

Characteristic	HER2-negative (n=5)	HER2-ultralow (n=3)	HER2-low (n=39)	HER2-positive (n=5)	p-value
Grade					0.530
G1	0 (0%)	0 (0%)	3 (7.7%)	0 (0%)	
G2	2 (40%)	2 (66.7%)	17 (43.6%)	0 (0%)	
G3	3 (60%)	1 (33.3%)	18 (46.2%)	5 (100%)	
ER positive, n (%)	5 (100%)	3 (100%)	39 (100%)	4 (80%)	0.250
Nodal status					0.616
Positive	3 (60%)	0 (0%)	16 (41.0%)	1 (20%)	
Negative	2 (40%)	2 (66.7%)	17 (43.6%)	3 (60%)	
Unknown	0 (0%)	1 (33.3%)	6 (15.4%)	1 (20%)	
OS event, n (%)	1 (20%)	0 (0%)	5 (12.8%)	0 (0%)	0.840
Genetic variant					0.506
Yes	1 (20%)	1 (33.3%)	4 (10.3%)	0 (0%)	
No	0 (0%)	1 (33.3%)	11 (28.2%)	1 (20%)	
Unknown	4 (80%)	1 (33.3%)	24 (61.5%)	4 (80%)	
Age, median (Q1–Q3)	76 (60.5–79.5)	81 (71–NA)	61 (55.8–72.5)	66 (55–74.5)	0.207
Ki67, median (Q1–Q3)	40 (25–50)	30 (30–NA)	32.5 (20–50)	30 (24.5–55)	0.897

Table S1 - Association between HER2 expression categories and clinicopathological characteristics.

Categorical variables were analyzed using the Fisher–Freeman–Halton exact test. Continuous variables were analyzed using the Kruskal–Wallis test. Q1–Q3: interquartile range.

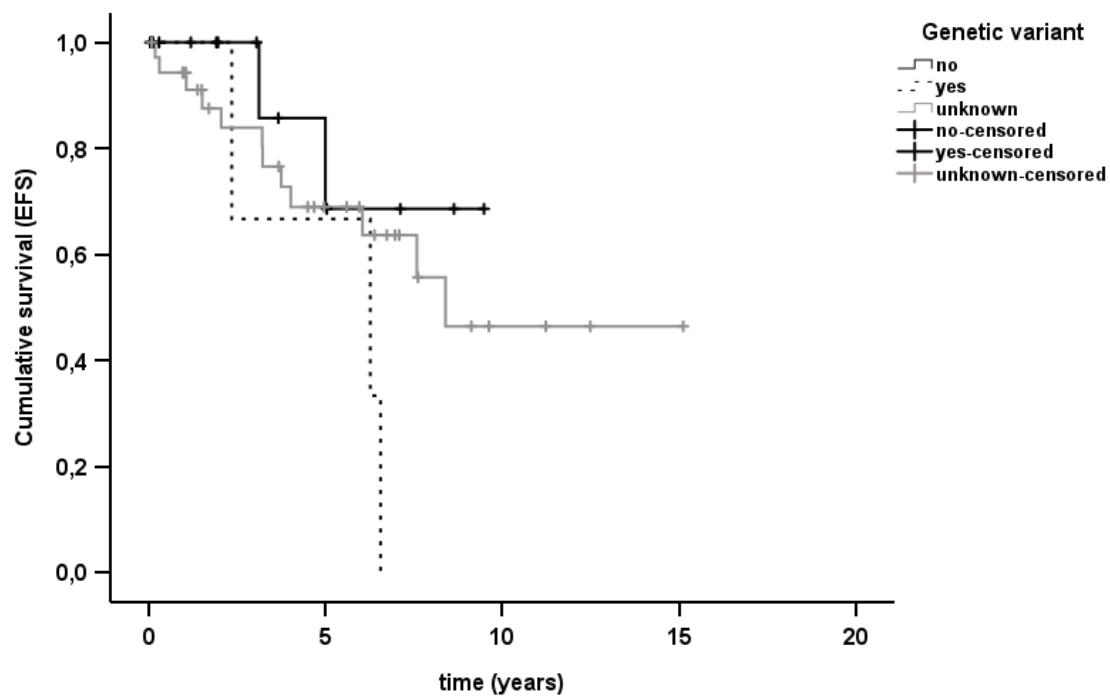


Figure S1 - Association between genetic variation and event-free survival (EFS) over time.

Y-axis shows percentage of total. No statistically significant differences in survival by genetic variant status were found within the study cohort (log-rank test, $p = 0.691$).