

Supplementary Materials: Value of Combined PET Imaging with [^{18}F]FDG and [^{68}Ga]Ga-PSMA-11 in mCRPC Patients with Worsening Disease during [^{177}Lu]Lu-PSMA-617 RLT

Fadi Khreish, Kalle Ribbat, Mark Bartholomä, Stephan Maus, Tobias Stemler, Ina Hierlmeier, Johannes Linxweiler, Mathias Schreckenberger, Samer Ezziddin and Florian Rosar

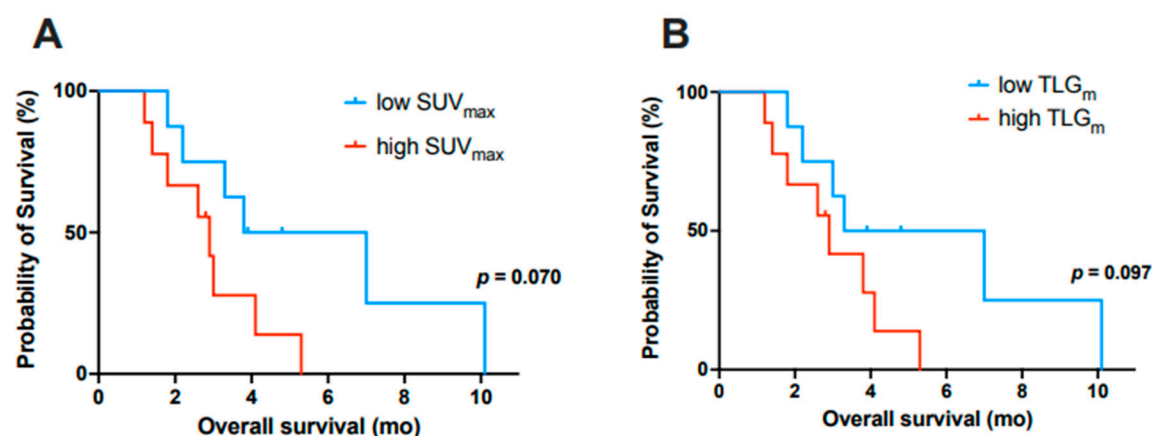


Figure S1. Kaplan-Meier curves for OS (from the time point of combined [^{18}F]FDG and [^{68}Ga]Ga-PSMA-11 PET imaging) in patients with mismatch findings ($n = 17$) stratified by (A) low/high SUV_{max} (cut-off value: 16.8): median OS 3.8 mo (95% CI 0.4–7.2 mo.)/ 2.9 mo (95% CI 2.2–3.6 mo.), (B) low/high TLG_m (cut-off value: 607.8 mL \times SUV): median OS 3.3 mo (95% CI 0–7.0 mo)/2.9 mo (95% CI 2.1–3.6 mo). OS: overall survival; SUV_{max} : maximal standardized uptake value of the mismatch lesion with the highest [^{18}F]FDG uptake; CI: confidence interval; TLG_m : total lesion glycolysis of all mismatch lesions.

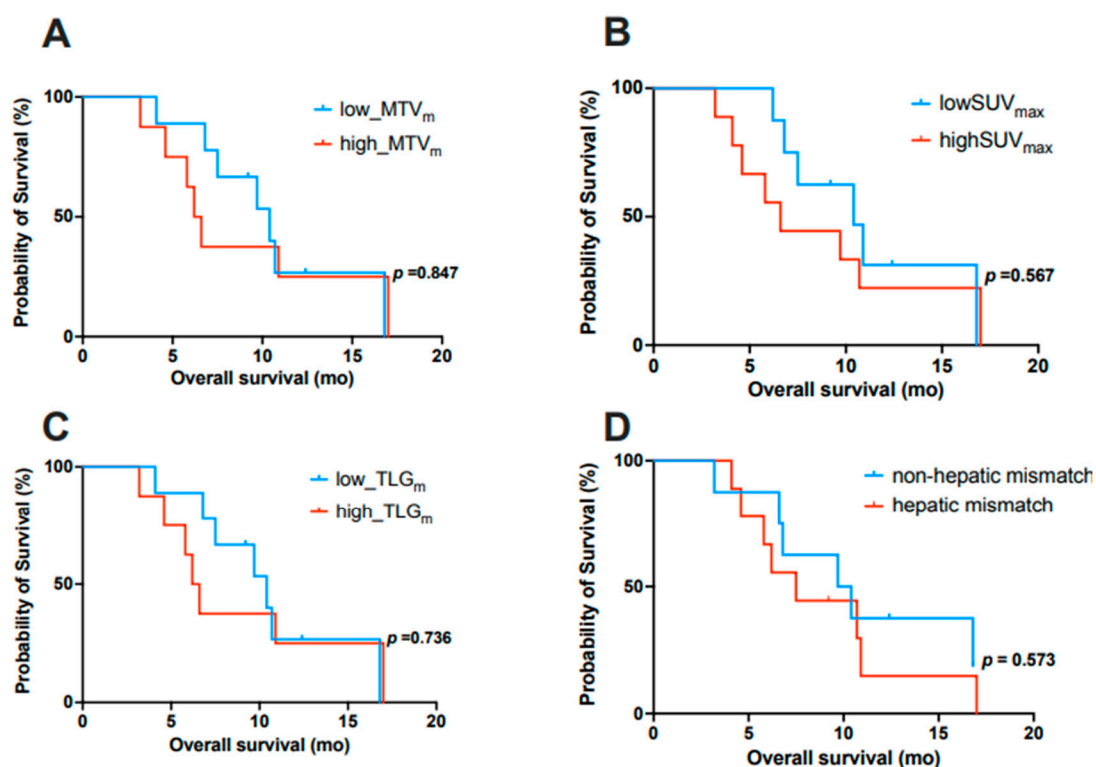


Figure S2. Kaplan-Meier curves for OS (from the start of [^{177}Lu]Lu-PSMA-617 radioligand therapy) in patients with mismatch findings ($n = 17$) stratified by (A) low/high MTV_m (cut-off value: 74.4 mL), (B) low/high SUV_{max} (cut-off value: 16.8), (C) low/high TLG_m (cut-off value: 607.8 mL \times SUV), (D) presence or absence of hepatic mismatch lesions. OS: overall survival; MTV_m: metabolic tumor volume of all mismatch lesions; SUV_{max}: maximal standardized uptake value of the mismatch lesion with the highest [^{18}F]FDG uptake; TLG_m: total lesion glycolysis of all mismatch lesions.