

Web Table F: Recurrence prediction results of 39 gene cross-validation loops.

Group	Patient	Tumour (date)	Prediction	Error	Prediction strength
A	968-1	Ta gr2	0		0.19
A	928-1	Ta gr2	0		0.49
A	934-1	Ta gr2 (220798)	0		1.73
A	709-1	Ta gr2 (210798)	0		0.45
A	930-1	Ta gr2 (300698)	0		0.82
A	524-1	Ta gr2 (201095)	0		0.14
A	455-1	Ta gr2 (060695)	1	*	0.68
A	370-1	Ta gr2 (100195)	0		0.32
A	810-1	Ta gr2 (031097)	0		0.45
A	1146-1	Ta gr2 (231199)	0		0.98
A	1161-1	Ta gr2 (101299)	0		0.03
A	1006-1	Ta gr2 (231198)	1	*	1.57
A	942-1	Ta gr2	0		0.31
A	1060-1	Ta gr2	1	*	0.81
A	1255-1	Ta gr2	1	*	0.71
B	441-1	Ta gr2	1		1.03
B	780-1	Ta gr2	1		0.37
B	815-2	Ta gr2	1		0.35
B	829-1	Ta gr2	1		0.75
B	861-1	Ta gr2	0	*	2.55
B	925-1	Ta gr2	1		0.78
B	1008-1	Ta gr2	0	*	0.12
B	1086-1	Ta gr2	0	*	0.51
B	1105-1	Ta gr2	1		0.37
B	1145-1	Ta gr2	1		0.44
B	1327-1	Ta gr2	1		1.96
B	1352-1	Ta gr2	0	*	0.97
B	1379-1	Ta gr2	1		0.67
B	533-1	Ta gr2	1		0.31
B	679-1	Ta gr2	1		0.82
B	692-1	Ta gr2	1		0.45

Group A: Primary tumours from patients with no recurrence of the disease for 2 years.

Group B: Primary tumours from patients with recurrence of the disease within 8 months.

Prediction: 0=no recurrence, 1=recurrence.

Prediction strength: The relative difference between the distance to the closest and the second closest group compared to the distance to the closest group.