Figure S1 Study flowchart. NGS, next-generation sequencing; FFPE, formalin-fixed paraffin-embedded; ctDNA, circulating tumor DNA; EMR, electronic medical records.
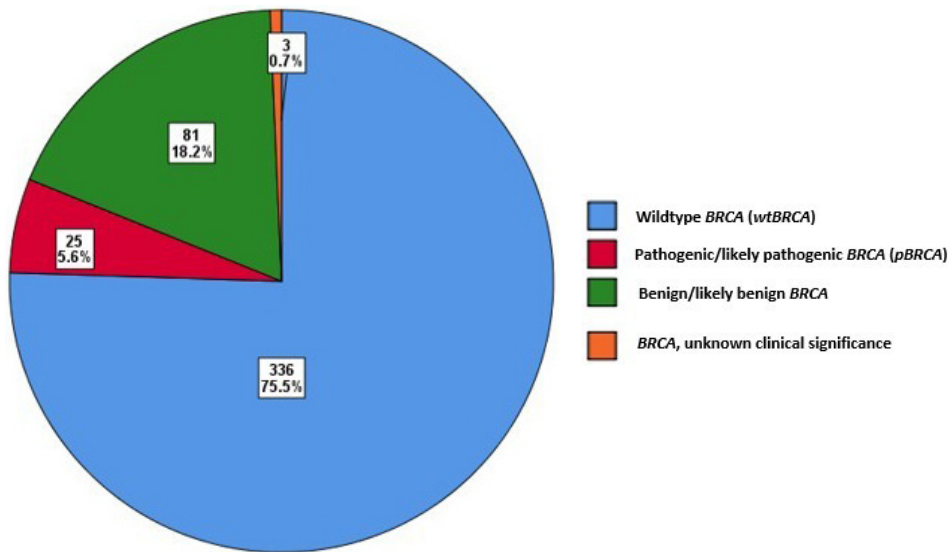
Figure S2 Patient distribution by tumor BRCA status. wtBRCA, wild-type BRCA; pBRCA, pathogenic/likely-pathogenic BRCA.
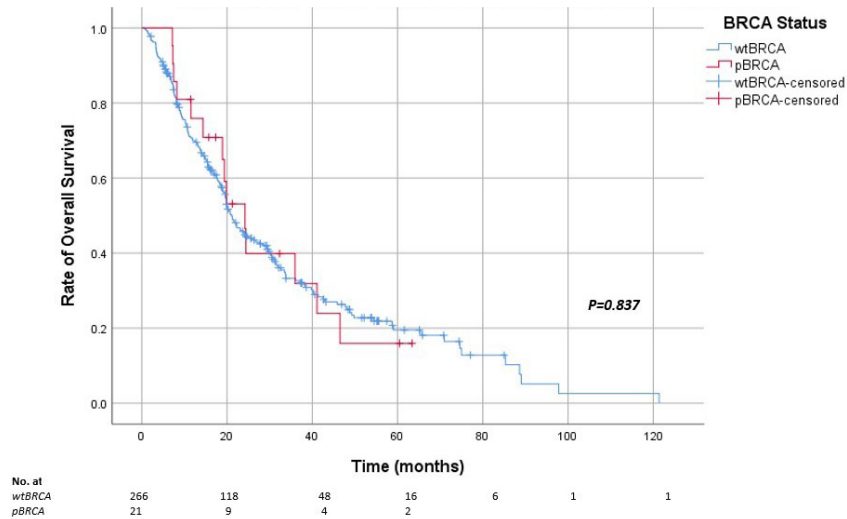

Figure S3 Overall survival from diagnosis of advanced disease. wtBRCA, wild-type BRCA; pBRCA, pathogenic/likely-pathogenic BRCA.

Table S1 Previously reported incidences of BRCA mutations in lung cancer patients

Study	Sample	Benign/likely benign/unknown clinical significance *BRCA*	Pathogenic *BRCA*
Variants identified in tumor tissue			
Remon 2020 (SAFIR02-Lung Trial)	n=379	n=12 (3.2%)	n=8 (2.1%)
Jordan 2017	n=860	Not reported	n=11 (1.3%)
Variants confirmed as germline			
Remon 2020 (SAFIR02-Lung Trial)	n=379	n=6 (1.6%)	n=2 (0.5%)
Kadouri 2019	n=248	n=1 (0.4%), BRCA1 Exon 6 delCTTT	n=12 (4.8%); BRCA1 185delAG PATH X2, BRCA1 5382insC PATH X2, BRCA2 6174delT PATH X7, BRCA2 IVS2+G>A PATH X
Tian 2020	n=1764	Not reported	n=20 (1.1%)
Hu 2019	n=6,220	Not reported	n=64 (1.03%)