	ROR to BaGTA	**ROR to rrs-1**	**ROR to trw**	**rrs-1 to trw**
BAnh1	23	151	100	258
BBb	29	239	-	345
BB	35	(59)[a]	-	(155)[a]
BC	26	75	-	162
BQ	32	174	122	306
BHH1	49	248	152	409
BVwin	30	197	138	344
BG	91	262	205	481
BT	82	319	280	615
Median	***32***	***197***	***145***	***344***
Median w/o BC and BB[b]	*31*	*218*	*145*	*344.5*

[a] Due to the large inversion in *B. bacilliformis*, these distances have been estimated from the second break-point of the inversion, located just upstream from rrs-2, and is thus artificially smaller.

[b] Due to the major rearrangements in *B. bacilliformis* and in group B strains, a separate statistic is shown for groups A, C and BAnh1.