr15:53341989-66107593	15	15q	15qD1	15qD1	0	0	0.3500	0	0.3400	0.4200
308	chr15:66107593	15	15q	15qD	15qD2	0	0	0.4300	0	0.4200	0.5000

	-68387165			2							
309	chr15:68387165-77049539	15	15q	15qD3	15qD3	0	0	0.4300	0	0.4200	0.5000
310	chr15:77049539-83432341	15	15q	15qE1	15qE1	0	0	0.4900	0	0.4200	0.5000
311	chr15:83432341-86623742	15	15q	15qE2	15qE2	0	0	0.4900	0	0.4200	0.5000
312	chr15:86623742-95286117	15	15q	15qE3	15qE3	0	0	0.4900	0	0.4200	0.5000
313	chr15:95286117-100757090	15	15q	15qF1	15qF1	0	0	0.4900	0	0.4200	0.5000
314	chr15:100757090-101668919	15	15q	15qF2	15qF2	0	0	0.4900	0	0.4200	0.5000
315	chr15:101668919-103492577	15	15q	15qF3	15qF3	0	0	0.4300	0	0.4200	0.5000
316	chr16:0-15439672	16	16q	16qA1	16qA1	0	0	0	0	0	0
317	chr16:15439672-16375409	16	16q	16qA2	16qA2	0	0	0	0	0	0
318	chr16:16375409-20586229	16	16q	16qA3	16qA3	0	0	0	0	0	0
319	chr16:20586229-26200655	16	16q	16qB1	16qB1	0	0	0	0	0	0
320	chr16:26200655-32282950	16	16q	16qB2	16qB2	0	0	0	0	0	0

321	chr16:32282950-38365245	16	16q	16qB3	16qB3	0	0	0	0	0	0
322	chr16:38365245-44915409	16	16q	16qB4	16qB4	1.0200	1.0000	0	0.9100	0	0
323	chr16:44915409-53804918	16	16q	16qB5	16qB5	0	0	0	0	0	0
324	chr16:53804918-58015737	16	16q	16qC1	16qC1.1	0	0	0	0	0	0
325	chr16:58015737-58951475	16	16q	16qC1	16qC1.2	0	0	0	0	0	0
326	chr16:58951475-66905245	16	16q	16qC1	16qC1.3	0	0	0	0	0	0
327	chr16:66905245-70648196	16	16q	16qC2	16qC2	0	0	0	0	0	0
328	chr16:70648196-79069836	16	16q	16qC3	16qC3.1	0	0	0	0	0	0
329	chr16:79069836-79537704	16	16q	16qC3	16qC3.2	0	0	0	0	0	0
330	chr16:79537704-91702295	16	16q	16qC3	16qC3.3	0	0	0	0	0	0
331	chr16:91702295-98252459	16	16q	16qC4	16qC4	0	0	0	0	0	0
332	chr17:0-13970997	17	17q	17qA1	17qA1	0	0	0	0	0	0
333	chr17:13970997	17	17q	17qA	17qA2	0	0	0	0	0	0

	-16153965			2							
334	chr17:16153965-17463746	17	17q	17qA3	17qA3.1	0	0	0	0	0	0
335	chr17:17463746-21829683	17	17q	17qA3	17qA3.2	0	0	0	0	0	0
336	chr17:21829683-31434744	17	17q	17qA3	17qA3.3	-0.5000	-0.5400	-0.5600	-0.5100	-0.5200	-0.5300
337	chr17:31434744-40166617	17	17q	17qB1	17qB1	0	0	0	0.9400	0	0
338	chr17:40166617-41476398	17	17q	17qB2	17qB2	0	0	0	0	0	0
339	chr17:41476398-45842335	17	17q	17qB3	17qB3	0	0	0	0	0	0
340	chr17:45842335-55883989	17	17q	17qC	17qC	0	0	0	0	0	0
341	chr17:55883989-60249926	17	17q	17qD	17qD	0	0	0	0	0	0
342	chr17:60249926-68108612	17	17q	17qE1	17qE1.1	0	0	0	0	0	0
343	chr17:68108612-68981799	17	17q	17qE1	17qE1.2	0	0	0	0	0	0
344	chr17:68981799-73347736	17	17q	17qE1	17qE1.3	0	0	0	0	0	0
345	chr17:73347736-78586860	17	17q	17qE2	17qE2	0	0	0	0	0	0

346	chr17:78586860-82952797	17	17q	17qE3	17qE3	0	0	0	0	0	0
347	chr17:82952797-89065108	17	17q	17qE4	17qE4	0	0	0	0	0	0
348	chr17:89065108-95177420	17	17q	17qE5	17qE5	0	0	0	0	0	0
349	chr18:0-19413462	18	18q	18qA1	18qA1	0	0	0	0	0	0
350	chr18:19413462-29542226	18	18q	18qA2	18qA2	0	0	0	0	0	0
351	chr18:29542226-35450671	18	18q	18qB1	18qB1	0	0	0	0	0	0
352	chr18:35450671-37138798	18	18q	18qB2	18qB2	0	0	0	0	0	0
353	chr18:37138798-45579434	18	18q	18qB3	18qB3	0	0	0	0	0	0
354	chr18:45579434-49799752	18	18q	18qC	18qC	0	0	0	0	0	0
355	chr18:49799752-54020070	18	18q	18qD1	18qD1	0	0	0	0	-0.6200	0
356	chr18:54020070-54442102	18	18q	18qD2	18qD2	0	0	0	0	0	0
357	chr18:54442102-60772579	18	18q	18qD3	18qD3	0	0	0	0	0	0
358	chr18:60772579	18	18q	18qE	18qE1	0	0	0	0	0	0

	-67947119			1							
359	chr18:67947119-75121660	18	18q	18qE2	18qE2	0	0	0	0	0	0
360	chr18:75121660-83562296	18	18q	18qE3	18qE3	0	0	0	0	0	0
361	chr18:83562296-90736837	18	18q	18qE4	18qE4	0	0	0	0	0	0
362	chr19:0-16650124	19	19q	19qA	19qA	0	0	-0.9900	-0.9900	-0.7500	-0.5600
363	chr19:16650124-25584337	19	19q	19qB	19qB	0	0	0	0	0	0
364	chr19:25584337-34924651	19	19q	19qC1	19qC1	0	0	0	0	0	0
365	chr19:34924651-38173456	19	19q	19qC2	19qC2	0	0	0	0	0	0
366	chr19:38173456-47513769	19	19q	19qC3	19qC3	0.9800	0.9900	1.0100	1.0400	0	1.2500
367	chr19:47513769-51574775	19	19q	19qD1	19qD1	0	0	0	0	0	0
368	chr19:51574775-58884586	19	19q	19qD2	19qD2	0	0	0	0	-0.7300	0
369	chr19:58884586-61321190	19	19q	19qD3	19qD3	0	0	0	0	-0.4200	0

Supplementary table 1: Chromosomal aberrations defined with the following parameters:

ADM2 method for segmentation with threshold 6, Log2 ratio > 0.25, and numbers of probes ≥ 5.

Average values are provided for tumours derived from irradiated TGFα-treated astrocytes

growing as adherent cells (n=5) and from irradiated TGFa-treated astrocytes growing as floating cells (n=3).