Supplementary materials

Comprehensive analysis of RNA expression correlations between biofluids and human tissues

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Table S1. Data source of collected biofluid transcriptome profile

Data source	Biofluid type
exRNA atlas	urine exRNA (n = 70) bile exRNA (n = 30)
GSE121869	serum exRNA (n = 54) plasma exRNA (n = 143)
GSE99573	stool seRNA (n = 111)
GSE131689	urine total RNA (n = 2) urine EV RNA (n = 2) platelet-rich plasma total RNA (n = 6) platelet-poor plasma total RNA (n = 14) platelet-rich plasma EV RNA (n = 2)
GSE145796	saliva EV RNA (n = 10)

EV RNA: extracellular vesicle RNA; exRNA: extracellular RNA; seRNA: stool-derived eukaryotic RNA

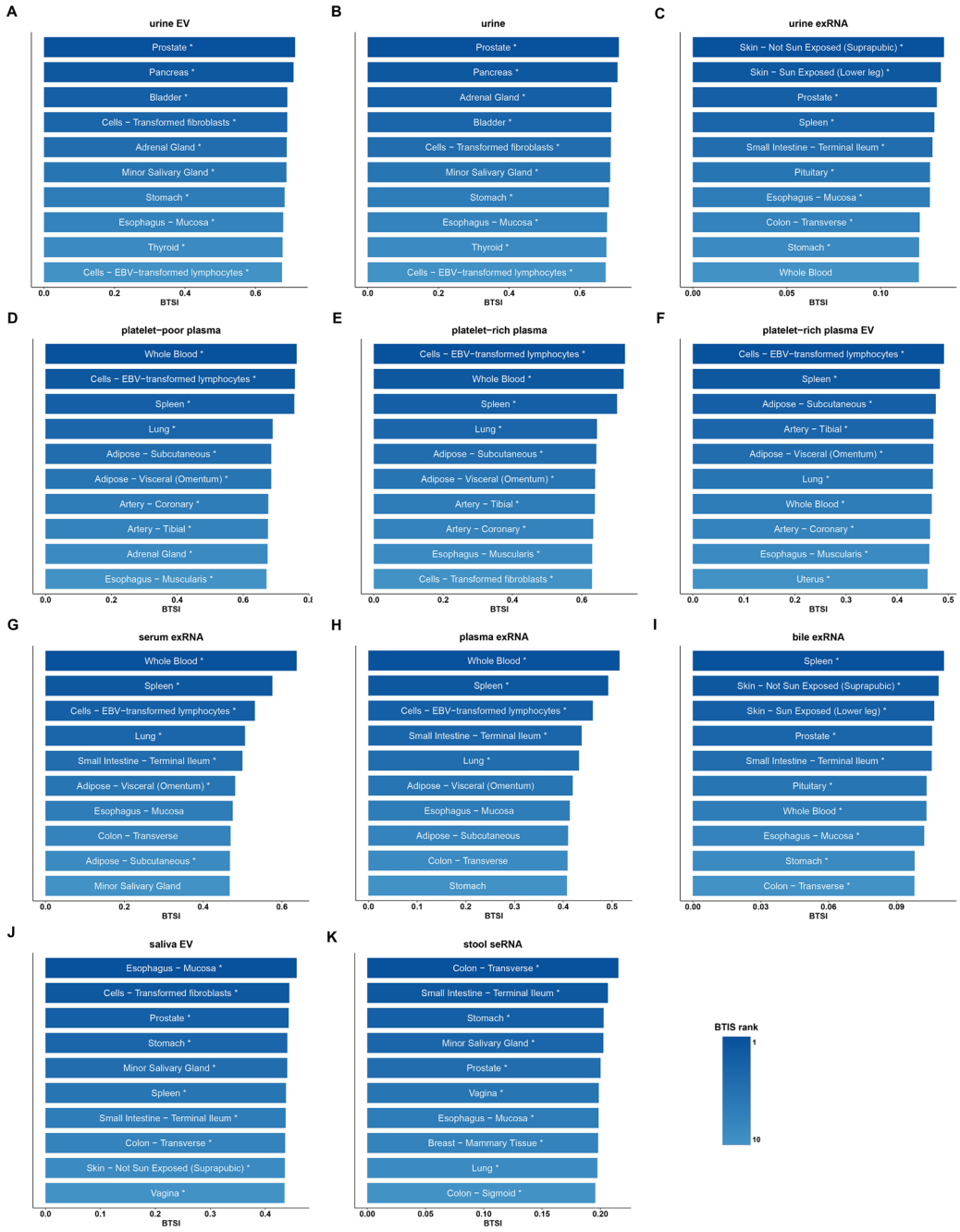

FIGURE S1. Tendency in BF-mRNAs T-mRNAs correlation. The bar plot shows the tissues of the top 10 highest BTSI value for each biofluid type from mRNA view. Only tissues significantly correlated with biofluid (Spearman's correlation, P-value < 0.05) and presented higher correlation with biofluid samples than randomized GTEx samples (n = 1000; t-test, 10 times repeat, P-value < 0.05) are labeled using '*'. The color of each bar represents the rank of the tissue BTSI value for the corresponding biofluid.

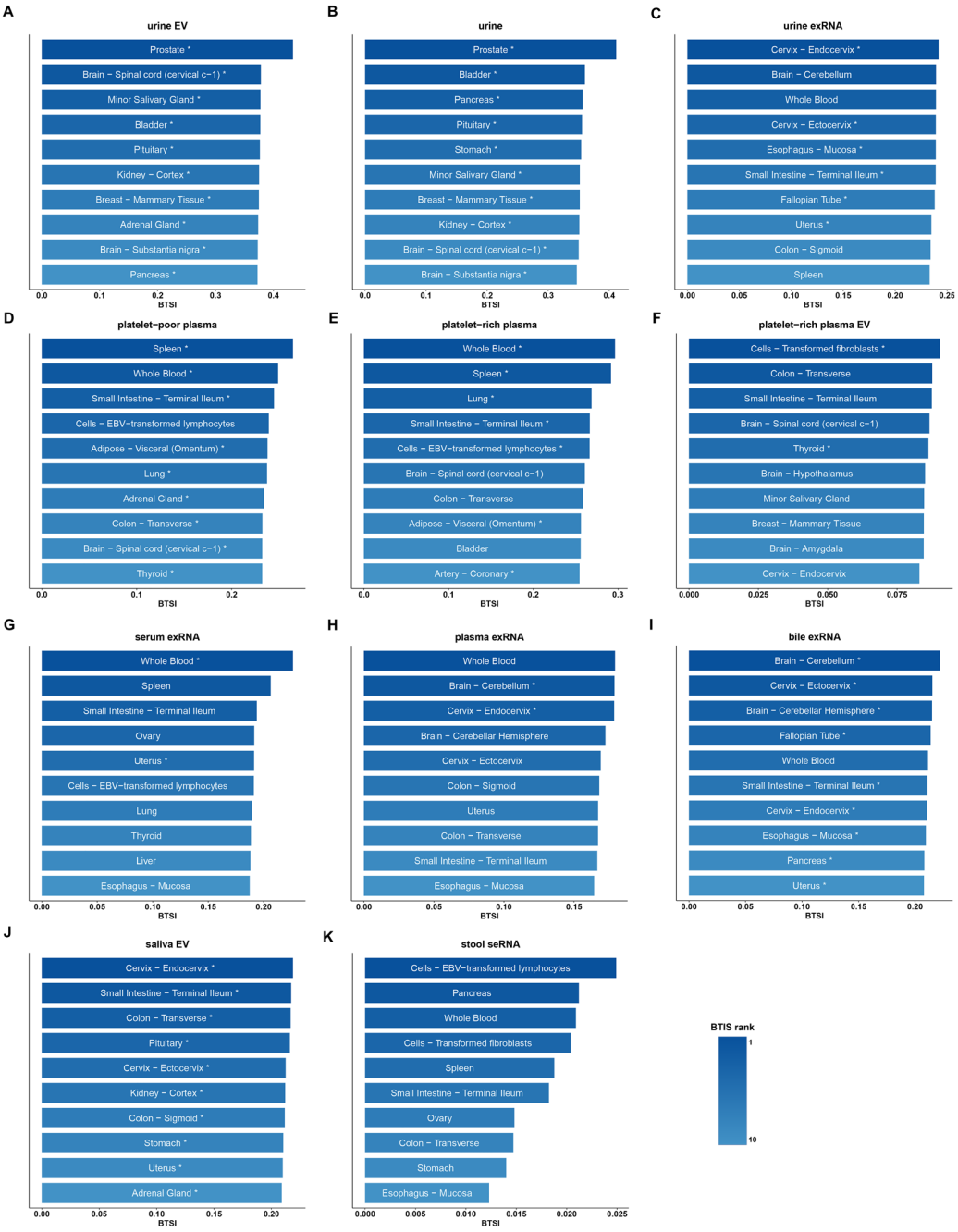

FIGURE S2. Tendency in BF-lncRNAs T-lncRNAs correlation. The bar plot shows the tissues of the top 10 highest BTSI value for each biofluid type from lncRNA view. Only tissues significantly correlated with biofluid (Spearman's correlation, P-value < 0.05) and presented higher correlation with biofluid samples than randomized GTEx samples (n = 1000; t-test, 10 times repeat, P-value < 0.05) are labeled using '*'. The color of each bar represents the rank of the tissue BTSI value for the corresponding biofluid.