medp\_verca-20110208

mod\_readcounts/\*.dat

Read counts obtained by post hoc alignment of reads to reported contigs,

per sample, via gsnap with default parameters. Tab-delimited columns

with the format

sample contig\_id contig\_len all\_aligned unique\_aligned paired\_aligned

where sample indicates the sample, library, tissue, etc.; contig\_id is

the contig identifier (e.g., my\_species-20111231|1234); contig\_len is the

bp length of the contig; all\_aligned is the number of reads aligned to this

contig; unique\_aligned is the number of reads that aligned uniquely to this

contig; and paired\_aligned is the number of pairs aligned to this contig.