Genetic Testing for Fanconi Anemia

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Line(s) of Business: HMO; PPO; QUEST; Medicare; FEP	**Precertification:** Refer to the GTM Utilization Review Matrix

I. Policy Description

Fanconi anemia (FA) is an inherited disorder in which cells cannot correctly repair inter-strand crosslinks (ICLs), a specific type of DNA damage that results in genomic instability. This can lead to bone marrow failure (such as aplastic anemia), leukemia, and/or solid tumors. FA is rare, occurring in one in 100,000 to 250,000 births, with an increased incidence in populations such as Ashkenazi Jews and South African Afrikaner populations.[1]

For guidance on prenatal or preconception screening for FA, please see AHS-M2179-Prenatal Screening (Genetic).

II. Indications and/or Limitations of Coverage

Application of coverage criteria is dependent upon an individual's benefit coverage at the time of the request. Specifications pertaining to Medicare and Medicaid can be found in the "Applicable State and Federal Regulations" section of this policy document.

1) For individuals who have received genetic counseling and who have clinical signs and symptoms of Fanconi anemia (FA), chromosome breakage testing or gene sequencing (single gene or multi-gene panel testing) for the diagnosis of FA **MEETS COVERAGE CRITERIA**.

2) For all other situations not discussed above, genetic testing for the diagnosis of FA **DOES NOT MEET COVERAGE CRITERIA**.

NOTES:

Note: For two or more gene tests being run on the same platform, please refer to AHS-R2162 Reimbursement Policy.

III. Table of Terminology

Term	Definition
ACMG	American College of Medical Genetics and Genomics
ACOG	American College of Obstetricians and Gynecologists

AML	Acute myeloid leukemia
ATM	Ataxia-telangiectasia mutated
ATR	Ataxia-telangiectasia mutated and Rad3-related protein
BMF	Bone marrow failure
BRCA2	*Breast cancer 2 gene*
CAP	College of American Pathologists
CBT	Chromosome breakage test
CCO	Cancer Care Ontario
CDK	Cyclin-dependent kinase
CI	Confidence interval
CLIA '88	Clinical Laboratory Improvement Amendments of 1988
CMS	Centers for Medicare and Medicaid Services
CNV	Copy number variants
DEB	Diepoxybutane
DNA	Deoxyribonucleic acid
FA	Fanconi anemia
FA-A	Fanconi anemia complementation group A
FA-C	Fanconi anemia complementation group C
FA-D1	Fanconi anemia complementation group D1 (breast cancer 2 gene related)
FANCA	Fanconi anemia complementation group A
FANCC	Fanconi anemia complementation group C
FANCD1	Fanconi anemia complementation group D1
FANCD2	Fanconi anemia complementation group D2
FANCE	Fanconi anemia complementation group E
FANCF	Fanconi anemia complementation group F
FANCG	Fanconi anemia complementation group G
FANCI	Fanconi anemia complementation group I
FANCM	Fanconi anemia complementation group M
FANCP	Fanconi anemia complementation group P
FARF	Fanconi Anemia Research Fund
FDA	Food and Drug Administration
FISH	Fluorescence in situ hybridization
GCT	Germ line tumor
G2	Second growth phase of the cell
HCT	Hematopoietic cell transplant
HSC	Hematopoietic stem cell
IBMF	Inherited bone marrow failure
ICL	Inter-strand cross link
IFAR	The International Fanconi Anemia Registry
LDT	Laboratory-developed test

MDS	Myelodysplastic syndrome
MMC	Mitomycin C
NCCN	The National Comprehensive Cancer Network
NGS	Next-generation sequencing
NORD	The National Organization for Rare Disorders
P/LP	Pathogenic or likely pathogenic
ROS	Reactive oxygen species
SCC	Squamous cell carcinoma
SLX4	*SLX4 structure-specific endonuclease subunit*
USPSTF	U.S. Preventive Services Task Force
VACTERL-H	Vertebral anomalies, anal atresia, congenital heart disease, tracheoesophageal fistula, esophageal atresia, renal anomalies, limb anomalies, and hydrocephalus
WES	Whole exome sequencing
WGS	Whole-genome sequencing

IV. Scientific Background

Primarily inherited as an autosomal recessive disorder, Fanconi anemia (FA) is associated with known mutations in at least 22 FA identified genes.[2] It is found equally in males and females, as well as in different ethnic groups; approximately 50% of FA patients are diagnosed by age ten.[3] Jung, et al. (2020) also noted that siblings with FA often have similar hematological courses, potentially attributed to similarity in causative variants and environmental factors but have different presentations of congenital anomalies (except for kidney abnormalities and microcephaly to a moderate degree). The three most mutated genes in FA are *FANCA*, *FANCC*, and *FANCG*; these comprise up to 80-90% of all FA cases, with *FANCA* mutations accounting for approximately 60% of cases worldwide.[1,4] The main function of this set of proteins is to repair the inter-strand crosslinks (ICL) that typically form during DNA replication and transcription.[1] A cell is estimated to repair about 10 ICLs per day, but as few as 20-40 unresolved ICLs can lead to cell death.[5]

The FA pathway may also play a role in other functions, such as metabolizing alcohol, ensuring the stability of the replication fork during DNA replication, managing oxidative stress as in providing defense from reactive oxygen species (ROS)-induced cell death, and repairing double strand breaks.[1,6-8] For example, a mutation in the *FANCC* gene was found to impede the cell's ability to clear out damaged mitochondria and viruses, which could eventually lower immunity to viral infection and contribute to the characteristic bone marrow failure.[9,10]

Fanconi anemia may manifest in several ways with symptoms including short stature, skin findings such as hyper- or hypo- pigmentation and café-au-lait skin lesions, microcephaly, and abnormalities in the thumb, eye, axial skeleton, ear, renal system, or urinary tract. There is also a potential connection between FA and the VACTERL-H association (three or more of the following: vertebral anomalies, anal atresia, congenital heart disease, tracheoesophageal fistula, esophageal atresia, renal anomalies, limb anomalies, and hydrocephalus) as the percentage of FA patients also meeting the criteria for VACTERL-H was much higher than previously found.[11] However, up to 25-40% of FA patients look physically

normal.[12] At the physiological level, the most common symptoms are bone marrow failure and cytopenias, such as pancytopenia, macrocytic anemia, or thrombocytopenia.[1] Bone marrow failure is reportedly the most common primary symptom in FA and presents itself in 70-80% of patients by age ten.[4] Though the exact mechanism of premature hematopoietic stem cell (HSC) loss in FA remains unclear, it is thought to be impacted by defective DNA repair, causing increased damage and cell cycle arrest, increased levels of reactive oxygen species and inflammatory cytokines, and damage caused by reactive aldehydes in the absence of intact repair pathways.[1]

Aplastic anemia, another common FA side effect which causes the body to halt the production of red blood cells, also typically occurs early, either leading to death or to a HSC transplant. Endocrine issues, such as growth hormone deficiency, abnormal glucose/insulin metabolism, dyslipidemia, pubertal delay, and hypothyroidism are also commonly associated with an FA diagnosis (about 80% of FA children and adults have at least one endocrine defect) and often lead to a worsening life quality in FA patients.[8,13]

Screening for Fanconi Anemia

The most common screening assay for Fanconi anemia is the chromosome breakage test. A DNA crosslinking agent, such as mitomycin C (MMC) or diepoxybutane (DEB), is used to induce chromosome breakage, and the cells are evaluated at their respective stages in the cell cycle. FA cells typically have more DNA damage and are forced to arrest in the G2 phase when these cells can be observed. Tests may be positive, negative, or inconclusive; a positive test typically shows about 90% of lymphocytes with increased breakage, a negative test shows no increased breakage, and an inconclusive test cannot provide any definitive answer.[14] Normal cells have a mean baseline of <.05 breaks per cell while FA cells may range from 0.02 – 0.85 breaks per cell. DEB (the more sensitive and specific agent) typically has a mean baseline of <.10 breaks per normal cell and from 1.06 to 23.9 breaks per FA cell.[15] The International Fanconi Anemia Registry (IFAR) found the mean standard error of breaks per cell of 104 FA patients to be 8.96 ± 0.448 and the mean standard error of percentage of cells with breaks to be 85.15% ± 1.99%, compared to 0.06 ± 0.004 breaks and 5.12% ± 0.28% of 224 non-FA patients.[16]

Inconclusive results are typically due to one of two possibilities—one is "mosaicism," where two separate populations of lymphocytes in the blood occur, and the other is where the patient has another underlying condition causing chromosome breakage. However, a mutation analysis can corroborate a diagnosis or provide further information. This can be particularly helpful in assessing the patient's family members, such as potential carriers, asymptomatic family members, or members who may develop clinical symptoms.[17]

More recently, researchers have utilized whole exome sequencing as a diagnostic method for FA. Historically, molecular diagnostics regarding FA have been challenging for the medical community because the disease is caused by hereditary patterns featuring point mutations and large genomic deletions in an estimated 22 genes.[18] Nonetheless, the whole exome sequencing method used in this study identified 93.3% of deletions and mutated alleles when compared to a previously validated method, leading the researchers to the conclusion that whole exome sequencing is efficient enough to characterize patients with FA.[18]

Clinical Utility and Validity

Due to the increased instability of an FA patient's genome, it is common to see an increased risk of cancer in patients with FA, particularly bone marrow cancers such as leukemia. A study found the observed to expected ratio of all cancers to be as high as 48 (i.e., the observed rate was 48 times higher than expected after controlling for factors such as age and sex).[19] The same study found the likelihood that an FA patient would develop acute myeloid leukemia (AML) to be 700 times higher than normal and the likelihood to develop any myelodysplastic syndrome (MDS) to be 6000 times higher.[19] Underlying FA disease mechanisms may also be causing patients to develop cancers at a much earlier age than typically observed. A study focusing on 35 FA patients found that when compared to the general population, those afflicted by FA were, on average, diagnosed with head and neck squamous cell carcinoma 31 years earlier than controls (32 years for FA patients, 63 years for general population). FA mutation type may also play a factor in cancer development as another study found that FA patients with *FANCA* mutations developed cancer at a significantly older age than those with other mutations; however, mutation type did not seem to affect the overall survival rates of FA cancer patients.[20] Furthermore, the common risk factors, such as tobacco or alcohol consumption, were typically not a factor for the FA patients as is usually seen in the general population.[21]

Another example of how intertwined the FA proteins and pathway is with cancer is found in the *FANCD1* (Fanconi anemia complementation group D1) gene. The *FANCD1* gene, also known as *BRCA2*, is a gene whose mutations often lead to a higher risk of breast cancer. The *BRCA2* (-/-) cell reacts the same way an FA cell does when treated with the crosslinking agents and *BRCA2* co-localizes with *FANCD2* at damaged sections of DNA. The patients with heterozygous genotypes of *BRCA2* are historically more likely to have a higher risk of breast and ovarian cancer.[12]

Novel studies have further demonstrated the risk of germline mutations in FA complementation group (FANC) of the FA pathway in cancer. *FANCD2* (Fanconi anemia complementation group D2) was found to confer a malignant phenotype in esophageal squamous cell carcinoma, and cyclin-cyclin-dependent kinase (CDK) and ataxia-telangiectasia RAD3-related/ataxia-telangiectasia mutated (ATR/ATM) signaling was shown to help in depletion of FANCD2 protein expression and suppress cancer cell proliferation.[22] In a different study done on a Han Chinese population, Yu, et al. (2020) identified that Fanconi anemia complement group F (*FANCF*), though already known to impact cell proliferation and DNA repair, can increase risk of colorectal cancer if hypomethylated. Aberrant methylation of *FANCF* was also observed in ovarian tumors, non-small-cell lung cancer, cervical cancer, and oral cancer previously in general populations.[23] This conveys the markedly increased predisposition to cancer via mutations in FA and FA pathway components.

Chang, et al. (2021) discusses novel diagnostic approaches for FA by single-cell sequencing and capillary nano-immunoassay. Next-generation sequencing (NGS) has been widely utilized for FA diagnosis but has limitations that may lead to unconfirmed genetic subtypes. Chang, et al. (2021) studies one FA cause with *FANCM* mutation by conducting the capillary-nano-immunoassay to analyze the expression profile of FA-associated proteins. This assay is designed to detect 417 blood disease genes, including the 17 known FA-related genes. In this case, Chang, et al. (2021) observed two homozygous mutations of the *FANCM* and *FANCD1* genes and abnormal expression of both genes simultaneously existed, diagnosing the patient as a FA-D1/FA-M dual subtype. According to the author, "compared with mixed cell sequencing, single-cell sequencing data shows more accuracy for the FA subtype evaluation, while the

capillary nano-immunoassay is a good method to detect the expression profile of abnormal or modified FA protein."[24]

Chan, et al. (2021) studied the genetic spectrum of FA-associated genes across populations of varying ancestries to explore potential genotype-phenotype associations in cancer. A total of 3,523 subjects in Singapore, of varying ancestry, were assessed for carrier frequency and variant spectrum of potentially pathogenic variants in 17 FA genes. The data suggested higher germline and somatic mutation burden between *FANCA* and *FANCC* with head and neck and lung squamous cell carcinomas and *FANCI* and *SLX4/FANCP* with uterine cancer. Additionally, Chan, et al. (2021) highlighted the differences in carrier frequencies in non-European populations, considering the fact that our knowledge about the clinical and genetic spectrum of FA is derived predominantly from populations of European ancestry. Consequently, "given the variable distribution of germline pathogenic variant carriers across different ancestries, genetic testing for molecular diagnosis should not be restricted to *FANCA*, *FANCC*, and *FANCG*, which are reported more frequently in FA patients of European descent, but should include all known FA genes."[25]

Alter, et al. (2022) classified patients by age of diagnosis as part of a National Cancer Institute IBMFS cohort that included 178 pediatric patients and 26 adult patients. The authors were investigating whether FA cases could be distinguished and placed into subgroups by age diagnosed. The various features that were compared included the cumulative incidences of first adverse events (severe BMF leading to hematopoietic cell transplant or death, leukemia, or solid tumors) between an adult cohort and the pediatric cohort. The adult group did not consistently have the traditional FA features of birth defects, early-onset bone marrow failure or leukemia, and the group had more patients with the *FANCA* genotype. This adult group developed more head and neck squamous cell carcinoma and/or gynecological cancers (as compared to the pediatric group). The overall conclusion is Hematology and Oncology providers should investigate an FA diagnosis in adult patients that present with early-onset head and neck squamous cell carcinoma or gynecological cancer (with or without hematologic issues).[26]

Wang, et al. (2025) studied germline pathogenic or likely pathogenic (P/LP) variants in FA genes and the relative risk of developing germ line tumors (GCTs) using next-generation sequencing (NGS) in Chinese patients. A total of 68 samples from 66 patients with GCTs were analyzed using DNA-based targeted NGS. In total, 12.12% (8/66) carried heterozygous germline P/LP variant in FA genes, including *FANCA, BRCA2, FANCD2, FANCE,* and *SLX4*. The frequencies of germline P/LP variants were compared, "overall five FA genes were associated with a relative risk of GCT, with an odds ratio (OR) of 10.17 (95% CI, 4.87 to 21.27, P 5 2.90E-06."[27] Specifically, "P/LP variants in *FANCA, FANCD2,* and *SLX4* genes were associated with a relative risk, with ORs of 6.81 (95% CI, 1.67 to 27.73, P 5 .038), 13.92 (95% CI, 3.43 to 56.56, P 5 .0098), and 19.71 (95% CI, 4.87 to 79.89, P 5 .005), respectively."[27] These results shows that the carriers of heterozygous germline P/LP variants in a subset of FA genes are at an increased risk of developing GCTs. Wang, et al. (2025) concluded that GCT patients with these variants exhibited a higher mutational burden, more frequent gene fusion, and greater genomic instability compared to those without FA germline variant.

V. Guidelines and Recommendations

American College of Medical Genetics and Genomics (ACMG)

The guidelines for clinical genetics laboratories are specified in the 2018 (revised January 2021) edition of the ***Standards and Guidelines for Clinical Genetics Laboratories*** by the ACMG. The guidelines on FA state that:

- A cytogenetic evaluation for FA should include an induction of breakage with a crosslinking agent such as MMC or DEB (in addition to a baseline chromosome breakage).
- A well-established negative and positive control should be present and multiple cultures are recommended (if there is enough specimen available).
- At least 50 different cells (banded or unbanded) in the metaphase stage of the cell cycle should be analyzed, and the percentage of cells with aberration should reported.[28]

In 2021, ACMG released an updated guideline for screening for autosomal recessive and X-linked conditions during pregnancy and preconception. Their practice resource reviews aim to recommend "a consistent and equitable approach for offering carrier screening to all individuals during pregnancy and preconception" and replaces any earlier ACMG position statements on prenatal/preconception expanded carrier screening and provide the following recommendations:

- "Analytical validity of carrier screening is to be established by a laboratory in compliance with CLIA/CAP regulations and adhering to ACMG Laboratory Standards and Guidelines."
- "As evidence evolves, ClinVar and ClinGen continually update pathogenicity of variants and the association between genes and conditions, respectively."
- "Carrier screening enables those screened to consider their reproductive risks, reproductive options, and to make informed decisions."
- "Published evidence supports clinical utility for carrier screening of multiple conditions simultaneously."
- "The phrase 'expanded carrier screening' be replaced by 'carrier screening.'"
- "Adopting a more precise tiered system based on carrier frequency:
  - Tier 4: <1/200 carrier frequency (includes Tier 3) genes/condition will vary by lab
  - Tier 3: ≥ 1/200 carrier frequency (includes Tier 2) includes X-linked conditions
  - Tier 2: ≥1/100 carrier frequency (includes Tier 1)
  - Tier 1: CF [Cystic Fibrosis] + SMA [spinal muscular atrophy] + Risk Based Screening"

Fanconi anemia falls into Tier 2 carrier screening, according to the ACMG recommendation. For purposes of Fanconi anemia screening, this policy focuses on Tier 2 and Tier 3 carrier screening (as Tier 3 is inclusive of Tier 2). ACMG recommends that:

- "Tier 2 carrier screening stems from an ACOG recommendation for conditions that have a severe or moderate phenotype and a carrier frequency of at least 1/100." However, "data demonstrate that carrier screening for two common conditions using a carrier frequency threshold of 1/100 may not be equitable across diverse populations. Others have shown that limiting the carrier frequency to ≥1/100 creates missed opportunities to identify couples at risk for serious

conditions."

- "We define Tier 3 screening as carrier screening for conditions with a carrier frequency ≥1/200 . . . Tier 2 and Tier 3 screening prioritize carrier frequency as a way to think about conditions most appropriate for screening in the general population. However, when ACOG proposed this level, they did not specify whether it was thinking about carrier frequency in terms of the global population or subpopulations. We use "carrier frequency" to mean in any ethnic group with reasonable representation in the United States."
- "All pregnant patients and those planning a pregnancy should be offered Tier 3 carrier screening."
- ACMG does NOT recommend:
  - Offering Tier 1 and/or Tier 2 screening, because these do not provide equitable evaluation of all racial/ethnic groups.
  - Routine offering of Tier 4 panels.
- "Carrier screening paradigms should be ethnic and population neutral and more inclusive of diverse populations to promote equity and inclusion."
- "All pregnant patients and those planning a pregnancy should be offered Tier 3 carrier screening for autosomal recessive (Tables 1–5) and X-linked (Table 6) conditions."
- "Reproductive partners of pregnant patients and those planning a pregnancy may be offered Tier 3 carrier screening for autosomal recessive conditions (Tables 1–5) when carrier screening is performed simultaneously with their partner."
- "All XX patients should be offered screening for only those X-linked genes listed in Table 6 as part of Tier 3 screening."
- "When Tier 1 or Tier 2 carrier screening was performed in a prior pregnancy, Tier 3 screening should be offered."[29]

ACMG table 2 lists autosomal recessive genes for screening with carrier frequency and includes Fanconi anemia, complementation C, as reported below.[29]

Table 2. Autosomal recessive genes for screening with carrier frequency <1/50 to ≥1/100.

OMIM gene	OMIM gene name	Maximum carrier frequency[a]	OMIM phenotype	Conditions
610142	*CEP290*	0.014422	610188	Joubert syndrome 5
			611755	Leber congenital amaurosis 10
607839	*GBE1*	0.013799	232500	Glycogen storage disease, type IV
			263570	GBE1-related disorders
606800	*GAA*	0.013565	232300	Glycogen storage disease, type II (Pompe disease)
100725	*CHRNE*	0.013526	100725	Myasthenic syndrome, congenital, 4A, slow-channel
				Myasthenic syndrome, congenital, 4B, fast-channel
613742	*G6PC*	0.013401	232200	Glycogen storage disease type IA
611409	*OCA2*	0.013113	203200	Oculocutaneous albinism brown and type II
120120	*COL7A1*	0.012995	226600	Recessive dystrophic epidermolysis bullosa
600509	*ABCC8*	0.012242	618857	Diabetes mellitus, permanent neonatal 3
612724	*ALDOB*	0.012119	229600	Hereditary fructosuria
613899	*FANCC*	0.011992	227645	Fanconi anemia, complementation group C
604597	*GRIP1*	0.011989	617667	Fraser syndrome
248611	*BCKDHB*	0.011760	245600	Maple syrup urine disease
613726	*ANO10*	0.010781	613728	Spinocerebellar ataxia 10
104170	*NAGA*	0.010637	609241	Schindler disease, type 1
				Schindler disease, type 3
607608	*SMPD1*	0.010259	257200	Niemann–Pick disease, type A
			607616	Niemann–Pick disease, type B
608400	*USH2A*	0.010203	276901	Usher syndrome, type 2A
609058	*MMUT*	0.009999	251000	Methylmalonic aciduria–methylmalonyl–CoA mutase deficiency
600650	*CPT2*	0.009742	600649	Carnitine palmitoyltransferase II deficiency, infantile
			608836	Carnitine palmitoyltransferase II deficiency, lethal neonatal
608894	*AHI1*	0.009740	608629	Joubert syndrome 3

OMIM Online Mendelian Inheritance in Man.[55]
[a]After rounding values are < 0.02 and ≥ 0.01 (two decimal places).

American College of Obstetricians and Gynecologists (ACOG) Committee Opinion on Carrier Screening for Genetic Conditions

In March 2017, ACOG issued a Committee Opinion on Carrier Screening for Genetic Conditions. Regarding Fanconi anemia, ACOG asserts the following:

"Fanconi anemia can be caused by mutations in at least 15 different genes, but 80–90% of cases are due to mutation in one of three genes: 1) *FANCA*, 2) *FANCC*, and 3) *FANCG*. Affected individuals can experience bone marrow failure; increased risk of cancer, including leukemia and solid tumors; and structural defects such as short stature, skin pigment changes, nervous system abnormalities (including central nervous system malformations), eye and ear malformations and hearing loss, skeletal abnormalities in particular affecting the thumb or forearms, gastrointestinal abnormalities (including effects on the oral cavity), and others. Of note, 25–40% of affected individuals do not have any physical abnormalities."[30]

These ACOG guidelines were reaffirmed in 2023.

Second Pediatric Blood and Marrow Transplant Consortium International Conference on Late Effects after Pediatric HCT

Due to recent increase in survival following a hematopoietic cell transplant (HCT), the conference recommends continued screening and follow up with a wide variety of specialists, with focus on the late side-effects of HCT. The conference emphasizes the importance of screening for cancer due to the increased cumulative risk.[31]

The National Organization for Rare Disorders (NORD)

The National Organization for Rare Disorders has published several recommendations for testing patients with suspected FA. These recommendations state that "FA should be suspected and tested for in any infant born with the thumb and arm abnormalities described previously. Anyone developing aplastic anemia at any age should be tested for FA, even if no other defects are present. Any patient who develops squamous cell carcinoma of the head and neck, gastrointestinal or gynecologic system at an early age with or without a history of tobacco or alcohol use, should be tested for FA. Many FA patients show no other abnormalities. It is essential to test for FA before contemplating stem cell transplantation for aplastic anemia or treatment for cancer, as standard chemotherapy and radiation protocols may prove toxic to FA patients."[3]

"Complementation testing is usually done first in order to identify which FA gene is mutated. Sequence analysis of the appropriate gene can then be done to determine the specific mutation in that gene. If a mutation is not identified, deletion/duplication analysis is available clinically for the genes associated with FA. Targeted mutation analysis is available for the common Ashkenazi Jewish FANCC mutation."[3]

Cancer Care Ontario (CCO)

In December 2016, the CCO published recommendations for malignant hematology conditions. It is stated that patients aged <50 years with suspected aplastic anemia may be tested for FA via a peripheral blood chromosomal breakage analysis, such as the diepoxybutane test (DEB Test). However, "it would also be indicated to screen older patients if FA is clinically suspected. It is difficult to set an upper age limit for FA screening, as anecdotal cases have been diagnosed in the fifth decade (unpublished observations). Screen all patients who are transplant candidates and siblings of FA patients." An abdominal ultrasound scan and echocardiogram is also indicated in some instances as "an enlarged spleen and/or lymph nodes raise the possibility of a malignant haematological disorder as the cause of the pancytopenia. In younger patients, abnormal or anatomically displaced kidneys are features of FA."[32]

The National Comprehensive Cancer Network (NCCN)

As FA often results in higher incidence of cancers, the NCCN has noted some observations regarding this condition. In the guideline for Esophageal and Esophagogastric Junction Cancers, the NCCN stated that

"The genes involved in Fanconi anemia (FA) include FA complementation groups A–E, with FA-A (FANCA) located at 16q24.3; FA-B (FANCB), unknown; FA-C (FANCC) at 9q22.3; FA-D (FANCD) at 3p26–p22; and FA-E (FANCE), unknown. Mutations in FANCA and FANCC have been identified. Individuals are identified by pancytopenia and chromosome breakage and hematologic abnormalities, including anemia, bleeding, and easy bruising. Increased frequency of SCC of the esophagus as well as other squamous epithelium is observed. Karyotyping does not identify individuals with FA, but enhanced chromosome breakage with mitomycin C can identify homozygotes but not heterozygotes."[33]

United Kingdom National Multidisciplinary Guidelines

These recommendations were specifically made in the context of head and neck cancers. The recommendations for Fanconi anemia (FA) are as follows:

- "FA patients should receive prophylactic vaccination against high-risk HPV virus."
- "FA patients should have quarterly screening for head and neck squamous cell carcinoma and an aggressive biopsy policy…treatment for head and neck squamous cell carcinoma with surgery alone where possible."
- "FA patients should follow up with a specialty Fanconi clinic."[34]

U.S. Preventive Services Task Force (USPSTF)

No U.S. Preventive Services Task Force recommendations for genetic testing for FA have been identified. A search for "Fanconi" on the USPSTF website turned up no results on October 15, 2024.

Fanconi Anemia Research Fund (FARF)

In 2023, the Fanconi Anemia Research Fund updated their recommendations on testing and genetic counseling. For a patient suspected of having FA:[35]

- "Any patient suspected of having FA should be referred to a hematologist and/or clinical geneticist or genetic counselor, who can arrange for diagnostic testing. As FA testing is highly specialized, particularly the evaluation of chromosome breakage in response to DNA damage, only laboratories with extensive experience should undertake this testing."
- "The recommended testing procedures are outlined in the flow chart in Figure 1. The flow chart presents one potential algorithm for testing, starting with chromosome breakage testing and ending with genotyping. However, genetic testing has become increasingly utilized as a first-line diagnostic test, especially for newborns and pediatric patients with multiple congenital anomalies. Regardless of the order of testing, it is important that both chromosome breakage and germline genetic testing be performed to obtain a precise diagnosis in all persons with suspected FA."
- The gold-standard test for diagnosing Fanconi anemia (FA) is the chromosome breakage test using DNA crosslinking agents, specifically diepoxybutane (DEB). Mitomycin C (MMC) may also be used, but it has a higher potential for false-positive results. Dotted line: If chromosome breakage testing is unavailable, a diagnosis of FA can be directly confirmed by genetic testing. If peripheral blood testing is negative but clinical suspicion for FA remains high, the negative result may be a false negative because of somatic mosaicism in the peripheral blood. Therefore, repeat testing on fibroblasts cultured from a skin biopsy should be performed. If the chromosome breakage testing is positive, FA panel testing should be performed. If FA panel testing is negative, whole exome sequencing (WES) and/or research testing should be considered. In cases where chromosome breakage testing on both blood and skin cells is negative, referral for evaluation of conditions that overlap clinically with FA should be considered."
- "Following a positive chromosome breakage test, NGS panel testing for clinically relevant FANC genes should be offered as the next step. Clinical laboratories have evolved to offer two types of panel tests: dedicated panels (laboratory pre-selected genes associated with a patient's

phenotype) and custom panels (self-selection of relevant genes from a large list of genes). When selecting a panel, it is important to consider whether the test has been designed to address variant hotspots and/or gene regions known to present reporting challenges. As an example, the FANCD2 gene has two pseudogenes that can complicate the accuracy and interpretation of test results. Because of rapidly evolving knowledge of FA, many laboratories have not yet added the more recently discovered FANC genes to their panels. Thus, most currently available panels evaluate only a subset of the 22 known FANC genes."

- "Following the diagnosis of FA, cytogenetic analysis of chromosomes in bone marrow cells should be performed using standard G-banding methodology. The goal of this analysis is to investigate for the presence of a clone with acquired chromosome abnormalities and, if present, to characterize the observed abnormalities. Identification of a clone, which involves the presence of the same numerical and/or structural chromosomal abnormalities in multiple cells, is an indication of an abnormal hematologic process. The significance of cytogenetic findings must be interpreted within the context of the clinical findings, bone marrow morphologic findings from hematopathology examination, and immunophenotyping results."

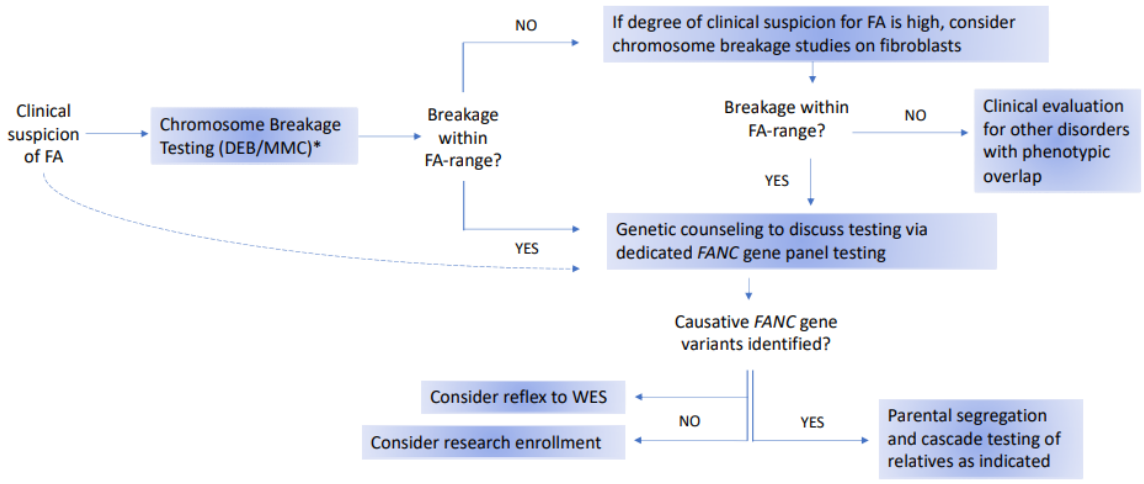


Figure 1: *Schematic representing a suggested algorithm for Fanconi anemia testing.*[35]

VI. Applicable State and Federal Regulations

DISCLAIMER: If there is a conflict between this Policy and any relevant, applicable government policy for a particular member [e.g., Local Coverage Determinations (LCDs) or National Coverage Determinations (NCDs) for Medicare and/or state coverage for Medicaid], then the government policy will be used to make the determination. For the most up-to-date Medicare policies and coverage, please visit the Medicare search website: https://www.cms.gov/medicare-coverage-database/search.aspx. For the most up-to-date Medicaid policies and coverage, visit the applicable state Medicaid website.

Food and Drug Administration (FDA)

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). LDTs are not approved or cleared by the U. S. Food and Drug Administration; however, FDA clearance or approval is not currently required for clinical use.

VII. Important Reminder

The purpose of this Medical Policy is to provide a guide to coverage. This Medical Policy is not intended to dictate to providers how to practice medicine. Nothing in this Medical Policy is intended to discourage or prohibit providing other medical advice or treatment deemed appropriate by the treating physician.

Benefit determinations are subject to applicable member contract language. To the extent there are any conflicts between these guidelines and the contract language, the contract language will control.

This Medical Policy has been developed through consideration of the medical necessity criteria under Hawaii's Patients' Bill of Rights and Responsibilities Act (Hawaii Revised Statutes §432E-1.4) or for QUEST members, under Hawaii Administrative Rules (HAR 1700.1-42), generally accepted standards of medical practice and review of medical literature and government approval status.

HMSA has determined that services not covered under this Medical Policy will not be medically necessary under Hawaii law in most cases. If a treating physician disagrees with HMSA's determination as to medical necessity in a given case, the physician may request that HMSA reconsider the application of the medical necessity criteria to the case at issue in light of any supporting documentation.

Genetic testing is covered for level 1 or 2A recommendations of the National Comprehensive Cancer Network (NCCN and in accordance with Hawaii's Patients' Bill of Rights and Responsibilities Act (Hawaii Revised Statutes §432E-1.4) or for QUEST members, the Hawaii Administrative Rules (HAR 1700.1-42).

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IX. Applicable CPT/HCPCS Procedure Codes

CPT	Code Description
81242	FANCC (Fanconi Anemia, complementation group C) (e.g.: Fanconi Anemia, type C) gene analysis, common variant (e.g.: IVS4+4A>T)
81412	Ashkenazi Jewish associated disorders (eg, Bloom syndrome, Canavan disease, cystic fibrosis, familial dysautonomia, Fanconi anemia group C, Gaucher disease, Tay-Sachs

CPT	Code Description
	disease), genomic sequence analysis panel, must include sequencing of at least 9 genes, including ASPA, BLM, CFTR, FANCC, GBA, HEXA, IKBKAP, MCOLN1, and SMPD1
81443	Genetic testing for severe inherited conditions (eg, cystic fibrosis, Ashkenazi Jewish-associated disorders [eg, Bloom syndrome, Canavan disease, Fanconi anemia type C, mucolipidosis type VI, Gaucher disease, Tay-Sachs disease], beta hemoglobinopathies, phenylketonuria, galactosemia), genomic sequence analysis panel, must include sequencing of at least 15 genes (eg, ACADM, ARSA, ASPA, ATP7B, BCKDHA, BCKDHB, BLM, CFTR, DHCR7, FANCC, G6PC, GAA, GALT, GBA, GBE1, HBB, HEXA, IKBKAP, MCOLN1, PAH)
88230	Tissue culture for non-neoplastic disorders; lymphocyte
88248	Chromosome analysis for breakage syndromes; baseline breakage, score 50-100 cells, count 20 cells, 2 karyotypes (eg, for ataxia telangiectasia, Fanconi anemia, fragile X)
88249	Chromosome analysis for breakage syndromes; score 100 cells, clastogen stress (eg, diepoxybutane, mitomycin C, ionizing radiation, UV radiation
88291	Cytogenetics and molecular cytogenetics, interpretation and report

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Procedure codes appearing in Medical Policy documents are included only as a general reference tool for each policy. They may not be all-inclusive.

X. Policy History

Action Date	Action
June 01, 2023	Policy created
March 17, 2026	Policy approved by Medical Directors
March 27, 2026	Policy approved at UMC
August 1, 2026	Policy effective date following notification period