

Update: RACE-454 in 5 tissues

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Encode Gencode experimental call
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Oct 23, 2012

Primerdesign Gencode 14PRE/Batch XI - Done

- ▶ data released: Oct. 10, 2010
- ▶ exon gtf gen14.exon.gtf
- ▶ exon junction file gen14.ej.gtf
- ▶ primer annotation gtf file gen14.p3primer.gtf
- ▶ selectd primer annotation gtf file gen14.p3primer.set.gtf
- ▶ 966 (gen13) + 640 (gen14) = **1,606 targets for batch XI**

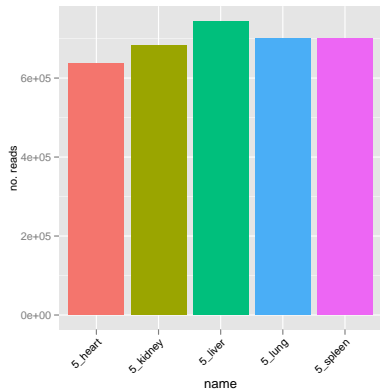
	input	primer design mus		select targets mus
total tx	189,882	125,355	66.02%	601
total exon	551,771	275,338	49.90%	1,192
multiexonic tx	167,139	125,355	75.00%	601
total ej	506,970	211,690	41.76%	640
total sj	340,988	150,872	44.25%	640
tx with unique sj	99,784	46,663	46.76%	601
unique sj	154,586	61,043	39.49%	640
total primer	-	309,516	-	1,228

race454 Data

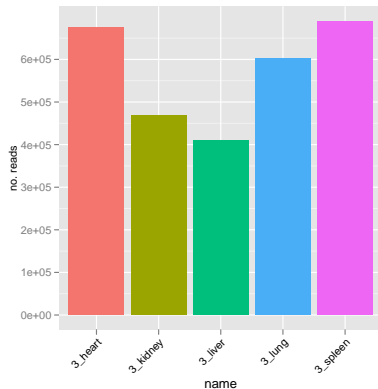
- ▶ 5 additional tissues: heart, kidney, lung, liver, spleen
- ▶ 5p and 3p RACE
- ▶ 500 targets
- ▶ raw reads, trimming, mapping
- ▶ reads available on Oct 11, 2012
- ▶ download started Oct 12, 2012
- ▶ analysis started Oct 15, 2012

Read Statistics - Raw Reads Counts

5p RACE

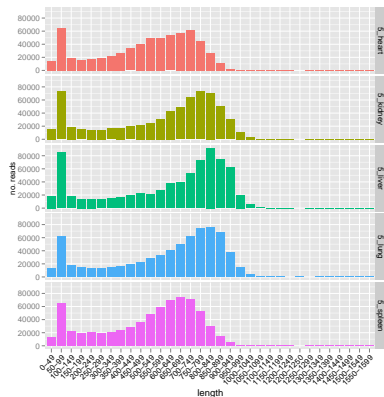


3p RACE



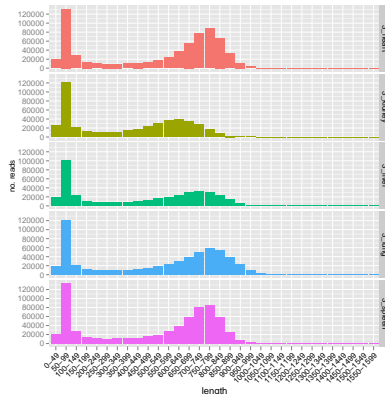
Read Statistics - Raw Reads Length

5p RACE



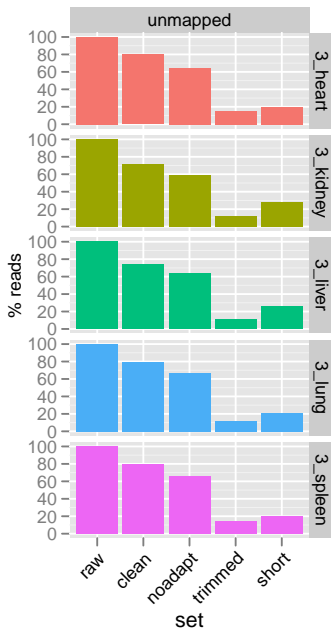
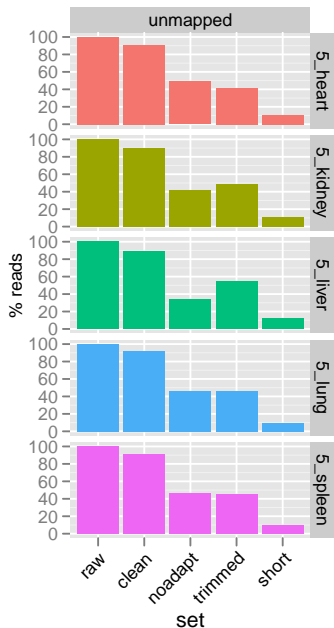
no fragmentation of RACE products

3p RACE

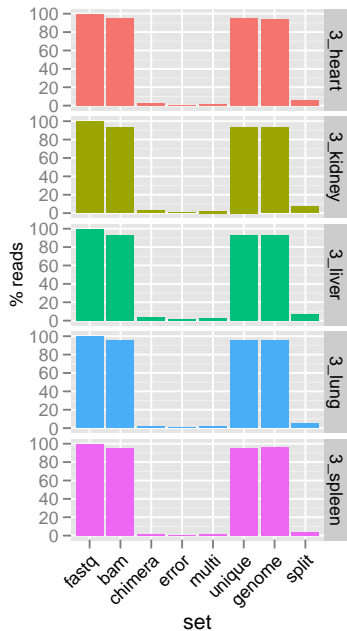
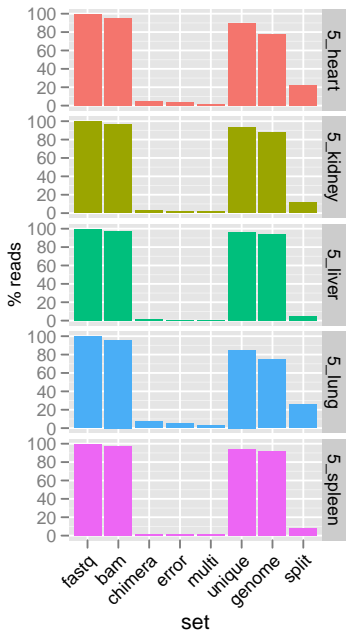


RACE product too long for library preparation
⇒ fragmented

Read Statistics - Trimming the Adaptor



Read Statistics - Mapped Reads



Next Steps

- ▶ optimize mapping parameters
- ▶ more split mapped reads?
- ▶ filter for off-target effects?
- ▶ clustering
- ▶ compare to targets and primers