Hereditary spastic paraplegias (HSPs) are neurodegenerative motor neuron diseases characterized by progressive age-dependent loss of corticospinal motor tract function. Although the genetic basis is partly understood, only a fraction of cases can receive a genetic diagnosis, and a global view of HSP is lacking. By using whole-exome sequencing in combination with network analysis, we identified 18 previously unknown HSP genes and generated a HSP interactome, demonstrating that many of known and candidate HSP genes are highly interconnected.
Our network analysis links HSP to other neurodegenerative disorders and can facilitate gene discovery and mechanistic understanding of disease