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Annexure

MedGenome Labs Ltd.
Sy. Nos. 94/1C and 94/2, Tower 1, Ground Floor, Veerasandra Village,
Attibele Hobli, Electronic City Phase-1, Electronics City, Bangalore,
Bangalore South, Karnataka, India, 560100.
Tel : 1800 296 9696, Web: www.medgenome.com

MEDGENOME

DNA TEST REPORT - MEDGENOME LABS

Full Name / Ref No:	**PROF DR. ASHA SUNDARAM**	Order ID/Sample ID:	**1458742/9415283**
Gender:	Female	Sample Type:	Blood
Date of Birth / Age:	48 years	Date of Sample Collection:	24th September 2025
Referring Clinician:	Dr. Asha Sundaram, Saveetha School of Law - Chennai,	Date of Sample Receipt:	25th September 2025
		Date of Order Booking:	25th September 2025
		Date of Report:	11th November 2025
Test Requested:	**Whole exome sequencing (80-100x)[Extended TAT]**		

CLINICAL DIAGNOSIS / SYMPTOMS / HISTORY

Prof Dr. Asha Sundaram is suspected to be harbor mutations in *CRHR1, CRHR2, NR3C1, FKBP5, SLC6A4, MAOA, BDNF, COMT, TPH2* genes and has been evaluated for pathogenic variations.

RESULTS

NO PATHOGENIC OR LIKELY PATHOGENIC VARIANTS CAUSATIVE OF THE REPORTED PHENOTYPE WERE DETECTED

VARIANT INTERPRETATION AND CLINICAL CORRELATION

No significant variant(s) for the given clinical indications that warrants to be reported was detected.
There are no clinically relevant variants in coding region and exon-intron boundaries of *CRHR1, CRHR2, NR3C1, FKBP5, SLC6A4, MAOA, BDNF, COMT, TPH2* genes and the genes are 100% covered.

ADDITIONAL INFORMATION

- No significant SNV(s)/INDELS or CNV(s) that warrants to be reported were detected. All the genes covered in this assay have been screened for the given clinical indications. To view the coverage of all genes Click here. NGS test methodology details of this assay are given in the appendix.
- With regard to ACMG recommendations for reporting of incidental findings in clinical exome and genome sequencing (PMID: 35802134; ACMG SF v3.1), we report significant pathogenic and/ or likely pathogenic variants in the recommended genes for the recommended phenotypes, only if informed consent is given by the patient.
- Please write an email to genetic.counseling@medgenome.com in case you need assistance for genetic counselling. For any further technical queries please write an email to techsupport@medgenome.com

RECOMMENDATIONS

- Genetic counselling is advised.

CAP ACCREDITED

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MEDGENOME

DNA TEST REPORT - MEDGENOME LABS

Full Name / Ref No:	**GIRIJA ANIL KUMAR**	Order ID/Sample ID:	**1458644/9415294**
Gender:	Female	Sample Type:	Blood
Date of Birth / Age:	51 years	Date of Sample Collection:	24th September 2025
Referring Clinician:	Dr. Asha Sundaram, Saveetha School of Law, Chennai	Date of Sample Receipt:	25th September 2025
		Date of Order Booking:	25th September 2025
		Date of Report:	11th November 2025
Test Requested:	**Whole Exome Sequencing**		

CLINICAL DIAGNOSIS / SYMPTOMS / HISTORY

Ms. *Girija Anil Kumar* is suspected to harbour mutations in *CRHR1*, CRHR2, *NR3C1, FKBP5, SLC6A4 (5-HTTLPR), MAOA, BDNF, COMT, TPH2* genes and has been evaluated for pathogenic variations.

RESULTS

NO PATHOGENIC OR LIKELY PATHOGENIC VARIANTS CAUSATIVE OF THE REPORTED PHENOTYPE WERE DETECTED

VARIANT INTERPRETATION AND CLINICAL CORRELATION

No significant variant(s) for the given clinical indications that warrants to be reported was detected.
There are no clinically relevant variants in coding region and exon-intron boundaries of in *CRHR1, CRHR2, FKBP5, SLC6A4 (5-HTTLPR), MAOA, BDNF, COMT, TPH2* genes and the genes are 100% covered.

ADDITIONAL INFORMATION

- **A heterozygous nonsense variant in the *HTRA1* gene (c.1120G>T, p.Gly374Ter) has been detected in this assay. Kindly correlate clinically.**
- **A heterozygous variant (p.Ala49Val; c.146C>T) in the *NR3C1* gene was also detected in this assay. However, it has high MAF.**
- No significant SNV(s)/INDELS or CNV(s) that warrants to be reported were detected. All the genes covered in this assay have been screened for the given clinical indications. To view the coverage of all genes Click here. NGS test methodology details of this assay are given in the appendix.
- With regard to ACMG recommendations for reporting of incidental findings in clinical exome and genome sequencing (PMID: 35802134; ACMG SF v3.1), we report significant pathogenic and/ or likely pathogenic variants in the recommended genes for the recommended phenotypes, only if informed consent is given by the patient.
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RECOMMENDATIONS

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