MedGenome Labs Ltd.
#258/A, Bommasandra, Hosur Road, Bangalore – 560 099, India.
Tel : +91 (0)80 67154932 / 933

MEDGENOME

DNA TEST REPORT - MEDGENOME LABORATORIES

Full Name / Ref No:		Order ID/Sample ID:	
Date of Birth / Age:		Gender:	
Parental Sample ID:		Sample Type:	
Referring Clinician:		Date of Sample Collection:	
		Date of Sample Receipt:	
		Date of Order:	
		Date of Report:	
Test Requested:	***HBB* Gene Analysis [Trio] [MGM1872]**		

CLINICAL DIAGNOSIS / SYMPTOMS / HISTORY

Mr. Vasu Dadoo and his wife are presented with Beta Thalassemia Minor. Mr. Vasu Dadoo is being evaluated for the pathogenic variations in the *HBB* gene.

RESULTS

CARRIER OF PATHOGENIC VARIANT CAUSATIVE OF THE REPORTED PHENOTYPE

Gene (Transcript) #	Location	Variant	Zygosity	Disease (OMIM)	Inheritance	Classification
***HBB* (-)** (ENST00000335295.4)	Intron 1	**c.92+5G>C (Splice variant)**	Heterozygous	Beta Thalassemia	Autosomal recessive	Pathogenic

[$]Genetic test results are reported based on the recommendations of American College of Medical Genetics [1].

ADDITIONAL FINDINGS: NO VARIANT(S) OF UNCERTAIN SIGNIFICANCE (VUS) DETECTED

No other variant that warrants to be reported was detected. Variations with high minor allele frequencies which are likely to be benign will be given upon request.

The *HBB* gene is 100% covered in this assay (include the promoter, exon, intron, upstream & downstream regions). 619 bp deletion beta 0 type deletion in the *HBB* gene is also covered in this assay. However, the deletion/duplication analysis of *HBB* gene cannot be rule out by this method.

VARIANT INTERPRETATION AND CLINICAL CORRELATION

NGS

Variant description: A heterozygous 5' splice variation in Intron 1 of the ***HBB*** gene **(chr11:g.5248155 C>G; Depth: 4283x)** that affects the position 5 nucleotides downstream of donor splice site of exon 1 **(c.92+5G>C; ENST00000335295.4)** was detected in this subject. This splice variant, commonly known as [IVS1-5G>C] results in aberrant processing of precursor RNA transcripts and leads to β0 phenotype (23, 24). This variation has been reported in homozygous state or compound heterozygous state with other HBB variants in β-Thalassemia+ patients (23). The variant has a minor allele frequency of 0.1% and 0.07% in the 1000 genomes and ExAC databases respectively. The reference base is conserved across species.

OMIM phenotype: Autosomal recessive Beta Thalassemia (OMIM#613985) is caused by homozygous or compound heterozygous variations in the *HBB* gene (OMIM+141900).

Based on the above evidences[$], ***the variation detected in this subject is classified as a heterozygous pathogenic variation and this variation has to be carefully correlated with the clinical symptoms observed.***

TEST FOR 619bp Del

The 619 bp deletion Beta 0 type was not detected in this subject.

RECOMMENDATIONS

Genetic counselling is advised.

If results obtained do not match the clinical findings, additional testing should be considered as per referring clinician's recommendations.

LIMITATIONS

- Genetic testing is an important part of the diagnostic process. However, genetic tests may not always give a definitive answer. In some cases, testing may not identify a genetic variant even though one exists. This may be due to limitations in current medical knowledge or testing technology. Accurate interpretation of test results may require knowing the true biological relationships in a family. Failing to accurately state the biological relationships in {my/my child's} family may result in incorrect interpretation of results, incorrect diagnoses, and/or inconclusive test results.
- Test results are interpreted in the context of clinical findings, family history and other laboratory data. Only variations in genes potentially related to the proband's medical condition are reported. Rare polymorphisms may lead to false negative or positive results. Misinterpretation of results may occur if the information provided is inaccurate or incomplete.
- Specific events like copy number variations, translocations, repeat expansions and chromosomal rearrangements may not be reliably detected with targeted sequencing. Variants in untranslated region, promoters and intronic variants are not assessed using this method.
- Genetic testing is highly accurate. Rarely, inaccurate results may occur for various reasons. These reasons include, but are not limited to: mislabeled samples, inaccurate reporting of clinical/medical information, rare technical errors or unusual circumstances such as bone marrow transplantation, blood transfusion; or the presence of change(s) in such a small percentage of cells that may not be detectable by the test (mosaicism).

DISCLAIMER

- Interpretation of variants in this report is performed to the best knowledge of the laboratory based on the information available at the time of reporting. The classification of variants can change over time and MedGenome cannot be held responsible for this. Please feel free to contact MedGenome Labs (techsupport@medgenome.com) in the future to determine if there have been any changes in the classification of any variations. Re-analysis of variants in previously issued reports in light of new evidence is not routinely performed, but may be available upon request.
- Incidental or secondary findings (if any) that meet the ACMG guidelines [2] can be given upon request.

- The report shall be generated within turnaround time (TAT), however, such TAT may vary depending upon the complexity of test(s) requested. MedGenome under no circumstances will be liable for any delay beyond afore mentioned TAT.
- It is hereby clarified that the report(s) generated from the test(s) do not provide any diagnosis or opinion or recommends any cure in any manner. MedGenome hereby recommends the patient and/or the guardians of the patients, as the case may be, to take assistance of the clinician or a certified physician or doctor, to interpret the report(s) thus generated. MedGenome hereby disclaims all liability arising in connection with the report(s).
- In a very few cases genetic test may not show the correct results, e.g. because of the quality of the material provided to MedGenome. In case where any test provided by MedGenome fails for unforeseeable or unknown reasons that cannot be influenced by MedGenome in advance, MedGenome shall not be responsible for the incomplete, potentially misleading or even wrong result of any testing if such could not be recognised by MedGenome in advance.
- MedGenome is not liable to provide diagnosis, opinion or recommendation related to disease, in any manner. MedGenome hereby recommends the Patient and/or the guardians of the Patient to contact clinician for further interpretation of the test results.
- This is a laboratory developed test and the development and the performance characteristics of this test was determined by MedGenome.

BACKGROUND

Beta thalassemia is an inherited blood disorder that reduces the production of hemoglobin. Mutations in the HBB gene cause beta thalassemia. The HBB gene is responsible for the synthesis of a protein called beta-globin which is a component (subunit) of hemoglobin. Mutations in this gene can result in decreased (β+) or no (β0) β-globin production leading to autosomal recessive disorders like β-thalassemia and sickle cell anemia. Approximately 20 mutations, including deletions, insertions, base substitutions and alternate splice variants, are known to be responsible for abnormal β-globin production in South-East Asians. Of these, del619bp, IVS1-5 G>C; nt 147, IVS1-1 G>T; nt 143, codon 8/9 (+G) and codon 41/42(-TTCT) are more prevalent in the Indian population. HBB genetic testing can be used for diagnostic purposes in individuals with clinical symptoms of β-thalassemia or a haemoglobinopathy. Parents who have symptoms, family history of the disorder, or are known carriers of the disease, can benefit from prenatal testing for mutations in this gene.

Jahnavi K
Program Manager – Genomic Medicine

Dr. Vasundhara Parag Tamhankar
DNB (Paediatrics), DCH, MBBS, Fellowship in Genetics, Consultant Clinical Geneticist

Sakthivel Murugan, SM PhD
VP-Operations (Lab and Genomic Medicine)

TEST METHODOLOGY

NGS

Targeted gene sequencing: Selective amplification and sequencing of the targeted region of the genome/genes is performed. Targeted sequencing represents a cost-effective approach to detect variants present in multiple/large genes in an individual. DNA was used to perform targeted amplification of the complete *HBB* gene. Libraries were prepared using the amplified product and sequenced to mean coverage of >100x on Illumina sequencing platform.

The sequences obtained are aligned to human reference genome (GRCh37/hg19) using BWA program [2, 3] and analyzed using Picard and Sentieon version 201808.01 to identify variants relevant to the clinical indication. We follow the GATK

best practices framework for identification of variants in the sample. Gene annotation of the variants is performed using VEP program [6] against the Ensembl release 87 human gene model [7]. Clinically relevant mutations were annotated using published variants in literature and a set of diseases databases - ClinVar, OMIM, GWAS, HGMD and SwissVar [8-15]. Common variants are filtered based on allele frequency in 1000Genome Phase 3, ExAC, EVS, dbSNP147, 1000 Japanese Genome and our internal Indian population database [16-20]. Non-synonymous variants effect is calculated using multiple algorithms such as PolyPhen-2, SIFT, Mutation Taster2, Mutation Assessor, and LRT. Only non-synonymous variants, splice site variants and previously reported intronic, silent and promoter variants found in the *HBB* gene were used for clinical interpretation.

Molecular genetic testing is performed in order to obtain information for genetic counselling of at-risk family members. It is indicated for prognostication in individuals who represent a simplex case (i.e., who are the only affected member in a family or carrier), identification of the *HBB*-619 deletion mutation can help predict the clinical phenotype and assess the risk of developing this in progeny.

***Genetic test results are reported based on the recommendations of American College of Medical Genetics [1], as described below:**

Variant	A change in a gene. This could be disease causing (pathogenic) or not disease causing (benign).
Pathogenic	A disease-causing variation in a gene which can explain the patients' symptoms has been detected. This usually means that a suspected disorder for which testing had been requested has been confirmed.
Likely Pathogenic	A variant which is very likely to contribute to the development of disease however, the scientific evidence is currently insufficient to prove this conclusively. Additional evidence is expected to confirm this assertion of pathogenicity.
Variant of Uncertain Significance	A variant has been detected, but it is difficult to classify it as either pathogenic (disease causing) or benign (non-disease causing) based on current available scientific evidence. Further testing of the patient or family members as recommended by your clinician may be needed. It is probable that their significance can be assessed only with time, subject to availability of scientific evidence.

[¥]The transcript used for clinical reporting generally represents the canonical transcript (according to Ensembl release 87 gene model), which is usually the longest coding transcript with strong/multiple supporting evidence. However, clinically relevant variants annotated in alternate complete coding transcripts could also be reported.

Variants annotated on incomplete and nonsense mediated decay transcripts will not be reported.

[#]The *in silico* predictions are based on Variant Effect Predictor, Ensembl release 87 (SIFT version - 5.2.2; PolyPhen - 2.2.2); LRT version - November, 2009 release from dbNSFPv3.1 and Mutation Taster2 based on build NCBI 37 / Ensembl 69 [21].

For any further technical queries please contact techsupport@medgenome.com**.**

REFERENCES

1. Richards S, Aziz N, Bale S, *et al*. Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology, Genetics in Medicine, 2015 May;17 (5):405-24.
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DNA TEST REPORT - MEDGENOME LABORATORIES

Full Name / Ref No:		Order ID/Sample ID:	
Date of Birth / Age:		Gender:	
Parental Sample ID:		Sample Type:	
Referring Clinician:		Date of Sample Collection:	
		Date of Sample Receipt:	
		Date of Order:	
		Date of Report:	
Test Requested:	***HBB* Gene Analysis [Trio] [MGM1872]**		

CLINICAL DIAGNOSIS / SYMPTOMS / HISTORY

Mrs. Mehak Dadoo and her husband are presented with Beta Thalassemia Minor. Mrs. Mehak Dadoo is being evaluated for the pathogenic variations in the *HBB* gene.

RESULTS

CARRIER OF PATHOGENIC VARIANT CAUSATIVE OF THE REPORTED PHENOTYPE

Gene (Transcript) #	Location	Variant	Zygosity	Disease (OMIM)	Inheritance	Classification
***HBB* (-)** (ENST00000335295.4)	Intron 1	**c.92+5G>C (Splice variant)**	Heterozygous	Beta Thalassemia	Autosomal recessive	Pathogenic

[$]Genetic test results are reported based on the recommendations of American College of Medical Genetics [1].

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VARIANT INTERPRETATION AND CLINICAL CORRELATION

NGS

Variant description: A heterozygous 5' splice variation in Intron 1 of the ***HBB*** gene **(chr11:g.5248155 C>G; Depth: 4225x)** that affects the position 5 nucleotides downstream of donor splice site of exon 1 **(c.92+5G>C; ENST00000335295.4)** was detected in this subject. This splice variant, commonly known as [IVS1-5G>C] results in aberrant processing of precursor RNA transcripts and leads to β0 phenotype (23, 24). This variation has been reported in homozygous state or compound heterozygous state with other HBB variants in β-Thalassemia+ patients (23). The variant has a minor allele frequency of 0.1% and 0.07% in the 1000 genomes and ExAC databases respectively. The reference base is conserved across species.

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Based on the above evidences[$], ***the variation detected in this subject is classified as a heterozygous pathogenic variation and this variation has to be carefully correlated with the clinical symptoms observed.***

TEST FOR 619bp Del

The 619 bp deletion Beta 0 type was not detected in this subject.

RECOMMENDATIONS

Genetic counselling is advised.

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LIMITATIONS

- Genetic testing is an important part of the diagnostic process. However, genetic tests may not always give a definitive answer. In some cases, testing may not identify a genetic variant even though one exists. This may be due to limitations in current medical knowledge or testing technology. Accurate interpretation of test results may require knowing the true biological relationships in a family. Failing to accurately state the biological relationships in {my/my child's} family may result in incorrect interpretation of results, incorrect diagnoses, and/or inconclusive test results.
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BACKGROUND

Beta thalassemia is an inherited blood disorder that reduces the production of hemoglobin. Mutations in the HBB gene cause beta thalassemia. The HBB gene is responsible for the synthesis of a protein called beta-globin which is a component (subunit) of hemoglobin. Mutations in this gene can result in decreased (β+) or no (β0) β-globin production leading to autosomal recessive disorders like β-thalassemia and sickle cell anemia. Approximately 20 mutations, including deletions, insertions, base substitutions and alternate splice variants, are known to be responsible for abnormal β-globin production in South-East Asians. Of these, del619bp, IVS1-5 G>C; nt 147, IVS1-1 G>T; nt 143, codon 8/9 (+G) and codon 41/42(-TTCT) are more prevalent in the Indian population. HBB genetic testing can be used for diagnostic purposes in individuals with clinical symptoms of β-thalassemia or a haemoglobinopathy. Parents who have symptoms, family history of the disorder, or are known carriers of the disease, can benefit from prenatal testing for mutations in this gene.

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TEST METHODOLOGY

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best practices framework for identification of variants in the sample. Gene annotation of the variants is performed using VEP program [6] against the Ensembl release 87 human gene model [7]. Clinically relevant mutations were annotated using published variants in literature and a set of diseases databases - ClinVar, OMIM, GWAS, HGMD and SwissVar [8-15]. Common variants are filtered based on allele frequency in 1000Genome Phase 3, ExAC, EVS, dbSNP147, 1000 Japanese Genome and our internal Indian population database [16-20]. Non-synonymous variants effect is calculated using multiple algorithms such as PolyPhen-2, SIFT, Mutation Taster2, Mutation Assessor, and LRT. Only non-synonymous variants, splice site variants and previously reported intronic, silent and promoter variants found in the *HBB* gene were used for clinical interpretation.

Molecular genetic testing is performed in order to obtain information for genetic counselling of at-risk family members. It is indicated for prognostication in individuals who represent a simplex case (i.e., who are the only affected member in a family or carrier), identification of the *HBB*-619 deletion mutation can help predict the clinical phenotype and assess the risk of developing this in progeny.

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Variants annotated on incomplete and nonsense mediated decay transcripts will not be reported.

[#]The *in silico* predictions are based on Variant Effect Predictor, Ensembl release 87 (SIFT version - 5.2.2; PolyPhen - 2.2.2); LRT version - November, 2009 release from dbNSFPv3.1 and Mutation Taster2 based on build NCBI 37 / Ensembl 69 [21].

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REFERENCES

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DNA TEST REPORT - MEDGENOME LABORATORIES

Full Name / Ref No:		Order ID/Sample ID:	
Date of Birth / Age:		Gender:	
Parental Sample ID:		Sample Type:	
Referring Clinician:		Date of Sample Collection:	
		Date of Sample Receipt:	
		Date of Order:	
		Date of Report:	
Test Requested:	***HBB* Gene Analysis [Trio] [MGM1872]**		

CLINICAL DIAGNOSIS / SYMPTOMS / HISTORY

Parents of *Fetus Of Mehak Dadoo* are Thalassemia Minor on HPLC. Fetus Of Mehak Dadoo is being evaluated for the pathogenic variations in the *HBB* gene.

RESULTS

NO PATHOGENIC OR LIKELY PATHOGENIC VARIANTS CAUSATIVE OF THE SUSPECTED PHENOTYPE HAVE BEEN IDENTIFIED

[$]Genetic test results are reported based on the recommendations of American College of Medical Genetics [1].

The potential presence of maternal cell contamination (MCC) of the Chorionic Villus Sample has been ruled out [MedGenome: 494216 /7687218; Dated: 09th September 2022].

ADDITIONAL FINDINGS: NO VARIANT(S) OF UNCERTAIN SIGNIFICANCE (VUS) DETECTED

No other variant that warrants to be reported was detected. Variations with high minor allele frequencies which are likely to be benign will be given upon request.

The *HBB* gene is 100% covered in this assay (include the promoter, exon, intron, upstream & downstream regions). 619 bp deletion beta 0 type deletion in the *HBB* gene is also covered in this assay. However, the deletion/duplication analysis of *HBB* gene cannot be rule out by this method.

TEST FOR 619bp Del

The 619 bp deletion Beta 0 type was not detected in this subject.

RECOMMENDATIONS

Genetic counselling is advised.

If results obtained do not match the clinical findings, additional testing should be considered as per referring clinician's recommendations.

LIMITATIONS

- Genetic testing is an important part of the diagnostic process. However, genetic tests may not always give a definitive answer. In some cases, testing may not identify a genetic variant even though one exists. This may be due to limitations in current medical knowledge or testing technology. Accurate interpretation of test results may require knowing the true biological relationships in a family. Failing to accurately state the biological relationships in {my/my child's} family may result in incorrect interpretation of results, incorrect diagnoses, and/or inconclusive test results.
- Test results are interpreted in the context of clinical findings, family history and other laboratory data. Only variations in genes potentially related to the proband's medical condition are reported. Rare polymorphisms may lead to false negative or positive results. Misinterpretation of results may occur if the information provided is inaccurate or incomplete.
- Specific events like copy number variations, translocations, repeat expansions and chromosomal rearrangements may not be reliably detected with targeted sequencing. Variants in untranslated region, promoters and intronic variants are not assessed using this method.
- Genetic testing is highly accurate. Rarely, inaccurate results may occur for various reasons. These reasons include, but are not limited to: mislabeled samples, inaccurate reporting of clinical/medical information, rare technical errors or unusual circumstances such as bone marrow transplantation, blood transfusion; or the presence of change(s) in such a small percentage of cells that may not be detectable by the test (mosaicism).

DISCLAIMER

- **In accordance to the Pre-Conception and Pre-Natal Diagnostic Testing (PCPNDT) Act, 1994- Govt. of India; MedGenome Labs Ltd. does not disclose the gender of the fetus.**
- Interpretation of variants in this report is performed to the best knowledge of the laboratory based on the information available at the time of reporting. The classification of variants can change over time and MedGenome cannot be held responsible for this. Please feel free to contact MedGenome Labs (techsupport@medgenome.com) in the future to determine if there have been any changes in the classification of any variations. Re-analysis of variants in previously issued reports in light of new evidence is not routinely performed, but may be available upon request.
- Incidental or secondary findings (if any) that meet the ACMG guidelines [2] can be given upon request.
- The report shall be generated within turnaround time (TAT), however, such TAT may vary depending upon the complexity of test(s) requested. MedGenome under no circumstances will be liable for any delay beyond afore mentioned TAT.
- It is hereby clarified that the report(s) generated from the test(s) do not provide any diagnosis or opinion or recommends any cure in any manner. MedGenome hereby recommends the patient and/or the guardians of the patients, as the case may be, to take assistance of the clinician or a certified physician or doctor, to interpret the report(s) thus generated. MedGenome hereby disclaims all liability arising in connection with the report(s).
- In a very few cases genetic test may not show the correct results, e.g. because of the quality of the material provided to MedGenome. In case where any test provided by MedGenome fails for unforeseeable or unknown reasons that cannot be influenced by MedGenome in advance, MedGenome shall not be responsible for the incomplete, potentially misleading or even wrong result of any testing if such could not be recognised by MedGenome in advance.
- MedGenome is not liable to provide diagnosis, opinion or recommendation related to disease, in any manner. MedGenome hereby recommends the Patient and/or the guardians of the Patient to contact clinician for further interpretation of the test results.
- This is a laboratory developed test and the development and the performance characteristics of this test was determined by MedGenome.

BACKGROUND

Beta thalassemia is an inherited blood disorder that reduces the production of hemoglobin. Mutations in the HBB gene cause beta thalassemia. The HBB gene is responsible for the synthesis of a protein called beta-globin which is a component (subunit) of hemoglobin. Mutations in this gene can result in decreased (β+) or no (β0) β-globin production leading to autosomal recessive disorders like β-thalassemia and sickle cell anemia. Approximately 20 mutations, including deletions, insertions, base substitutions and alternate splice variants, are known to be responsible for abnormal β-globin production in South-East Asians. Of these, del619bp, IVS1-5 G>C; nt 147, IVS1-1 G>T; nt 143, codon 8/9 (+G) and codon 41/42(-TTCT) are more prevalent in the Indian population. HBB genetic testing can be used for diagnostic purposes in individuals with clinical symptoms of β-thalassemia or a haemoglobinopathy. Parents who have symptoms, family history of the disorder, or are known carriers of the disease, can benefit from prenatal testing for mutations in this gene.

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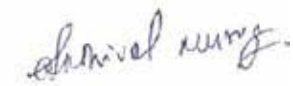

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TEST METHODOLOGY

NGS

Targeted gene sequencing: Selective amplification and sequencing of the targeted region of the genome/genes is performed. Targeted sequencing represents a cost-effective approach to detect variants present in multiple/large genes in an individual. DNA was used to perform targeted amplification of the complete *HBB* gene. Libraries were prepared using the amplified product and sequenced to mean coverage of >100x on Illumina sequencing platform.

The sequences obtained are aligned to human reference genome (GRCh37/hg19) using BWA program [2, 3] and analyzed using Picard and Sentieon version 201808.01 to identify variants relevant to the clinical indication. We follow the GATK best practices framework for identification of variants in the sample. Gene annotation of the variants is performed using VEP program [6] against the Ensembl release 87 human gene model [7]. Clinically relevant mutations were annotated using published variants in literature and a set of diseases databases - ClinVar, OMIM, GWAS, HGMD and SwissVar [8-15]. Common variants are filtered based on allele frequency in 1000Genome Phase 3, ExAC, EVS, dbSNP147, 1000 Japanese Genome and our internal Indian population database [16-20]. Non-synonymous variants effect is calculated using multiple algorithms such as PolyPhen-2, SIFT, Mutation Taster2, Mutation Assessor, and LRT. Only non-synonymous variants, splice site variants and previously reported intronic, silent and promoter variants found in the *HBB* gene were used for clinical interpretation.

Molecular genetic testing is performed in order to obtain information for genetic counseling of at-risk family members. It is indicated for prognostication in individuals who represent a simplex case (i.e., who are the only affected member in a family or carrier), identification of the *HBB*-619 deletion mutation can help predict the clinical phenotype and assess the risk of developing this in progeny.

***Genetic test results are reported based on the recommendations of American College of Medical Genetics [1], as described below:**

Variant	A change in a gene. This could be disease causing (pathogenic) or not disease causing (benign).
Pathogenic	A disease causing variation in a gene which can explain the patients' symptoms has been detected. This usually means that a suspected disorder for which testing had been requested has been confirmed.

Likely Pathogenic	A variant which is very likely to contribute to the development of disease however, the scientific evidence is currently insufficient to prove this conclusively. Additional evidence is expected to confirm this assertion of pathogenicity.
Variant of Uncertain Significance	A variant has been detected, but it is difficult to classify it as either pathogenic (disease causing) or benign (non-disease causing) based on current available scientific evidence. Further testing of the patient or family members as recommended by your clinician may be needed. It is probable that their significance can be assessed only with time, subject to availability of scientific evidence.

[¥]The transcript used for clinical reporting generally represents the canonical transcript (according to Ensembl release 87 gene model), which is usually the longest coding transcript with strong/multiple supporting evidence. However, clinically relevant variants annotated in alternate complete coding transcripts could also be reported.

Variants annotated on incomplete and nonsense mediated decay transcripts will not be reported.

[#]The *in silico* predictions are based on Variant Effect Predictor, Ensembl release 87 (SIFT version - 5.2.2; PolyPhen - 2.2.2); LRT version - November, 2009 release from dbNSFPv3.1 and Mutation Taster2 based on build NCBI 37 / Ensembl 69 [21].

For any further technical queries please contact techsupport@medgenome.com**.**

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END OF REPORT