The impact of whole genome and transcriptome analysis (WGTA) on predictive biomarker discovery and diagnostic accuracy of advanced malignancies

B Tessier-Cloutier, JK Grewal *et al*. *J Pathol Clin Res* DOI: 10.1002/cjp2.265

Supplementary Figures

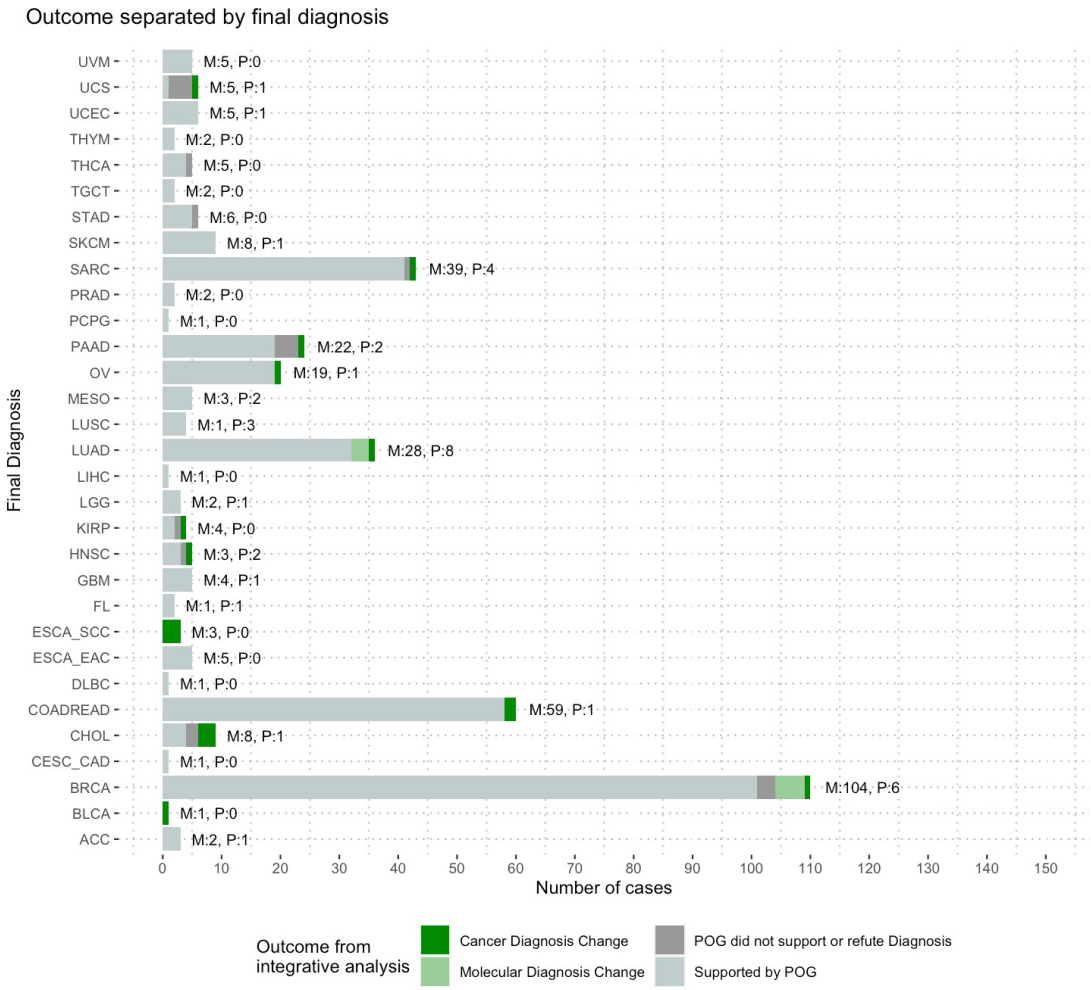

Figure S1. Impact of cancer type on the ability of an automated RNA-Seq based classifier (SCOPE) to provide the correct putative diagnosis in the POG cohort. The outcomes are shown separated by cancer type. M and P indicate the number of metastatic and primary/relapse samples respectively.

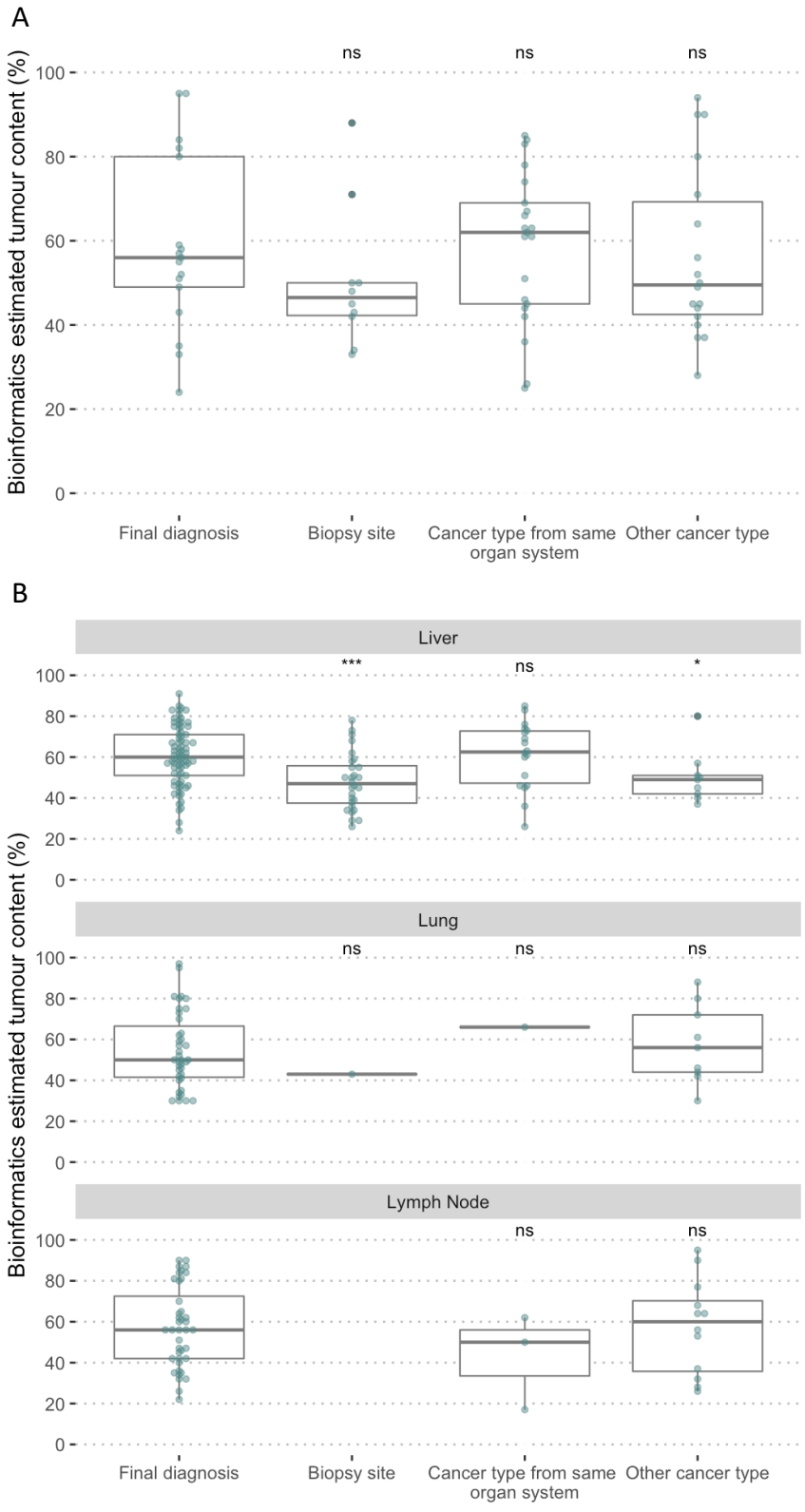

Figure S2. Impact of tumor content on the ability of an automated RNA-Seq based diagnostic (SCOPE) to provide the correct putative diagnosis in the POG cohort; (A) agnostic of tumor site and (B) from the main 3 most common biopsy sites. Wilcox test for significance between SCOPE outcome matching final diagnosis, versus each of the other categories: * p =< 0.05; ** p =< 0.01; *** p =< 0.001; ns p > 0.05.