

Case	Neuropath Dx	Age	RIN	Braak Staging	CERAD Criteria
138	AD	78	4.0		
156	AD	77	4.0		
178	AD	77	6.9		
190	AD	78	4.0		
196	AD	66	5.0		AD
208	AD	92	5.1		AD
212	AD	90	4.3		
215	AD	73	4.4	V/VI	AD
223	AD	69	4.4		AD
248	AD	81	4.8	V/VI	AD
<b>mean</b>		<b>78.1</b>	<b>4.7</b>		
<b>std dev</b>		<b>8.2</b>	<b>0.9</b>		
<b>ADvsCTL RNAseq p (t-test)</b>		<b>0.18</b>	<b>0.97</b>		

#### RNAseq CTLs

137	CTL	63	5	N/A	N/A
144	CTL	83	4.9	N/A	N/A
147	CTL	53	4.9	N/A	N/A
151	CTL	88	4.7	N/A	N/A
161	CTL	87	4.6	N/A	N/A
164	CTL	70	4	N/A	N/A
191	CTL	71	4	N/A	N/A
150	CTL	53	5.3	N/A	N/A
216	CTL	71		N/A	N/A
<b>mean</b>		<b>71</b>	<b>4.7</b>		
<b>std dev</b>		<b>12.5</b>	<b>0.5</b>		

#### Mito Prep and immunoblot CTLs

137	CTL	63		N/A	N/A
144	CTL	83		N/A	N/A
142	CTL	62		N/A	N/A
159	CTL	45		N/A	N/A
213	CTL	61		N/A	N/A
164	CTL	70		N/A	N/A
191	CTL	71		N/A	N/A

<b>150</b>	CTL	53	N/A	N/A
<b>216</b>	CTL	71	N/A	N/A
<b>228</b>	CTL	64	N/A	N/A
<b>mean</b>		<b>64</b>		
<b>std dev</b>		<b>10</b>		
<b>ADvsCTL Immunoblot p (t-test)</b>		0.008		

```
cd <path to trimmed fastq files (can be gz compressed)>
hisat21 -p 4 --dta-cufflinks -x <path to genome_tran files> -1 x.forward_paired.fq -2
x.reverse_paired.fq -S <path to HISAT2 output> x.sam
cd <path to x.sam> samtools view -bS x.sam > x.bam
samtools sort -T PREFIX -o x.sorted.bam x.bam
cufflinks -o <path to cufflinks output> -G <path to genes.gtf3> genes.gtf --library-
type fr-firststrand -p 4 -u -b <path to genome.fa> genome.fa4 <path to
x.sorted.bam> x.sorted.bam
```

<sup>1</sup> download executable file and genome-tran files from  
<https://ccb.jhu.edu/software/hisat2/index.shtml> for Windows, Linux or Mac OSX.

Be sure executable file is in \$PATH

<sup>2</sup> use latest version of Samtools and be sure file is in \$PATH

<sup>3</sup> reference gene transcript file in gtf format

<sup>4</sup> reference genome file in FASTA (.fa or .fna) format



