



Pairwise aligned fraction (AF)

1	0.94	0.94	0.94	0.94	0.94	0.94	0.94	0.9	0.74	0.42	0.34	saccharibacter_am169
0.94	1	0.96	0.96	0.96	0.96	0.94	0.94	0.9	0.74	0.42	0.34	parasaccharibacter_apium
0.94	0.96	1	0.99	0.99	0.96	0.94	0.94	0.9	0.74	0.42	0.34	parasaccharibacter_apium_a2
0.94	0.96	0.99	1	0.99	0.96	0.94	0.94	0.9	0.74	0.32	0.34	parasaccharibacter_apium_b8
0.94	0.96	0.99	0.99	1	0.96	0.94	0.94	0.9	0.74	0.32	0.34	parasaccharibacter_apium_c6
0.94	0.96	0.96	0.96	0.96	1	0.96	0.94	0.9	0.74	0.42	0.34	saccharibacter_3.A.1
0.94	0.94	0.94	0.94	0.94	0.96	1	0.94	0.9	0.72	0.42	0.33	saccharibacter_m18
0.9	0.9	0.9	0.9	0.9	0.9	0.9	1	0.94	0.74	0.46	0.29	bombella_intestini
0.74	0.74	0.74	0.74	0.74	0.74	0.72	0.75	1	0.5	0.21	0.21	parasaccharibacter_apium_as
0.42	0.42	0.42	0.42	0.42	0.42	0.42	0.46	0.5	1	0.23	0.23	sacchariabcter_floricola
0.34	0.34	0.34	0.34	0.34	0.34	0.34	0.29	0.21	0.23	1	0.23	gluconobacter_oxydans