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High-Throughput, Motility-Based Sorter for Microswimmers and Gene Discovery Platform[1] JINZHOU YUAN, DAVID RAIZEN, HAIM BAU, University of Pennsylvania — Animal motility varies with genotype, disease progression, aging, and environmental conditions. In many studies, it is desirable to carry out high throughput motility-based sorting to isolate rare animals for, among other things, forward genetic screens to identify genetic pathways that regulate phenotypes of interest. Many commonly used screening processes are labor-intensive, lack sensitivity, and require extensive investigator training. Here, we describe a sensitive, high throughput, automated, motility-based method for sorting nematodes. Our method was implemented in a simple microfluidic device capable of sorting many thousands of animals per hour per module, and is amenable to parallelism. The device successfully enriched for known *C. elegans* motility mutants. Furthermore, using this device, we isolated low-abundance mutants capable of suppressing the somnogenic effects of the *flp-13* gene, which regulates sleep-like quiescence in *C. elegans*. Subsequent genomic sequencing led to the identification of a *flp-13*-suppressor gene.

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