AACC 2021 CLFS Recommendations

Code	Code Desciption	AACC Crosswalk Recommendation	Rationale	Proposed NLA
Reconsiderati	on			
81307	PALB2 (partner and localizer of BRCA2) (eg, breast and pancreatic cancer) gene analysis; full gene sequence	81317	The work and resources align with the number of exons studied in the PALB2 gene analysis, full gene sequence.	\$676.50
Molecular Pat				
8XX00	SF3B1 (splicing factor [3b] subunit B1) (eg, myelodysplastic syndrome/acute myeloid leukemia) gene analysis, common variants (eg, A672T, E622D, L833F, R625C, R625L)	81120	The methodology, resources, and amount of genetic material sequenced are comparable to that of IDH1 common variants. Both assess genes for an oncology disorder and similar number of variants.	\$193.25
8XX01	SRSF2 (serine and arginine-rich splicing factor 2) (eg, myelodysplastic syndrome, acute myeloid leukemia) gene analysis, common variants (eg, P95H, P95L)	81233	The methodology, resources, and amount of genetic material sequenced are comparable to that of BTK common variants. Both assess genes for an oncology disorder and similar number of variants.	\$175.40
8XX02	U2AF1 (U2 small nuclear RNA auxiliary factor 1) (eg, myelodysplastic syndrome, acute myeloid leukemia) gene analysis, common variants (eg, S34F, S34Y, Q157R, Q157P)	81120	The methodology, resources, and amount of genetic material sequenced are comparable to that of IDH1 common variants. Both assess genes for an oncology disorder and similar number of variants.	\$193.25
8XX03	ZRSR2 (zinc finger CCCH-type, RNA binding motif and serine/arginine-rich 2) (eg, myelodysplastic syndrome, acute myeloid leukemia) gene analysis, common variant(s) (eg, E65fs, E122fs, R448fs)	81120	The methodology, resources, and amount of genetic material sequenced are comparable to that of IDH1 common variants. Both assess genes for an oncology disorder and similar number of variants.	\$193.25
8X000	NTRK1 (neurotrophic receptor tyrosine kinase 1) (eg, solid tumors) translocation analysis	81315	The methodology, resources, and amount of genetic material sequenced are comparable to that of PML/RARalpha translocation analysis	\$207.31
8X001	NTRK2 (neurotrophic receptor tyrosine kinase 2) (eg, solid tumors) translocation analysis	81315	The methodology, resources, and amount of genetic material sequenced are comparable to that of PML/RARalpha translocation analysis.	\$207.31
8X002	NTRK3 (neurotrophic receptor tyrosine kinase 3) (eg, solid tumors) translocation analysis	81315	The methodology, resources, and amount of genetic material sequenced are comparable to that of PML/RARalpha translocation analysis.	\$207.31

BX003 TP31 (tumor protein 53) (eg. Li-Fraumeni syndrome) gene analysis; full gene sequence analysis; fund gene sequence analysis; trageted sequence analysis (eg. 4 oncology) B1298 The methodology, resources, and amount or genetic material sequence analysis (eg. 4 oncology) S041.85 BX004 TP53 (tumor protein 53) (eg. Li-Fraumeni syndrome) gene analysis; trageted sequence analysis (eg. 4 oncology) B1334 The methodology, resources, and amount or genetic material sequenced are comparable to that of MSH 6 hown familial variants. Both assess thrown familial sequence analysis. S308.00 BX005 MPL (MPL, proto-oncogene, thrombopoletin r	8X020	NTRK (neurotrophic-tropomyosin receptor tyrosine kinase 1, 2, and 3) (eg, solid tumors) translocation analysis	81315 X 2.5	The methodology, resources, and amount of genetic material sequenced are comparable to that of 81315 X 2.5	\$207.31 X 2.5 = \$518.26
8X004analysis; targeted sequence analysis [eg. 4 oncology]81334of genetic material sequenced are comparable to that of K96 known familial variants. Both assess targeted sequences in carcer-related genes.8X005analysis; known familial variant81299The methodology, resources, and amount of genetic material sequenced are comparable to that of K96 known familial variant.5329.518X006MPL (MPL proto-oncogene, thrombopoletin receptor) [eg. wyeloproliferative disorder) gene analysis; common variants81120The methodology, resources, and amount of genetic material sequenced are comparable to that of K96 known familial variants.5329.518X006MPL (MPL proto-oncogene, thrombopoletin receptor) [eg. wyeloproliferative disorder) gene analysis; sequence analysis.81120The methodology, resources, and amount of genetic material sequenced are comparable to that of KPM1 gene analysis.5246.528X007MPL (MPL proto-oncogene, thrombopoletin receptor) (eg. wyeloproliferative disorder) gene analysis; sequence analysis.81130The methodology, resources, and amount of genetic material sequenced are comparable to that of NPM1 gene analysis.5246.528X008MPL (AMPL proto-oncogene, thrombopoletin receptor) (eg. wyeloproliferative disorder) targeted sequence analysis.8133081330S246.528X008Genetic material sequenced are comparable to that of NPM1 gene analysis.S246.52S246.528X008Genetic material sequenced are comparable to that of NPM1 gene analysis.S329.518X009Genetic material sequenced are comparable to that of NPM1 gene analysis.S329.518X009Genetic material sequenced are comparable to th	8X003		81298	of genetic material sequenced are comparable to that of MSH6 full sequence analysis. Both assess germline cancer disposition genes and are relatively the	\$641.85
8X005analysis; known familial variant81299of genetic material sequenced are comparable to that of MSH6 known familial variants. Both assess known familial variants. Both assess known familial variants. Both assess known familial variants. Both assess known familial explored liferative disorder) gene analysis; common variants (eg. W515A, W515K, W515K)S308.008X006MPL (MPL proto-oncogene, thrombopoietin receptor) (eg, myeloproliferative disorder) gene analysis; common variants (eg. W515A, W515K, W515K)S193.25S193.258X007MPL (MPL proto-oncogene, thrombopoietin receptor) (eg, myeloproliferative disorder) gene analysis; sequence analysis exon 1081310The methodology, resources, and amount of genetic material sequenced are comparable to that of NPM1 gene analysis (81310)S246.528X008JAK2 (lanus kinase 2) (eg, myeloproliferative disorder) targeted sequence analysis (eg, exons 12 and 13)81272The methodology, resources, and amount of genetic material sequenced are comparable to that of KIT targeted sequence analysis, major breakpoints, qualitative or quantitative (eg on (mr) breakpoints, qualitative or quantitative, if erigo (mcr) breakpoints, qualitative or quantitative, if eperformed81315The methodology, resources, and amount of genetic material sequenced are comparable to that of translocation analysis, major breakpoint, qualitative and quantitative, if eperformed81315The methodology, resources, and amount of genetic material sequenced are comparable to that of translocation analysis, major breakpoint, qualitative and quantitative, if eperformed81315The methodology, resources, and amount of genetic material sequenced are comparable to that of translocat	8X004		81334	of genetic material sequenced are comparable to that of MSH6 known familial variants. Both assess targeted sequences in	\$329.51
8X006myeloproliferative disorder) gene analysis; common variants (eg. W515A, W515K, W515L, W515R)81120of genetic material sequenced are comparable to that of IDH1 common variants (81120)\$193.258X007MPL (MPL proto-oncogene, thrombopoletin receptor) (eg. myeloproliferative disorder) gene analysis; sequence analysis; exon 1081310The methodology, resources, and amount of genetic material sequenced are comparable to that of NPM1 gene analysis (81310)\$246.528X008JAK2 (Janus kinase 2) (eg. myeloproliferative disorder) targeted sequence analysis (eg. exons 12 and 13)81272The methodology, resources, and amount of genetic material sequenced are comparable to that of KIT targeted sequence analysis, major breakpoint, gualitative or quantitative\$329.518X009IGH@/BCL2(t(14:18)) (eg, follicular lymphoma) translocation analysis, major breakpoint, gualitative or quantitative81315The methodology, resources, and amount of genetic material sequenced are comparable to that of translocation analysis, major breakpoint, gualitative or quantitative\$207.318X010CCND1/IGH(t(11:14)) (eg, mante cell lymphoma) translocation analysis, major breakpoint, qualitative and quantitative, if performed81315The methodology, resources, and amount of genetic material sequenced are comparable to that of translocation analysis for PML-RARA\$207.31	8X005		81299	of genetic material sequenced are comparable to that of MSH6 known familial variants. Both assess known familial	\$308.00
8X007myeloproliferative disorder) gene analysis; sequence analysis, exon 1081310of genetic material sequenced are comparable to that of NPM1 gene analysis (81310)\$246.528X008JAK2 (Janus kinase 2) (eg, myeloproliferative disorder) targeted sequence analysis (eg, exons 12 and 13)81272The methodology, resources, and amount of genetic material sequenced are comparable to that of KIT targeted 	8X006	myeloproliferative disorder) gene analysis; common variants	81120	of genetic material sequenced are comparable to that of IDH1 common	\$193.25
8X008sequence analysis (eg, exons 12 and 13)81272of genetic material sequenced are comparable to that of KIT targeted sequence analysis.\$329.518X009IGH@/BCL2(t(14;18)) (eg, follicular lymphoma) translocation analysis, major breakpoint region (MBR) and minor cluster region (mcr) breakpoints, qualitative or quantitative81315The methodology, resources, and amount of genetic material sequenced are comparable to that of translocation analysis for PML-RARA\$207.318X010CCND1/IGH(t(11;14)) (eg, mantle cell lymphoma) translocation analysis, major breakpoint, qualitative and quantitative, if performed81315The methodology, resources, and amount of genetic material sequenced are comparable to that of translocation of genetic material sequenced are comparable to that of translocation analysis for PML-RARA\$207.31	8X007	myeloproliferative disorder) gene analysis; sequence analysis,	81310	of genetic material sequenced are comparable to that of NPM1 gene analysis	\$246.52
8X009analysis, major breakpoint region (MBR) and minor cluster region (mcr) breakpoints, qualitative or quantitative81315of genetic material sequenced are comparable to that of translocation analysis for PML-RARA\$207.318X010CCND1/IGH(t(11;14)) (eg, mantle cell lymphoma) translocation analysis, major breakpoint, qualitative and quantitative, if performedThe methodology, resources, and amount of genetic material sequenced are comparable to that of translocation\$207.31	8X008		81272	of genetic material sequenced are comparable to that of KIT targeted	\$329.51
analysis, major breakpoint, qualitative and quantitative, if performed81315of genetic material sequenced are comparable to that of translocation\$207.31	8X009	analysis, major breakpoint region (MBR) and minor cluster	81315	of genetic material sequenced are comparable to that of translocation	\$207.31
	8X010	analysis, major breakpoint, qualitative and quantitative, if	81315	of genetic material sequenced are comparable to that of translocation	\$207.31

87635	Infectious agent detection by nucleic acid (DNA or RNA); severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]), amplified probe technique	87502	This code represents similar methodology and resources to perform the testing.	\$95.80
Immunology				
86328	Immunoassay for infectious agent antibody(ies), qualitative or semiquantitative, single step method (eg, reagent strip); severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19])	86794 X 2.5	Qualitative or semiquantitative immunoassays for Zika virus IgM	\$16.85 X 2.5 = \$42.13
86769	Antibody; severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19])	86794 x 2.5	Qualitative or semiquantitative immunoassays for Zika virus IgM	\$16.85 X 2.5 = \$42.13
Chemistry				
81XX3	Alcohol (ethanol); any specimen except urine and breath, immunoassay (eg, IA, EIA, ELISA, RIA, EMIT, FPIA) and enzymatic methods (eg, alcohol dehydrogenase)	83520	Immunoassay for analyte other than infectious agent antibody or infectious agent antigen; quantitative, not otherwise specified represents the methodology being used for the assay. Similar resources required to perform assay.	\$17.27
82XX1	Estradiol; free, direct measurement (eg, equilibrium dialysis)	82670	Current coding is 82670. This code represents similar methodology and resources to perform the testing.	\$27.94
Therapeutic Dr	ug Assav			
80XXX	Acetaminophen	80299	This code represents similar methodology and resources to perform the testing.	\$18.64
80XX2	Amiodarone	80155	This code represents similar methodology and resources to perform the testing.	\$38.57
80XX1	Salicylate	80299	This code represents similar methodology and resources to perform the testing.	\$18.64

80XX3	Carbamazepine; 10,11-Epoxide	80155	This code represents similar methodology and resources to perform the testing.	\$38.57
80XX4	Felbamate	80199	This code represents similar methodology and resources to perform the testing and is used to treat seizures/epilepsy.	\$27.11
80XX5	Flecainide	80155	This code represents similar methodology and resources to perform the testing.	\$38.57
80XX6	Itraconazole	80187	This code represents similar methodology and resources to perform the testing and is used to treat antifungal infections.	\$27.11
80XX7	Leflunomide	80230	This code represents similar methodology and resources to perform the testing and is used for inflammatory disorders.	\$38.57
80XX8	Methotrexate	80230	This code represents similar methodology and resources to perform the testing and is used for inflammatory disorders.	\$38.57
802XX	Rufinamide	80199	This code represents similar methodology and resources to perform the testing and is used to treat seizures/epilepsy.	\$27.11