

Table 1. Genomic features of draft genome sequences		
Strains	<i>K. obscura</i> CBS 148926	<i>K. obscura</i> FJI-L2-BK-P2
Sequencing method	Oxford Nanopore	Illumina
Contig counts	54	140
Total Length	30507620	30336935
Min	4628	1007
Max	4888905	2043846
L50	6	12
N50	1876131	791130
L90	19	45
N90	458232	197538
GC (%)	50.64	50.69
Genome completeness (%)	90.7	91.1
T2T Scaffolds	0	1
Telomere Fwd	2	10
Telomere Rev	8	10
Genes	11327	11298
mRNA	11248	11220
tRNA	79	78
Average gene length	1519.2	1518.32
Total introns	9877	9858
Total exons	21125	21078
Average exon length	5519	532.84
Average protein length	482.91	482.8
GO terms	2697	2605
Interproscan	3735	3683
EggNOG	9301	9259
MEROPS	317	318
CAZYmes	325	322
BUSCO	3233	3263
Secretion	669	678