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

reads classified closer to *B. cereus* ".

	weight				
	14	16	18	20	22
contig hit nb	83/14	81/11	79/09	77/08	76/08
contig cover	78/17	80/12	79/09	77/08	76/08
contig Jaccard	87/13	87/11	85/09	83/08	82/08
spaced hit nb	83/13	82/11	80/09	79/09	79/08
spaced cover	80/15	81/11	80/09	79/09	79/08
spaced Jaccard	88/12	88/11	85/09	84/08	84/08