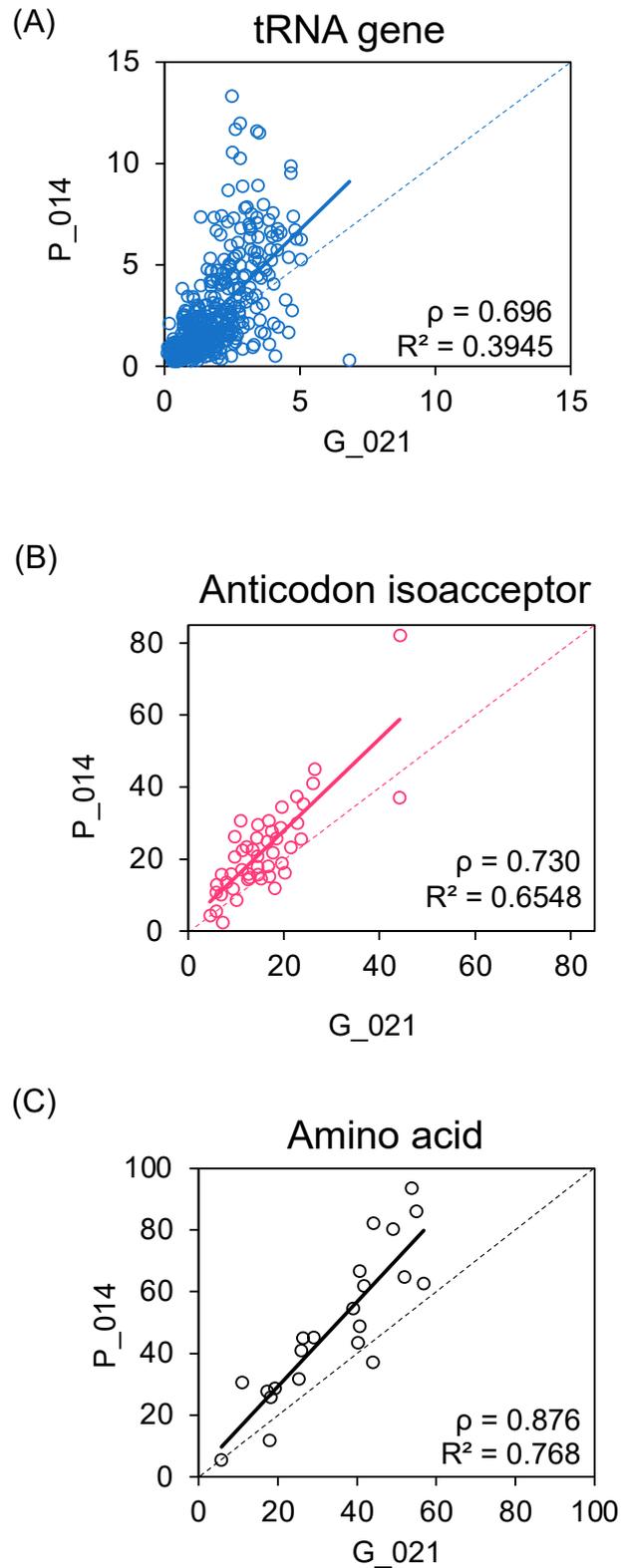
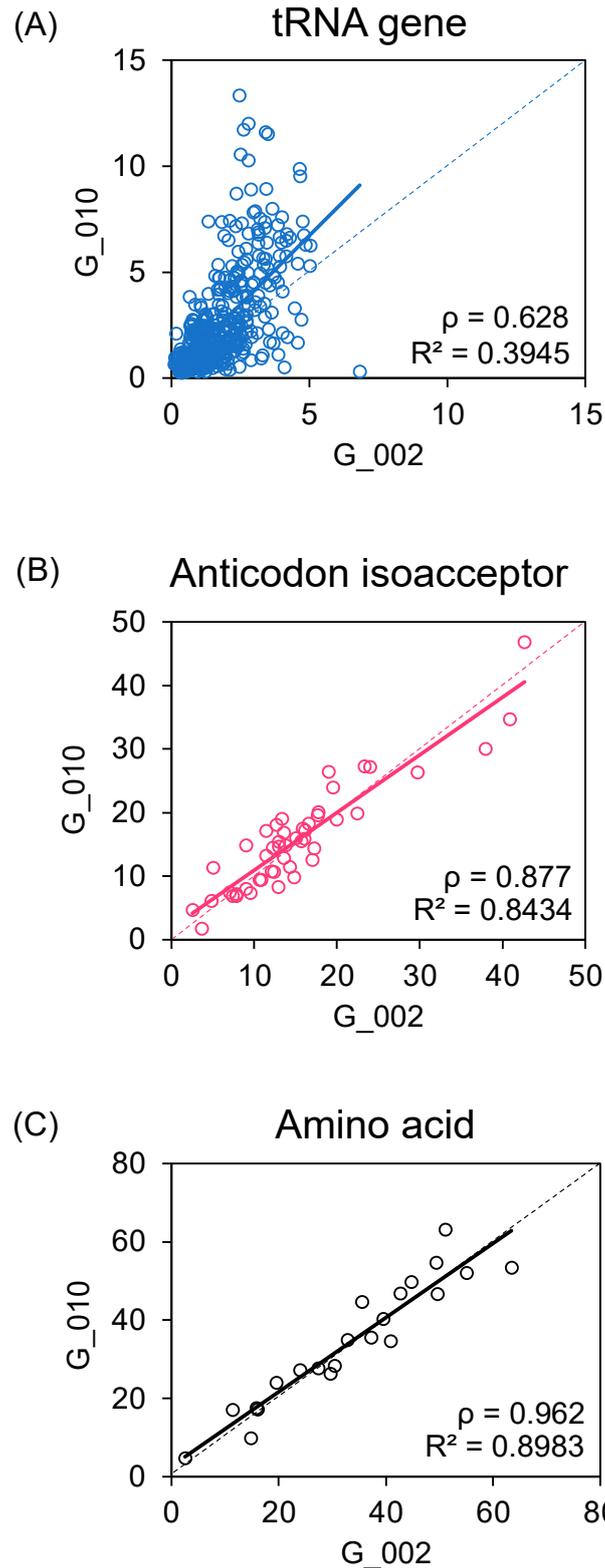


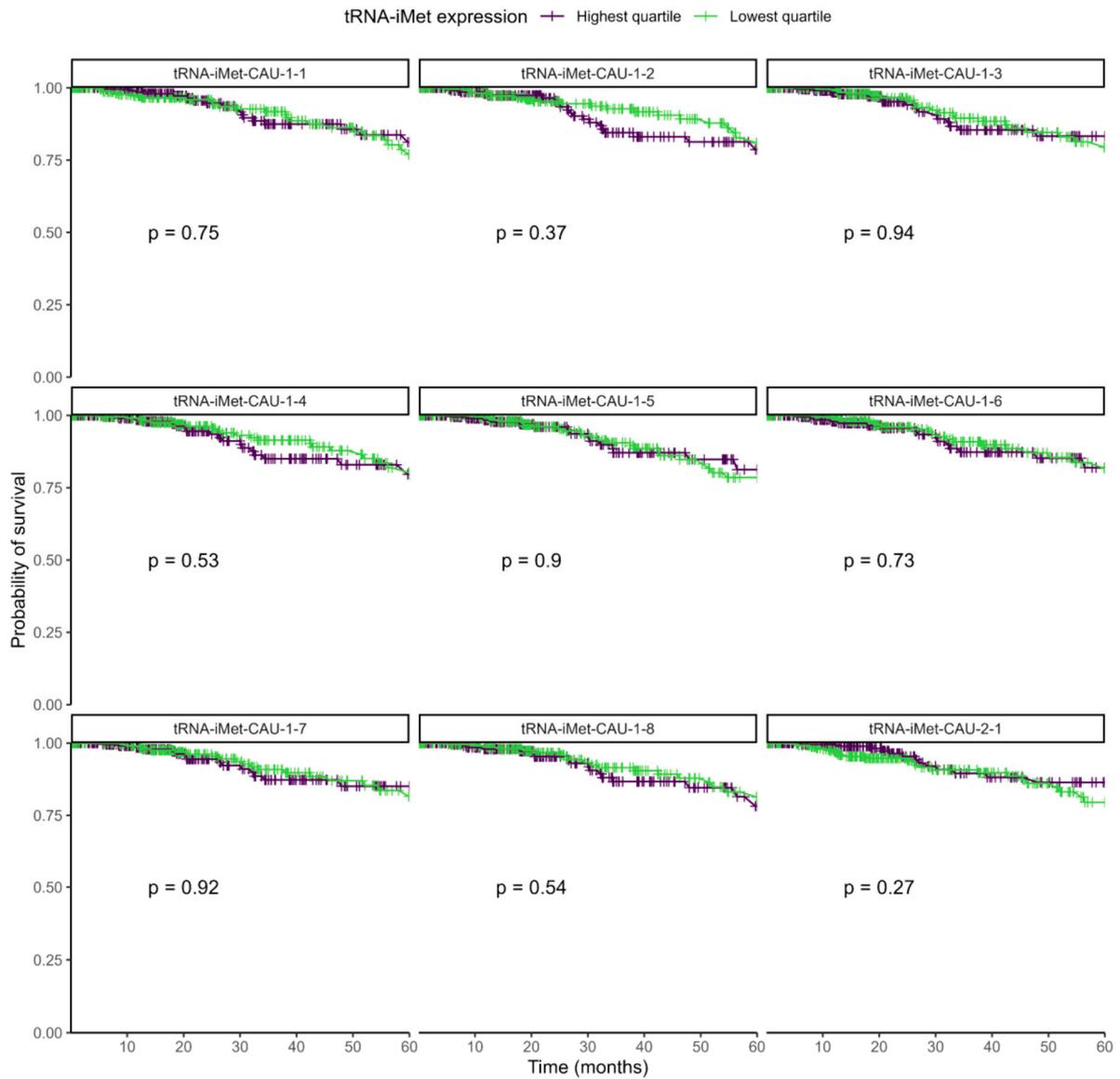
## Supplementary figures



**Supplementary Figure S1.** Variation between cancers P\_014 and G\_021 of H3K27ac enrichment at tRNA genes and families. (A-C) Plots comparing H3K27ac Q-values at 428 tRNA gene loci (A), 48 anticodon isoacceptor families (B), and 21 amino acid isotype families (C) in primary tumours P\_014 and G\_021, which had overall relative H3K27ac enrichment across the 40 tumours and 428 tRNA genes of 1076 and 754, respectively. Spearman's rank correlation coefficient is shown ( $\rho$ ).



**Supplementary Figure S2.** Variation between cancers G\_002 and G\_010 of H3K27ac enrichment at tRNA genes and families. (A-C) Plots comparing H3K27ac Q-values at 428 tRNA gene loci (A), 48 anticodon isoacceptor families (B), and 21 amino acid isotype families (C) in primary tumours G\_010 and G\_002, which were chosen because they share very similar overall H3K27ac enrichment across the 40 tumours and 428 tRNA genes (756 and 619, respectively). Spearman's rank correlation coefficient is shown ( $\rho$ ).



**Supplementary Figure S3.** Survival of patients with breast invasive carcinomas expressing upper quartile (purple) or lower quartile (green) levels of each individual tRNA-iMet-CAU.