Supplementary Material For:

Comparison of gene expression profiling by reverse transcription quantitative PCR between fresh frozen and formalin-fixed, paraffin embedded breast cancer tissues

Iker Sánchez-Navarro1*, Angelo Gámez-Pozo1*, Manuel González-Barón2, Álvaro Pinto-Marin3, David Hardisson3, Rocío López1, Rosario Madero4, Paloma Cejas1, Marta Mendiola1,3, Enrique Espinosa2, and Juan Ángel Fresno Vara1

1Laboratory of Molecular Pathology and Oncology, Research Unit, Hospital Universitario La Paz, Madrid, Spain, 2Department of Medical Oncology, Hospital Universitario La Paz, Madrid, Spain, 3Department of Pathology, Hospital Universitario La Paz, Madrid, Spain, and 4Biostatistics Unit, Hospital Universitario La Paz, Madrid, Spain


Keywords: breast cancer; gene expression profiling; RT-qPCR; FFPE; normalization; biomarkers

*I.S.-N. and A.G.-P. contributed equally to this work.

Supplementary Figure S1. Size distribution of FFPE RNA from tumor specimens. Total RNA extracted from breast cancer specimens was analyzed by capillary electrophoresis using an Agilent 2100 Bioanalyzer. RNA from a representative frozen breast tumor is also shown. The RNA from FFPE tissues is degraded and does not have detectable 28S and 18S ribosomal bands, as compared with FF-derived RNA.