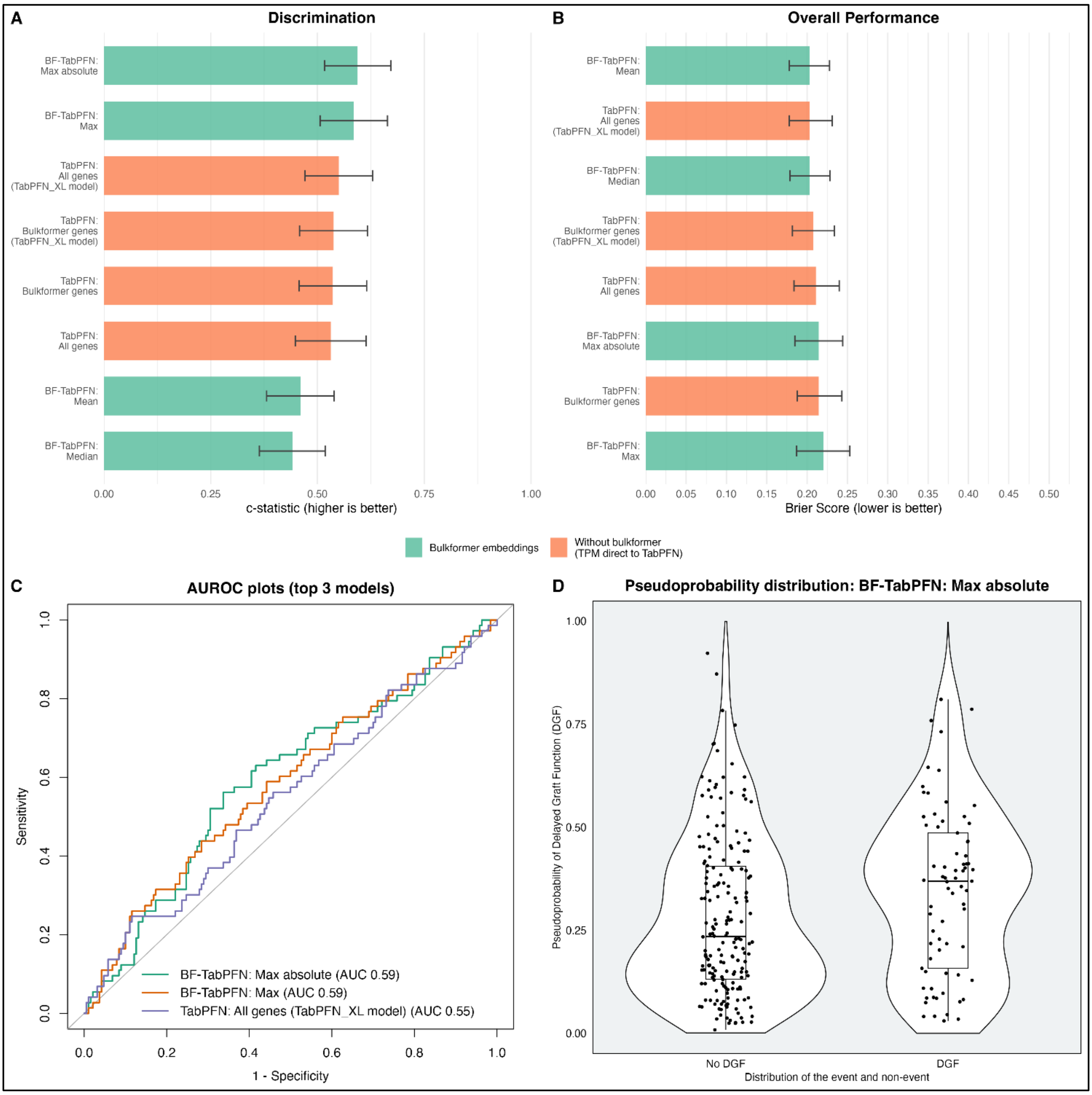
Supplementary Figures



Supplementary Figure 1 – Predictive performance for early post-transplant kidney function (defined as Delayed Graft Function; DGF) in the QUOD retrieval biopsy cohort. The discrimination (measured using c-statistic) and overall performance (Brier score) for each of the tested models are shown in panel A and B, and are ranked best to worst. Models using the full BulkFormer-TabPFN pipeline are shown in green, and are labelled with which BulkFormer method was used for aggregation of gene-level embeddings (e.g. Max absolute). Models using only TabPFN directly on the transcriptomic data (without BulkFormer) are shown in orange, and labelled with which genes were used, and whether the TabPFN default or high feature count (XL model) were used. C) Receiver-operating characteristic curves for the top three performing models by c-statistic. D) Distribution of predicted probabilities stratified by subsequent delayed graft function status.

Supplementary tables

Supplementary table 1 – All model performance metrics for all models in the NMP and QUOD cohorts. For models using the BulkFormer-TabPFN pipeline (BF-TabPFN) the labels reflect the BulkFormer method for aggregating gene-level embeddings. For models using the just TabPFN on the raw transcript per million data (without BulkFormer), the label represents which genes were used, and whether the TabPFN default or high feature count (XL model) were used.

Cohort	**n**	**Model label**	**c-statistic (95% CI)**	**AUPRC (95% CI)**	**AP (95% CI)**	**Brier (95% CI)**	**Log loss (95% CI)**	**Scaled Brier (95% CI)**	**McFadden R^2 (95% CI)**	**Cox-Snell R^2 (95% CI)**	**Nagelkerke R^2 (95% CI)**
NMP	34	BF-TabPFN: Max absolute	0.82 (0.67, 0.97)	0.52 (0.23, 0.90)	0.58 (0.30, 0.91)	0.15 (0.08, 0.22)	15.46 (9.77, 21.72)	0.22 (-0.25, 0.49)	0.21 (-0.14, 0.44)	0.22 (-0.15, 0.41)	0.32 (-0.23, 0.59)
NMP	34	BF-TabPFN: Max	0.76 (0.59, 0.93)	0.46 (0.21, 0.84)	0.52 (0.28, 0.85)	0.17 (0.10, 0.24)	17.10 (11.29, 23.43)	0.13 (-0.34, 0.40)	0.13 (-0.22, 0.35)	0.14 (-0.25, 0.34)	0.20 (-0.40, 0.49)
NMP	34	BF-TabPFN: Mean	0.55 (0.32, 0.77)	0.27 (0.12, 0.56)	0.31 (0.17, 0.61)	0.22 (0.14, 0.29)	21.35 (15.62, 27.80)	-0.11 (-0.55, 0.10)	-0.09 (-0.39, 0.09)	-0.10 (-0.48, 0.10)	-0.15 (-0.74, 0.14)
NMP	34	BF-TabPFN: Max (99.9)	0.54 (0.32, 0.77)	0.27 (0.12, 0.56)	0.31 (0.16, 0.60)	0.25 (0.15, 0.36)	26.14 (16.11, 37.58)	-0.29 (-1.04, 0.10)	-0.33 (-0.92, 0.05)	-0.47 (-1.68, 0.06)	-0.68 (-2.49, 0.08)
NMP	34	BF-TabPFN: Median	0.53 (0.30, 0.76)	0.27 (0.12, 0.57)	0.32 (0.15, 0.61)	0.21 (0.15, 0.29)	21.31 (15.55, 27.65)	-0.11 (-0.58, 0.10)	-0.09 (-0.41, 0.09)	-0.10 (-0.45, 0.09)	-0.15 (-0.72, 0.14)
NMP	34	BF-TabPFN: Max absolute (99.9)	0.49 (0.24, 0.75)	0.28 (0.11, 0.62)	0.33 (0.14, 0.65)	0.23 (0.15, 0.34)	25.66 (16.11, 38.34)	-0.21 (-0.84, 0.12)	-0.31 (-0.86, 0.07)	-0.42 (-1.70, 0.07)	-0.62 (-2.45, 0.11)
NMP	34	TabPFN: All genes	0.43 (0.17, 0.69)	0.26 (0.10, 0.61)	0.31 (0.14, 0.63)	0.22 (0.14, 0.30)	22.17 (15.79, 28.83)	-0.14 (-0.57, 0.07)	-0.13 (-0.44, 0.04)	-0.16 (-0.52, 0.04)	-0.23 (-0.82, 0.07)
NMP	34	TabPFN: Bulkformer genes	0.42 (0.15, 0.69)	0.25 (0.10, 0.58)	0.30 (0.14, 0.61)	0.23 (0.15, 0.31)	23.20 (15.97, 30.67)	-0.16 (-0.56, 0.07)	-0.18 (-0.49, 0.03)	-0.23 (-0.68, 0.04)	-0.34 (-1.02, 0.05)
NMP	34	TabPFN: All genes (TabPFN_XL model)	0.39 (0.13, 0.65)	0.23 (0.09, 0.55)	0.28 (0.12, 0.59)	0.22 (0.15, 0.30)	22.32 (16.51, 28.68)	-0.15 (-0.53, 0.03)	-0.14 (-0.41, 0.02)	-0.17 (-0.48, 0.02)	-0.25 (-0.79, 0.03)
NMP	34	TabPFN: Bulkformer genes (TabPFN_XL model)	0.38 (0.12, 0.63)	0.22 (0.09, 0.53)	0.27 (0.12, 0.56)	0.23 (0.15, 0.31)	23.09 (16.66, 30.74)	-0.16 (-0.49, -0.00)	-0.17 (-0.46, -0.01)	-0.22 (-0.63, -0.01)	-0.33 (-0.96, -0.02)
QUOD	263	BF-TabPFN: Max absolute (99.9)	0.60 (0.51, 0.68)	0.43 (0.32, 0.55)	0.44 (0.34, 0.56)	0.20 (0.18, 0.23)	162.91 (144.07, 184.85)	-0.01 (-0.13, 0.09)	-0.05 (-0.16, 0.05)	-0.06 (-0.20, 0.05)	-0.09 (-0.30, 0.08)
QUOD	263	BF-TabPFN: Max (99.9)	0.59 (0.52, 0.67)	0.39 (0.29, 0.50)	0.40 (0.30, 0.51)	0.20 (0.18, 0.23)	165.19 (142.99, 187.78)	-0.02 (-0.13, 0.07)	-0.06 (-0.18, 0.03)	-0.08 (-0.23, 0.04)	-0.11 (-0.33, 0.06)

Cohort	n	Model label	c-statistic (95% CI)	AUPRC (95% CI)	AP (95% CI)	Brier (95% CI)	Log loss (95% CI)	Scaled Brier (95% CI)	McFadden R² (95% CI)	Cox-Snell R² (95% CI)	Nagelkerke R² (95% CI)
QUOD	263	BF-TabPFN: Max absolute	0.59 (0.52, 0.67)	0.34 (0.26, 0.45)	0.35 (0.27, 0.47)	0.21 (0.18, 0.24)	168.62 (147.29, 190.09)	-0.07 (-0.19, 0.04)	-0.09 (-0.20, 0.02)	-0.11 (-0.26, 0.03)	-0.15 (-0.37, 0.04)
QUOD	263	BF-TabPFN: Max	0.58 (0.51, 0.66)	0.34 (0.26, 0.45)	0.35 (0.27, 0.47)	0.22 (0.19, 0.25)	178.86 (152.96, 207.86)	-0.10 (-0.23, 0.02)	-0.15 (-0.29, -0.02)	-0.20 (-0.42, -0.02)	-0.28 (-0.60, -0.03)
QUOD	263	TabPFN: All genes (TabPFN_XL model)	0.55 (0.47, 0.63)	0.33 (0.24, 0.44)	0.34 (0.26, 0.45)	0.20 (0.18, 0.23)	157.77 (142.34, 175.44)	-0.01 (-0.08, 0.04)	-0.02 (-0.07, 0.03)	-0.02 (-0.09, 0.03)	-0.03 (-0.13, 0.05)
QUOD	263	TabPFN: Bulkformer genes (TabPFN_XL model)	0.54 (0.46, 0.62)	0.31 (0.23, 0.40)	0.31 (0.24, 0.41)	0.21 (0.18, 0.23)	160.72 (144.87, 176.38)	-0.04 (-0.10, 0.02)	-0.04 (-0.09, 0.02)	-0.04 (-0.11, 0.02)	-0.06 (-0.16, 0.03)
QUOD	263	TabPFN: Bulkformer genes	0.54 (0.46, 0.61)	0.30 (0.23, 0.39)	0.31 (0.24, 0.40)	0.21 (0.19, 0.24)	166.33 (148.36, 185.07)	-0.07 (-0.15, 0.01)	-0.07 (-0.15, -0.00)	-0.09 (-0.20, -0.00)	-0.13 (-0.28, -0.00)
QUOD	263	TabPFN: All genes	0.53 (0.45, 0.61)	0.33 (0.25, 0.45)	0.34 (0.27, 0.46)	0.21 (0.18, 0.24)	165.08 (146.42, 184.60)	-0.05 (-0.14, 0.03)	-0.06 (-0.14, 0.01)	-0.08 (-0.18, 0.01)	-0.11 (-0.27, 0.01)
QUOD	263	BF-TabPFN: Mean	0.46 (0.38, 0.54)	0.25 (0.19, 0.33)	0.26 (0.20, 0.34)	0.20 (0.18, 0.23)	156.84 (142.61, 171.23)	-0.01 (-0.03, -0.00)	-0.01 (-0.03, -0.00)	-0.01 (-0.04, -0.00)	-0.02 (-0.05, -0.00)
QUOD	263	BF-TabPFN: Median	0.44 (0.36, 0.52)	0.24 (0.19, 0.30)	0.24 (0.20, 0.31)	0.20 (0.18, 0.23)	157.22 (143.05, 171.51)	-0.01 (-0.04, -0.01)	-0.01 (-0.03, -0.00)	-0.01 (-0.04, -0.01)	-0.02 (-0.05, -0.01)