Elucidating the mechanisms governing biological processes relies heavily on our ability to characterize the physical features and traits of organisms. Today, a significant amount of biological readouts are based on fluorescent reporters. Studies that make use of these markers typically depend on changes perceivable by human observers. In the multicellular organism *Caenorhabditis elegans*, fluorescent markers can be visualized in intact animals with subcellular resolution. However, obtaining high-content data from high-resolution images of live animals is challenging due to the manual labor required, as well as the non-quantitative and biased nature of human vision. Coupling microfluidics with external hardware and custom automation software, we are able to acquire images in a high-throughput, fully automated manner. In addition, we develop algorithms to extract complex information from images of fluorescently labeled synaptic patterns in *C. elegans*. Using our integrated approach, we are able to isolate mutants that exhibit extremely subtle phenotypes, hidden to human vision. These mutants, nonetheless, reproducibly show measurable phenotypic differences. Making use of mathematical algorithms and visualization tools, we identify the characteristic traits of these mutants and predict altered genetic pathways. The novel alleles should aid in finding the missing players in synaptic establishment and maintenance, and thus propose candidate genes important for neurotransmission disorders.