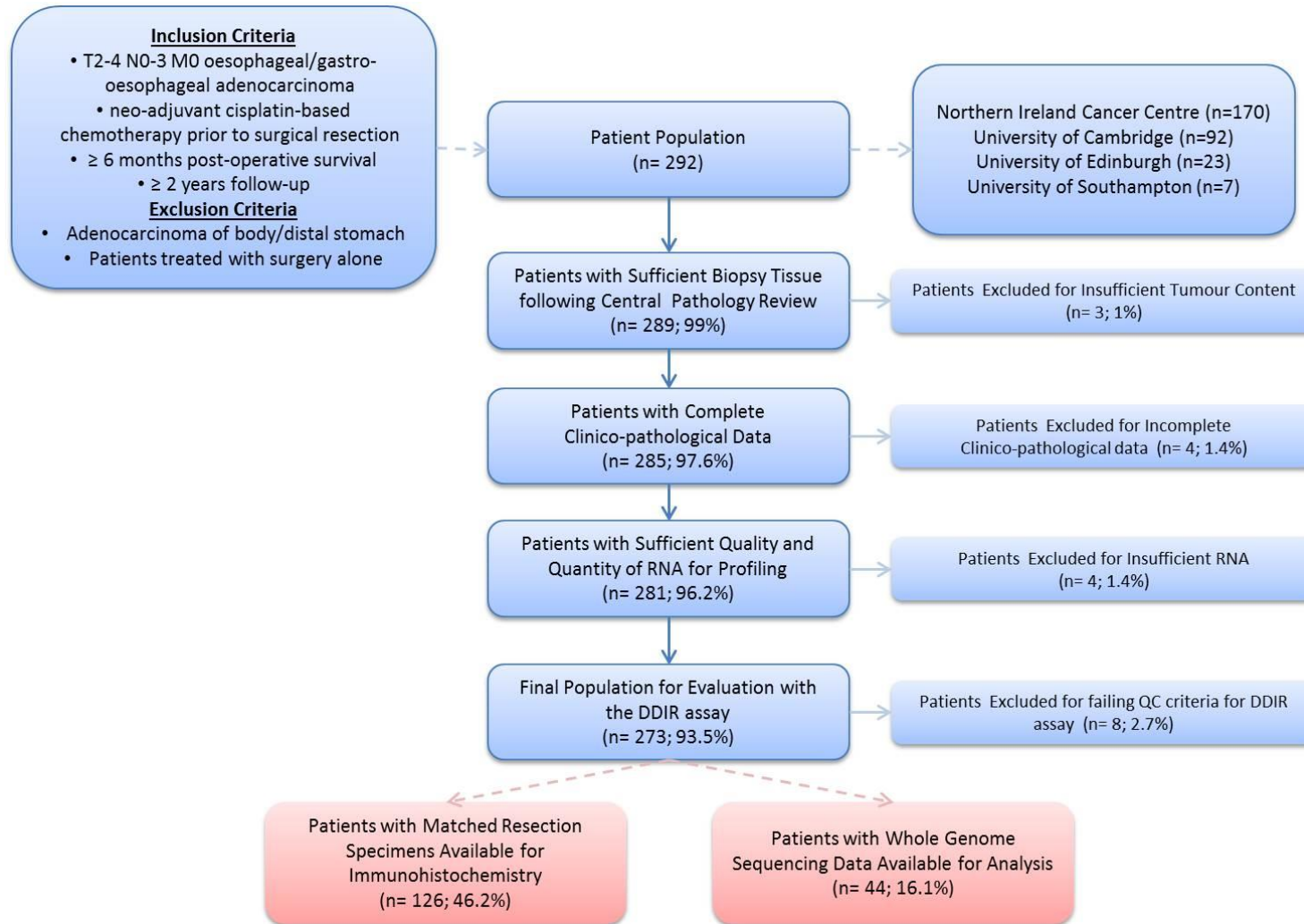
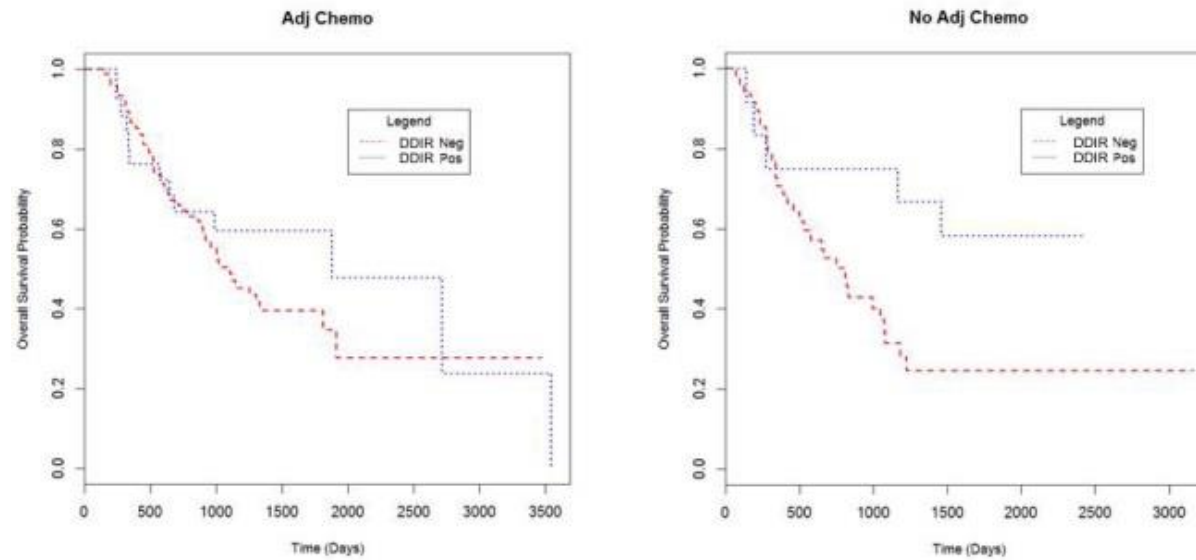


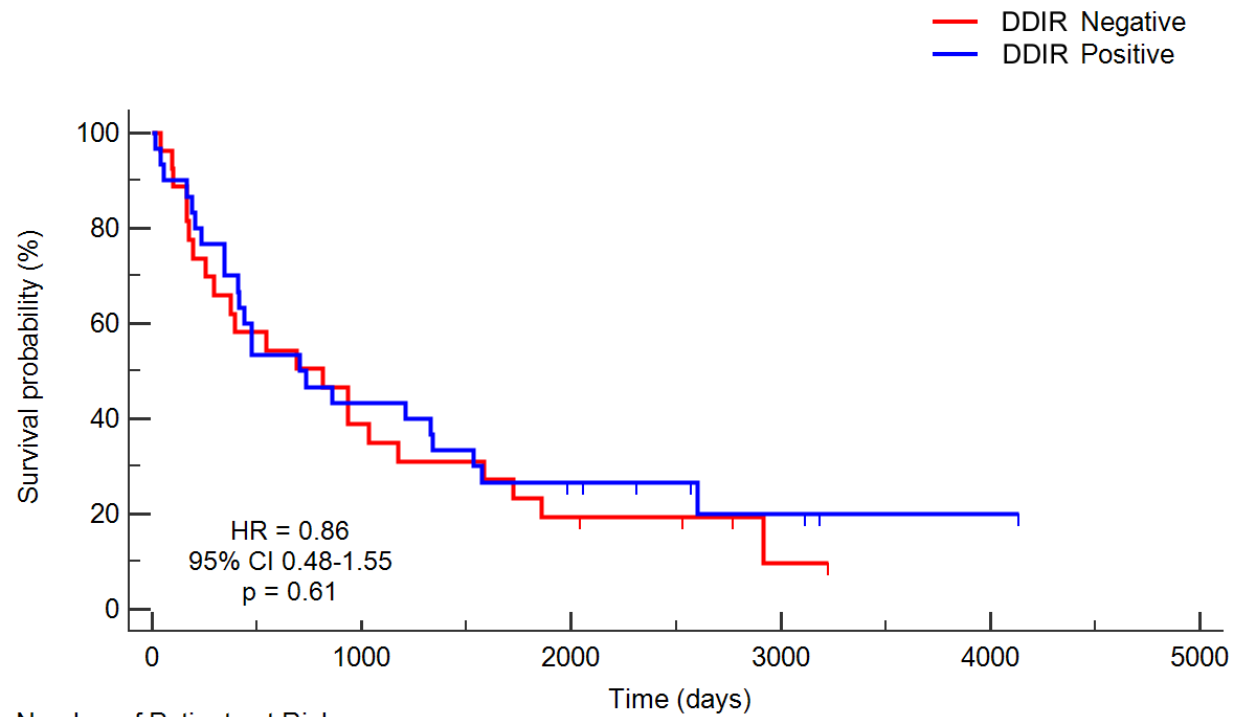
Supplementary Figures



Supplementary Figure 1- REMARK diagram

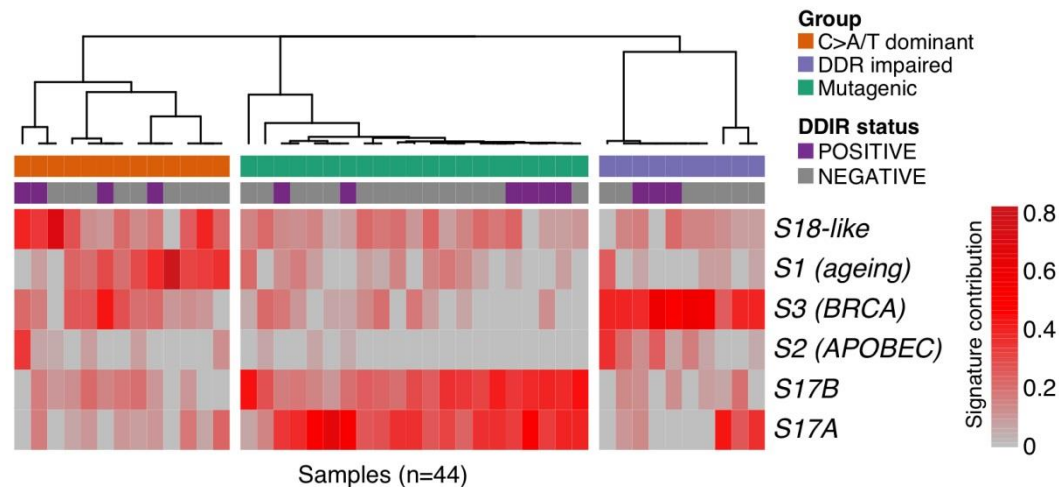


Supplementary Figure 2: Kaplan-Meier curves stratified by the DNA Damage Immune Response (DDIR) assay for overall survival for 101 OAC patients treated with adjuvant chemotherapy following surgical resection and 60 OAC patients who did not receive further chemotherapy following surgical resection.

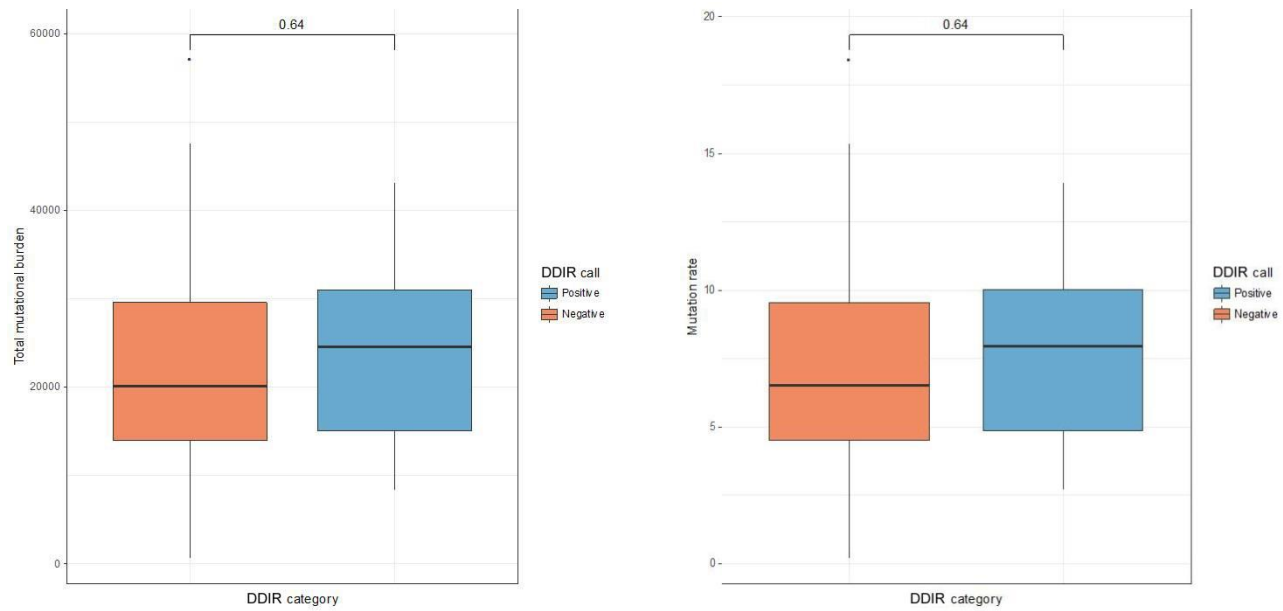


Number of Patients at Risk					
	0	1000	2000	3000	4000
DDIR Negative	27	10	5	1	0
DDIR Positive	30	13	7	3	1

Supplementary Figure 3: Kaplan-Meier curves stratified by the DNA Damage Immune Response (DDIR) assay for overall survival for 57 oesophageal adenocarcinoma patients treated with surgical resection alone.



Supplementary Figure 4: Mutational signature-based clustering of 44 OAC patients analysed by whole genome sequencing. The strength of the exposure to each mutational process associated with distinct risk factors of cancer (0-100%) was calculated using the non-negative matrix factorization (NMF) methodology and hierarchical clustering was used to group the samples based on their mutational signature profiles. Samples were assigned to one of three subgroups reported in Secier, Li et al, Nat Genet 2016 based on the dominant mutational process in the respective genome as follows: C>A/T dominant (S18-like/S1-ageing; 30%), DDR Impaired (S3-BRCA; 23%) and Mutagenic (S17A/B; 47%). For cases where more than one tumour sample had been whole-genome sequenced, the sample with the highest tumour purity (estimated by ASCAT) was used in the analysis. DDIR status is annotated for each sample.



Supplementary Figure 5: Boxplots of (A) Tumour Mutational Burden and (B) Mutational Rate grouped by DDIR status