Supplementary Table S13

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

Patient ID	GGI	70-gene	p53	RS*	Sorlie‡	Hu‡	Parker‡	Ki8§	Ki10§	Ki18§	Ki20§	Ki27§	Ki28§	% Good Prognosis	% Poor Prognosis	Overall Prognostic Risk
003Wi	1	1	0	1	0	1	1	1	1	0	0	0	0	46	54	Poor
005Jo	0	0	0	1	0	0	1	1	1	0	0	0	0	69	31	Good
014Er	1	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
018Gu	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
019Er	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
026Na	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
027Jo	0	1	0	1	1	1	1	1	1	0	0	0	0	46	54	Poor
028Ja	0	0	0	0	0	0	0	1	1	0	0	0	0	85	15	Good
031Er	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
035Si	0	0	0	0	0	0	0	1	1	0	0	0	0	85	15	Good
036Ar	1	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
040Th	1	1	0	1	1	1	1	1	1	1	1	1	1	8	92	Poor
041La	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
045Ol	1	1	1	1	1	1	1	1	1	0	0	0	0	31	69	Poor
052Za	1	1	0	1	1	1	1	1	1	0	0	0	0	38	62	Poor
055Sv	1	1	0	0	0	1	1	1	1	1	1	1	1	23	77	Poor
059Ho	0	1	0	1	-	0	0	1	1	0	0	0	0	69	31	Good
063Pe	0	1	0	0	0	0	1	1	1	0	0	0	0	69	31	Good
069Ek	1	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
071Av	1	1	0	1	0	1	1	1	1	1	1	1	1	15	85	Poor
072Te	1	1	0	1	0	1	1	1	1	1	1	1	1	15	85	Poor
076Er	0	0	0	0	0	0	1	1	1	0	0	0	0	77	23	Good
081Ul	0	1	0	1	0	0	0	1	1	0	0	0	0	69	31	Good
085Ry	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good

086Li	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
087Bu	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
089Ho	1	1	0	1	0	1	1	1	1	0	0	0	0	46	54	Poor
092No	0	1	0	0	0	0	0	0	0	0	0	0	0	92	8	Good
101Gl	0	0	0	0	0	0	1	1	1	1	1	0	0	62	38	Good
112Fr	0	0	0	0	0	0	0	1	1	1	1	0	0	69	31	Good
113So	1	1	1	1	1	1	1	0	0	0	0	0	0	46	54	Poor
117Ko	1	1	0	1	1	1	1	1	0	0	0	0	0	46	54	Poor
121Le	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
123Er	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
125Wa	1	0	0	1	1	1	1	0	0	0	0	0	0	62	38	Good
126As	0	0	0	0	0	0	0	1	1	0	0	0	0	85	15	Good
128Sa	1	1	1	1	1	1	1	0	0	0	0	0	0	46	54	Poor
132Vi	0	0	0	0	0	0	0	1	1	1	1	1	1	54	46	Good
136Er	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
142Sw	1	0	0	1	0	1	1	1	1	1	1	1	0	31	69	Poor
146Ho	0	0	0	1	-	0	0	0	0	0	0	0	0	92	8	Good
157Ha	0	0	0	0	0	0	0	1	1	0	0	0	0	85	15	Good
158Ku	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
160Lu	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
161Jo	1	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
164My	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
165An	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
166Jo	1	1	1	1	1	1	1	1	0	0	0	0	0	38	62	Poor
170Fa	1	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
171So	1	1	0	1	0	1	1	1	1	1	0	0	0	38	62	Poor
172Sa	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good

174He	0	1	0	1	0	0	0	1	0	0	0	0	0	77	23	Good
176Th	0	1	1	1	1	0	0	0	0	0	0	0	0	69	31	Good
178Wa	0	0	0	0	0	0	0	1	0	0	0	0	0	92	8	Good
183An	1	1	1	1	1	1	1	0	0	0	0	0	0	46	54	Poor
185Ny	1	1	0	1	1	1	1	1	1	1	1	1	0	15	85	Poor
187Ol	1	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
188Ah	1	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
192La	1	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
196Sa	0	0	0	1	0	0	0	1	1	1	1	1	1	46	54	Poor
199Po	0	0	0	0	0	0	0	1	1	1	1	1	1	54	46	Good
202Ni	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
204Fa	0	0	0	0	-	0	0	1	1	0	0	0	0	85	15	Good
206Ri	0	0	0	0	0	0	0	1	1	1	0	0	0	77	23	Good
211Wa	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
215He	0	1	0	1	0	1	0	0	0	0	0	0	0	77	23	Good
216An	1	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
218Be	0	0	0	1	0	0	0	1	0	0	0	0	0	85	15	Good
219Wo	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
221Lu	1	1	0	1	1	1	1	1	1	0	0	0	0	38	62	Poor
223Li	1	1	0	1	0	1	1	0	0	0	0	0	0	62	38	Good
229La	0	0	0	0	-	0	0	0	0	0	0	0	0	100	0	Good
231Ca	0	0	0	1	0	0	0	0	0	0	0	0	0	92	8	Good
240Sm	0	0	0	0	-	0	0	0	0	0	0	0	0	100	0	Good
243Be	0	0	0	0	-	0	0	1	1	1	1	0	0	69	31	Good
246Ta	1	1	0	1	0	1	1	1	0	0	0	0	0	54	46	Good
249Lu	0	1	0	0	0	0	0	1	0	0	0	0	0	85	15	Good
258Ve	1	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor

260Li	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
261En	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
262Sp	0	1	0	1	1	0	1	1	1	0	0	0	0	54	46	Good
264La	0	0	0	0	0	0	0	1	1	1	1	0	0	69	31	Good
268Ar	0	0	0	0	0	0	1	1	1	0	0	0	0	77	23	Good
275We	1	1	0	1	1	1	1	1	1	1	1	1	1	8	92	Poor
276Ek	1	0	0	0	0	0	1	0	0	0	0	0	0	85	15	Good
281Br	0	0	0	0	0	0	0	1	1	1	1	1	0	62	38	Good
282Wi	1	0	0	0	0	0	1	1	1	1	0	0	0	62	38	Good
283An	0	0	0	1	-	0	0	1	1	1	1	0	0	62	38	Good
284Je	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
285Fl	0	1	0	0	0	0	1	1	1	1	1	0	0	54	46	Good
296Ny	1	1	1	1	-	1	1	1	1	1	1	1	1	8	92	Poor
297Pe	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
298La	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
307Eg	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
309Ev	0	0	0	1	0	0	0	0	0	0	0	0	0	92	8	Good
310Wi	0	0	0	0	0	0	0	1	1	0	0	0	0	85	15	Good
318Ki	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
319An	1	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
327En	1	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
331Ha	1	1	0	1	0	1	1	1	0	0	0	0	0	54	46	Good
333Si	0	0	0	0	-	0	0	1	1	0	0	0	0	85	15	Good
336Mo	1	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
342Bl	1	1	0	1	1	0	1	1	1	1	1	0	0	31	69	Poor
345Vi	0	1	0	0	0	0	0	1	1	0	0	0	0	77	23	Good
347Ja	1	1	1	1	1	1	1	1	1	0	0	0	0	31	69	Poor

351Ol	1	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
352An	0	1	0	0	0	0	0	1	1	1	1	1	1	46	54	Poor
356Al	1	1	1	1	1	1	1	1	1	0	0	0	0	31	69	Poor
365Ma	1	1	0	1	1	1	1	0	0	0	0	0	0	54	46	Good
372Lu	1	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
373Li	1	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor
379Ba	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	Good
382Gu	1	1	1	1	1	1	1	1	1	1	1	1	1	0	100	Poor

* High recurrence score grouping; others as reference.

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

§Note: Each Ki67 cutoff is paired to a gene signature. E.g. Tumour 003Wi has a Ki67 value of 14% 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 18% in the Stockholm dataset. Thus, for the GGI-Ki67 pairing, Ki67 designates this sample as good prognosis (as it is *less than* 18%). In contrast, the 70-gene signature is paired with a ROC defined Ki67 cutoff of 8%, meaning for the 70-gene/Ki67 pairing, Ki67 designates the same sample as poor prognosis (as it is *greater than* 8%).