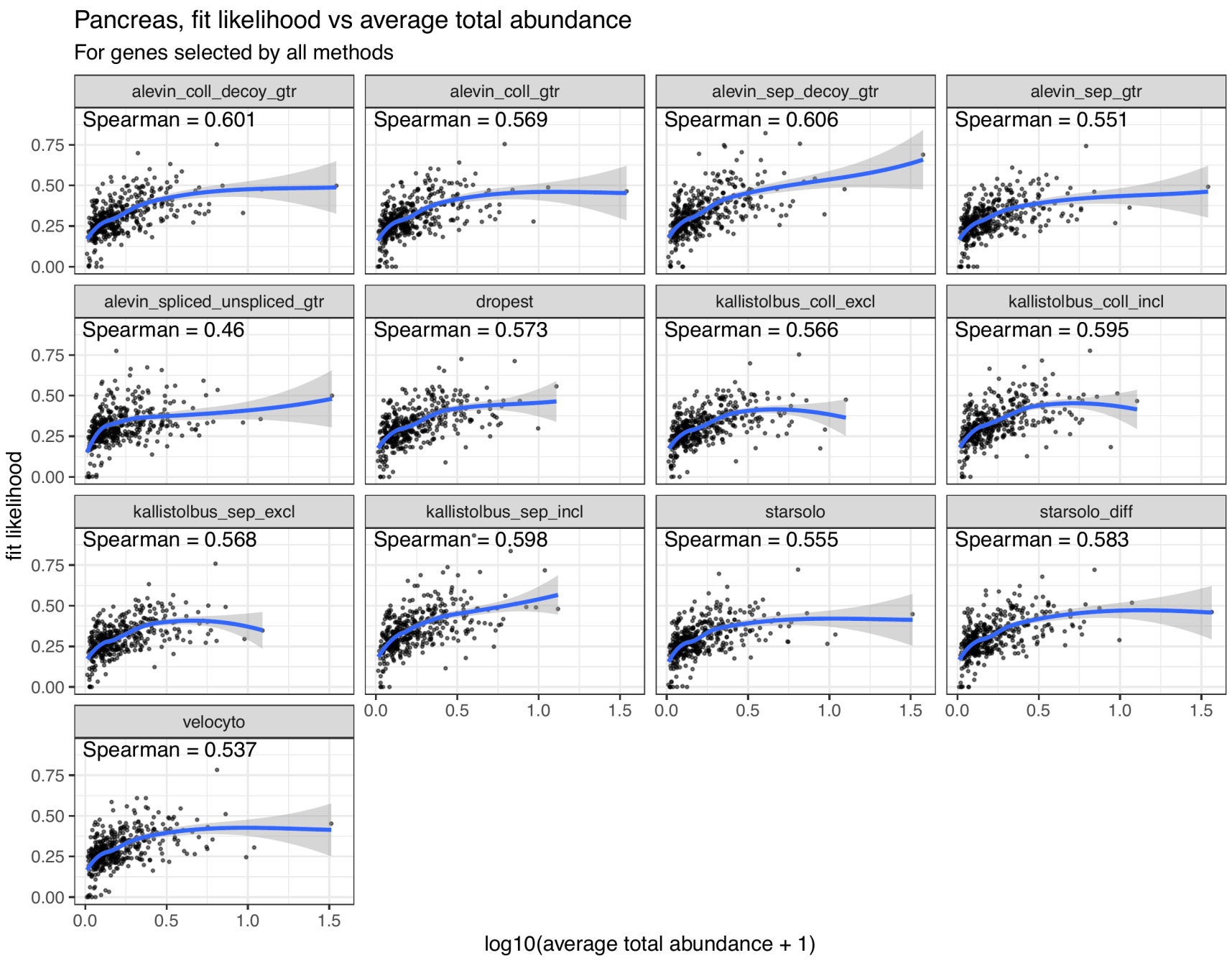
Pancreas, fit likelihood vs average total abundance
For genes selected by all methods
alevin_coll_decoy_gtr
Spearman = 0.601
alevin_coll_gtr
Spearman = 0.569
alevin_sep_decoy_gtr
Spearman = 0.606
alevin_sep_gtr
Spearman = 0.551
alevin_spliced_unspliced_gtr
Spearman = 0.46
dropest
Spearman = 0.573
kallistolbus_coll_excl
Spearman = 0.566
kallistolbus_coll_incl
Spearman = 0.595
kallistolbus_sep_excl
Spearman = 0.568
kallistolbus_sep_incl
Spearman = 0.598
starsolo
Spearman = 0.555
starsolo_diff
Spearman = 0.583
velocyto
Spearman = 0.537
fit likelihood
0.00
0.25
0.50
0.75
0.0
0.5
1.0
1.5
log10(average total abundance + 1)