

Differences in gene expressions between adult and fetus brains

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TASK 3

1. Does the document appear to have an appropriate QC?

Yes the document have very good QC for both the fetal samples and the Adult samples. FastQC was used to QC the samples. See the FASTQC results below.

2. Is the mapping rates similar for fetal and adult samples?

The mapping rates are similar for both fetal and adult samples. Both have mapping rate of about > 95%

3. Is there a trend in the average quality score of mapped reads?

Yes, the average quality score of mapped reads are between 34-38 Phred's score for all the samples. One would think that the adult samples will have lower quality scores because of the lower RIN score indicating poor quality of the RNA. However, their adult samples have about the same quality scores falling in the range above. All mean quality Phred's Score are in the range of 34-40, indicating good quality.

The Quality results:

Adult samples:

```
##FastQC    0.11.8
>>Basic Statistics    pass
#Measure    Value
Filename    HISAT2 on data 2 and data 1_ aligned reads _BAM_
File type    Conventional base calls
Encoding    Sanger / Illumina 1.9
Total Sequences 45183379
Sequences flagged as poor quality    0
Sequence length 100
%GC    46
```

```
##FastQC    0.11.8
>>Basic Statistics    pass
#Measure    Value
Filename    HISAT2 on data 4 and data 3_ aligned reads _BAM_
File type    Conventional base calls
Encoding    Sanger / Illumina 1.9
Total Sequences 80441231
Sequences flagged as poor quality    0
Sequence length 100
%GC    47
```

```
##FastQC    0.11.8
>>Basic Statistics    pass
```

```

#Measure      Value
Filename      HISAT2 on data 10 and data 9_ aligned reads _BAM_
File type     Conventional base calls
Encoding       Sanger / Illumina 1.9
Total Sequences 70679196
Sequences flagged as poor quality      0
Sequence length 100
%GC           48

```

Fetal samples:

```

##FastQC      0.11.8
>>Basic Statistics      pass
#Measure      Value
Filename      HISAT2 on data 10 and data 9_ aligned reads _BAM_
File type     Conventional base calls
Encoding       Sanger / Illumina 1.9
Total Sequences 70679196
Sequences flagged as poor quality      0
Sequence length 100
%GC           48

```

```

##FastQC      0.11.8
>>Basic Statistics      pass
#Measure      Value
Filename      HISAT2 on data 8 and data 7_ aligned reads _BAM_
File type     Conventional base calls
Encoding       Sanger / Illumina 1.9
Total Sequences 146274535
Sequences flagged as poor quality      0
Sequence length 100
%GC           47

```

```

##FastQC      0.11.8
>>Basic Statistics      pass
#Measure      Value
Filename      HISAT2 on data 8 and data 7_ aligned reads _BAM_
File type     Conventional base calls
Encoding       Sanger / Illumina 1.9
Total Sequences 146274535
Sequences flagged as poor quality      0
Sequence length 100
%GC           47

```

```

##FastQC      0.11.8
>>Basic Statistics      pass
#Measure      Value
Filename      HISAT2 on data 12 and data 11_ aligned reads _BAM_
File type     Conventional base calls
Encoding       Sanger / Illumina 1.9
Total Sequences 147946732
Sequences flagged as poor quality      0
Sequence length 100
%GC           46

```