**LETTER OF MEDICAL NECESSITY**

**For**

**Chromosomal Microarray Analysis**

To: ***[Insurance Company Name]***

**STAT Review Request**

***[Address]***

***[City, State, ZIP]***

***[Fax]***

Re: ***[Patient Name, DOB]***

***[Member ID Number]***

[Date]

Dear Medical Director:

I am writing this letter on behalf of my patient and your subscriber, listed above, to request coverage of medically-indicated Chromosomal Microarray Analysis (CMA) in support of the diagnosis and/or treatment of **[Insert indication(s)]**.This genetic test will be performed by Baylor Genetics, LLC.

Chromosomal Microarray Analysis (CMA) analyzes the genome for gains or losses of genetic material at a much higher resolution than standard karyotype analysis. CMA has the ability to detect small gains or losses in genetic material that may have been missed on standard blood chromosome analysis alone. The diagnostic yield was 12.2% higher than that of a G-banded karyotype in a review of 21,698 patients referred for developmental delay/intellectual disability (DD/ID), multiple congenital anomalies, and/or autism spectrum disorders (ASDs) (Miller et al Genet Med. 2010.12(11):742-5). Citing large-scale studies such as these, the American College of Medical Genetics has officially endorsed CMA as a “first line test” in the evaluation of individuals with unexplained developmental delays, autism and multiple congenital anomalies (Manning and Hudgins. Genet in Med. 2010. 12(11): 742-745).

For this patient, I have determined that this genetic test is medically necessary based on [his/her] clinical symptoms, history, and/or family history.Significant aspects of my patient’s personal and/or family medical history that raise reasonable suspicion of an underlying genetic diagnosis are as follows:

Due to the heterogeneous nature of my patient’s symptoms, there is a reasonable probability of detecting a causative chromosomal abnormality using this test. Per American Academy of Pediatrics and American College of Medical Genetics and Genomics guidelines, CMA analysis is recommended as a first-tier test for my patient.

The CMA test provided by Baylor Genetics, LLC. extends its detection capability to identify losses or gains involving at least one exon and as small as several hundred base pairs in size by using custom-designed, exon-targeted oligonucleotide arrays. The two current microarrays, CMA-HR (v8.1.1) and CMA-comprehensive-SNP (v11.2), have ~1,700 or ~42,00 disease genes or disease candidate genes, respectively, covered at the exon level. Copy-number changes have been detected within a gene known to be causative of the observed clinical phenotype, demonstrating the utility of the CMA-HR array to detect intragenic copy-number changes in patients with various clinical phenotype (Boone et al. Human Mutation 201031(12): 1326–1342) In addition to exon level copy number analysis, the CMA-comprehensive-SNP array also includes 60,000 probes used for SNP analysis for the detection of uniparental disomy (UPD) and copy-neutral absence of heterozygosity (AOH) (Wiszniewska et al. European Journal of Human Genetics. 2014. 22(1), 79–87).

Specifically for this patient, the results of the CMA test are necessary to consider in the following areas **[check all that apply]**:

* Genetic testing will lead to changes in my medical management strategies; AND/OR
* Genetic testing will lead to changes in diagnostic procedures such that more potentially invasive alternative procedures could be avoided, reducing unnecessary tests and cost; AND/OR
* Genetic testing will lead to informed decisions for other family members with similar conditions, or that may be at risk for similar conditions

Due to the medical risks associated with chromosomal alterations and available interventions, this genetic testing is medically indicated. As such, I am ordering this test and affirm that my patient/patient’s family member has provided informed consent for genetic testing.

A positive test result would confirm a genetic diagnosis and/or risk in my patient, and would ensure my patient is being managed appropriately. Similarly, a negative CMA result would also be clinically useful as it would rule out chromosomal abnormalities and focus our efforts to find a diagnosis in other areas, such as metabolic or single gene disorders. I am specifying Baylor Genetics because this laboratory has highly-sensitive and cost-effective CMA analysis, along with a large database of approximately 70,000 tested patients to ensure highly validated, accurate, and informative test interpretation.

Please review this information and provide support for this request for coverage of diagnostic genetic testing for my patient. Coordinating and completing complex testing of this nature can sometimes take up to several months; we are requesting that the authorization be valid for at least 4 months.

Thank you for your time and further consideration. If you have any questions, please do not hesitate to contact me at the numbers below.

Patient Diagnosis:

*[Patient name]* is a *[insert age]* year old female with the following diagnoses:

1. **[ICD10 code]**

2. **[ICD10 code]**

Thank you for your consideration. I look forward to receiving a timely response given the time sensitive nature of my patient’s condition. Please feel free to contact me at **[Phone number]** for additional information.

Sincerely,

**[GC Name]**

Genetic Counselor

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**[Signature of ordering physician]**

**[Name of Ordering Physician]**

*CPT Codes:* ***[Insert CPT codes]***

*Laboratory: Baylor Molecular Genetics Laboratories*

References

1. Boone PM, Bacino CA, Shaw CA, Eng PA, Hixson PM, Pursley AN, Kang SH, Yang Y, Wiszniewska J, Nowakowska BA, del Gaudio D, Xia Z, Simpson-Patel G, Immken LL, Gibson JB, Tsai AC, Bowers JA, Reimschisel TE, Schaaf CP, Potocki L, Scaglia F, Gambin T, Sykulski M, Bartnik M, Derwinska K, Wisniowiecka-Kowalnik B, Lalani SR, Probst FJ, **Bi W**, Beaudet AL, Patel A, Lupski JR, Cheung SW, Stankiewicz P (2010). Detection of clinically relevant exonic copy-number changes by array CGH. Hum Mutat. 31:1326-1342.

2. Wiszniewska J, **Bi W**, Shaw C, Stankiewicz P, Kang SH, Pursley AN, Lalani S, Hixson P, Gambin T, Tsai CH, Bock HG, Descartes M, Probst FJ, Scaglia F, Beaudet AL, Lupski JR, Eng C, Wai Cheung S, Bacino C, Patel A. (2014). Combined array CGH plus SNP genome analyses for optimized clinical diagnostics. Eur J Hum Genet. 22:79-87.