CRM ID	: 0000000	Sample Type	: NA
Name	: DUMMY	Date & Time Collected	: DD-MM-YYYY
Sex/Age	: NA	Date & Time Received	: DD-MM-YYYY
Bill. Loc.	: NA	Date & Time Reported	: DD-MM-YYYY
Ref. By	: NA		

MECP2 (RETT SYNDROME) Deletion/Duplication Report by MLPA

Clinical History

NA

Result summary

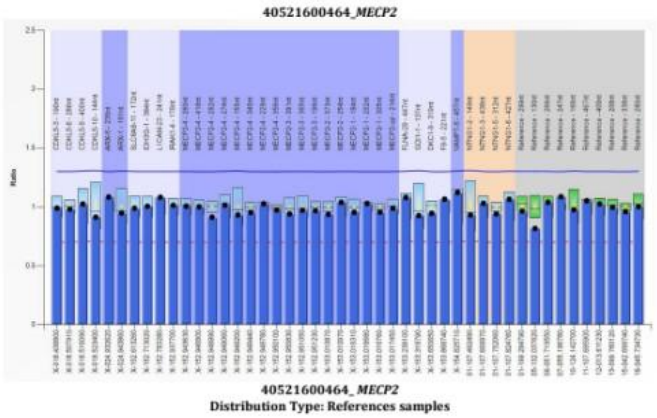
Normal

(No deletions or duplication were detected, within the detection limits of MLPA, in MECP2 gene of this subject)

Sr. No.	Gene	Deletion/Duplication	No. of Exons deleted/Duplicated	Dosage Quotient
1	MECP2	--	--	1.0

Data from Clinical sample:

MECP2-MLPA Result Figure
Fig.1- 40521600464_MLPA Ratio Chart: MECP2



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Interpretation Reference:	
Dosage Quotient [DQ] Distribution	**Copy Number Status**
DQ = 0	0 copies (homozygous deletion)
0.40 < DQ < 0.65	2 – 1 copy (heterozygous deletion)
0.80 < DQ < 1.20	NORMAL (identical to reference samples)
1.30 < DQ < 1.65	2 – 3 copies (heterozygous duplication)
1.75 < DQ < 2.15	2 – 4 copies (or 1 – 2copies)
MLPA ratios below 0.7 or above 1.3 indicate a heterozygous deletion or duplication respectively.	

Background:

Rett syndrome (RTT) is a severe progressive neurodevelopmental disorder that presents early in childhood and affects primarily females. This X-linked dominant disorder affects 1:10,000-1:15,000 girls. In classic RTT, normal growth and development occurs during approximately the first 6-18 months of life.
This is followed by an arrest in development and subsequent progressive loss of acquired motor skills and language and the onset of stereotypical hand movements. Rett syndrome is caused by mutations in the methyl CpG binding protein 2 (MECP2) located at chromosome Xq28.

Test Methodology:

Multiplex ligation-dependent probe amplification (MLPA) is a variation of the multiplex polymerase chain reaction that permits multiple targets to be amplified with only a single primer pair. Each probe consists of two oligonucleotides which recognize adjacent target sites on the DNA. One probe oligonucleotide contains the sequence recognized by the forward primer, the other the sequence recognized by the reverse primer.

Only when both probe oligonucleotides are hybridised to their respective targets, can they be ligated into a complete probe. The advantage of splitting the probe into two parts is that only the ligated oligonucleotides, but not the unbound probe oligonucleotides, are amplified. Each complete probe has a unique length, so that its resulting amplicons can be separated and identified by (capillary) electrophoresis. Comparing the peak pattern obtained on a given sample with that obtained on various reference samples, the relative quantity of each amplicon can be determined. This ratio is a measure for the ratio in which the target sequence is present in the sample DNA.
MECP2 gene Deletion/Duplication Analysis is based on the MLPA technology (Multiplex Ligation-dependent Probe Amplification) and employs the SALSA® MLPA® probe mixes available from MRC(Holland).

Recommendations:

Genetic counseling is advised.
Sequencing of MECP2 genes is recommended to rule out point variations.

Disclaimer:

Sequence changes (SNPs, point mutations) in the target sequence detected by a probe can cause false positive MLPA results.
Mutations/SNPs close to the ligation site (1-5 nt) can reduce or prevent the probe signal by preventing ligation of the two probe oligonucleotides.
In a portion of the cases, the cause of genetic defects in the MECP2 gene is small (point) mutations, most of which will not be detected by using SALSA MLPA probemix P015-F2 MECP2.
MLPA cannot detect any changes that lie outside the target sequence of the probes and will not detect most inversions or translocations. Even when MLPA did not detect any aberrations, the possibility remains that biological changes in that gene or chromosomal region do exist but remain undetected.
For questions about this report, or for assistance in locating nearby genetic counselling services, please contact the Laboratory: contact@Redcliffelab.com.
Although all precautions are taken during DNA tests the currently available data indicate that the technical error rate for all types of DNA analysis is approximately 2%. It is important that all clinicians or persons requesting DNA diagnostic tests are aware of these data before acting upon these results.

***References*:**

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2. *Shahbazian MD, Zoghbi HY: Molecular genetics of Rett syndrome and clinical spectrum of MECP2 mutations. Curr Opin Genet Dev 2001; 14:171-176.*
3. *Wan M, Lee SS, Zhang X, Houwink-Manville I, Song HR, Amir RE, Budden S, Naidu S, Pereira JL, Lo IF, Zoghbi HY, Schanen NC, Francke U: Rett syndrome and beyond: recurrent spontaneous and familial MECP2 mutations at CpG hotspots. Am J Hum Genet 1999; 65:1520–1529.*
4. *Cheadle JP, Gill H, Fleming N, Maynard J, Kerr A, Leonard H, Krawczak M, Cooper DN, Lynch S, Thomas N, Hughes H, Hulten M, Ravine D, Sampson JR, Clarke A: Long read sequence analysis of the MECP2 gene in Rett syndrome patients: correlation of disease severity with mutation type and location. Hum Mol Genet 2000: 9:1119–1129.*
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End Of Report

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Disclaimer: Method given in report are only indicative and can be changed depending upon type of machine and kit available at time of testing.

Not all tests at all locations are under NABL scope. Availability of tests under NABL scope varies from lab to lab.