reads against *Bacillus anthracis* and *Bacillus pumilus* genomes. Each entry contains a pair "Fraction (in classified closer to *B.anthracis* / Fraction of reads classified closer to *B.pumilus* ".

	weight				
	14	16	18	20	22
contig hit nb	47/40	24/25	04/07	0.9/3.8	0.3/2.4
contig cover	49/46	24/25	04/07	0.9/3.8	0.3/2.4
contig Jaccard	37/62	24/30	04/08	0.8/4.0	0.3/2.6
spaced hit nb	49/33	22/27	04/10	1.0/5.4	0.4/3.3
spaced cover	53/39	23/27	04/10	1.0/5.4	0.5/3.3
spaced Jaccard	41/59	22/35	04/10	0.9/4.6	0.4/3.5