Corporate Medical Policy

General Genetic Testing, Somatic Disorders AHS-M2146

File Name: general_genetic_testing_somatic_disorders
Origination: 01/2019
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Next CAP Review: 03/2021
Last Review: 04/2020

Description of Procedure or Service

Genetic testing refers to the use of technologies that identify genetic variation, which include genomic, transcriptional, proteomic, and epigenetic alterations, for the prevention, diagnosis, and treatment of disease (Li et al., 2017; B. Raby, Kohlman, & Venne, 2018). Somatic variations or mutations are defined as a genetic alteration that occurs after conception in any of the cells of the body, except the germ cells, and therefore are not passed on to offspring (Li et al., 2017).

Related Policies
General Genetic Testing, Germline Disorders AHS – M2145
Whole Genome and Whole Exome Sequencing AHS – M2032
Molecular Panel Testing of Cancers for Diagnosis, Prognosis, and Identification of Targeted Therapy AHS – M2109

***Note: This Medical Policy is complex and technical. For questions concerning the technical language and/or specific clinical indications for its use, please consult your physician.

Policy

BCBSNC will provide coverage for general genetic testing for somatic disorders when it is determined the medical criteria or reimbursement guidelines below are met.

Benefits Application

This medical policy relates only to the services or supplies described herein. Please refer to the Member's Benefit Booklet for availability of benefits. Member's benefits may vary according to benefit design; therefore member benefit language should be reviewed before applying the terms of this medical policy.

When General Genetic Testing, Somatic Disorders is covered

1. Genetic testing is covered for a specific genetic mutation or mutations that have documented clinical utility for diagnosis, selection of therapy, or prognostication when there is a documented benefit based on the presence of such mutations in the tumor, or neoplastic hematologic cells.

2. Repeat testing is covered for recurrence monitoring, OR

3. Repeat testing is covered when there is the possibility of further genetic alterations in the hematologic malignancy, primary tumor or metastasis AND knowledge of these changes would result in the addition, elimination or alteration of non-investigational therapies.
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4. MSI testing for all solid tumors is considered medically necessary for individuals being considered for pembrolizumab (Keytruda) therapy.

Note: For more than 5 gene tests being run on a tumor specimen (i.e. non-liquid biopsy) on the same platform, such as multi-gene panel next generation sequencing, please refer to policy AHS-R2162 Laboratory Procedures Reimbursement Policy.

When General Genetic Testing, Somatic Disorders is not covered

Testing with a gene panel containing genes that do not meet the criteria in item 1 above is not covered.

Policy Guidelines

Background

Gene mutations are referred to as “somatic” if they are not within the germline (i.e. within gametes); therefore, these mutations are not passed on from parent to offspring. These mutations may arise de novo or later in life and are very common in neoplasms (B. Raby, Blank, Robert, 2019). There are many different types of somatic mutations, including single nucleotide polymorphisms (SNPs); structural variations such as deletions, inversions, or translocations; and smaller chromosomal abnormalities such as short tandem repeats or gene fusions. Most mutations do not result in disease (B. Raby, 2018).

SNPs are the most common type of genetic mutation, including missense mutations. These mutations are single base-pair changes where one nucleotide replaces a different nucleotide. More than 65% of the diseases caused by genetic mutations are due to SNPs (B. Raby, 2018). Estimates based on whole genome sequencing have placed the average amount of SNPs in any given individual at 2.8 to 3.9 million (B. Raby, 2018). Insertion/deletion (indel) polymorphisms are often a single nucleotide but may be up to four nucleotides. SNPs often lead to frameshift mutations that can cause premature stop codons and the failure of the allele (B. Raby, 2018).

Structural variations are usually classified as larger than 1000 base pairs. These include deletions, duplications, inversions, translocations, or ring chromosome formations. Due to the large number of genes affected, these variations commonly lead to severe genetic abnormalities; for example, a major cause of chronic myeloid leukemia is due to the translocation between chromosomes 9 and 22, resulting in a fused gene. The most common structural variation is the copy number variant (CNV), referring to a differing number of DNA segment copies in different individuals. For example, one person may have three copies of a particular segment whereas another may only have two. These variations may lead to dysregulation, gain-of-function, or loss-of-function of the affected genes (B. Raby, 2018). The sensitive genes that require or produce precise quantities of a protein product tend to suffer more from these variations (Bacino, 2017).

Any size mutation may be pathogenic and must be categorized as to how likely the mutation is to cause disease. The American College of Medical Genetics (ACMG) has classified mutations in five categories, which are as follows: pathogenic, likely pathogenic, uncertain significance, likely benign, and benign. The “likely pathogenic” and “likely benign” refer to weaker evidence than their respective pathogenic and benign categories, and “uncertain significance” refers to evidence that does not meet criteria for benignity or pathogenicity or has conflicting evidence from both sides (B. Raby, 2018). Prediction algorithms have been used to interpret variants and to predict whether a variant will affect the gene function or splicing of the gene. These algorithms are publicly available but have a tendency of predicting the harmful impact of a variant. The specificity of these databases has been estimated at 60-80% (Li et al., 2017).
Due to the enormous number of variants, as well as the rate that variants are discovered, comprehensive databases of genetic variants have been published and are easily available. For example, the Genome-Wide Repository of Associations Between SNPs and Phenotypes (GRASP) database includes information from over 2000 studies and over one million variant-related results (B. Raby, 2018). Databases focusing on cancer-specific variants, reference sequences, and the general population are all available publicly (Li et al., 2017).

Spontaneous mutations accumulate in somatic cells over a lifetime. Early somatic mutations can cause developmental disorders while the accumulation of mutations throughout life can lead to cancer and contribute to aging (Martincorena & Campbell, 2015). Molecular profiles of tumors have clinical utility in guiding the clinical management of cancer patients, providing diagnostic or prognostic information, or identifying a potential treatment regimen (Li et al., 2017). Increasingly, somatic mutations are being identified in diseases other than cancer, such as neurodevelopmental diseases (Poduri, Evrony, Cai, & Walsh, 2013).

A malignant neoplasm is another term for cancer, which may encompass many types including breast, prostate, skin, lung, rectum, colon, and brain. Gastrointestinal stromal tumors (GISTs) are considered rare neoplasms with approximately 95% of these cancers non-hereditary; GISTs are mainly identified by KIT protein expression with typical mutations in the KIT or platelet-derived growth factor receptor alpha (PDGFRA) genes (Morgan, Raut, Duensing, & Keedy, 2018). These GISTs are the most common mesenchymal tumor of the gastrointestinal tract that originate from the cell of Cajal (Comandini, Damiani, & Pastorino, 2017). Primary prostate and lung tumors have been associated with different types of GISTs such as gastric and small bowel; genetic analysis of one patient found “that the gastric GIST and abdominal tumors were characterized by two different c-KIT mutations (Comandini et al., 2017).” Extragastrintestinal stromal tumors (EGISTs) are another type of rare neoplasm which also arise in the gastrointestinal tract. Liu et al. (2014) report that an EGIST was identified in the prostate of a male patient. “The results of immunohistochemical staining showed positive immunoreactivity for cluster of differentiation (CD)117 (c-kit), CD34 and DOG1 in the tumor. On mutation analysis, loss of heterozygosity of the c-kit gene was observed in the prostatic EGIST; however, the platelet-derived growth factor receptor-α (PDGFRA) gene was considered to be normal (Liu et al., 2014).” Due to the rarity of EGIST of the prostate, immunohistochemistry analysis is important to confirm a diagnosis.

Mutations of the KIT and PDGFRA genes in small cell neuroendocrine carcinoma (SCNEC) of the prostate have been researched by Terada (2012). A total of 706 malignant prostate tumors were identified, and four of these tumors were classified as SCNEC. Of these four tumors, three tumors were positive for KIT, and PDGFRA, among other genes. Molecular genotyping via PCR showed no KIT or PDGFRA mutations (Terada, 2012). Another study completed by McCabe, Spyropoulos, Martin, and Moreno (2008) noted that homeobox C6 (HOXC6) is overexpressed in prostate cancers and completed an analysis of prostate cancer cells to identify which promoters are bound by HOXC6. “We show that HOXC6 directly regulates expression of bone morphogenetic protein 7, fibroblast growth factor receptor 2, insulin-like growth factor binding protein 3, and platelet-derived growth factor receptor alpha (PDGFRA) in prostate cells (McCabe et al., 2008).” The researchers also note that PDGFRA is able to reduce the proliferation of prostate cancer cells, and that if HOXC6 is overexpressed, the effects of PDGFRA inhibition may be overcome. The fusion gene FIP1L1-PDGFRα has also been associated with chronic eosinophilic leukemia (Legrand et al., 2013).

Clinical Validity and Utility

Advancements in technology and availability of sequencing, previously constrained by limitations of sequential single-gene testing on limited patient samples, have led to significant strides in our understanding of the genetic basis of inherited and somatic conditions. Variants detected by genetic testing include inherited germline variants and somatic mutations; next generation sequencing (NGS) has allowed for superior detection of these mutations (Konnick & Pritchard, 2016). The accuracy of NGS varies depending on how many genes are sequenced; fewer genes tends to result
in higher accuracy since there will be more “probe-template overlap.” Although Sanger sequencing remains the most accurate at >99.99% accuracy, it cannot sequence a large amount of genes in a timely fashion and is best used for sequencing of a specific gene (Hulick, 2019).

NGS has been used to identify several types of somatic mutations associated with cancer and may help to single out therapeutic targets. Genetic mutations in \textit{BRCA1} & \textit{2} are associated with breast and ovarian cancer. Kowalik et al. (2019) have identified somatic genetic mutations in \textit{BRCA1} & \textit{2} for ovarian cancer prognostic purposes using NGS. Ovarian cancer tissue samples were used for the analysis. A total of 3\% of mutations (6/201) were identified as somatic; with only 24\% (49/201) of samples identified with a pathogenic mutation overall (Kowalik et al., 2019). The other 35 mutations were of germline origin. This is similar to the report by Nagahashi et al. (2019) which states that approximately 2.5\% of \textit{BRCA1} & \textit{2} mutations are somatic.

The clinical validity of a genetic test depends primarily on the expressivity and penetrance of a given phenotype. Penetrance refers to the likelihood of developing a disease when the pathogenic mutation is present, and expressivity refers to the variations in the way the disease is expressed. For example, virtually any mutation in the \textit{APC} gene will cause symptoms of familial adenomatous polyposis, thereby increasing the clinical validity of an \textit{APC} assessment. Some conditions may not clinically manifest at all despite a mutated genotype (B. Raby, Kohlmann, Wendy, Venne, Vickie, 2018).

The clinical utility of a genetic test generally relies on available treatments for a condition. Conditions such as Huntington’s Disease that do not have many options for treatment will have limited clinical utility compared to another condition even though the actual test is highly valid. Factors such as severity of the disease and management options affect the clinical utility of a genetic test (B. Raby, Kohlmann, Wendy, Venne, Vickie, 2018).

Hayano et al. (2016); McCabe et al. (2008) noted that homeobox C6 (HOXC6) is overexpressed in prostate cancers and completed an analysis of prostate cancer cells to identify which promoters are bound by HOXC6.

\textbf{Guidelines and Recommendations}

\textbf{Association for Molecular Pathology (AMP), American Society of Clinical Oncology (ASCO), and College of American Pathologists (CAP) (Li et al., 2017)}

The Joint Commission recommended that somatic variants be categorized by and reported based on their impact on clinical care. The Joint Commission notes that somatic variants include indels, SNVs, fusion genes from genomic rearrangements, and CNVs and should focus on their impact on clinical care. Any variant may be considered a biomarker if it predicts response to therapy, influences prognosis, diagnosis, treatment decisions, or the gene function itself. The Joint Commission proposes four levels for these biomarkers which are as follows:

1. Level A, biomarkers that predict response or resistance to US FDA-approved therapies for a specific type of tumor or have been included in professional guidelines as therapeutic, diagnostic, and/or prognostic biomarkers for specific types of tumors;

2. Level B, biomarkers that predict response or resistance to a therapy based on well-powered studies with consensus from experts in the field, or have diagnostic and/or prognostic significance of certain diseases based on well-powered studies with expert consensus;

3. Level C, biomarkers that predict response or resistance to therapies approved by FDA or professional societies for a different tumor type (ie, off-label use of a drug), serve as inclusion criteria for clinical trials, or have diagnostic and/or prognostic significance based on the results of multiple small studies;
4. Level D, biomarkers that show plausible therapeutic significance based on preclinical studies, or may assist disease diagnosis and/or prognosis themselves or along with other biomarkers based on small studies or multiple case reports with no consensus (Li et al., 2017).

The Joint Commission also includes variants in different tiers based on the amount of evidence there is to support its significance. For example, tier 1 variants include significance of levels A and B and tier 2 includes significance of levels C and D. Tier 3 is variants of unknown significance (VUS), such as variants in cancer genes that have not been reported in any other cancers. These variants are not typically seen in significant frequencies in the general population. When evaluating these variants, the type of mutation and gene function should be considered. Tier 4 is benign variants or likely benign variants. These alleles are often observed in significant amounts in general populations. Tier 3 variants should be reported while ensuring that the most important information is communicated to the patient (Li et al., 2017).

National Comprehensive Cancer Network (NCCN) (NCCN, 2018, 2020)

Multiple somatic mutations have been incorporated into the diagnostic workups recommended by the NCCN. Furthermore, the NCCN has several guidelines which recommend that gene expression profiling, or multiple gene testing, may be helpful, more efficient and/or cost-effective for selected patients (NCCN, 2018, 2020). Please see the individual policies.

American College of Medical Genetics and Genomics (ACMG) and the Association for Molecular Pathology (AMP) (Richards et al., 2015)

The ACMG and AMP released criteria on the types and severity of mutations, which are as follows:

- **Very strong evidence of pathogenicity**: Null variants (nonsense, frameshifts, canonical +/- 1-2 splice sites, initiation codon, exon deletions) in a gene where loss of function (LOF) is a known mechanism of disease. The guidelines note to use caution in genes where LOF is not a mechanism, if LOF variants are at the 3’ end, if exon skipping occurs, and if multiple transcripts are present.

- **Strong**: Amino acid change to a pathogenic version, de novo mutations, established studies supporting a damaging gene or gene product, or if the prevalence of the variant is increased in affected individuals compared to healthy controls. The guidelines note to be careful of changes impacting splicing and if only the paternity has been confirmed.

- **Moderate**: Located in a mutational hot spot or well-established functional domain (e.g., active site of an enzyme) without a benign variation, absent from controls in Exome Sequencing Project, 1000 Genomes Project, or Exome Aggregation Consortium, detected in trans with pathogenic variants for a recessive disorder, protein length changes, novel missense changes where a different missense change has been pathogenic before, and a possible de novo mutation.

- **Supporting**: Co-segregation with disease in multiple affected family members in a gene definitively known to cause the disease, missense variant in a gene with low rate of benign missense variation, if the mutation has evidence that it is deleterious, if the patient’s phenotype is highly specific for disease with a single genetic cause.

The guidelines also list criteria for benign gene variants.

- **Stand-alone evidence of benignity**: Allele frequency is >5% in Exome Sequencing Project, 1000 Genomes Project, or Exome Aggregation Consortium
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- **Strong**: Allele frequency is greater than expected for disorder, observed in healthy adult with full penetrance at early age, lack of segregation in affected family members (although pathogenic variants may masquerade as nonsegregated), or well-established studies that show no damaging effect on protein production.

- **Supporting**: Missense variant of a gene for which truncating mutations are pathogenic, indels in repetitive region of unknown function, silent variants, variants of unknown significance, or a *trans* version of a *cis* mutation (Richards et al., 2015).

**American College of Medical Genetics (ACMG) (Kalia et al., 2016)**

The ACMG has released a list of genes for which secondary findings should be disclosed. Secondary findings refer to incidental findings unrelated to why a genetic test was originally ordered but are of significant clinical value to the patient. The portion of the table containing the conditions, the associated genes, and which variants should be report is listed below (Kalia et al., 2016):

<table>
<thead>
<tr>
<th>Condition</th>
<th>Gene(s)</th>
<th>Variants to Report</th>
</tr>
</thead>
<tbody>
<tr>
<td>Breast/ovarian cancer</td>
<td>BRCA1, BRCA2</td>
<td>KP, EP</td>
</tr>
<tr>
<td>Li-Fraumeni syndrome</td>
<td>TP53</td>
<td>KP, EP</td>
</tr>
<tr>
<td>Peutz-Jeghers syndrome</td>
<td>STK11</td>
<td>KP, EP</td>
</tr>
<tr>
<td>Juvenile polypsis</td>
<td>BMPR1A, SMAD4</td>
<td>KP, EP</td>
</tr>
<tr>
<td>PTEN hamartoma syndrome</td>
<td>PTEN</td>
<td>KP, EP</td>
</tr>
<tr>
<td>Lynch syndrome</td>
<td>MLH1, MSH2, MSH6, PMS2,</td>
<td>KP, EP</td>
</tr>
<tr>
<td>Familial adenomatous polyposis</td>
<td>APC</td>
<td>KP, EP</td>
</tr>
<tr>
<td>MYH-associated polyposis</td>
<td>MUTYH</td>
<td>KP, EP</td>
</tr>
<tr>
<td>Von Hippel Lindau syndrome</td>
<td>VHL</td>
<td>KP, EP</td>
</tr>
<tr>
<td>Retinoblastoma</td>
<td>RB1</td>
<td>KP, EP</td>
</tr>
<tr>
<td>Tuberous sclerosis complex</td>
<td>TSC1, TSC2</td>
<td>KP, EP</td>
</tr>
<tr>
<td>Wilms tumor</td>
<td>WT1</td>
<td>KP, EP</td>
</tr>
<tr>
<td>Multiple endocrine neoplasia 1 or 2</td>
<td>MEN1 (1), RET (2)</td>
<td>KP</td>
</tr>
<tr>
<td>Familial medullary thyroid cancer</td>
<td>RET</td>
<td>KP</td>
</tr>
<tr>
<td>Hereditary paraganglionoma-pheochromocytoma syndrome</td>
<td>SDHD, SDHAF2, SDHC, SDHB</td>
<td>KP, EP for all but SDHAF2 (KP only)</td>
</tr>
<tr>
<td>Neurofibromatosis type 2</td>
<td>NF2</td>
<td>KP, EP</td>
</tr>
<tr>
<td>Hypertrophic or dilated cardiomyopathy</td>
<td>MYBPC3, MYH7, TNNT2, TNN13, TPM1, MYL3, ACTC1, PRKAG2, GLA, MYL2, LMNA</td>
<td>KP, EP for LMNA, GLA, MYBPC3, TNNT2, KP only for MYH7, TNN13, MYL2</td>
</tr>
</tbody>
</table>

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<table>
<thead>
<tr>
<th>Condition</th>
<th>Genes</th>
<th>Coverage</th>
</tr>
</thead>
<tbody>
<tr>
<td>Catacholamnergic polymorphic ventricular tachycardia</td>
<td>RYR2</td>
<td>KP</td>
</tr>
<tr>
<td>Arrhythmogenic right ventricular cardiomyopathy</td>
<td>PKP2, DSP, DSC2, TMEM43, DSG2</td>
<td>KP, EP for all but DSP (KP only)</td>
</tr>
<tr>
<td>Romano-Ward Long QT syndromes, Brugada syndrome</td>
<td>KCNQ1, KCNH2, SCN5A</td>
<td>KP, EP for all</td>
</tr>
<tr>
<td>Familial hypercholesterolemia</td>
<td>LDLR, APOB, PCSK9</td>
<td>KP, EP for LDLR, KP only for APOB and PCSK9</td>
</tr>
<tr>
<td>Ehlers Danlos syndrome</td>
<td>COL3A1</td>
<td>KP, EP</td>
</tr>
<tr>
<td>Marfan syndrome, Loeys-Dietz syndrome, familial thoracic aortic aneurysms and dissections</td>
<td>FBN1, TGFBR1, TGFBR2, SMAD3, ACTA2, MYH11</td>
<td>KP, EP for all</td>
</tr>
<tr>
<td>Malignant hyperthermia sensitivity</td>
<td>RYR1, CACNA1S</td>
<td>KP only</td>
</tr>
<tr>
<td>Wilson disease (copper metabolism)</td>
<td>ATP7B</td>
<td>KP, EP</td>
</tr>
<tr>
<td>Ornithine transcarbamylase deficiency (urea cycle)</td>
<td>OTC</td>
<td>KP, EP</td>
</tr>
</tbody>
</table>

**American Society of Clinical Oncology (ASCO) (Robson et al., 2015)**

The ASCO published guidelines regarding genetic and genomic testing for cancer susceptibility. These guidelines state that the “ASCO recognizes that concurrent multigene testing (ie, panel testing) may be efficient in circumstances that require evaluation of multiple high-penetration genes of established clinical utility as possible explanations for a patient’s personal or family history of cancer. Depending on the specific genes included on the panel employed, panel testing may also identify mutations in genes associated with moderate or low cancer risks and mutations in high-penetration genes that would not have been evaluated on the basis of the presenting personal or family history… ASCO affirms that it is sufficient for cancer risk assessment to evaluate genes of established clinical utility that are suggested by the patient’s personal and/or family history (Robson et al., 2015).”

**European Society for Medical Oncology (ESMO) (Casali et al., 2018)**

The ESMO recommends that “Mutational analysis inclusion in the diagnostic work-up of all GISTs should be considered standard practice [II, A] (with the possible exclusion of < 2 cm non-rectal GISTs) (Casali et al., 2018).” The article also states that “Mutational analysis for known mutations involving KIT and PDGFRA can confirm the diagnosis of GIST, if doubtful (particularly in rare CD117/DOG1-negative suspect GIST). Mutational analysis has a predictive value for sensitivity to molecular-targeted therapy and to prognostic value. Its inclusion in the diagnostic work-up of all GISTs should be considered standard practice (Casali et al., 2018).”

**British Sarcoma Group (BSG) (Judson et al., 2017)**

The BSG has published guidelines on the management of GIST and state that the majority of GIST cases are associated with a KIT or PDGFRA mutation. The guidelines recommend the following:

- “The diagnosis should be made by a pathologist experienced in the disease and include the use of immunohistochemistry and mutational analysis, which should be performed by an accredited laboratory.”
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- If neoadjuvant treatment with imatinib is planned, it is vital to confirm the diagnosis, since there is a wide differential. It may be necessary to perform a percutaneous core needle biopsy if the tumour is inaccessible to endoscopic ultrasound-guided biopsy. Mutational analysis is obligatory, since some GISTs are insensitive to imatinib (e.g. those with D842V mutation in exon 18 of PDGFRA) (Judson et al., 2017)."

Applicable Federal Regulations

A search for the phrase “somatic mutation” yielded 17 results on 1/17/2020. Additionally, many labs have developed specific tests that they must validate and perform in house. These laboratory-developed tests (LDTs) are regulated by the Centers for Medicare and Medicaid (CMS) as high-complexity tests under the Clinical Laboratory Improvement Amendments of 1988 (CLIA ’88). As an LDT, the U. S. Food and Drug Administration has not approved or cleared this test; however, FDA clearance or approval is not currently required for clinical use.

Billing/Coding/Physician Documentation Information

This policy may apply to the following codes. Inclusion of a code in this section does not guarantee that it will be reimbursed. For further information on reimbursement guidelines, please see Administrative Policies on the Blue Cross Blue Shield of North Carolina web site at www.bcbsnc.com. They are listed in the Category Search on the Medical Policy search page.

Applicable service codes: 81175, 81176, 81233, 81236, 81261, 81262, 81263, 81264, 81265, 81266, 81267, 81268, 81301, 81305, 81314, 81315, 81316, 81340, 81341, 81342, 81370, 81371, 81372, 81373, 81374, 81375, 81376, 81377, 81378, 81379, 81380, 81381, 81382, 81400, 81401, 81402, 81403, 81405, 81479, 81599, 88237, 88239, 88240, 88241, 88241, 88240, 88241, 88269, 88271, 88272, 88273, 88275, 88280, 88283, 88285, 88289, 88291, 88299, 96040, S0265

BCBSNC may request medical records for determination of medical necessity. When medical records are requested, letters of support and/or explanation are often useful, but are not sufficient documentation unless all specific information needed to make a medical necessity determination is included.

Scientific Background and Reference Sources


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Policy Implementation/Update Information

1/1/2019  New policy developed. BCBSNC will provide coverage for general genetic testing for somatic disorders when it is determined to be medically necessary because the medical criteria and guidelines are met. Medical Director review 1/1/2019. Policy noticed 1/1/2019 for effective date 4/1/2019. (jd)

5/14/19    Reviewed by Avalon 1st Quarter 2019 CAB. Added “Related Policies” to Description section. Added item 4 under the When Covered section: “MSI testing for all solid tumors is considered medically necessary for individuals being considered for pembrolizumab (Keytruda) therapy”, along with statement regarding 5 gene tests to refer to policy AHS-M2109 Molecular Panel Testing of Cancers to Identify Targeted
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10/1/19  Reviewed by Avalon 2nd Quarter 2019 CAB. Minor revisions only: Changed item #5 under the When Covered section to a “Note” and minor update to the Related Policies section. No change to policy statement intent. Medical Director review 9/2019. (jd)

11/12/19  Wording in the Policy, When Covered, and/or Not Covered section(s) changed from Medical Necessity to Reimbursement language, where needed.


5/12/20  Reviewed by Avalon 1st Quarter 2020 CAB. Policy guidelines and references updated. The following updates were made to the Billing/Coding section: added 81314, 81233, 81236, 81305, and removed G0452. Medical Director review 4/2020. (jd)

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