Letter of Medical Necessity Test Code 2000

<<Today’s Date>>

<<Insurance Company Name>>

<<Address 1>>

<<Address 2>>

<<City, State ZIP>>

**Regarding:** <<Patient full name>>

**DOB:** <<MM/DD/YYYY>>

**Subscriber ID:** <<Member ID#>>

**Group ID:** <<Group ID#>>

**Re:** Request for prior authorization coverage for PreventionGenetics’ Whole-Genome Chromosomal Microarray. Billing is through <<billing institution>> with testing performed at PreventionGenetics, LLC. CPT codes for PreventionGenetics test code #2000 include: 81229. The ICD 10 code(s) associated with the patient’s diagnosis include <<ICD code(s)>>.

**Rationale for Whole-Genome Chromosomal Microarray Analysis (CMA)**

Chromosomal Microarray Analysis is designed to detect microdeletions and duplications of DNA segments as small as 500 bp to 30 kb and larger. By comparing <<Mr/Mrs/Ms/Miss patient’s last name’s>> genome to a reference sequence, deletions and/or duplications, also known as copy number variants (CNVs), can be detected within <<his/her>> genome1. The detection of CNVs can provide a diagnosis for an existing, unexplained, abnormal phenotype. CMA has been proven to be a first-tier diagnostic test that is useful in the detection of CNVs associated with intellectual disability, developmental delay, and autism spectrum disorder2, 3, 4, as well as revealing the underlying causes of heart defects, epilepsy, and seizures. It can also provide important information in the evaluation of stillbirth, spontaneous pregnancy loss, and genetically heterogeneous disorders.

In addition to the detection of CNVs, the absence/loss of heterozygosity (AOH/LOH), also described as long contiguous stretches of homozygosity (LCSH), may be detected by the use of single nucleotide polymorphism (SNP) probes. Concurrent analysis of CGH and SNP data allows for the detection of UPD, AOH/LOH, parental consanguinity, and ploidy changes.

CMA has proven to be more successful than the alternative means of deletion and duplication analysis, G-banded karyotyping3, 5. G-banded karyotyping is capable of detecting large chromosomal abnormalities, but fails to detect smaller CNVs. The ability of CMA to detect smaller CNVs increases the likelihood of a conclusive diagnosis after a negative karyotype.

Detection rates of CMA have been found to be 10-20% higher than those of conventional karyotyping methods and therefore, CMA increases the likelihood of detecting pathogenic variants6. In one study, CMA increased detection rates from 2.9% to 9.6%7. In another study, the detection rate was 17.1%, much higher than the detection of abnormalities by other methods, and this rate would be expected to be even higher with use of a SNP aCGH, depending on the clinical presentation of the patient8.

In the case of incidental findings the American College of Medical Genetics and Genomics guidelines will be followed9. Appropriate consent forms allow for discussion and disclosure of incidental findings as needed.

**Personal History**

<<Personal Medical History: Include details of patient’s relevant medical history>>

<<Insert a relevant work up including previous testing and negative results and/or further rationale for the CMA request>>

**Family History**

<<Family History: Include list of relevant family history information if applicable. Appropriate risk assessment models or limited history should be noted >>

Given <<Mr/Mrs/Ms/Miss patient’s last name’s>> phenotype, the most efficient and cost effective method that would result in a potentially conclusive diagnosis would be CMA.

The laboratory providing the genetic testing is PreventionGenetics, LLC, (Tax ID: 83 0343803) who is a sponsor of Pediatric Lab Utilization Guidance Services ([PLUGS®](http://www.seattlechildrenslab.org/plugs.aspx)).  PreventionGenetics is committed to providing comprehensive, high quality, and affordable genetic testing that adds value to patient care.  Through utilization management strategies at PreventionGenetics, over 1.3 million healthcare dollars are saved annually.

I am hopeful that we can work together for <<Mr/Mrs/Ms/Miss patient’s last name’s>> benefit.  Please contact me at <<Phone #>> with the result of this prior authorization and/or if you need additional information.

Sincerely,

<<Name, credentials>>

<<Title>>

<<Institution>>

References

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5. Shin, S., et al. (2015). *Annals of Laboratory Medicine, 35,* 510-518. PubMed ID: 26206688
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