From Farm to Clinic? Soil organisms have long been assumed to be an important source of antibiotic resistance genes, in part because of antibiotic-treated livestock and in part because of the natural ecology of antibiotic production in the soil. Forsberg et al. (p. 1107) developed a metagenomic protocol to assemble short-read sequence data after antibiotic selection experiments, using 12 different drugs in all antibiotic classes, and compared antibiotic resistance gene sequences between soil bacteria and clinically occurring pathogens. Sixteen sequences, representing seven gene products, were discovered in farmland soil bacteria within long stretches of perfect nucleotide identity with pathogenic proteobacteria.