

**Table 3.** Cox regression analysis for breast cancer death for patients with gene expression data (n=69-77)

	(a) Univariate analysis			(b) Multivariate analysis		
	<i>RR</i>	<i>95% CI</i>	<i>P</i>	<i>RR</i>	<i>95% CI</i>	<i>P</i>
Age, $\geq 55$ years vs $< 55$ years	1.22	0.52-2.84	0.65			
Tumor type (overall effect)			0.32			
Lobular (vs ductal)	0.65	0.28-1.51	0.31			
Other (vs ductal)	0.34	0.05-2.53	0.29			
Tumor size (overall effect)			0.014			
T2 (vs size T1)	2.63	0.88-7.86	0.085			
T3-T4 (vs size T1)	5.27	1.61-17.2	0.006			
Lymph node status (overall effect)			0.016			0.004
pN1 (vs pN0)	0.45	0.16-1.26	0.13	0.47	0.17-1.33	0.15
pN2-pN3 (vs pN0)	2.41	0.95-6.08	0.064	3.42	1.29-9.05	0.013
Other* (vs pN0)	2.12	0.75-5.98	0.16	2.70	0.93-7.78	0.067
Histological grade (overall effect)			0.68			
G2 (vs G1)	2.20	0.30-16.3	0.44			
G3 (vs G1)	2.07	0.25-16.8	0.50			
TP53, mutation (vs wild type)	3.46	1.66-7.21	0.002	4.43	2.04-9.64	0.0004
ER, positive (vs negative)	0.75	0.35-1.63	0.48			
PR, positive (vs negative)	0.71	0.33-1.51	0.38			
Gene expression (overall effect)			0.006			
Highly prolif. lum. (vs Luminal A)	6.59	1.79-24.3	0.005			
Normal like (vs LuminalA)	2.82	0.71-11.3	0.14			
Basal like (vs Luminal A)	6.93	1.79-26.8	0.005			
ERRB2 <sup>+</sup> (vs Luminal A)	5.82	1.30-26.2	0.022			

\*Lymph nodes not removed