

Name :  
Sex/Age :  
Date Received :  
Indication :

Whole Exome Sequencing on the Illumina Novaseq 6000 NGS Platform

Clinical Indication:

\*

Variant Interpretation & Clinical correlation:

Signature 1

Signature 2

Signature 3

Nucleome Address

Name :  
Sex/Age :  
Date Received :  
Indication :

Variant Evidence			Gene Impact													
Chromosome: Position: NC_000017.11(GRCh38 Chr17):			RefSeq Gnese 110, NCBI													
<table border="1"> <thead> <tr> <th>Allele</th> <th>DP</th> <th>%</th> </tr> </thead> <tbody> <tr><td> </td><td> </td><td> </td></tr> <tr><td> </td><td> </td><td> </td></tr> <tr><td> </td><td> </td><td> </td></tr> </tbody> </table>			Allele	DP	%										Gene:	Transcript:
Allele	DP	%														
			Effect:	Protein:												
			Exon:	Coding:												
Genotype:                      phred quality score:																

Based on the evidence, this variant is classified as likely to be variant

OMIM Phenotype:

Case Specific Recommendations:

Recommendations

Name :  
Sex/Age :  
Date Received :  
Indication :

Methodology:

Limitations/Disclaimer:

Variant Classification as per ACMG guidelines:


References:

Appendix 1: Sample Data and Statistics

Signature 1

Signature 2

Signature 3

Nucleome Address

Name :  
Sex/Age :  
Date Received :  
Indication :

Title	Data

#### Appendix 2: Coverage Summary

Mean Depth	Percentage target base pairs covered

#### Appendix 3: Coverage of Analyzed Genes (Percentage of coding region covered)

Gene	Region Covered	Gene	Region Covered	Gene	Region Covered