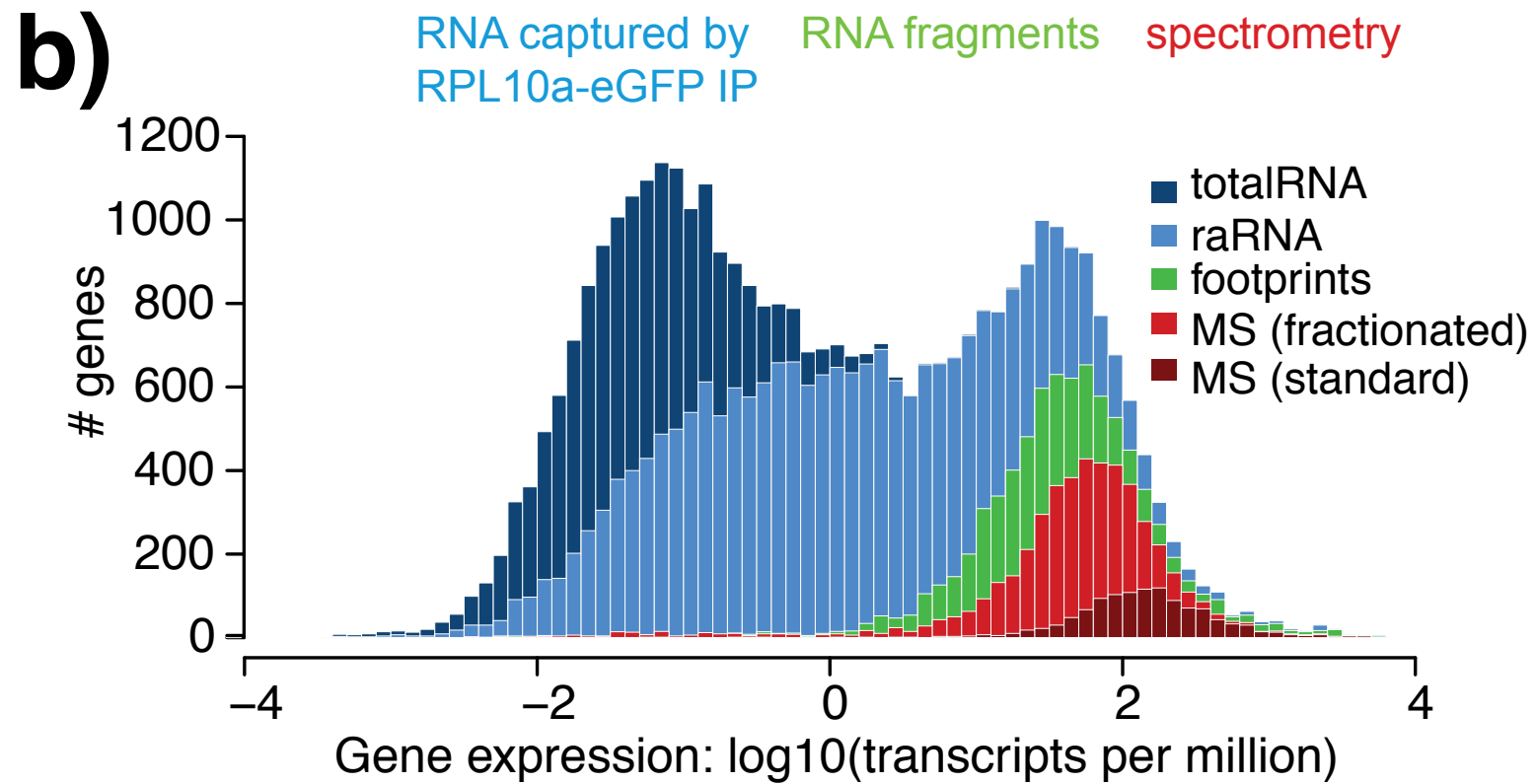
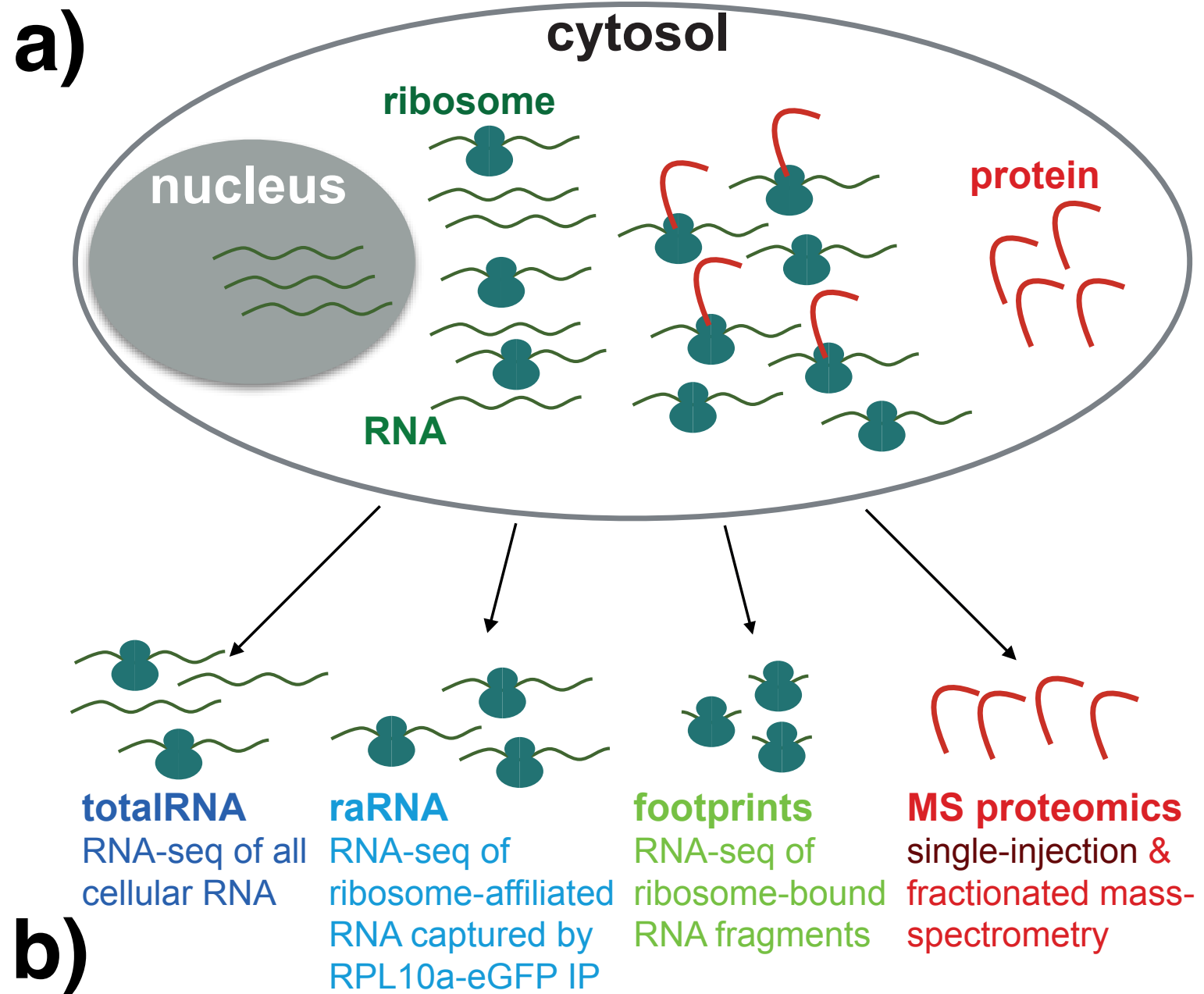
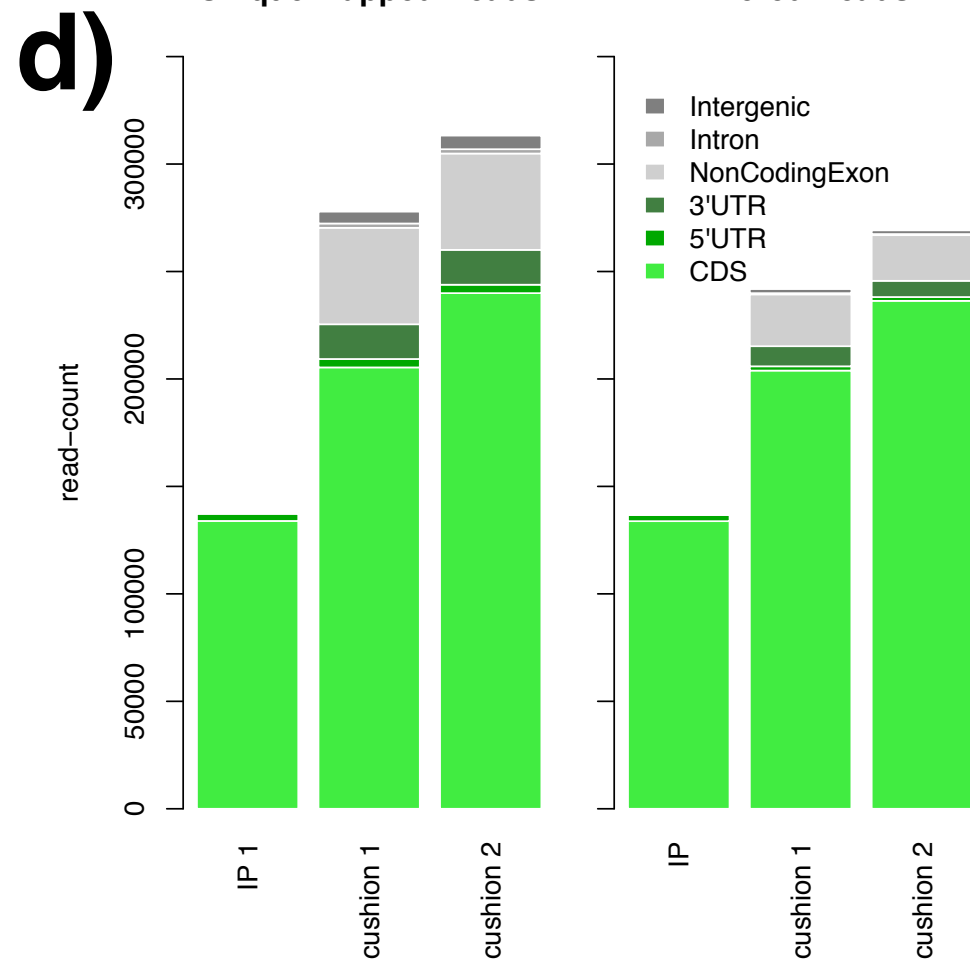
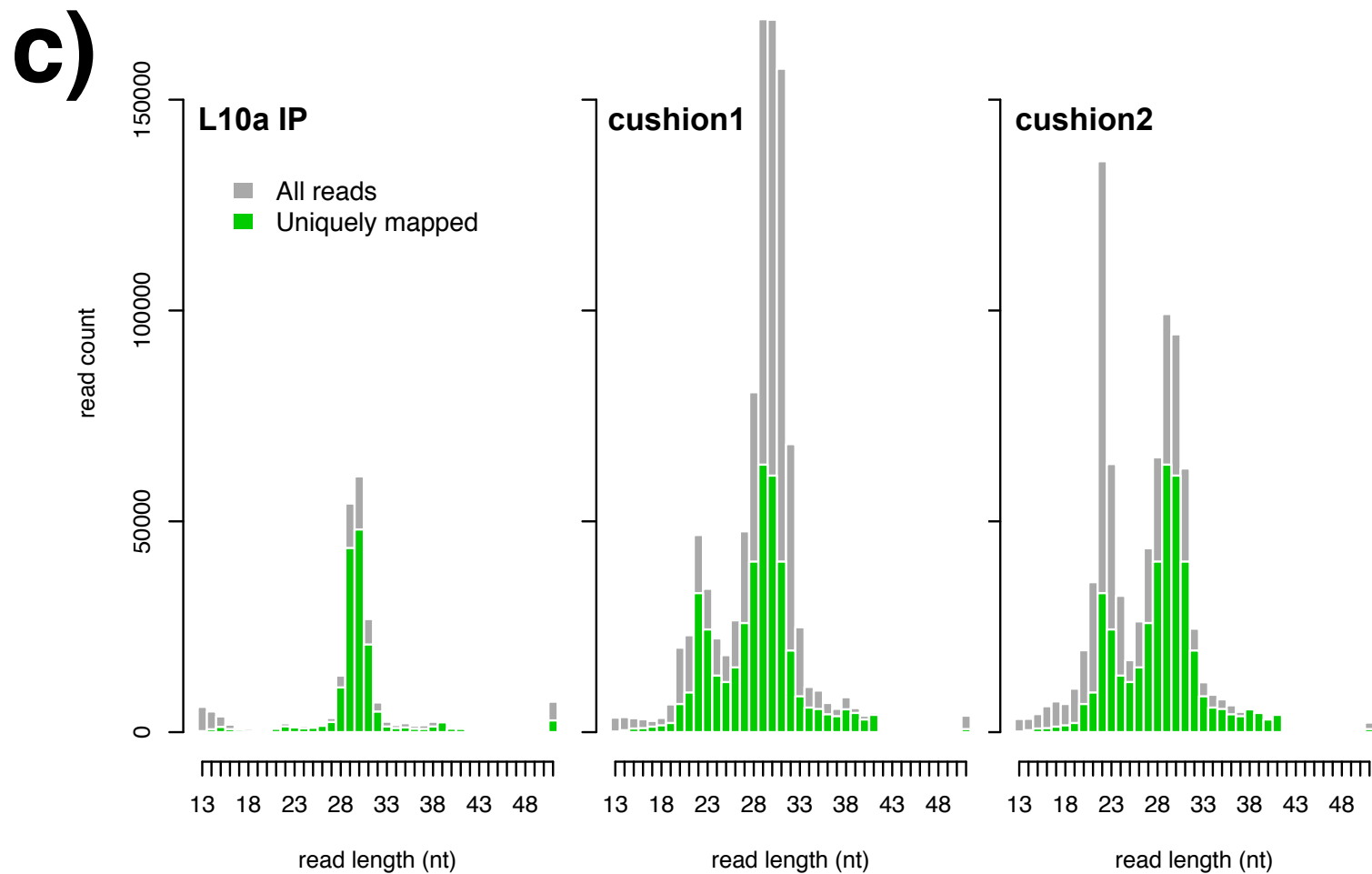
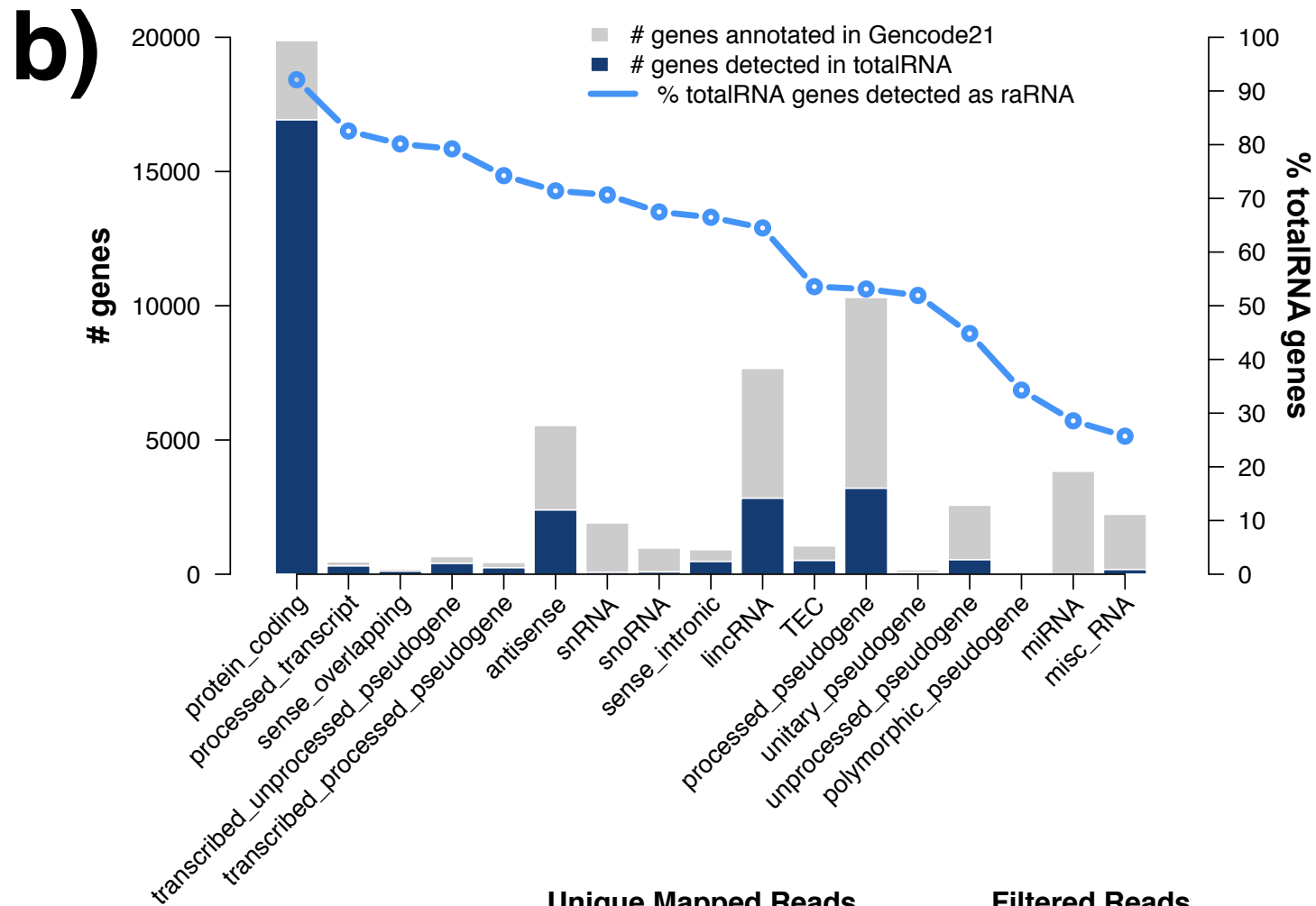
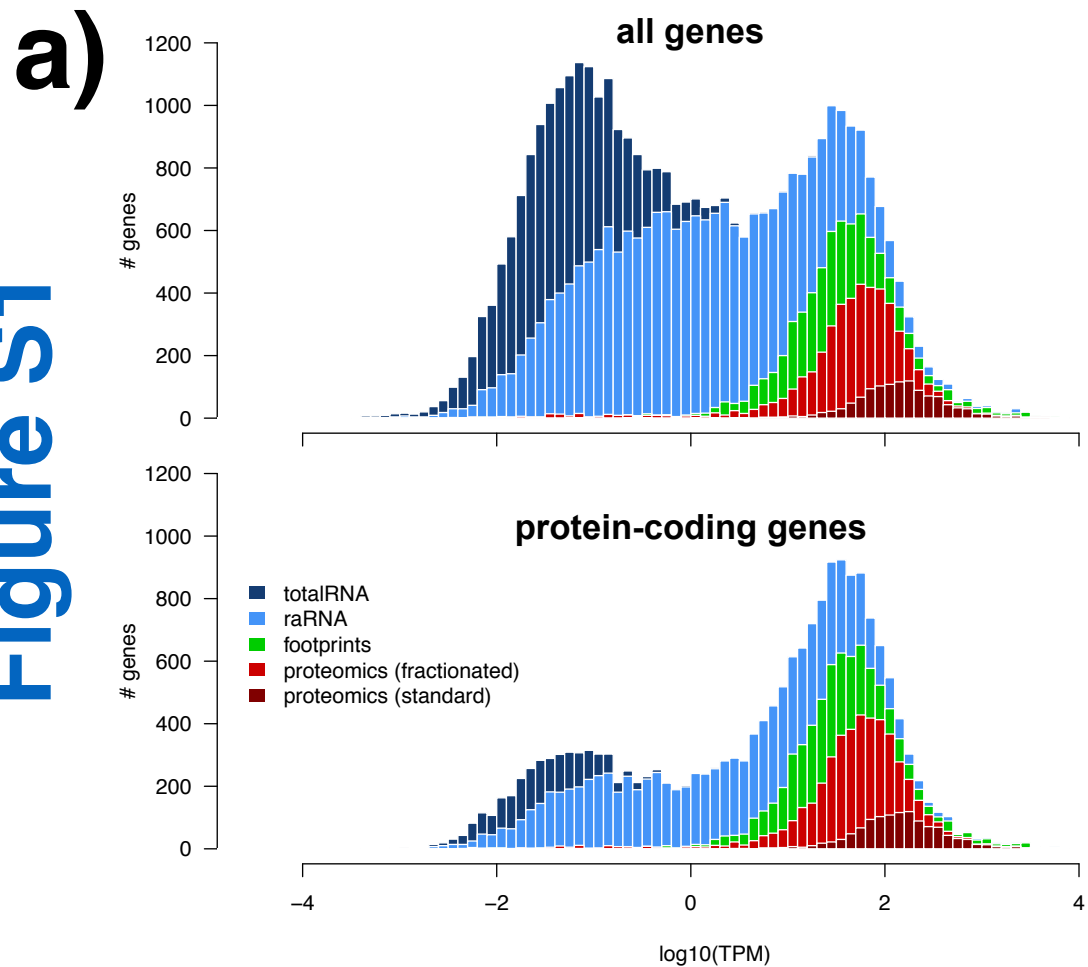
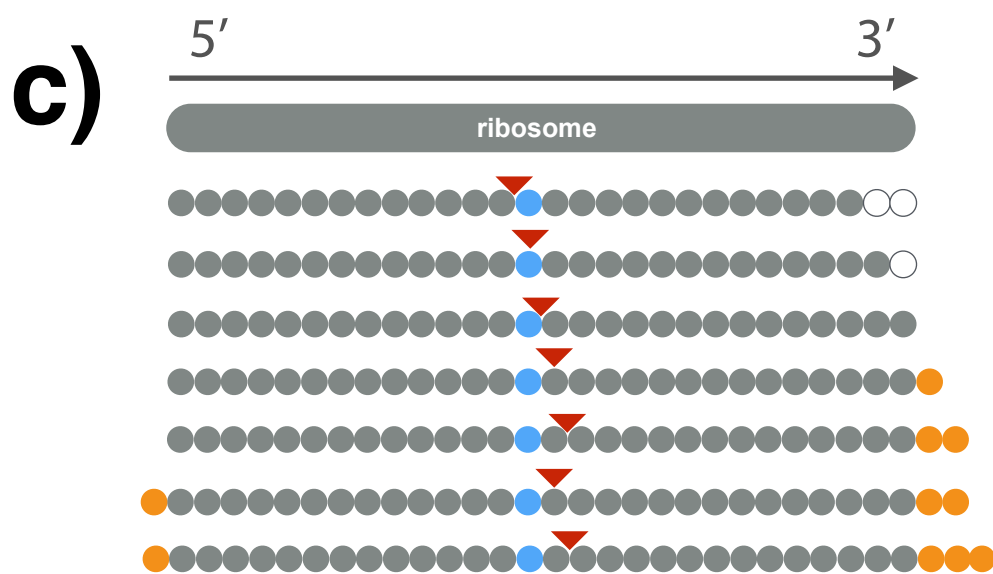
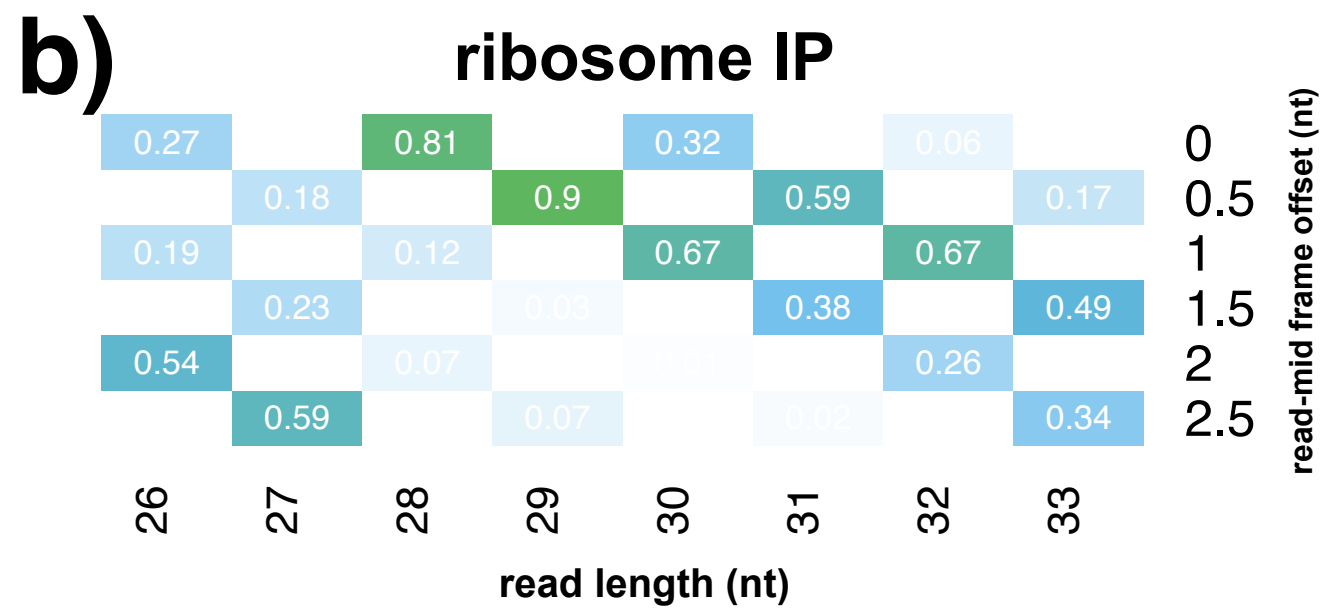
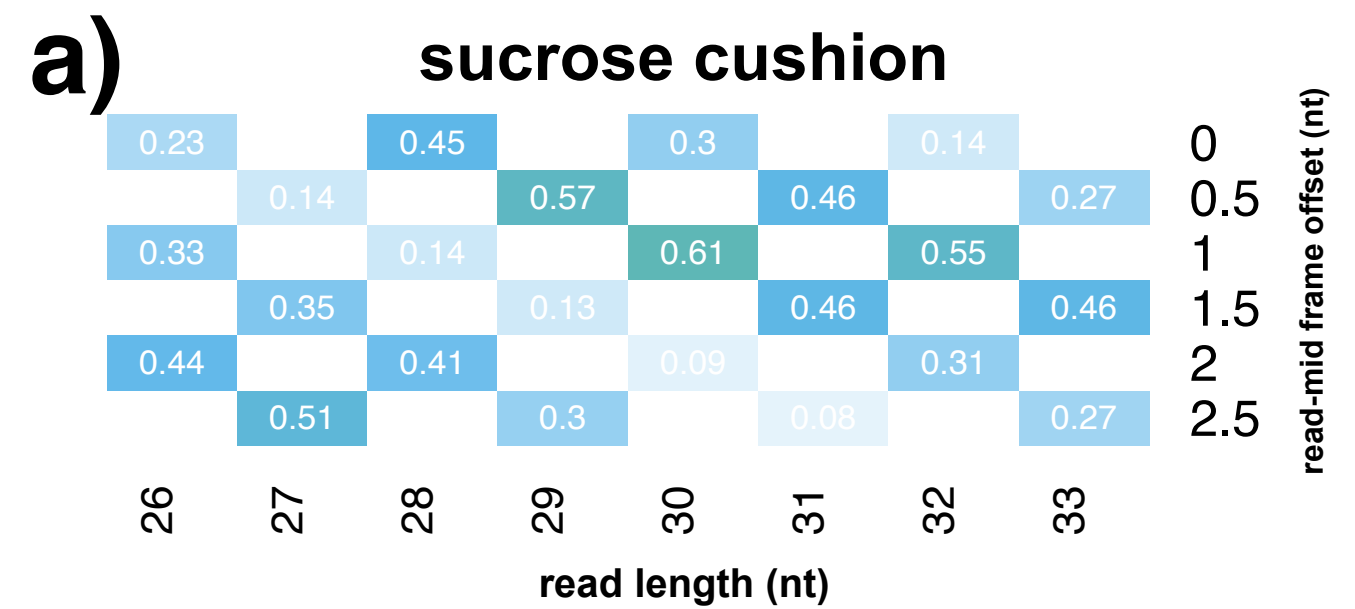


Figure 1







read length	% reads in frame cushion	% reads in frame IP
26nt	44%	54%
27nt	51%	59%
28nt	45%	81%
29nt	57%	90%
30nt	61%	67%
31nt	46%	59%
32nt	55%	67%

eligible reads:
- in CDS
- >50% in correct frame

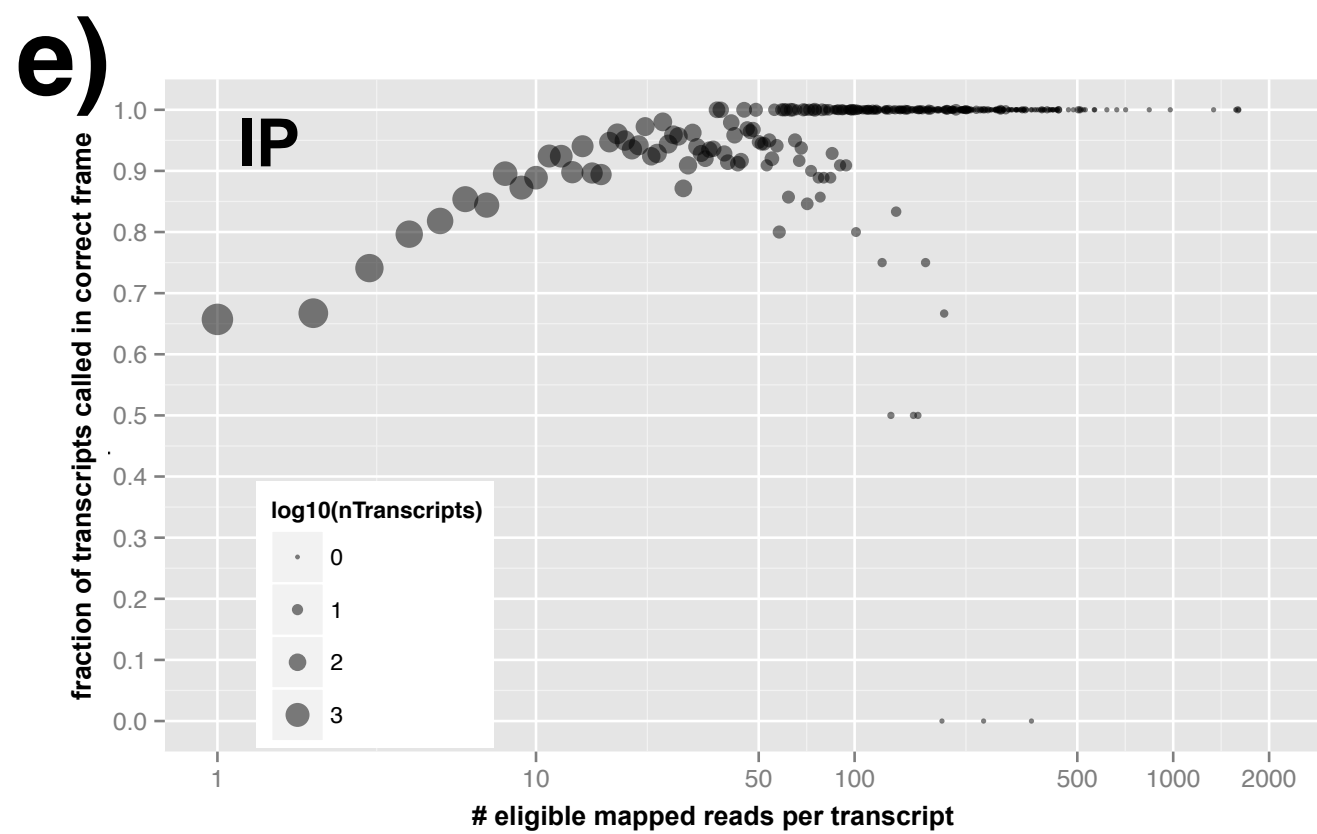
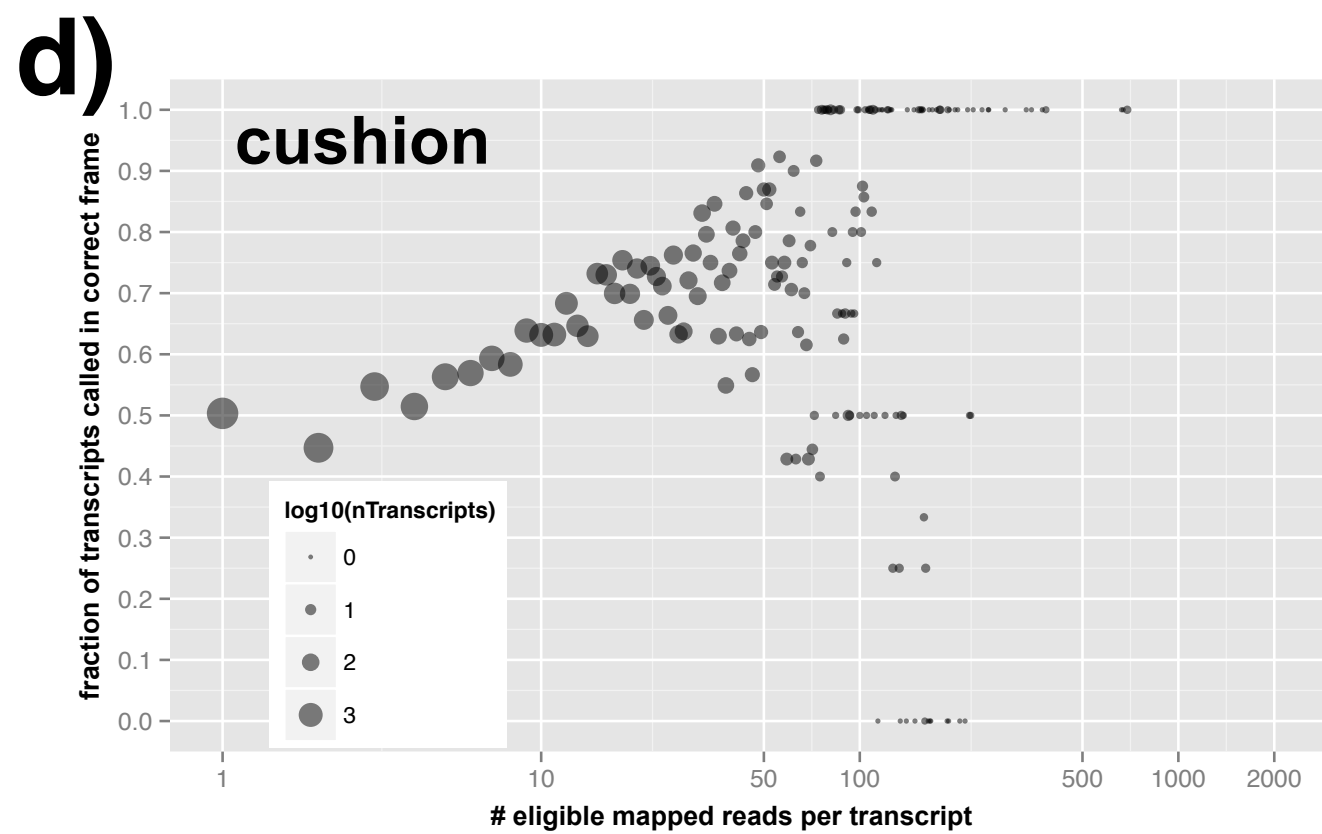
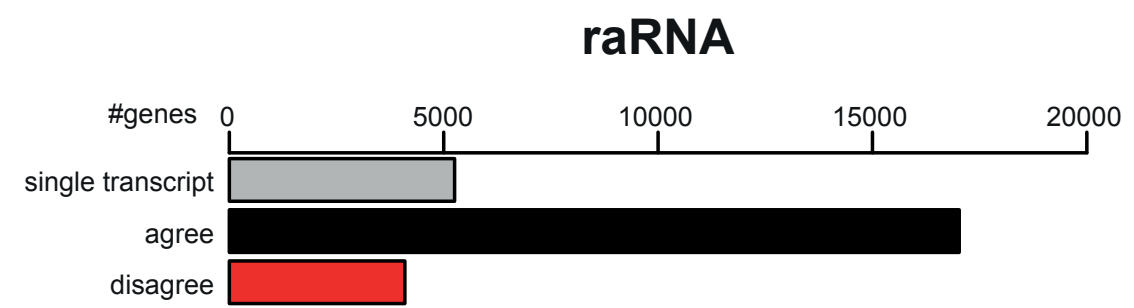
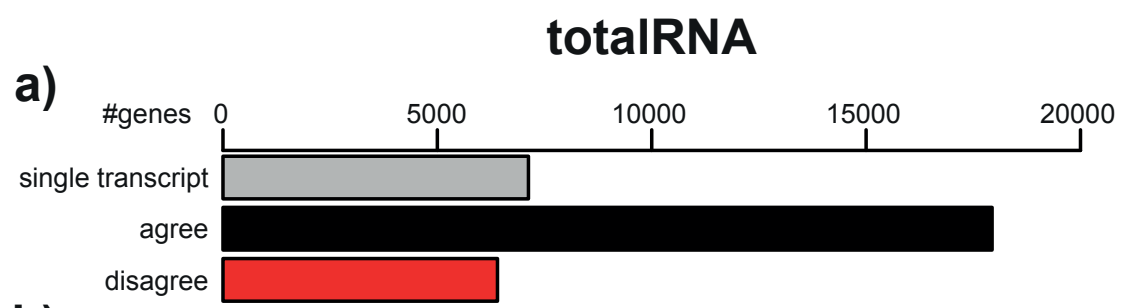


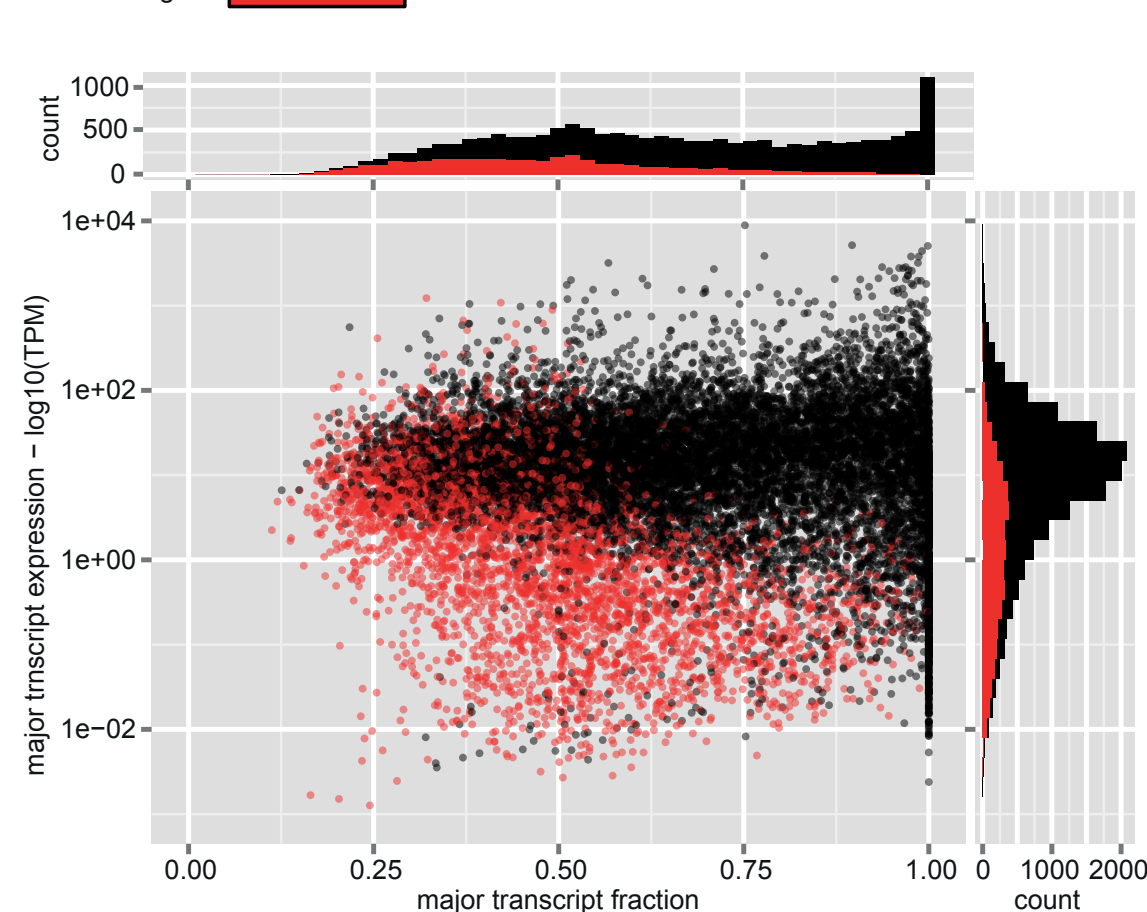
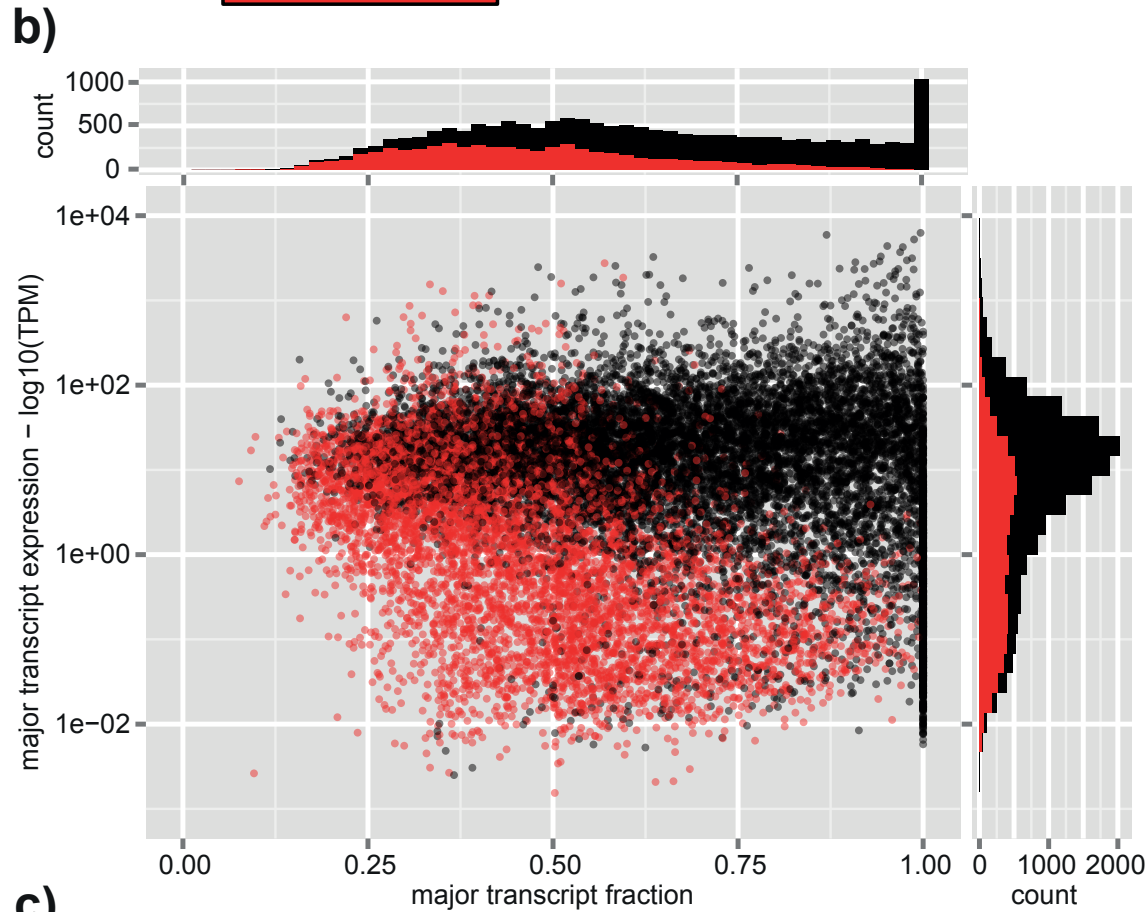
Figure 2



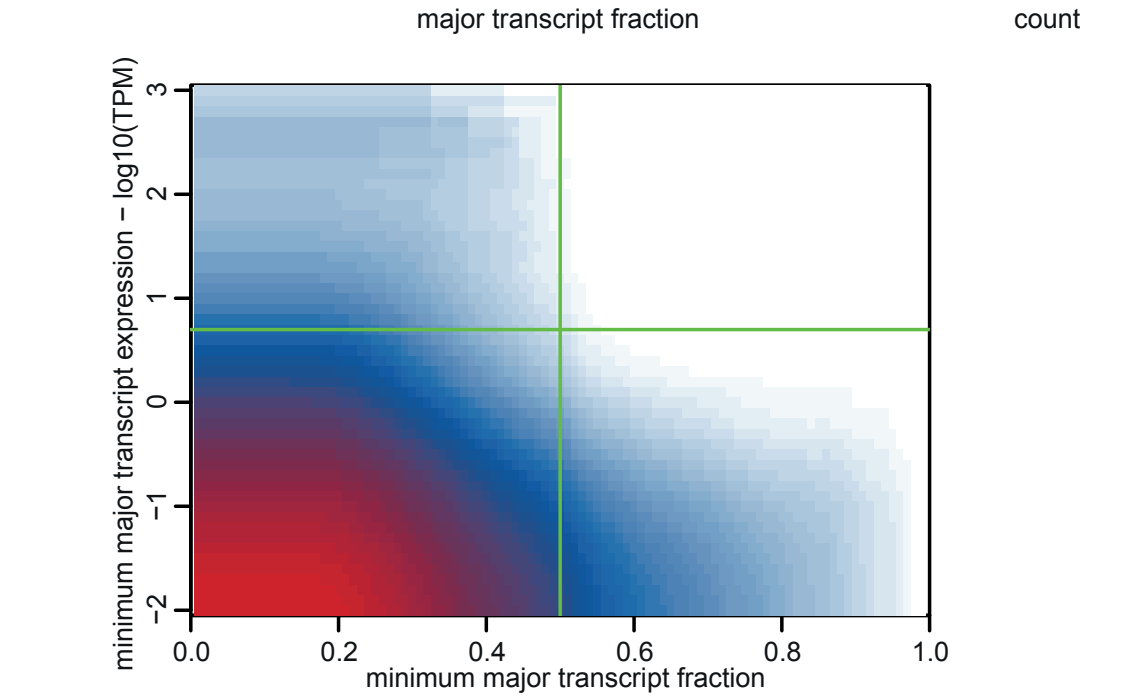
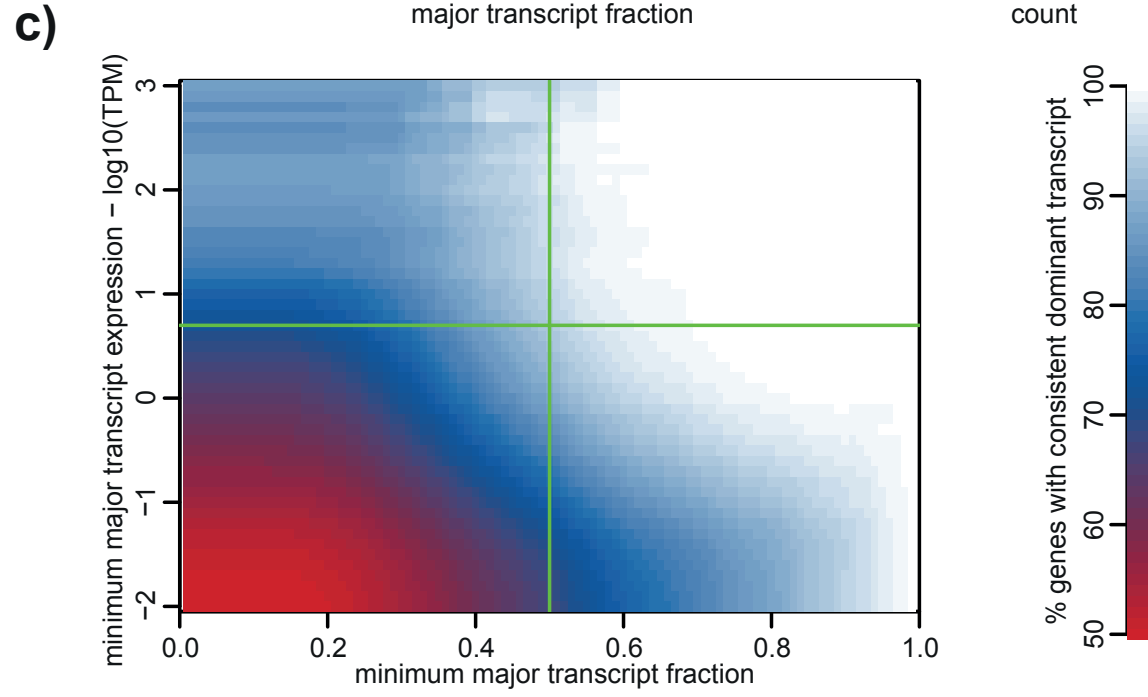
basic agreement in major transcript over 3 replicate samples:

totalRNA: 74% genes

raRNA: 81% genes



agreement depends on transcript dominance -and- transcript expression

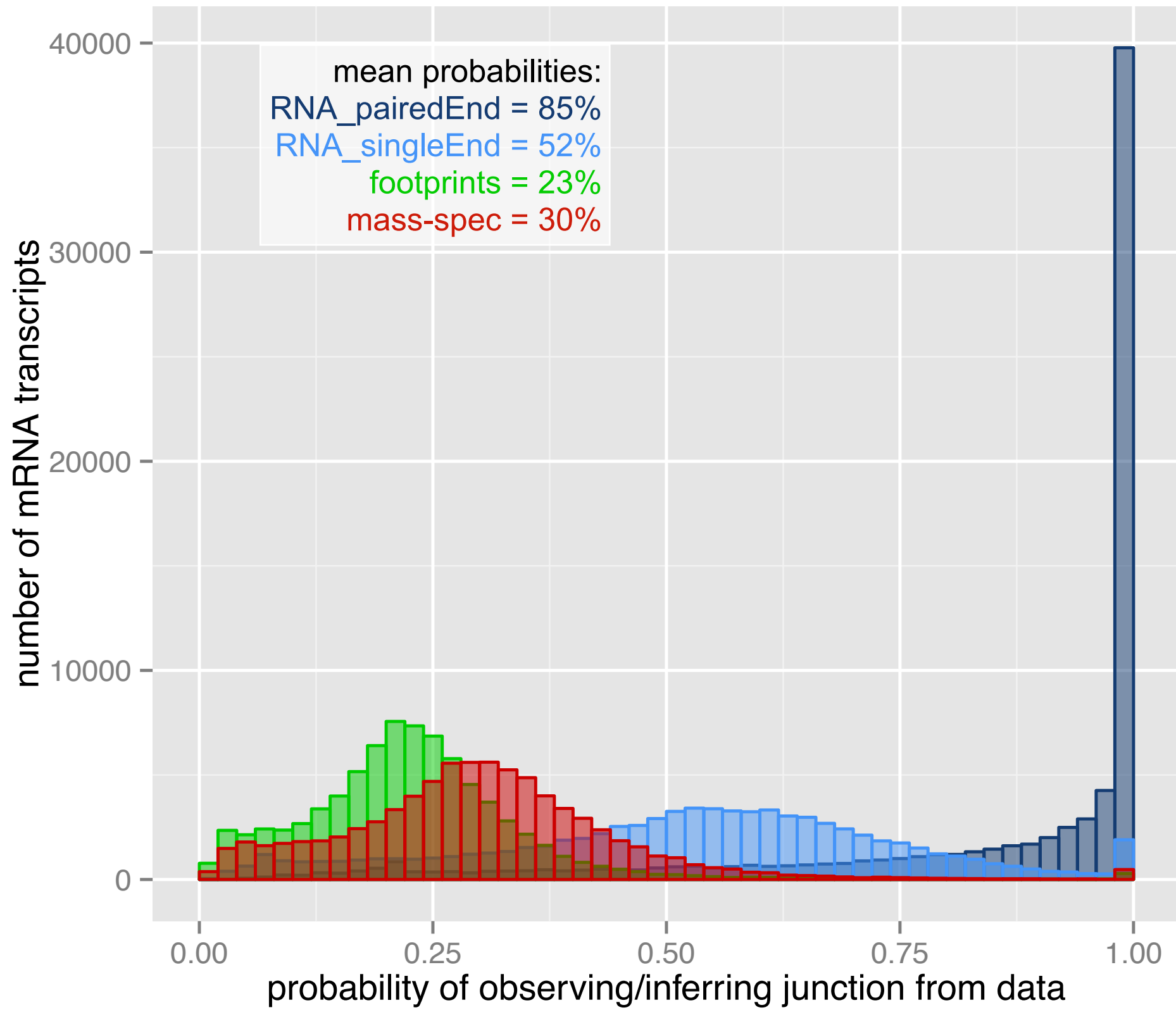


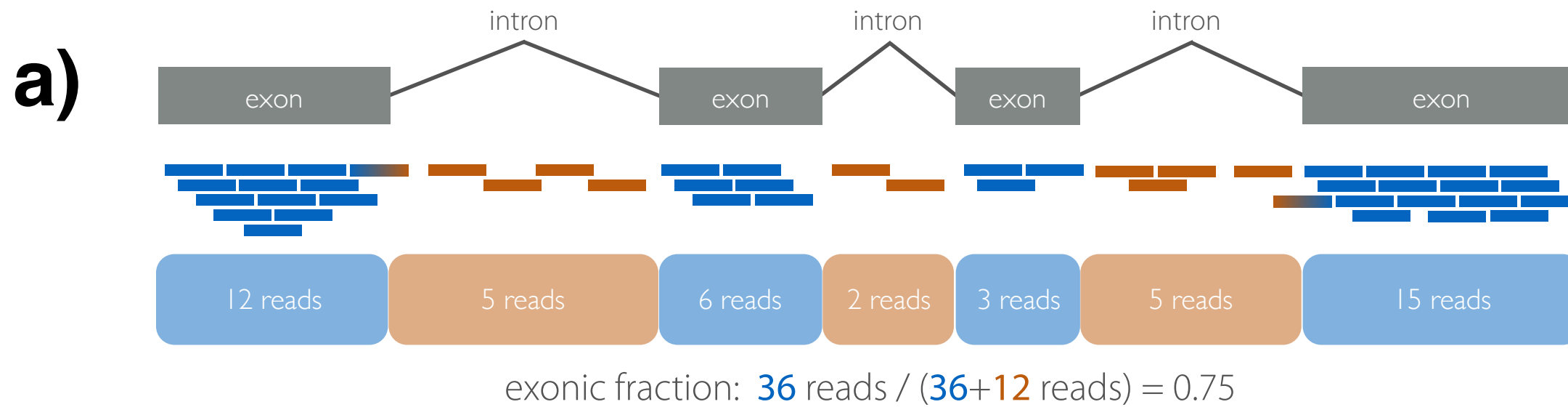
using genes with a major isoform expressed ≥ 5 TPM and comprising $\geq 50\%$ of the overall gene abundance the agreement between replicate samples increases:

totalRNA: 93% genes

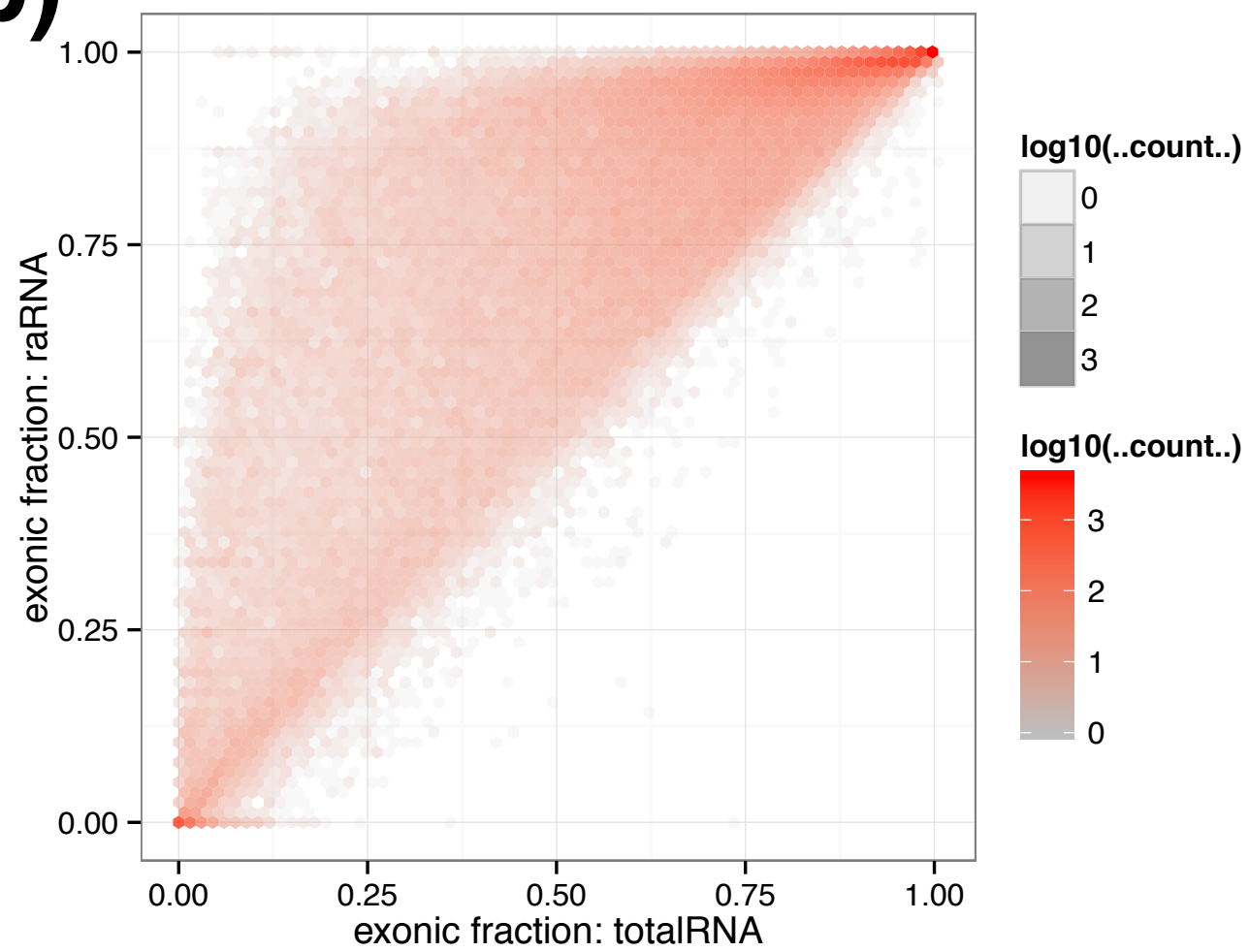
raRNA: 97% genes

Figure S3





b)



c)

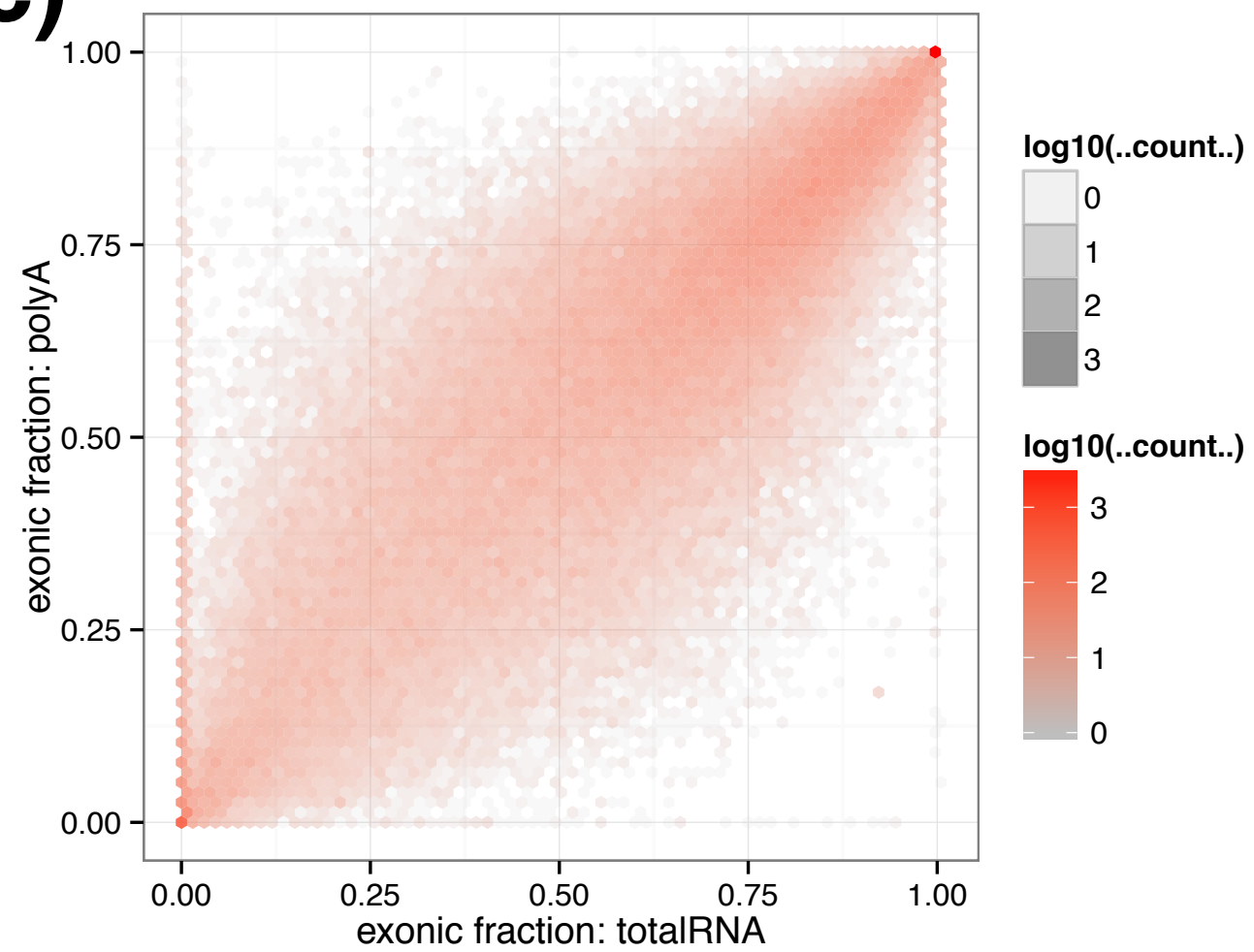
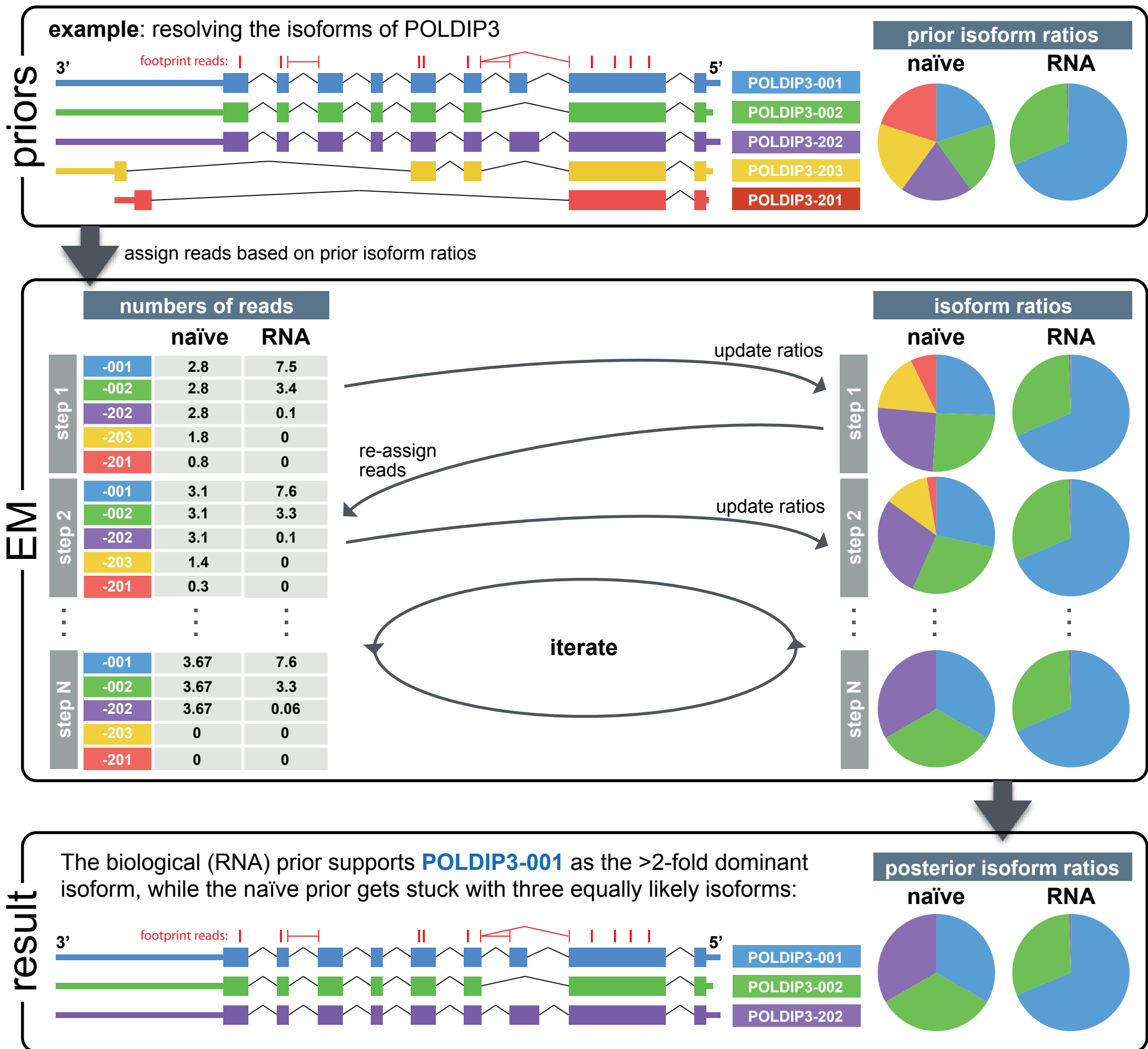


Figure 3



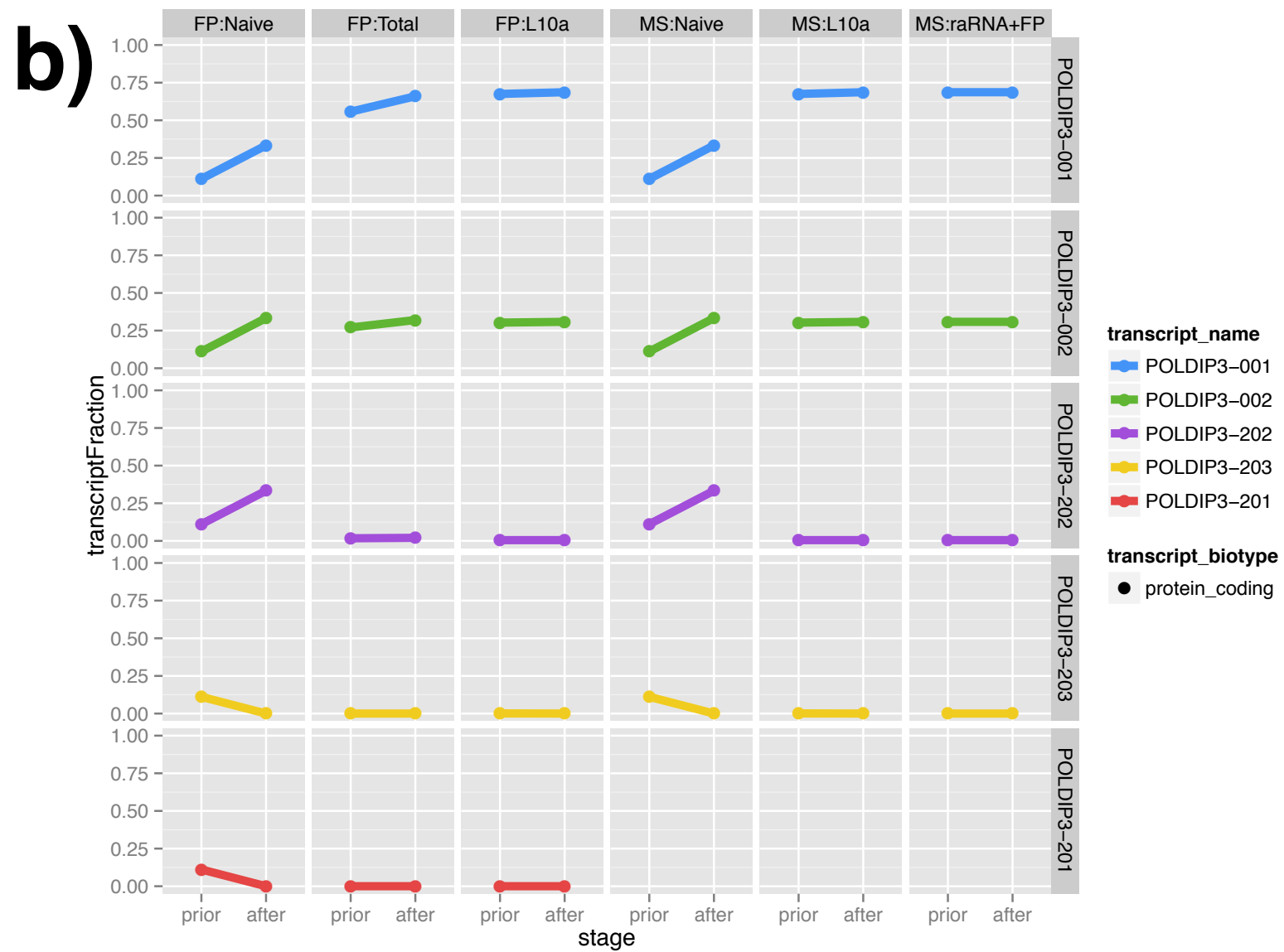
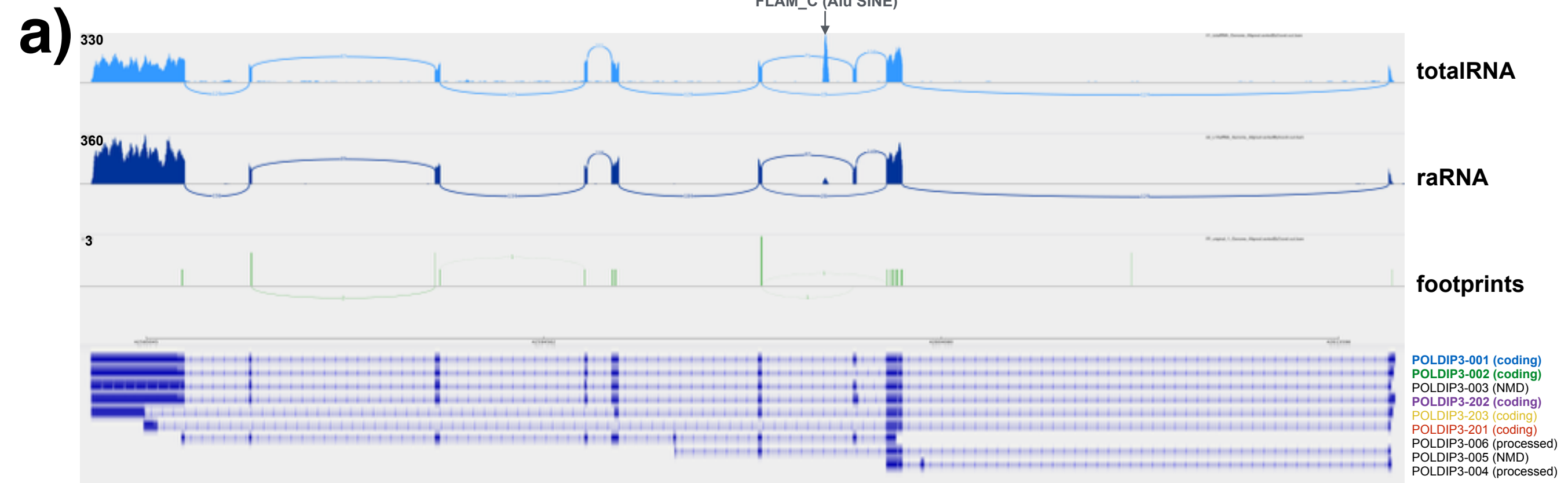
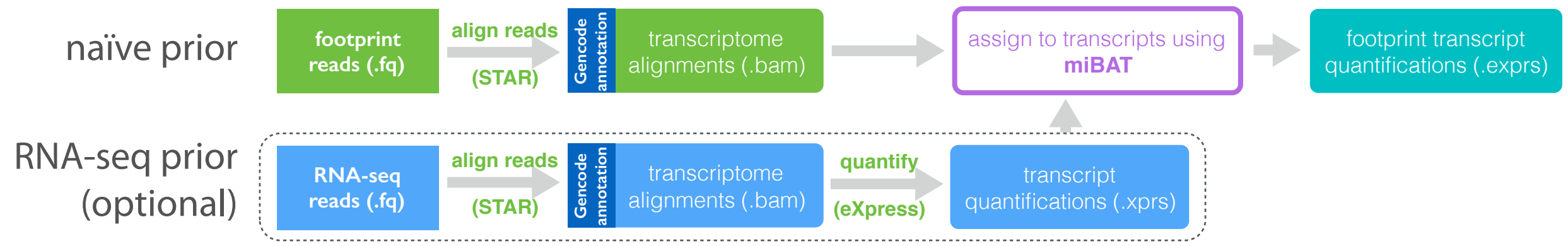
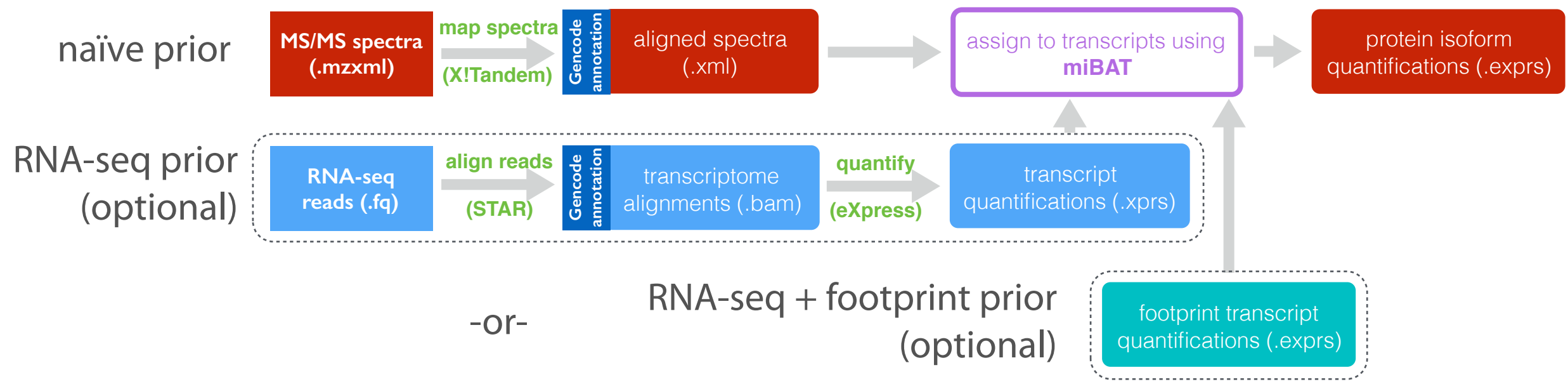


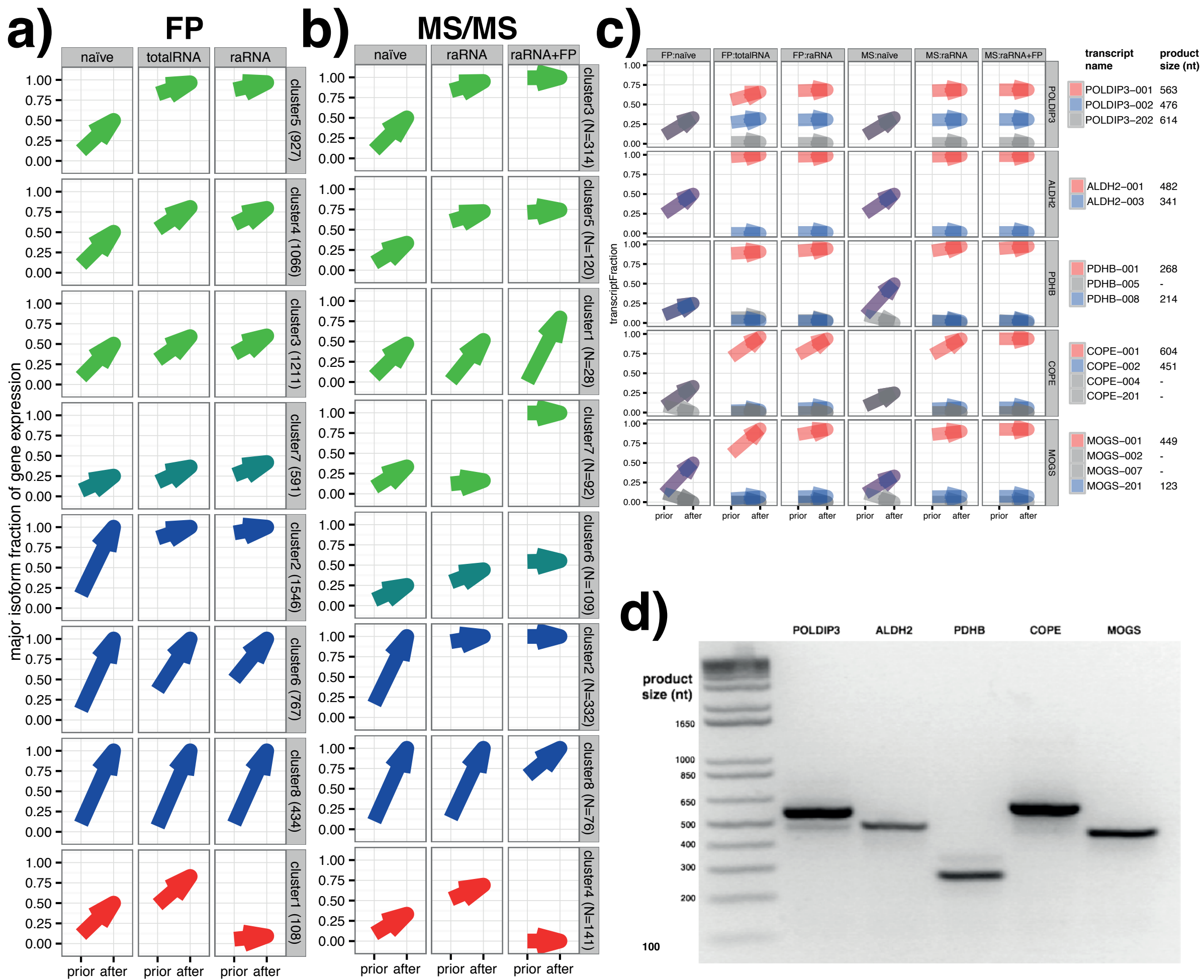
Figure S6

a) ribosome footprint EM



b) mass-spec proteomics EM





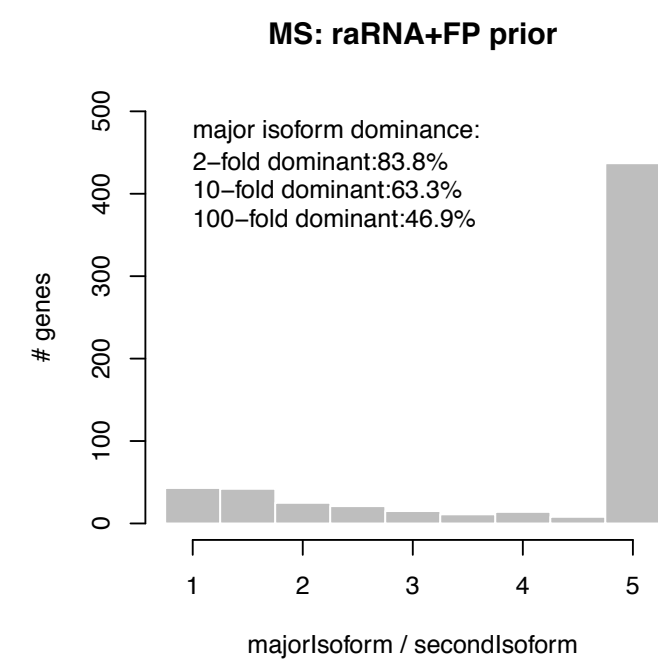
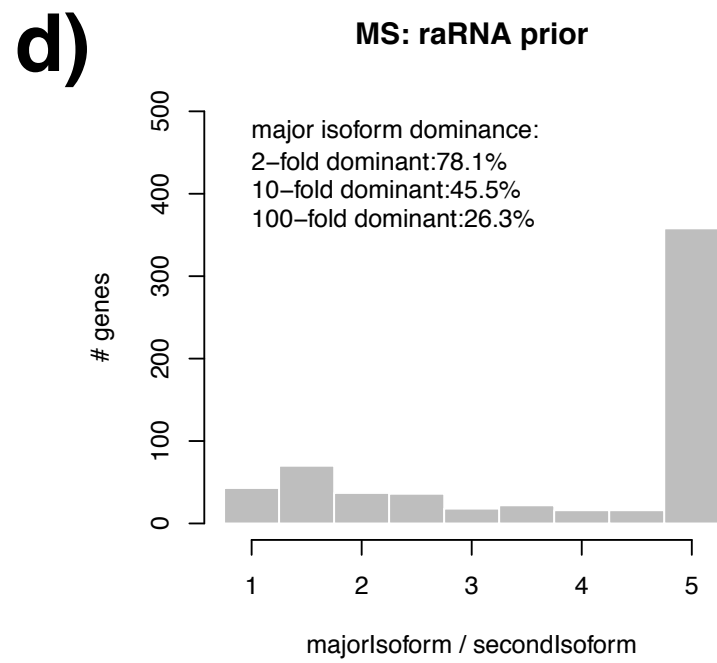
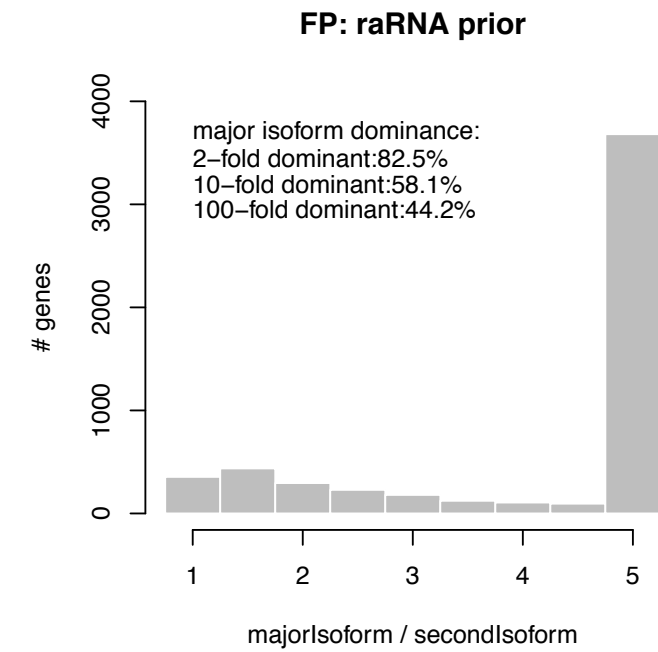
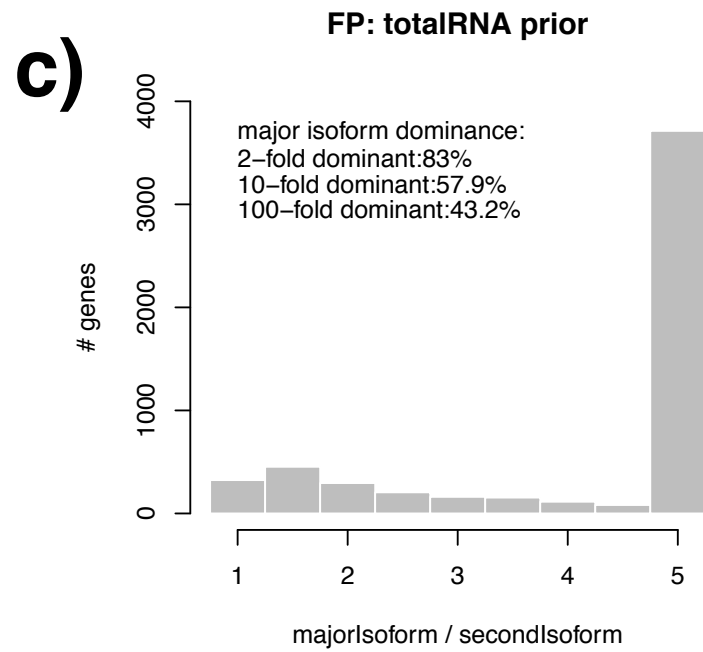
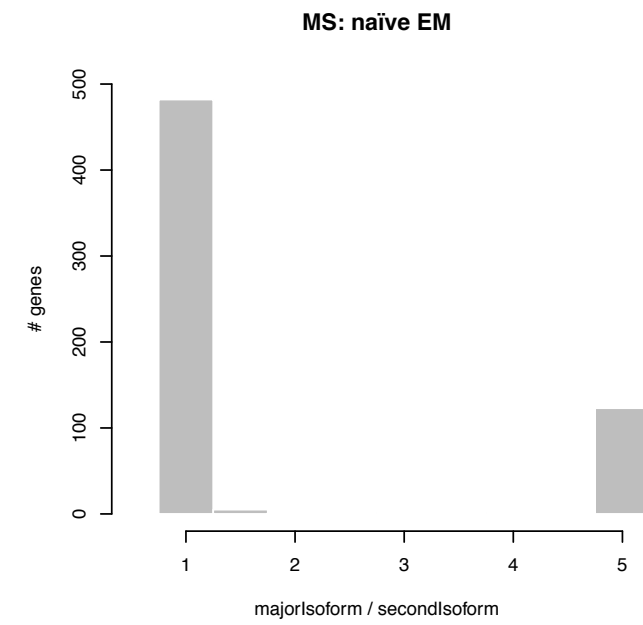
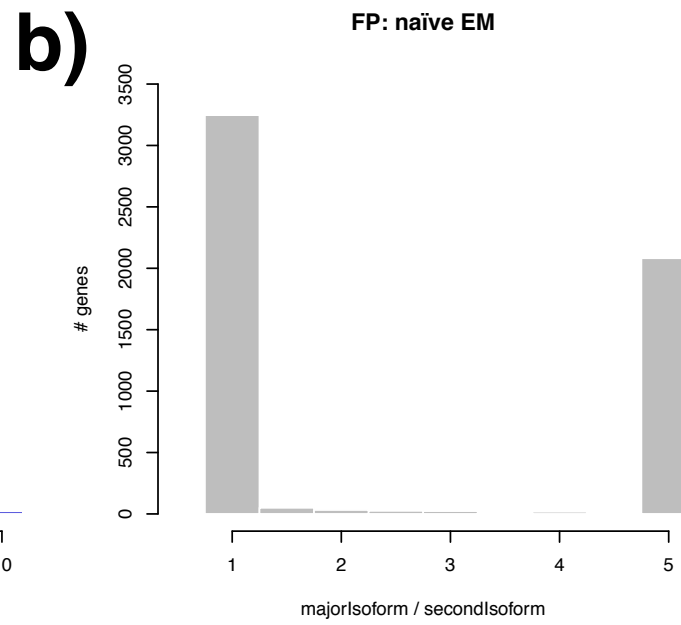
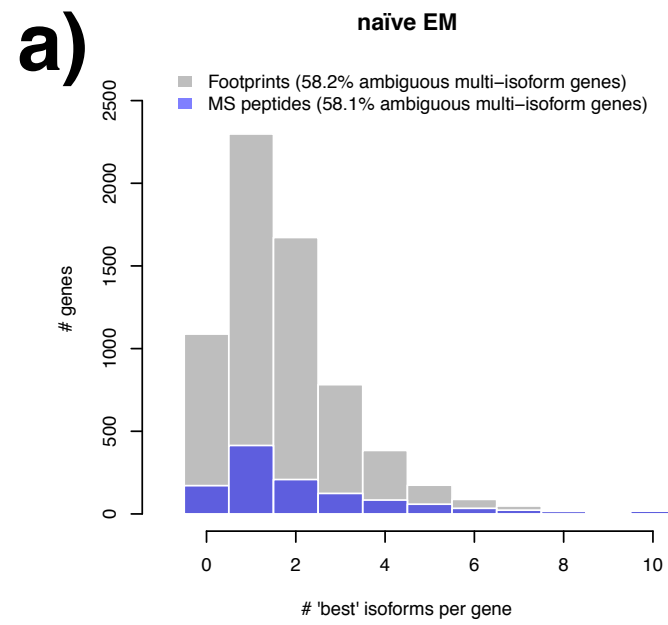


Figure S8

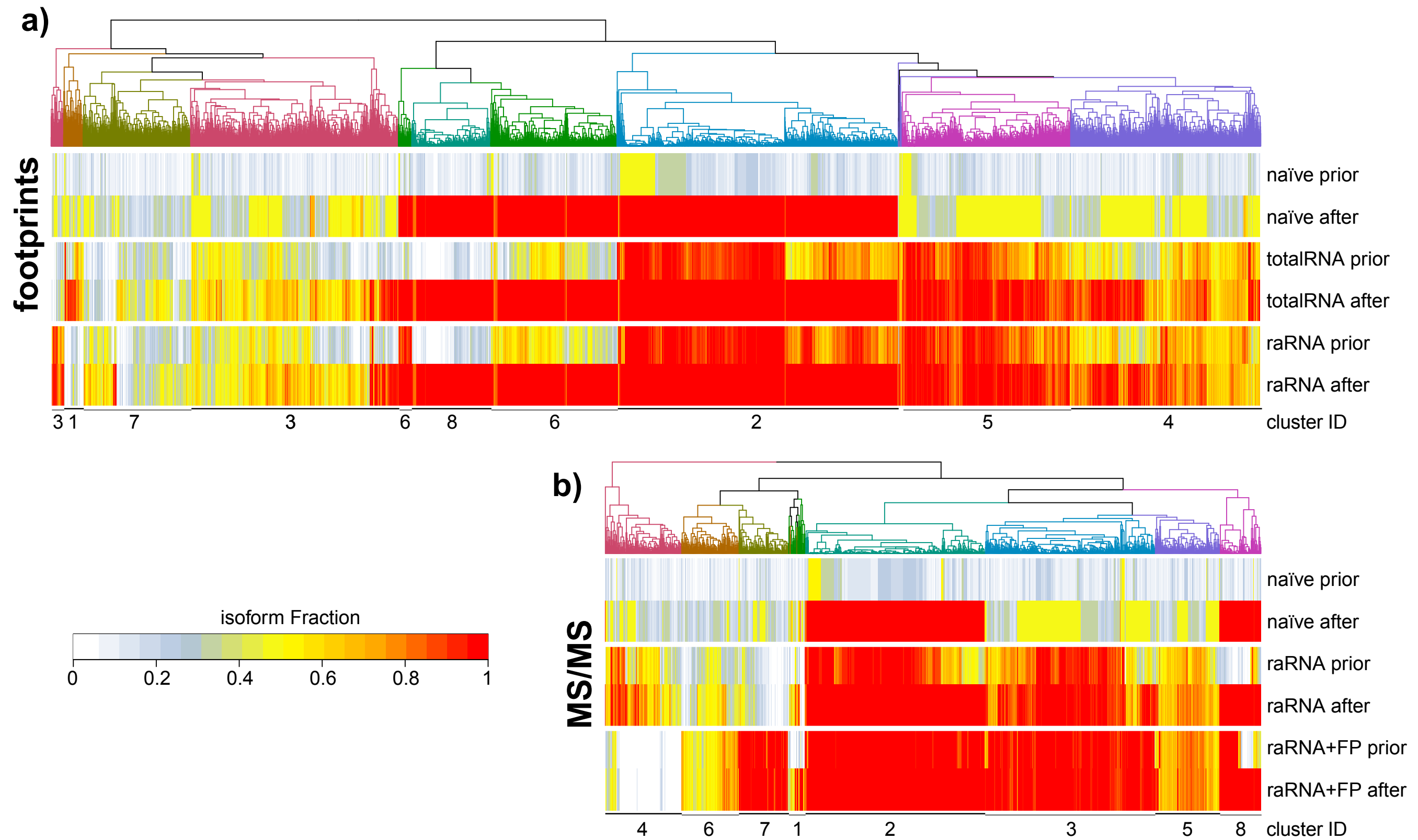


Figure S9

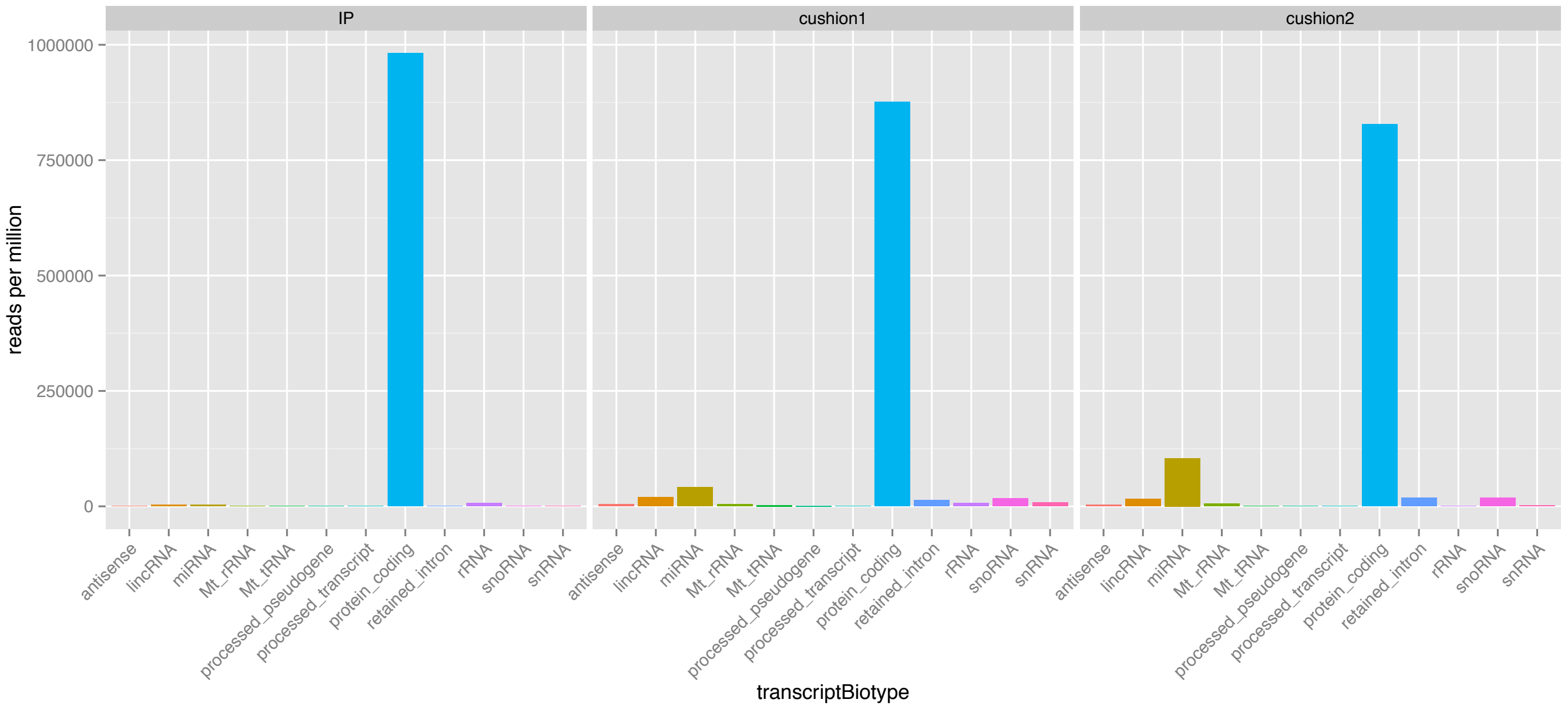
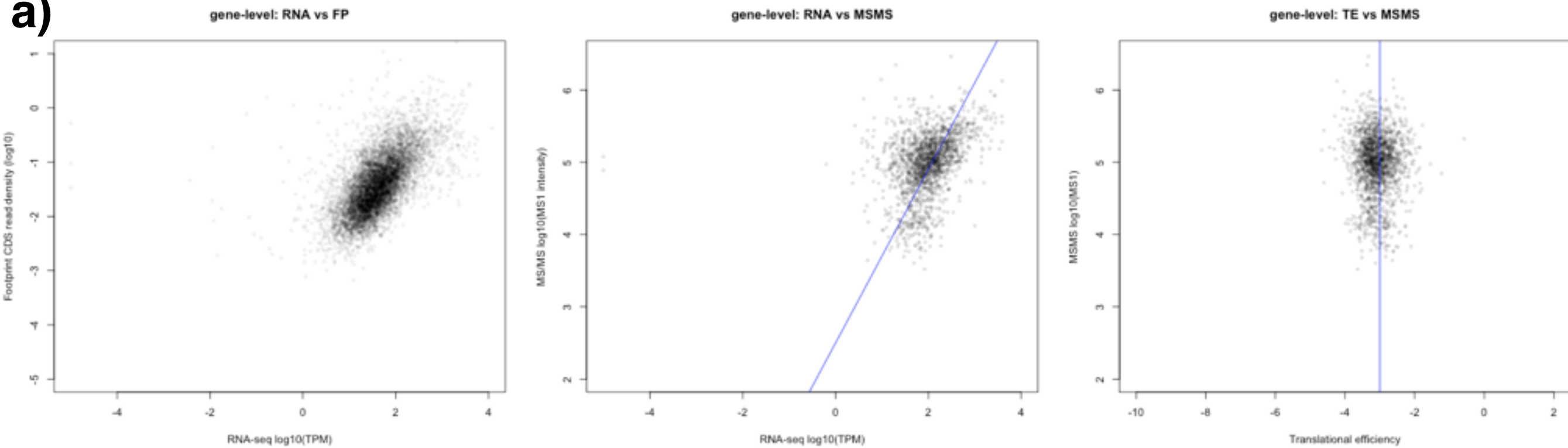


Figure S10

a)



b)

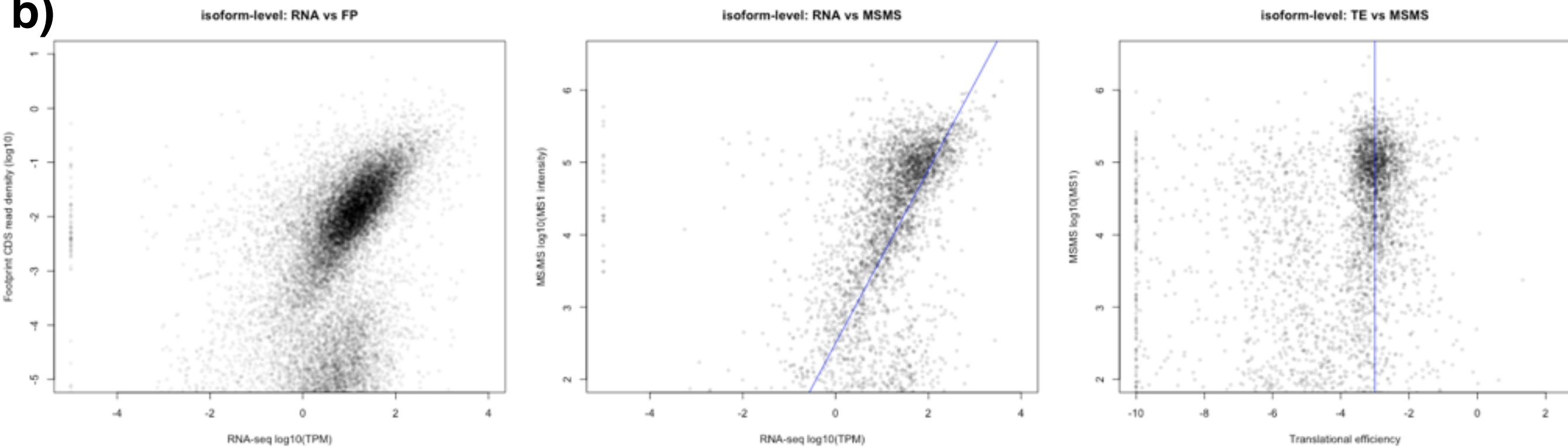
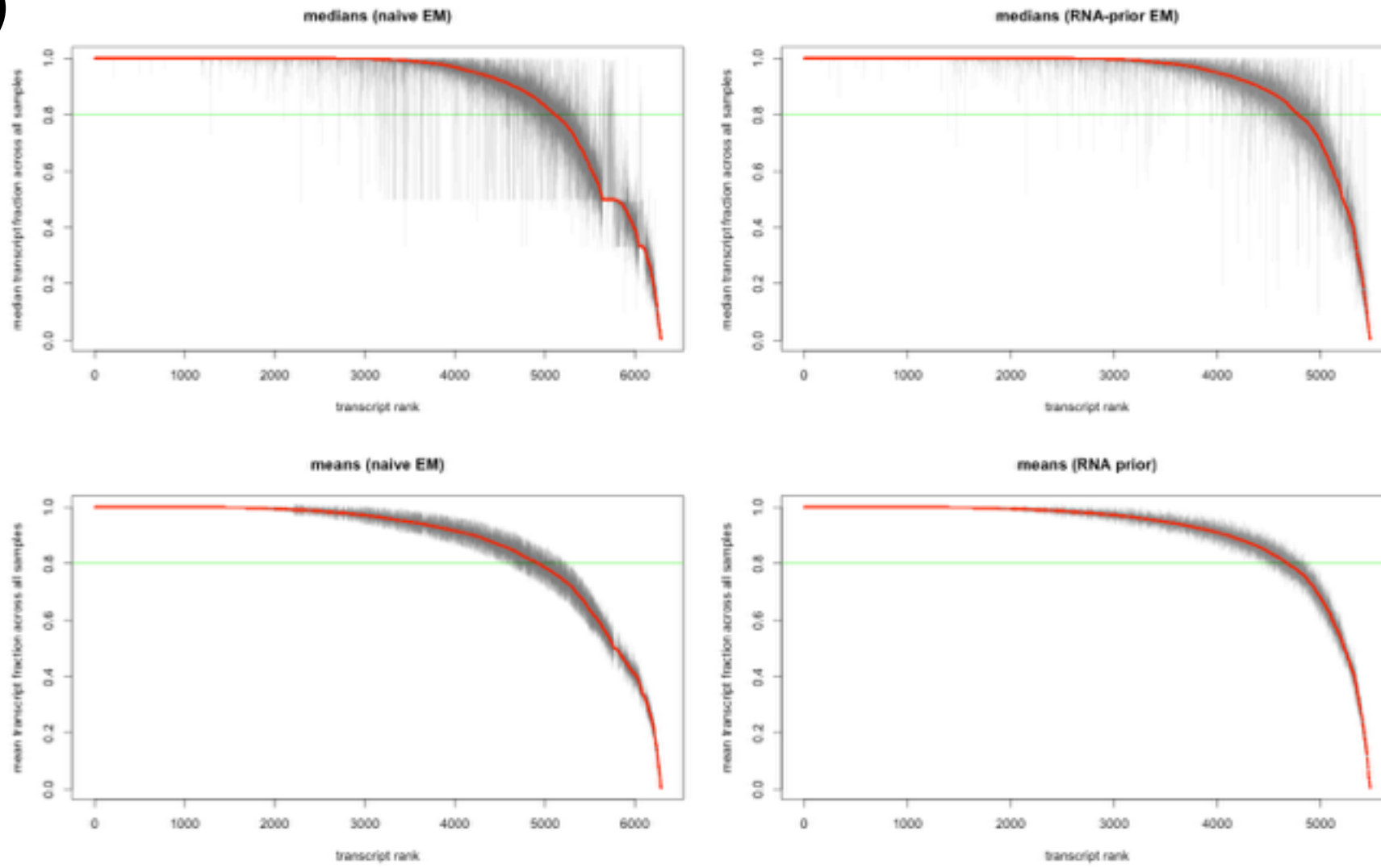


Figure S11

a)



b)

