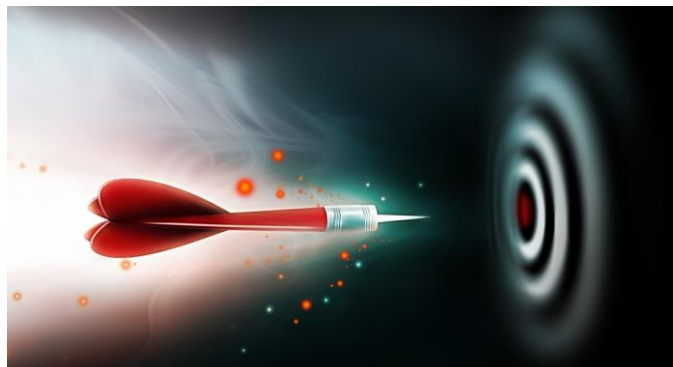


Chromosomal Amplicon QC Report Targeted Bisulfite Sequencing



SHAKHAWAN K. MAWLOOD

Appendices-2-
Of
PhD Thesis

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1. Sequences Regions of Interest ROI Overview

To get DNA sequence around interested CpG site, the assembly of genome reference consortium human Build38 (GRCh38 or hg38) was used in the assembly. The GRCh38 assembly offers an "analysis set" that was created to accommodate next generation sequencing read alignment pipelines. Some common features were used and applied to all amplicon. Small letter is for repeat sequence and capital letter is unique sequence. Dark grey means, regions not covered by target sequencing amplicons and Light grey indicates region of interest. The methylated CpG sites were coloured in red and underlined CG.

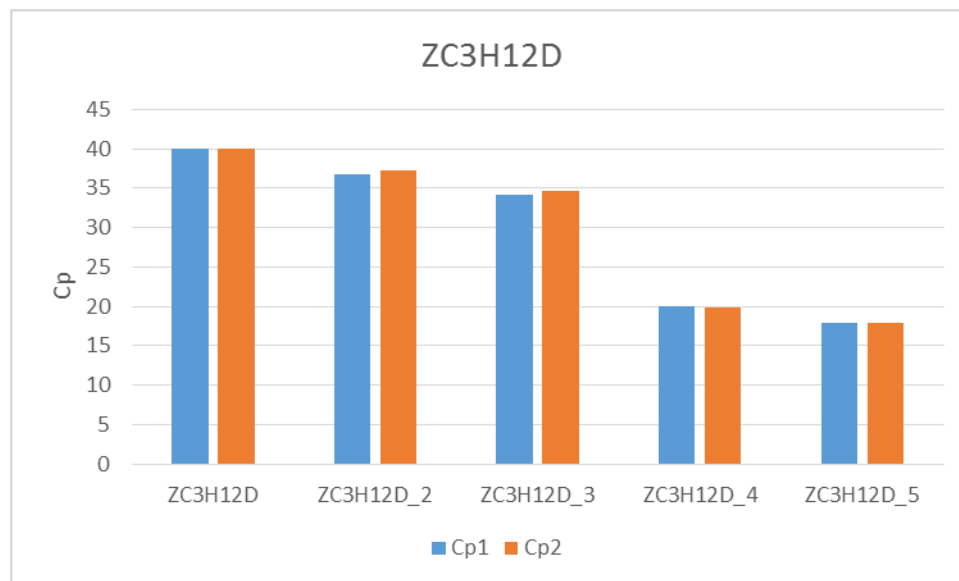
Region of Interest (ROI) ID	Number of Amplicons that passed QC
ZC3H12D	5
BCAS4	2
AHRR	1
NPTX2	2
EDARADD	1
EDARADD_promoter-2	1
TOM1L1	1
TOM1L1-2	2
GRIA2	1
GRIA2_Promoter-1	2
TRIM58	3
KCNQ1DN	4
ITGA2B	1
ASPA	1
PDE4C	1

Total

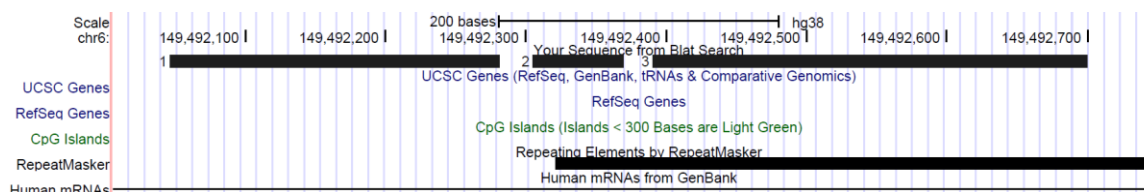
28

1.1. ZC3H12D

1.1.1. QC Data



1.1.2. ROI Genomic Sequence



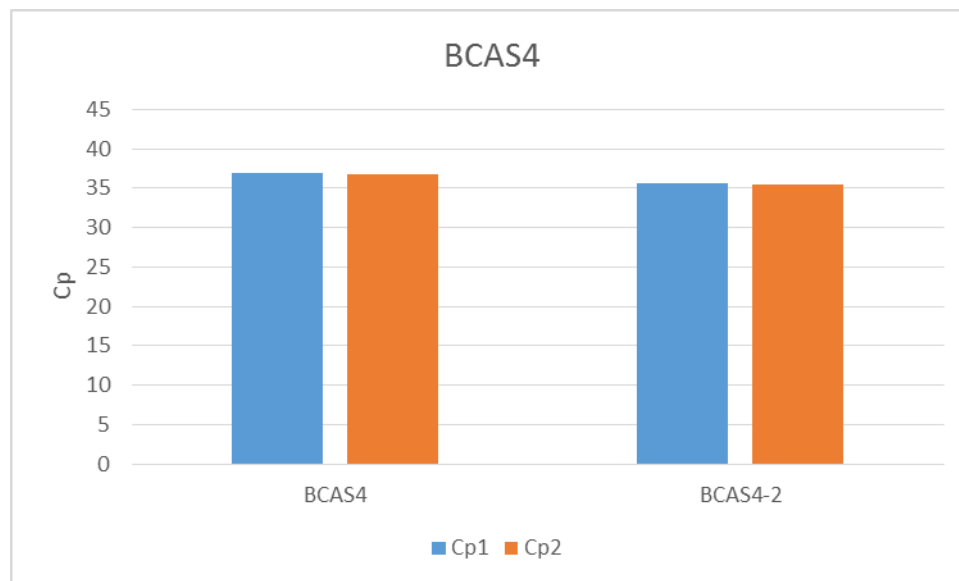
Light Gray= Regions of Interest; **Green**= ROI Covered with Amplicons that passed QC; **CG**= CG of interest

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repeatMasking=lower
```

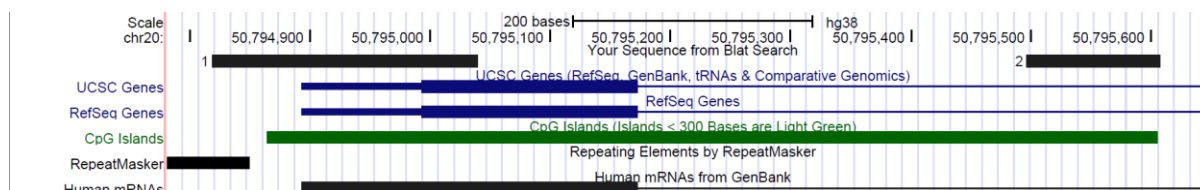
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ATTCCAGTGACCGTTTGGGCCTTCTTTTCCTTCCTAGCAATTTCTTTTAACTTTGCTGTATTCTCAGTTTTCTTC
GAAAAGCAAAGCCTTGTCCTTGCGAACGCTCCCCACGAAGGCTTGCGGGTGGTTAGGC CGCATGTCTTCTGTT
TCACATTCTTATTCTGTACCCGAACGCTGGAACCCCTTCACCACGACCTCAAAACCACCAGGC CGCACTTCG
CGCCCGCCTCACCGGCACCATTGCAGCCAACCTAAGTGGTCATCGACATGGGGTttttctttttctttttttttt
tttttttgagacgggagtcctcgctgtcgccaggctggagtgagtgaggacgacatcgggctcactgcaagctcggc
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ttatgttactcaggctggtctcgaaaggcctggcctcaagcaatcctcccaccttggtctcccaaagtgtctgggat
tataggtgtaagccacgatgtccaaccTTGTtttaagtcacccctgcttatggtagtttgttgtgacgggtcctagg
aaactaatacacCCTTCAAGCCCACAAACACTTTCCCTCAGAGCTCTTAGTTGTGATAACCATTACTCACAGCT
AAGCACATTCTCGCTGTCTAATGAGAAGACTGTG
```

1.2. BCAS4-2

1.2.1. QC Data



1.2.2. ROI Genomic Sequence



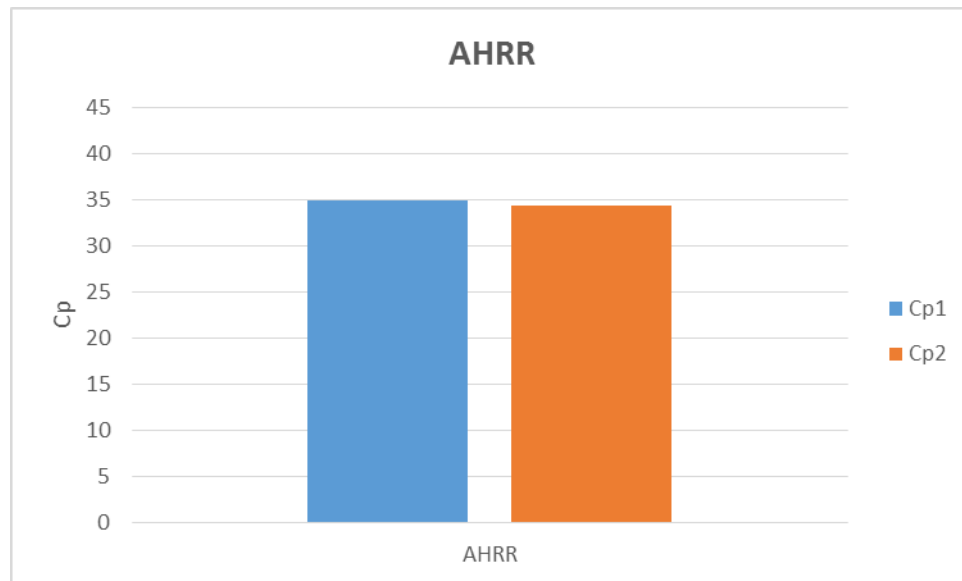
Light Gray= Regions of Interest; **Green**= ROI Covered with Amplicons that passed QC; **CG**= CG of interest

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repeatMasking=lower
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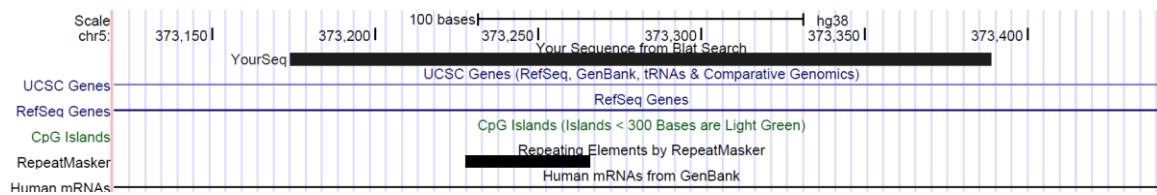
```
GAGGGGTGGCTTGCCCaatagttctcaaatttagctttgggtcaacaatctggttggaaacacctaacaacat
caaaagatcctgatgccaggtcttaaccagagacggtgtggtccaggcttgggaaattctaaaagagctccag
gtgactgccaatctgcaagcgagtttgcaagcactgATGCCAGGTGCTGCGGGGGCGGGCGCAGCGCGCCCGC
TCCCACTGGGTGGCGCTGCCCGCTCGGCCCGGGCTCCTGGAGCTGCGAGCGGGACCGCGGGAGCGCACCTG
CCCCCGCTTCGCCAGGCGGTCCCGGGGCATGCAGCGGACCGGGGGCGGGGCTCCGAGGCCCGGGCGCAACCA
GGCTCCCAAGCAGCCTCCGCCAGCCGCGACCCCGTCGCCCTCCTGATGCTGCTCGTGGAAGCTGATCAGCCGAGC
CCATGCGCAGCGGGGCGCGCGAGCTCGCGCTCTTCCTGACCCCGAGCCTGGGGCGAGGTAGGGGAAGGGGCTG
TGGAGTTGGAGGAGAGGGTTCTCGCGGTTAGGGGTCGGGCCCGGACCCTCGGCTTCCCAGGAGCATCCTCTCG
CTCCCGAGTGGGGGGCCCGGGGATTCCCCCTTCTGAAGGGTGGCTCGGGGGCGCCAAGCAGAGATGTGCAGC
GGGTCTGCTCCTCGCTCCTCGGGCGACACCGGGCCCAGGAGGCCAGGCTCGCTTTCCTCCCCACCAGGGT
CCCCCAGCATCCGCGGGTCTCAGGCGCGCCCTTTGCCAGGCAGGCCCTGGGAGAGGCGGACCCCGGGACCTC
TGCTGCCCGGGCTACCTCCGAGCGGTGCCCGGGCGAGCGGCGCTCAGGCTGCGGCTGTGCGGCGGGCTGCG
CTGCTGCAGCTCGGAGCGAAACACCAAGCCTCTGTCTGCGCTTTCTATTTTAAAGCACCAAGTGAAAGCAGA
TCTAAACGAGACCCTCTACCTTCCGGCTGGAGGCATCTGTGACGCTGTTGTGAAAAAGTTATTTGTCTGAGTT
CACTAGGAGTTATTTACGGTCAGAAATTCAACCCATTCTCTTTTAAACCACAAAAGCAGTACAGGAGTATTTAA
CATAAAGGCTATGCAC
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1.3. AHRR

1.3.1. QC Data



1.3.2. ROI Genomic Sequence



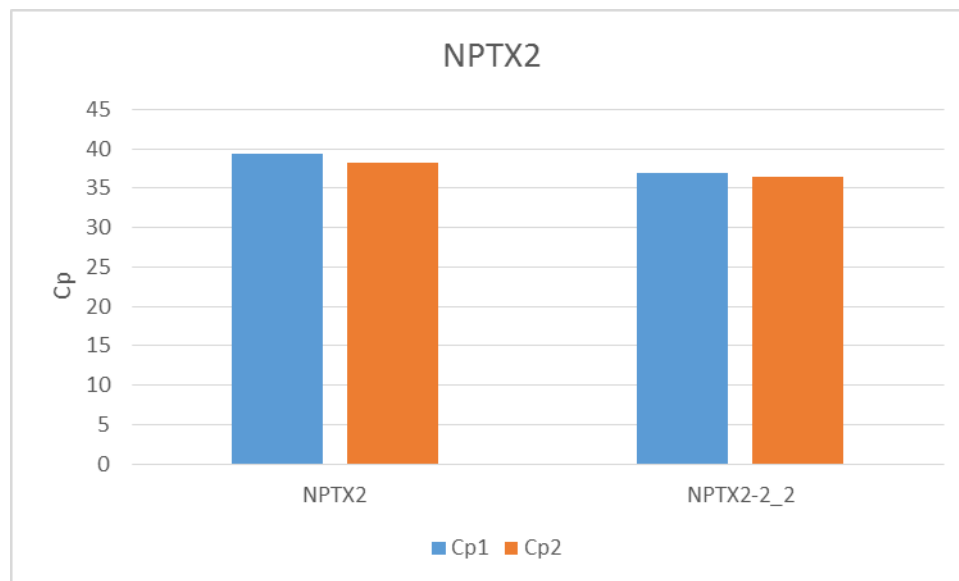
Light Gray= Regions of Interest; **Green**= ROI Covered with Amplicons that passed QC; **CG**= CG of interest

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repeatMasking=lower
```

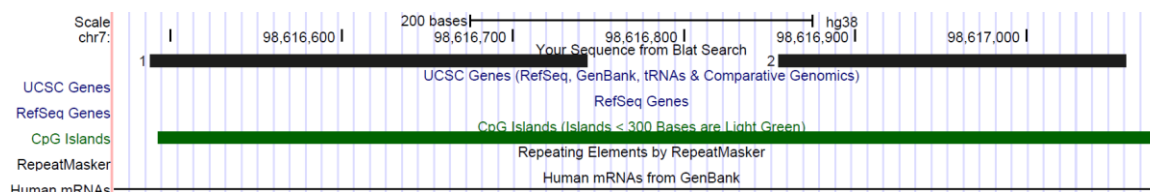
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TTGGCAGAGTGCTGGCAGGACACAGGGGTTGCCAGG CTACAGATC CGGGTTCAGGCCCCAGC CGTGGGGACTGTT
CACCTCTGAGAGGGCAGCCCTGCCC CGCGGGCCCTGGCCCTGCCCTGCACC CGGCTGGGTCTCATCTGACA CGCAG
CCTTCCAGCCTCTCATTGCC CGAGGGGTGGGCCCTGGGAGTGGTCTCTGGCAGGGCCCCCTCTCTGCAGACCCTG CG
GGACCAGCAGGC CGGGCGGTGGCTGGGAGGCAGGGGACAGGTTGGCCCTCTG CGGTCTTGGAGGCACAGAGCTCCT
CCCGCCCTGGGCCTGTGGCCCCCTC
```

1.4. NPTX2

1.4.1. QC Data



1.4.2. ROI Genomic Sequence



Light Gray= Regions of Interest; **Green**= ROI Covered with Amplicons that passed QC; **CG**= CG of interest

>hg38_dna range=chr7:98616285-98617284 5'pad=0 3'pad=0 strand=+

repeatMasking=lower

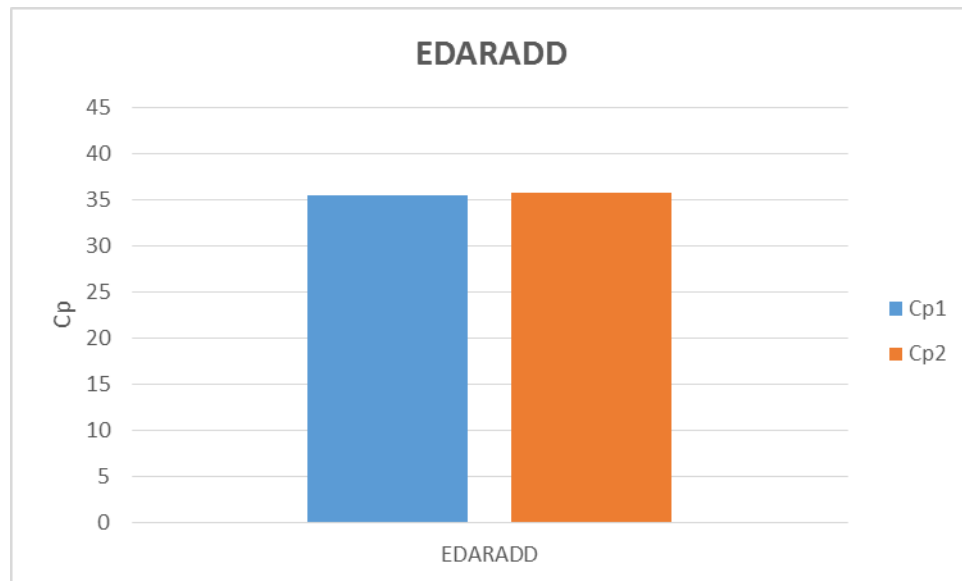
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TTCGAGGAAGTGGTGACACTGCGGGGCCCTCCTGGTTACAAGGACCGGGCACTGTTGGACCACGTGGCTCCATCAT
GATGACTCCAGTTAGATGTCACCCCGCCCCCTGAGCTCAGGTCTTGCTGAATAAGGTCACCGCCAGGGGGCAGTCG
SATGAACACCGCGCGCGAGGGCTCTGCGAGTGGCCTCGTGACTTTGTCCCTAACTCCGGGTGTCCCTCCTTCCCA
TCAGCGTCCGGGCGCCTGGTCCTGGTCCCGGTCCCCGAGGCCCCCGGGATTCTTCCCGAGCGTTTTCCGAGTTGGCG
CGGGGGGGTGGAGGCGGGGCCATGGAGCGCGCTCCCGGGGACCGTTGCATCCGGAGGCGGCCGTCGTGCGGCTCCT
TCCCGCCTCGGAGAGTGAGGTGGCCGGGCCTTGACCGAGAAGGCCCACGCCTGCCGCGGGGGTGGCTCGCGATGGCA
GTCGGGGTTCGAGTCCCGCCTGGGGGGCTGCTCCTGCTGGAGAAACGCCTCCCTGAGGGCGCGCGCAAACGCGC
AGCGAGGCCCGGTGCGCGCGCCAGAAGCCACCCTGAGAAAGGGGCACCGGGACACCGAGGGGTTCCTACTTTCTCC
TCAGCCTGTGACCGCCCGCGTCTCCGGGTGGGTTCGAGGGGCGCCTGGGCACGGCCAGCCGAGGCTCTCGAGAGCC
CCAGTGTCGTTTTCCACCTCAGGCCTCCTTTCTGAGGCAGAGCCCGGGACCTCGCGCTCTCGCCTCAGGCTCCG
GCCCACCGCTCCCGCCCGCGCCAGGCGCGCAACCGGAAAGCGCcccCGcccCGcccCGctcCGcccACTGCGTGA
CGCGCACCCCGGCCGAGCCAATCAGAGCTCGTGGCGCGCGCCCCACACCGCGCGCCCCCTCCGCCCCTCAGCTTAAG
AAAGGGCGCGCGGACCCCGGCAGGCC

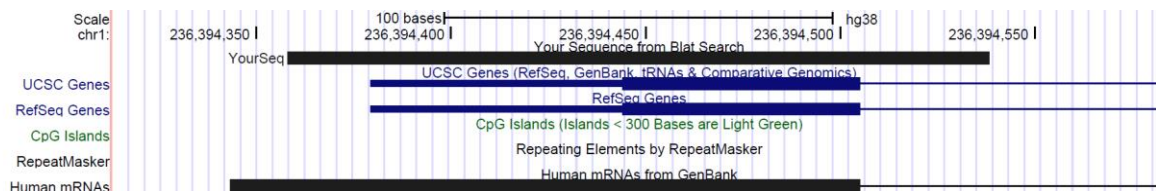
```


1.5. EDARADD

1.5.1. QC Data



1.5.2. ROI Genomic Sequence



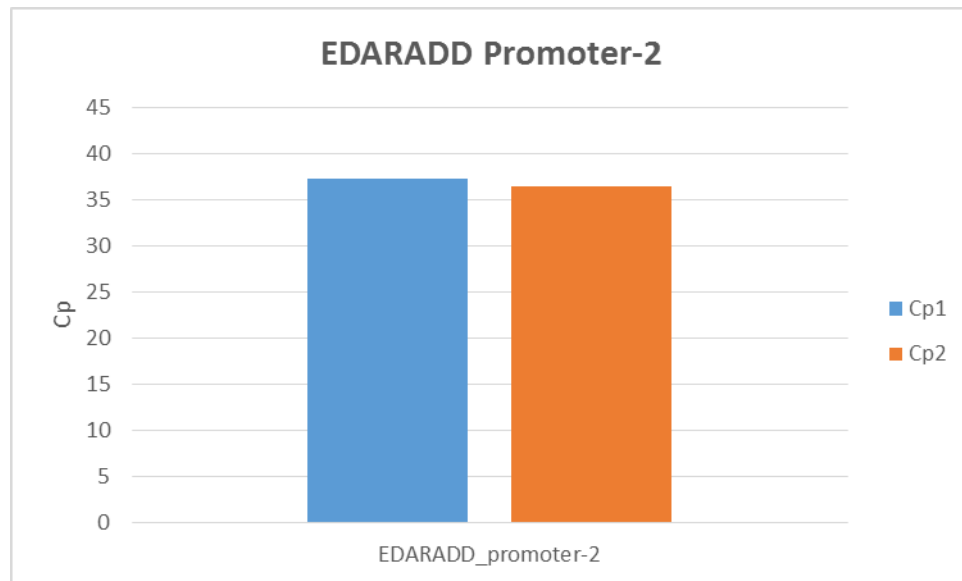
Light Gray= Regions of Interest; **Green**= ROI Covered with Amplicons that passed QC; **CG**= CG of interest

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repeatMasking=lower
```

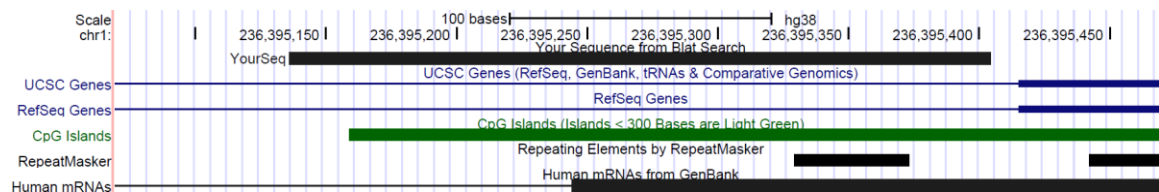
```
ATTCCATCTCCATGAGAAGTACAGAAAGAACCAAAACCAACCTCCAAATTGATTCTAAGATAAAATACCCCTTA
AAAAAAATTTCCCTTCCTATCCGAAGGCAGACCAAGAGGAAGTTTATCCTCCCACCTACAAATTTCCCAGAGAGC
TTTCATCTAGAAGGTTTGACTCTGGCCAGACAACCAGCGAGCATCTTCTCGCAATCTGTTGCTTCTTCCATGGCA
AACTCCAGAGAATTAAGAAGCCAACTCAACATCGCCATGGGCCTCAGGAGGACTAAACAGATGGGGAGAGGCAC
TAAAGCTCCTGGTCACCAAGAGGGTATGTAGGCATTTGCTGTCTTCTGGATTCTTCAGAGCTGAGTTTTTAGCC
AGAGGTTGCTTATTTACGATAATTCTTGGATATATTATACACTAAA
```

1.6. EDARADD Promoter-2

1.6.1. QC Data



1.6.2. ROI Genomic Sequence



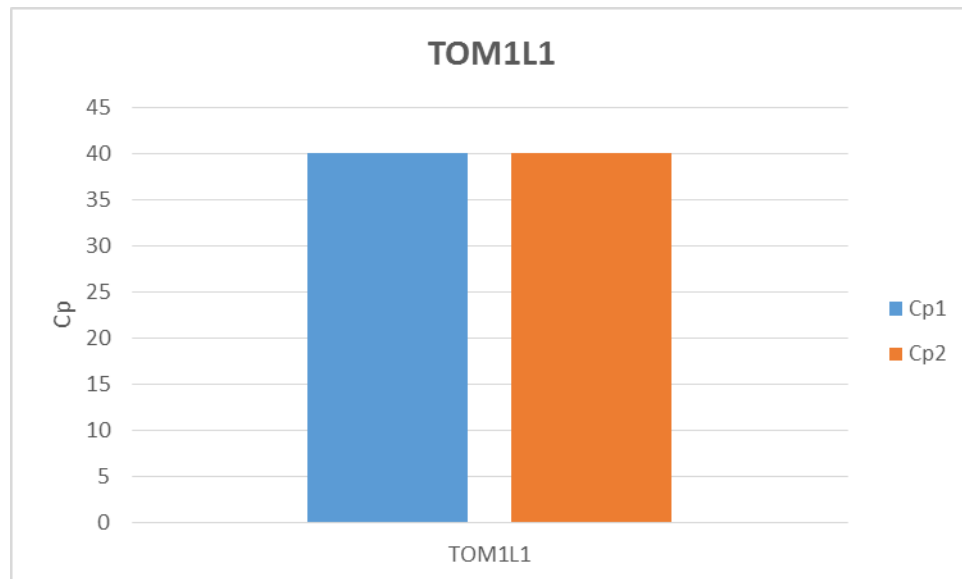
Light Gray= Regions of Interest; **Green**= ROI Covered with Amplicons that passed QC; **CG**= CG of interest

```
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repeatMasking=lower
```

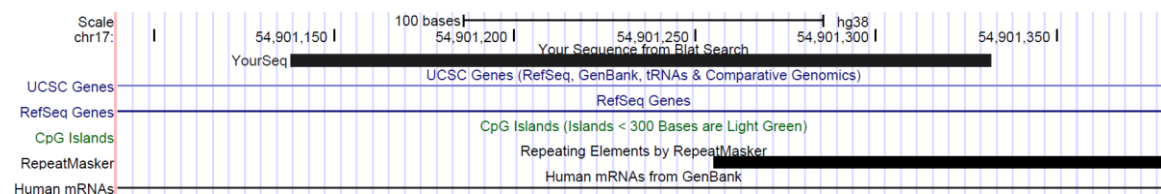
```
CCTGGAGGTCATGTAGTAATAATGCCAAAGAAAAATCAAAATAGAAAGTACCAGCGTGTGCCATCATGCAGCGG
CAGAGCCTGCTTAAAGATCAGGAAATTTGTCTAAATATCAGATCGCCGGCGGGCATCTCAGCCCAGGCCTGTGTA
AGGGGAGTTCTGGTGTCTCAGCTGAGGCGGTGAGTAGGGAGCCAGGAAAGCGACCGGACTGCAGCCGTTTCTT
AAGGCCAGTCCTTCGCTCGCAGTCTGTCCGGGGCGCAGTGGTGTGAGCCCCCGCTAGGACCCCGCCAGGGGGA
CGTGGGTACCGGGCAGGACCGCGCTCTGGGGCGCTGGGGAGCCCGGGACACTCGGGGCCCGCCTTGCGTCCCA
GCCCCGGGTCCCGCACCCCGGCTCCCGCCCCCGCCCTCTGGAGGGAGGTACCGAGGGAAGCGCAGCGAAAGGGGC
TTTGCTAATTGCCAAAGCAGGAAGTGAGCTCGTggaagaagCGaaggaggagaagaagaaggaggaggaggaggCG
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CCAAGGTCCTCCCGCGCCCCCGGAGGCCTGCCAGCCCCGCTCGGACGCTCGTTTGCCCCCTAACC CGCGCCATGGC
TTCACCGGACGACCCTCTGCGCGCAGGTAAAGGGACACAGCGCCGCGCCGCTCCTGGAGCGAGCACCGCGGGGC
GGGAGCTCGGGAGGCGCTCGCAGCAGCCGAGGGCTATCGAGGCGGGCCTCGGCGACCCCGAGGGAGGCCCGG
GAACCACCCCGACCCAGGCGCCAGACC CGAGT CGACCGGGCTCCAGTCCAGCCC CGCGAGCGGCTGCTGAC
CGCCCCCTCCCGGCTCGCCAGGGCCCCCTGCCC CGGTCAGCCACCGCGCGCCTTCCCCCTGCCATGCGCGAGCC
CCCGTGGCTTTTGTCTGGAATCGGGATGCCAGGTTGAGACACGTCCTGCAAACCTCTGGCAGAAATGGGCGCAA
GGGGGTGGATTTTCTTTTTCGCTCCCGGGCTTTTCTTTCTCCCCGCTCACATGCCTTCTCATTACTCCTCTTCC
TCTCTCCATTGCACTTTGATGAAATGGTTTGTCTGTCTAAACATTGGCCCTCGGAGCTATTTTCATCAGATAGT
ATCCGCAGAATCGAGAGGCGGATCCACCTGTGGGATCCCATCTGTGATTAGAATGGCCTCTAGTTCTGTCTTTA
TT
```

1.7. TOM1L1

1.7.1. QC Data



1.7.2. ROI Genomic Sequence



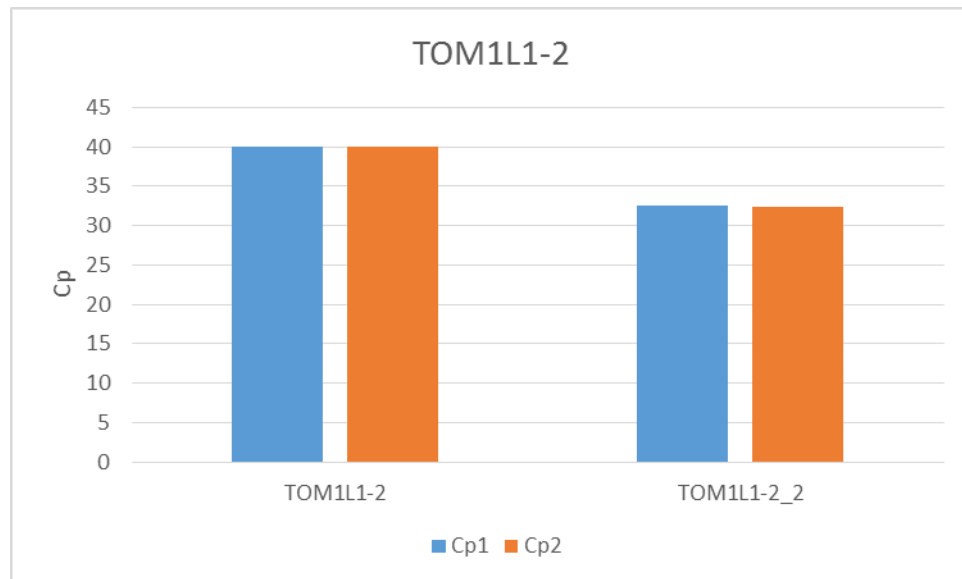
Light Gray= Regions of Interest; **Green**= ROI Covered with Amplicons that passed QC; **CG**= CG of interest

```
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repeatMasking=lower
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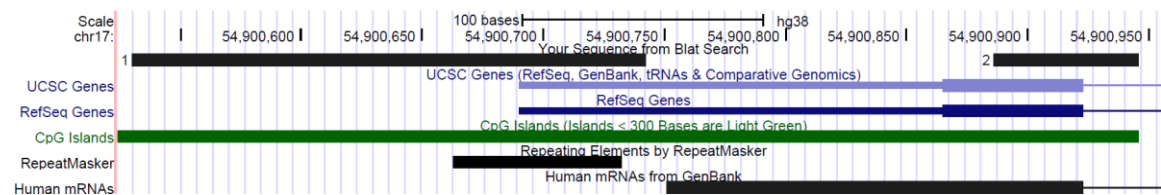
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TTTCGTCGTTTTCCTTCTTGGCCAACCTCACTGTAGAACCTCAGTCCTCAAAAAATGTACCTTCCTTTCGATGCCGCC
TGGGGAGTGGAACCAACAGGTGAACCGCGGGAGTCAGGCATGGAGTGTGGGGCTCCACGAGGAGACACCAGA
AACTTCTCGGTAGGGGAAGttattcctaaaggcacattctccagggcacggtattgttatgcccgttttacagat
cagaagaggaggctctgggagactaagtgatgtggccttactgtgaggggcaggtctccccaaccagttttctc
tagtgccaagCTTATACAACCTGGATTACTTTTCTGGGTAAACAAA
```

1.8. TOM1L1-2

1.8.1. QC Data



1.8.2. ROI Genomic Sequence



Light Gray= Regions of Interest; **Green**= ROI Covered with Amplicons that passed QC; **CG**= CG of interest

```
>hg38_dna range=chr17:54900306-54901146 5'pad=0 3'pad=0 strand=+
repeatMasking=lower
```

```
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ttggtctacccagggcagccaaagaggcgagagaagaatgacaaggtgcccagcaagcggcaggatcaaagcct
gggtctctataattcccaggcTGGAGATTCTGGGCTGCCTGCTCCTCTGCACGGGGCGAAAAAGCCACCTGGGATC
CGAGCGGGCGGCCGCCACTCTCGCAGGCTCCATACACCGCCACTACCCTGTACCACCTGCAGCCGCGCAG
CGCAGCCTCCTCGCGGGTCCCGCAGGGCGCGCTGCAGGTGGCTGGGCGTCCCGAAGCcccgccctcggttcctt
gcccgggcccagctcctcaagctcggtgcccgggcccggcagggcagggcAGAAAGCACGCGCTCTGCCAGAG
CCCGGAAGCGCTCGGGCGAAGAGGAGGAGCAAGGTACCGAGCGGGTGGAGTGGGAGCCGAGAGCGGTGGA
GGCGGATTTCTGGGCCCGGCCCTCTGGCGCTACCATTGGCTTTGGCAAGAGTCACCGGATCCCTACCGCACCT
CGGTGGGCCACCTCATAGGTAAGGAGGCGCGGGGAGAGACCGCCAGGCAGGCAGGGGACCGTGGGATCCTTTCTT
GCTTGATCCATTCTCGGCCTGCAGAGGACGGAGTTAGTCCAACCTTGAAAAAATTATTCCCCCTCCCCCGCAACTT
TCCCAAGGCACCCGCATTCCACCCGCCCCCTTTTCGTCGTTTCTTCTTGGCCAACTCACTGTAGAACCCTCAGTC
CTCAAAAATGTACCTT
```

1.9.1. QC Data



1.10.1. QC Data

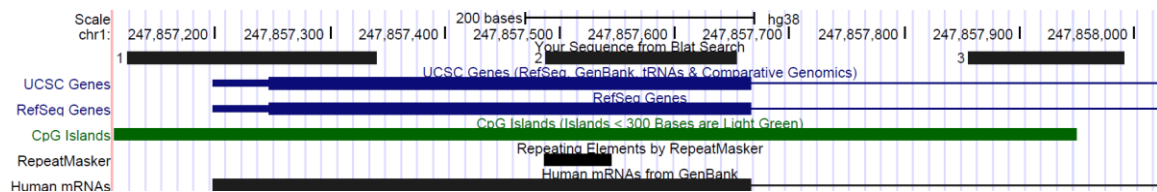


1.11. TRIM58

1.11.1. QC Data



1.11.2. ROI Genomic Sequence



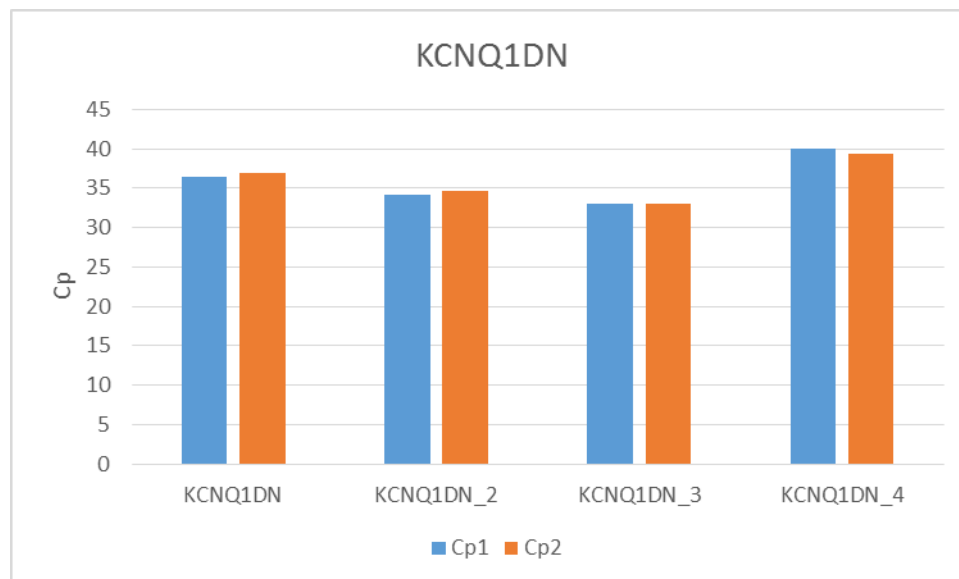
Light Gray= Regions of Interest; **Green**= ROI Covered with Amplicons that passed QC; **CG**= CG of interest

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repeatMasking=lower
```

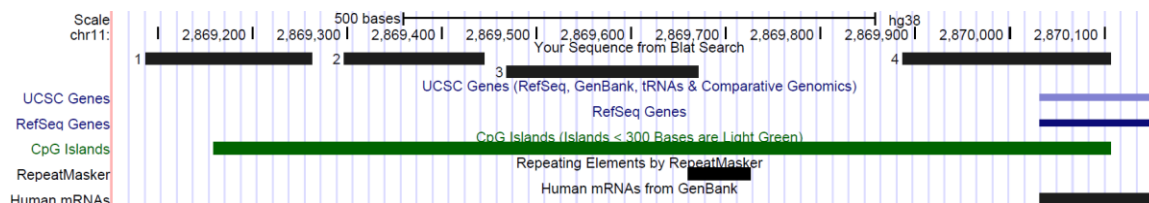
```
agtgagccgagatcgcgccaccgcactccagcctgggcgacagagcgagactccctctcaaaaaacaaaaacaa
aaacaaacaaaCAAAGATGGAAGGAAGGAGGGAATTTAGCAATTCTCCAGATCTACTGCCAGTGAAAAATAGCATA
TGAGGAGGGATTCCAGTTAGAAATGCCAGTTTCTGGGTGTGTGTGTGACGGGGGCGGGGAACCACAACGTTAA
TTTTATCCCCGACATAGGGAGCGCCTGAGTGGTGGCTTTTCACCGGGTGTGGCTCGTCTGAGCTCTTGAACTGAA
GCCAGCGACACCACCGTCTGGCGCCTGCTTTCTGGGGCGTGGGCTCCTCCCCCTGTGCAGACCGCGAGGGGAG
ACGGTGCCGGGCGCGGGAGCGCAGCCCTCCGGGAGCGGGTCATGGCCTGGGCGCCCGCGGGAGCGGCTGCG
CGAGGATGCGCGGTGCCCGGTGTGCCTGGATTTCCTGCAGGAGCGGTTCAGCGTGGACTGCGGCCACAGCTTCTG
CCTCAGGTGCATCTCCGAGTTCTGCGAGAAGTCGACCGCGCGCAGGGCGGCGTCTACCGCCTGTCCGCAGTGCCG
GGGCCCCCTTCCGGCCCTCGGGCTTTTCCCCCAACCGGCAGCTGGCGGGCCTGGTGGAGAGCGTGCGCGGCTGGG
GTTgggCGCGgggcccCGgggCGCGgCGATGCGCGCGCACGCGCGAGGACCTGAGCGCTTCTGCGAGGAGGACGA
GGCGGCGCTGTGCTGGGTGTGCGACCGCGGCCCGAGCACAGGACGCACCGACCGCGCGCTGCAGGAGGCCGC
CGGCAGCTACCAGGTGAggCGccccCGgCGggggctgCGggCGcTGCGGTGACCGGGAAGCGGGCGACAGTCCG
GAGCGGAGCGCGCGAGGCCACCGTCTCCTGAGCGGCTCCACCGGCCGCTCCCCCACCGCGCGCGTCCCCCCC
GCCCCCGCGGCTCACTCAGTGTGGGTCTCTTTGCCTTGGCTGTGGTAACCCCCTTTGCGACACACACCCATTATT
TTACACCTCTCGCCCTCCCCCAAGCACTCTCCTGTCTTGAAGTCTGGCTGGGCTGGTTCTCCCGATGCGGAT
AGTCTGGTCCCTCAGCTGGGCTCTGGTCGGGAGGGCTGTGTGGTCCAGTTCATTCTTGGTAACAATTGTACGTCT
ATATCGTAAACTTGCCATAATAATTCTCATTTGTGCAATGCTTTGCTTTTGCACAGTGTTTACATTAAATGAGTG
TTGTCAGCAAAGCAACCCTCGGGTTTGGGCGTTGTTAAGAAGAGTGT
```

1.12. KCNQ1DN

1.12.1. QC Data



1.12.2. ROI Genomic Sequence



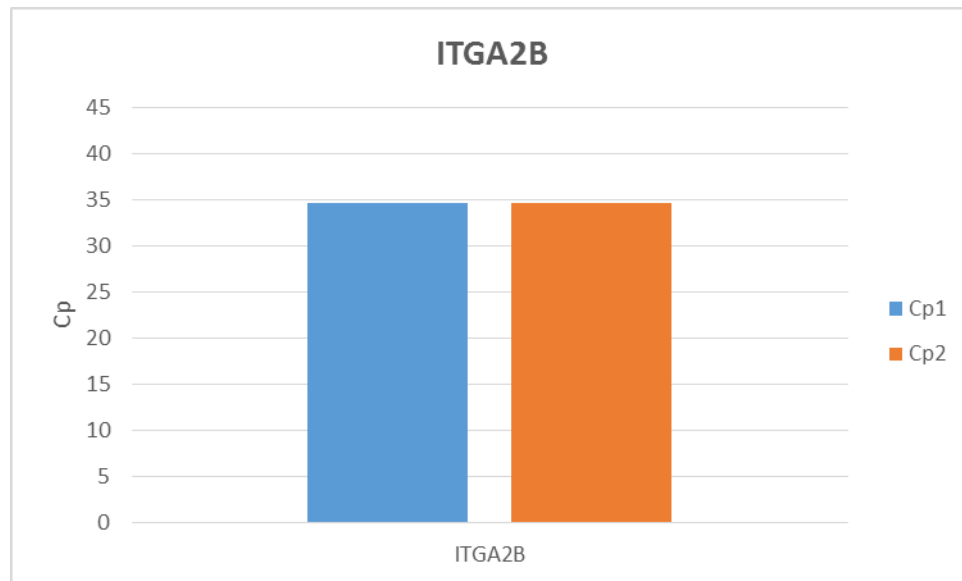
Light Gray= Regions of Interest; Green= ROI Covered with Amplicons that passed QC; CG= CG of interest

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repeatMasking=lower
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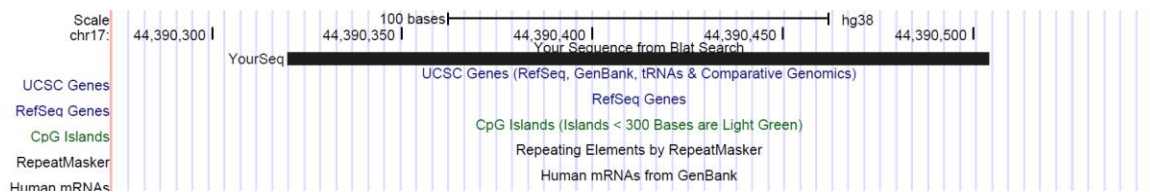
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CGCCCCACAGAGCCACACCGTGACCCTCGGAGGCACCCCTGAAGCATAACTGGGCCAACCGTGCCTGCAGGAAGC
CCCTTTGTTCTCCTTGGGGCCCCAGAGCACCTGAGTGAAAGAGTCTGAGACCGGAGGGGCAGCCAGAGGGGGCC
CTGGAGGGAGGCGGAGGGACCCCTCCCTGGGCCAGCCAGGCCAGCGTCTGCCAGAGTCTGTTGCTAAGTCCCT
CTTCTTGCAGCCTGGGGATCCCAGAGGACCCTGGCCCCAGTCCATCAGCTGGGCTGGGTCTTTAATATTTAAAGAG
CTCTCCCGGACATTTCAAGAACTCCCCTGACACGATTTTCTGTGATGCTGGGCTGTCTGGACATCTGTCTTCTAT
ACCTAATAAAGTCCCGGACGAGCAGAATGAACTCCTCGGCATCGCTTTGAATCCGGGCTCACATATGGTTGCTAAT
TAGCTGGCTATCTCTTGGAGTTAAATGATTTTTTTTCTCGCCCCGTTCCATCCATAATAGAAGGAAACAGAGTCT
GTGATTGTTCCCTGTTGGGGACATTTCTGCGCCTGAATGAGCGGGGGCTGCTGTGTGACGCGGATTGCCATAT
GGTTGCGCGAGCCAGGAAGAATGGGCCCCCTGTGTGTGGACCGGAGCCAGCGCGCGGGCGTGCACGCGG
CGAGAGCTGGGTGCCCTGACGGCGCAGGACGAGCGGGCGCAGGACGAGCGAGCGAGCGGGCGCGGGCGCACGCTCG
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CGTggacaggCGGCGGgagggcagcaggacCGatgcacCGaCGgaCGcacCGaCGgaCGCGCGgacagatgCGCC
GACCGCAGGCTCTCCCGCGTCCCGGGGCGCTCGTGCCCGTGAGGCAGCGCGAGCAGCGGCGGGGCAGGCTCTGCG
GCTGCAGCAGCCCCATTGTGAGGCAGGCGAGACAATGGGCGGCCAGGAGGCACCTGCTCGCTGAAAGGCCCA
TAAATCGCGCGCGCTCCAGCTGCCTTCCCGCCCCCTCCCGCGGACCCTAGCGGGAAGCGCGCGCGCGCG
GAGGGGGAGGCTCGGTCCGACAGTGGGGCAGGGCGCCTGGGGCCACCGCGCGCGCTCCCTCCCGCTGGGCGCA
GCTGCCCGCAGCGCCCGACGGGAGCTGCGCCAGCCTCCCTCTGGAGTGGCGCTCCAGGCTGCTGCCCGCGCG
GTGGCCAAGGCCCCAGCACCACCGTCCCTCCTGCAGGGCATCCAGCACCTACCCTTCCACTGGGCGGCTCCTGGT
TCTGGTCCCGGCTGGCTCACTCAGGCTGCCTTTGGACCAGATTCTTGAACCTTTTCCACCAAGGATGTTGCTGCTG
TTTGTAGCGTCGGATCCTGGAATATCGCTGTGTTGGGGAGCAGCAGGCTC
```


1.13. ITGA2B

1.13.1. QC Data



1.13.2. ROI Genomic Sequence



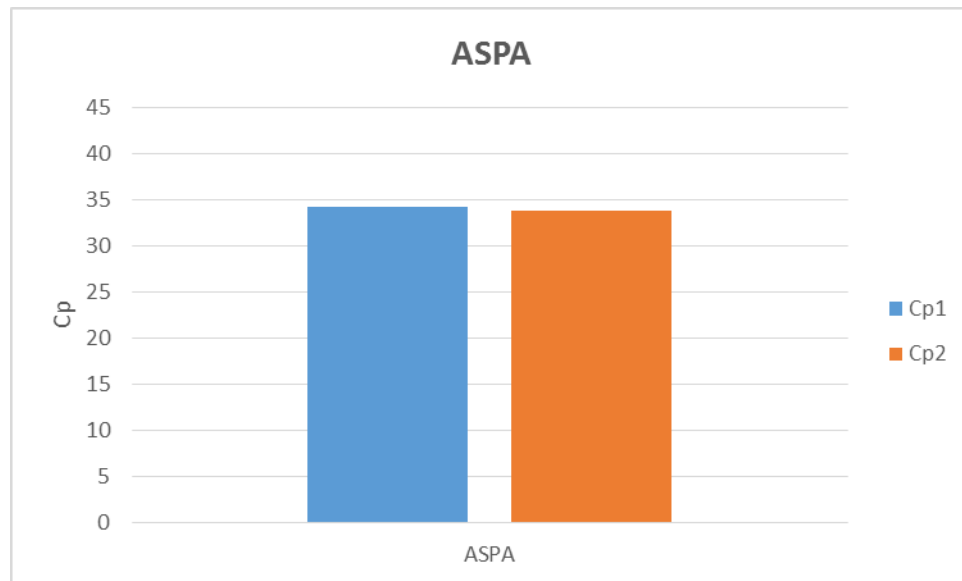
Light Gray= Regions of Interest; Green= ROI Covered with Amplicons that passed QC; CG= CG of interest

```
>hg38_dna range=chr17:44390160-44390559 5'pad=100 3'pad=100 strand=+
repeatMasking=lower
```

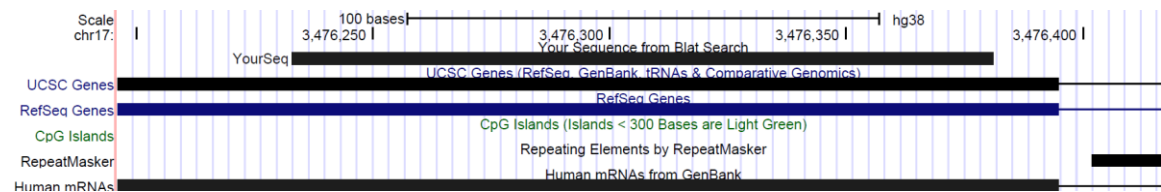
```
CTAGGTGGCAAGGAGATTGGGGATAAAGTGGAGTTATTCCAGGGAATTTTGACTCACAGTTTCTGAGATTATGCA
TTAGCTGTTTCAGTTGAAGGTAGGCCCTCAATCCTTTTTGGGTGATGGAGCTCTTTAACCATTAAGACTTGATTCT
GGTTGGGGGCTTTGCCTAGGGGAGCCTTCCCTGACTCCTCAGGCTGGCCGCGTGGGCTAACACACGTAGGCACAG
CATTGAGCACACTGTTTACTCTTGGTCCGTTTACAGGATTGTGTAAATGAGTCCCTTGGGAGCAAGGCTCCTTGC
TACAGCCCTAGAGACTACCCAAGAGTCCAATGTGTAGTACGTGTACGTTGCTGAAAGACTGGATGGAAACACACACT
AAGGATGGAAGATGCAAACATAGGG
```

1.14. ASPA

1.14.1. QC Data



1.14.2. ROI Genomic Sequence



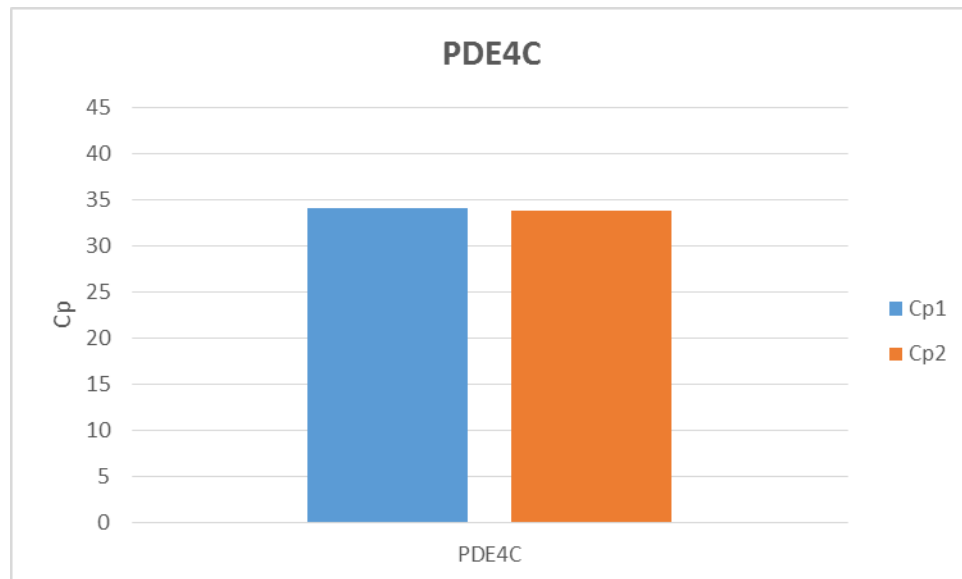
Light Gray= Regions of Interest; **Green**= ROI Covered with Amplicons that passed QC; **CG**= CG of interest

>hg38_dna range=chr17:3476073-3476472 5'pad=100 3'pad=100 strand=+
repeatMasking=lower

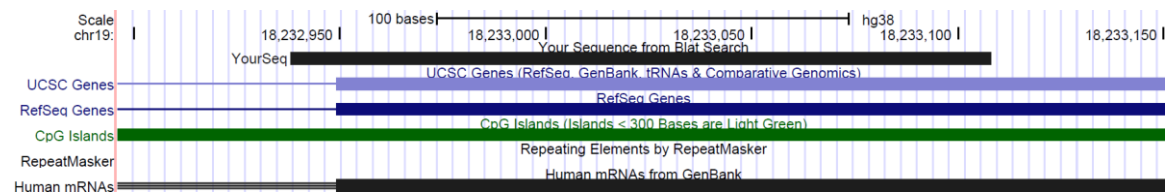
```
TACATTTCTAACCTTTCTTAAGAAAATCGAATTTCTTTGATCTCTTCTGAATTGCAGAAATCAGATAAAAA
CTACTTGGTGAAATGACTTCTTGTCACATTGCTGAAGAACATATACAAAAGGTTGCTATCTTTGGAGGAACCCAT
GGGAATGAGCTAACCGGAGTATTTCTGGTTAAGCATTGGCTAGAGAATGCGCTGAGATTTCAGAGAACAGGGCTG
GAGGTAAAACCATTTATTACTAACCCAGAGCAGTGAAGAAGTGTACCAGATATATTGACTGTGACCTGAATCGC
ATTTTTGACCTTGAAAATCTTGGGTAAGACTATGCTTTGTATTGTATATGTATGTATGTTGTGTGAAAAGTGGA
GGTGTGTGAAAGAGAACACATATAT
```

1.15. PDE4C

1.15.1. QC Data



1.15.2. ROI Genomic Sequence



Light Gray= Regions of Interest; **Green**= ROI Covered with Amplicons that passed QC; **CG**= CG of interest

```
>hg38_dna range=chr19:18232892-18233291 5'pad=100 3'pad=100 strand=+
repeatMasking=lower
```

```
GCCAGGCCCGCGCGCCCCCTCCCCGCGCTGCAGGAGGCCCTGCCCGGCCACCTACCGCCTGCAGGAGGAAAC
GGGCCAGGAGAGCCGCGACTTCTCTGAGCTCCGGCCGCGGGCTCAGGTCCCTCTCGCGGCAGCCCCGCGGACTTGTC
CGGATCCGAATAGAAGCGCTGTTGGATGCGGATGGGGCGCCGGGGTTGCGGCCACAGGTGCTTCGGGGCTCTGGT
CATGCTGTGGCGGCCGCGAGAGCGACTCAACCTGCTGCAAGCCTCTGCCCTTCGCCGACCCCCAGGTTCTCCAT
GCGCCAGAGAAAGGGTCTGGGATAGCAGGGAGCAGGACTCGTCCCCGTGAGCGGGCGCCGAGGAGCGTCTGCTC
CCGGGTCCGGCCAGGGCCGGGAGT
```