

Table 2. Analyses of genome-wide population genetic measures using 10 kb genomic windows of the European and Japanese populations of *Serpula lacrymans*. Specific information for the two loci detected in Bayescan to significantly deviate from the expectations are included. # of SNPs for the Full genome is the number of variable SNPs within the populations, for the specific loci it indicates the total number of SNPs in the dataset for this region.

Genomic region	# SNPs	#SNPs	Tajimas	Tajimas	π	π Japan	D_{XY}	F_{ST}
	Europe	Japan	D	D	Europe			
			Europe	Japan				
Full genome	18982	231952	-0.079	0.724	0.00028	0.0023	0.518	0.57
						4		
Scaff 8: 2440001-2450000	163	163	-2.388	2.042	0.00025	0.0056	0.525	0.45
						0		
Scaff 27: 1-10000	101	101	0.829	-0.648	0.00186	0.0024	0.478	0.36
						5		