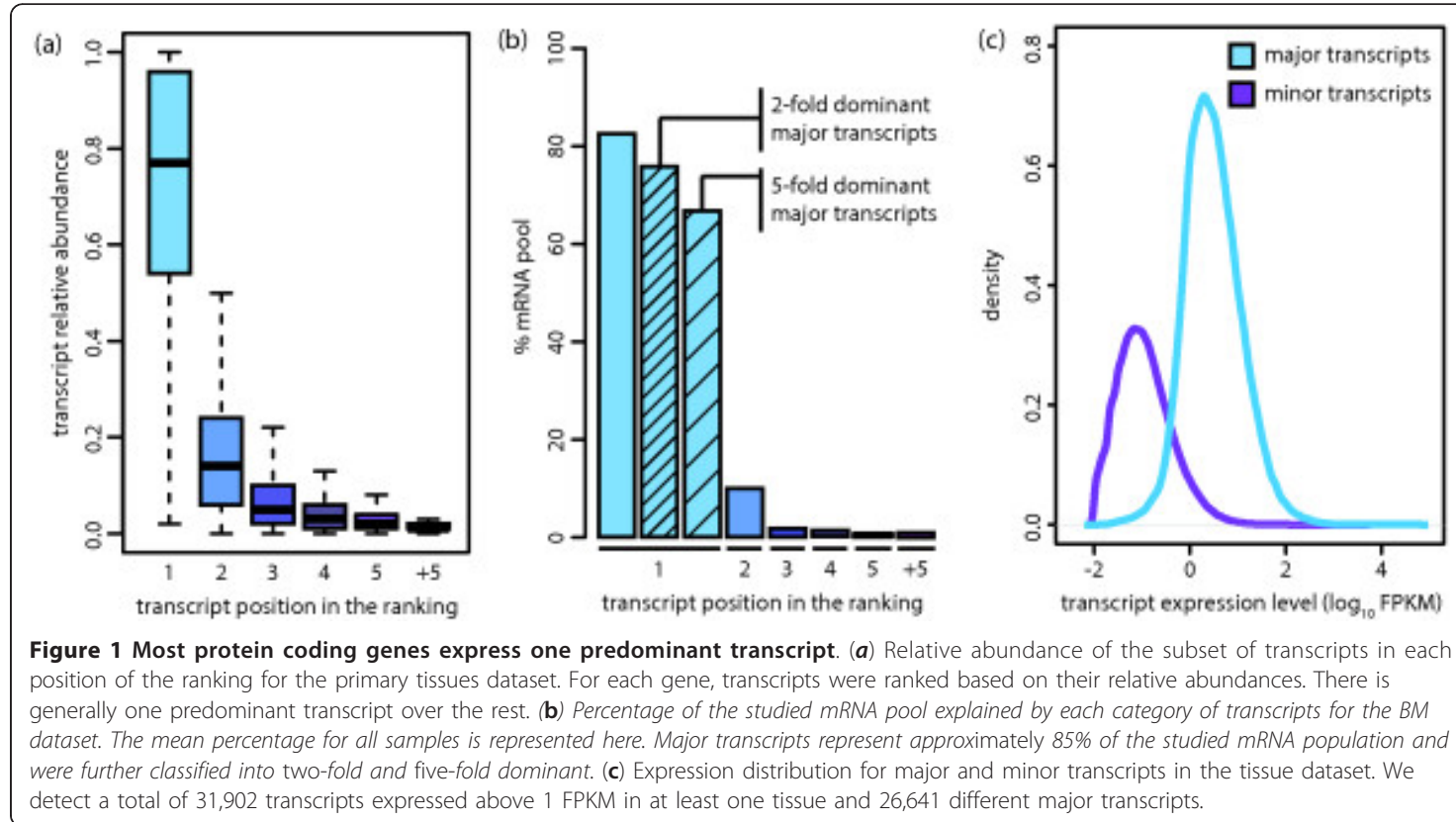


RESEARCH

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Transcriptome analysis of human tissues and cell lines reveals one dominant transcript per gene

Mar González-Porta¹, Adam Frankish², Johan Rung¹, Jennifer Harrow² and Alvis Brazma^{1*}

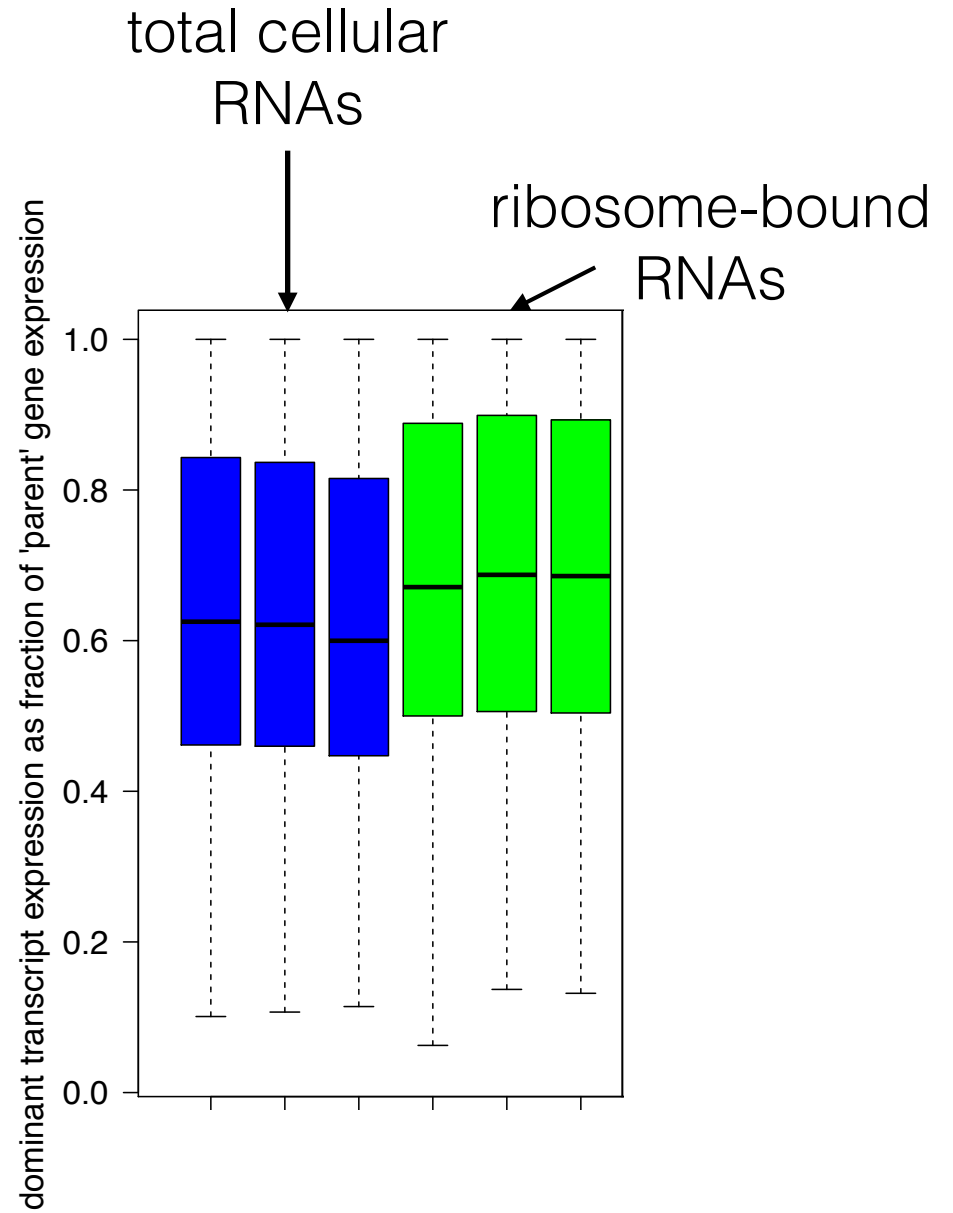
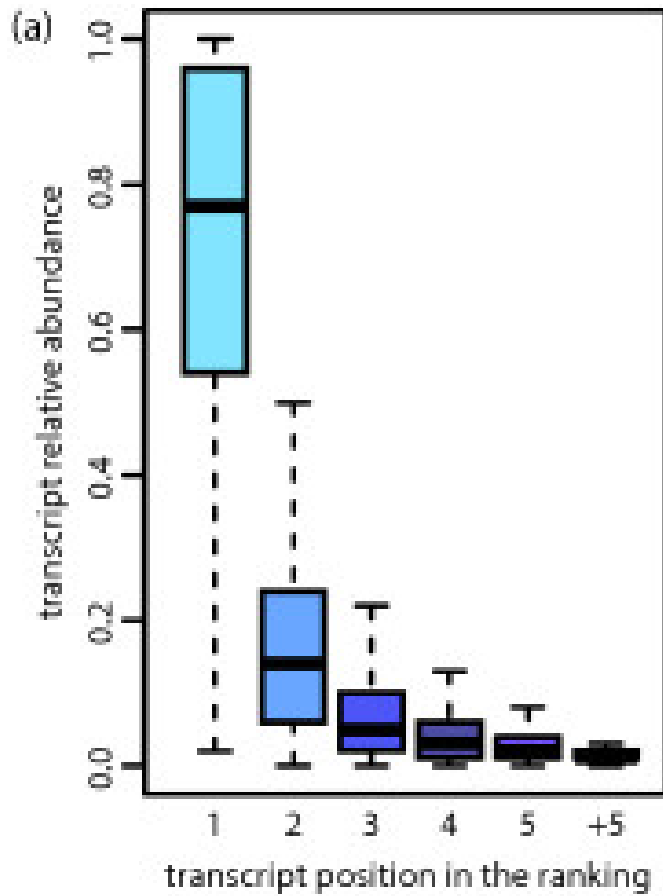


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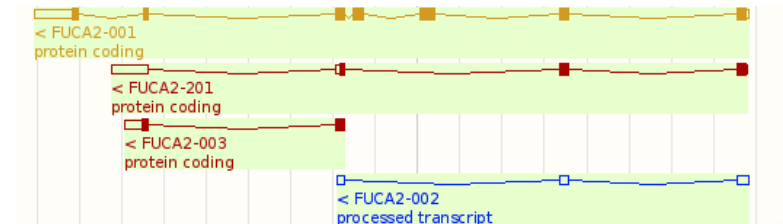
Transcriptome analysis of human tissues and cell lines reveals one dominant transcript per gene

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fucosidase, alpha-L-2, plasma

ENSG0000001036.8



		YEDFGPLFTAK	FFNANQWADIFQASGAK	WPTSGQLFLGHPK	HGGFYTCSDR
001	ENST00000002165.5	1	1	1	1
002	ENST00000367585.1	1	1	0	0
201	ENST00000438118.2	1	1	1	0
003	ENST00000451668.1	0	0	1	0

- 4 transcripts, 4 peptides
- 'best' transcript (ENST00000002165.5) supports 100% of these spectra

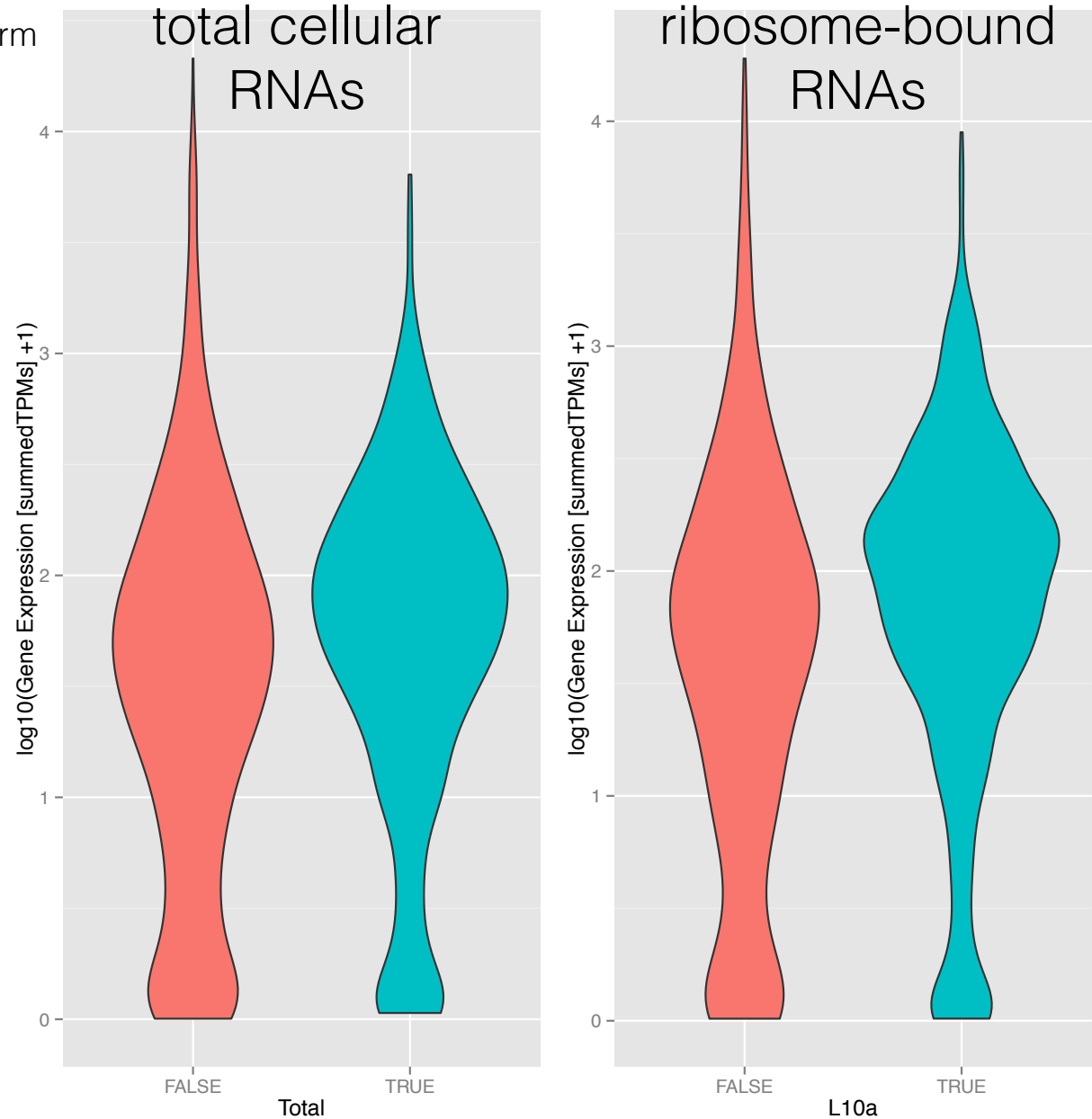
Dominant isoform agreement

- **5,522** genes observed in both RNA-seq and MSMS, use the **4,839** of these that have >1 isoform
- only consider (for now) the **2,328** genes for which the MSMS suggest a single dominant isoform (**926** genes peptides support only 1 isoform!)
- ~50% of these genes have same dominant isoform reported by both RNA-seq and MSMS
 - Total: **1,141** genes agree with MSMS
 - L10a: **1,158** genes agree with MSMS
 - Y10B: **1,159** genes agree with MSMS

Dominant isoform agreement

- RNA-seq / proteomics **disagree** on major isoform
- RNA-seq / proteomics **agree** on major isoform

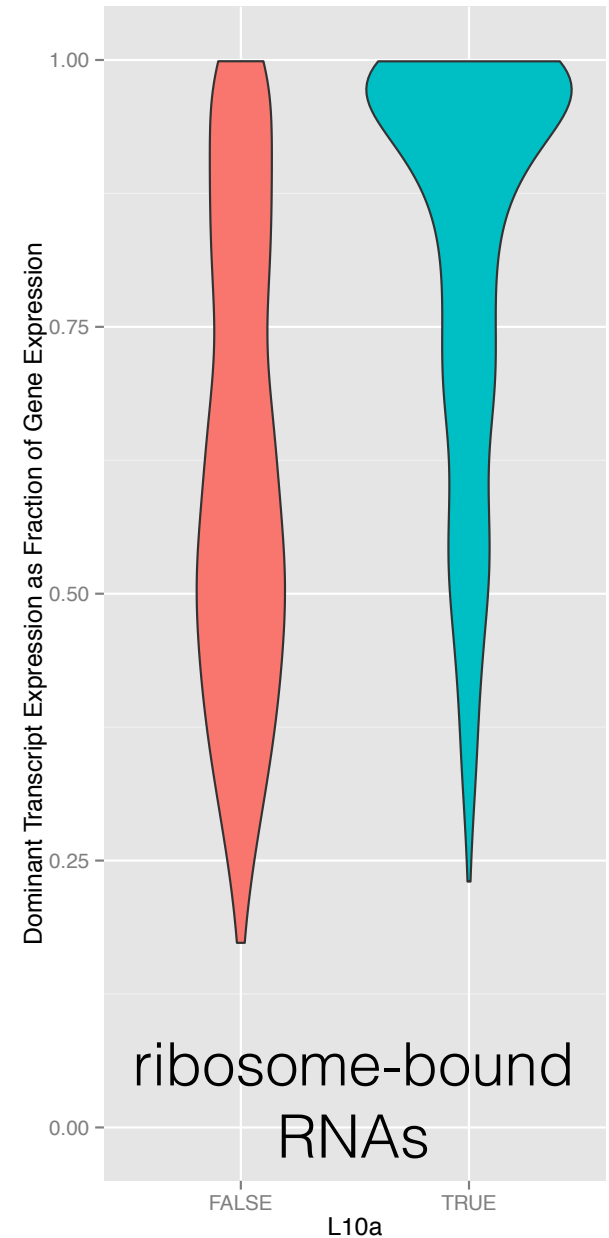
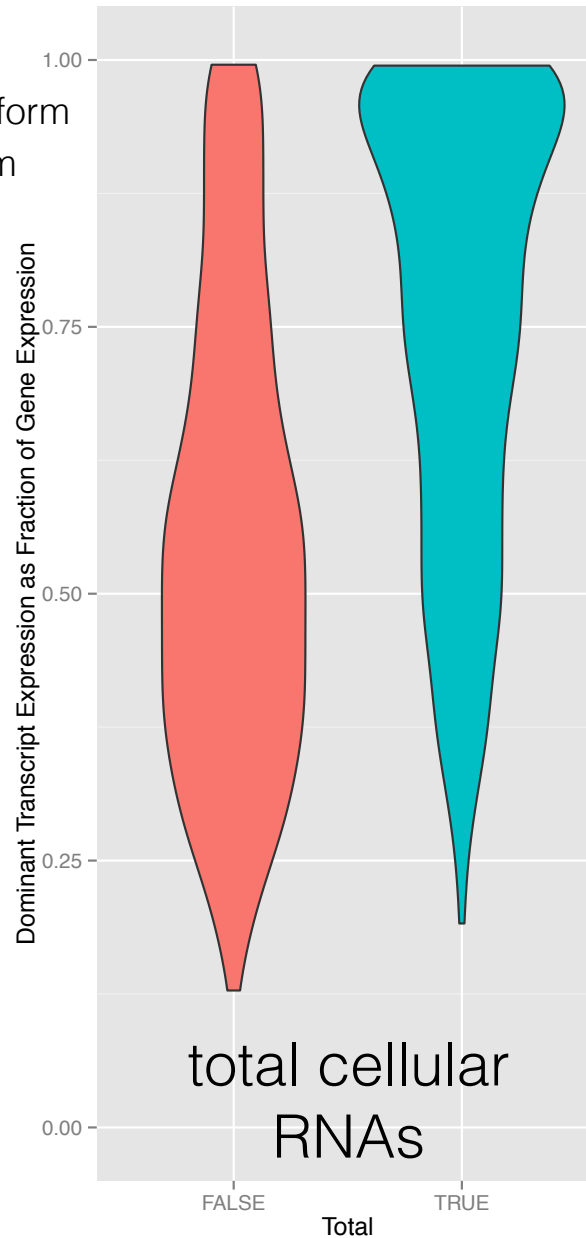
Agreement based on RNA-seq gene expression



Dominant isoform agreement

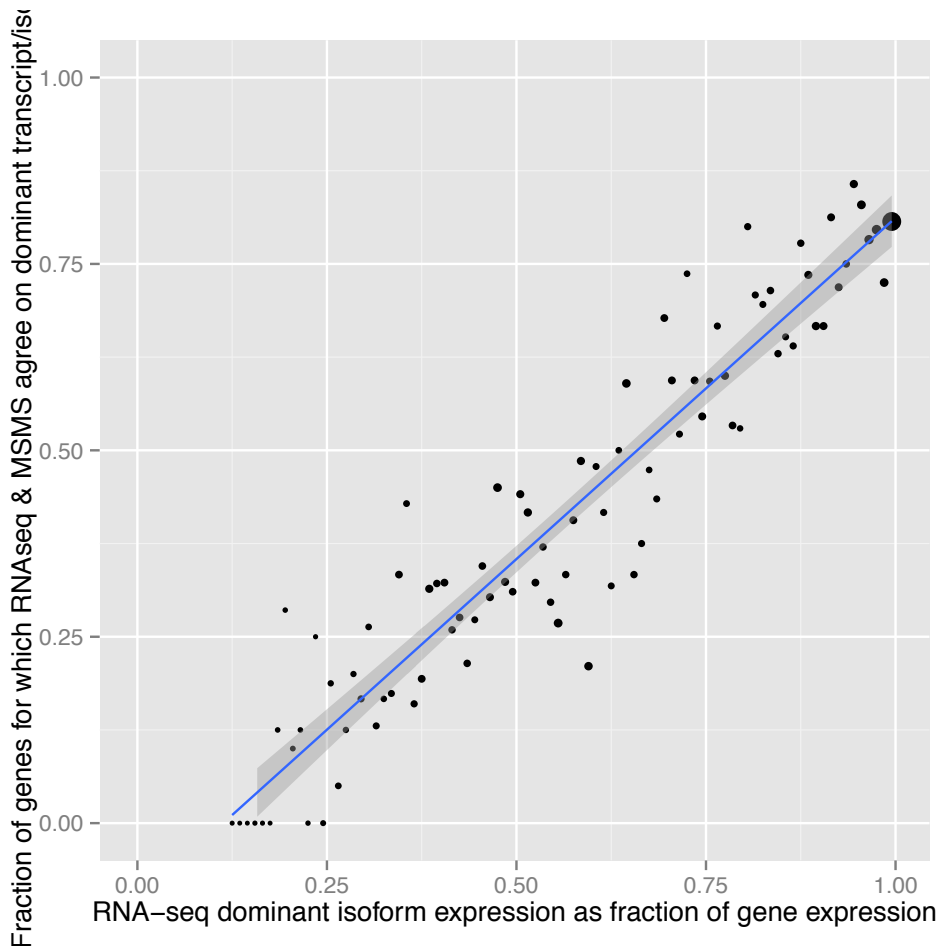
- RNA-seq / proteomics **disagree** on major isoform
- RNA-seq / proteomics **agree** on major isoform

Agreement based on RNA-seq dominant isoform expression as a fraction of the gene's expression

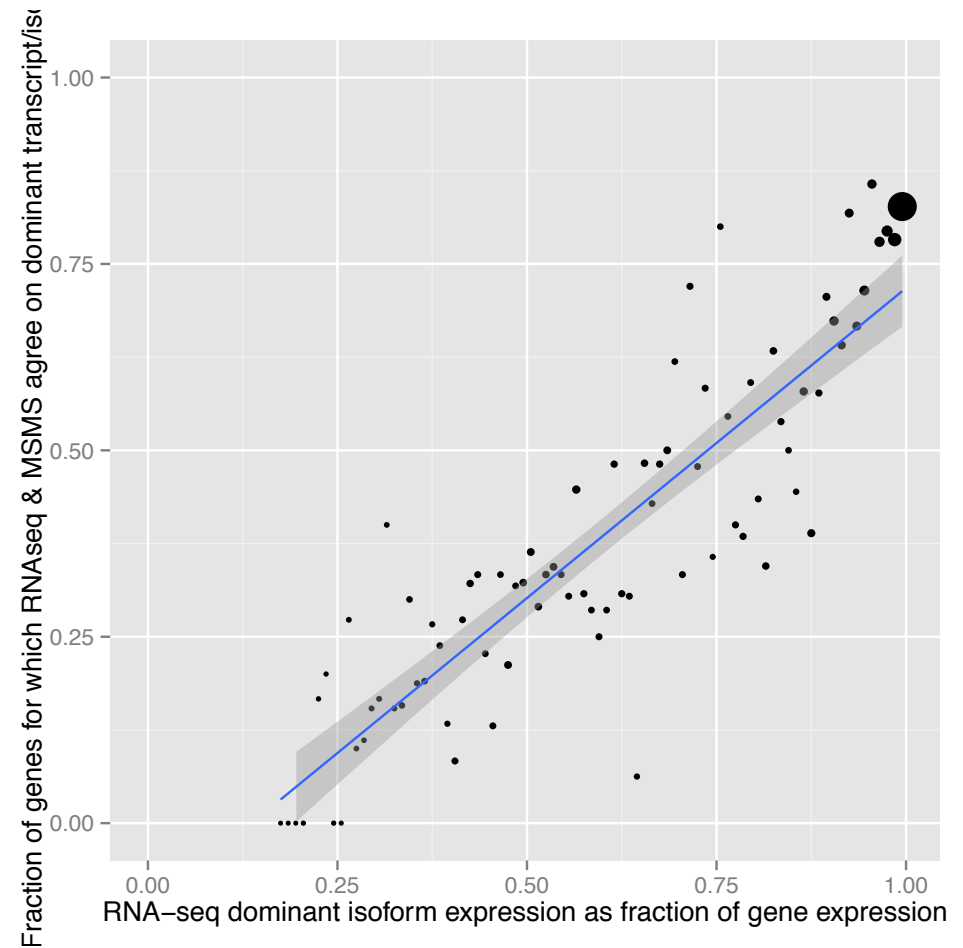


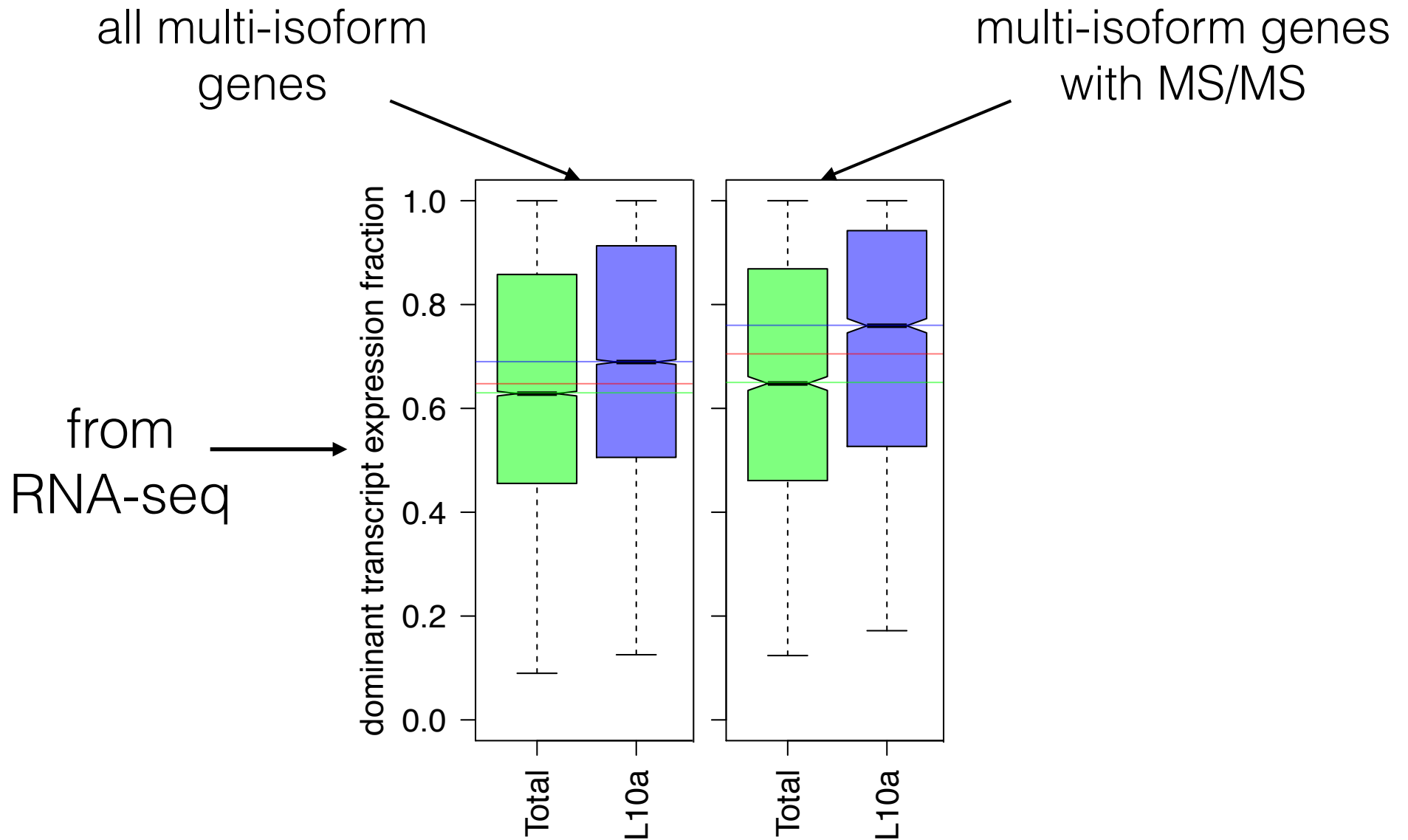
Dominant isoform agreement

total cellular RNAs



ribosome-bound RNAs





- dominant isoform becomes more dominant in ribosome-associated RNAs
- becomes even more dominant in genes for which we see peptides