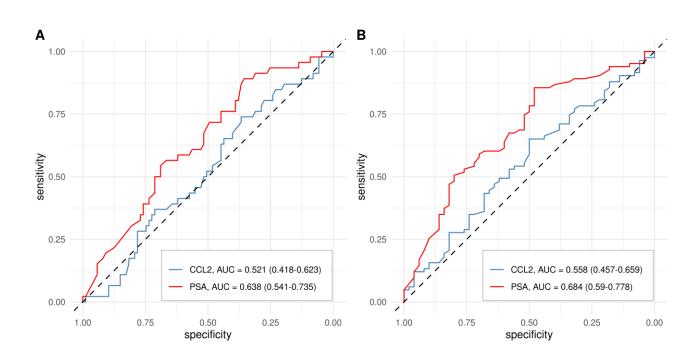
Supplemental material

R Session log

```
## R version 4.1.2 (2021-11-01)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Big Sur 10.16
Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRblas.0.
dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRlapac
k.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/c/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats graphics grDevices utils datasets methods base
##
## other attached packages:
## [1] pROC_1.18.0 qwraps2_0.5.2 forcats_0.5.1 stringr_1.4.0
## [5] dplyr_1.0.7 purrr_0.3.4 readr_2.1.1 tidyr_1.1.4
## [9] tibble 3.1.6 tidyverse 1.3.1 cowplot 1.1.1 ggpubr 0.4.0
## [13] ggplot2_3.3.5
##
## loaded via a namespace (and not attached):
## [1] Rcpp_1.0.7 svglite_2.0.0 lubridate_1.8.0 assertthat_0.2.1
## [5] digest_0.6.29 utf8_1.2.2 plyr_1.8.6 R6_2.5.1
```



	Non-significant Cance (n=87)	Significan Cancer (n = 46)	t Median of the Difference 95% CI	p-value
Median PSA, ng/ml	7.0	8.4	1.4 [0.3,2.6]	0.00913*
Median CCL2, pg/ml	130.8	133.0	2.2 [-10.6,14.4]	0.698
	Neg. biopsy (n = 50)	Cancer (n = 83)	Median of the Difference 95% CI	p-value
Median PSA, ng/ml	6.2	8.2	1.8 [0.8,2.9]	0.000389*
Median CCL2, pg/ml	126.5	134	6.6 [-5.2,18.4]	0.262

Supplementary Figure 1 CCL2 & PSA levels ROC

A: PSA and CCL2 receiver operating characteristic curve for significant cancer versus Gleason Score 6 (3+3) or negative biopsies and ability to predict significant cancer, B: as above with any cancer compared to negative biopsies. Wilcoxon nonparametric test was used for two-group comparison, p-values < 0.05 were considered significant (*). Confidence bands for area under the curve (AUC) for receiver operating characteristic (ROC) curves were compared using DeLongs's nonparametric approach.