Supplementary material has been published as submitted. It has not been copyedited, or typeset by Acta Oncologica

SUPPLEMENTAL FIGURE 1: ASSOCIATION OF NER AND IMDC RISK GROUPS. COMPARISON AND P-VALUE AS CALCULATED BY ANOVA.







- -- IMDC poor NER<median (<33.8): mOS 20 mo
- --- IMDC poor NER>median (>33.8): mOS 10 mo



PFS (%) all patients







PFS (%) all patients



SUPPLEMENTAL FIGURE 7: PANEL A-C: KAPLAN-MEIER ESTIMATES OF THE IMPACT OF NER, NLR AND EOSINOPHILS ON DISEASE-FREE SURVIVAL POST-NEPHRECTOMY

a Metastasis-free survival after initial diagnosis (%)



C Metastasis-free survival after initial diagnosis (%)



b Metastasis-free survival after initial diagnosis (%)





SUPPLEMENTAL FIGURE 9: PANEL A-B: KAPLAN-MEIER ESTIMATES OF THE IMPACT OF EOSINOPHILS ON PROGRESSION-FREE SURVIVAL AND OVERALL SURVIVAL IN ALL PATIENTS TREATED WITH VEGFR-TKIS



а

b OS (%) on 1st line VEGFR-TKIs



SUPPLEMENTAL FIGURE 10: PANEL A-B: KAPLAN MEIER ESTIMATES OF PFS AND OS BASED ON NER AT WEEK 6. PANEL C-D: KAPLAN MEIER ESTIMATES OF PFS AND OS BASED ON EOSINOPHIL COUNT AT WEEK 6.

a PFS (%) all patients (NER at week 6)



b OS (%) all patients (NER at week 6)



C PFS (%) all patients (EOSINOs at week 6)



d OS (%) all patients (EOSINOs at week 6)



SUPPLEMENTAL FIGURE 11: Transcriptomic correlates of baseline eosinophil counts. PANEL A, Dotplot showing correlation coefficient and p values of spearman correlation between baseline eosinophil count and tumour immune cell estimates (CIBERSORTx). PANEL B: Dotplot showing correlation coefficient and p values of spearman correlation between baseline eosinophil count and PD-L1 (by *CD274* expression), tLHP and Javelin101 and IMmotion150 gene signatures. PANEL C: GSEA leveraging Hallmark gene sets, comparing patients with high vs. low eosinophil count (by median, also for panels D-F). PANEL D, GSEA leveraging Reactome gene sets. PANEL E, GSEA leveraging Gene Ontology BP gene sets. PANEL F, GSEA leveraging ImmuneSigDB gene sets. For panels D-F, only top 25 gene sets enriched in high eosinophil count and top 25 enriched in low eosinophil count are shown. NES: normalized enrichment score.



SUPPLEMENTAL FIGURE 12: Gene set enrichment analysis (GSEA) comparing NER^{HIGH} vs. NER^{LOW} groups

(dichotomized by median). PANEL A, GSEA leveraging Hallmark gene sets. PANEL B, GSEA leveraging Reactome gene sets. PANEL C, GSEA leveraging Gene Ontology BP gene sets. PANEL D, GSEA leveraging ImmuneSigDB gene sets. For b-d, only top 25 gene sets enriched in NER^{HIGH} and top 25 enriched in NER^{LOW} are shown. NES: normalized enrichment score.



SUPPLEMENTAL FIGURE 13: Gene set enrichment analysis (GSEA) comparing NLR^{HIGH} vs. NLR^{LOW} groups

<u>(dichotomized by median)</u>. PANEL A, GSEA leveraging Hallmark gene sets. PANEL B, GSEA leveraging Reactome gene sets. PANEL C, GSEA leveraging Gene Ontology BP gene sets. PANEL D, GSEA leveraging ImmuneSigDB gene sets. For b-d, only top 25 gene sets enriched in NLR^{HIGH} and top 25 enriched in NLR^{LOW} are shown. NES: normalized enrichment score.

