Figure 1

Diagram of the workflow for processing metagenomic samples:

1. **Short reads from metagenomic samples**
   - ReadPicker: Choose number of reads to analyze
   - Map against NCBI ref using BLAST*
   - BLAST hits (E<1e-6)
   - Tax2Lim: Retrieve specified taxonomy nodes
   - Taxonomic distribution

2. **Random reads**

3. **Unaligned reads**
   - Clinical samples pipeline

4. **HIVE hexagon**: map against Human genome

5. **Coagulated taxonomic distribution from multiple iterations**

*Can be replaced with other mapping programs*