

Outline

tRNA - contaminant mapping

QC

Correlation between data types

Ratio CDS/UTR - riboprofiling VS RNAseq

Ratio protein coding/long non coding RNA

tRNA - contaminant mapping

	6h	18h	120h
Reads	42,130,444	45,982,977	44,077,266
Size selected (25-44)	34,439,444	39,441,134	32,501,482
After rRNA filtering	4,928,271	26,687,975	18,992,877
Aligned (-rRNA, 10mm)	2,022,381 (41.04%)	6,718,578 (25.17%)	9,117,294 (48.00%)
Uniquely aligned (-rRNA, 10mm)	1,095,120 (54.15%)	3,543,776 (52.75%)	4910138 (53.86%)
tRNA (-rRNA, 10mm)	33,333 (1.65%)	114,375 (1.70%)	111,788 (1.23%)
Exonic mapping primary alignment	918,722	3,241,787	3,881,137
Exonic uniquely mapped	697,556	2,486,593	3,071,028

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Correlation between data types

Ratio CDS/UTR - riboprofiling VS RNAseq

Ratio protein coding/long non coding RNA

H006 (6,109 genes) - Spearman

RP VS RNASeq

id	H006.1RP
H006.1RP	1
H000.2C	0.85
H000.3C	0.81
H003.2C	0.862
H003.3C	0.847
H006.2C	0.879
H006.3C	0.853
H009.2C	0.862
H009.3C	0.844
H012.2C	0.847
H012.3C	0.838
H018.2C	0.845
H018.3C	0.83
H024.2C	0.839
H024.3C	0.793
H036.2C	0.828
H036.3C	0.774
H048.2C	0.8
H048.3C	0.752
H072.2C	0.742
H072.3C	0.705
H120.2C	0.689
H120.3C	0.639
H168.2C	0.682
H168.3C	0.663

RP VS Proteomics

id	H006.1RP
H006.1RP	1
H000.2P	0.469
H003.2P	0.447
H006.2P	0.454
H009.2P	0.462
H012.2P	0.466
H018.2P	0.484
H024.2P	0.484
H036.2P	0.448
H048.2P	0.448
H072.2P	0.41
H120.2P	0.335
H168.2P	0.329

RNASeq VS Proteomics

id	H006.2C
H006.2C	1
H000.2P	0.421
H003.2P	0.403
H006.2P	0.407
H009.2P	0.418
H012.2P	0.418
H018.2P	0.436
H024.2P	0.443
H036.2P	0.406
H048.2P	0.405
H072.2P	0.364
H120.2P	0.284
H168.2P	0.277

id	H006.3C
H006.3C	1
H000.2P	0.397
H003.2P	0.377
H006.2P	0.38
H009.2P	0.391
H012.2P	0.392
H018.2P	0.412
H024.2P	0.421
H036.2P	0.386
H048.2P	0.384
H072.2P	0.35
H120.2P	0.282
H168.2P	0.276

H018 (6,109 genes) - Spearman

RP VS RNASeq

id	H018.1RP
H018.1RP	1
H000.2C	0.839
H000.3C	0.805
H003.2C	0.848
H003.3C	0.839
H006.2C	0.862
H006.3C	0.841
H009.2C	0.862
H009.3C	0.844
H012.2C	0.863
H012.3C	0.851
H018.2C	0.874
H018.3C	0.855
H024.2C	0.872
H024.3C	0.825
H036.2C	0.863
H036.3C	0.81
H048.2C	0.833
H048.3C	0.788
H072.2C	0.781
H072.3C	0.743
H120.2C	0.73
H120.3C	0.68
H168.2C	0.72
H168.3C	0.703

RP VS Proteomics

id	H018.1RP
H018.1RP	1
H000.2P	0.448
H003.2P	0.426
H006.2P	0.431
H009.2P	0.44
H012.2P	0.44
H018.2P	0.466
H024.2P	0.474
H036.2P	0.446
H048.2P	0.454
H072.2P	0.42
H120.2P	0.352
H168.2P	0.348

RNASeq VS Proteomics

id	H018.2C
H018.2C	1
H000.2P	0.391
H003.2P	0.372
H006.2P	0.372
H009.2P	0.385
H012.2P	0.383
H018.2P	0.409
H024.2P	0.424
H036.2P	0.401
H048.2P	0.405
H072.2P	0.376
H120.2P	0.31
H168.2P	0.302

id	H018.3C
H018.3C	1
H000.2P	0.379
H003.2P	0.359
H006.2P	0.358
H009.2P	0.37
H012.2P	0.371
H018.2P	0.396
H024.2P	0.411
H036.2P	0.388
H048.2P	0.389
H072.2P	0.364
H120.2P	0.303
H168.2P	0.296

H120 (6,109 genes) - Spearman

RP VS RNASeq

id	H120.1RP
H120.1RP	1
H000.2C	0.625
H000.3C	0.603
H003.2C	0.638
H003.3C	0.636
H006.2C	0.655
H006.3C	0.643
H009.2C	0.665
H009.3C	0.652
H012.2C	0.676
H012.3C	0.667
H018.2C	0.702
H018.3C	0.684
H024.2C	0.719
H024.3C	0.676
H036.2C	0.753
H036.3C	0.692
H048.2C	0.75
H048.3C	0.704
H072.2C	0.822
H072.3C	0.764
H120.2C	0.852
H120.3C	0.774
H168.2C	0.857
H168.3C	0.823

RP VS Proteomics

id	H120.1RP
H120.1RP	1
H000.2P	0.292
H003.2P	0.267
H006.2P	0.266
H009.2P	0.279
H012.2P	0.278
H018.2P	0.309
H024.2P	0.328
H036.2P	0.323
H048.2P	0.354
H072.2P	0.401
H120.2P	0.404
H168.2P	0.412

RNASeq VS Proteomics

id	H120.2C
H120.2C	1
H000.2P	0.267
H003.2P	0.245
H006.2P	0.241
H009.2P	0.253
H012.2P	0.255
H018.2P	0.282
H024.2P	0.306
H036.2P	0.303
H048.2P	0.325
H072.2P	0.367
H120.2P	0.372
H168.2P	0.38

id	H120.3C
H120.3C	1
H000.2P	0.233
H003.2P	0.212
H006.2P	0.207
H009.2P	0.219
H012.2P	0.223
H018.2P	0.248
H024.2P	0.271
H036.2P	0.267
H048.2P	0.285
H072.2P	0.326
H120.2P	0.334
H168.2P	0.342

Outline

tRNA - contaminant mapping

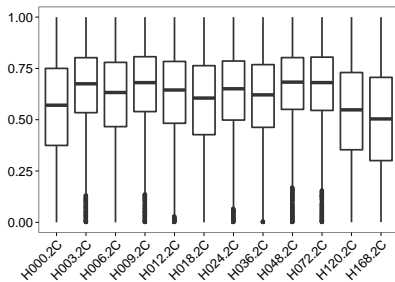
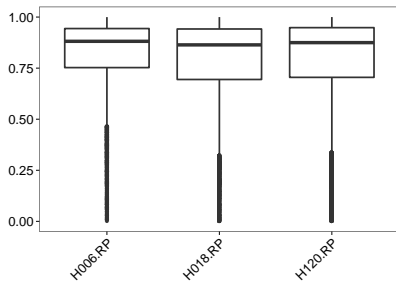
QC

Correlation between data types

Ratio CDS/UTR - riboprofiling VS RNAseq

Ratio protein coding/long non coding RNA

Ratio CDS/UTR: riboprofiling VS all time points RNAseq cytoplasmic fraction



Outline

tRNA - contaminant mapping

QC

Correlation between data types

Ratio CDS/UTR - riboprofiling VS RNAseq

Ratio protein coding/long non coding RNA

Ratio protein coding/long non coding RNA

		Whole cell fraction		cytoplasmic fraction	
		sum PC	sum lncRNA	sum PC	sum lncRNA
ENCODEv19 IDR \leq 0.1, polyA+ 20345 PC, 13870 lncRNA	McF-7	671,592	12,921.9	1,040,080	15,924.1
	A549	797,591	14,007	1,056,900	14,948.3
	GM12878	747,946	13,864.5	948,485	17,570.7
ERC - RNAseq 19815 PC, 15935 lncRNA	H000.rep2	793,260	15,955	986,133	12,822
	H000.rep3	728,367	10,802	1087,439	11,941
	H003.rep2	815,928	14,688	995,406	8,935.8
	H003.rep3	748,292	9,418.6	1096,988	12,004
	H006.rep2	825,798	11,829	991,627	9,817.3
	H006.rep3	737,896	8,805.9	1035,817	9,777
	H009.rep2	795,112	11,358	975,828	8,859.3
	H009.rep3	726,807	8,892.7	998,428	9,098.3
	H012.rep2	758,863	11,076	964,975	9,019.3
	H012.rep3	883,194	10,771	964,230	8,832.8
	H018.rep2	778,990	11,467	989,046	10,109
	H018.rep3	721,733	9,295.8	954,880	9,249.3
	H024.rep2	743,191	11,403	928,758	9,487.4
	H024.rep3	729,061	8,829.4	990,018	9,302
	H036.rep2	820,256	10,314	945,639	9,339.5
	H036.rep3	725,228	8,958.2	1,064,567	9,148.1
	H048.rep2	801,333	9,809.9	941,293	7,623.6
	H048.rep3	718,885	8,214	1,026,083	8,157.8
	H072.rep2	772,403	7,245.4	936,454	5,930.2
	H072.rep3	712,192	6,704.3	1,026,260	6,577.1
H120.rep2	759,301	6,576.7	1,004,718	9,942.8	
H120.rep3	715,442	7,800.2	1,020,129	7,199.2	
H168.rep2	827,355	8,484.3	1,024,853	12,182	
H168.rep3	773,405	8,630.3	1,098,374	9,996.8	

ENCODE v24 - K562

19815 PC, 15935 lncRNA

cytosol						
id	sum PC	sum lncRNA	library	depletion	size range	stranded
ENCSR384ZXD-rep1-1	1,136,058	23,981	polyadenylated mRNA	NA	> 200	true
ENCSR384ZXD-rep2-1	1,182,877	25,450	polyadenylated mRNA	NA	> 200	true
ENCSR860DWK-rep1-1	605,907	79,388	RNA	rRNA	> 200	true
ENCSR860DWK-rep2-1	608,815	73,664	RNA	rRNA	> 200	true
insoluble cytoplasmic fraction						
ENCSR594NJP-rep1-1	907,866	15,048	polyadenylated mRNA	NA	> 200	true
ENCSR594NJP-rep2-1	935,157	16,255	polyadenylated mRNA	NA	> 200	true
ENCSR696YIB-rep1-1	700,349	14,355	RNA	rRNA	> 200	true
ENCSR696YIB-rep2-1	681,177	14,894	RNA	rRNA	> 200	true
nucleus						
ENCSR040YBR-rep1-1	491,528	67,311	RNA	rRNA	> 200	true
ENCSR040YBR-rep2-1	476,521	73,323	RNA	rRNA	> 200	true
ENCSR530NHO-rep1-1	676,217	24,724	polyadenylated mRNA	NA	> 200	true
ENCSR530NHO-rep2-1	632,591	28,824	polyadenylated mRNA	NA	> 200	true
whole cell						
ENCSR000AEN-rep1-1	606,747	31,077	RNA	rRNA	> 200	true
ENCSR000AEN-rep2-1	586,627	35,319	RNA	rRNA	> 200	true
ENCSR000AEO-rep1-1	845,995	15,030	polyadenylated mRNA	NA	> 200	true
ENCSR000AEO-rep2-1	876,457	14,941	polyadenylated mRNA	NA	> 200	true

Ratio protein coding/long non coding RNA

RNAseq fraction: nucleus

19815 PC

15935 lncRNA

	sum PC	sum lncRNA	nb-map-read	nb-uniq-read	prop-map-read	prop-uniq-read
H000.2N.8998	608,031	26,231	532,137,564	510,899,794	94.94	96.01
H000.3N.9845	904,210	27,182	487,204,530	463,915,578	96.19	95.22
H003.2N.8999	573,806	24,290	457,834,678	442,563,104	95.09	96.66
H003.3N.9846	813,617	25,051	480,864,798	461,445,362	96.62	95.96
H006.2N.9000	543,965	26,886	409,004,302	380,826,896	96.17	93.11
H006.3N.9847	702,063	17,045	458,003,976	438,009,398	97.10	95.63
H009.2N.9001	530,339	22,321	469,159,974	453,953,132	96.87	96.76
H009.3N.9848	633,340	16,369	460,678,002	441,727,036	97.50	95.89
H012.2N.9002	668,684	24,536	431,462,588	413,926,962	91.73	95.94
H012.3N.12109	654,835	18,008	447,404,662	428,869,558	96.25	95.86
H018.2N.9003	622,039	24,915	475,133,588	456,571,028	91.87	96.09
H018.3N.9850	723,133	16,233	496,376,108	474,842,632	96.97	95.66
H024.2N.9004	577,529	24,319	458,348,070	441,625,248	94.48	96.35
H024.3N.9851	647,133	19,722	440,641,690	422,959,520	95.50	95.99
H036.2N.9005	597,786	24,146	445,262,254	429,047,826	95.37	96.36
H036.3N.9852	698,159	15,859	414,013,216	397,850,754	95.85	96.10
H048.2N.9006	582,878	19,861	475,824,414	460,121,628	95.93	96.70
H048.3N.9853	616,362	11,872	430,922,498	412,949,360	87.89	95.83
H072.2N.9007	593,984	13,212	485,613,606	470,547,586	95.00	96.90
H072.3N.9854	738,629	11,126	414,833,046	398,514,902	95.45	96.07
H120.2N.9008	801,007	17,385	443,898,168	422,008,490	94.23	95.07
H120.3N.9855	720,797	12,961	433,448,692	414,729,854	95.69	95.68
H168.2N.9009	925,825	18,902	473,360,988	439,534,450	95.40	92.85
H168.3N.9856	851,323	13,140	444,776,158	421,244,798	97.07	94.71

Ratio protein coding/long non coding RNA

19815 PC
15935 lncRNA

		sum PC	sum lncRNA
Riboprofiling	H006	1,002,966	821,368
	H018	1,149,118	144,690
	H120	1,072,901	94,444
RNAseq Cytoplasmic Fraction	H000.2C.8986	986,133	12,822
	H000.3C.9539	1,087,439	11,941
	H003.2C.8987	995,406	8,935.8
	H003.3C.9540	1,096,988	12,004
	H006.2C.8988	991,627	9,817.3
	H006.3C.9541	1,035,817	9,777
	H009.2C.8989	975,828	8,859.3
	H009.3C.9542	998,428	9,098.3
	H012.2C.8990	964,975	9,019.3
	H012.3C.9543	964,230	8,832.8
	H018.2C.8991	989,046	10,109
	H018.3C.9544	954,880	9,249.3
	H024.2C.8992	928,758	9,487.4
	H024.3C.9911	990,018	9,302
	H036.2C.8993	945,639	9,339.5
	H036.3C.9912	1,064,567	9,148.1
	H048.2C.8994	941,293	7,623.6
	H048.3C.9913	1,026,083	8,157.8
	H072.2C.8995	936,454	5,930.2
	H072.3C.9914	1,026,260	6,577.1
H120.2C.8996	1,004,718	9,942.8	
H120.3C.9915	1,020,129	7,199.2	
H168.2C.8997	1,024,853	1,2182	
H168.3C.9916	1,098,374	9,996.8	