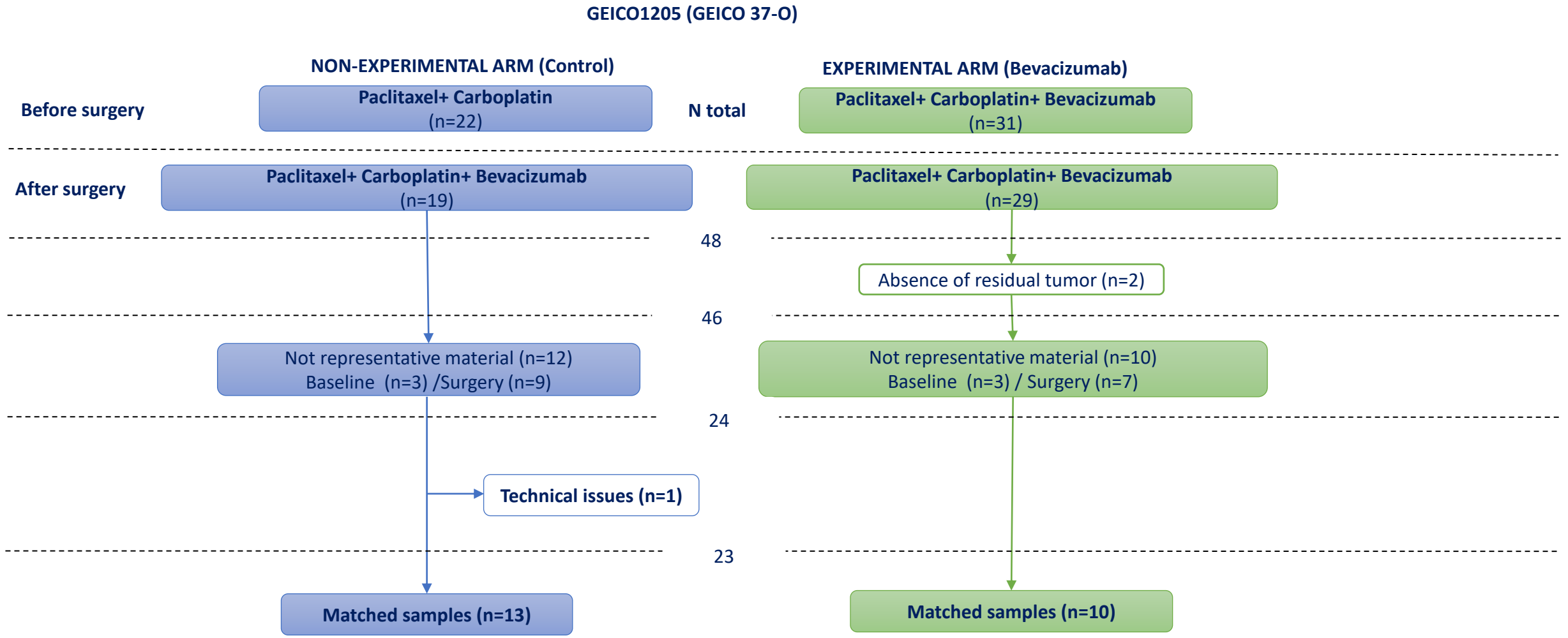

Supplementary Figure 1: Sample selection workflow for MINOVA study from GEICO-1205 clinical trial.

From the initial set of patients included in GEICO-1205 (n=71), a total number of 23 matched samples (13 patients in the control arm/ 10 patients in the bevacizumab arm, total n =46) from primary (ovary) or metastasic sites (e.g., peritoneum, omentum) were finally available for the study. From this initial cohort, 3 patients were excluded for ineligible tumors (n= 68). In the control group (chemotherapy alone) 22 patients underwent surgery meanwhile 31 individuals were included in the bevacizumab group (chemotherapy+ bevacizumab). After surgery, 19 from the control group and 29 from the bevacizumab group started adjuvant therapy, being this population our starting cohort for this translational study (n=48). From this cohort of 48 patients, only 2 individuals belonging to the bevacizumab group have been reported as having an "absence of residual tumor" in the clinical files (n=46). For the rest of the samples, the Department of Pathological Anatomy indicated that in 22 patients "there was no representative material" meaning the sample was not collected either at baseline (n=6) or post-surgery (n=16). The original cohort was reduced to 24 paired samples. Due to technical reasons (quality of the sample), 1 sample from the chemotherapy group was excluded (n=23). The samples remaining were paired by the patient but not by tumor site.