Supplementary Table S5

Paired gene signature and signature specific Ki67 prognostic classifications for each patient of the Uppsala Cohort (0=Good, 1= Poor Prognosis)

Patient ID	GGI	70-gene	p53	RS*	Sorlie†	Hu[‡]	Parker[‡]	Ki11[§]	Ki12[§]	Ki13[§]	Ki15[§]	Ki16[§]	% Good Prognosis	% Poor Prognosis	Overall Prognostic Risk
100B08	0	0	0	1	0	0	0	0	0	0	0	0	92	8	Good
101B88	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor
102B06	1	1	1	1	0	1	1	1	1	1	1	1	8	92	Poor
103B41	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor
104B91	1	1	0	1	1	0	1	1	1	0	0	0	42	58	Poor
105B13	0	0	0	1	0	0	0	0	0	0	0	0	92	8	Good
106B55	0	0	0	1	0	0	0	1	1	1	1	0	58	42	Good
10B88	0	0	0	0	0	0	1	0	0	0	0	0	92	8	Good
111B51	1	1	1	1	1	1	1	1	1	1	1	0	8	92	Poor
112B55	0	0	0	0	0	1	1	1	1	1	1	1	42	58	Poor
113B11	1	1	0	1	1	1	1	1	1	1	1	1	8	92	Poor
114B68	0	1	0	0	0	0	1	0	0	0	0	0	83	17	Good
11B47	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
120B73	1	1	0	1	0	1	1	1	1	1	1	1	17	83	Poor
122B81	0	0	0	0	0	0	0	1	1	1	1	0	67	33	Good
124B25	0	0	0	1	0	0	0	0	0	0	0	0	92	8	Good
127B00	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
128B48	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
130B92	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
132B80	1	1	0	1	1	1	1	1	1	1	1	1	8	92	Poor
134B33	1	1	0	1	1	1	1	1	1	1	1	1	8	92	Poor
135B40	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
136B04	0	1	0	1	0	1	1	0	0	0	0	0	67	33	Good
137B88	0	0	1	1	0	1	1	0	0	0	0	0	67	33	Good

138B34	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
139B03	1	0	0	1	0	1	1	0	0	0	0	0	67	33	Good
13B79	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
140B91	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
142B05	1	1	1	1	0	1	1	1	1	1	1	1	8	92	Poor
143B81	1	1	1	1	0	1	1	1	1	1	0	0	25	75	Poor
144B49	0	0	0	1	0	0	1	1	1	1	1	1	42	58	Poor
145B10	1	1	1	1	1	0	1	1	1	1	1	1	8	92	Poor
146B39	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor
147B19	1	1	1	1	0	1	1	0	0	0	0	0	50	50	Equal
148B49	0	1	0	0	0	0	0	1	1	1	1	1	50	50	Equal
14B98	0	0	0	0	0	0	0	1	1	1	1	1	58	42	Good
150B81	0	0	0	1	0	1	1	1	1	1	0	0	50	50	Equal
151B84	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
152B99	0	0	0	1	0	0	1	0	0	0	0	0	83	17	Good
153B09	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor
154B42	1	1	0	1	1	1	1	1	1	1	1	1	8	92	Poor
155B52	0	0	0	1	0	0	0	0	0	0	0	0	92	8	Good
156B01	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
158B84	0	1	0	1	0	0	0	0	0	0	0	0	83	17	Good
159B47	1	1	0	1	0	1	1	1	1	1	1	0	25	75	Poor
15C94	0	0	0	0	0	0	0	1	1	1	1	1	58	42	Good
160B16	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
161B31	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
162B98	0	1	0	0	0	1	1	1	1	1	1	1	33	67	Poor
164B81	1	1	1	1	0	0	1	1	1	1	1	1	17	83	Poor
165B72	0	1	0	1	0	1	1	0	0	0	0	0	67	33	Good

166B79	0	0	0	0	0	1	1	0	0	0	0	0	83	17	Good
168B51	0	0	0	0	0	0	0	1	1	0	0	0	83	17	Good
169B79	0	0	0	1	0	0	1	0	0	0	0	0	83	17	Good
16C97	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
170B15	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
171B77	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
172B19	1	1	1	1	0	0	0	1	1	0	0	0	50	50	Equal
173B43	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
174B41	0	0	0	1	0	0	0	1	1	0	0	0	75	25	Good
175B72	0	1	0	1	0	0	1	0	0	0	0	0	75	25	Good
176B74	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
177B67	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
179B28	0	1	0	1	0	1	1	1	1	1	1	1	25	75	Poor
17C40	0	0	0	1	0	0	0	0	0	0	0	0	92	8	Good
180B38	0	1	0	0	0	0	0	0	0	0	0	0	92	8	Good
182B43	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor
183B75	0	1	0	1	0	1	1	1	1	1	1	1	25	75	Poor
184B38	0	0	0	1	0	0	0	0	0	0	0	0	92	8	Good
186B22	1	1	0	1	0	1	1	1	1	1	0	0	33	67	Poor
187B36	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
188B13	0	1	1	1	0	1	1	1	1	1	1	1	17	83	Poor
189B83	1	1	1	1	1	0	1	1	1	1	1	1	8	92	Poor
18C56	0	0	0	0	0	1	0	1	1	1	0	0	67	33	Good
191B79	1	1	0	1	1	1	1	0	0	0	0	0	50	50	Equal
192B69	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
193B72	0	1	1	1	0	0	1	1	1	1	1	1	25	75	Poor
195B75	0	0	0	0	0	0	1	0	0	0	0	0	92	8	Good

198B90	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
199B55	0	1	0	1	0	0	1	1	1	1	1	1	33	67	Poor
19C33	0	1	1	1	0	0	0	0	0	0	0	0	75	25	Good
200B47	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
201B68	0	0	0	1	1	0	0	0	0	0	0	0	83	17	Good
203B49	0	0	0	1	0	0	0	0	0	0	0	0	92	8	Good
204B85	0	0	0	0	-	0	0	0	0	0	0	0	100	0	Good
205B99	1	0	0	0	0	0	0	1	0	0	0	0	83	17	Good
206C05	0	0	0	0	0	1	1	1	1	1	0	0	58	42	Good
207C08	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
208C06	1	1	1	1	0	1	1	1	1	1	1	1	8	92	Poor
209C10	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
210C72	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
211C88	0	0	0	0	0	0	1	1	1	1	1	1	50	50	Equal
212C21	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
213C36	1	1	0	1	0	1	0	1	1	1	0	0	42	58	Poor
216C61	0	0	0	1	0	0	1	0	0	0	0	0	83	17	Good
217C79	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
218C29	0	0	0	0	0	0	1	0	0	0	0	0	92	8	Good
21C28	0	0	0	1	-	0	0	0	0	0	0	0	91	9	Good
220C70	0	0	0	1	0	0	0	0	0	0	0	0	92	8	Good
221C14	0	1	0	1	1	0	1	1	1	1	0	0	42	58	Poor
222C26	0	0	0	0	0	0	1	0	0	0	0	0	92	8	Good
223C51	0	0	0	1	0	0	0	0	0	0	0	0	92	8	Good
224C93	0	1	1	1	0	0	1	1	0	0	0	0	58	42	Good
225C52	1	1	0	1	1	1	1	1	1	1	1	1	8	92	Poor
226C06	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor

227C50	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
229C44	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
22C62	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
230C47	1	1	1	1	0	1	1	0	0	0	0	0	50	50	Equal
231C80	0	0	0	0	0	0	0	1	1	1	0	0	75	25	Good
232C58	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
233C91	0	0	0	0	0	0	0	1	1	1	0	0	75	25	Good
234C15	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor
235C20	1	1	0	1	0	0	1	0	0	0	0	0	67	33	Good
236C55	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
237C56	1	1	0	1	1	1	1	1	1	1	1	1	8	92	Poor
238C87	1	1	1	1	0	0	0	0	0	0	0	0	67	33	Good
239C32	0	1	0	1	0	0	0	1	1	1	1	1	42	58	Poor
23C52	1	1	0	1	1	1	1	1	1	1	1	1	8	92	Poor
240C54	1	1	1	1	-	0	1	1	1	1	1	1	9	91	Poor
241C01	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
242C21	1	1	0	0	0	1	0	1	1	1	1	1	33	67	Poor
243C70	0	0	0	1	-	0	0	0	0	0	0	0	91	9	Good
244C89	1	1	0	1	0	1	1	1	1	1	1	1	17	83	Poor
245C22	1	1	1	1	0	0	0	1	1	0	0	0	50	50	Equal
246C75	0	0	0	1	0	0	0	0	0	0	0	0	92	8	Good
247C76	0	0	0	0	0	1	0	0	0	0	0	0	92	8	Good
248C91	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
249C42	1	1	1	1	0	0	1	1	1	1	1	1	17	83	Poor
24C30	0	1	0	0	0	0	0	1	1	0	0	0	75	25	Good
250C78	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor
251C14	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good

252C64	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor
254C80	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
255C06	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
256C45	1	1	1	1	0	0	1	1	1	1	1	1	17	83	Poor
257C87	0	0	0	1	0	0	0	1	1	1	0	0	67	33	Good
258C21	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
259C74	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
260C91	0	1	1	1	0	0	1	1	1	1	1	1	25	75	Poor
261C94	0	0	0	1	0	0	0	0	0	0	0	0	92	8	Good
262C85	0	1	0	0	0	0	0	0	0	0	0	0	92	8	Good
263C82	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
265C40	1	1	0	0	0	1	1	1	1	0	0	0	50	50	Equal
266C51	0	0	0	1	0	0	0	0	0	0	0	0	92	8	Good
267C04	0	0	0	0	0	1	0	0	0	0	0	0	92	8	Good
268C87	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor
269C68	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor
26C23	0	1	1	1	0	0	0	1	1	1	1	1	33	67	Poor
270C93	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor
271C71	1	1	1	1	0	1	1	1	1	1	1	1	8	92	Poor
272C88	0	0	0	0	0	0	0	1	1	1	1	1	58	42	Good
274C81	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
275C70	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
277C64	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
278C80	0	1	1	1	0	0	1	1	1	1	1	1	25	75	Poor
279C61	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor
27C82	0	1	0	1	-	0	0	1	1	0	0	0	64	36	Good
282C51	0	0	0	1	0	0	0	0	0	0	0	0	92	8	Good

283C22	0	1	0	1	0	1	1	0	0	0	0	0	67	33	Good
284C63	0	0	0	1	0	0	0	0	0	0	0	0	92	8	Good
287C67	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor
289C75	0	0	0	0	0	0	0	1	1	0	0	0	83	17	Good
28C76	0	0	0	1	0	0	0	1	1	1	1	0	58	42	Good
290C91	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
296C95	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
297C26	0	0	0	1	0	0	0	0	0	0	0	0	92	8	Good
298C47	0	1	0	0	1	1	1	1	1	1	0	0	42	58	Poor
301C66	0	1	1	1	0	0	0	0	0	0	0	0	75	25	Good
303C36	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor
304C89	0	0	0	1	0	0	0	1	1	1	1	1	50	50	Equal
307C50	0	1	0	1	0	0	1	0	0	0	0	0	75	25	Good
308C93	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor
309C49	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor
311A27	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
313A87	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
314B55	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor
315C75	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
316C65	0	0	0	1	0	0	0	0	0	0	0	0	92	8	Good
33C30	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
34C80	0	0	0	1	0	0	0	0	0	0	0	0	92	8	Good
35C29	0	0	0	1	0	0	0	0	0	0	0	0	92	8	Good
36C17	0	0	0	1	-	0	0	0	0	0	0	0	91	9	Good
40C57	0	0	0	1	0	0	0	1	1	0	0	0	75	25	Good
41C65	0	1	0	1	-	0	1	0	0	0	0	0	73	27	Good
42C57	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good

43C47	0	1	0	0	0	0	0	1	0	0	0	0	83	17	Good
44A53	0	0	0	0	0	0	0	1	1	1	0	0	75	25	Good
45A96	0	0	0	0	0	1	1	0	0	0	0	0	83	17	Good
46A25	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
47A87	1	1	1	1	1	0	1	0	0	0	0	0	50	50	Equal
48A46	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
49A07	0	1	0	1	0	0	0	0	0	0	0	0	83	17	Good
50A91	0	1	0	1	1	0	0	1	1	1	1	1	33	67	Poor
51A98	1	0	0	1	0	1	0	0	0	0	0	0	75	25	Good
52A90	0	0	0	0	-	0	0	1	0	0	0	0	91	9	Good
53A06	1	1	0	1	1	1	1	1	1	1	1	1	8	92	Poor
54A09	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor
55A79	1	1	0	1	0	1	1	0	0	0	0	0	58	42	Good
56A94	0	1	0	1	0	0	0	0	0	0	0	0	83	17	Good
58A50	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
5B97	1	1	1	1	0	1	1	1	1	1	1	1	8	92	Poor
60A05	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
61A53	0	0	0	1	0	0	1	1	1	1	0	0	58	42	Good
62A02	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor
63A62	0	0	0	1	0	0	0	1	1	0	0	0	75	25	Good
64A59	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor
65A68	0	0	0	1	1	0	0	0	0	0	0	0	83	17	Good
66A84	1	1	1	1	1	1	1	1	1	0	0	0	25	75	Poor
67A43	1	1	1	1	1	0	1	1	1	1	1	1	8	92	Poor
69A93	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor
6B85	1	1	0	1	0	1	1	1	1	1	1	1	17	83	Poor
70A79	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor

72A92	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
73A01	0	1	1	1	0	1	1	1	1	1	1	1	17	83	Poor
74A63	0	0	0	1	0	0	0	0	0	0	0	0	92	8	Good
75A01	0	0	0	1	0	0	1	0	0	0	0	0	83	17	Good
76A44	1	1	0	1	0	1	1	1	1	1	1	1	17	83	Poor
77A50	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
79A35	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
7B96	0	1	1	1	0	1	1	1	1	1	1	1	17	83	Poor
82A83	1	0	1	1	1	0	1	1	1	1	1	1	17	83	Poor
83A37	0	0	NA	0	0	0	0	0	0	0	0	0	100	0	Good
84A44	1	0	0	0	0	0	1	1	1	1	1	0	50	50	Equal
85A03	1	1	0	1	1	1	1	0	0	0	0	0	50	50	Equal
86A40	1	1	1	1	0	0	0	1	1	1	1	1	25	75	Poor
88A67	0	0	0	1	1	1	1	1	1	1	1	1	25	75	Poor
89A64	1	1	NA	1	1	0	0	1	1	1	1	1	25	75	Poor
8B87	0	0	0	1	0	0	0	0	0	0	0	0	92	8	Good
94A16	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
96A21	0	0	0	0	0	0	0	1	1	1	0	0	75	25	Good
99A50	0	1	0	1	0	0	0	1	0	0	0	0	75	25	Good
9B52	0	1	0	1	1	1	1	0	0	0	0	0	58	42	Good

* High or intermediate recurrence score grouping; low as reference.

† Luminal B subtype grouping; others as reference.

‡ Luminal B or HER2 subtype grouping; others as reference.

§Note: Each Ki67 cutoff is paired to a gene signature. E.g. Tumour 104B91 has a Ki67 value of 12% as defined on a whole-tumour section by a trained pathologist. For the purposes of our analysis GGI is paired with a ROC defined Ki67 cutoff of 15% in the Uppsala dataset. Thus, for the GGI-Ki67 pairing, Ki67 designates this sample as good prognosis (as it is *less than* 15%). In contrast, the 70-gene signature is paired with a ROC defined Ki67 cutoff of 11%, meaning for the 70-gene/Ki67 pairing, Ki67 designates the same sample as poor prognosis (as it is *greater than* 11%).