Description of Additional Supplementary Files

Supplementary Data 1. Participant Characteristics (n=1,930, MESA Exam 1)
Study participant demographics for all participants, and the subset of 1,889 participants included in QTL mapping analyses. Ancestry cluster assignment based on similarity to 1000G ancestry cluster (>0.5 similarity to one cluster). Quantitative phenotypes reported as mean (SD).1000G ancenstry groups are: AFR = African. AMR = Admixed American. EAS = East Asian. EUR = European. UNK = Unassigned.

Supplementary Data 2. Protein Pearson's r Correlation Estimates Overall, Per-Ancestry Estimates and Inter-ancestry Heterogeneity for all 2,708 probe pairs
Pearson's r correlation for SomaScan and Olink protein measures. "SMP-normalized SomaScan" indicates that underlying SomaScan measures had company-performed adaptive-normalization by maximum likelihood (ANML) transformations on all participant samples. "non-SMP-normalized SomaScan" indicates that underlying SomaScan measures had ANML applied only to quality control samples.
Pair rank refers to the relative ordering of correlation strength between all SeqID–OlinkID measurement pairs that target the same protein UniProt ID. For example, pair rank of 1 indicates the most correlated probe pair for a given UniProt ID. Pair rank of 2 denotes the second most correlated probe pair for a given UniProt ID, etc.
"Cross_Ancestry_Heterogeneity_p0.05" and "Cross_Ancestry_Heterogeneity_pBonferroni" columns indicate whether protein measure correlations across ancestry groups were heterogeneous, according to Cochran's Q test of heterogeneity (one-sided) with Cochran's Q p-value <0.05 or Cochran's Q p-value < 1.8×10^{-5} (Bonferroni significant at α=0.05, with correction for 2,708 probe pairs), respectively.
Previously reported inter-platform correlations across studies were derived from Fenland study [1] (SomaScan v4 vs. 1,069 Olink measures in 485 participants), JHS [2] (SomaScan 1.3k vs. Olink Explore 1.5k, n=568 participants), ARIC [3](SomaScan v4 vs. 500 Olink measured proteins in 427 participants), and deCODE [4](SomaScan v4. vs. Olink Explore 3072 in N=1,514 participants), and were matched to proteins by UniProt ID (given the differences in probe IDs between different versions of the platforms used).

Supplementary Data 3. 80 proteins with Bonferroni-significant heterogenity in inter-platform correlation estimates across contributing ancestry groups. (One-Probe-Per-UniProt ID)
Displayed here are the 80 proteins with Bonferroni-significant (Cochran's Q p-value<1.8×10^{-5}, significant at α=0.05 with correction for 2,708 probe pairs tested) heterogeneity in inter-

platform Pearson's r correlation estimates across the 4 ancestry groups represented in this study, acording to the Cochran's Q test of heterogeneity (one-sided). "QTL Summary" columns denote whether a given probe associates with a cis-pQTL, a cis-pQTL driven by a variant with ancestry-differentiated allele frequencies, a protein-altering variant (PAV) cis-pQTL with ancestry-differentiated allele frequencies, a trans-pQTL, and/or a trans-pQTL with ancestry-differentiated allele frequencies. pQTL were generated with linear regression under an additive model (two-sided test of significance). Variants with ancestry-differentiated allele frequencies were determined according to Chi-square test using allele frequencies derived in each contributing ancestry group (significance defined as a X^2 value in the 75th percentile).
AFR = African, AMR = Admixed American, EAS = East Asian, EUR = European Ancestry.

Supplementary Data 4. SomaScan Significant cis-pQTL SuSiE Credible Sets For Main Analysis SeqIDs

Each row shows cis-pQTL association statistics (generated with linear regression under an additive model, two-sided test of significance) for an individual variant with a protein measure. Variants are grouped according to SuSiE credible set (Credible_Set_ID). Only significant SomaScan cis-pQTL credible sets are shown (credible sets containing at least one variant p-value<$5x10^{-8}$, i.e. significant at a traditional genome-wide significance threshold). Variants with ancestry-differentiated allele frequencies were determined according to Chi-square test using allele frequencies derived in each contributing ancestry group (significance defined as a X^2 value in the 75th percentile). * Non-abundance protein-altering variants (PAVs) are PAVs associated with differences in peptide abundances as measured by mass-spectrometry in the QMDiab study (n= 345), but not protein abundances [5], and are postulated to drive assay interference QTL.

Supplementary Data 5. Olink Significant SuSiE cis-pQTL Credible Sets For Main Analysis Olink IDs

Each row shows cis-pQTL association statistics (generated with linear regression under an additive model, two-sided test of significance) for an individual variant with a protein measure. Variants are grouped according to SuSiE credible set (Credible_Set_ID). Only significant Olink cis-pQTL credible sets are shown (credible sets containing at least one variant p-value<$5x10^{-8}$, i.e. significant at a traditional genome-wide significance threshold). Variants with ancestry-differentiated allele frequencies were determined according to Chi-square test using allele frequencies derived in each contributing ancestry group (significance defined as a X^2 value in the 75th percentile). * Non-abundance protein-altering variants (PAVs) are PAVs associated with differences in peptide abundances as measured by mass-spectrometry in the QMDiab

study (n= 345), but not protein abundances [5], and are postulated to drive assay interference QTL.

Supplementary Data 6. PAV cis-pQTL and Epidemiological Association Summary Statistics for Proteins with Platform-Discordant cis-pQTL containing a PAV in discordant credible set (Results for all probe pairs)

Proteins associated with a platform-discordant pQTL (overlapping credible sets between platforms, at least one platform's lead in the other platform's credible set, discordant pQTL effect-size directions between platforms) containing a protein altering variant (PAV). cis-pQTL were generated with linear regression under an additive model, two-sided test of significance. Protein associations with phenotypes were assessed with linear or logistic regression (two-sided test of significance). Protein-phenotype associations were significant at α=0.05 correcting for the 2,708 probe pairs tested ($p<1.8x10-5$). The PAV and association statistics for each platform's measure are shown, as well as the associated probe, encoded consequence (according to Variant Effect Predictor), the correlation of each platform's measures without adjustment for PAV, and with adjustment for the PAV, intra-ancestry correlations and cross-ancestry heterogeneity without and with adjustment for the PAV, and protein-phenotype association statistics for each platform when using protein measures not adjusted for the PAV and adjusted for the PAV. Phenotypes assessed were age, sex, body mass index (BMI), and type 2 diabetes (T2D).

Supplementary Data 7. SomaScan 7k and Olink Explore 3072 Correlation by Inter-platform Concordance -- Comparison by Protein (Main Analysis Probes - 1 probe per UniProt ID)

Correlation of proteins according to whether they have a cis-pQTL on both platforms, a platform-concordant cis-pQTL (credible sets overlap between platforms, concordant directions of pQTL effect on both platforms), platform-discordant cis-pQTL (credible sets overlap between platforms, discordant directions of pQTL effect on both platforms), a platform-specific cis-pQTL (a given credible set for one platform's protein measure does not overlap the other platform's), or no cis-pQTL at all. cis-pQTL were generated with linear regression under an additive model, two-sided test of significance. PAV = Protein-altering Variant. * Non-abundance protein-altering variants (PAVs) are PAVs associated with differences in peptide abundances as measured by mass-spectrometry in the QMDiab study (n= 345), but not protein abundances [5], and are posutlated to drive assay interference QTLs. Mass-spectrometry pQTL signals were derived from the QMDiab study, n=345 participants [5], and the Tarkin study, n=1,260 participants [6].

Supplementary Data 8. Characterizing cis-pQTL By Signal -- Main Analysis Results (One Probe-Per-UniProt ID)

Counts of cis-pQTL credible sets containing a protein-altering variant (PAV), expression quantitative trait locus lead variant (eQTL) reported in GTEx v8 [7], or a mass-spectrometry (MS) pQTL or non-abundance PAV lead variant. Credible sets are categorized by platform-concordance of the genetic signal, and the direction of pQTL effects ere compared to the eQTL or MS-QTL directions of effect. * Non-abundance protein-altering variants (PAVs) are PAVs associated with differences in peptide abundances as measured by mass-spectrometry in the QMDiab study (n= 345), but not protein abundances [5], and are posutlated to drive assay interference QTLs. Mass-spectrometry pQTL signals were derived from the QMDiab study, n=345 participants [5], and the Tarkin study, n=1,260 participants [6].

Supplementary Data 9. SomaScan Significant SuSiE trans-pQTL Credible Sets For Main Analysis SeqIDs (One-Probe-Per-UniProt ID)

Legend: Each row shows trans-pQTL association statistics for an individual variant with a protein measure. Variants are grouped according to SuSiE credible set (Credible_Set_ID). Only significant SomaScan trans-pQTL credible sets are shown (credible sets containing at least one variant p-value<$1x10^{-11}$, i.e. genome-wide significant at a traditional threshold with correction for 2,157 proteins tested). trans-pQTL were generated with linear regression under an additive model, two-sided test of significance. * Non-abundance protein-altering variants (PAVs) are PAVs associated with differences in peptide abundances as measured by mass-spectrometry in the QMDiab study (n= 345), but not protein abundances [5], and are postulated to drive assay interference QTL.

Supplementary Data 10. Olink Significant SuSiE trans-pQTL Credible Sets For Main Analysis OlinkIDs

Each row shows trans-pQTL association statistics for an individual variant with a protein measure. Variants are grouped according to SuSiE credible set (Credible_Set_ID). Only significant Olink trans-pQTL credible sets are shown (credible sets containing at least one variant p-value<$1x10^{-11}$, i.e. genome-wide significant at a traditional threshold with correction for 2,157 proteins tested). trans-pQTL were generated with linear regression under an additive model, two-sided test of significance. * Non-abundance protein-altering variants (PAVs) are PAVs associated with differences in peptide abundances as measured by mass-spectrometry in the QMDiab study (n= 345), but not protein abundances [5], and are postulated to drive assay interference QTL.

Supplementary Data 11. Inter-platform Correlation by Trans-pQTL Signal Presence and Pleiotropy (One-probe-per-UniProt ID Analysis Counts)

Correlation of protein measures according to whether they have a signfiicant cis-pQTL credible set (credible set lead significant at a traditional genome-wide threshold, $p<5x10^{-8}$) and/or trans-pQTL credible set (credible set lead significant at a traditional genome wide threshold further corrected for 2,157 proteins tested $p<1x10^{-11}$) on one, both, or neither platform. pQTL were generated with linear regression under an additive model (two-sided test of significance). Trans-pQTL are further categorized according to pleiotropy, with a pleiotropic locus defined as a trans-pQTL sliding window region associated with at least 5 probes on a given platform. A platform-shared pleiotropic trans-pQTL region is defined as one that overlaps on both platforms and is associated with at least 5 proteins on each platform (these do not need to be the same 5 proteins on each platform). A platform-differentiated pleiotropic trans-pQTL locus is a region that is associated with at least 5 proteins on one platform, and less than 5 on the other (or no overlapping trans-pQTL in the region).

Supplementary Data 12. Summary of Pleiotropic Regions Identified in Main (One-Probe-Per-UniProt) Analysis

Counts of proteins and inter-platform Pearson's r correlation of proteins associated with platform shared or platform-differentiated pleiotropic loci on each platform, and a summary of one gene contained in the trans-pQTL region for each platform. A pleiotropic locus is defined as a trans-pQTL sliding window region associated with at least 5 probes on a given platform. A platform-shared pleiotropic trans-pQTL region is defined as one that overlaps on both platforms and is associated with at least 5 proteins on each platform (these do not need to be the same 5 proteins on each platform). A platform-differentiated pleiotropic trans-pQTL locus is a region that is associated with at least 5 proteins on one platform, and less than 5 on the other (or no overlapping trans-pQTL in the region).

Supplementary Data 13. trans-pQTL Regions Identified on SomaScan and Olink, Aligned by Platform Overlap

List of sliding window trans-pQTL regions identified on SomaScan and Olink. Each row represents a region identified on each platform. Rows where Region_ID_SomaScan and Region_ID_Olink are both non-NA valuesdenote trans-pQTL regions that had at least one significant trans-pQTL on each platform and overlapped between platforms. Credible sets and association statistics for trans-pQTL contained in each region can be found in Supplemental Table 9 (SomaScan) and Supplemental Table 10 (Olink), respectively.

Supplementary Data 14. pQTL status by Limit of Detection (LOD). Proteins with a significant cis- or trans- pQTL credible set on each platform, according to whether at least 50% of protein measures on a given platform was above the platform's LOD (Main Analysis - One Probe per UniProt).

Supplementary Data 15. Protein Measure Correlation by LOD
Protein measure correlation (Pearson's r) according to whether at least 50% of a platform's measures were above the limit of detection (LOD), and or whether a significant cis- or trans- pQTL was detected -- One Probe per UniProt.

Supplementary Data 16. Limit of Detection (LOD) Values by platform
LOD Values for each platform and summary of percentage of measures below LOD on each platform (All probes per UniProt ID).

Supplementary Data 17. Summary of Phenotypic Associations for each Platform -- Main Analysis Results (One Probe Per UniProt)
Protein associations with phenotypes were assessed with linear or logistic regression (two-sided test of significance). Protein-phenotype associations were significant at $p<0.05$, or $p<1.8x10\text{-}5$ ($\alpha=0.05$ correcting for the 2,708 probe pairs tested). Count of proteins associated with age, sex, body mass index (BMI), and type 2 diabetes (T2D) at two significance thresholds (denoted by column): $p<0.05$ or Bonferroni-significance threshold ($p<0.05/2,708$ probe pairs). In each category, we report the number of proteins with a significant association on a given platform that also have a cis-pQTL. We also report the number of proteins with a significant association on both platforms that have inter-platform effect-size heterogeneity (according to the Cochran's Q test, with significance defined as $\alpha=0.05$, correcting for 2,708 probe pairs tested ($p<1.8x10\text{-}5$)), and correlation of effect sizes for proteins with a significant association on both platforms. Results used to generate this table can be found in Supplemental Table 18.

Supplementary Data 18. Summary of Phenotypic Associations for each Platform -- Main Analysis Results (One Probe Per UniProt)
Legend: Protein associations with phenotypes were assessed with linear or logistic regression (two-sided test of significance). Protein-phenotype associations were signfiicant at $p<0.05$, or $p<1.8x10\text{-}5$ ($\alpha=0.05$ correcting for the 2,708 probe pairs tested, Bonferroni significance). Effect sizes, standard errors, and p-values for each platform's protein measure association with age,

sex, body mass index (BMI), and type 2 diabetes (T2D) as well as cross-platform heterogeneity of effect-sizes obtained (Cochran's Q test of heterogeneity).

Supplementary Data 19. Comparing MESA SomaScan significant cis-pQTL SuSiE credible sets associated with proteins with a platform-discordant PAV without and with-PAV adjustment (For all probes-per-UniProt ID)

Each row shows SomaScan cis-pQTL summary statistics for individual SNPs in significant credible sets (at least one variant with $p<5x10^{-8}$, traditional genome-wide significance threshold) identified in pQTL mapping in two versions of the analysis, one without adjustment for platform-discordant PAVs in pQTL mapping (left) , and one with adjustment for platform-discordant PAVs (right) in pQTL mapping. pQTL were generated with linear regression under an additive model (two-sided test of significance). Rows are grouped by credible set IDs. If a variant was in a significant credible set in one analysis, but not the other, association statistics are listed as "NA" for the analysis where there was no significant credible set at that SNP.

Supplementary Data 20. Comparing MESA Olink significant cis-pQTL SuSiE credible sets associated with proteins with a platform-discordant PAV without and with-PAV adjustment (For all probes-per-UniProt ID)

Each row shows Olink cis-pQTL summary statistics for individual SNPs in significant credible sets (at least one variant with $p<5x10^{-8}$, significant at traditional genome-wide significance threshold) identified in pQTL mapping in two versions of the analysis: one without adjustment for platform-discordant PAVs in pQTL mapping (left), and one with adjustment for platform-discordant PAVs in pQTL mapping(right). pQTL were generated with linear regression under an additive model (two-sided test of significance). Rows are grouped by credible set IDs. If a variant was in a significant credible set in one analysis, but not the other, association statistics are listed as "NA" for the analysis where there was no significant credible set at that SNP.

Supplementary Data 21. SomaScan cis-pQTL Credible Sets that Become More Significant in pQTL mapping Adjusted for Platform-Discordant PAVs (All Probes)

Each row shows the lead variant from a cis-pQTL credible set that was significantly (credible sets containing at least one variant p-value$<5x10^{-8}$, traditional genome-wide significance threshold) associated with a SomaScan measure in a cis-pQTL analysis prior to adjusting for a PAV, but became more significantly associated with the given SomaScan protein measure following adjustment for a platform-discordant cis-pQTL protein-altering variant (PAV) in pQTL mapping (shown in PAV_Adjusted_For_in_pQTL_Mapping). pQTL were generated with linear

regression under an additive model (two-sided test of significance). pQTL summary statistics for the lead variant from pQTL analysis without PAV and with PAV adjustment ("_PAV_Adj" column suffix) are shown.

Supplementary Data 22. Olink cis-pQTL Credible Sets that Become More Significant in pQTL mapping Adjusted for Platform-Discordant PAVs (All Probes)

Each row shows the lead variant from a cis-pQTL credible set that was significantly (credible sets containing at least one variant p-value<$5x10^{-8}$, traditional genome-wide significance threshold) associated with an Olink measure in a cis-pQTL analysis prior to adjusting for a PAV, but became more significantly associated with the given Olink protein measure following adjustment for a platform-discordant cis-pQTL protein-altering variant (PAV) in pQTL mapping (shown in PAV_Adjusted_For_in_pQTL_Mapping). pQTL summary statistics for the lead variant from pQTL analysis without PAV and with PAV adjustment ("_PAV_Adj" column suffix) are shown. pQTL were generated with linear regression under an additive model (two-sided test of significance).

Supplementary Data 23. Credible sets that are significant in cis-pQTL analysis adjusting for platform-discordant protein altering variants (PAVs) but have no overlapping significant credible sets in pQTL mapping without adjusting for platform-discordant PAVs

Each row shows the lead variant from a cis-pQTL credible set that was not significantly associated with a protein measure in a cis-pQTL analysis prior to adjusting for a PAV, but was significantly associated (credible sets containing at least one variant p-value<$5x10^{-8}$, traditional genome-wide significance threshold) with the protein measure following adjustment for a platform-discordant cis-pQTL protein-altering variant (PAV) in pQTL mapping (shown in PAV_Adjusted_For). pQTL summary statistics for the lead variant from pQTL analysis without PAV and with PAV adjustment ("_PAV_Adj" column suffix) are shown. pQTL were generated with linear regression under an additive model (two-sided test of significance).

Supplementary Data 24. Protein-altering variants (PAVs) significantly associated in cis- with SomaScan protein measures only and the associated protein's platform-measure-correlation and association statistics from phenotypic regressions (with and without adjustment for PAV) (All Probes Per UniProt ID)

Significant cis-pQTL associations are those within a cis-pQTL SuSiE credible set where at least one variant has p<$5x10^{-8}$ (traditional genome-wide significance threshold). Here, only the PAVs that were in significant SomaScan cis-pQTL credible sets that did not overlap significant Olink

credible sets are shown. pQTL were generated with linear regression under an additive model (two-sided test of significance).

Supplementary Data 25. Protein-altering variants (PAVs) significantly associated in cis- with Olink protein measures only and the associated protein's platform-measure-correlation and association statistics from phenotypic regressions (with and without adjustment for PAV) (All Probes Per UniProt ID)

Significant cis-pQTL associations are those within a cis-pQTL SuSiE credible set where at least one variant has $p<5x10^{-8}$ (traditional genome-wide significance threshold). Here, only the PAVs that were in significant Olink cis-pQTL credible sets that did not overlap significant SomaScan credible sets are shown. pQTL were generated with linear regression under an additive model (two-sided test of significance).

Supplementary Data 26. Two-Sample Inverse-Variance Weighted (IVW) Mendelian Randomization Results for Alzheimer's Disease (AD) using MESA SomaScan cis-pQTL instruments ($p<5x10^{-8}$) available in Bellenguez et al., 2022 [8] **AD GWAS-Meta Analysis**

Results from IVW MR analyses (two-sided test of significance) for each protein using pQTL instruments obtained from SomaScan pQTL analyses. Here, we considered a nominal MR p-value ($p<0.05$) significant. For each probe, 3 MR analyses were run. (1) IVW with all significant cis-pQTL (most significant variant available in outcome GWAS chosen for each credible set) (2) IVW with all cis-pQTL EXCEPT for platform-discordant protein altering variants (PAVs) (3) IVW with all cis-pQTL EXCEPT for platform-discordant PAVs and platform-specific PAVs.

Supplementary Data 27. Two-Sample Inverse-Variance Weighted (IVW) Mendelian Randomization Results for Alzheimer's Disease (AD) using MESA Olink cis-pQTL instruments ($p<5x10^{-8}$) available in Bellenguez et al., 2022 [8] **AD GWAS-Meta Analysis**

Results from IVW MR analyses (two-sided test of significance) for each protein using pQTL instruments obtained from Olink pQTL analyses. Here, we considered a nominal MR p-value ($p<0.05$) significant. For each probe, 3 MR analyses were run. (1) IVW with all significant cis-pQTL (most significant variant available in outcome GWAS chosen for each credible set) (2) IVW with all cis-pQTL EXCEPT for platform-discordant protein altering variants (PAVs) (3) IVW with all cis-pQTL EXCEPT for platform-discordant PAVs and platform-specific PAVs

Supplementary Data 28. Protein measures associated with a trans-pQTL in region pleiotropic for SomaScan protein measures only in analysis including all probes-per-UniProt ID, and protein measure correlation without and with adjustment for the lead trans-pQTL SNP
trans-pQTL were generated with linear regression under an additive model (two-sided test of significance). Significant trans-pQTL credible sets were defined as those containing at least one variant $p<1x10^{-11}$ (traditional genome-wide significance threshold, corrected for 2,157 proteins tested). Pleiotropic trans-pQTL were those significantly associated with at least 5 proteins on a given platform.

Supplementary Data 29. Comprehensive summary of protein annotations, cross-platform protein measure correlation, pQTL presence/absence and pQTL annotations (All 2,708 Probe Pairs for the 2,157 unique UniProt IDs assessed)
For each probe from each platform (paired according to UniProt ID targeted, this table shows a comprehensive summary of protein location and whether or not secreted, percentage of measures above limit of detection, protein-measure correlation across platforms, both across all participants (with ANML-normalization applied to all SomaScan samples, and with ANML-normalization applied to SomaScan QC samples only) and within each contributing ancestry. cis-pQTL and trans-pQTL associations and annotations for each probe are summarized. The tables where more information can be found for each protein are found in the column descriptions. Our hope is that this table can help researchers quickly assess all cross-platform correlation and genetic associations for a given protein target / probe of interest.
Pair rank refers to the relative ordering of correlation strength between all SeqID–OlinkID measurement pairs that target the same protein UniProt ID. For example, pair rank of 1 indicates the most correlated probe pair for a given UniProt ID. Pair rank of 2 denotes the second most correlated probe pair for a given UniProt ID, etc.
"Cross_Ancestry_Heterogeneity_p0.05" and "Cross_Ancestry_Heterogeneity_pBonferroni" columns indicate whether protein measure correlations across ancestry groups were heterogeneous with Cochran's Q p-value <0.05 or Cochran's Q p-value < 0.05/2,708 (Bonferroni significant, a=0.05 correcting for 2,708 probe pairs tested), respectively.
Previously reported inter-platform correlations across studies were derived from Fenland study (Pietzner et al, 2021: SomaScan v4 vs. 1,069 Olink measures in 485 participants), JHS (Katz et al., 2022, SomaScan 1.3k vs. Olink Explore 1.5k, n=568 participants), ARIC (Rooney et al., 2023, SomaScan v4 vs. 500 Olink measured proteins in 427 participants), and deCODE (Eldjarn et al., 2023, SomaScan v4. vs. Olink Explore 3072 in N=1,514 participants), and were matched to proteins by UniProt ID (given the differences in probe IDs between different versions of the platforms used). pQTL were generated with linear regression under an additive model (two-sided test of significance). cis-pQTL were considered sigificant at a traditional genome-wide

significance p-value threshold (p<5x10-8). trans-pQTL were considered sigificant at a traditional genome-wide significance threshold further corrected for the 2,708 probe pairs tested (p<1x10-11).

Supplementary Data 30. Summary of pQTL Signals identified by Platform

cis- and trans-pQTL credible set characteristics and overlap with previously identified expression quantitative trait loci (eQTL) [7], affinity-based pQTL identified in deCODE [9] or UK BioBank [10], mass-spectrometry based pQTL (MS-pQTL) and non-abundance MS-PAVs from the QMDiab Study (n=345 paricipants, [5]) and/or from the Tarkin Study (n=1,260 participants, [6]) and GWAS catalog variants. pQTL were generated with linear regression under an additive model (two-sided test of significance). cis-pQTL were considered sigificant at a traditional genome-wide significance p-value threshold (p<5x10-8). trans-pQTL were considered sigificant at a traditional genome-wide significance threshold further corrected for the 2,708 probe pairs tested (p<1x10-11). Signals identified in the present study were compared to previously reported signals either with a signal level approach, in which we assessed overlap between previously reported lead variants and credible sets identified here, or with a region based approach, where we assessed whether previously reported lead variants fell within a 1 Megabase (Mb) window of the lead variants for the signals identified here

[a] Counts correspond to results from all probes per UniProt ID

[b] PAV = Protein Altering Variant

[c] Ancestry-differentiated = Variants with ancestry-differentiated allele frequencies were determined with the Chi-square test using allele frequencies derived in each contributing ancestry group (significance defined as a X^2 value in the 75th percentile).

[d] Plasma mass-spectrometry (MS) pQTL lead variants were obtained from two previous studies published by Suhre et al, using data from Qatar Metabolomics Study of Diabetes (QMDiab) [5] and the Tarkin study [6].

[e] Plasma MS- Potential Non-abundance QTL lead variants were generated in the QMDiab study by Suhre et al [5] and are considered most-likely to impact peptide measurements (and potentially, protein measurements), rather than circulating protein abundances.

[f] Pleiotropic regions are defined as signal regions collectively associated with at least 5 proteins on the platform.

[g] Platform-shared pleiotropic regions are defined as platform-overlapping regions associated with at least 5 proteins (but not necessarily the same proteins) on both platforms.

[h] Platform "specific" pleiotropic regions are defined as regions associated with at least 5 proteins on one platform, and 0 or 1 proteins on the other platform.

Supplementary Data 31. SomaScan cis-pQTL Credible Sets For All SeqIDs
Each row shows cis-pQTL association statistics for an individual variant with a protein measure. cis-pQTL were generated with linear regression under an additive model (two-sided test of significance). Variants are grouped according to SuSiE credible set (Credible_Set_ID). Only significant SomaScan cis-pQTL credible sets are shown (credible sets containing at least one variant p-value<$5x10^{-8}$, traditional genome-wide significance threshold).
* Non-abundance protein-altering variants (PAVs) are PAVs associated with differences in peptide abundances as measured by mass-spectrometry in the QMDiab study (n= 345), but not protein abundances [5] and are postulated to drive assay interference QTLs.

Supplementary Data 32. Olink cis-pQTL Credible Sets For All Olink IDs
Each row shows cis-pQTL association statistics for an individual variant with a protein measure. cis-pQTL were generated with linear regression under an additive model (two-sided test of significance). Variants are grouped according to SuSiE credible set (Credible_Set_ID). Only significant Olink cis-pQTL credible sets are shown in this table (credible sets associated with an Olink protein measure containing at least one variant p-value<$5x10^{-8}$, traditional genome-wide significance threshold).
* Non-abundance protein-altering variants (PAVs) are PAVs associated with differences in peptide abundances as measured by mass-spectrometry in the QMDiab study (n= 345), but not protein abundances [5], and are postulated to drive assay interference QTLs.

Supplementary Data 33. Significant SomaScan trans-pQTL Credible Sets For All SeqIDs
Each row shows trans-pQTL association statistics for an individual variant with a SomaScan protein measure. trans-pQTL were generated with linear regression under an additive model (two-sided test of significance). Variants are grouped according to SuSiE credible set (Credible_Set_ID). Only significant SomaScan trans-pQTL credible sets are shown (credible sets containing at least one variant p-value<$1x10^{-11}$, traditional genome-wide significance threshold corrected for 2,157 proteins tested). * Non-abundance protein-altering variants (PAVs) are PAVs associated with differences in peptide abundances as measured by mass-spectrometry in the QMDiab study (n=345), but not protein abundances [5], and are postulated to drive assay interference QTL.

Supplementary Data 34. Significant Olink trans-pQTL SuSiE Credible Sets For All OlinkIDs
Each row shows trans-pQTL association statistics for an individual variant with an Olink protein measure. trans-pQTL were generated with linear regression under an additive model (two-sided

test of significance). Variants are grouped according to SuSiE credible set (Credible_Set_ID). Only significant Olink trans-pQTL credible sets are shown (credible sets containing at least one variant p-value<$1x10^{-11}$, traditional genome-wide significance threshold further corrected for 2,157 proteins tested).

Supplementary Data 35. pQTL by Limit of Detection (LOD) -- All Probes per UniProt.
pQTL status by platform LOD for set of probes targeting overlapping UniProt IDs on each platform.

Supplementary Data References

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