Phosphorus Diagnostics

REPRODUCTIVE HEALTH

PERFORMED AT PHOSPHORUS DIAGNOSTICS,
3 REGENT STREET, LIVINGSTON, NJ 07039

ORDERING PRACTICE

Practice Code: 5000
Advanced Reproductive World
25 W 26th St, 3rd Floor
New York, NY 10010
Physician: Dr. Bisignano
Report Generated: 1/3/2017

FEMALE PARTNER

Name: Jane Doe
Patient ID: 43527
DOB: 1987-06-07
Donor Gamete: No
Procedure ID: 53787
Kit Barcode: 201729301294
Specimen: Blood, 45679
Date Collected: 1/1/2017
Date Received: 1/2/2017
Date Analyzed: 1/3/2017

MALE PARTNER

Name: John Doe
Patient ID: 43526
DOB: 1987-07-04
Donor Gamete: No
Procedure ID: 53786
Kit Barcode: 201729301293
Specimen: Blood, 45679
Date Collected: 1/1/2017
Date Received: 1/2/2017
Date Analyzed: 1/3/2017

SUMMARY OF GENETIC RESULTS

Positive: Increased Reproductive Risk

INDICATION	JANE DOE	JOHN DOE
Thrombophilia-Related Recurrent Pregnancy Loss	Normal reproductive risk profile	N/A
Ovarian Hyperstimulation Syndrome	Normal reproductive risk profile	N/A
Polycystic Ovary Syndrome	Normal reproductive risk profile	N/A
Premature Ovarian Insufficiency	Increased reproductive risk profile	N/A
Sex Chromosome Aneuploidy	Normal reproductive risk profile	Normal reproductive risk profile
Y-Chromosome Microdeletions	N/A	Normal reproductive risk profile
Congenital Absence of the Vas Deferens (CAVD)	N/A	Normal reproductive risk profile
Other Male Factor Infertility	N/A	Normal reproductive risk profile

INTERPRETATION

Jane Doe is a carrier of an FMR1 premutation (68 CGG repeats).

This result is consistent with an increased risk for FMR1-Related Premature Ovarian Insufficiency.

FMR1 premutations are also associated with increased risk of Fragile X-associated Tremor Ataxia Syndrome. Female carriers of premutations are at increased risk to have a child with Fragile X syndrome.

RECOMMENDATIONS

Clinical follow-up is recommended for appropriate management and reproductive counseling.

Genetic counseling is recommended.

CLIA #31D2123554

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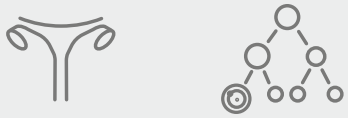
JANE DOE DETAILED RESULTS

PREMATURE OVARIAN INSUFFICIENCY (POI)

GENE(S)	RESULT	INTERPRETATION	MECHANISM
FMR1	68 CGG Repeats - Premutation	Jane Doe carries an expanded FMR1 allele of 68 CGG repeats, which is consistent with a premutation. This is consistent with an increased risk for premature ovarian insufficiency, as well as an increased risk for Fragile X-associated tremor ataxia syndrome, and the risk to have a child with Fragile X syndrome.	In women with POI, the ovaries prematurely stop producing important hormones, which stops oocytes from maturing correctly, leading to decreased fertility.  Functional Gonad Oogenesis
BMP15	No pathogenic variant(s) identified		
CYP17A1	No pathogenic variant(s) identified		
CYP19A1	No pathogenic variant(s) identified		
FOXL2	No pathogenic variant(s) identified		
FSHB	No pathogenic variant(s) identified		
FSHR	No pathogenic variant(s) identified		
GALT	No pathogenic variant(s) identified		
GDF9	No pathogenic variant(s) identified		
GNAS	No pathogenic variant(s) identified		
GNRHR	No pathogenic variant(s) identified		
KISS1R	No pathogenic variant(s) identified		
LHCGR	No pathogenic variant(s) identified		
NOBOX	No pathogenic variant(s) identified		
NR5A1	No pathogenic variant(s) identified		
STAG3	No pathogenic variant(s) identified		
ZP1	No pathogenic variant(s) identified		

ABOUT FMR1-RELATED PREMATURE OVARIAN INSUFFICIENCY:

The average individual has <45 CGG repeats in the promoter region of the FMR1 gene. Sometimes, the number of repeats in this region can expand, leading to negative health outcomes. Women who have 55-200 CGG repeats, called a premutation, are at increased risk for premature ovarian insufficiency, where affected females will experience Diminished Ovarian Reserve significantly earlier in life than expected. There is no known cure for FMR1-related POI, thus earlier detection is the best way to maintain the most reproductive options. Female carriers of FMR1 premutations are also at risk for Fragile X-associated tremor/ataxia synrome (FXTAS), and are at risk to have children with Fragile-X syndrome, as premutations can expand to full mutations when passed down to offspring.

FOLLOW-UP:

Clinical evaluation is recommended. All clinical management decisions should be based on the patient's specific clinical history. Genetic counseling is recommended.

THROMBOPHILIA-RELATED RECURRENT PREGNANCY LOSS

GENE(S)	RESULT	INTERPRETATION
F2	No pathogenic variant(s) identified	Normal risk profile. Patient is not at increased risk for thrombophilia-related pregnancy loss based on these results.
F5	No pathogenic variant(s) identified	
PROC	No pathogenic variant(s) identified	
PROS1	No pathogenic variant(s) identified	
SERPINC1	No pathogenic variant(s) identified	

OVARIAN HYPERSTIMULATION SYNDROME

GENE(S)	RESULT	INTERPRETATION
FSHR	No pathogenic variant(s) identified	Normal risk profile. Patient is not at increased risk for ovarian hyperstimulation syndrome based on these results.

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JANE DOE DETAILED RESULTS

POLYCYSTIC OVARY SYNDROME

GENE(S)	RESULT	INTERPRETATION
CAPN10	No pathogenic variant(s) identified	Normal risk profile. Patient is not at increased risk for polycystic ovary syndrome based on these results.
CYP11A1	No pathogenic variant(s) identified	
DENND1A	No pathogenic variant(s) identified	
FSHR	No pathogenic variant(s) identified	
GDF9	No pathogenic variant(s) identified	
LHCGR	No pathogenic variant(s) identified	
THADA	No pathogenic variant(s) identified	

SEX CHROMOSOME ANEUPLOIDY

REGION	RESULT	INTERPRETATION
Sex chromosomes	No aneuploidy detected	Normal risk profile. Patient result is consistent with typical female sex chromosomes (X,X).

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JOHN DOE DETAILED RESULTS

SEX CHROMOSOME ANEUPLOIDY

REGION	RESULT	INTERPRETATION
Sex chromosomes	No aneuploidy detected	Normal risk profile. Patient result is consistent with typical male sex chromosomes (X,Y).

CONGENITAL ABSENCE OF THE VAS DEFERENS (CAVD)

GENE(S)	RESULT	INTERPRETATION
CFTR	No pathogenic variant(s) identified	Normal risk profile. Patient is not at increased risk for CFTR-related absence of the vas deferens based on these results.

Y-CHROMOSOME MICRODELETIONS

REGION	RESULT	INTERPRETATION
AZF region of Y chromosome	No microdeletions	Normal risk profile. No Y-chromosome microdeletions identified.

OTHER MALE FACTOR INFERTILITY

GENE(S)	RESULT	INTERPRETATION
AR	No pathogenic variant(s) identified	Normal risk profile. Patient is not at increased risk for azoo- or oligospermia related to mutations in the genes assayed.
AURKC	No pathogenic variant(s) identified	
CATSPER1	No pathogenic variant(s) identified	
DPY19L2	No pathogenic variant(s) identified	
FSHB	No pathogenic variant(s) identified	
FSHR	No pathogenic variant(s) identified	
LHCGR	No pathogenic variant(s) identified	
SRY	No pathogenic variant(s) identified	
USP9Y	No pathogenic variant(s) identified	

METHODS

Sequencing is performed using a custom next-generation sequencing platform. Only the specified regions of genes are assayed via next-generation sequencing. This methodology may not detect low-level mosaicism. Exons containing only untranslated regions are not assayed. Sensitivity to detect insertions and deletions larger than 15 base pairs but smaller than a full exon may be reduced. Some exons of a few individual genes have inherent sequence properties that yield suboptimal data, and mutations in those regions may not be reliably identified. All mutations included within the genes assayed may not be detected. All clinically significant observations are confirmed by orthogonal techniques as part of our ongoing quality managment process.

LIMITATIONS

This test is designed to detect specific mutations associated with specific forms of hereditary risk for infertility. It cannot detect every mutation associated with this disease, nor does it look for all known genetic diseases. Therefore, a negative result on this test is risk reducing but not risk eliminating. Although this test is highly accurate, no genetic test is 100% accurate. Novel sequence changes in the promoter region and other non-coding regions will not be detected by this assay. This methodology may not detect low-level mosaicism. Exons containing only untranslated regions are not assayed. Sensitivity to detect insertions and deletions larger than 15 base pairs but smaller than a full exon may be reduced. Some exons of a few individual genes have inherent sequence properties that yield suboptimal data, and mutations in those regions may not be reliably identified. All mutations included within the genes assayed may not be detected.

For some genes, only specific variants are assayed. The possibility that other variants within these genes contribute to disease cannot be excluded. As new information becomes available, variant classification may evolve over time. Providers are encouraged to contact support@phosphorus.com to obtain updated information.

This report does not constitute medical advice. Any questions or concerns regarding the contents of this report should be directed to a qualified medical geneticist, genetic counselor, or reproductive endocrinologist. This report reflects the analysis of an extracted DNA sample. In very rare cases, the analyzed DNA may not represent that patient's constitutional genome. Examples include but are not limited to: circulating hematolymphoid neoplasm, bone marrow transplantation, blood transfusion, sample contamination, sample mix-up, and technical errors.

This test was developed and its performance determined by Phosphorus, Inc., and has not been approved by the U.S. Food and Drug Administration (FDA). The FDA has determined that such approval is not necessary.

SIGNED BY

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