Online Resource 9 Discrepancies in predictions of hormone receptor status and *ERBB2* status determined from microarray and RT-qPCR, and from microarray and IHC

	No. of samples			microarray positive, RT-qPCR/ IHC negative		microarray negative, RT-qPCR/ IHC positive	
Validation set 1	**N** (total)	**N** (discrepant)	**%** (of total)	**N**	**%** (of total)	**N**	**%** (of total)
microarray *vs.* RT-qPCR							
ERBB2	133	11	8	7	5	4	3
ESR1	127	11	9	8	6	3	2
PGR	66	12	18	3	5	9	14
microarray *vs.* IHC							
ERBB2	133	9	7	4	3	5	4
ESR1	133	5	4	4	3	1	1
PGR	87	15	17	4	5	11	13

ESR1: estrogen receptor α, *ERBB2*: human epidermal growth factor receptor 2, *PGR*: progesterone receptor

Number of discrepant samples between predictions of hormone- and *ERBB2* status from fresh frozen tissue, analyzed using microarray, and RT-qPCR from a corresponding whole slide, paraffin embedded section and IHC, respectively, for validation set 1 (total of 133 samples)

Reliable PCR quantitation of estrogen-, progesterone and ERBB2 receptor mRNA from formalin-fixed, paraffin-embedded tissue is independent of prior macro-dissection. Trine Tramm, Guido Hennig, Marianne Kyndi, Jan Alsner, Flemming Brandt Sørensen, Simen Myhre, Therese Sørlie, Jens Overgaard

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