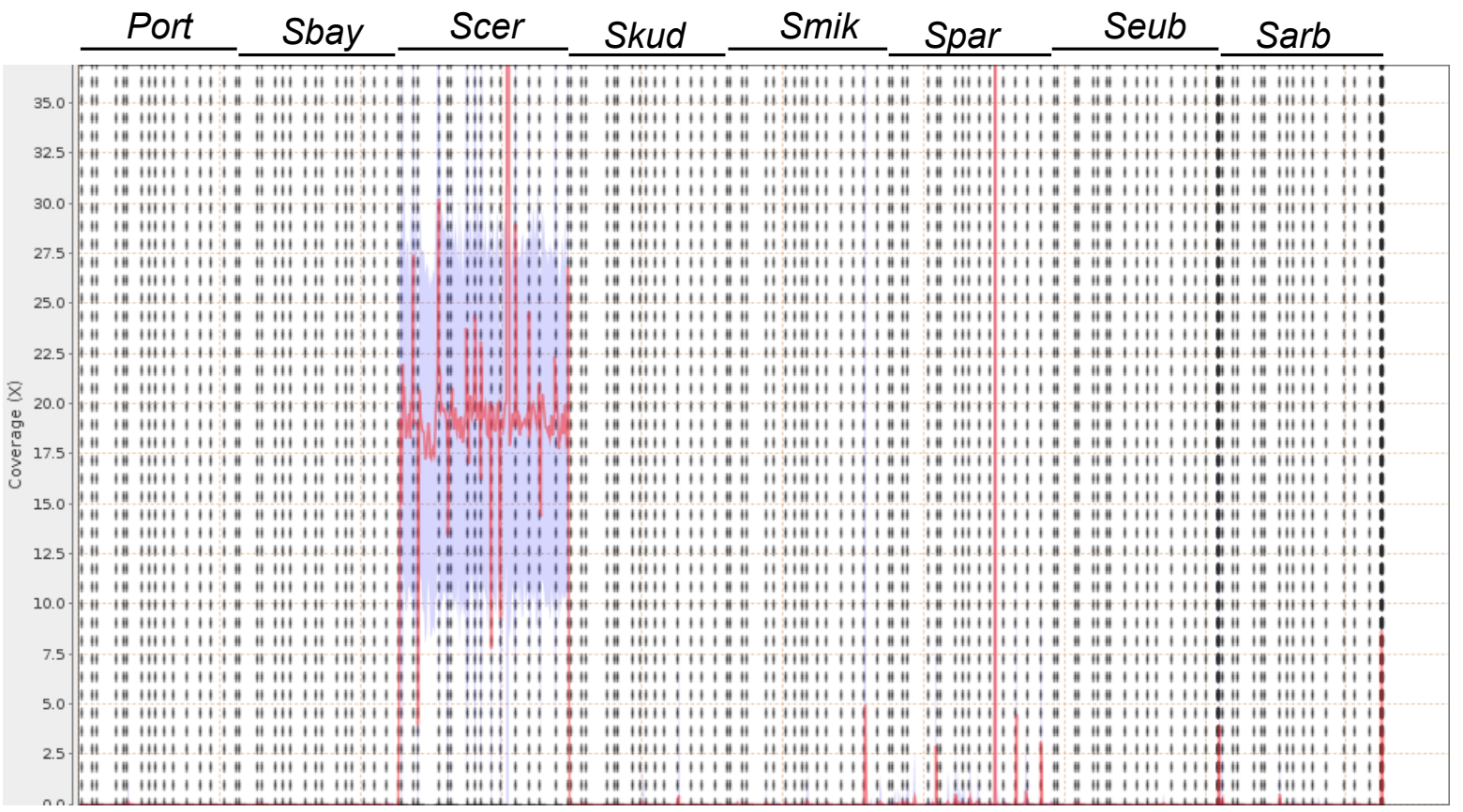
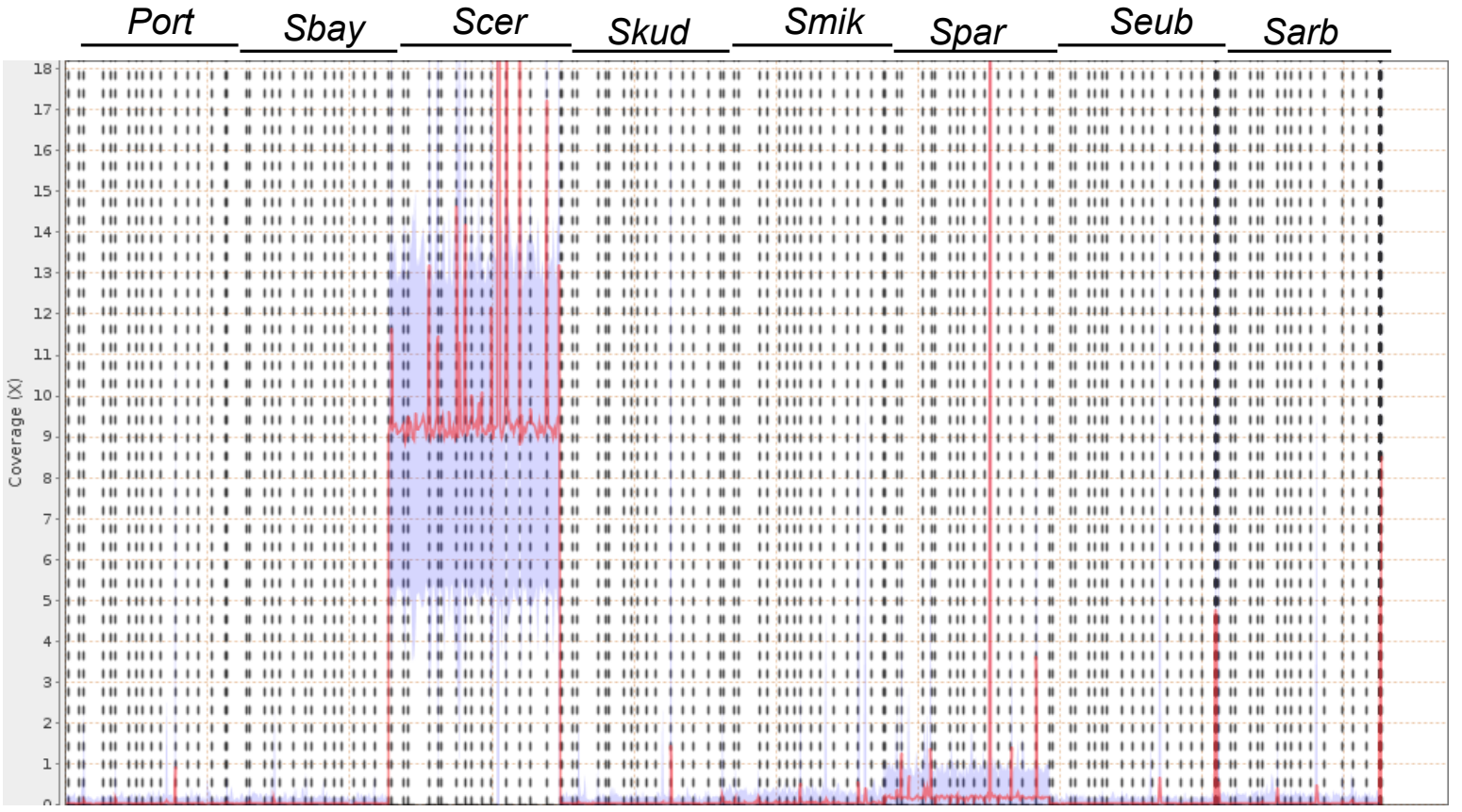
A 15V-P4



B S288C



C YJM248

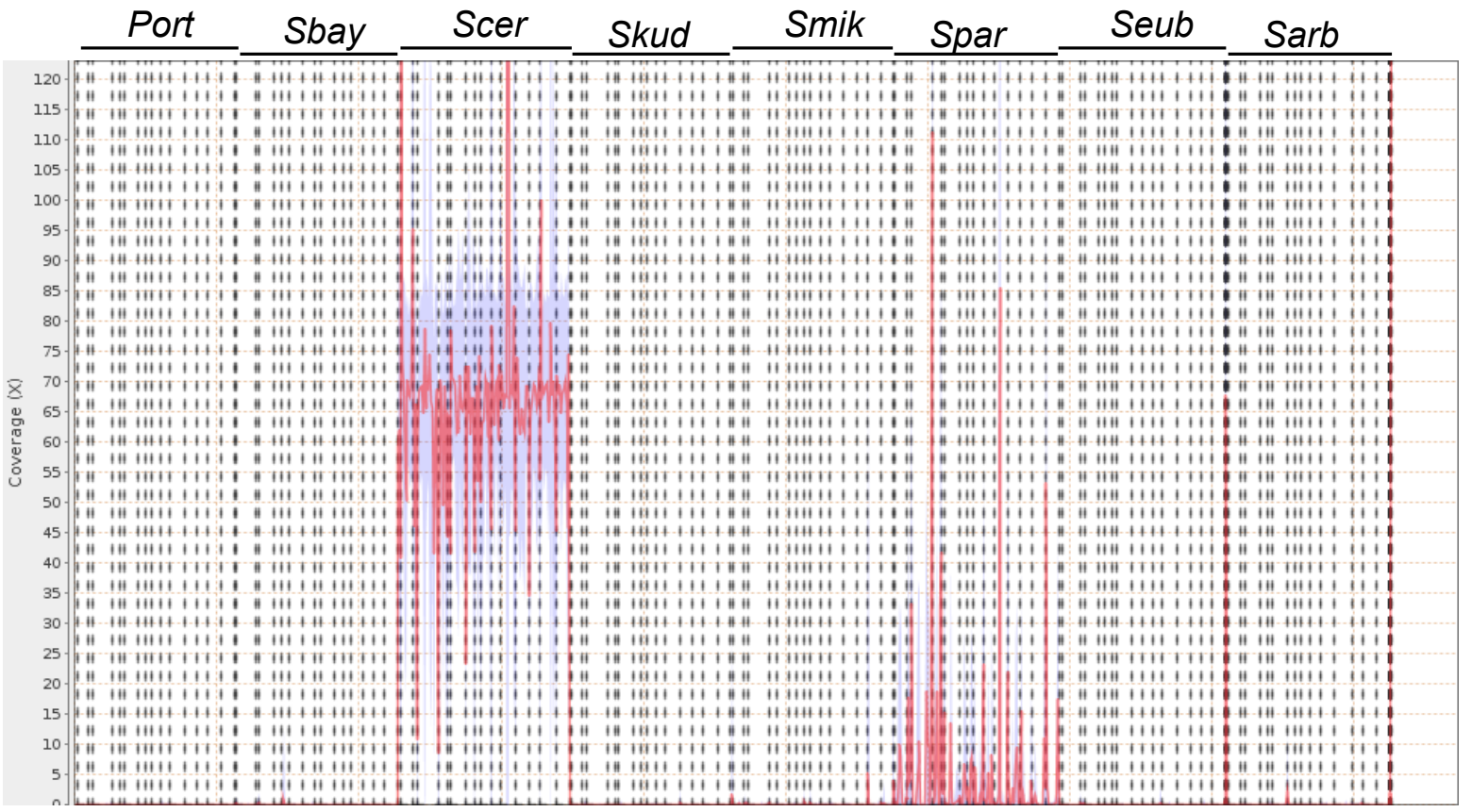


Figure S3. Coverage of *Saccharomyces sensu stricto* genomes with short reads for 15V-P4 does not reveal introgression from any of the closely related species. Short reads for the 15V-P4 genome were aligned to concatenated genomes of *S. sensu stricto* species with bowtie2. S288C and YJM248 were used as a negative and positive controls for introgression, respectively.
Port, *S. kudriavzevii* ZP 591
Sbay, *S. bayanus var. uvarum* CBS 7001
Scer, *S. cerevisiae* S288C
Skud, *S. kudriavzevii* IFO1802^{T}
Smik, *S. mikatae* IFO1815^{T}
Spar, *S. paradoxus* CBS432
Seub, *S. eubayanus* FM1318
Sarb, *S. arboricolus* H-6