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BRAIN COMMUNICATIONS

SCFD1 expression quantitative trait loci in amyotrophic lateral sclerosis are differentially expressed

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Evidence indicates that common variants found in genome-wide association studies increase risk of disease through gene regulation via expression Quantitative Trait Loci. Using multiple genome-wide methods, we examined if Single Nucleotide Polymorphisms increase risk of Amyotrophic Lateral Sclerosis through expression Quantitative Trait Loci, and whether expression Quantitative Trait Loci expression is consistent across people who had Amyotrophic Lateral Sclerosis and those who did not. In combining public expression Quantitative Trait Loci data with Amyotrophic Lateral Sclerosis genome-wide association studies, we used Summary-data-based Mendelian Randomization to confirm that *SCFD1* was the only gene that was genome-wide significant in mediating Amyotrophic Lateral Sclerosis risk via expression Quantitative Trait Loci (Summary-data-based Mendelian Randomization beta = 0.20, standard error = 0.04, *P*-value = 4.29×10^{-6}). Using *post-mortem* motor cortex, we tested whether expression Quantitative Trait Loci showed significant differences in expression between Amyotrophic Lateral Sclerosis ($n = 76$) and controls ($n = 25$), genome-wide. Of 20 757 genes analysed, the two most significant expression Quantitative Trait Loci to show differential in expression between Amyotrophic Lateral Sclerosis and controls involve two known Amyotrophic Lateral Sclerosis genes (*SCFD1* and *VCP*). *Cis*-acting *SCFD1* expression Quantitative Trait Loci downstream of the gene showed significant differences in expression between Amyotrophic Lateral Sclerosis and controls (top expression Quantitative Trait Loci beta = 0.34, standard error = 0.063, *P*-value = 4.54×10^{-7}). These *SCFD1* expression Quantitative Trait Loci also significantly modified Amyotrophic Lateral Sclerosis survival (number of samples = 4265, hazard ratio = 1.11, 95% confidence interval = 1.05–1.17, *P*-value = 2.06×10^{-4}) and act as an Amyotrophic Lateral Sclerosis trans-expression Quantitative Trait Loci hotspot for a wider network of genes enriched for *SCFD1* function and Amyotrophic Lateral Sclerosis pathways. Using gene-set analyses, we found the genes that correlate with this trans-expression Quantitative Trait Loci hotspot significantly increase risk of Amyotrophic Lateral Sclerosis (beta = 0.247, standard deviation = 0.017, $P = 0.001$) and schizophrenia (beta = 0.263, standard deviation = 0.008, *P*-value = 1.18×10^{-5}), a disease that genetically correlates with Amyotrophic Lateral Sclerosis. In summary, *SCFD1* expression Quantitative Trait Loci are a major factor in Amyotrophic Lateral Sclerosis, not only influencing disease risk but are differentially expressed in *post-mortem* Amyotrophic Lateral Sclerosis. *SCFD1* expression Quantitative Trait Loci show distinct expression profiles in Amyotrophic Lateral Sclerosis that correlate with a wider network of genes that also confer risk of the disease and modify the disease's duration.

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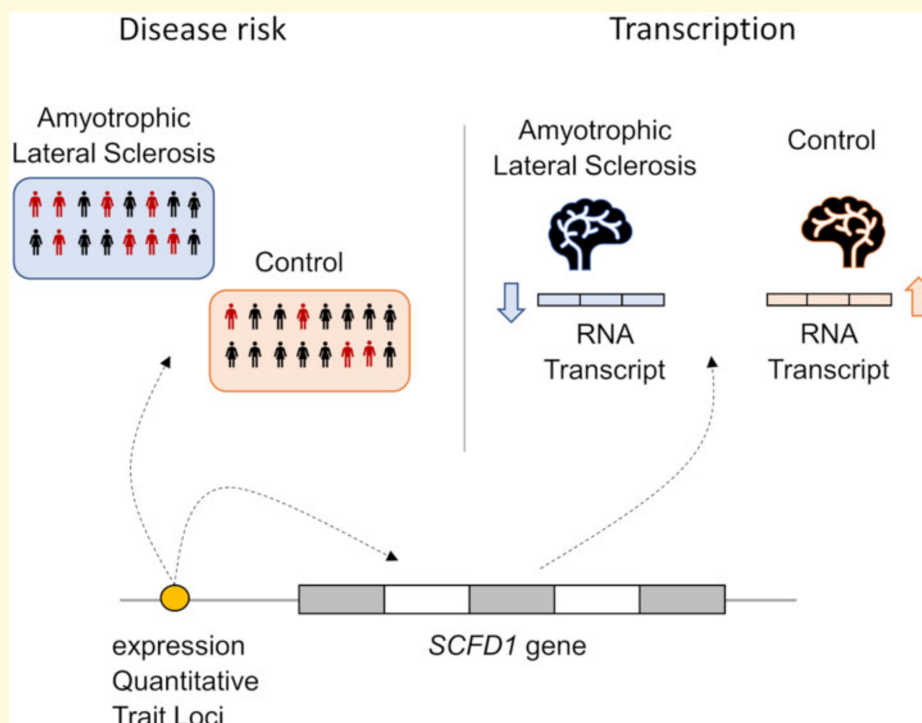
Abbreviations: ALS = amyotrophic lateral sclerosis; GWAS = genome-wide association study; CI = confidence Interval; D′ = D-prime; eQTL = expression Quantitative Trait Loci; ER = endoplasmic reticulum; FDR = false discovery rate; FTD = frontotemporal dementia; GO = gene ontology; GRCh37 = Genome Reference Consortium human build 37; GTEx = genotype-tissue expression project; HG19 = human genome build 19; hp-τ = hyperphosphorylated tau; KB = kilobase; NES = normalized effect size; r^2 = R-squared; RIN = RNA integrity number; rsID = reference SNP identifier; SD = standard deviation; SE = standard error; SMR = summary-data-based Mendelian Randomization; SNP = single nucleotide polymorphism; VST = variance stabilizing transformation

Graphical Abstract



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Introduction

Amyotrophic lateral sclerosis (ALS) is characterized by the progressive degeneration of upper and lower motor neurons, which leads to muscle weakness and loss of voluntary control of the limbs. More than 50% of people with ALS have extra-motor symptoms including cognitive and behavioural impairments. Multiple genetic, environment and lifestyle factors coincide to cause the disease. Most of our understanding of what causes ALS is derived from genetic, proteomic, functional and epidemiological research. Two disease-modifying treatments are licensed for ALS, Riluzole[1] and Edaravone,[2] but their exact molecular effects on the disease mechanism remain unclear.

Our genetic understanding of ALS is derived from rare variants that co-segregate with disease in families and variants common in the population [single nucleotide polymorphism (SNPs)] that associate with disease risk. Rare variants often provide a link between genes and protein dysfunction. Genes implicated in ALS that have rare deleterious mutations, such as *TARDBP*,[3–5] *FUS*,[6,7] *SOD1*,[8] *OPTN*,[9] *ANXA11*,[10] *UBQLN2*,[11] suggest protein dysfunction in RNA metabolism, protein homeostasis, oxidative stress and vesicle transport.

SNPs that associate with disease risk, typically identified through genome-wide association studies (GWAS), can have a less obvious relationship with disease mechanism. SNPs often implicate multiple genes within a genomic region and can be very common in the general population where the increase in disease risk is marginal. For ALS there is also little reconciliation between with pathways identified through rare, large effect variants and genes identified using GWAS.

There is increasing evidence that most common SNPs that associate with disease regulate gene expression.[12] One method in identifying regulatory SNPs is to analyse whether changes in genotype correlate with changes in gene expression; referred to as expression Quantitative Trait Loci (eQTL). eQTLs can help clarify which gene(s) in a genomic region are modifying disease risk, can provide insights into how, and also provide information on which tissues and cells are affected.[13] eQTLs have been associated with increased risk of schizophrenia,[14] Alzheimer's disease[15] and Parkinson's disease,[16] as examples.

Using public GWAS and eQTL data, we confirmed the most significant gene to increase risk of ALS via eQTLs is *SCFD1*, which concurs with previous studies using different methods.[17,18] In an independent analysis, we find *SCFD1* eQTL expression is significantly different in *post-mortem* ALS compared to controls. And that *SCFD1* eQTLs are hotspot in ALS that significantly correlate with major ALS pathways and ALS survival. Our findings indicate that while *SCFD1* eQTLs increase risk of ALS, the expression profile of these eQTLs is different in ALS compared to controls, and these changes correlate with disease duration and pathways known to be compromised in the disease, namely vesicle-mediated transport, RNA metabolism and transmembrane trafficking.

Materials and methods

Samples and cohorts

Genomic datasets

We used the largest ALS GWAS[19] for which summary statistics were publicly available, which included 80 610 individuals (20 806 cases and 59 804 controls) of European ancestry and 10 031 417 SNPs. In this study, the authors compared allelic frequency between ALS cases and controls from the UK, USA, Italy, France and Belgium (8229 cases and 36 329 controls in total) by logistic regression and a fixed-effects meta-analysis, integrating our antecedent European ALS GWAS (12 577 cases and 23 475 controls).[20]

For the survival analysis, we used the largest ALS survival GWAS available.[21] In this study, the authors analysed if alleles associated with changes in ALS survival (from date of diagnosis to date of death) for 4256 ALS patients and 7 174 392 SNPs, using genome-wide Cox proportional hazards regression and controlling for age of onset, sex, and four principal components.

Publicly available eQTL datasets

eQTL data were downloaded from the Genotype-Tissue Expression (GTEx) portal,[13] for frontal cortex (BA9), cortex, cerebellum and cerebellar hemisphere. We used the GTEx Analysis V8 (dbGaP Accession phs000424. v8. p2 accessed 10/05/2020), the latest release at the time. For consistency with genotype datasets used in this study, we mapped the hg38 genomic coordinates of the GTEx V8 data onto hg19 using the liftover tool in UCSC Genome Browser.

Post-mortem samples

Post-mortem motor cortex was provided by the MRC London Neurodegenerative Diseases Brain Bank based at the Institute of Psychiatry, Psychology & Neuroscience, King's College London. Ethical approval was granted via local committee at King's College London and MRC London Neurodegenerative Diseases Brain Bank. Tissue was flash frozen and stored at −80°C. One hundred milligrams of tissue blocks were excised. RNA and DNA were isolated from the same tissue block.

Samples were selected based on availability. The cohort was age-sex matched manually ($n = 108$) and sex, age and *post-mortem* delay were analysed for statistically significant differences using a Student's t-test (Supplementary Results). Five samples were removed as they were outliers in the genomic principal components' analyses (indicating non-European ancestry) and two samples removed showing significant shared identity by

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descent (indicating familial relations); see Supplementary Methods 3 and Results 2. The final cohort consisted of 76 ALS and ALS-FTD donors, and 25 non-ALS age-sex matched controls with no known neurological disease (pathology below hp-τ and BNE\Braak stages 2; Supplementary Table 1). Owing to clinical data collected at the time of donation, we are unable to estimate the proportion of pure ALS compared to ALS patients who had FTD involvement. The ALS cohort was screened for ALS mutations, where 5 donors had the *C9orf72* repeat mutation, one donor had an *ANXA11* D40G mutation, and one donor had a *PFN1* E117G mutation.

Statistical analyses

Genome-wide eQTL analyses using genomic summary-statistics and GTEx

See Supplementary Methods 1 for gene-level genome-wide association study.

Mendelian Randomization analyses

To analyse the effects that eQTLs have on ALS risk we performed summary-data-based Mendelian Randomization (SMR) with Heidi tests, using the SMR tool.[22] We used eQTL summary statistics from the GTEx Portal for cortical and cerebellar tissues as exposure, and the ALS GWAS disease status as an outcome. We selected frontal cortex and cerebellar eQTLs from GTEx with a *P*-value $< 5 \times 10^{-8}$ and cortex eQTLs with *P*-value $< 5 \times 10^{-7}$. SNPs extracted from the ALS GWAS that were not present in the GTEx eQTL dataset were removed.

Direction of effects between exposure and SNP allele were harmonized. A total of 11 728 eQTL gene-targets were tested and 11 198 passed the heterogeneity filter ($P_{HEIDI} > 0.05$, with number of SNPs > 2). We set the significant threshold at $P = 0.05/11{,}198$ (4.5×10^{-6}) to correct for multiple-testing. To confirm these results, we used an eQTL dataset from Braineac[16] (see Supplementary Methods and Supplementary Results).

Genome-wide QTL analyses in *post-mortem* motor cortex

See Supplementary Methods for RNA-sequencing, genotyping and imputation methods.

Statistically significant eQTLs, with a nominal *P*-value = 1×10^{-5}, identified in GTEx were downloaded for cortex, frontal lobe (BA9), cerebellum and cerebellar hemisphere. These eQTLs were extracted from our *post-mortem* genotype imputation dataset based on their reference SNP identifier, position and effect allele. The resulting file was a post-mortem genotype dataset consisting of GTEx brain-specific eQTLs only.

Post-mortem motor cortex RNA-sequence data were normalized using variance stabilizing transformation (VST) at the gene-level (Ensembl GRCh37). Genes with a read-count less than 10, normalized expression for genes at a minimal value, and genes showing variance within the lower quartile genome-wide, were removed, resulting in 20 757 testable Ensembl gene IDs. For distribution, minimum, quartile and maximum normalized expression estimates see Supplementary Fig. 1A.

Matrix eQTL[23] was used to import and analyse eQTLs genome-wide. Genotype data, gene expression data, SNP maps and gene locations were standardized to GRCh37 (hg19). Matrix eQTL uses an additive linear least squares model to test for association between SNPs and gene-level expression. We removed SNPs with a minor allele count less than five in cases and controls separately, to allow sufficient statistical power to detect variation in gene expression that correlated with genotypes. We also removed outlier samples and SNPs (see Supplementary Methods). See previous paragraph on removing genes with insufficient variation after normalization.

Given that we were interested in identifying eQTLs that had differential expression in ALS donors compared to controls, our model tested for an interaction between genotype and disease status on the gene expression, genome-wide. This model incorporated covariates: sex, age of death, *post-mortem* delay and surrogate variables (see Supplementary Fig. 1B). Surrogate variable analysis was calculated using SVA[24] and SVASeq.[25] We also implemented a model with covariates RNA integrity number (RIN) and flow-cell ($n = 2$), and these covariates did not show significant impact on gene expression. As our library preparation protocols accounted for RNA fragmentation profiles and surrogate variable analysis controls for RNA degradation effects, we omitted RIN from the final analysis. Reported fold-changes, beta values, standard error and *P*-values are from the interaction term in additive linear model. *P*-values were adjusted for multiple testing using false discovery rate (FDR).

Evidence indicates that the correlation between SNPs and gene expression beyond 850 kb becomes marginal,[12] therefore, *cis*-acting eQTLs were categorized as being within an 850 kb region from SNP to gene boundary (determined by Ensembl gene GRCh37coordinates). eQTLs were categorized as *trans*-acting if greater than this region.

Analyses above were implemented using DESeq2[26] and MatrixEQTL.[23] eQTL and Manhattan plots were created using ggplots in R,[27] LocusZoom[28] and rMVP (https://github.com/xiaolei-lab/rMVP Accessed 13 October 2021).

Post-mortem cell deconvolution analysis

BRETIGEA was used to estimate cell composition per sample using BRETIGEA's cell marker dataset (50 markers).[29] To analysis differences in cell composition by type across samples, we used a linear regression model to compare cell-type estimates between ALS and controls controlling for variables age of death, post-mortem delay, RIN, and surrogate variables from the previous analysis. We report beta, standard error and non-adjusted *P*-values from these analysis in the Supplementary Results.

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ALS survival genotype and gene-level analysis

To analyse the effect of eQTLs on ALS survival, we used Cox proportional hazards GWAS summary statistics[21]; see *Genomic Datasets*.

For gene-level and gene-set analyses, we used MAGMA[30] incorporating a flanking region of 40 kb downstream and upstream of the genes, to cover the *SCFD1* eQTL haplotype. The ALS survival GWAS summary results were used to assess change in survival as a function of eQTLs and raw genotype data used for Kaplan–Meier plots (using R) to show changes in survival as a function of *SCFD1* eQTL genotypes.

Co-expression analyses

To identify genes that co-express with *SCFD1* and correlate with *SCFD1* eQTLs, we incorporated a Pearson's r correlation analysis using normalized expression values from *post-mortem* ALS RNA-sequence data. This created a one-to-many correlation matrix, where *SCFD1* r and P-values were calculated for each *trans*-acting gene that associated with *post-mortem* ALS via *SCFD1* downstream eQTLs. Because we are interested in a wider network of genes, we report non-adjusted P-values unless stated others. Correlation matrices were plotted using Performance Analytics and ggplots in R.

Gene function enrichment and over-representation analyses

We implemented three gene function enrichment analyses. The first was a rank-ordered analysis using g: profiler (https://biit.cs.ut.ee/gprofiler/gost). Categories with a g: profiler adjusted P-value < 0.05 were deemed statistically significant. Generic Enrichment Map (GEM) and Gene Matrix Transposed (GMT) files from this analysis were used for the Gene Set Enrichment Analyses (GSEA) analyses.[31] For the second enrichment analysis, we used Enrichr (https://amp.pharm.mssm.edu/Enrichr/), where categories with rank-based adjusted P-values < 0.05 were regarding as statistically significant unless stated otherwise. The third function enrichment analysis was performed on *SCFD1* positively and negatively co-expressed genes, using 5000 permutations and GMT files generated from g: profiler. Gene ontology (GO) categories with an FDR corrected q-value < 0.05 were deemed statistically significant, unless stated otherwise. To test if genes significantly overlapped between two gene-sets we implemented an over-representation adapted from: http://nemates.org/MA/progs/overlap_stats.html (Supplementary Methods).

Data availability

Datasets are available, on reasonable request. The post-mortem genetic and RNA-sequence datasets are available from the corresponding author, the GWAS survival datasets are available through Dr Isabella Fogh, and the Braineac eQTL datasets are available through the UK Brain Expression Consortium.

Results

ALS GWAS and eQTLSCFD1 eQTLs increase risk of ALS

To confirm and contextualize which SNPs increase risk of ALS via eQTLs, we performed genome-wide summary-data-based Mendelian Randomization (SMR) using eQTLs derived from cortex, cerebellum and blood as instrumental variables, gene expression as exposure, and ALS disease status as outcome. Here, SMR is testing the likelihood that SNPs that increase risk of ALS do so through modifying gene expression. Filtering for genes with $P_{HEIDI} > 0.05$, we found *SCFD1* was the only gene to show genome-wide significant association with ALS in cerebellum [SMR beta = 0.20, SMR standard error (SE) = 0.043, SMR P-value = 4.29×10^{-6}]. In addition, *SCFD1* eQTLs showed association with ALS with the lowest genome-wide P-values in frontal cortex (SMR beta = 0.27, SMR SE = 0.072, SMR P-value = 1.34×10^{-4}). In GTEx, there are no cortical *SCFD1* eQTLs with a P-value $< 5 \times 10^{-8}$ so we ran the SMR analysis using a GTEx P-value threshold = 5×10^{-7}, where *SCFD1* had the second lowest association P-value (SMR beta = 0.30, SMR SE = 0.085, SMR P-value = 3.81×10^{-4}); see Table 1 and Supplementary Fig. 2, and see Supplementary Table 2 for the genome-wide gene-level association analysis.

SCFD1 eQTLs that increase risk of ALS do not correlate with SCFD1 expression in ALS motor cortex

The most significant *SCFD1* SNP to associate with ALS is rs10139154.[20] It is a significant eQTL in GTEx (V8) for cerebellum [Normalized Effect Size (NES) = 0.330, SE = 0.033, P-value = 7.54×10^{-19}], cerebellar hemisphere (NES = 0.314, SE = 0.036, P-value = 1.33×10^{-14}), frontal cortex (NES = 0.233, SE = 0.046, P-value = 1.7×10^{-6}) and cortex (NES = 0.18, SE = 0.041, P-value = 2.2×10^{-5}). In GTEx, for each rs10139154 T allele there is an increase in *SCFD1* expression. Using our *post-mortem* control data, we confirmed this correlation (beta = 0.16, SE = 0.047, P-value = 0.03). However, the rs10139154 eQTL in our *post-mortem* ALS cohort we did not find significant correlation with *SCFD1* expression (beta = 0.02, P-value = 0.12) (Supplementary Fig. 3). This finding indicates *SCFD1* eQTLs that associate with disease risk may have a different relationship between genotype and expression in post-mortem ALS compared to controls.

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Post-mortem differential eQTL expression

SCFD1 eQTLs show significant differences in expression in post-mortem ALS

Given eQTLs that increase risk of ALS showed differences in the relationship between genotype and expression in patients compared to controls, we performed a *post-mortem* eQTL differential expression analysis modelling the effect of disease status by genotype. We ran this analysis genome-wide for *cis*-acting eQTLs in *post-mortem* motor cortex comparing age and sex matched ALS ($n = 76$ and) non-ALS control donors ($n = 25$) (see Supplementary Result and Supplementary Table 1).

The most statistically significant *cis*-acting eQTL to show differential expression was for gene *C9orf24*. The eQTL locus was upstream of *C9orf24* and formed a haplotype over ALS genes *VCP* and *DNAJB5*. For the most significant eQTL rs2782401, the addition of each G allele correlated with an increase in *C9orf24* expression in ALS donors, in contrast to controls where G alleles correlated with a decrease in *C9orf24* expression (top eQTL = rs2782401, beta = 0.44, SE = 0.076, P-value = 6.30×10^{-8}); see Fig. 1A and B. rs2782401 is a significant GTEx eQTL for *VCP* (NES = 0.10, SE = 0.018, P-value = 3.57×10^{-9}) and *DNAJB5* (NES = −0.186, SE = 0.037, P-value = 7.07×10^{-7}).

The second most significant *cis*-acting eQTL to show differential expression in ALS was for *SCFD1*. These eQTLs were approximately 500 kb downstream of *SCFD1* and were largely concentrated across genes *HEATR5A*, *DTD2*, *HECTD1* and *NUBPL* (top eQTL = rs8005942, beta = 0.34, SE = 0.063, P-value = 4.54×10^{-7}); see Fig. 1C and D. While a decrease in *SCFD1* gene expression significantly correlated with each additional in rs8005942 A allele in controls, the opposite was found for ALS samples, where an increase in *SCFD1* expression was found with each additional A allele (see Supplementary Table 3).

Post-mortem cell deconvolution analysis

In our *post-mortem* differential eQTL expression analysis, we have used surrogate variable analysis to control for differences in cell heterogeneity across samples and sample groups. To further examine if the above findings could be explained by differences in cell composition, we performed cell deconvolution analysis to estimate the presence of cell types across all samples. In comparing ALS samples with controls, we found that disease status in our model did not predict differences in cell estimates for any cell type (see Supplementary Table 4). Furthermore, there were no significant differences in RIN estimates between ALS and controls (beta = 0.299, SE = 0.230, P-value = 0.190).

Differentially expressed *SCFD1* eQTLs significantly modify ALS survival

In our first analysis (SMR using GTEx-derived eQTLs), we confirmed eQTLs either within or immediately adjacent to *SCFD1* increased risk of ALS. In our second *post-mortem* analysis, testing for differences in eQTL expression between ALS and control donors, we identified an additional locus of *SCFD1* eQTLs downstream of the gene that associated with disease status. These two *SCFD1* eQTL loci are not in linkage disequilibrium. Given that the *SCFD1* downstream eQTLs do not necessarily increase risk of ALS we examined their influence on survival.

We used summary statistics from a 2016 ALS GWAS[21] that estimated the effect of genotypes on ALS survival. We filtered SNPs within a 1 Mb flanking region of *SCFD1*. The most significant SNP to modify ALS survival in the region was rs35330064, which is linkage disequilibrium with eQTLs that show differences in expression *post-mortem*. Homozygosity for the rs35330064 minor allele (AA) reduced survival in ALS by a median of 4.8 months (Hazard ratio = 1.11, 95% CI 1.05–1.17, P-value = 2.06×10^{-4}); see Fig. 2. rs35330064 was in linkage disequilibrium with the eQTLs that showed differential expression. For example, rs35330064 homozygosity (AA) showed significant linkage disequilibrium with rs8005942 (AA) ($r^2 = 0.687$, $D' = 1$, Chi-Square = 125.10, P-value $< 1 \times 10^{-4}$), the most significant eQTL to show differential expression in ALS in this region (see Supplementary Fig. 4).

rs35330064 and rs8005942 eQTLs are a part of a haplotype spanning genes *HEATR5A*, *DTD2*, *NUBPL* AND *GPR33* (see Fig. 2A). To understand if the region was influencing ALS survival, we performed a gene-set analysis of SNPs in these four genes using summary statistics from the 2016 ALS survival GWAS. Collectively, these four genes significantly influenced survival, where beta = 2.20, SE = 0.032, P-value = 3.45×10^{-5}. The most significant gene to show association with changes in ALS survival was for *HEATR5A* (Z Statistic = 2.38, P-value = 0.007), where most of the eQTLs that show differential expression in *post-mortem* donors are concentrated. In general, the directionality of genotypes indicates that increased *SCFD1* expression may reduce ALS survival.

SCFD1 eQTLs form a *trans*-QTL hotspot that associates with *post-mortem* ALS

We used the *post-mortem* motor cortex dataset to test for *trans*-acting eQTLs that show significant differences in expression between ALS ($n = 76$) and non-ALS donors ($n = 25$). The most significant *trans*-acting eQTLs that was differentially expressed in ALS, after genome-wide FDR correction, was for gene *PPP1R8* (top eQTL = rs56314035_C, beta = −0.371, SE = 0.053, P-value = 3.55×10^{-10}); Supplementary Fig. 5. Notably, the base pair locations and genotypes for these *PPP1R8 trans*-acting eQTLs were the same as the *SCFD1* eQTLs (from

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Table 1 Results from genome wide SMR analysis using GTEx eQTLs from Cortex, Cerebellum, Frontal Cortex, and Blood, and ALS GWAS SNPs, where SMR *P*-value $< 1 \times 10^{-3}$

Gene	Chr.	Top SNP BP	GWAS *P*-value	eQTL *P*-value	SMR Beta	SMR SE	SMR *P*-value	Heidi *P*-value	Heidi N SNPs
Cerebellum									
SCFD1	14	30622112	2.64×10^{-7}	3.14×10^{-24}	0.197	0.043	4.29×10^{-6}[a]	0.695	20
TRIM65	17	75880335	6.36×10^{-5}	1.76×10^{-30}	−0.083	0.022	1.62×10^{-4}	0.869	20
TRIP11	14	91965991	8.08×10^{-6}	2.45×10^{-8}	0.265	0.072	2.16×10^{-4}	0.765	18
MESDC2	15	80946289	4.51×10^{-4}	1.04×10^{-13}	0.109	0.034	1.50×10^{-3}	0.634	20
Cortex									
FBF1	17	75909574	8.54×10^{-5}	4.41×10^{-22}	−0.104	0.028	2.63×10^{-4}	0.686	20
SCFD1	14	30622112	1.09×10^{-6}	2.11×10^{-7}	0.301	0.085	3.81×10^{-4}	0.513	13
ZNF391	6	27374615	1.63×10^{-4}	4.39×10^{-11}	−0.159	0.049	1.07×10^{-3}	0.495	20
PLEKHG5	1	6466196	1.36×10^{-4}	1.16×10^{-7}	0.271	0.087	1.93×10^{-3}	0.297	7
Frontal cortex									
SCFD1	14	30622112	2.24×10^{-7}	1.41×10^{-8}	0.273	0.072	1.34×10^{-4}	0.945	20
DENND6B	22	50309030	1.17×10^{-4}	7.99×10^{-16}	0.182	0.052	5.25×10^{-4}	0.731	20
GOLGA6L10	15	82339998	2.34×10^{-4}	3.16×10^{-18}	0.064	0.019	6.80×10^{-4}	0.753	20
TESC	12	117038923	1.96×10^{-4}	1.69×10^{-10}	−0.171	0.053	1.29×10^{-3}	0.123	20
Blood									
SCFD1	14	30622112	3.87×10^{-7}	1.88×10^{-56}	−0.258	0.053	1.38×10^{-6}[a]	0.634	20
GGNBP2	17	36544888	3.27×10^{-6}	1.83×10^{-27}	0.434	0.102	1.90×10^{-5}	0.279	20
TNIP1	5	151029945	7.14×10^{-7}	1.52×10^{-15}	−0.45	0.107	2.56×10^{-5}	0.538	7
PLXNB2	22	50274979	7.45×10^{-6}	3.72×10^{-12}	−0.547	0.146	1.71×10^{-4}	0.236	20

For Cerebellum, Frontal Cortex and Blood, SCFD1 eQTLs showed the most significant association with ALS genome wide. For Cortex SCFD1 eQTLs were second most significant to associate ALS genome-wide. Genes with $P_{HEIDI} < 0.05$ (Heidi *P*-value) were removed. Genes organized by their GWAS *P*-value association. Chr: Chromosome. Top SNP BP: Genomic base-pair location of most significantly associated SNP with ALS.
[a]Genome-wide significant.

the *post-mortem cis*-acting eQTL analyses); Fig. 1A. *SCFD1* significantly co-expressed with *PPP1R8* in our *post-mortem* ALS samples, where Pearson's $r = 0.386$ and P-value $= 6.18 \times 10^{-4}$.

Similar to *PPP1R8*, we found that many of the *trans*-acting eQTLs that show differences in expression in *post-mortem* ALS, significantly overlapped with *SCFD1* eQTLs. To explore this, we expanded our search for *trans*-acting eQTLs that were differentially expressed in ALS, by increasing the *P*-value to $P < 5 \times 10^{-5}$. We then mapped each of these *trans*-acting eQTLs by their genomic location and calculated the number genes the eQTLs correlated with. We found that the number of genes ($n = 382$) that were differentially expressed via *trans*-acting eQTLs in ALS, and which were located in *SCFD1* eQTL locus downstream of the gene, to be the highest in the genome compared to other loci (see Fig. 3). These 382 genes also show significant levels of co-expression with *SCFD1* (see Supplementary Results; see Supplementary Fig. 6).

In summary, *SCFD1 cis*-acting eQTLs that show significant differences in expression between ALS and controls are not just correlated with *SCFD1*, but correlate with a wider network of genes that show expression changes in *post-mortem* ALS. And the number of genes that associate with *post-mortem* ALS via *trans*-acting eQTLs are most concentrated in this *SCFD1* locus, more than anywhere else on the genome. These results suggest that *SCFD1* eQTLs are having a wider impact on transcriptional pathways, that are specific to ALS, which we will explore next. We will refer to this *SCFD1* eQTL locus as the *SCFD1 trans*-eQTL hotspot.

Genes that associate with the *SCFD1 trans*-eQTL hotspot are enriched for ALS pathways

To assess the wider effects of the *SCFD1 trans*-eQTL hotspot in ALS, we selected genes with differentially expressed *trans*-acting eQTLs where $P < 5 \times 10^{-5}$. We also included an additional 8 genes which are proximal to the *SCFD1 trans*-eQTL hotspot and show differences in

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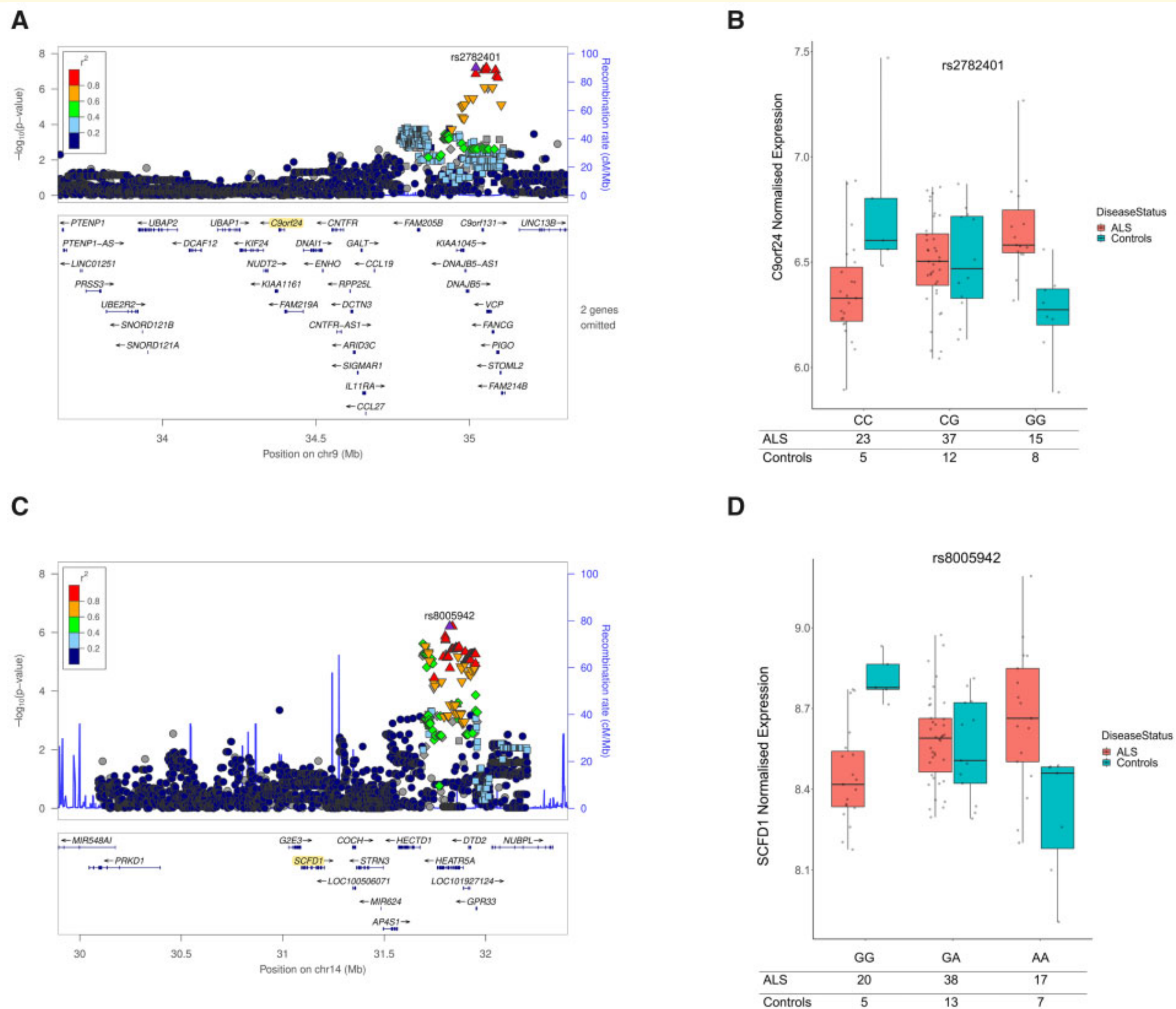

Figure 1 The most significant eQTL loci differentially expressed in *post-mortem* ALS compared to controls. (**A**) Locus plot of *C9orf24* eQTLs, where *P*-values are derived from differences in *C9orf24* eQTL expression between ALS cases and controls. Points are *C9orf24* eQTLs, point-colour represent r^2 LD with the most significant *C9orf24* eQTL (rs2782401) to associate with ALS, the *x*-axis is the genomic location of the eQTLs, and the *y*-axis is the −log10(*P*-value) of the eQTL association test. Upward-triangles LD $r^2 > 0.8$, downward-triangles LD r^2 between 0.8 and 0.6, rhombi LD r^2 between 0.6 and 0.4, and squares LD r^2 between 0.4 and 0.2. **(B)** Jitter-boxplot of *C9orf24* eQTL rs2782401 expression by genotype (beta = 0.44, *P*-value = 6.30×10^{-8}). Statistics taken from the linear additive model testing eQTL association with ALS modelling genotype by disease status. *X*-axis: rs2782401 genotypes; *y*-axis: normalized *C9orf24* expression; Points: *C9orf24* expression estimates by sample, differentiated into controls (red) and ALS cases (blue). **(C)** Locus plot of *SCFD1* eQTLs, where *P*-values are derived from differences in *SCFD1* eQTL expression between ALS cases and controls. Dots are *SCFD1* eQTLs, dot-colour represent r^2 LD with the most significant *SCFD1* eQTL (rs8005942) to associate with ALS, the *x*-axis is the genomic location of the eQTLs, and the *y*-axis is the −log10(*P*-value) of the eQTL association test. Upward-triangles LD $r^2 > 0.8$, downward-triangles LD r^2 between 0.8 and 0.6, rhombi LD r^2 between 0.6 and 0.4, and squares LD r^2 between 0.4 and 0.2. **(D)** Jitter-boxplot of *SCFD1* eQTL rs8005942 expression by genotype (beta = 0.34, *P*-value = 4.45×10^{-7}). Statistics taken from the linear additive model testing eQTL association with ALS modelling genotype by disease status. *X*-axis: rs8005942 genotypes; *y*-axis: normalized *SCFD1* expression; Points: *SCFD1* expression estimates by sample, differentiated into controls (red) and ALS cases (blue). In summary, this figure. shows that there are eQTLs that are differentially expressed in ALS compared to controls. The top two most significant loci both implicate ALS genes, with the first loci (A) located at ALS gene *VCP* and the second loci (C) showing differential eQTL expression of ALS gene *SCFD1*.

expression in ALS compared to controls: *SCFD1*, G2E3, *HEATR5A*, *HECTD1*, *NUBPL*, *COCH* and *DTD2*.

Using a final list of 389 genes, we performed gene function enrichment analyses (see Table 2A and Supplementary Table 5). We found genes that associate with *post-mortem* ALS via the *SCFD1 trans*-eQTL hotspot were significantly enriched for *SCFD1* function and ALS pathways. *SCFD1* is involved in retrograde vesicle-

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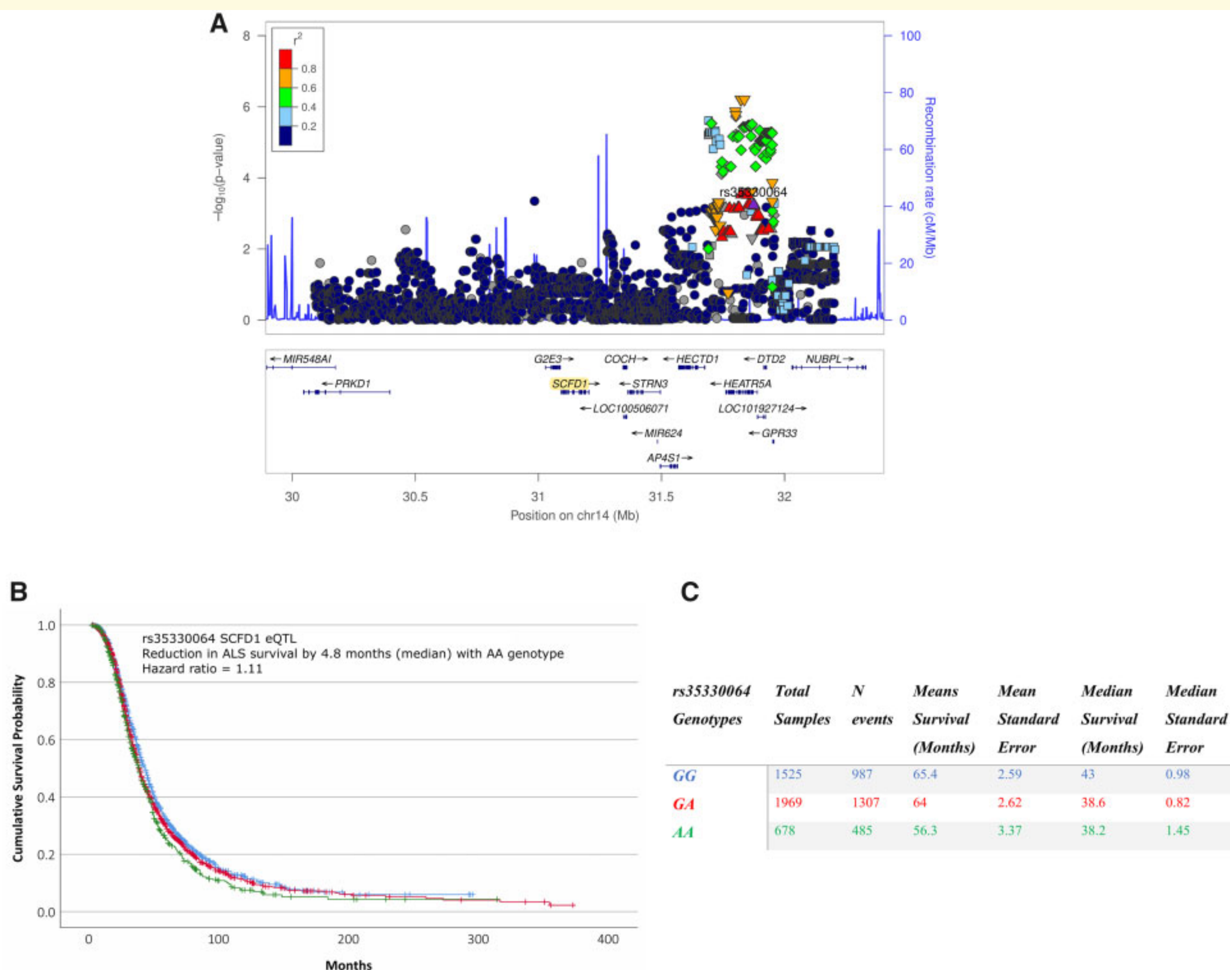

rs35330064 Genotypes	*Total Samples*	*N events*	*Means Survival (Months)*	*Mean Standard Error*	*Median Survival (Months)*	*Median Standard Error*
GG	1525	987	65.4	2.59	43	0.98
GA	1969	1307	64	2.62	38.6	0.82
AA	678	485	56.3	3.37	38.2	1.45

Figure 2 The relationship between SCFD1 eQTLs and SNPs that modify ALS survival. (**A**) Locus plot of SCFD1 eQTLs, where *P*-values are derived from differences in SCFD1 eQTL expression between ALS cases and controls. Points are SCFD1 eQTLs, point-colour represent r^2 LD with the most significant SCFD1 eQTL (rs35330064) to associate with ALS survival, the *x*-axis is the genomic location of the eQTLs, and the *y*-axis is the $-\log10$(*P*-value) of the eQTL association test. Upward-triangles LD $r^2 > 0.8$, downward-triangles LD r^2 between 0.8 and 0.6, rhombi LD r^2 between 0.6 and 0.4, and squares LD r^2 between 0.4 and 0.2. (B) Kaplan–Meier plot and table results showing the effect of rs35330064 genotypes on ALS survival. Kaplan–Meier *x*-axis show ALS survival in months, *y*-axis is the cumulative survival probability, and legend table displays in the effect of rs35330064 genotypes on ALS survival. In summary, this figure. shows that SCFD1 eQTLs that are differentially expressed in ALS significantly influence the disease duration of ALS.

mediated protein transport from the ER-to-Golgi, and the regulation of synaptic vesicle docking and exocytosis. These results indicate that *SCFD1* eQTLs do not only correlate with *SCFD1* expression but with a wider functional pathway that is differentially expressed in *post-mortem* ALS.

Genes that associate with the ALS *SCFD1 trans*-eQTL hotspot are enriched for disease risk

Our previous analysis of *SCFD1 trans*-eQTL genes ($n = 389$) identified significant enrichment of genes involved in schizophrenia risk (Table 2A). Genetic correlation between ALS and schizophrenia risk has been previously shown, where *SCFD1* was identified as a candidate gene driving risk of both diseases.[32] Performing gene-set analysis on the latest publicly available schizophrenia GWAS,[33] we found that the 389 genes that associated with *post-mortem* ALS via the *SCFD1 trans*-eQTL hotspot were enriched for SNPs that modify schizophrenia risk [beta = 0.263, standard deviation (SD) = 0.036, *P*-value = 1.18×10^{-5}]. Thirteen genes from this set had a statistically significant association below the standard GWAS threshold of $P \leq 5 \times 10^{-8}$, 38 genes below the MAGMA genome-wide threshold of $P \leq 2.7 \times 10^{-5}$, and 148 genes below $P < 0.05$.

Using results from the 2018 ALS GWAS,[19] we performed gene-set analysis on the 387 genes that associated with *post-mortem* ALS status via the *SCFD1 trans*-eQTL hotspot (we removed *SCFD1* and G2E3 from the gene-set, due to their significant association with the disease).

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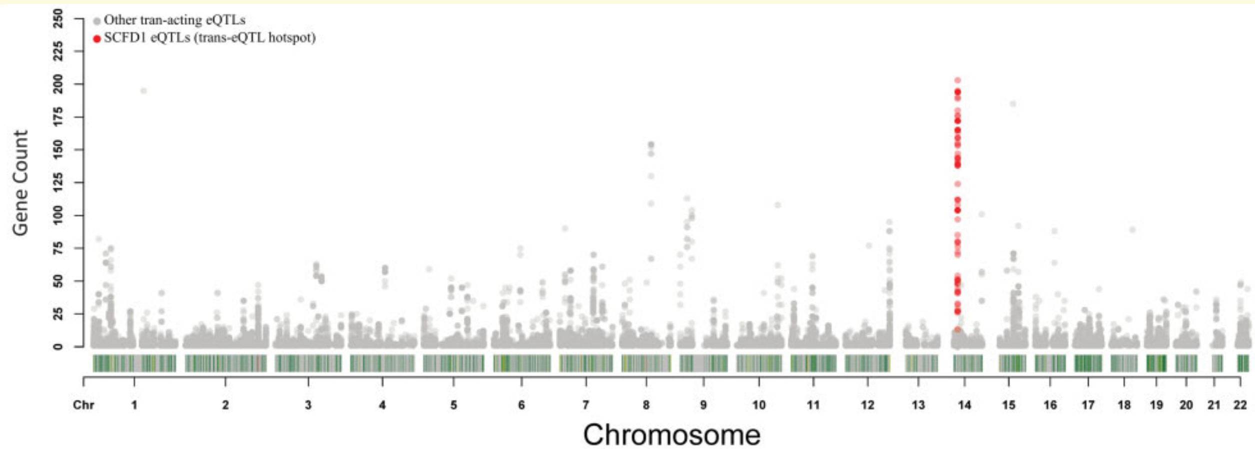

Figure 3 Count of genes that show association with ALS via *trans*-acting eQTLs by genomic location. Dots represent *trans*-acting eQTLs that show significant differences in expression comparing *post-mortem* ALS to controls. The *x*-axis is the genomic locations of these ALS-associated *trans*-acting eQTLs. The *y*-axis displays the number of genes that correlate with these ALS-associated *trans*-acting eQTLs. The highlighted dots (red) are the *cis*-acting *SCFD1* eQTLs that associated with *post-mortem* ALS, from the *post-mortem* genome-wide *cis*-eQTL analysis. In summary, this figure displays the genomic locations of *trans*-acting eQTLs that show significant differences in expression between ALS and controls. *Trans*-acting eQTLs that correlate with the expression of multiple genes are called *trans*-eQTL hotspots. We found that *SCFD1* eQTLs (red dots) formed a *trans*-eQTL hotspot that showed significant differences in expression in ALS, for a large number of genes throughout the genome. This indicates that *SCFD1* eQTLs that associate with ALS are impacting the transcription of other genes at a distance, and that these changes in expression significantly associate with ALS disease status.

This analysis revealed a marginal increase in ALS risk, where beta = 0.05, SD = 0.008, $P = 0.094$. However, we found that the top 100 genes from this list (ranked by their association with *post-mortem* ALS) were significantly enriched for SNPs that increased ALS risk, where beta = 0.247, SD = 0.017, $P = 0.001$.

Discussion

In our first analysis, we confirm that *SCFD1* was the only gene that is genome-wide significant in mediating ALS risk via eQTLs. While we were able to confirm a correlation between ALS risk eQTLs and *SCFD1* expression in our *post-mortem* controls, in our ALS donors the correlation was lost, indicating that *SCFD1* eQTL expression may be influenced by other factors related to the disease.

In our second analysis using motor cortex, we tested if *cis*-acting eQTLs showed differences in expression between ALS and control donors, genome-wide. The top two most significant eQTL loci that show differential expression were for *SCFD1* and *C9orf24*. Differentially expressed *SCFD1* eQTLs significantly associated with ALS survival, as well as a number of differentially expressed *trans*-acting eQTLs across the genome. The genes that correlate with *trans*-acting eQTL ALS-specific changes were highly enriched for *SCFD1* function, ALS pathways, and risk of schizophrenia and ALS. ALS and schizophrenia genetically correlate, where *SCFD1* is a candidate overlapping gene.[32]

In addition to the gene-targets, the genomic location of the top two eQTLs to show differential expression in ALS are relevant to the disease as well. For *C9orf24*, the eQTLs are localized nearby in genes *VCP* and *DNAJB5*. *VCP* is an ALS gene first implicated in the disease in 2010 through the identification of an autosomal dominant point mutation in familial ALS (Johnson et al., 2010). Genomic variants in *DNAJB5* have shown association with neuromuscular diseases, including Charcot-Marie-Tooth disease.[34] The genomic location of differentially expressed *SCFD1* eQTLs, span a number of nearby genes including *NUBPL*, which itself has shown association with ALS via a TDP-43 conditional FDR analysis.[35]

Factors influencing differential eQTL expression

SCFD1 alleles that increase ALS risk via GWAS, increase *SCFD1* expression in brain in non-ALS controls. We confirmed this using two sets of *post-mortem* controls: GTEx and our non-ALS cohort. When we examine ALS donors in our *post-mortem* data, the correlation between ALS *SCFD1* risk alleles and *SCFD1* expression is not present. In addition, we show *cis*-acting eQTLs downstream of *SCFD1* are differentially expressed in ALS. These results indicate the genomic regulation of *SCFD1* eQTLs, in ALS specifically, may be influenced by additional factors.

There are a number of factors that can influence eQTL expression, which show complex relationships between

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Table 2 (A–D) Gene function enrichment results from various analyses

A. Functional categories enriched for genes that are differentially expressed in ALS via the *SCFD1 trans*-eQTL hotspot			
Term Name	**Term ID**	**Adj. *P*-value**	**Tool**
Regulation of vesicle mediated transport[a]	GO:0060627	2.24×10^{-5}	g:profiler
Cellular, protein and organelle localisation[a]	GO:0051641	7.08×10^{-7}	g:profiler
Cytoplasmic vesicles[a]	GO:0031410	0.004	g:profiler
Vesicle mediated transport in synapse	GO:0099003	7.58×10^{-7}	g:profiler
Vesicle docking involved in exocytosis\exocytic vesicles	GO:0070382	3.30×10^{-5}	g:profiler
Calcium/calmodulin signalling	KEGG:04020	0.006	g:profiler
The glutamatergic synapse	GO:0098978	4.20×10^{-6}	g:profiler
mRNA splicing via spliceosome	GO:0048024	0.001[b]	g:profiler
Microtubule genes	GO:0005874	0.002[b]	g:profiler
Schizophrenia	NA	3.99×10^{-4}	Enrichr: DisGeNET
Motor neuron	NA	2.78×10^{-14}	Enrichr: ARCHS4
Brain	NA	3.56×10^{-43}	Enrichr: ARCHS4
Cerebral cortex	NA	1.35×10^{-34}	Enrichr: ARCHS4
Spinal cord	NA	7.86×10^{-20}	Enrichr: ARCHS4
Prefrontal cortex	NA	4.10×10^{-9}	Enrichr: ARCHS4
Abnormal CNS synaptic transmission	NA	4.05×10^{-3}	Enrichr: MGI
Impaired motor coordination	NA	0.064	Enrichr: MGI
B. Functional categories enriched for *trans*-acting genes that negatively co-express with SCFD1			
Term name	**Term ID**	**FDR *q*-value**	**Tool**
Regulation of vesicle mediated transport[a]	GO:0060627	0.004	GSEA
Regulation of localization[a]	GO:0032879	0.03	GSEA
Integral component of membrane[a]	GO:0016021	2.262×10^{-5}	GSEA
Secretion[a]	GO:0046903	0.004	GSEA
Regulation of *trans*-synaptic signalling	GO:0099177	3.926×10^{-4}	GSEA
Exocytic vesicles	GO:0070382	0.001	GSEA
Glutamatergic synapse	GO:0098978	0.01	GSEA
C. Functional categories enriched for *trans*-acting genes that positively co-express with SCFD1			
Term name	**Term ID**	**FDR *q*-value**	**Tool**
RNA-binding	GO:0003723	$<1 \times 10^{-5}$	GSEA
Ribonucleoprotein complex	GO:1990904	$<1 \times 10^{-5}$	GSEA
Nuclear lumen	GO:0031981	9.617×10^{-5}	GSEA
Negative regulation of gene expression	GO:0010629	0.001	GSEA
RNA splicing	GO:0008380	0.002	GSEA
D. Functional categories enriched for genes that co-express with SCFD1 and modify schizophrenia risk			
Term name	**Term ID**	**FDR *q*-value**	**Tool**
Voltage-gated potassium channel activity	GO:0022843	2.21×10^{-5}	g:profiler
Potassium ion transmembrane transporter activity	GO:0015079	3.46×10^{-5}	g:profiler
Synaptic signalling	GO:0099536	6.95×10^{-8}	g:profiler
Regulation of vesicle mediated transport[a]	GO:0060627	0.002	g:profiler
Cholinergic Synapse	KEGG:04725	6.36×10^{-4}	g:profiler
Negative regulation of NMDA receptor-mediated neuronal transmission	REAC	0.007	g:profiler
Unblocking of NMDA receptors, glutamate binding and activation	REAC	0.007	g:profiler

[a]Functional category of which SCFD1 is a member.
[b]Raw *P*-value reported.

SNPs and gene expression similar to our findings. These include epistatic interactions,[36,37] environmental factors,[36] methylation,[38] chromatin interactions,[39] and drug-eQTL interactions.[40] An additional factor may involve pre-disease processes influencing the genomic regulation of *SCFD1* in ALS, as has been found with TDP-43 depletion and decreased expression of ALS GWAS gene *UNC13A*.[41]

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Our finding that differentially expressed *SCFD1* eQTLs influence ALS survival suggests that the genomic regulation of *SCFD1* expression is important to the disease process. Through the analysis of *trans*-acting eQTLs in the *SCFD1* locus, our results indicate differences the regulation of *SCFD1* and *SCFD1* eQTLs are to likely involve functional pathways known to ALS pathology. Research, explored below, shows modifying *SCFD1* expression can be both protective and toxic to cells under stress, and it is plausible that how this regulatory response occurs depends on a person's genotypes proximal to *SCFD1*, thereby modifying disease vulnerability and duration.

Changes in *SCFD1* expression are functionally relevant to ALS

SCFD1 is a key component in Endoplasmic Reticulum (ER) to Golgi retrograde vesicle transport,[42,43] vesicle docking in exocytosis,[44] collagen/procollagen ER export[45] and autophagy. These pathways have been a major focus in ALS research. Mutations found in genes that play a major role in these pathways cause ALS. The most recent was for gene *ANXA11*,[10] a protein essential for stabilization of SEC31A at ER exit sites,[46] a process critical in ER-Golgi vesicle-mediated trafficking.

Previous research into *SCFD1* function found that knockdown in zebrafish embryos significantly disrupts ER-to-Golgi transport, leading to intracellular protein build-up and an unfolded protein response.[47] In a study using SH-SY5Y cells, *SCFD1* expression significantly responds to neurotoxin-induced oxidative stress, where increased expression exhibited anti-apoptotic effects by supressing morphological changes to the ER, where *SCFD1*-antisense transfected cells accelerated apoptosis.[48] *SCFD1* also colocalizes with SEC31 at ER exit sites, similarly to *ANXA11*, although *SCFD1* knockdown in HeLa cells did not disrupt SEC31 ER localization.[45]

In our *in silico* study, vesicle-mediated transport genes involved in cytoplasmic vesicles, localization, and exocytosis, significantly correlated with *SCFD1* eQTL expression. Given that *SCFD1* eQTLs increase ALS risk and were differentially expressed, these pathways may be differentially regulated depending a person's genotypes, which confers risk of the disease.

We also found *SCFD1* eQTLs significantly correlated with pathways involved in ALS but not attributed to *SCFD1* function itself, including glutamatergic and GABAergic synapses, calcium signalling, microtubule genes, RNA-binding and mRNA splicing. The relationship between synaptic glutamate and Ca^{2+} signalling is believed to selectively predispose motor neurons to excitotoxicity in ALS and is the putative mechanism of the ALS drug Riluzole.[1] We found *SCFD1* expression negatively correlated with genes involved in synaptic glutamate, GABA and calcium signalling. This included *ADCY1*, the gene to most significantly negatively co-express with *SCFD1*. *ADCY1* is almost exclusively expressed in brain, regulated by calcium, and is involved in regulation of synaptic vesicle exocytosis, and calcium-responsive adenylate cyclase binding. Similarly, we found ALS gene *UNC13A*[49] negatively correlated with *SCFD1* expression, which is also involved in glutamatergic-mediated synapses and synaptic vesicles.

Schizophrenia, ALS and *SCFD1*

Genes that associated with ALS in our *post-mortem* analysis via *SCFD1* eQTLs, significantly overlap with genes that increase schizophrenia risk. Higher incidences of schizophrenia in families with a history of ALS have been shown since 2013.[50] Genetic correlation between ALS and schizophrenia risk was also identified in 2017,[32] where *SCFD1* was one of 31 candidate genes that overlapped between the diseases. Why this correlation exists is not understood.

Our results support that *SCFD1* has role in both ALS and schizophrenia and provides insights into the pathways that links them. We found (i) genes that correlate with *SCFD1* eQTLs increase risk of both diseases and (ii) these genes were significantly enriched for pathways known to be involved in the pathology of both diseases, specifically cholinergic synapses, synaptic signalling, potassium transmembrane activity, NMDA-receptor activity and glutamate-binding, and vesicle-mediated transport. Our results indicate that the genetic correlation between ALS and schizophrenia may be driven by shared genomically regulated pathways, which, given the higher incidence of the schizophrenia in ALS families, is heritable risk factor. Further clarification of regulatory loci shared across these diseases could help prioritize drug therapies used in schizophrenia as candidate targets for ALS.

Limitations

A concern in using *post-mortem* whole-tissue samples is that differences in cell heterogeneity between ALS and control cohorts may lead to confounding results. We have used two methods to control and analyse differences in cell composition between samples and sample groups. We have integrated surrogate variables into our model when testing for differences in eQTL expression between ALS and controls. SVA controls for differences in heterogeneity caused by unavailable confounding factors.[24] We performed cell deconvolution analysis to estimate cell composition for each sample and found no significant differences in cell-type between ALS and control groups in our model. If *SCFD1* was a marker for motor neuron loss then we would expect gene-level differential expression between ALS and control cohorts, regardless of patient genotypes, which we did not. It is also worth noting that there is significant variability in motor neuron loss across ALS patients.[51]

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In our *post-mortem* analysis, we identified significant differences in *SCFD1* expression between ALS and control donors for both homozygotes of the rarer genotype and the common genotype. Using the *post-mortem* analysis only, it is unclear how increased or decreased expression of *SCFD1* associates with increased ALS risk. Our survival analysis showed increased *SCFD1* expression correlated with a quicker disease duration, which given alleles that increase risk of ALS via GWAS also increase *SCFD1* expression, may initially indicate that over-expression contributes to the disease onset and process. However, this does not necessarily concur with *in vivo* and *in vitro* functional analyses of *SCFD1* that indicate increased expression can act as a protective factor against oxidative stress and apoptosis, while a decrease in *SCFD1* can lead to cell stress vulnerability. Therefore, an alternative explanation is that increased *SCFD1* expression could be reflecting a response to another unknown factor which is accelerating the disease process.

Summary

We confirmed and expanded *SCFD1*'s involvement in ALS. We confirm that *SCFD1* eQTLs significantly increase ALS risk but are differentially expressed in *post-mortem* ALS, which correlates with the disease's duration. *SCFD1* is a key component in a large transcriptional network that correlates with ALS pathways and genes enriched for schizophrenia risk, a disease known to genetically correlate with ALS.

Supplementary material

Supplementary material is available at *Brain Communications* online.

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Competing interests

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Appendix

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