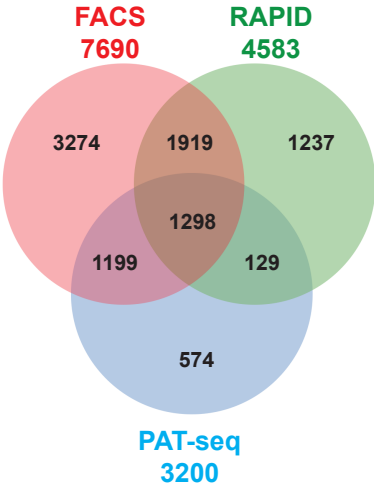
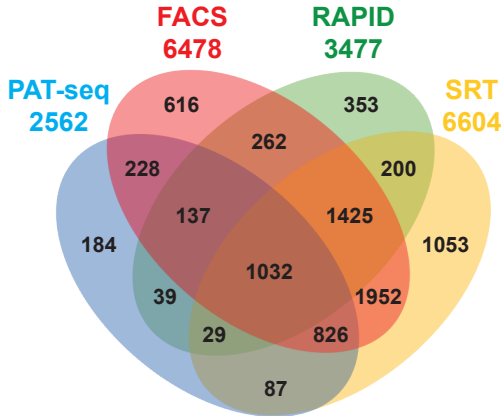


Figure S5

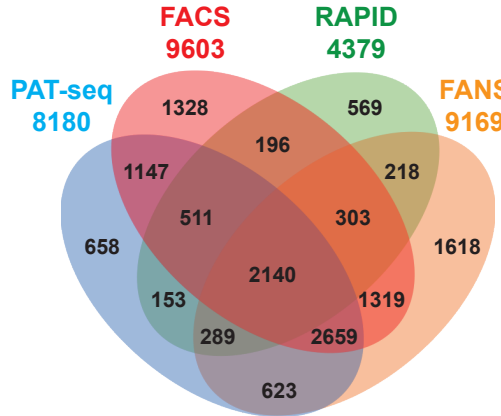
A Muscle



B Muscle (SL1)



C Intestine



D

Muscle	In common with		
	RAPID	FACS-seq	PAT-seq
Fraction of RAPID genes	100%	70%	31%
Fraction of FACS-seq genes	42%	100%	32%
Fraction of PAT-seq genes	45%	78%	100%

Muscle (SL1)	In common with			
	RAPID	FACS-seq	PAT-seq	SRT
Fraction of RAPID genes	100%	82%	36%	77%
Fraction of FACS-seq genes	44%	100%	34%	81%
Fraction of PAT-seq genes	48%	87%	100%	77%
Fraction of SRT genes	41%	79%	30%	100%

Intestine	In common with			
	RAPID	FACS-seq	PAT-seq	FANS-seq
Fraction of RAPID genes	100%	72%	71%	67%
Fraction of FACS-seq genes	33%	100%	67%	67%
Fraction of PAT-seq genes	38%	79%	100%	70%
Fraction of FANS-seq genes	32%	70%	62%	100%

E

Muscle	Cross-method consistency		
	Not detected by other methods	Detected by one other method	Detected by the two other methods
Fraction of RAPID genes	27%	45%	28% $\Sigma=73\%$
Fraction of FACS-seq genes	43%	40%	17% $\Sigma=57\%$
Fraction of PAT-seq genes	18%	41%	41% $\Sigma=82\%$

Muscle (SL1)	Cross-method consistency			
	Not detected by other methods	Detected by one other method	Detected by two other methods	Detected by the three other methods
Fraction of RAPID genes	10%	14%	46%	30% $\Sigma=90\%$
Fraction of FACS-seq genes	9%	38%	37%	16% $\Sigma=91\%$
Fraction of PAT-seq genes	7%	14%	39%	40% $\Sigma=93\%$
Fraction of SRT genes	16%	34%	34%	16% $\Sigma=84\%$

Intestine	Cross-method consistency			
	Not detected by other methods	Detected by one other method	Detected by two other methods	Detected by the three other methods
Fraction of RAPID genes	13%	13%	25%	49% $\Sigma=87\%$
Fraction of FACS-seq genes	14%	28%	36%	22% $\Sigma=86\%$
Fraction of PAT-seq genes	8%	24%	42%	26% $\Sigma=92\%$
Fraction of FANS-seq genes	18%	24%	35%	23% $\Sigma=82\%$