595 eligible patients included in the clinical trial

FFPE tissue samples available:
\[ n = 367 \text{ (62\% of the patients)} \]

Insufficient tumor tissue on sections

At least one value for HER2 or TOP2A available:
\[ n = 352 \text{ (96\% of the FFPE blocks)} \]

Template abundance, method eligibility criteria

CISH analysis
- HER2: \( n = 285 \) (81%)
- TOP2A: \( n = 266 \) (76%)
- HER2/TOP2A: \( n = 266 \) (76%)

qRT-PCR (mRNA expression)
- HER2: \( n = 314 \) (89%)
- TOP2A: \( n = 314 \) (89%)
- HER2/TOP2A: \( n = 314 \) (89%)

IHC analysis
- HER2: \( n = 297 \) (84%)
- TopoIIa: \( n = 273 \) (78%)
- HER2/TopoIIa: \( n = 269 \) (76%)

Profiled HER2 variables
- HER2 CISH/mRNA: \( n = 249 \) (70%)
- HER2 CISH/IHC: \( n = 278 \) (79%)
- HER2 mRNA/IHC: \( n = 261 \) (74%)
- HER2, all: \( n = 243 \) (69%)

Profiled TOP2A variables
- TOP2A CISH/mRNA: \( n = 232 \) (66%)
- TOP2A CISH/IHC: \( n = 249 \) (70%)
- TOP2A mRNA/IHC: \( n = 240 \) (68%)
- TOP2A, all: \( n = 217 \) (62%)