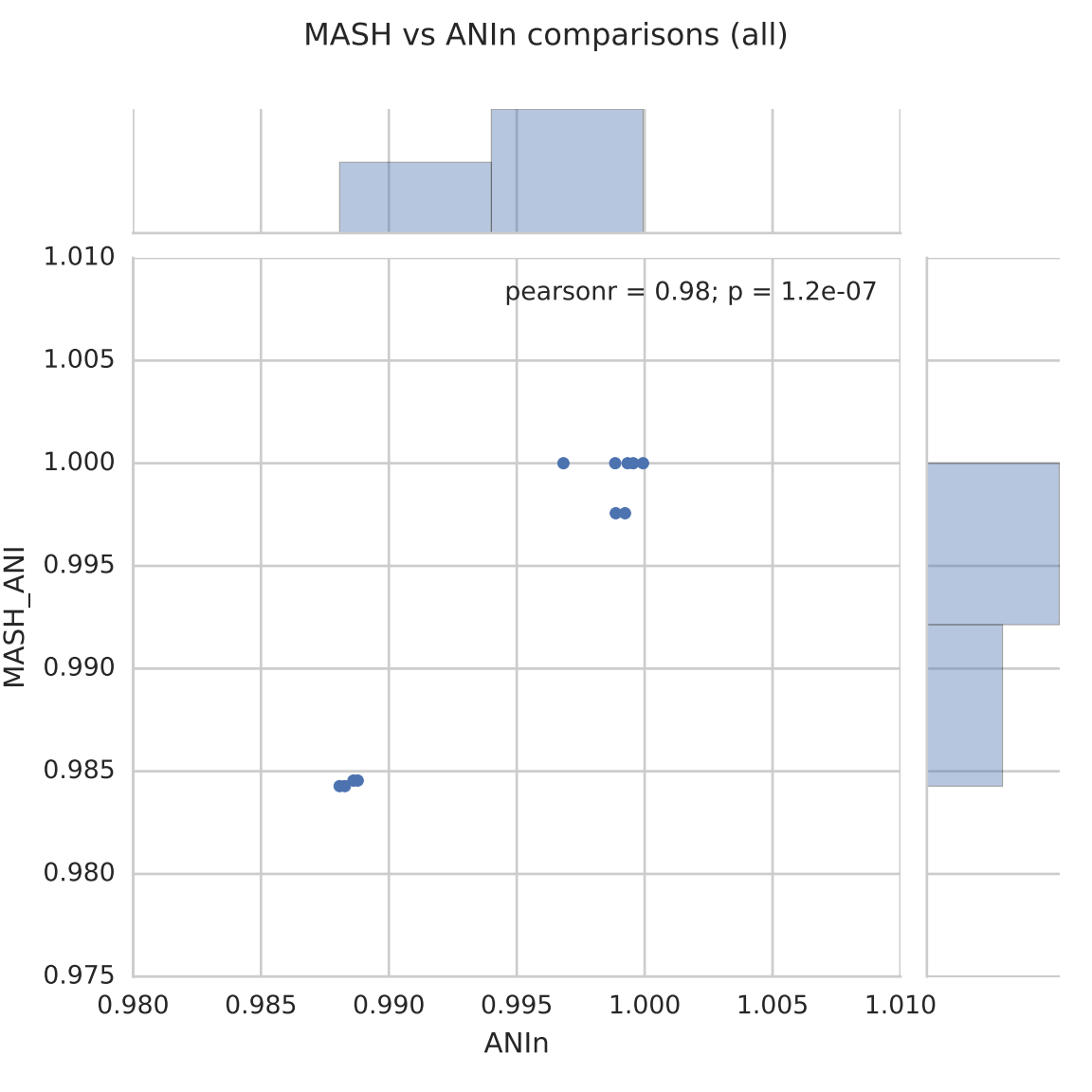
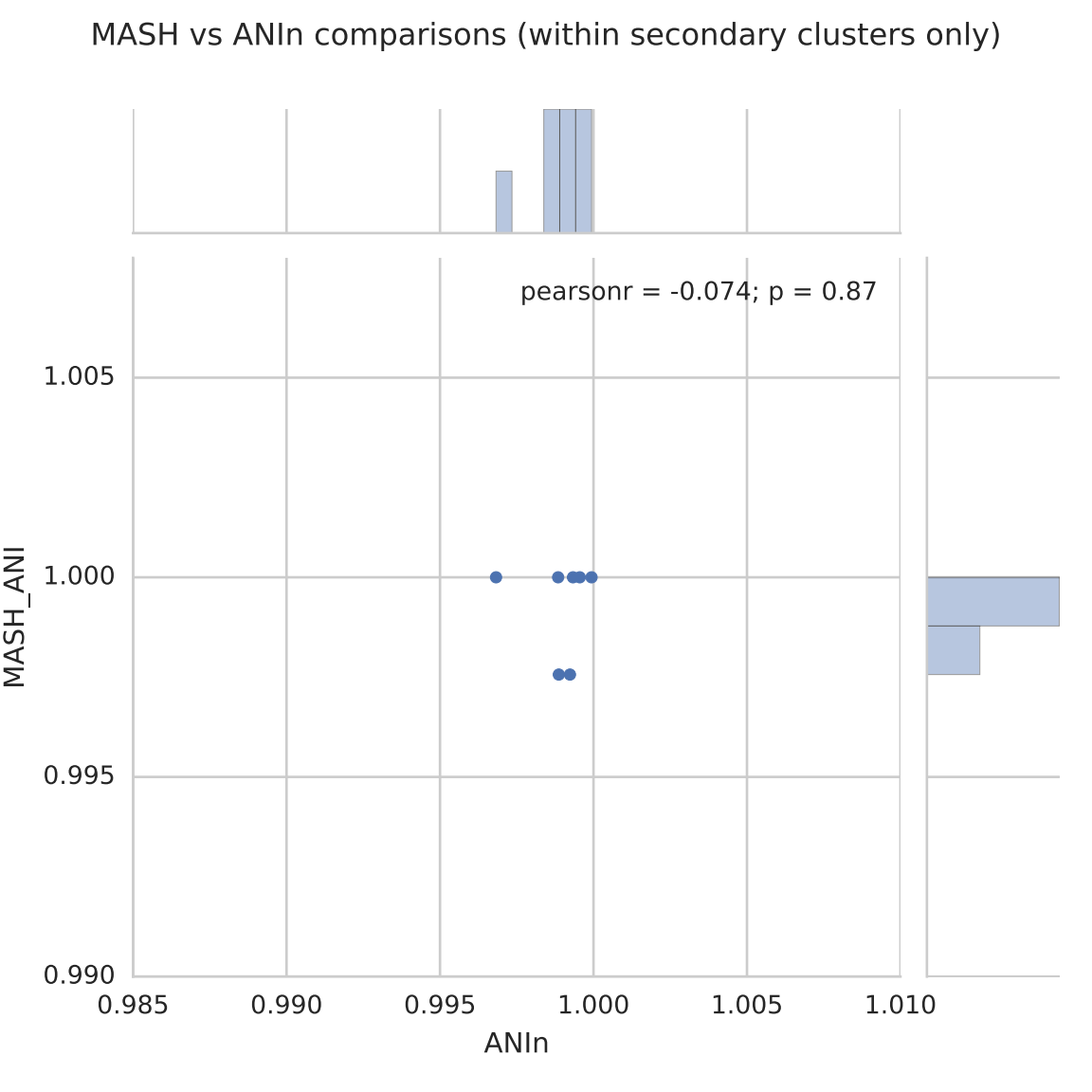
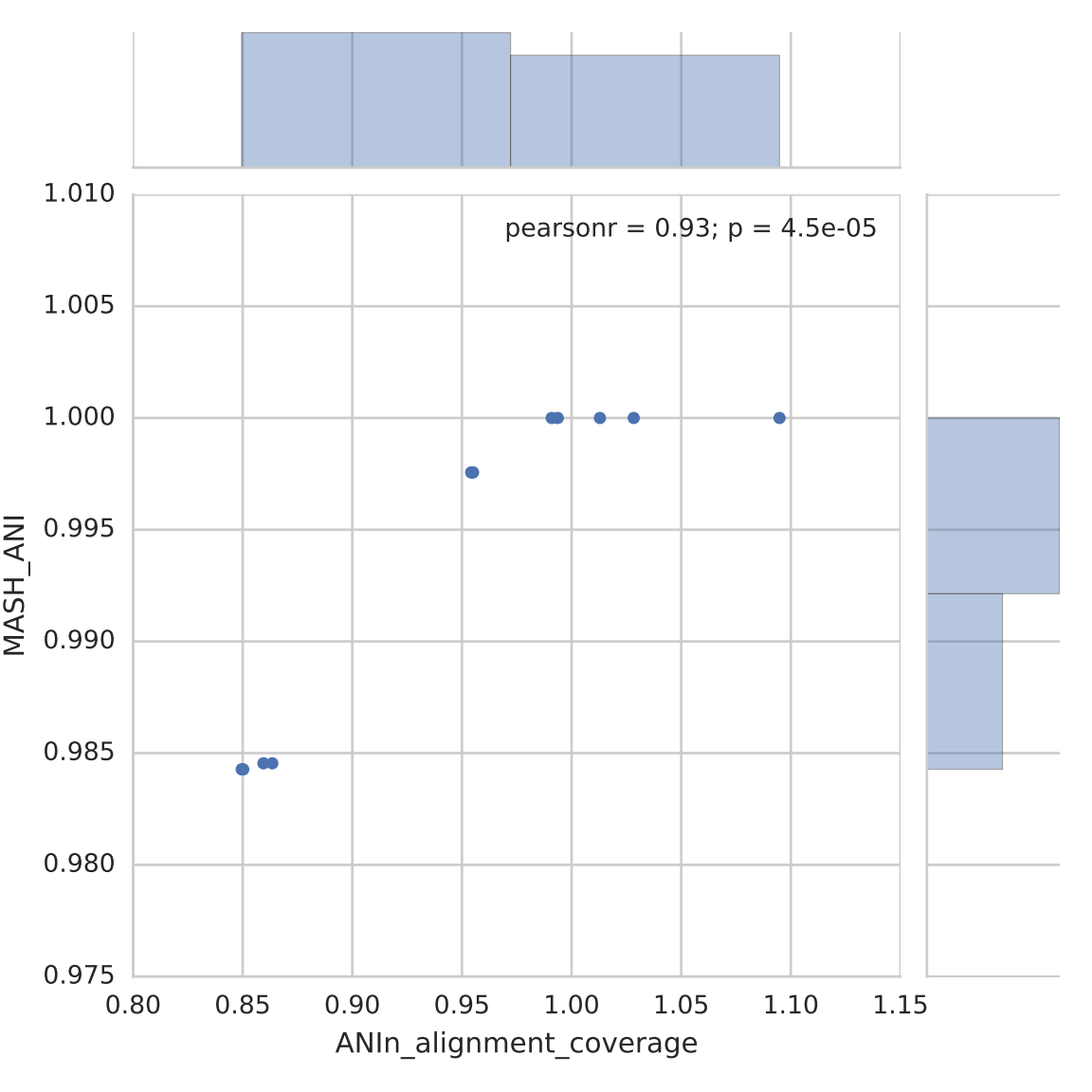
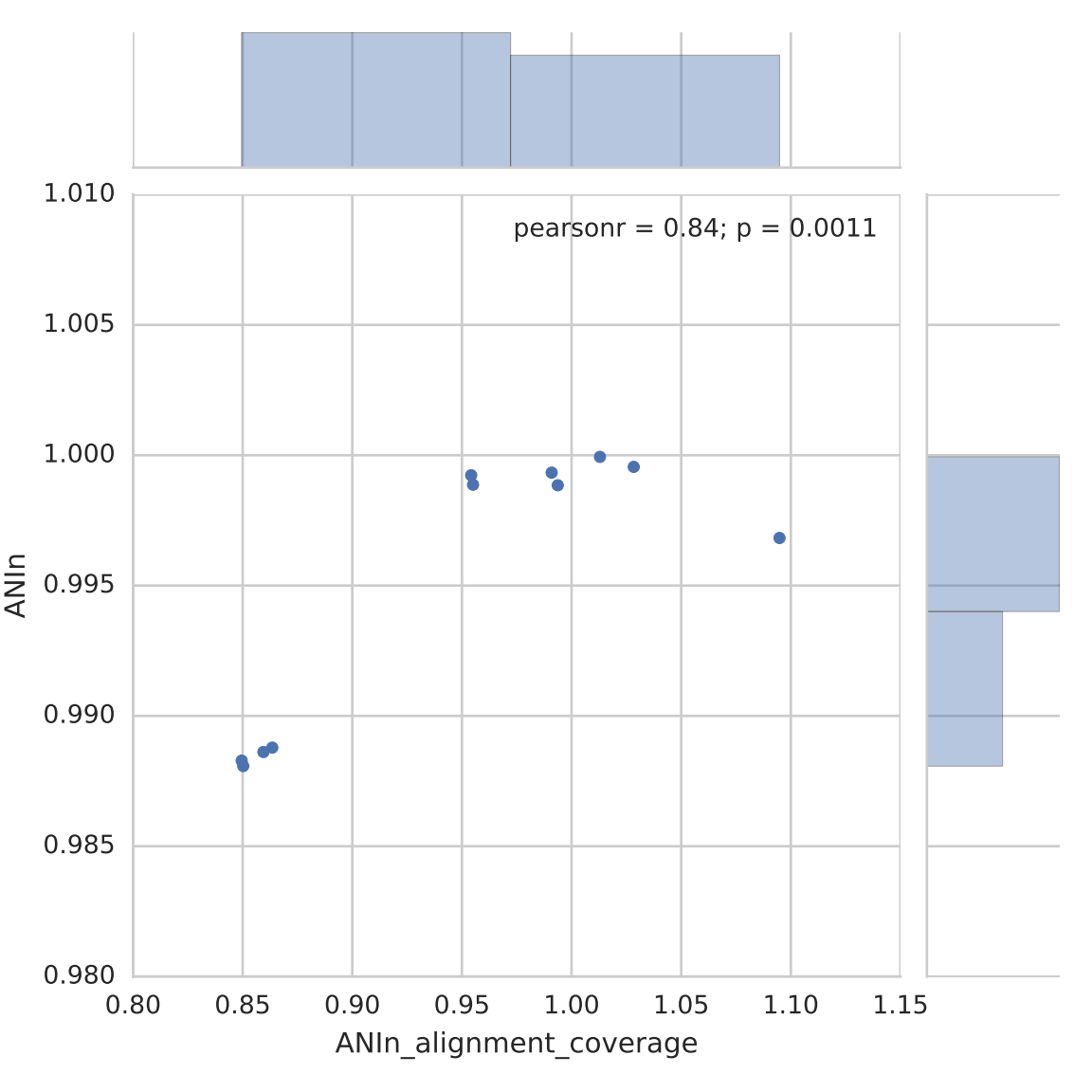
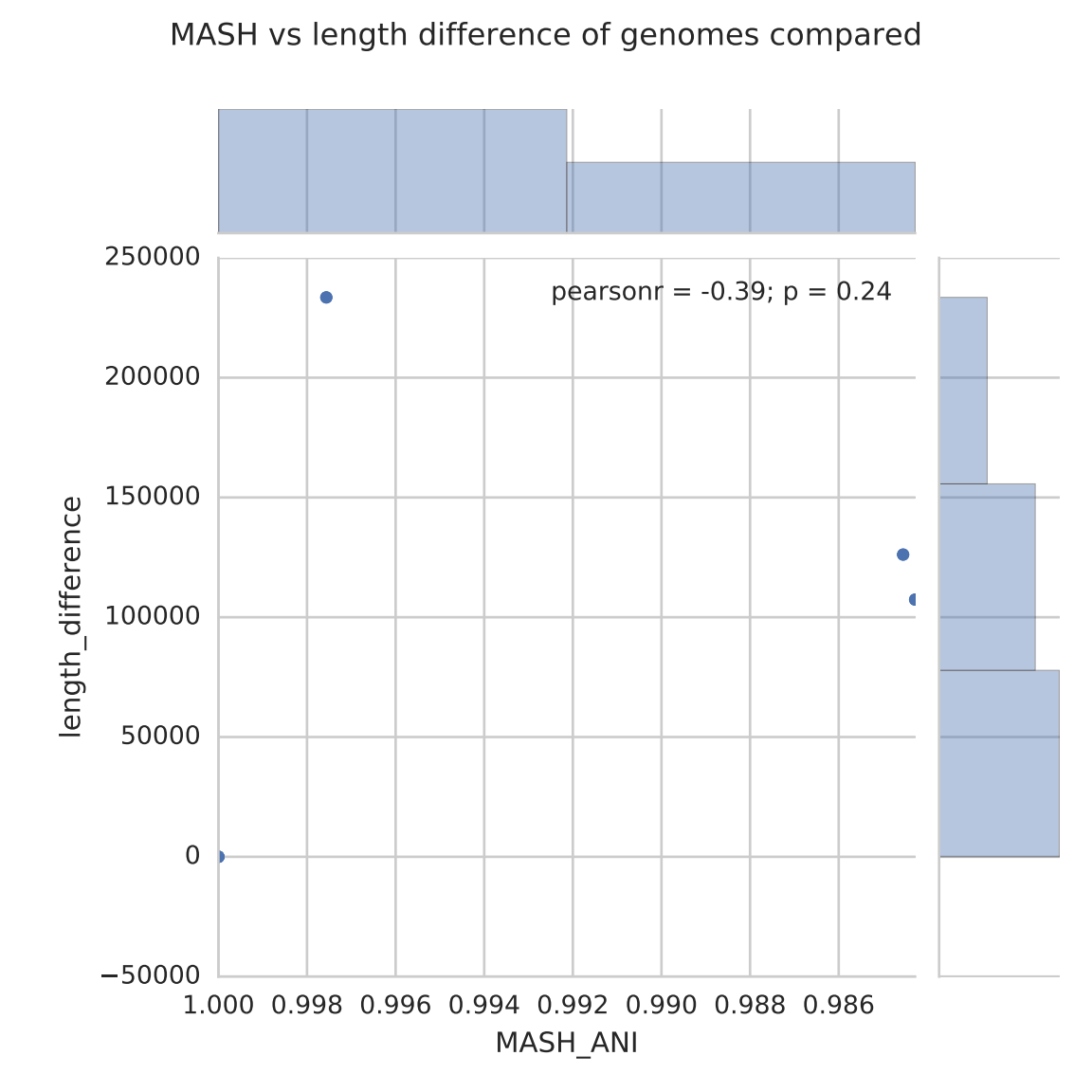
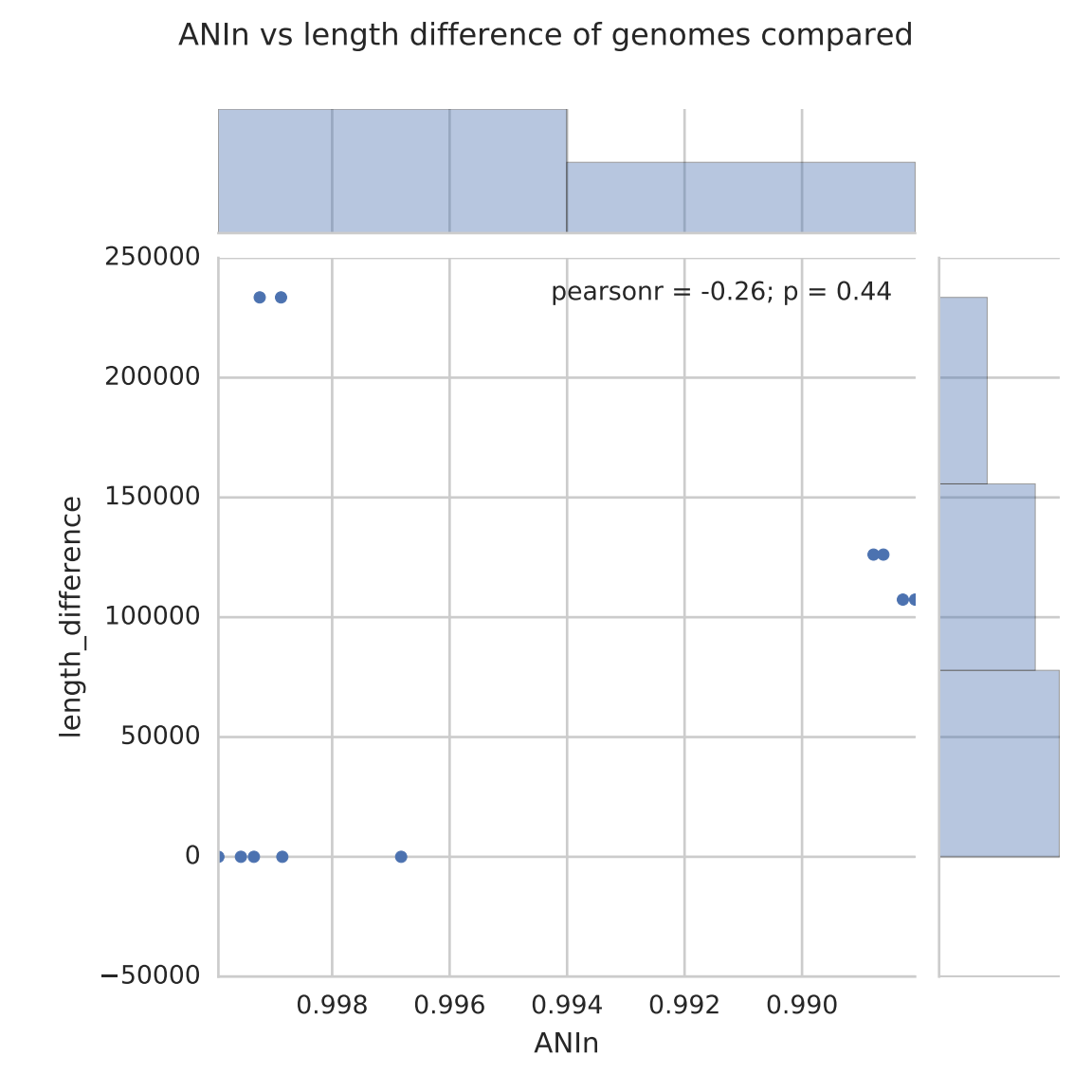

MASH vs ANIn comparisons (all)
pearsonr = 0.98; p = 1.2e-07
MASH_ANI
ANIn
1.010
1.005
1.000
0.995
0.990
0.985
0.980
0.975
0.980
0.985
0.990
0.995
1.000
1.005
1.010


MASH vs ANIn comparisons (within secondary clusters only)
pearsonr = -0.074; p = 0.87
MASH_ANI
1.005
1.000
0.995
0.990
0.985
0.990
0.995
1.000
1.005
1.010
ANIn


pearsonr = 0.93; p = 4.5e-05
MASH_ANI
1.010
1.005
1.000
0.995
0.990
0.985
0.980
0.975
0.80
0.85
0.90
0.95
1.00
1.05
1.10
1.15
ANIn_alignment_coverage


pearsonr = 0.84; p = 0.0011
1.010
1.005
1.000
0.995
0.990
0.985
0.980
ANIn
0.80
0.85
0.90
0.95
1.00
1.05
1.10
1.15
ANIn_alignment_coverage


MASH vs length difference of genomes compared
pearsonr = -0.39; p = 0.24
length_difference
250000
200000
150000
100000
50000
0
−50000
1.000
0.998
0.996
0.994
0.992
0.990
0.988
0.986
MASH_ANI


ANIn vs length difference of genomes compared
pearsonr = -0.26; p = 0.44
length_difference
250000
200000
150000
100000
50000
0
−50000
0.998
0.996
0.994
0.992
0.990
ANIn