



Research article

Systems-wide analysis unravels the new roles of CCM signal complex (CSC)

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ABSTRACT

Cerebral cavernous malformations (CCMs) are characterized by abnormally dilated intracranial capillaries that result in increased susceptibility to stroke. Three genes have been identified as causes of CCMs; KRIT1 (CCM1), MGC4607 (CCM2) and PDCD10 (CCM3); one of them is disrupted in most CCM cases. It was demonstrated that both CCM1 and CCM3 bind to CCM2 to form a CCM signaling complex (CSC) to modulate angiogenesis. In this report, we deployed both RNA-seq and proteomic analysis of perturbed CSC after depletion of one of three CCM genes to generate interactomes for system-wide studies. Our results demonstrated a unique portrait detailing alterations in angiogenesis and vascular integrity. Interestingly, only in-direct overlapped alterations between RNA and protein levels were detected, supporting the existence of multiple layers of regulation in CSC cascades. Notably, this is the first report identifying that both β 4 integrin and CAV1 signaling are downstream of CSC, conveying the angiogenic signaling. Our results provide a global view of signal transduction modulated by the CSC, identifies novel regulatory signaling networks and key cellular factors associated with CSC.

1. Introduction

Cerebral cavernous malformations (CCMs), abnormally dilated intracranial capillaries, result in focal neurological defects and increased susceptibility to strokes, presenting patients with seizures, headaches and cerebral hemorrhage (Otten et al., 1989). Roughly around 0.5% of the general population are said to have these microvascular malformations, although this number is estimated to be low since many patients with CCMs are asymptomatic (Flemming et al., 2017). Familial forms of the disease, accounting for around 55% of patients, results from a predisposition of genetic mutations in three known CCM loci while the etiology of remaining 45% of CCM cases are still unknown (Batra et al., 2009; Hayman et al., 1982; Rigamonti et al., 1988). Interestingly, the Hispanic population has a higher percentage (1 in 70) of harboring a potential mutation in one of the three CCM genes compared to non-Hispanic populations (1 in 200) (Günel et al., 1996). CCM induced dilated capillaries, detected in the clinical setting through magnetic resonance imaging (MRI), eventually induce lesions in the central nervous system (CNS), skin and liver. These lesions have characteristic densely packed microvessels and deficient interstitial brain parenchyma (Cavalcanti et al., 2012). Treatment for patients suffering from CCM's ranges from antiepileptic drugs for seizures to surgical excision for those suffering from seizures or hemorrhage (Günel et al., 1996). It has been shown that in addition to cerebral hemorrhagic strokes and seizures, CCM2 variants

have been linked to cerebral microbleeds and suggest a link to preclinical Alzheimer's disease as a result of the CCM2 variant in patients (Cohn-Hokke et al., 2017).

The CCM signaling complex (CSC) is composed of all three CCM genes KRIT1 (CCM1), MGC4607 (CCM2) and PDCD10 (CCM3); in which CCM2 functions as the docking site (Padarti and Zhang, 2018). The CSC interacts with other proteins and has affinity for a wide range of ligands; interactions with ligands contribute to cellular processes including cell migration, adhesion and apoptosis (Hilder et al., 2007; Zhang et al., 2001a, 2008, 2017). CCM proteins have been shown to alter pathways associated with angiogenesis, the process of new blood vessel development (Faurobert and Albiges-Rizo, 2010; He et al., 2010; Plummer et al., 2005; Scimone et al., 2015; Stockton et al., 2010), vascular angiogenesis (Zhang et al., 2005; Zhang et al., 2001a, b), blood vessel stability (Liu et al., 2010), cell adhesion to extracellular matrix, tube formation and endothelial cell morphogenesis (Faurobert and Albiges-Rizo, 2010; Liu et al., 2011). An association between vascular endothelial growth factor (VEGF) and CCM's have also been correlated to angiogenesis pathways, creating a more complex understanding of how all these pathways coordinate together (Distefano et al., 2014; He et al., 2010; Hoeben et al., 2004; Sun et al., 2003).

Integrins, cell surface receptors for extracellular matrix (ECM), regulate angiogenesis, along with lymphangiogenesis by promoting events such as pro-angiogenic cell trafficking and endothelial cell (EC)

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survival and migration (Avraamides et al., 2008). Integrin signaling is known to be important for angiogenesis, specifically for ECs survival, growth and migration (Avraamides et al., 2008; Brooks et al., 1994). Angiogenesis is an essential component of regulating blood brain barrier (BBB) involving integrin (Zhu et al., 2002). In fibronectin binding integrins, $\alpha 5\beta 1$ or $\alpha \nu\beta 3$ integrins are known to bind to fibronectin while $\alpha 5\beta 1$ is crucial to regulate levels of $\alpha \nu\beta 3$ in stimulating RhoA-mediated signaling (Danen et al., 2002). In laminin binding integrins, $\alpha 2\beta 1$ are known to enhance vascular endothelial growth factor receptor 1 (VEGFR1) signaling, while $\alpha 6\beta 1$ has been shown to block tube formation and ECs migration (Lee et al., 2006). The $\beta 4$ integrin, also part of the laminin binding Integrins, are known to mediate hemidesmosome assembly and promote Raf-ERK and Rac-JNK signaling; mice deficient in the $\beta 4$ integrin C-terminus (cytoplasmic tail) had reduced angiogenic response to VEGF, confirming the essential role of $\beta 4$ integrin in promoting angiogenesis (Dans et al., 2001; Dowling et al., 1996; Nikolopoulos et al., 2004).

Angiogenesis has also been found to share common signaling pathways involved with inflammation. Inflammation, essential for defending the body from pathogens, has negative effects on tissue including the ability to induce angiogenesis (Imhof and Aurrand-Lions, 2006). It has been shown that regulators of angiogenesis, such as angiopoietin-2 (ANGPT2) upregulates inflammatory responses (Imhof and Aurrand-Lions, 2006). Chemokines and cytokines, which have a large part to play with inflammation, are also important for angiogenesis. One example includes members of the CC chemokine family, such as CCL2, which along with IL-8 mediates localization of endothelial cells to sites of inflammation (Granger and Senchenkova, 2010). Increased VEGF-A expression by CCL2 leads to induced angiogenesis, which reinforces CCL2's role in promoting angiogenesis during inflammation (Granger and Senchenkova, 2010). IL-1 proteins, also involved with inflammatory responses, have been reported to stimulate release of collagenase and prostaglandin from synovial cells, which is known to stimulate expression of VEGF (Dalton et al., 1989; Lefebvre et al., 1990; Tolnay et al., 1997). To our knowledge, this is the first attempt in systems biology, analyzing CCMs deficient models in human brain microvascular endothelial cells (HBMVEC) *in-vitro* and zebrafish lines *in-vivo*. Our results elucidate a very unique and interconnected story demonstrating alterations in various signaling cascades, both in cerebral neovascular angiogenesis as well as developmental angiogenesis with disruption of the CSC signaling cascade. Our goal is to provide a global view of alterations at both the proteome and transcriptome level resulting from deficiencies in CCM expression in both *in-vitro* and *in-vivo* models. Integrative proteomic and genomic analysis of CCM deficiencies in HBMVEC allow us to investigate effects on cerebral microvascular angiogenesis while our zebrafish models allow us to investigate effects on developmental angiogenesis resulting from a disrupted CSC.

2. Materials and methods

2.1. Generation of CCM deficient cells and zebrafish strains

CCM deficient cells were generated by silencing *CCM1*, *CCM2* and *CCM3* genes respectively in human brain microvascular endothelial cells (HBMVEC) as described (Zhang et al., 2001a, 2005) and *Ccm1*-knockout (*Ccm1*-KO, *san*) and *Ccm2*-knockout (*Ccm2*-KO, *vtn*) zebrafish embryos were produced by crossing the hemizygous parents in our lab as described (Liu et al., 2010, 2011).

2.2. RNA extraction and RNA-seq for HBMVEC cells and zebrafish embryos

Total RNAs were extracted with TRIZOL reagent (Invitrogen) following the manufacturer's protocol. For cultured HBMVEC, cell monolayer was rinsed with ice cold PBS once. Cells were lysed directly in a culture dish by adding 1 ml of TRIZOL reagent per flask and scraping

with cell scraper. The cell lysate was passed several times through a pipette and vortexed thoroughly. For zebrafish embryos, tissue samples were homogenized in 1 ml of TRIZOL reagent per 50–100 mg of tissue, using a glass-Teflon or power homogenizer. The quality (purity and integrity) of each RNA sample was assessed using a Bioanalyzer (Agilent) before RNA-seq. All RNA-seq data were produced using Illumina HiSeq 2000; clean reads for all samples were over 99.5%. 60–80% of reads were mapped to respective reference genomes (Human or zebrafish).

2.3. RNA-seq processing of files to assemble interactomes for HBMVEC and zebrafish embryos

The RNA-seq files for the HBMVEC samples were obtained through paired-end (PE) sequencing with 100 bp reads (2×100) in Illumina HiSeq 2000. The data consisted of 8 FASTQ files, 2 PE FASTQ files for each of the four cohorts: KD-CCM1, KD-CCM2, KD-CCM3 and WT (wild type). All cohorts consisted of one sample, with CCM2 acting as a replicate for both CCM1 and CCM3, as CCM2 functions as the docking site for the CSC (Padarti and Zhang, 2018). The zebrafish data consisted of 6 FASTQ files, 2 PE FASTQ files for each of the three cohorts: KO-Ccm1 (*san*, Z1), KO-Ccm2 (*vtn*, Z2), and WT (wild type, Zc). Comparisons among the zebrafish samples were made as well (Z1 vs Z2, Z2 vs Zc, and Z1 vs Zc). For Zebrafish-Human comparisons, the genes were converted to human homologs and processed the same way as the endothelial cell samples above.

RNA data were cleaned and passed quality control before starting the analysis. After extracting the FASTQ files, the RNA-seq FASTQ files were aligned to the Human genome using HISAT2. This generated two SAM files per cohort that were converted to SAM using SAMtools 1.9. SAMtools quick check was then used to ensure the files were complete. The SAM files were then converted to BAM files and sorted. Cufflinks was used to assemble transcripts for each cohort and cuffmerge to merge all the transcript files. These files were analyzed for differential gene expression with CuffDiff.

After importing the gene exp.diff output file from cuffdiff into Excel, data was filtered for significant 2X and 3X changes in expression. A Python script was created to identify shared differentially expressed genes between cohorts. These were annotated in Excel, and simple set operations were used to find exclusions between the sets. The overlaps were inputted into the Human Reference Protein Interactome Mapping Project database (HURI) and using external links, were sent along with the rest of the genes to Genemania. If there were any identified genes not present in the HURI database, these were copied and manually added to the Genemania network before extracting using Cytoscape. The output from Genemania with query and interactor genes then input into STRING database to obtain the KEGG pathways, GO cellular components, GO molecular functions and GO biological processes.

Identified overlaps were compared between proteomics and RNA-seq data, with KD of either CCM1, CCM2, or CCM3 in HBMVEC and to the zebrafish KO data with KO of *Ccm1* (*san*) or *Ccm2* (*vtn*). The goal was to identify similarities between cohorts at both the protein and transcription level. Those that were shared with zebrafish were said to be zebrafish validated. The agreements in differential expression were noted through the use of the Python comparison script.

2.4. Protein extraction for HBMVEC cells and zebrafish embryos

HBMVEC cells and zebrafish embryos were lysed using a digital sonifier cell disruptor (Branson model 450 with model 102C converter and double step microtip) in ice cold lysis buffer containing 50 mM Tris-HCl (pH 7.5), 150 mM NaCl, 0.5% NP-40 (Sigma), 50 mM sodium fluoride (Sigma), 1 mM PMSF (Sigma), 1 mM dithiothreitol (Invitrogen) and EDTA-free complete protease inhibitor (Roche). The concentration of protein lysates were measure by Qubit assay (Invitrogen) before analysis.

2.5. Liquid chromatography-tandem mass spectrometry (LC-MS/MS)

The cell lysates were generated from the four cohorts (KD-CCM1, KD-CCM2, KD-CCM3 and WT) in HBMVEC cells and three cohorts (KO-Ccm1 or *san*, KO-Ccm2 or *vtn*, and WT) in zebrafish embryos. All cohorts consisted of three samples. The cell lysates (20–25 µg of protein) were subjected to trypsin digestion using the FASP method (Wisniewski et al., 2009), following the manufacturer's protocol (Expedion Inc, San Diego, Ca). Four microliters of each digested sample (100 ng/µl) was loaded onto a 25-cm custom-packed porous silica Aqua C18, 125Å, 5 µm (Phenomenex) column. The porous silica was packed into a New Objective PicoTip Emitter, PF360-100-15-N-5, 15 ± 1 µm and pre-equilibrated with 95% solvent A (100% water, 0.1% formic acid) and 5% solvent B (90% acetonitrile, 10% water, 0.1% formic acid) before injection of the digested peptides, respectively. Liquid Chromatography (LC) separation of the peptides was performed on an Ultimate 3000 Dionex RSLC-nano UHPLC (Thermo Fisher Scientific), equilibrated with 95% solvent A and 5% solvent B (equilibration solution). Samples were loaded onto the column for 10 min, at a constant flow rate of 0.5 µL/min, before beginning the elution gradient. Solvent B was then increased from 5% to 35% over 85 min, followed by increase to 95% solvent B over 5 min. The plateau was maintained at 95% solvent B for 9 min, followed by a sharp decrease to 5% solvent B over 1 min. The column was then re-equilibrated with 5% solvent B for 10 min. The total runtime consisted of 120 min. Peptides were analyzed using a Q Exactive Plus Hybrid Quadrupole-Orbitrap Mass Spectrometer (Thermo Fisher Scientific), equipped with a Nanospray Flex Ion Source (Thermo Fischer Scientific). Parameters for the mass spectrometer were as follows: full MS; resolution was set at 70,000 and 17,500, for MS1 and MS2, respectively; AGC target was set at 3e⁶ and 1e⁵ for MS1 and MS2, respectively; Max IT at 50 ms; scan range from 350 to 1600 *m/z* dd-MS²; Max IT at 100 ms; isolation window at 3.0.

2.6. Processing of proteomics analysis data to assemble interactomes for perturbed CSC

Proteomic data analysis was performed using the Proteome Discoverer (PD) 2.1.1.21 (Thermo Fisher Scientific), with an estimated false-discovery rate (FDR) of 1%. The Human Database was downloaded in FASTA format on December, 1, 2018, from UniProtKB; <http://www.uniprot.org/>; 177,661 entries. Common contaminants such as trypsin autolysis fragments, human keratins, and protein lab standards were included in the contaminants database which may be found in the cRAP contaminant database and a couple in house contaminants (Fenyó, 1999). The following parameters were used in the PD: HCD MS/MS; fully tryptic peptides only; up to 2 missed cleavages; parent-ion mass tolerance of 10 ppm (monoisotopic); and fragment mass tolerance of 0.6 Da (in Sequest) and 0.02 Da (in PD 2.1.1.21) (monoisotopic). A filter of two-high confidence peptides per protein were applied for identifications. PD dataset was further processed through Scaffold Q+ 4.8.2 (Proteome Software, Portland, OR) to obtain the protein quantification. A protein threshold of 99%, peptide threshold of 95%, and a minimum number of 2 peptides were used for protein validation. The quantitation was performed using empAI values for comparisons. Statistical analysis was carried out using Student's *t*-test and a significance level of *p* < 0.05. After files were extracted, they were analyzed through proteome discover (described above) to compare differences between mutant and wild type samples. Identified proteins were pooled together by sample, based on significance of the protein being either under-expressed or over-expressed compared to the control samples. Once these datasheets were available, a Python script was created to identify shared differentially expressed genes between cohorts and used to identify important proteins involved in the CSC, second layer interactors of the CSC, or proteins well-known to have significance in human brain microvascular endothelial cells (Dib et al., 2012; Ghosh et al., 1998; Goddard et al., 2014; Kar et al., 2017; Salazar et al., 2016; Wallerath et al., 1999; Xu

et al., 2002). Identified proteins were assembled into a separate sheet, which were used to generate the interactomes. Interactomes were made for individual pathways (CSC, CSC second layer and proteins well-known to have significance in human brain microvascular endothelial cells). To simplify the generated interactomes, all identified query proteins were pooled together to generate figures illustrated. In addition, proteins found up-regulated or down-regulated in more than one CCM KD/KO strains were combined to show alterations to these pathways when either of the resulting genes are deficient in expression.

To generate interactomes, identified proteins from above criteria were inputted into HuRI database and using external links, were sent along with the interactors to Genemania (identical to generation of transcriptomes). If there were any identified proteins not present in the HURI database, these were manually added to the Genemania network before extracting using Cytoscape. The output from Genemania with query and interactor proteins was then input into STRING database to obtain the KEGG pathways, GO cellular components, GO molecular functions and GO biological processes identical to the processing of the RNA-seq data.

3. Results

3.1. Gene expression profiling by RNA-seq in the deficiency of CCM1

Genomic and interactomic effects of alterations detected through RNA-seq with the knockdown (KD) of CCM1 in HBMVEC are illustrated in Figure 1. Altered cellular processes related to these genes include various regulation of intrinsic and extrinsic apoptotic signaling pathways, RNA and mRNA processing, RNA and mRNA splicing, spliceosomal tri-snRNP complex assembly, membrane docking, ribonucleoprotein complex assembly, negative regulation of response to stimulus, vesicle docking and regulation of I-κB kinase/NF-κB signaling (suppl. Table 1A). Affected KEGG pathways include spliceosome and NOD-like receptor signaling pathways (suppl. Table 1B). Significantly down-regulated genes unique in CCM1 mutant included a neuronal adaptor protein, Amyloid β Precursor Protein Binding Family A Member 2 (APBA2); a group of inflammatory factors: Interleukin 1α (IL1A), Moesin (MSN), C-C Motif Chemokine Ligand 2 (CCL2), BCL2 Related Protein A1 (BCL2A1); and a cellular transporter, Lectin Mannose Binding 1 (LMAN1). Significantly up-regulation of genes, found only in CCM1 deficient cells, were not as prominent as down-regulated genes but included a pre-mRNA splicing factor, Pre-mRNA Processing Factor 8 (PRPF8); two well-known angiogenic factors: Nephroblastoma Overexpressed (NOV), and Kruppel Like Factor 8 (KLF8) and a cellular factor involving autophagy, Dehydrogenase/Reductase X-Linked (DHRSX) (Figure 1).

To compare CCM1 interactomes, we also evaluated Ccm1-knockout (KO) zebrafish strain (*san*) and found correlations among 2 genes unique in only CCM1 deficient conditions, either CCM1-KD HBMVEC or CCM1-KO zebrafish (Figure 1, suppl. fig. 1). Affected cellular processes associated with these two genes included vesicle docking (suppl. Table 1C). These 2 gene correlations between our models included down-regulation of a transcriptional factor, Early Growth Response 1 (EGR1) in both CCM1-KD HBMVEC cells and Ccm1-KO zebrafish, and down-regulation of a cellular factor in vesicle transport, Exocyst Complex Component 5 (EXOC5) in CCM1-KD HBMVEC cells, but up-regulation in Ccm1-KO zebrafish (Figure 1, suppl. fig. 1). It must be noted however, that we were unable to obtain significant P-values or Q-values from our RNA-seq analysis with zebrafish data for these two genes (Figure 1, suppl. fig. 1).

3.2. Gene expression profiling by RNA-seq in the deficiency of CCM2

Figure 2 shows pathways affected by alterations in CCM2-KD HBMVEC cells detected by RNA-seq. Affected cellular processes associated with these genes included RNA and mRNA splicing, RNA and mRNA processing, RNA localization and metabolic process, RNA and poly(A) RNA binding, mRNA export from nucleus, mRNA-containing

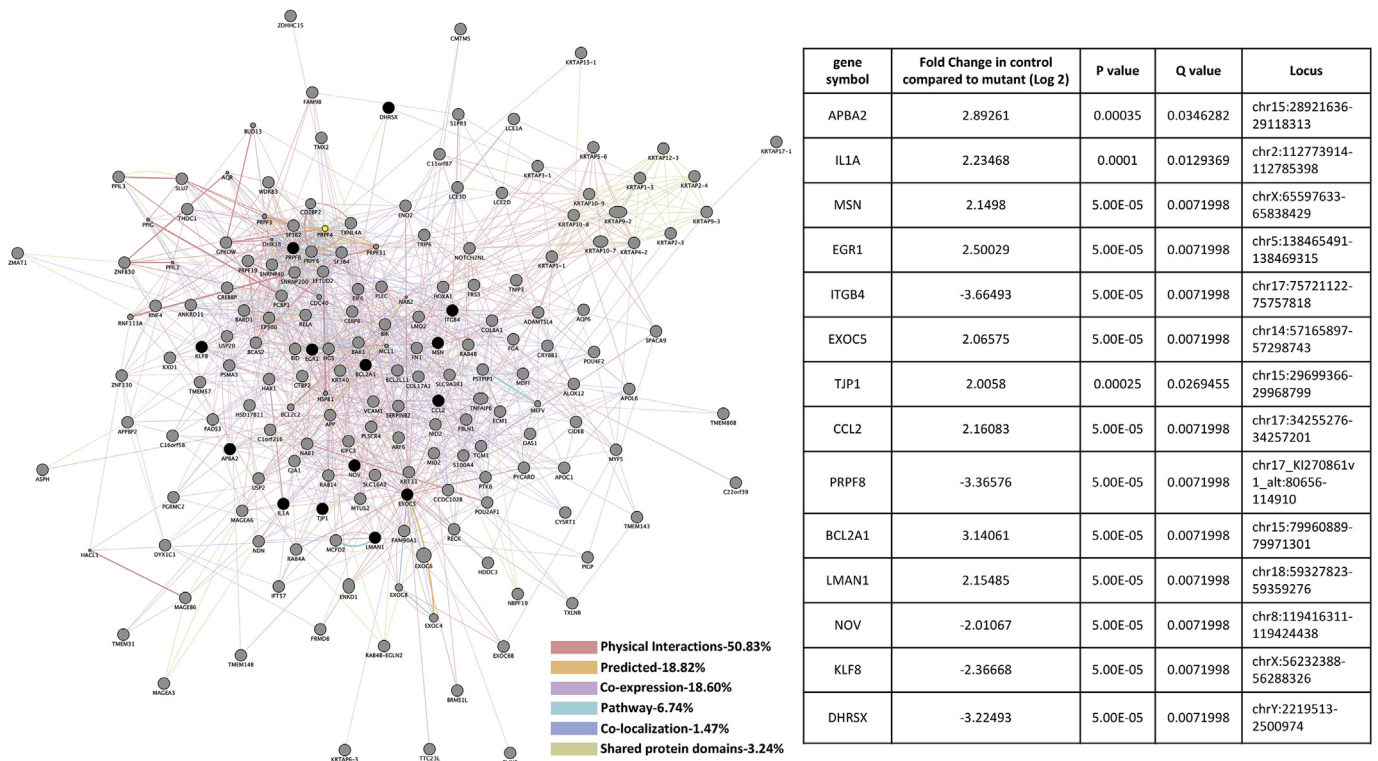


Figure 1. Perturbed transcriptomes in the deficiency of CCM1 in human brain microvascular endothelial cells (HBMVEC). A total of 14 genes were identified with significant expression changes in CCM1 deficient HBMVEC. Data table on right illustrates gene symbol, fold change in control/mutant, P-value and Q-value's to determine significance and locus identification. RNA-seq results were filtered for significant 2X changes in expression. Interactomes were constructed using cytoscape software equipped with genemania application. Interactomes illustrate affected pathways with both query (●) and interactors (●). Interaction descriptions with percentages and coordinating line colors are displayed below figures. Significances were determined using Cuffdiff software, depending on whether $p > FDR$ (false discovery rate) after Benjamini-Hochberg correction for multiple-testing and, if Q -value < 0.05 .

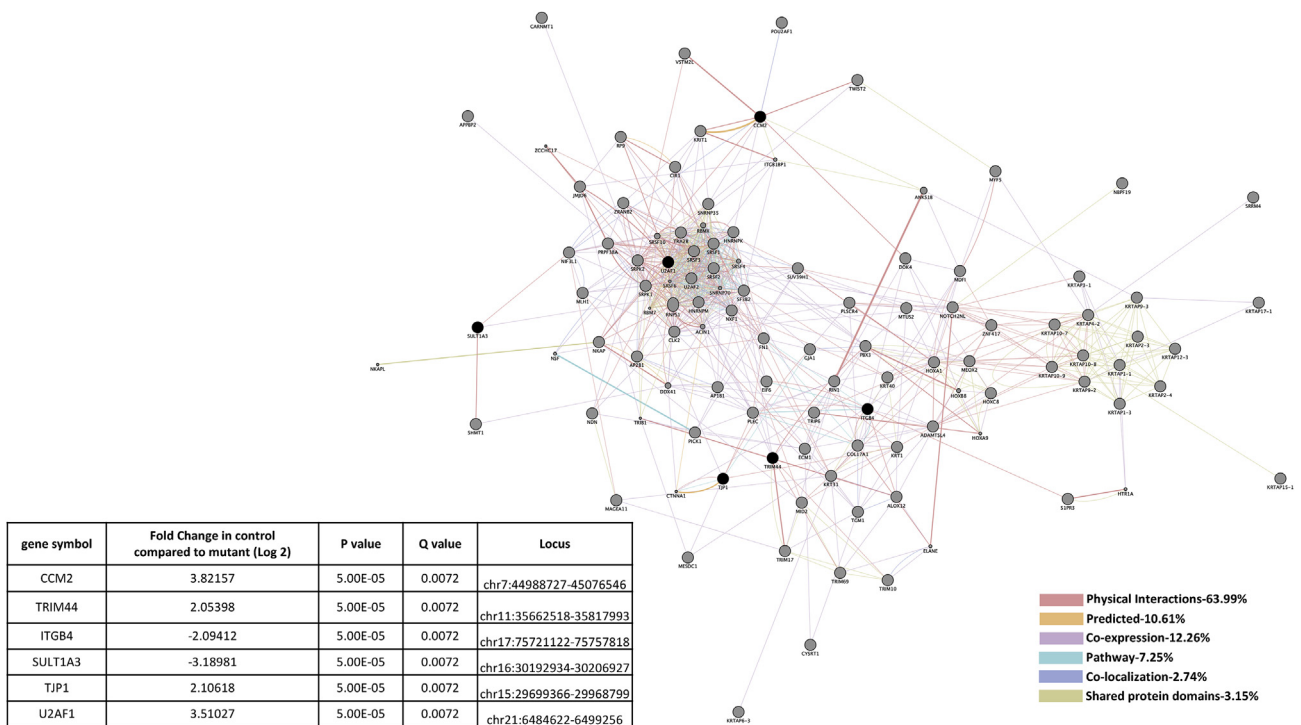


Figure 2. Perturbed transcriptomes in the deficiency of CCM2 in (HBMVEC). A total of 6 genes were identified with significant expression changes in CCM1 deficient HBMVEC. Data table on left illustrates gene symbol, fold change in control/mutant, P-value and Q-value's to determine significance and locus identification. RNA-seq results were filtered identical to Fig. 1. Interactomes were constructed identical to Fig. 1. Interactomes illustrations are identical to Fig. 1. Significances were determined identical to Fig. 1.

ribonucleoprotein complex export from nucleus, termination of RNA polymerase II transcription, mRNA 3'-end processing, transcription from RNA polymerase II promoter, nitrogen compound transport, ribonucleoprotein complex export from nucleus, ribonucleoprotein complex localization, cell junction organization, cytoplasmic transport, and multiple cellular metabolic processes (suppl. Table 2A, 2B). Down-regulated genes unique in CCM2 deficiency included an epithelial-to-mesenchymal transition (EMT) marker, Tripartite Motif Containing 44 (TRIM44); and a pre-mRNA splicing factor, U2 Small Nuclear RNA Auxiliary Factor 1 (U2AF1). Interestingly, a cellular regulator of neurotransmitters, Sulfo-transferase Family 1A Member 3 (SULT1A3) was the only gene found to be up-regulated unique in CCM2 deficient HBMVEC cells (Figure 2).

To compare CCM2 interactomes, we also examined expression levels of CCM2 gene among tissues/cells, and found the expression levels of CCM2 gene were significantly down in both CCM2-KD HBMVEC cells and Ccm2-KO zebrafish (Figure 2, suppl. fig. 2), validating the efficiency of our CCM2 gene silencing (KD) and KO technique, and the accuracy of our RNA-seq data. Affected cellular process associated with CCM2-deficiency target cell junction organization (suppl. Table 2A, 2B).

3.3. Gene expression profiling by RNA-seq in the deficiency of CCM1 and CCM2

Similarities in altered gene expression in CCM1 and CCM2 deficient HBMVEC cells included down-regulation of Tight Junction Protein 1 (TJP1) (Figure 3). It should be mentioned that these shared gene alterations were detected separately in individual knockdown experiments, not as a result of a double knockdown strain. Perturbed expression of two EC markers involved in vascular integrity were also observed. First, down-regulation of TJP1 in both CCM1-KD and CCM2-KD HBMVEC cells but was unable to be replicated in *san* or *vtm* zebrafish strains (Figure 3, suppl. fig. 3). Up-regulation of Integrin $\beta 4$ (ITGB4), a key component of hemidesmosome, among CCM1-KD and CCM2-KD HBMVEC cells and Ccm1-KO zebrafish (*san*) was observed, but ITGB4 was interestingly

down-regulated in Ccm2-KO zebrafish (*vtm*) (Figure 3, suppl. fig. 3). Affected cellular processes include hemidesmosome assembly, cell junction organization and assembly, cell-substrate junction assembly, cell-matrix adhesion and extracellular matrix organization (suppl. table 3A, 3C). Altered KEGG pathways include ECM-receptor interaction, P13K-Akt signaling pathway, and focal adhesion (suppl. table 3B, 3D).

3.4. Gene expression profiling by RNA-seq in the deficiency of CCM3

Heme oxygenase (HMOX2) was the only down-regulated gene detected in CCM3-KD HBMVEC cells (Figure 4). With its highest expression in the cerebrovasculature in the brain (Kang et al., 2013; Sun et al., 1990), HMOX2 has a role in neovascularization and heme oxygenase (decyclizing) activity (suppl. table 4).

3.5. Perturbed protein interactome pathways in the deficiency of CCM1

Proteins altered that were unique in CCM1-KD HBMVEC cells included down-regulation of Calpain-2 (CAPN2), endothelial cell specific chemotaxis regulator (ECSCR), Glyceraldehyde-3-Phosphate Dehydrogenase (GAPDH) and Cathepsin B (CTSB) (Figure 5). At the protein level, the majority of altered cellular processes due to CCM1 deficiency lay in the area of vascular angiogenesis, including angiogenesis, blood vessel development and morphogenesis, circulatory system development, tube development and morphogenesis, cellular developmental process, cell differentiation, chemical response, chordate embryonic development, neuron apoptotic process and microtubule cytoskeleton organization (suppl. table 5A). Altered molecular functions of interest included cytoskeletal protein binding, ion binding and calcium ion binding (suppl. table 5B). Affected KEGG pathways included cellular senescence, Alzheimer's disease, focal adhesion, apoptosis and HIF-1 signaling pathway (suppl. table 5C).

To compare CCM1 interactomes, we also evaluated Ccm1-KO zebrafish strain (*san*) which gave less interactome data than with CCM1-KD

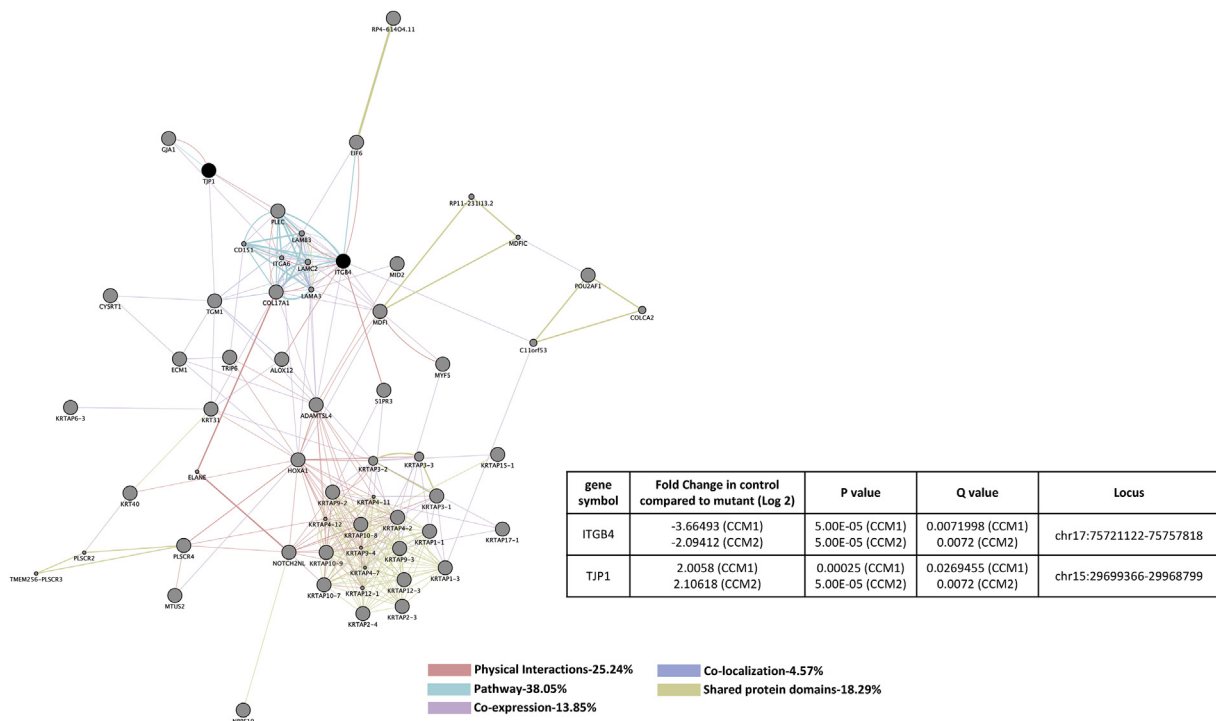


Figure 3. Perturbed transcriptomes shared in the deficiency of CCM1 or CCM2 in (HBMVEC). Two genes were identified with significant expression changes in both CCM1 and CCM2 deficient HBMVEC. Data table on right illustrates gene symbol, fold change in control/mutant, P-value and Q-value's to determine significance and locus identification. RNA-seq results were filtered identical to Fig. 1. Interactomes were constructed identical to Fig. 1. Interactomes illustrations are identical to Fig. 1. Significances were determined identical to Fig. 1.

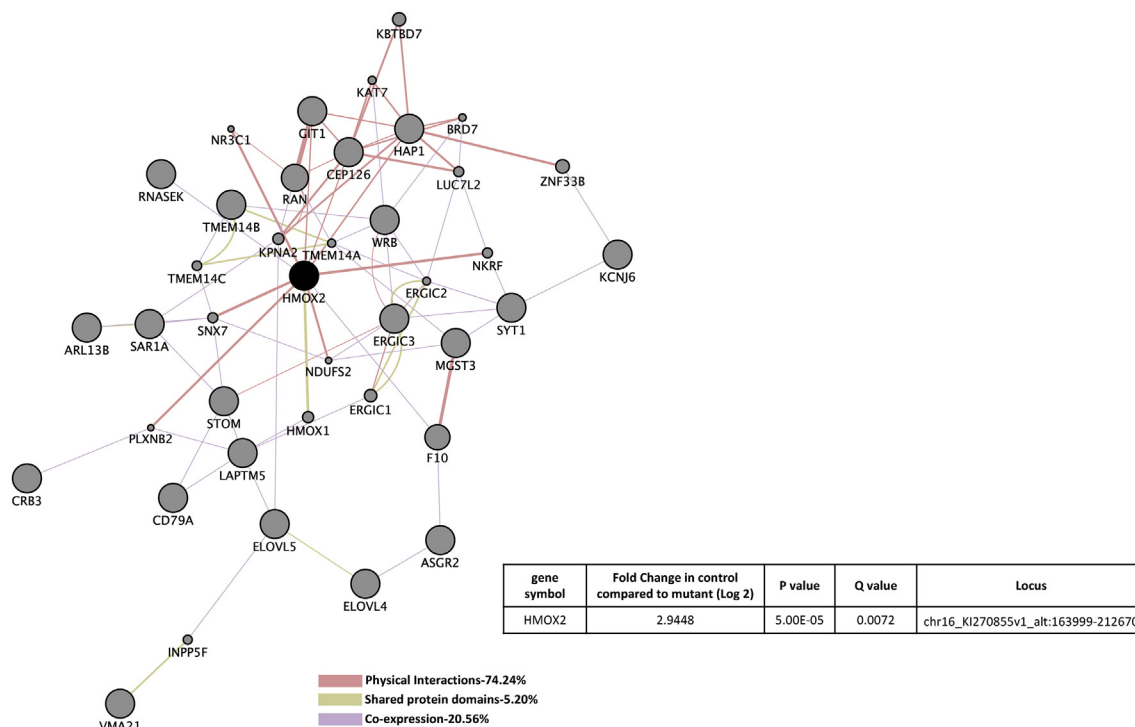


Figure 4. Perturbed transcriptomes in the deficiency CCM3 in (HBMVEC). HMOX2 was the only identified gene with significant expression changes in CCM3 deficient HBMVEC. Data table on right illustrates gene symbol, fold change in control/mutant, P-value and Q-value's to determine significance and locus identification. RNA-seq results were filtered identical to Fig. 1. Interactomes were constructed identical to Fig. 1. Interactomes illustrations are identical to Fig. 1. Significances were determined identical to Fig. 1.

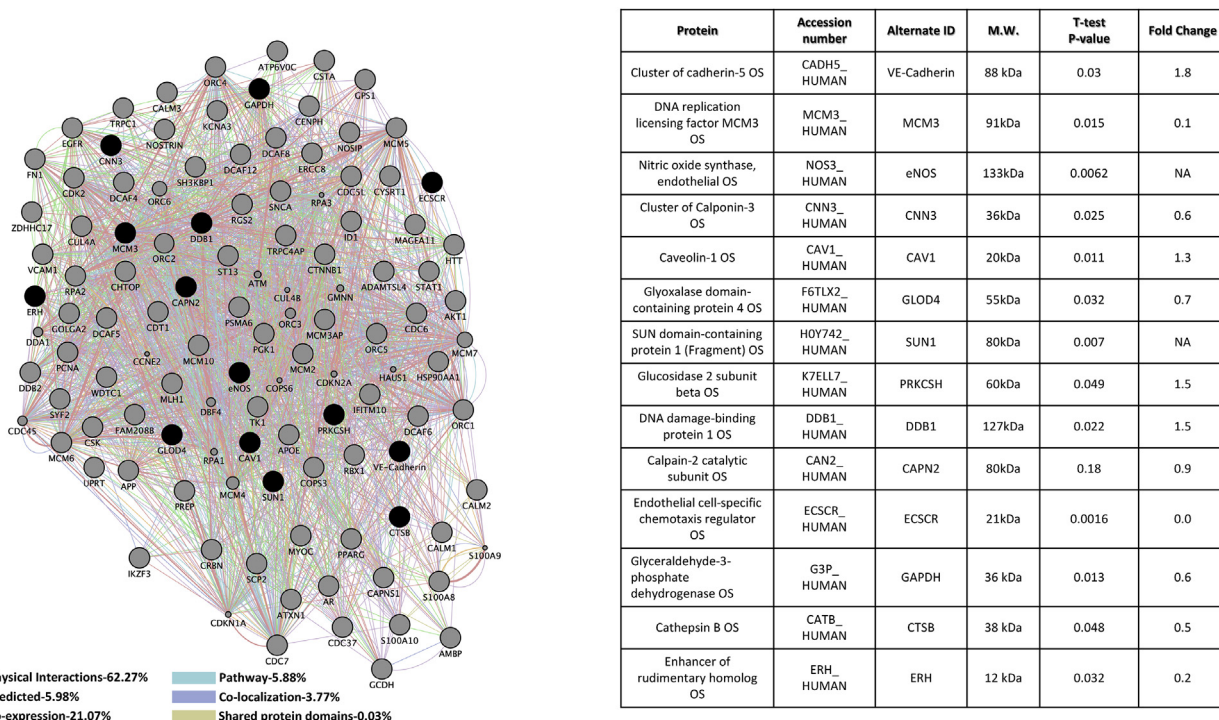


Figure 5. Perturbed protein interactome pathways in the deficiency of CCM1 in (HBMVEC). Fourteen proteins were identified with significant expression changes in CCM1 deficient HBMVEC. Table on the right illustrates details of query proteins identified in the samples through mass spectrometry with accession number, alternate ID, Molecular Weight (M.W.), p-values and fold changes in mutant/controls. NA = not found in WT samples. Interactomes were built using proteomic data and constructed using cytoscape software equipped with genemania application. Interactomes illustrations are identical to Fig. 1. All samples were run in triplicates. Significances were determined using student's t-test with p values <0.05.

HBMVEC (suppl. fig. 4). Alterations in genes unique in Ccm1-KO zebrafish involved multiple disrupted metabolic processes as well as negative regulation of cellular process (suppl. table 5D). Molecular functions potentially affected included binding mechanisms as well as hydrolase activity and catalytic activity (suppl. table 5E). Similar to down-regulated Calpain-2 (CAPN2), found in CCM1-KD HBMVEC (Figure 5), Calpain-9 (CAPN9) was found to be down-regulated in CCM1-KD zebrafish (suppl. fig. 4).

3.6. Perturbed protein interactome pathways in the deficiency of CCM2

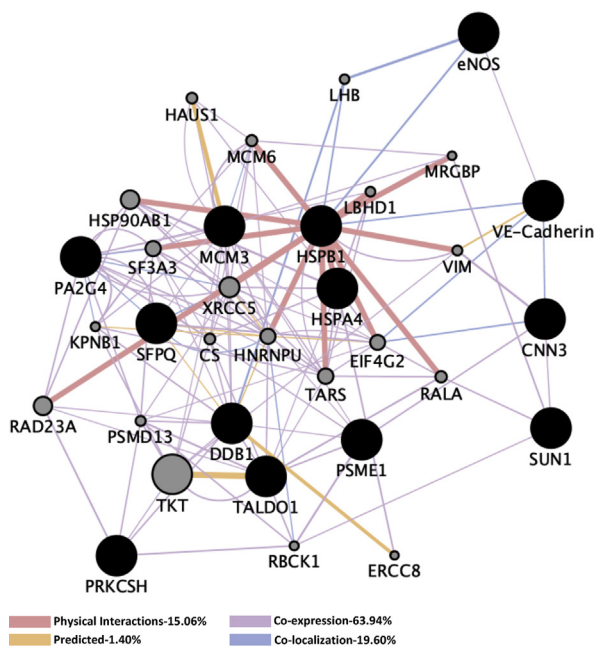
In CCM2 deficient HBMVEC, five unique affected proteins were found, including up-regulation of three proteins controlling cellular protein stability: Splicing Factor Proline And Glutamine Rich (SFPQ), Heat Shock Protein Family A Member 4 (HSPA4), Heat Shock Protein Family B (Small) Member 1 (HSPB1) and one blood coagulating factor, Trans aldolase 1 (TALDO1); down-regulation of an RNA-binding protein, Proliferation-Associated 2G4 (PA2G4) was also observed (Figure 6). Cellular processes potentially affected in the deficiency of CCM2 included cell cycle process, cellular component organization or biogenesis, response to organic substance, various metabolic processes, regulation of oxidative stress-induced intrinsic apoptotic signaling pathway and neutrophil degranulation (suppl. table 6A). Molecular functions included transferase activity, transferring aldehyde or ketonic groups and various binding pathways (suppl. table 6B). Interestingly, KEGG pathways affected in CCM2 deficient HBMVEC included biosynthesis of amino acids, carbon metabolism, pentose phosphate pathway, antigen processing and presentation and VEGF signaling pathway (suppl. table 6C).

Only one down-regulated protein, Small Glutamine Rich Tetrapeptide Repeat Containing Alpha (SGTA), in Ccm2-null zebrafish (*vtm*) was identified (suppl. fig. 5), which was not observed with CCM2 deficient HBMVEC (Figure 6). Cellular processes associated with SGTA included cellular regulations in response to stimulus, in responses to stress; in responses to metabolic and catabolic processes and ERAD pathway regulation (suppl. table 6D). Molecular functions of SGTA included protein binding and are mainly associated with protein stability and ER-associated autophagy processes (suppl. table 6E).

3.7. Perturbed protein interactome pathways in the deficiency of CCM1 and CCM2

There was an overlapped group of proteins that were perturbed in deficiencies in either CCM1 or CCM2 expression in HBMVEC (Figure 7). Among these shared group of altered genes, Cadherin 5 (CDH5, VE-Cadherin) is up-regulated in CCM1-KD but slightly down-regulated in CCM2-KD. VE-Cadherin, a key player in endothelial adherens junction assembly and maintenance (Dejana and Orsenigo, 2013), is involved in BBB integrity, ERK signaling and immune cell transmigration through VCAM-1/CD106 signaling pathways (Bartaula-Brevik et al., 2014; Gaston et al., 2017; Lee et al., 2015). Nitric oxide synthase 3 (NOS3, eNOS) is up-regulated in both CCM1-KD and CCM2-KD HBMVEC cells. eNOS participates in VEGF induced angiogenesis (Saleh et al., 2015), while altered eNOS expression levels are associated with strokes (Dahiyat et al., 1999; Du et al., 2008; Hua et al., 2014; Morris et al., 2011; Turkanoglu Ozcelik et al., 2014). Both Calponin-3 (CNN3) that is highly expressed in brain and Minichromosome Maintenance Complex Component 3 (MCM3) that is involved in DNA replication (Gibson et al., 1990; Lei et al., 2002) are down regulated in both CCM1-KD and CCM2-KD HBMVEC cells. Cellular processes involving these 4 proteins include various cell cycle pathways, numerous metabolic pathways, VEGFR signaling pathway, negative regulation of ion transport, regulation of cell proliferation and cell activation, second-messenger-mediated signaling, blood circulation and coagulation, RTK signaling pathway, *in-utero* embryonic development, negative regulation of platelet activation, regulation of heart contraction, blood vessel development and various DNA replication pathways (suppl. table 7A). Molecular functions of these proteins mainly included various binding pathways, DNA helicase activity and nucleoside-triphosphatase activity (suppl. table 7B). Potentially affected KEGG pathways included cell cycle, DNA replication, PI3K-Akt signaling pathway, estrogen signaling pathway and HIF-1 signaling pathway (suppl. table 7C).

MCM3 is the only gene found to have shared down-regulation in protein level in CCM1 and CCM2 mutants in HBMVEC. MCM3 protein level was also altered in Ccm1-KO zebrafish (Figure 7 and suppl. fig. 6). This alteration, however, was only demonstrated for Ccm1-KO zebrafish



Protein	Accession number	Alternate ID	M.W.	T-test P-value	Fold Change
Cluster of cadherin-5 OS	CADH5_HUMAN	VE-Cadherin	88 kDa	0.02	0.8
DNA replication licensing factor MCM3 OS	MCM3_HUMAN	MCM3	91kDa	0.02	0.3
Nitric oxide synthase, endothelial OS	NOS3_HUMAN	eNOS	133kDa	0.00013	NA
Cluster of Calponin-3 OS	CNN3_HUMAN	CNN3	36kDa	0.00	0.7
Splicing factor, proline- and glutamine-rich OS	SFPQ_HUMAN	SFPQ	76 kDa	0.037	1.2
Cluster of Proliferation-associated protein 2G4 OS	PA2G4_HUMAN	PA2G4	44 kDa	0.04	0.8
SUN domain-containing protein 1 (Fragment) OS	HOY742_HUMAN	SUN1	80kDa	0.039	NA
Glucosidase 2 subunit beta OS	K7ELL7_HUMAN	PRKCSH	60kDa	0.007	1.4
DNA damage-binding protein 1 OS	DDB1_HUMAN	DDB1	127kDa	0.05	1.2
Cluster of Transaldolase OS	TALDO_HUMAN	TALDO1	38 kDa	0.04	1.6
Heat shock 70 kDa protein 4 OS	HSP74_HUMAN	HSPA4	94 kDa	0.034	1.3
Heat shock protein beta-1 OS	HSPB1_HUMAN	HSPB1	23 kDa	0.041	1.2
Proteasome activator complex subunit 1 OS	PSME1_HUMAN	PSME1	29 kDa	0.00	0.7

Figure 6. Perturbed protein interactome pathways in the deficiency of CCM2 in HBMVEC. Thirteen proteins were identified with significant expression changes in CCM2 deficient HBMVEC. Table on the right illustrates details of query proteins identified in the samples through mass spectrometry with accession number, alternate ID, Molecular Weight (M.W.), p-values and fold changes in mutant/controls. NA = not found in WT samples. Interactomes were constructed identical to Fig. 5. Interactomes illustrations are identical to Fig. 5. All samples were run in triplicates. Significances were determined identical to Fig. 5.

but not Ccm2-KO zebrafish (suppl. fig. 6). It must also be noted that MCM3, in CCM1-KO zebrafish, was up-regulated but was down-regulated in both CCM1-KD and CCM2-KD HBMVEC cells (compare Figure 7 and suppl. fig. 6), perhaps suggesting a different level of feed-back regulation for this protein between cerebral vascular angiogenesis and developmental angiogenesis. Cellular processes in CCM1-KD and CCM2-KD HBMVEC cells validated in Ccm1-KO zebrafish included metabolic processes, DNA replication processes and various cell cycle processes (suppl. table 7D). Zebrafish conferred molecular functions mainly included binding pathways and DNA helicase activity (suppl. table 7E). Validated KEGG pathways included cell cycle and DNA replication (suppl. table 7F).

3.8. Perturbed protein interactome pathways in the deficiency of CCM3

Down-regulated expression of two interesting proteins, unique in CCM3-deficient HBMVEC cells, Serine/Threonine Kinase 24 (STK24) and Procollagen-Lysine, 2-Oxoglutarate 5-Dioxygenase 2 (PLOD2), were observed (Figure 8). STK24 is among the first group of proteins identified to bind to CCM3 protein (Rual et al., 2005; Zhang et al., 2013), which further validates our current data. Metabolic processes, various regulations of kinase activity, various responses to stress, regulation of mitotic cell cycle, regulation of MAPK cascade, response to stimulus, regulation of transferase activity, intracellular signal transduction processes, activation of MAPKKK activity and various apoptotic signaling pathways are associated with these two genes (suppl. table 8A). Molecular functions affected included MAPKKK activity (suppl. table 8B).

3.9. Perturbed protein interactome pathways in the deficiency of CCM1 and CCM3

Up-regulation of the scaffolding protein, Caveolin-1 (CAV1), was observed for CCM1 mutants, while down-regulation in CCM3 mutants was observed (Figure 9), suggesting a potentially intricate feed-back

regulation within the CSC. Interestingly, down-regulation of Glyoxalase Domain Containing 4 (GLOD4) was shared in both CCM1 and CCM3 mutants (Figure 9). Cellular processes associated with these two genes were vast, but included neurogenesis, nervous system development, cellular response to hormone stimulus, negative regulation of signal transduction, circulatory system development, regulation of cell proliferation, apoptotic processes, membrane biogenesis, regulation of MAPK cascade, caveola assembly, blood vessel development and morphogenesis and vasculature development (suppl. table 9A). Molecular functions potentially affected mainly included binding pathways (suppl. table 9B). The main KEGG pathway of interest affected for these mutants included focal adhesion pathway (suppl. table 9C).

3.10. Perturbed protein interactome pathways shared in the deficiency of CCM2 and CCM3

Proteasome Activator Subunit 1 (PSME1), which controls cellular protein stability and found at high concentrations throughout eukaryotic cells, was down-regulated in both CCM2 and CCM3 mutants (Figure 10). Potentially affected cellular processes included various cell cycle pathways, apoptotic processes, several DNA damage pathways, antigen processing and presentation, Wnt signaling pathways, cellular response to stress pathways and several signal transduction pathways (suppl. table 10A). Endopeptidase activator activity functions are also associated with altered PSME1 levels (suppl. table 10B) as well as proteasome and antigen processing and presentation pathways (suppl. table 10C).

3.11. Perturbed protein interactome pathways shared in the deficiency of CCM1, CCM2 and CCM3

Up-regulation of SUN Domain-Containing Protein 1 (SUN1), a component of the linker of nucleoskeleton and cytoskeleton (LINC) complex that connects the cytoskeleton and nuclear lamina, was observed in all three CCM-KD HBMVEC cells (Figure 11). Interestingly,

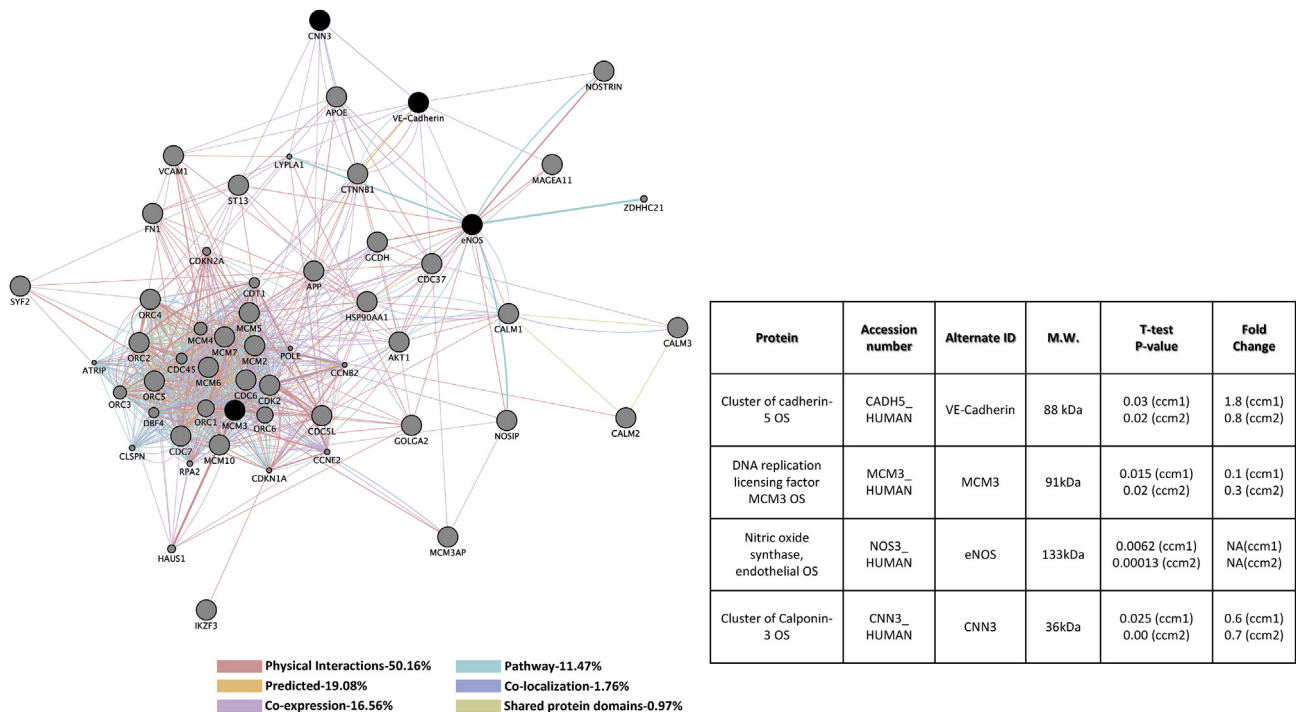


Figure 7. Perturbed protein interactome pathways in the deficiency of CCM1 or CCM2 in (HBMVEC). Four proteins were identified with significant expression changes in CCM1 or CCM2 deficient HBMVEC. Table on the right illustrates details of query proteins identified in the samples through mass spectrometry with accession number, alternate ID, Molecular Weight (M.W.), p-values and fold changes in mutant/controls. NA = not found in WT samples. Interactomes were constructed identical to Fig. 5. Interactomes illustrations are identical to Fig. 5. All samples were run in triplicates. Significances were determined identical to Fig. 5.

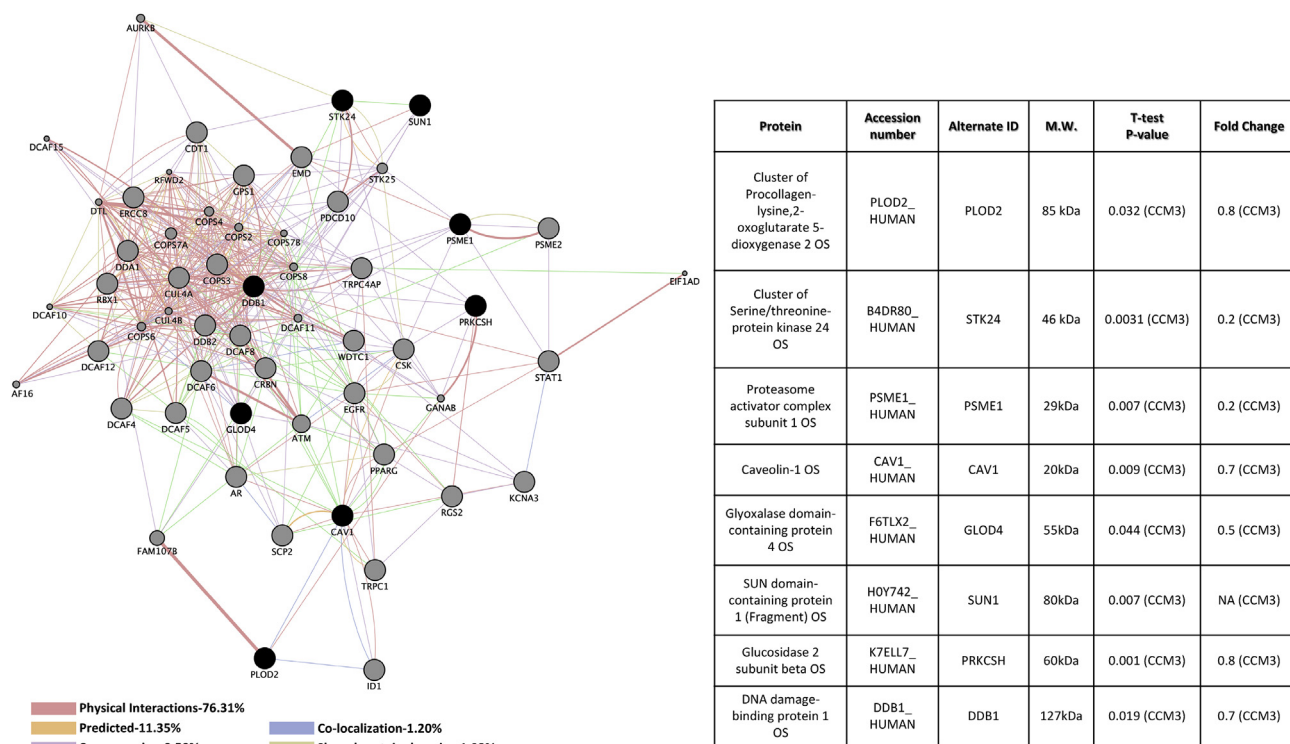


Figure 8. Perturbed protein interactome pathways in the deficiency of CCM3 in (HBMVEC). Eight proteins were identified with significant expression changes in CCM3 deficient HBMVEC. Table on the right illustrates details of query proteins identified in the samples through mass spectrometry with accession number, alternate ID, Molecular Weight (M.W.), p-values and fold changes in mutant/controls. NA = not found in WT samples. Interactomes were constructed identical to Fig. 5. Interactomes illustrations are identical to Fig. 5. All samples were run in triplicates. Significances were determined identical to Fig. 5.

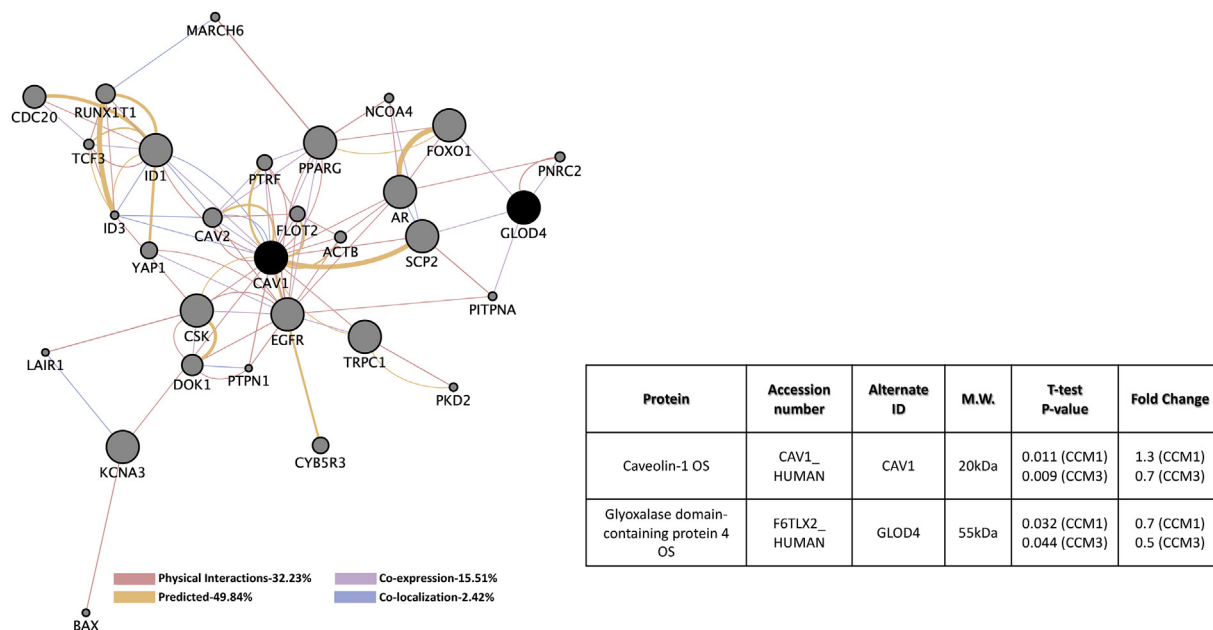


Figure 9. Perturbed protein interactome pathways in the deficiency of CCM1 or CCM3 in (HBMVEC). Two proteins were identified with significant expression changes in CCM1 or CCM3 deficient HBMVEC. Table on the bottom right illustrates details of query proteins identified in the samples through mass spectrometry with accession number, alternate ID, Molecular Weight (M.W.), p-values and fold changes in mutant/controls. Interactomes were constructed identical to Fig. 5. Interactomes illustrations are identical to Fig. 5. All samples were run in triplicates. Significances were determined identical to Fig. 5.

up-regulation of Glucosidase 2 (PRKCSH) in both CCM1-KD and CCM2-KD HBMVEC cells but down-regulation in CCM3-KD cells were observed (Figure 11). Lastly, DNA damage binding protein (DDB1) was also up-regulated in both CCM1-KD and CCM2-KD HBMVEC cells, but down-regulated in CCM3-KD cells (Figure 11). Numerous metabolic

processes, protein modification processes, proteolysis, DNA damage response and repair, cytoskeletal anchoring at nuclear membrane, translation synthesis and cell cycle regulation pathways are potentially affected in these CCMs-KD HBMVEC cells (suppl. table 11A). KEGG pathways include nucleotide excision repair and ubiquitin mediated

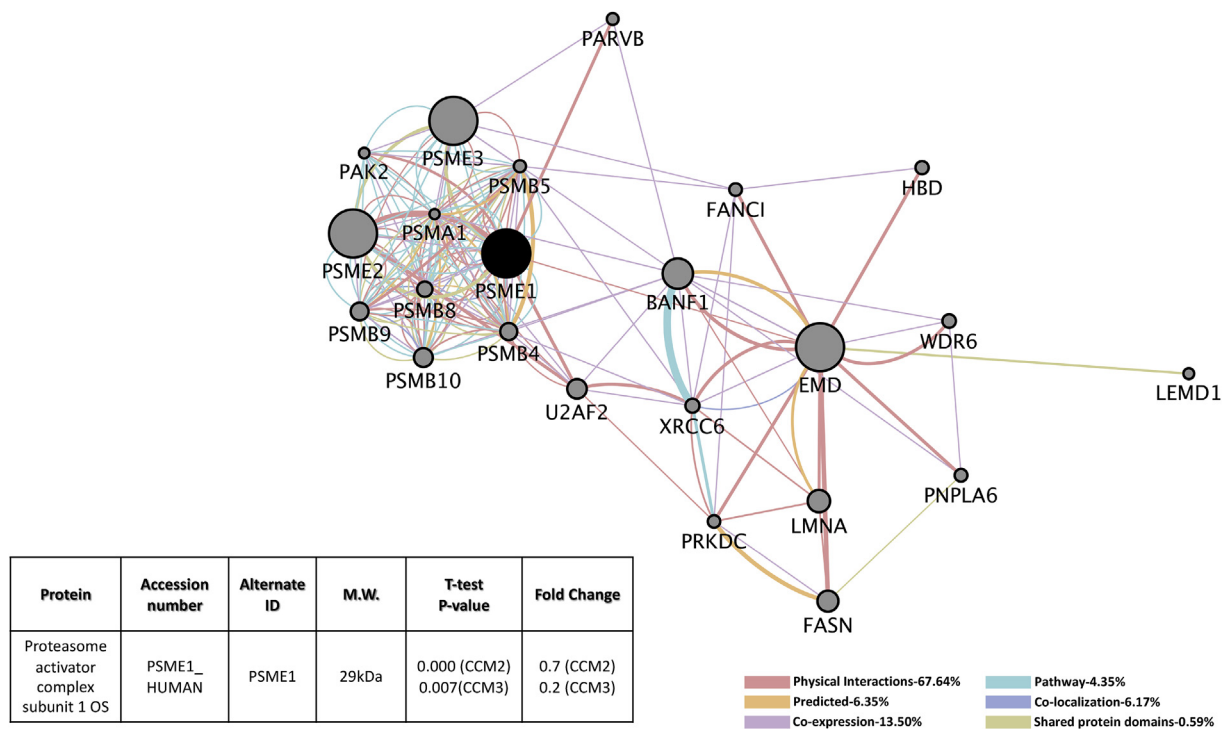


Figure 10. Perturbed protein interactome pathways in the deficiency of CCM2 or CCM3 in (HBMVEC). PSME1 was identified with significant expression changes in CCM2 or CCM3 deficient HBMVEC. Table on the bottom left illustrates details of query proteins identified in the samples through mass spectrometry with accession number, alternate ID, Molecular Weight (M.W.), p-values and fold changes in mutant/controls. Interactomes were constructed identical to Fig. 5. Interactomes illustrations are identical to Fig. 5. All samples were run in triplicates. Significances were determined identical to Fig. 5.

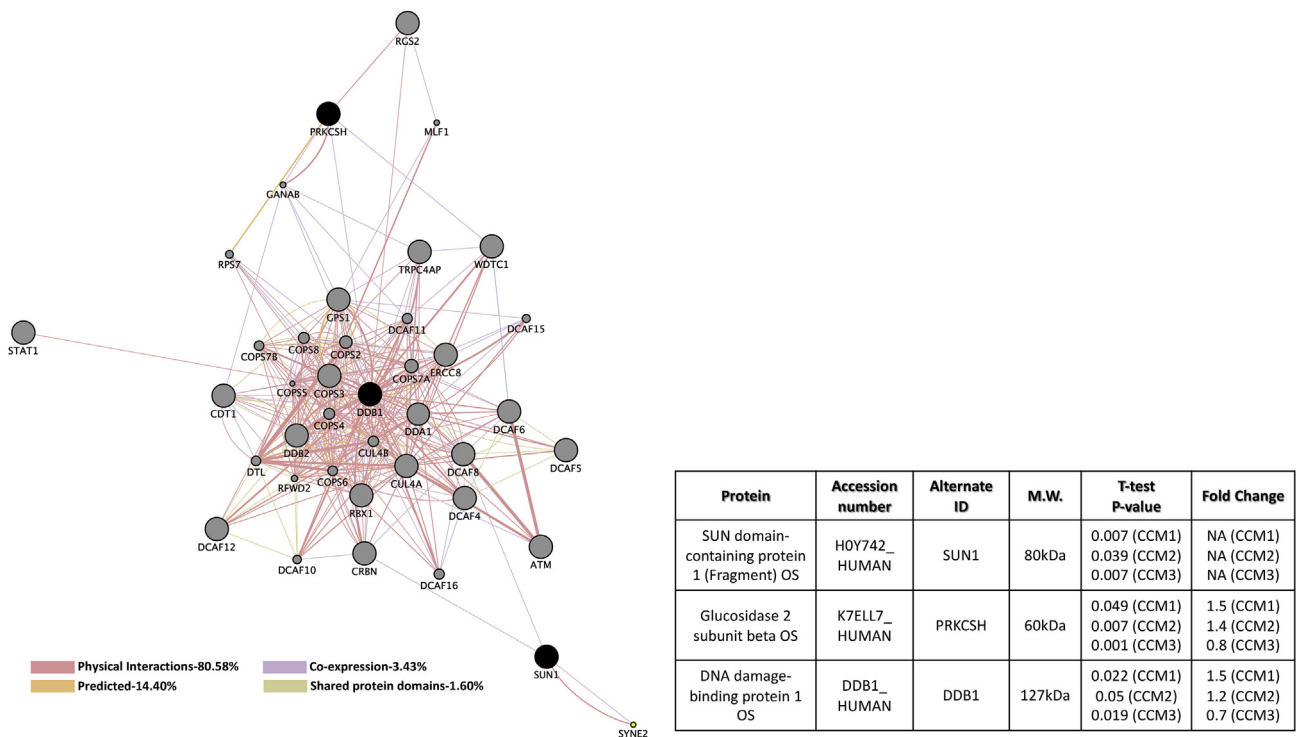


Figure 11. Perturbed protein interactome pathways in the deficiency of CCM1, CCM2 or CCM3 in (HBMVEC). Three proteins were identified with significant expression changes in CCM1, CCM2 or CCM3 deficient HBMVEC. Table on the bottom right illustrates details of query proteins identified in the samples through mass spectrometry with accession number, alternate ID, Molecular Weight (M.W.), p-values and fold changes in mutant/controls. NA = not found in WT samples. Interactomes were constructed identical to Fig. 5. Interactomes illustrations are identical to Fig. 5. All samples were run in triplicates. Significances were determined identical to Fig. 5.

proteolysis with DDB1 altered levels in our mutant strains (suppl. table 11B).

4. Discussion

4.1. No apparent correlations between proteomic and transcriptomic results

It is highly anticipated the integrated transcriptomic and proteomic approach employed in the study will provide a systems-level understanding of cellular functions of the CSC. By comparing both transcriptomic and proteomic data, we found no overlaps between proteomic and RNA-seq results, which is not totally surprising. Messenger RNA levels do not necessarily correlate with their coded protein levels at steady state, but we must also acknowledge the limitation and interpretation of transcriptomics results due to the small sampling size ($n = 1$) compared to proteomics analysis ($n = 3$). There are several other possible explanations for this discrepancy as well. First, there may be various regulation mechanisms existing at both RNA and protein levels for the CSC. Second, RNA-seq transcriptome profiling is not able to detect the expressional adjustment by post-transcriptional mechanisms (Schwanhausser et al., 2011, 2013; Tebaldi et al., 2012). Third, there are major post-transcriptional (King and Gerber, 2016; Spangenberg et al., 2013) and post-translational mechanisms to separate the RNA expression and protein abundance at static state (Sampath et al., 2008), such as protein synthesis control pathways and protein degradation control pathways. Fourth, these results might also indicate a form of feedback inhibitory mechanisms on transcriptional regulation based on protein abundance at static state. Finally, RNA-seq approach is more sensitive than proteomic techniques, especially in detecting low-expressed species, such as CCMs (only detected in RNA-seq in this study). However, among identified targets, there are some possible noise-like responses at both transcriptional and translational levels, due to some adaptive responses to physiological and pathological situations (Sharma et al., 2017), unrelated to CSC alterations.

Although we were unable to find direct overlaps of altered gene expression between the RNA and protein levels, in-direct overlapped alterations were frequently seen. For example, protein level of Calpain-2 (CAPN2) was down-regulated while down-regulated RNA transcripts of Moesin (MSN), one of the interactors of CAPN2, were detected in CCM1-KD HBMVEC cells. Also, detected protein levels of Minichromosome Maintenance Complex Component 3 (MCM3) was down-regulated in both CCM1-KD and CCM2-KD HBMVEC cells while down-regulated RNA transcripts of C-C Motif Chemokine Ligand 2 (CCL2), one of the interactors of MCM3, was detected in CCM1-KD HBMVEC cells. Interestingly, in CCM2 deficient HBMVEC cells, Splicing Factor Proline and Glutamine Rich (SFPQ) protein levels were up-regulated, while down-regulated transcript levels of U2 Small Nuclear RNA Auxiliary Factor 1 (U2AF1), one of the interactors of SFPQ, was observed, suggesting that there may be a feedback regulation between SFPQ protein level and U2AF1 RNA transcript level. Our data further support the existence of multiple layers of regulation between the proteins and RNAs associated with the functions of the CSC during angiogenesis.

4.2. Most alterations occur in angiogenic signaling cascades in perturbed CSC conditions

4.2.1. Alterations in angiogenesis at the transcript level

A significant amount of alterations at both RNA and protein levels represent an interesting outcome on potential effects concerning angiogenesis in both HBMVEC (cerebral neovascular angiogenesis) and zebrafish models (developmental angiogenesis) (Figs. 12 and 13). NOV is known to play an important role in fibrosis, skeletal development and cardiovascular development (Bleau et al., 2005; Heath et al., 2008; Jiang et al., 2004; Lafont et al., 2005; Moussad and Brigstock, 2000; Perbal, 2001). Several integrins (ITG α V, ITG β 3, ITG α 5 and ITG β 1) are known

ligands that interact with NOV to stimulate pro-antigenic activities and induce angiogenesis in endothelial cells (Lin et al., 2003, 2005; van Roeyen et al., 2012). NOV RNA being down-regulated in CCM1-KD HBMVEC might suggest that the loss of CCM1 leads to reduced NOV transcription during angiogenesis.

Down regulation of IL1 α transcripts in CCM1 deficient HBMVEC cells potentially alters Vascular Endothelial Growth Factor A (VEGF-A) since IL1 α stimulates VEGF-A expression. VEGF-A is one of the 6 members of the VEGF family which has been shown to be one of the most important factors during angiogenesis (Hoeben et al., 2004). IL1 α proteins stimulate release of collagenase, a protease used to enable endothelial cell migration by breaking up the basement membrane (Dalton et al., 1989; Lefebvre et al., 1990). IL1 α has also been shown to induce release of fibroblast growth factor (FGF), an angiogenic molecule, influencing tissue and urokinase type plasminogen activators in endothelial cells used to generate plasmin to degrade the extracellular matrix (Cozzolino et al., 1993; Hoeben et al., 2004). FGF has also been shown to increase hypoxia-inducible protein complex HIF-1 α which in turn, can promote VEGF-A expression, since this complex binds to the enhancer of VEGF-A (Hoeben et al., 2004). Alterations in both EGR1 and EXOC5 also confirmed potential effects on angiogenesis through VEGF signaling in CCM1 deficient zebrafish embryos. Focal cerebral Ischemia, one of the major diseases associated with EGR1, stimulates VEGF expression in the brain, in an effort to promote formation of new blood vessels (Lee and Bondy, 1993; Sun et al., 2003). EXOC5, part of the exocyst complex, is involved in docking of vesicles on the plasma membrane (Lipschutz et al., 2003; Mukerji et al., 2012). EXOC5 is reported to be an essential component for biogenesis of epithelial cell surface polarity, reported to interact with vesicle transport machinery and involved in actin cytoskeletal remodeling (Lipschutz et al., 2000). Altered EXOC5 expression, involved in actin cytoskeletal remodeling, could also indirectly affect VEGF, since the process of cytoskeletal remodeling involves interactions of p38 MAPK with VEGFR-2 (Hoeben et al., 2004). Down-regulated CCL2, which is linked to Rheumatoid Arthritis (RA), Psoriasis and amyotrophic lateral sclerosis (ALS), is also associated with VEGF and angiogenesis signaling pathways (Gupta et al., 2011; Hoeben et al., 2004). VEGF-A isoform 165, VEGFR-2 and neuropilin-1 are associated with synovial angiogenesis in RA; VEGF-A in RA will eventually stimulate generation of plasmin which leads to production of matrix metalloproteinases (MMPs) that are involved in destruction of arthritic joints characteristic in RA (Zhao and Guan, 2011). VEGF-A, inhibiting apoptosis of endothelial cells (ECs) through VEGFR-2 activation, is essential in remodeling new vasculature in RA (Hoeben et al., 2004). Psoriasis is characterized by skin plaques along with neovascularization and proliferation of blood vessels; VEGF/VEGFR-1/VEGFR-2 are all overexpressed by keratinocytes in epidermis and fibroblasts influencing neovascularization at a dermal level (Hoeben et al., 2004). Both VEGF-A and CCL2 were found to be up regulated in cerebral spinal fluid in patients suffering from ALS, suggesting angiogenic responses as well as involvement of adult neural stem cells and microglial activation in pathogenesis of ALS (Gupta et al., 2011).

Down regulation of TJP1, essential for tight junction function by coordinating binding of cytosolic proteins, F-actin and transmembrane proteins as well as a component of both human and rat BBB, was demonstrated in both CCM1 and CCM2 deficient HBMVEC. Potential alterations to focal adhesion pathways identified in CCM1 and CCM2 deficient HBMVEC interactome data, suggest a possible connection with VEGF induced cytoskeletal reorganization through its interaction of focal adhesion kinase (FAK) with paxillin (Rousseau et al., 1997). Altered protein expression of ITGB4 was observed in CCM1 and CCM2 deficient HBMVEC as well as CCM1 deficient zebrafish, indicating an important role of ITGB4 in the CSC. ITGB4 signaling pathway plays an essential role in the integrity of the BBB. This data suggests overlaps in potential alterations in tight junction, focal adhesion and BBB pathways when either CCM1 or CCM2 expression levels are altered in HBMVEC and zebrafish model.

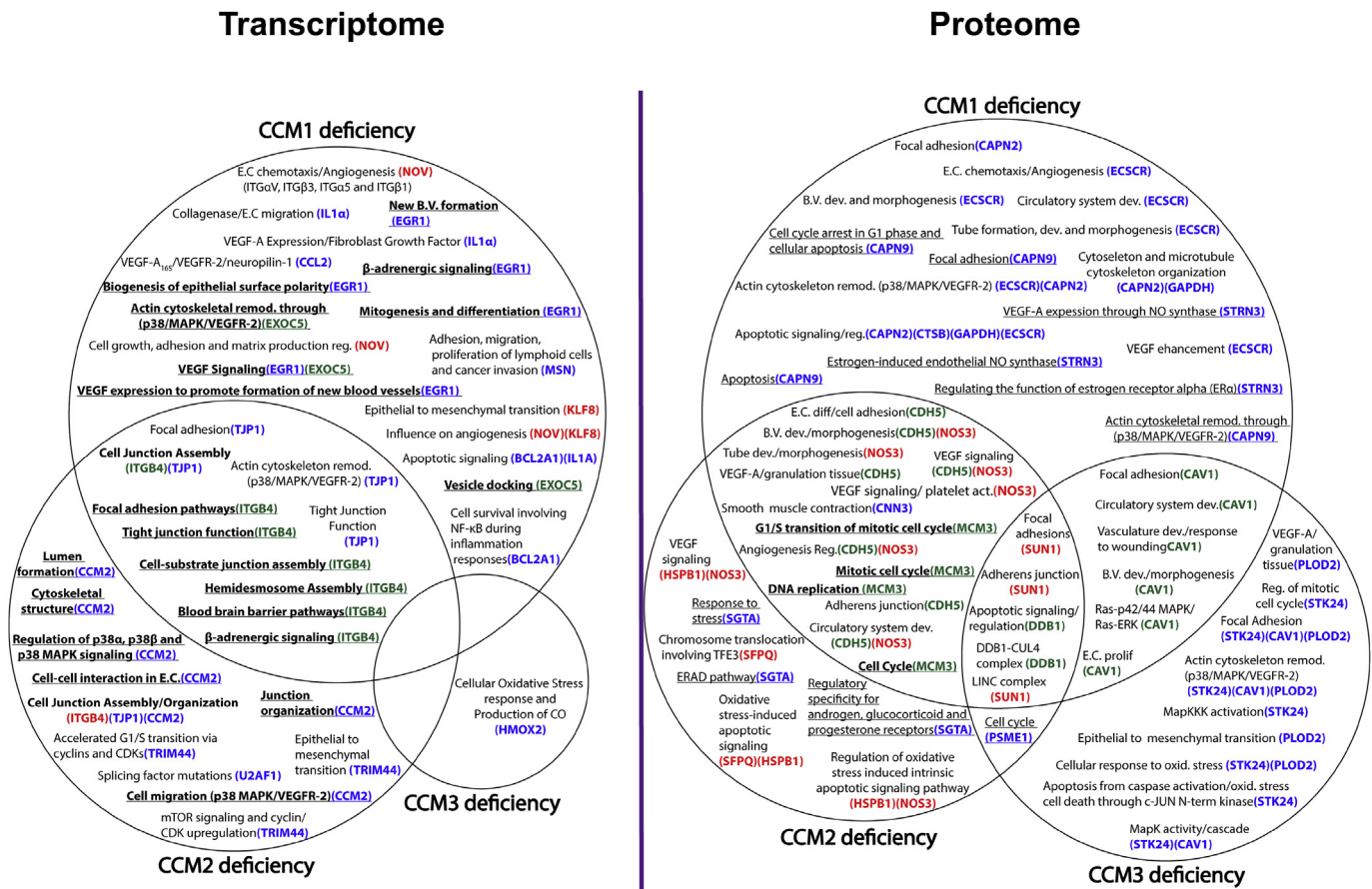


Figure 12. Pathways summary associated with perturbed CSC. Signaling cascades impacted with perturbed CSC in human brain microvascular endothelial cells (HBMVEC) and zebrafish strains (*san*, *vtm*). Venn diagram illustrates affected pathways with observed down-regulated (blue), up-regulated (red), or oppositely regulated (green) genes between CCM mutants. Diagram is divided into transcriptome (altered transcriptional data analysis) and proteome (altered translational data analysis). Pathways that are underlined are zebrafish specific while pathways that are in bold and underlined are shared between zebrafish (*in-vivo*) and HBMVEC (*in-vitro*) models. Abbreviations: Endothelial cells (E.C.), development (dev.), blood vessel (B.V.), remodeling (remod.), differentiation (diff.), activation (act.), regulation (reg.), vascular endothelial growth factor (VEGF), linker of nucleoskeleton and cytoskeleton (LINC), proliferation (prolif.) and oxidative (oxid.).

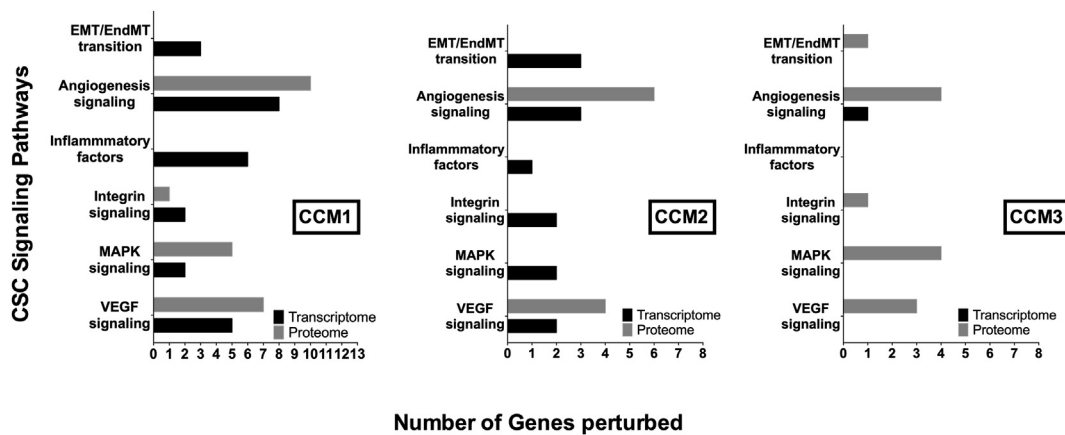


Figure 13. Summarized CSC signaling pathways and number of genes perturbed in each model. Pathways impacted in our models with perturbed CSC signaling in human brain microvascular endothelial cells (HBMVEC) and zebrafish strains (*san*, *vtm*) in this study were summarized based off of Fig. 12. Bar graph demonstrates the number of perturbed genes found in each of the major CSC signaling pathways. Angiogenesis and VEGF signaling appeared to be the signaling pathways with the greatest number of perturbed genes across all three mutants. Genes that are involved in more than one signaling pathway were counted and added to each pathway. Missing bars indicate a lack of perturbed genes (for either proteomics or transcriptomics) for that particular pathway in this study.

4.2.2. Potential alterations in angiogenesis at the proteome level

Correlating with affected pathways concerning angiogenesis at the transcription level, there was a number of affected pathways at the

protein level that reinforces CCM genes' involvement in angiogenesis in both HBMVEC and zebrafish models (Figs. 12 and 13). Down-regulated in CCM1-KD, ECSCR is known to regulate tube formation as well as

endothelial chemotaxis and interact with filamin A (Armstrong et al., 2008), and is involved in EGF-induced cell migration and cell shape alterations. ECSCR is primarily found in blood vessels and ECs (Wu et al., 2012), asserting its role in angiogenesis through modulation of actin cytoskeleton, and enhances VEGF (Kilari et al., 2013). Down-regulation of CAPN2 potentially affects focal adhesion pathways associated with CAPN2. This data, similar to that mentioned above with RNA transcript analysis of CCM1 and CCM2 deficient models, suggests a possible connection with VEGF induced cytoskeletal reorganization (Rousseau et al., 1997). Down-regulation of CAPN2 and GAPDH illustrated potential alterations to regulation of cytoskeleton and microtubule organization. Down-regulated Striatin 3 (STRN3), unique in zebrafish Ccm1 mutant only, is suspected to function as a signaling or scaffold protein, and shown to have a role in regulating the function of estrogen receptor alpha (ER α) and acts as a scaffold for assembly of proteins necessary for rapid activation of ER α -induced eNOS (Lu et al., 2004). VEGFR-2 also activates eNOS which aids in generating nitric oxide to increase vascular permeability and cellular migration. Overexpression of cyclooxygenase (COX)-2, an enzyme induced by eNOS, stimulates tube formation and EC motility through increased production of VEGF-A (Hoeben et al., 2004). Up-regulation of Heat Shock Protein Family B Small Member 1 (HSPB1), as seen in CCM2 deficient HBMVEC lines, is shown to be involved in VEGF signaling pathways. Up-regulation of eNOS, in both CCM1 and CCM2 HBMVEC mutants, promotes blood clotting by activating platelets, and participating in VEGF induced angiogenesis (Saleh et al., 2015). Further demonstration of alterations in angiogenesis involving eNOS include potentially affected pathways involved in regulation of blood circulation, blood vessel diameter, blood coagulation, blood vessel EC migration, and platelet activation. VE-Cadherin, up-regulated in CCM1 and down-regulated in CCM2 deficient HBMVEC, is a key player in endothelial adherens junction assembly and maintenance. VEGF-A disorganizes endothelial junction proteins, including cadherin proteins such as VE-Cadherin, to allow for decreased barrier properties and gap formation between ECs, thereby enhancing supply of proteins and cells to form granulation tissue (Hoeben et al., 2004). VE-Cadherin alterations potentially affect pathways including cell-cell adhesion and regulation of EC differentiation. Altered pathways involving both eNOS and VE-Cadherin expression levels include blood vessel development, circulatory system development, VEGF receptor signaling pathway and regulation of angiogenesis. Calponin-3 (CNN3), down-regulated in both CCM1 and CCM2 HBMVEC mutants, is a cytoskeleton protein and has been shown to regulate actin cytoskeleton functions and smooth muscle contraction. When looking at CCM3 deficiency, down-regulation of STK24 expression levels present a potential effect on axon regeneration in the radial and optic nerves. STK24 promotes apoptosis in response to caspase activation and stress stimuli, as well as mediating oxidative stress induced cell death by modulating c-Jun N-terminal kinase (JNK) activation (Chen et al., 2009; Lin et al., 2010). In regards to angiogenesis, binding of VEGF to VEGFR-2 results in a downward signaling cascade that eventually activates p42/44 MAPK that phosphorylates and activates c-JUN (Hoeben et al., 2004). Altered gene expression of STK24 affects several kinase cascade pathways including activation of MAPKKK and various regulation of both MAPK activity and MAPK cascade. VEGF-A and its target receptors, VEGFR-1 and VEGFR-2, undergoes increased expression when cells are undergoing hypoxia; in several *in-vivo* models (Hoeben et al., 2004). Interestingly, alterations in STK24 affect several pathways associated with oxidative stress including intrinsic apoptotic signaling pathways in response to oxidative stress.

Down-regulation of PLOD2 is also expected to alter angiogenesis through VEGF induced cytoskeletal reorganization through VEGFR-2/p38MAPK/focal adhesion interactions in HBMVEC lines. PLOD2 facilitates hydroxylation of lysyl residues in collagen-like peptides and is involved in degradation of the ECM and collagen chain trimerization, an important step for transforming fibrin-fibronectin stroma into granulation tissue of healing wounds (Hoeben et al., 2004). PLOD2 is also implicated in response to oxidative stress, similar to STK24 mentioned

above. One of the main functions of the multidomain scaffolding protein TJP1, is to help regulate movement of macromolecules and ions between endothelial and epithelial cells (Anderson and Van Itallie, 1995). TJP1 is essential for tight junction function, and has been shown to be a key component for human and rat BBB integrity (Watson et al., 1991; Xu et al., 2012; Yu et al., 2010).

Altered protein expression of CAV1 was defined in CCM1 and CCM3 deficient cells, CAV1 negatively regulate Ras-p42/44 mitogen-activated protein kinase (MAPK) cascade, promotes cell cycle progression and participates in coupling integrins signaling to the Ras-ERK pathway. The p42/44 MAPK pathway is involved as a downstream effect to the binding of VEGF to VEGFR-2 and also to binding of VEGF to VEGFR-3. Altered levels of CAV1 could therefore indirectly provide some feedback inhibition signaling for altered VEGF/VEGFR-2 binding, influencing blood vessel EC proliferation, migration and survival; while VEGF/VEGFR-3 binding, influences survival of blood and lymphatic EC survival, migration and proliferation (Hoeben et al., 2004). Additionally, multiple pathways potentially affected by CAV1 expression, reinforces its role in angiogenesis, including circulatory system development, blood vessel development and morphogenesis, vasculature development, nitric oxide biosynthetic process, response to wounding, focal adhesion pathways and EC proliferation.

Shared alterations in SUN1 levels were observed in CCM1, CCM2 and CCM3 deficient HBMVEC cells, suggesting its major role in CSC-mediated angiogenesis signaling. SUN1 is a component of the linker of nucleoskeleton and cytoskeleton (LINC) complex that connects the cytoskeleton and nuclear lamina. The cytoskeleton, important for various steps in angiogenesis, cell motility and membrane protrusion events are essential for establishing successful angiogenic responses (Bayless and Johnson, 2011). Furthermore, it has been demonstrated that the focal adhesions at cell-matrix and adherens junctions at cell-cell contacts that tether the cytoskeleton to the plasma membrane are essential for angiogenic responses; it was demonstrated that when cadherin's, focal adhesions and integrins are inhibited, angiogenic responses are blocked (Bach et al., 1998; Carmeliet et al., 1999; Liao et al., 2000).

4.3. Altered $\beta 4$ integrin signaling in all perturbed CSC conditions is a surprise

Perturbation of integrin β -4 (ITGB4) signaling was consistently observed in both CCMs-KD HBMVEC cells and CCMs-KO zebrafish embryos; which is the only signaling cascade validated in both human and animal models (Figs. 3 and 13 and suppl. fig. 3). Up-regulation was observed among CCM1-KD and CCM2-KD HBMVEC cells and Ccm1-KO zebrafish (*san*) but down-regulated in Ccm2-KO zebrafish (*vtn*) (Figure 3 and suppl. fig. 3). ITGB4 is different from other β subunits for its extra-large cytoplasmic tail (over 1,000 amino acid long), docking to intermediate filaments through plectin (Dans et al., 2001; Walko et al., 2015), while cytoplasmic tails of other β subunits (~50 amino acids) bind to actin cytoskeletons. As a laminin-5 (LN5) receptor and a key component of hemidesmosome (HD) (Wang et al., 2012c), ITGB4 is mainly located in the adhesion structure of HD, contributing to the maintenance of integrity of epithelium (Walko et al., 2015), especially the epidermis (Dowling et al., 1996; van der Neut et al., 1996). In angiogenesis, ITGB4 was initially found to be located predominantly on the matured vasculature where it is negatively regulated, suggesting ITGB4 as a negative regulator of angiogenesis at quiescent state (Hiran et al., 2003). Up-regulated integrin β 4 was suggested to be associated with vascular disease related to aging (Sun et al., 2010).

One mutagenesis study demonstrated that ITGB4 could promote cancer angiogenesis in tumorigenesis (Nikolopoulos et al., 2004), suggesting its potentially versatile roles in angiogenesis in various conditions. ITGB4, which binds to the basal lamina of blood vessels, was initially found to be expressed in small vessels (Cremona et al., 1994; Hiran et al., 2003) but recently, ITGB4 was found to be highly expressed in the brain. Initial studies suggested that ITGB4 is expressed by astrocyte

end-feet that run along the vascular basal lamina (Previtali et al., 1997; Wagner et al., 1997), which was supported by animal studies showing transgenic mice deficient in astrocyte or pericyte laminin displayed defective BBB integrity (Chen et al., 2013b; Menezes et al., 2014). Pathways associated with ITGB4 include BBB and β -adrenergic signaling pathways (Braadland et al., 2015; Welser-Alves et al., 2013). A recent study found that ITGB4 is highly expressed in ECs in cerebral vessels, specifically in arteriolar ECs (Welser-Alves et al., 2013), raising the possible existence and important role of the adhesive HD structure in cerebrovascular ECs and BBB. However, further study found that ITGB4 is not essential for localization or regulation of expression of key HD structural proteins, plectin and CD151 (Welser-Alves et al., 2016), making the function of ITGB4 interestingly elusive in cerebral vessels.

Intriguingly, we just reported that the cytoplasmic tail of ITGB4 binds to CCM2 protein (submitted). Up-regulation of ITGB4 observed in CCM1 and CCM2 deficient HBMVEC as well as CCM1 deficient zebrafish, but down regulation in CCM2 deficient zebrafish strains offer an interesting and contradicting regulation mechanism for ITGB4 whose main pathways lay on cerebral vessels and the integrity of BBB. Since three CCM proteins influence each other within the CSC, there might be a “paradoxical regulation of ITGB4”, mimicking regulation of CAV1, as described below. Therefore, in the perturbed CSC, we postulate that ITGB4 likely functions as a cellular sensor guarding for the integrity of BBB in cerebrovascular ECs. In response to environmental cues, CSC signaling can modulate BBB status by regulating ITGB4 expression level in ECs. In an effort to enhance the weakened BBB integrity of cerebral vessels, ITGB4 expression in ECs can be enhanced by CSC, increasing the ability of anchoring to the basal lamina. ITGB4 also plays many other important roles in ECs cell physiology, including survival, proliferation, apoptosis, autophagy, angiogenesis, and senescence. Recently, reported up-regulation of ITGB4 expression in cerebrovascular ECs has been associated with neuroinflammatory events (Hashimoto et al., 2006; Milner and Campbell, 2006; Welser et al., 2017), raising the possible role of ITGB4 in connection between neuroinflammation and perturbation of CSC as discussed below.

4.4. CSC might be a master-regulator for CAV1-mediated signaling

CAV1 is an essential component of caveolae that are 60–80 nm wide, bulb-shaped pits in the plasma membrane (Parton and del Pozo, 2013). Each caveola has an estimated 140–150 Cav1 molecules, which usually form oligomers in the plasma membrane (Parton and Simons, 2007; Pelkmans and Zerial, 2005); genetic ablation of CAV1 causes loss of caveolae (Drab et al., 2001; Razani et al., 2002). It has been demonstrated that β 1 integrin regulates caveola formation (Singh et al., 2010), and caveolar density decreases when integrin-mediated adhesion to the extracellular matrix (ECM) is disrupted (del Pozo et al., 2005). Reciprocally, caveolin can also contribute to β 1 integrin endocytosis to influence β 1 integrin signaling in either positive (Du et al., 2011; Shi and Sottile, 2008) or negative (Arjonen et al., 2012) fashions, depending on specific cell types (Upla et al., 2004). Cav1 plays an important role in endocytosis, and caveolin-dependent endocytosis is modulated through RAC1–p21-activated kinase (PAK), PI3K–AKT and RAS–ERK signaling cascades (Cerezo et al., 2009; del Pozo et al., 2005). These reports are fully in concordance with our previous observations that perturbation of CSC signaling leads to disruption of β 1 integrin-mediated angiogenesis (Liu et al., 2010; Liu et al., 2011; Zhang et al., 2004; Zhang et al., 2005, 2008; Zhang et al., 2001a, b), altered RAC1–p21-activated kinase (PAK), PI3K–AKT and RAS–ERK signaling cascades (Liu et al., 2010, 2011; Zhang, 2011; Zhang et al., 2004, 2005). This data strongly suggests that CAV1 signaling is downstream of CSC signaling complex.

It has been well defined that CAV1 directly interacts with endothelial nitric oxide synthase (eNOS) through its binding to caveolin-binding motifs (CBM) in eNOS (Collins et al., 2012; Garcia-Cardena et al., 1997) and inhibits eNOS signaling (Bucci et al., 2000; Garcia-Cardena et al., 1997; Sowa et al., 2001). Intriguingly in this study, eNOS was

found to be up-regulated in both CCM1-KD and CCM2-KD HBMVEC cells (Figure 7), further enhancing our previous conclusion that CAV1 signaling is modulated by CSC as one of its downstream signaling targets. Interestingly, CAV1 protein level was up-regulated in CCM1 deficiency, while down-regulation of CAV1 protein in CCM3 depletion was observed (Figure 9). This contradicting phenomena has been well described as the caveolar “paradox” (Sbaa et al., 2005). In this paradoxical regulation, there is a coexistence of the “signaling inhibitory” paradigm allosteric inhibition of eNOS proportional to caveolin levels and the “signaling promoting” effect of caveolin through compartmentation of eNOS according to the abundance of caveolin. Therefore, there is a typical bell-shaped relationship between the abundance of CAV1 and NO-driven angiogenesis, in which there is only a narrow center-region of pro-angiogenic effects for CAV1-eNOS signaling. Anti-angiogenic effects will be observed when CAV1 expression level shifts out of the normal range, as up-regulation leads to an exacerbated inhibitory clamp, while down-regulation leads to loss of compartmentation (Dessy et al., 2010). Therefore, CSC can be a master regulator to either positively (via CCM3) or negatively (via CCM1) regulate CAV1 expression to fine-tune the intricate balance of CAV1-eNOS signaling cascades.

Likewise, canonical Wnt signaling is essential for both brain specific angiogenesis and blood brain barrier genesis (Daneman et al., 2009; Stenman et al., 2008), in which β -catenin signaling may mediate BBB functions (Liebner et al., 2008), and phosphorylated CAV1 can sequester β -catenin and thus decrease BBB function (Kronstein et al., 2012). Interestingly, pathway analysis showed that perturbed Wnt signaling pathways were found to be shared in the deficiency of CCM2 and CCM3 (suppl. table 10A). One report described that EC-specific Ccm3-KO led to activation of β -catenin, preceding the initiation of TGF- β /BMP signaling (Bravi et al., 2015), which might add more evidence that CSC signaling is upstream of Wnt signaling pathways in modulating the activity of β -catenin. These observations have expanded our view about the relationship and signal flow direction among CSC signaling, CAV1 signaling and Wnt signaling cascades during angiogenesis.

Oxidative stress has been defined as molecular insults resulting from excessive and/or cumulative production of reactive species, such as reactive oxygen species (ROS) and reactive nitrogen species (RNS) (Gupta et al., 2014). Cav-1 has been shown to have regulatory feedback functioning on oxidative stress status. As discussed before, as a molecular hub, Cav-1 can bind and negatively regulate the activity of eNOS, therefore, loss of Cav-1 will lead to up-regulation of eNOS activity and increased NO production, which could lead to accumulation of RNS. Further, Cav-1 regulates a variety of cellular signaling, such as RAS-MAPKs signaling (Sundaresan et al., 1996) and AKT signaling pathways (Nogueira et al., 2008; Venema et al., 1997), therefore silencing Cav-1 could result in enhanced oxidative stress (Wang et al., 2017).

Chronic inflammation has been proven to be associated with elevated oxidative stress in cardiovascular diseases (Szczyrek and Szygula-Jurkiewicz, 2015). A group of inflammatory factors, including CCL2, IL1 α , MSN, BCL2A1 and LMAN1, were all significantly down-regulated in CCM1-KD HBMVEC cells. CCL2 has a specific role as a chemotactic factor attracting basophils and monocytes (Wu et al., 2018). CCL2 expression is up-regulated during degenerative and inflammatory conditions in the CNS (Prinz and Priller, 2014), and is associated with RA, atherosclerosis and psoriasis (O'Connor et al., 2015; Zhang et al., 2015). IL1 α , through maturation and proliferation of B-cells and induction of IL-2 release and fibroblast growth factor activity, is able to stimulate inflammation (Boraschi et al., 1990; Cozzolino et al., 1993; Rupp et al., 1986). Being involved in inflammatory responses, IL1 α has been reported to stimulate release of collagenase and prostaglandin from synovial cells (Dalton et al., 1989; Lefebvre et al., 1990). MSN, involved in adhesion, migration and proliferation of human lymphoid cells, are known to contribute to immunologic synapse formation (Charrin and Alcover, 2006; Chen et al., 2013a; Ilani et al., 2007). RhoA signaling and actin nucleation by ARP-WASP are all pathways involving participation

of MSN (Simoncini et al., 2006; Wang et al., 2012b). Dysregulation of MSN might be associated with immunodeficiency (Kobayashi et al., 2003; Lagresle-Peyrou et al., 2016). BCL2A1, being a direct target of NF- κ B during inflammation responses, is believed to have a cyto-protective function essential for cell survival and lymphocyte activation; BCL2A1 is up-regulated in the presence of signals such as IL1 α and TNF (Kloosterboer et al., 2005; Mandal et al., 2005; Rasooly et al., 2005).

Previous reports indicate that CCM1 plays a protective role against oxidative stress in the cell by utilizing anti-inflammatory and anti-oxidant pathways (Goitre et al., 2010). CCM1 deficient cells have increased activity of COX-2, a mediator of inflammatory pathways (Hsieh et al., 2012); furthermore, Ccm1-KO mice had hyper-exaggerated responses to inflammatory agents (Corr et al., 2012), suggesting that neuroinflammatory events might be associated with CCM lesion formation (Retta and Glading, 2016). Further, we observed that regulation of oxidative stress-induced signaling pathway was changed in CCM2 deficient HBMVEC. This current study falls in line with these previous findings.

4.5. Protein stability regulation in perturbed CSC condition

Heat shock proteins (HSPs), mainly functioning as chaperones, whose altered expression levels can result in misfolded proteins and lead to degradation. Up-regulation of both HSPA4 and HSPB1 was observed in CCM2 deficient HBMVEC lines, contradicting to previous report that CCM1 deficient cells have decreased levels of heat shock proteins (HSP, Hsp70 and Hsp27), which have a protective role in handling cellular stress (Antognelli et al., 2018). DDB1, perturbed in all three CCMs-KD HBMVEC cells, is a part of the DDB1-CUL4 ubiquitin ligase complex, a key factor in autophagy. Autophagy removes protein aggregates and damaged organelles from cells and helps to recycle lipids and protein building blocks, a constitutively active, evolutionary conserved, catabolic process for maintaining homeostasis in cellular stress responses and cell survival. Regulatory mechanisms of this process are still largely unknown. LMAN1, down-regulated in CCM1-KD HBMVEC cells, functions as a cargo receptor for glycoprotein transport, cycles between cis-Golgi, the endoplasmic reticulum (ER), and the ER-Golgi intermediate compartment (Zheng et al., 2013), which might participate in ER stress-induced autophagy. SGTA, down-regulated in CCM2-KO zebrafish, is not characterized very well but has been shown to interact with 70-kDa heat shock cognate protein and hypothesized to serve housekeeping functions (Liu et al., 1999; Paul et al., 2014). DHRSX, up-regulated only in CCM1 deficient cells, is relatively uncharacterized other than being hypothesized in having a role in positive regulation of starvation-induced autophagy (Zhang et al., 2014). Previous data showed that down-regulation of integrin β 4 promotes sphingosylphosphorylcholine-induced autophagy (Ge et al., 2011), suggesting that perturbed autophagy can be observed in CCMs. Therefore, this data is in agreement with previous reports that defective autophagy is a key feature of CCMs (Marchi et al., 2015).

4.6. Endothelial-to-mesenchymal transition factors in perturbed CSC

Originally found in tumor research, endothelial-to-mesenchymal transition (EndMT) is a phenomena in which ECs change its organized vascular EC cell layer phenotype in losing cell-cell junctions into a mesenchymal phenotype of invasive and migratory properties to invade the underlying tumor tissue and is one of the major causes of fibroproliferative vascular disease (Jackson et al., 2017; Li et al., 2018; Moonen et al., 2015; Sanchez-Duffhues et al., 2018). EndMT accounts for up to 40% of cancer-associated fibroblasts (CAFs). EndMT is often considered as a specialized form of epithelial-to-mesenchymal transition (EMT), which has been extensively studied in cancer. Both EMT and EndMT generate cells that share a similar mesenchymal phenotype and utilize common signaling pathways (Potenta et al., 2008). Therefore, both share the same, if not identical, mesenchymal markers such as fibroblast-specific protein 1 (FSP1/S100A4), α -smooth muscle actin

(α SMA) or a group of transcription factors (Snail, Zeb1/2, Twist, Slug), making it difficult to distinguish both events (Souilhol et al., 2018; Wesseling et al., 2018).

High PLOD2 expression is associated with EMT (Okumura and Eguchi, 2018; Okumura et al., 2018). Likewise, TRIM44 acts as an EMT-promoting molecule (Kawaguchi et al., 2017; Peinado et al., 2007), with overexpression of TRIM44 inducing EMT transition (Peng et al., 2018; Xing et al., 2016). It has been reported that perturbed CSC was able to induce EndMT in brain microvascular ECs that plays a crucial role in the pathogenesis of CCMs (Maddaluno et al., 2013). It was further reported that EC-specific Ccm3-KO led to activation of β -catenin preceding the initiation of TGF- β /BMP signaling. A β -catenin-driven transcription program that leads ECs to EndMT in CCM3 deficient ECs, and pharmacological inhibitors of β -catenin signaling can significantly reduce progress of this EndMT transition (Bravi et al., 2015). Then, it was reported that transcription factors KLF 2/4 (Kruppel-like factor 2 or 4) can be strongly induced in CCM1-null ECs, which, in turn, promotes TGF β /BMP signaling, leading to EndMT (Cuttano et al., 2016; Zhou et al., 2015; Zhou et al., 2016a, b). These findings support a theory that the CSC has an inhibitory effect on the EndMT/EMT cellular processes.

Surprisingly in our data, the significantly changed expression levels of two EndMT/EMT factors identified, PLOD2 in CCM3-deficient HBMVEC and TRIM44 in CCM2-deficient HBMVEC cells, were both down-regulated, contradicting to the previous theory. Likewise, down-regulation of both TJP1 and ITGB4 was reported in platelet-derived growth factor-D (PDGF-D) induced EMT (Kong et al., 2010). TJP1 mRNAs have also been shown to have direct functional relations with miRNAs isolated from CCM patients (Kar et al., 2017). Interestingly, we observed down-regulation of TJP1 in both CCM1-KD and CCM2-KD HBMVEC cells and down-regulation of ITGB4 in Ccm2-KO zebrafish (vtn), however, up-regulation of ITGB4 was found among CCM1-KD, CCM2-KD HBMVEC cells and Ccm1-KO zebrafish (san) (Figure 3 and suppl. fig. 3), discordant to previous results. Although no KLF 2/4 was found in our data, increased expression of KLF8 was found in CCM1 deficient HBMVEC cells; whether this is a KLF 2/4 related pathway or a feedback regulation in the defective EndMT/EMT needs to be further investigated. In sum, our systems biological data suggests that pathogenesis of CCM seems unlikely to be directly associated with EndMT/EMT pathways in our current models (Figure 13).

4.7. Neurological conditions associated with perturbed CSC

CCM itself, as a neurological disorder, can certainly be associated with many other neurological conditions. APBA2 and CTSSB are known to interact with amyloid precursor protein (APP) associated with Alzheimer's disease (AD). CTSSB, down-regulated in CCM1-KD HBMVEC cells, is known for its role in proteolytic processing of APP, in which disruption of this process is suggested to play a major role in AD (Asai et al., 2011; Wang et al., 2012a; Wu et al., 2017). Interestingly, APBA2 also down-regulated in CCM1-KD HBMVEC cells, stabilizes APP to stop production of proteolytic fragments of APP often found in the brain of patient's suffering from AD (McLoughlin et al., 1999; Miller et al., 2006; Zhao et al., 2010). APBA2 is also hypothesized to function as a vesicular trafficking protein that couples synaptic vesicle exocytosis to neuronal cell adhesion (Biederer and Sudhof, 2000; Minami et al., 2010; Okamoto and Sudhof, 1997). AD is associated with dysregulated CAPN2 gene, and this family of proteins have been shown to play a major role in neuropathological events following traumatic brain injury (Adamec et al., 2002; Battaglia et al., 2003; Kuwako et al., 2002; Saatman et al., 2010; Shimohama et al., 1991). Perturbed expression levels of HSP protein can often be observed in ALS, AD and Huntington's disease. HSPA4 is known to interact with Parkin, PINK1 and DJ-1 of which all three genes have been linked with Parkinson disease and has been shown to interact with transcription factor C-myc, Creb1 and Egr1 (Van Der Merwe et al., 2015). GAPDH, down-regulated in CCM1-KD HBMVEC cells, by stimulating binding of CHP1 to microtubules, plays a major role in CHP-1 dependent

microtubule and membrane associations (Andrade et al., 2004). GAPDH is also a key player in assembly and organization of the cytoskeleton, and has been implicated in AD-related apoptotic cell death (Butterfield et al., 2010; Jung et al., 2014).

eNOS, up-regulated in both CCM1 and CCM2 HBMVEC mutants, mainly functions to produce nitric oxide. AD is also associated with altered eNOS expression levels (Dahiyat et al., 1999; Du et al., 2008; Hua et al., 2014; Morris et al., 2011; Turkanoglu Ozcelik et al., 2014). PRPF8, up-regulated in CCM1-KD HBMVEC cells, has been reported to be essential in pre-mRNA splicing processes, cell survival and myeloid differentiation (Keightley et al., 2013). This protein is associated with rare, genetic disorders involved in the breakdown and loss of cells in the retina (Martinez-Gimeno et al., 2003; Xu et al., 2018). TALDO1 is known to be a key player in both nucleic acid synthesis as well as lipid biosynthesis (Moriyama et al., 2016). Interestingly, multiple sclerosis (MS), transaldolase deficiency (TALDO1) and Ribose 5-Phosphate Isomerase Deficiency (RPIA) are associated with TALDO1 (Samland and Sprenger, 2009).

4.8. Proteomic and transcriptomic data confirmation

Several omics papers, recently published, also confirmed perturbation of many genes/pathways reported here, including direct overlaps in identified genes while many other genes belonging to the same family of genes identified here. Alterations at the RNA level included the family of Integrin's (ITGB and ITGA), Moesin (MSN), protein kinase C (PRKC) and tripartite motif containing (TRIM) proteins (Edelmann et al., 2014; Koskimäki et al., 2019). TJP1 mRNAs were also shown to have direct functional relations with miRNAs isolated from CCM patients (Kar et al., 2017), validating our observation of downregulated TJP1 RNA levels in CCM1 and CCM2 KD HBMVEC. Proteomic confirmation included alteration of Calponin, Glycerinaldehyde-3-Phosphate Dehydrogenase, Cathepsin, Glucosidase 2, Caveolin-1, Splicing Factor Proline And Glutamine Rich, Proteasome Activator Subunit 1, Trans aldolase 1, Procollagen-Lysine 2-Oxoglutarate 5-Dioxygenase 2 and Heat Shock Proteins (Edelmann et al., 2014).

5. Conclusion

Although there have been many efforts in elucidating the molecular and cellular effects of deficiency of each CCM protein, currently, there is no report yet on dissecting the perturbed CSC by utilizing a systems biology approach. This first effort of systems analysis on CCMs deficient models in HBMVEC (in-vitro) and zebrafish lines (in-vivo), elucidates a very unique and interconnected story demonstrating alterations in various signaling cascades both in cerebral neovascular angiogenesis as well as developmental angiogenesis with disruption of the CSC. These alterations mainly involved angiogenesis signaling cascades, VEGF pathways, $\beta 4$ integrin signaling, CAV1 signaling, autophagy and association with altered inflammatory factors (Figs. 12, 13, and 14). Alterations in angiogenic pathways mainly involved in 1). *Angiogenic cues*: endothelial cell chemotaxis, ECM, VEGF signaling, FGF signaling; 2). *Blood vessel formation*: cytoskeletal remodeling, endothelial cell migration, lumen formation, tube morphogenesis and development, vessel morphogenesis and development; 3). *blood vessel maintenances*: Blood circulation, regulation of blood vessel diameter, blood coagulation; 4). *Cell junction organization*: Focal adhesion pathways and tight junction function; and 5). *P38/MAPK cascade, response to oxidative stress* (Figs. 12, 13, and 14). To further elucidate these altered pathways, in-vivo mouse models in the deficiency of CCMs will be utilized to evaluate the impact of alterations of the CSC with various approaches to further dissect the underlying mechanism of CSC signaling during angiogenesis.

Declarations

Author contribution statement

Johnathan Abou-Fadel: Performed the experiments; Analyzed and interpreted the data; Contributed reagents, materials, analysis tools or data.

Mariana Vasquez, Brian Grajeda, Cameron Ellis: Performed the experiments; Analyzed and interpreted the data.

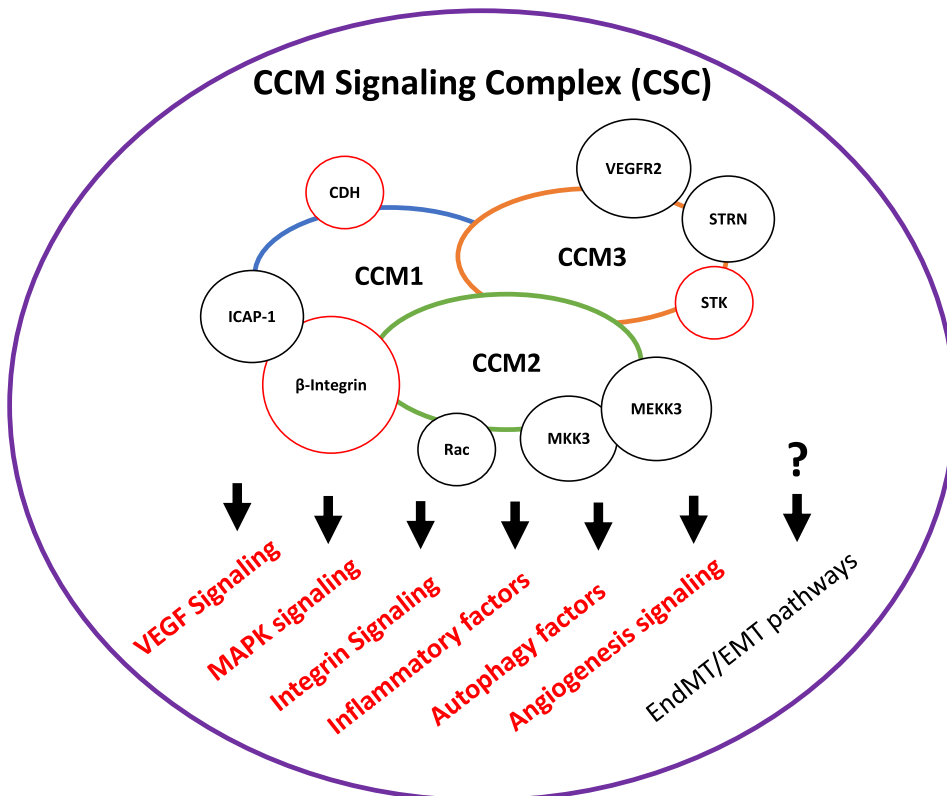


Figure 14. Summarized major signaling pathways associated with perturbed CSC. Pathways impacted in our models with perturbed CSC signaling in human brain microvascular endothelial cells (HBMVEC) and zebrafish strains (*san*, *vm*) in this study are labeled in red beneath the diagram. Diagram illustrates affected pathways in regards to angiogenesis with interactors bound to each CCM protein; interactors in red were found at altered levels in our current CCM mutagenesis study. Signaling cascade not supported in this study is labeled with a question mark.

Jun Zhang: Conceived and designed the experiments; Performed the experiments; Analyzed and interpreted the data; Contributed reagents, materials, analysis tools or data; Wrote the paper.

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Competing interest statement

The authors declare no conflict of interest.

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