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Article Title: Billing and Coding: Molecular Pathology and Genetic Testing

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Article Text:

This Billing and Coding Article provides billing and coding guidance for molecular pathology services, genomic sequencing procedures and other multianalyte assays, multianalyte assays with algorithmic analyses, and applicable proprietary laboratory analyses codes and Tier 1 and Tier 2 molecular pathology procedures. Consistent with CFR, Title 42, Section 414.502 Advanced diagnostic laboratory tests must provide new clinical diagnostic information that cannot be obtained from any other test or combination of tests.

This instruction focuses on coding and billing for molecular pathology diagnostics and genetic testing. Nothing stated in this instruction implies or infers coverage.

Molecular diagnostic testing and laboratory developed testing are rapidly evolving areas and thus present billing and coding challenges. Due to the rapid changes in this field, the CMS Clinical Laboratory Fee Schedule pricing methodology does not account for the unique characteristics of these tests. These challenges have led to services being incorrectly coded and improperly billed. It is the MAC's responsibility to pay for services that are medically reasonable and necessary and coded correctly. The intent of this billing and coding article is to provide guidance for accurate coding and proper submission of claims.

Prior to January 1, 2013, each step of the process of a molecular diagnostic test was billed utilizing a separate CPT code to describe that process. Such billing was termed "stacking" with each step of a molecular diagnostic test utilizing a different CPT code to create a "Stack". The updates to CPT after January 1, 2013, were to create a more granular, analyte and/or gene specific coding system for these services and to eliminate, or greatly reduce, the "stacking" of codes in billing for molecular pathology services. The current CPT and HCPCS codes include all analytic services and processes performed with the test. This approach has resulted in the following subgroups of CPT codes:

- Genomic Sequencing Procedures
- Multi-Analyte with Algorithmic Analyses (MAAA)
- Proprietary Laboratory Analyses (PLA codes)
- Tier 1 - Analyte Specific codes; a single test or procedure corresponds to a single CPT code
- Tier 2 – Rare disease and low volume molecular pathology services

However, the updates to CPT since 2013 have NOT resulted in the elimination or reduction of stacking of codes in billing. Rather the billing of multiple CPT codes for a unique molecular pathology or genetic test has significantly increased over the last two (2) years. Coding issues have been identified throughout all the molecular pathology coding subgroups, but these issues of billing multiple CPT codes for a specific test have been significant in the Tier 2 (81403 - 81408) and Not Otherwise Classified (81479) codes. Per Title 42 of the United States Code (USC) Section 1320c-5(a)(3), providers are required by law to "provide economical medical services and then, only where medically necessary." In keeping with Title 42 of the USC Section 1320c-5(a)(3), claims inappropriately billed utilizing stacking or unbundling of services will be rejected or denied.

Many applications of the molecular pathology procedures are not covered services given a lack of benefit category (e.g., preventive service or screening for a genetic abnormality in the absence of a suspicion of disease) and/or failure to meet the medically reasonable and necessary threshold for coverage (e.g., based on quality of clinical evidence and strength of recommendation or when the results would not reasonably be used in the management of a beneficiary). Furthermore, payment of claims in the past (based on "stacking" codes) or in the future (based on the new code series) is not a statement of coverage since the service may not have been audited for compliance with program requirements and documentation supporting the medically reasonable and necessary testing for the beneficiary. Certain molecular pathology procedures may be subject to medical review (medical records requested). The medical records must support the service billed.

Molecular pathology tests for diseases or conditions that manifest severe signs or symptoms in newborns and in early childhood or that result in early death (e.g., Canavan disease) are subject to automatic denials since these tests are generally not relevant to a Medicare beneficiary.

The following types of tests are examples of services that are not relevant to a Medicare beneficiary, are not considered a Medicare benefit (statutorily excluded), and therefore will be denied as Medicare Excluded Tests:

- Tests considered screening in the absence of clinical signs and symptoms of disease that are not specifically identified by the law
- Tests performed to determine carrier screening
- Tests performed for screening hereditary cancer syndromes
- Prenatal diagnostic testing
- Tests performed on patients without signs or symptoms to determine risk for developing a disease or condition
- Tests performed to measure the quality of a process
- Tests without diagnosis specific indications
- Tests identified as investigational by available literature and/or the literature supplied by the developer and are not a part of a clinical trial

Screening services such as pre-symptomatic genetic tests and services used to detect an undiagnosed disease or disease predisposition are not a Medicare benefit and are not covered.

In accordance with the Code of Federal Regulations, Title 42, Subchapter B, Part 410, Section 410.32, the referring/ordering practitioner must have an established relationship with the patient, and the test results must be used by the ordering/referring practitioner in the management of the patient's specific medical problem.

For ease of reading, the term "gene" in this document will be used to indicate a gene, region of a gene, and/or variant(s) of a gene.

Coding Guidance

Notice: It is not appropriate to bill Medicare for services that are not covered as if they are covered. When billing for non-covered services, use the appropriate modifier.

Code selection is based on the specific gene(s) that is being analyzed. Codes that describe tests to assess for the presence of gene variants use common gene variant names. All of the listed variants would usually be tested; however, these lists are not exclusive. If additional variants, for the same gene, are also tested in the analysis they are included in the procedure and are not reported separately.

Full gene sequencing is not reported using codes that assess for the presence of gene variants unless the CPT code specifically states full gene sequence in the descriptor.

Tier 1 codes generally describe testing for a specific gene or Human Leukocyte Antigen (HLA) locus. Tier 2 molecular pathology procedure codes (81400-81408) are used to report procedures not listed in the Tier 1 molecular pathology codes (81161, 81200-81383). These codes represent rare diseases and molecular pathology procedures that are performed in lower volumes than Tier 1 procedures. These codes should rarely, if ever, be used unless instructed by other coding and billing articles.

If billing utilizing the following Tier 2 codes, additional information will be required to identify the specific analyte/gene(s) tested in the narrative of the claim or the claim will be rejected:

- 81403
- 81404
- 81405
- 81406
- 81407
- 81408

Unlisted Molecular Pathology - CPT Code 81479

Providers are required to use a procedure code that most accurately describes the service being rendered. If the analyte being tested is not represented by a Tier 1 code or is not accurately described by a Tier 2 code, the unlisted molecular pathology procedure code 81479 should be reported.

However, when reporting CPT code 81479, the specific gene being tested must be entered in block 80 (Part A for the UBO4 claim), box 19 (Part B for a paper claim) or electronic equivalent of the claim. Failure to include this information on the claim will result in Part A claims being returned to the provider and Part B claims being rejected. In addition, medical records may be requested when 81479 is billed. The medical record must clearly identify the unique molecular pathology procedure performed, its analytic validity and clinical utility, and why CPT code 81479 was billed.

When multiple procedure codes are submitted on a claim (unique and/or unlisted), the documentation supporting each code must be easily identifiable. If on review the contractor cannot link a billed code to the documentation, these services will be denied based on Title XVIII of the Social Security Act, Section 1833(e).

Testing for Multiple Genes and Next Generation Sequencing (NGS) testing

A panel of genes is a distinct procedural service from a series of individual genes. All services billed to Medicare must be medically reasonable and necessary. As such, if a provider or supplier submits a claim for a panel, then the patient's medical record must reflect that the panel was medically reasonable and necessary. Alternatively, if a provider or supplier bills for individual genes, then the patient's medical record must reflect that each individual gene is medically reasonable and necessary.

Genes can be assayed serially or in parallel. Genes assayed on the same date of service are considered to be assayed in parallel if the result of one (1) assay does not affect the decision to complete the assay on another gene, and the two (2) genes are being tested for the same indication.

Genes assayed on the same date of service are considered to be assayed serially when there is a reflexive decision component where the results of the analysis of one (1) or more genes determines whether the results of additional analyses are medically reasonable and necessary.

If the laboratory method is NGS testing, and the laboratory assays two (2) or more genes in a patient in parallel, then those two (2) or more genes will be considered part of the same panel, consistent with the NCCI manual Chapter 10, Section F, number 8.

If the laboratory assays genes in serial, then the laboratory must submit claims for genes individually. The order by the treating clinician must reflect whether the treating clinician is ordering a panel or single genes, and additionally, the patient's medical record must reflect that the service billed was medically reasonable and necessary.

CMS payment policy does not allow separate payment for multiple methods to test for the same analyte.

We would not expect that a provider or supplier would routinely bill for more than one (1) distinct laboratory genetic testing procedural service on a single beneficiary on a single date of service. In the rare circumstance that more than one (1) distinct genetic test is medically reasonable and necessary for the same beneficiary on the same date of service, the provider or supplier must attest that each additional service billed is a distinct procedural service using the 59 modifier.

-59 Modifier; Distinct Procedural Service

This modifier is allowable for radiology services and it may also be used with surgical or medical codes in appropriate circumstances.

When billing, report the first code without a modifier. On subsequent lines, report the code with the modifier. Under certain circumstances, it may be necessary to indicate that a procedure or service was distinct or independent from other non-Evaluation and Management (E/M) services performed on the same day. Modifier 59 is used to identify procedures/services, other than E/M services, that are not normally reported together, but are appropriate under the circumstances. Documentation must support a different session, different procedure or surgery, different site or organ system, separate incision/excision, separate lesion, or separate injury (or area of injury in extensive injuries) not ordinarily encountered or performed on the same day by the same individual. However, when another already established modifier is appropriate it should be used rather than modifier 59. Only if a more descriptive modifier is unavailable, and the use of modifier 59 best explains the circumstances, should modifier 59 be used.

The use of the 59 modifier will be considered an attestation that distinct procedural services are being performed rather than a panel **and may result in the request for medical records**.

Frequent use of the 59 modifier may be subject to medical review.

Genomic Sequencing Profiles (GSP)

When a GSP assay includes a gene or genes that are listed in more than one code descriptor, the code for the most specific test for the primary disorder sought must be reported, rather than reporting multiple codes for the same gene(s). Reporting multiple codes for the same gene will result in claim rejection or denial.

Multianalyte Assays with Algorithmic Analyses (MAAAs) and Proprietary Laboratory Analyses (PLA)

A valid PLA code takes precedence over Tier 1 and Tier 2 codes and must be reported if available. Reporting of a Tier 1 or Tier 2 code in this circumstance or in addition to a PLA code is incorrect coding and will result in claim rejection or denial.

Per CPT, the results of individual component procedure(s) that are inputs to the MAAAs may be provided on

the associated reporting, however these assays are not reported separately using additional codes. Claims reporting such, will be rejected or denied.

Date of Service (DOS)

As a general rule, the DOS for either a clinical laboratory test or the technical component of a physician pathology service is the date the specimen was collected. In situations where a specimen is collected over a period of two calendar days, the DOS is the date the collection ended. There are some exceptions to the DOS policy. Please refer to the CMS IOM Publication 100-04, Chapter 16, Section 40.8 for complete information related to the DOS policy.

Documentation Requirements

1. All documentation must be maintained in the patient's medical record and made available to the contractor upon request.
2. Every page of the record must be legible and include appropriate patient identification information (e.g., complete name, dates of service[s]). The documentation must include the legible signature of the physician or non-physician practitioner responsible for and providing the care to the patient.
3. The submitted medical record must support the use of the selected ICD-10-CM code(s). The submitted CPT/HCPCS code must describe the service performed.
4. In accordance with CFR Section 410.32, the medical record must contain documentation that the testing is expected to influence treatment of the condition toward which the testing is directed and will be used in the management of the beneficiary's specific medical problem.
5. The medical record must support that the referring/ordering practitioner who ordered the test for a specific medical problem is treating the beneficiary for this specific medical problem. An example of documentation that could support the practitioner's management of the beneficiary's specific medical problem would be at least two E/M visits performed by the ordering/referring practitioner over the previous six months.
6. The medical record must include documentation of how the ordering/referring practitioner used the test results in the management of the beneficiary's specific medical problem.
7. The ordering physician/nonphysician practitioner (NPP) documentation in the medical record must include, but is not limited to, history and physical or exam findings that support the decision making, problems/diagnoses, relevant data (e.g., lab testing, imaging results).
8. The medical record from the ordering physician/NPP must clearly indicate all tests that are to be performed.
9. Documentation requirements of the performing laboratory (when requested) include, but are not limited to, lab accreditation, test requisition, test record/procedures, reports (preliminary and final), and quality control record.

Coding Information

CPT/HCPCS Codes:

Group 1 Paragraph:

Note: Providers are reminded to refer to the long descriptors of the CPT codes in their CPT book.

Providers should refer to the current CPT book for applicable CPT codes.

Group 1 CPT Codes:

0001U	RED BLOOD CELL ANTIGEN TYPING, DNA, HUMAN ERYTHROCYTE ANTIGEN GENE ANALYSIS OF 35 ANTIGENS FROM 11 BLOOD

	GROUPS, UTILIZING WHOLE BLOOD, COMMON RBC ALLELES REPORTED
0004M	SCOLIOSIS, DNA ANALYSIS OF 53 SINGLE NUCLEOTIDE POLYMORPHISMS (SNPS), USING SALIVA, PROGNOSTIC ALGORITHM REPORTED AS A RISK SCORE
0005U	ONCOLOGY (PROSTATE) GENE EXPRESSION PROFILE BY REAL-TIME RT-PCR OF 3 GENES (ERG, PCA3, AND SPDEF), URINE, ALGORITHM REPORTED AS RISK SCORE
0006M	ONCOLOGY (HEPATIC), MRNA EXPRESSION LEVELS OF 161 GENES, UTILIZING FRESH HEPATOCELLULAR CARCINOMA TUMOR TISSUE, WITH ALPHA-FETOPROTEIN LEVEL, ALGORITHM REPORTED AS A RISK CLASSIFIER
0007M	ONCOLOGY (GASTROINTESTINAL NEUROENDOCRINE TUMORS), REAL-TIME PCR EXPRESSION ANALYSIS OF 51 GENES, UTILIZING WHOLE PERIPHERAL BLOOD, ALGORITHM REPORTED AS A NOMOGRAM OF TUMOR DISEASE INDEX
0007U	DRUG TEST(S), PRESUMPTIVE, WITH DEFINITIVE CONFIRMATION OF POSITIVE RESULTS, ANY NUMBER OF DRUG CLASSES, URINE, INCLUDES SPECIMEN VERIFICATION INCLUDING DNA AUTHENTICATION IN COMPARISON TO BUCCAL DNA, PER DATE OF SERVICE
0008U	HELICOBACTER PYLORI DETECTION AND ANTIBIOTIC RESISTANCE, DNA, 16S AND 23S RRNA, GYRA, PBP1, RDXA AND RPOB, NEXT GENERATION SEQUENCING, FORMALIN-FIXED PARAFFIN EMBEDDED OR FRESH TISSUE OR FECAL SAMPLE, PREDICTIVE, REPORTED AS POSITIVE OR NEGATIVE FOR RESISTANCE TO CLARITHROMYCIN, FLUOROQUINOLONES, METRONIDAZOLE, AMOXICILLIN, TETRACYCLINE AND RIFABUTIN
0009U	ONCOLOGY (BREAST CANCER), ERBB2 (HER2) COPY NUMBER BY FISH, TUMOR CELLS FROM FORMALIN FIXED PARAFFIN EMBEDDED TISSUE ISOLATED USING IMAGE-BASED DIELECTROPHORESIS (DEP) SORTING, REPORTED AS ERBB2 GENE AMPLIFIED OR NON-AMPLIFIED
0010U	INFECTIOUS DISEASE (BACTERIAL), STRAIN TYPING BY WHOLE GENOME SEQUENCING, PHYLOGENETIC-BASED REPORT OF STRAIN RELATEDNESS, PER SUBMITTED ISOLATE
0011M	ONCOLOGY, PROSTATE CANCER, MRNA EXPRESSION ASSAY OF 12 GENES (10 CONTENT AND 2 HOUSEKEEPING), RT-PCR TEST UTILIZING BLOOD PLASMA AND URINE, ALGORITHMS TO PREDICT HIGH-GRADE PROSTATE CANCER RISK
0012M	ONCOLOGY (UROTHELIAL), MRNA, GENE EXPRESSION PROFILING BY REAL-TIME QUANTITATIVE PCR OF FIVE GENES (MDK, HOXA13, CDC2 [CDK1], IGFBP5, AND CXCR2), UTILIZING URINE, ALGORITHM REPORTED AS A RISK SCORE FOR HAVING UROTHELIAL CARCINOMA
0013M	ONCOLOGY (UROTHELIAL), MRNA, GENE EXPRESSION PROFILING BY REAL-TIME QUANTITATIVE PCR OF FIVE GENES (MDK, HOXA13, CDC2 [CDK1], IGFBP5, AND CXCR2), UTILIZING URINE, ALGORITHM REPORTED AS A RISK SCORE FOR HAVING RECURRENT UROTHELIAL CARCINOMA
0016M	ONCOLOGY (BLADDER), MRNA, MICROARRAY GENE EXPRESSION PROFILING OF 219 GENES, UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED TISSUE, ALGORITHM REPORTED AS MOLECULAR

	SUBTYPE (LUMINAL, LUMINAL INFILTRATED, BASAL, BASAL CLAUDIN-LOW, NEUROENDOCRINE-LIKE)
0016U	ONCOLOGY (HEMATOLYMPHOID NEOPLASIA), RNA, BCR/ABL1 MAJOR AND MINOR BREAKPOINT FUSION TRANSCRIPTS, QUANTITATIVE PCR AMPLIFICATION, BLOOD OR BONE MARROW, REPORT OF FUSION NOT DETECTED OR DETECTED WITH QUANTITATION
0017U	ONCOLOGY (HEMATOLYMPHOID NEOPLASIA), JAK2 MUTATION, DNA, PCR AMPLIFICATION OF EXONS 12-14 AND SEQUENCE ANALYSIS, BLOOD OR BONE MARROW, REPORT OF JAK2 MUTATION NOT DETECTED OR DETECTED
0018U	ONCOLOGY (THYROID), MICRORNA PROFILING BY RT-PCR OF 10 MICRORNA SEQUENCES, UTILIZING FINE NEEDLE ASPIRATE, ALGORITHM REPORTED AS A POSITIVE OR NEGATIVE RESULT FOR MODERATE TO HIGH RISK OF MALIGNANCY
0019U	ONCOLOGY, RNA, GENE EXPRESSION BY WHOLE TRANSCRIPTOME SEQUENCING, FORMALIN-FIXED PARAFFIN EMBEDDED TISSUE OR FRESH FROZEN TISSUE, PREDICTIVE ALGORITHM REPORTED AS POTENTIAL TARGETS FOR THERAPEUTIC AGENTS
0022U	TARGETED GENOMIC SEQUENCE ANALYSIS PANEL, CHOLANGIOCARCINOMA AND NON-SMALL CELL LUNG NEOPLASIA, DNA AND RNA ANALYSIS, 1-23 GENES, INTERROGATION FOR SEQUENCE VARIANTS AND REARRANGEMENTS, REPORTED AS PRESENCE/ABSENCE OF VARIANTS AND ASSOCIATED THERAPY(IES) TO CONSIDER
0023U	ONCOLOGY (ACUTE MYELOGENOUS LEUKEMIA), DNA, GENOTYPING OF INTERNAL TANDEM DUPLICATION, P.D835, P.I836, USING MONONUCLEAR CELLS, REPORTED AS DETECTION OR NON-DETECTION OF FLT3 MUTATION AND INDICATION FOR OR AGAINST THE USE OF MIDOSTAURIN
0026U	ONCOLOGY (THYROID), DNA AND MRNA OF 112 GENES, NEXT-GENERATION SEQUENCING, FINE NEEDLE ASPIRATE OF THYROID NODULE, ALGORITHMIC ANALYSIS REPORTED AS A CATEGORICAL RESULT ("POSITIVE, HIGH PROBABILITY OF MALIGNANCY" OR "NEGATIVE, LOW PROBABILITY OF MALIGNANCY")
0027U	JAK2 (JANUS KINASE 2) (EG, MYELOPROLIFERATIVE DISORDER) GENE ANALYSIS, TARGETED SEQUENCE ANALYSIS EXONS 12-15
0029U	DRUG METABOLISM (ADVERSE DRUG REACTIONS AND DRUG RESPONSE), TARGETED SEQUENCE ANALYSIS (IE, CYP1A2, CYP2C19, CYP2C9, CYP2D6, CYP3A4, CYP3A5, CYP4F2, SLCO1B1, VKORC1 AND RS12777823)
0030U	DRUG METABOLISM (WARFARIN DRUG RESPONSE), TARGETED SEQUENCE ANALYSIS (IE, CYP2C9, CYP4F2, VKORC1, RS12777823)
0031U	CYP1A2 (CYTOCHROME P450 FAMILY 1, SUBFAMILY A, MEMBER 2) (EG, DRUG METABOLISM) GENE ANALYSIS, COMMON VARIANTS (IE, *1F, *1K, *6, *7)
0032U	COMT (CATECHOL-O-METHYLTRANSFERASE) (DRUG METABOLISM) GENE ANALYSIS, C.472G>A (RS4680) VARIANT
0033U	HTR2A (5-HYDROXYTRYPTAMINE RECEPTOR 2A), HTR2C (5-HYDROXYTRYPTAMINE RECEPTOR 2C) (EG, CITALOPRAM METABOLISM) GENE ANALYSIS, COMMON VARIANTS (IE, HTR2A RS7997012 [C.614-2211T>C], HTR2C RS3813929 [C.-759C>T] AND RS1414334 [C.551-3008C>G])

0034U	TPMT (THIOPURINE S-METHYLTRANSFERASE), NUDT15 (NUDIX HYDROXYLASE 15)(EG, THIOPURINE METABOLISM), GENE ANALYSIS, COMMON VARIANTS (IE, TPMT *2, *3A, *3B, *3C, *4, *5, *6, *8, *12; NUDT15 *3, *4, *5)
0036U	EXOME (IE, SOMATIC MUTATIONS), PAIRED FORMALIN-FIXED PARAFFIN-EMBEDDED TUMOR TISSUE AND NORMAL SPECIMEN, SEQUENCE ANALYSES
0037U	TARGETED GENOMIC SEQUENCE ANALYSIS, SOLID ORGAN NEOPLASM, DNA ANALYSIS OF 324 GENES, INTERROGATION FOR SEQUENCE VARIANTS, GENE COPY NUMBER AMPLIFICATIONS, GENE REARRANGEMENTS, MICROSATELLITE INSTABILITY AND TUMOR MUTATIONAL BURDEN
0040U	BCR/ABL1 (T(9;22)) (EG, CHRONIC MYELOGENOUS LEUKEMIA) TRANSLOCATION ANALYSIS, MAJOR BREAKPOINT, QUANTITATIVE
0045U	ONCOLOGY (BREAST DUCTAL CARCINOMA IN SITU), MRNA, GENE EXPRESSION PROFILING BY REAL-TIME RT-PCR OF 12 GENES (7 CONTENT AND 5 HOUSEKEEPING), UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED TISSUE, ALGORITHM REPORTED AS RECURRENCE SCORE
0046U	FLT3 (FMS-RELATED TYROSINE KINASE 3) (EG, ACUTE MYELOID LEUKEMIA) INTERNAL TANDEM DUPLICATION (ITD) VARIANTS, QUANTITATIVE
0047U	ONCOLOGY (PROSTATE), MRNA, GENE EXPRESSION PROFILING BY REAL-TIME RT-PCR OF 17 GENES (12 CONTENT AND 5 HOUSEKEEPING), UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED TISSUE, ALGORITHM REPORTED AS A RISK SCORE
0048U	ONCOLOGY (SOLID ORGAN NEOPLASIA), DNA, TARGETED SEQUENCING OF PROTEIN-CODING EXONS OF 468 CANCER-ASSOCIATED GENES, INCLUDING INTERROGATION FOR SOMATIC MUTATIONS AND MICROSATELLITE INSTABILITY, MATCHED WITH NORMAL SPECIMENS, UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED TUMOR TISSUE, REPORT OF CLINICALLY SIGNIFICANT MUTATION(S)
0049U	NPM1 (NUCLEOPHOSMIN) (EG, ACUTE MYELOID LEUKEMIA) GENE ANALYSIS, QUANTITATIVE
0050U	TARGETED GENOMIC SEQUENCE ANALYSIS PANEL, ACUTE MYELOGENOUS LEUKEMIA, DNA ANALYSIS, 194 GENES, INTERROGATION FOR SEQUENCE VARIANTS, COPY NUMBER VARIANTS OR REARRANGEMENTS
0053U	ONCOLOGY (PROSTATE CANCER), FISH ANALYSIS OF 4 GENES (ASAP1, HDAC9, CHD1 AND PTEN), NEEDLE BIOPSY SPECIMEN, ALGORITHM REPORTED AS PROBABILITY OF HIGHER TUMOR GRADE
0055U	CARDIOLOGY (HEART TRANSPLANT), CELL-FREE DNA, PCR ASSAY OF 96 DNA TARGET SEQUENCES (94 SINGLE NUCLEOTIDE POLYMORPHISM TARGETS AND TWO CONTROL TARGETS), PLASMA
0060U	TWIN ZYGOSITY, GENOMIC-TARGETED SEQUENCE ANALYSIS OF CHROMOSOME 2, USING CIRCULATING CELL-FREE FETAL DNA IN MATERNAL BLOOD
0068U	CANDIDA SPECIES PANEL (C. ALBICANS, C. GLABRATA, C. PARAPSILOSIS, C. KRUSEII, C TROPICALIS, AND C. AURIS), AMPLIFIED PROBE TECHNIQUE WITH QUALITATIVE REPORT OF THE PRESENCE OR ABSENCE OF EACH SPECIES

0069U	ONCOLOGY (COLORECTAL), MICRORNA, RT-PCR EXPRESSION PROFILING OF MIR-31-3P, FORMALIN-FIXED PARAFFIN-EMBEDDED TISSUE, ALGORITHM REPORTED AS AN EXPRESSION SCO
0070U	CYP2D6 (CYTOCHROME P450, FAMILY 2, SUBFAMILY D, POLYPEPTIDE 6) (EG, DRUG METABOLISM) GENE ANALYSIS, COMMON AND SELECT RARE VARIANTS (IE, *2, *3, *4, *4N, *5, *6, *7, *8, *9, *10, *11, *12, *13, *14A, *14B, *15, *17, *29, *35, *36, *41, *57, *61, *63, *68, *83, *XN)
0071U	CYP2D6 (CYTOCHROME P450, FAMILY 2, SUBFAMILY D, POLYPEPTIDE 6) (EG, DRUG METABOLISM) GENE ANALYSIS, FULL GENE SEQUENCE (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
0072U	CYP2D6 (CYTOCHROME P450, FAMILY 2, SUBFAMILY D, POLYPEPTIDE 6) (EG, DRUG METABOLISM) GENE ANALYSIS, TARGETED SEQUENCE ANALYSIS (IE, CYP2D6-2D7 HYBRID GENE) (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
0073U	CYP2D6 (CYTOCHROME P450, FAMILY 2, SUBFAMILY D, POLYPEPTIDE 6) (EG, DRUG METABOLISM) GENE ANALYSIS, TARGETED SEQUENCE ANALYSIS (IE, CYP2D7-2D6 HYBRID GENE) (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
0074U	CYP2D6 (CYTOCHROME P450, FAMILY 2, SUBFAMILY D, POLYPEPTIDE 6) (EG, DRUG METABOLISM) GENE ANALYSIS, TARGETED SEQUENCE ANALYSIS (IE, NON-DUPLICATED GENE WHEN DUPLICATION/MULTIPLICATION IS TRANS) (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
0075U	CYP2D6 (CYTOCHROME P450, FAMILY 2, SUBFAMILY D, POLYPEPTIDE 6) (EG, DRUG METABOLISM) GENE ANALYSIS, TARGETED SEQUENCE ANALYSIS (IE, 5' GENE DUPLICATION/MULTIPLICATION) (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
0076U	CYP2D6 (CYTOCHROME P450, FAMILY 2, SUBFAMILY D, POLYPEPTIDE 6) (EG, DRUG METABOLISM) GENE ANALYSIS, TARGETED SEQUENCE ANALYSIS (IE, 3' GENE DUPLICATION/ MULTIPLICATION) (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
0078U	PAIN MANAGEMENT (OPIOID-USE DISORDER) GENOTYPING PANEL, 16 COMMON VARIANTS (IE, ABCB1, COMT, DAT1, DBH, DOR, DRD1, DRD2, DRD4, GABA, GAL, HTR2A, HTTLPR, MTHFR, MUOR, OPRK1, OPRM1), BUCCAL SWAB OR OTHER GERMLINE TISSUE SAMPLE, ALGORITHM REPORTED AS POSITIVE OR NEGATIVE RISK OF OPIOID-USE DISORDER
0079U	COMPARATIVE DNA ANALYSIS USING MULTIPLE SELECTED SINGLE-NUCLEOTIDE POLYMORPHISMS (SNPS), URINE AND BUCCAL DNA, FOR SPECIMEN IDENTITY VERIFICATION
0084U	RED BLOOD CELL ANTIGEN TYPING, DNA, GENOTYPING OF 10 BLOOD GROUPS WITH PHENOTYPE PREDICTION OF 37 RED BLOOD CELL ANTIGENS
0086U	INFECTIOUS DISEASE (BACTERIAL AND FUNGAL), ORGANISM IDENTIFICATION, BLOOD CULTURE, USING RRNA FISH, 6 OR MORE ORGANISM TARGETS, REPORTED AS POSITIVE OR NEGATIVE WITH PHENOTYPIC MINIMUM INHIBITORY CONCENTRATION (MIC)-BASED ANTIMICROBIAL SUSCEPTIBILITY

0087U	CARDIOLOGY (HEART TRANSPLANT), MRNA GENE EXPRESSION PROFILING BY MICROARRAY OF 1283 GENES, TRANSPLANT BIOPSY TISSUE, ALLOGRAFT REJECTION AND INJURY ALGORITHM REPORTED AS A PROBABILITY SCORE
0088U	TRANSPLANTATION MEDICINE (KIDNEY ALLOGRAFT REJECTION), MICROARRAY GENE EXPRESSION PROFILING OF 1494 GENES, UTILIZING TRANSPLANT BIOPSY TISSUE, ALGORITHM REPORTED AS A PROBABILITY SCORE FOR REJECTION
0089U	ONCOLOGY (MELANOMA), GENE EXPRESSION PROFILING BY RTQPCR, PRAME AND LINC00518, SUPERFICIAL COLLECTION USING ADHESIVE PATCH(ES)
0090U	ONCOLOGY (CUTANEOUS MELANOMA), MRNA GENE EXPRESSION PROFILING BY RT-PCR OF 23 GENES (14 CONTENT AND 9 HOUSEKEEPING), UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED (FFPE) TISSUE, ALGORITHM REPORTED AS A CATEGORICAL RESULT (IE, BENIGN, INTERMEDIATE, MALIGNANT)
0094U	GENOME (EG, UNEXPLAINED CONSTITUTIONAL OR HERITABLE DISORDER OR SYNDROME), RAPID SEQUENCE ANALYSIS
0096U	HUMAN PAPILLOMAVIRUS (HPV), HIGH-RISK TYPES (IE, 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66, 68), MALE URINE
0101U	HEREDITARY COLON CANCER DISORDERS (EG, LYNCH SYNDROME, PTEN HAMARTOMA SYNDROME, COWDEN SYNDROME, FAMILIAL ADENOMATOSIS POLYPOSIS), GENOMIC SEQUENCE ANALYSIS PANEL UTILIZING A COMBINATION OF NGS, SANGER, MLPA, AND ARRAY CGH, WITH MMRNA ANALYTICS TO RESOLVE VARIANTS OF UNKNOWN SIGNIFICANCE WHEN INDICATED (15 GENES [SEQUENCING AND DELETION/DUPLICATION], EPCAM AND GREM1 [DELETION/DUPLICATION ONLY])
0102U	HEREDITARY BREAST CANCER-RELATED DISORDERS (EG, HEREDITARY BREAST CANCER, HEREDITARY OVARIAN CANCER, HEREDITARY ENDOMETRIAL CANCER), GENOMIC SEQUENCE ANALYSIS PANEL UTILIZING A COMBINATION OF NGS, SANGER, MLPA, AND ARRAY CGH, WITH MMRNA ANALYTICS TO RESOLVE VARIANTS OF UNKNOWN SIGNIFICANCE WHEN INDICATED (17 GENES [SEQUENCING AND DELETION/DUPLICATION])
0103U	HEREDITARY OVARIAN CANCER (EG, HEREDITARY OVARIAN CANCER, HEREDITARY ENDOMETRIAL CANCER), GENOMIC SEQUENCE ANALYSIS PANEL UTILIZING A COMBINATION OF NGS, SANGER, MLPA, AND ARRAY CGH, WITH MMRNA ANALYTICS TO RESOLVE VARIANTS OF UNKNOWN SIGNIFICANCE WHEN INDICATED (24 GENES [SEQUENCING AND DELETION/DUPLICATION], EPCAM [DELETION/DUPLICATION ONLY])
0105U	NEPHROLOGY (CHRONIC KIDNEY DISEASE), MULTIPLEX ELECTROCHEMILUMINESCENT IMMUNOASSAY (ECLIA) OF TUMOR NECROSIS FACTOR RECEPTOR 1A, RECEPTOR SUPERFAMILY 2 (TNFR1, TNFR2), AND KIDNEY INJURY MOLECULE-1 (KIM-1) COMBINED WITH LONGITUDINAL CLINICAL DATA, INCLUDING APOL1 GENOTYPE IF AVAILABLE, AND PLASMA (ISOLATED FRESH OR FROZEN), ALGORITHM REPORTED AS PROBABILITY SCORE FOR RAPID KIDNEY FUNCTION DECLINE (RKFD)
0109U	INFECTIOUS DISEASE (ASPERGILLUS SPECIES), REAL-TIME PCR FOR DETECTION OF DNA FROM 4 SPECIES (A. FUMIGATUS, A. TERREUS, A. NIGER, AND A. FLAVUS), BLOOD, LAVAGE FLUID, OR TISSUE,

	QUALITATIVE REPORTING OF PRESENCE OR ABSENCE OF EACH SPECIES
0111U	ONCOLOGY (COLON CANCER), TARGETED KRAS (CODONS 12, 13, AND 61) AND NRAS (CODONS 12, 13, AND 61) GENE ANALYSIS UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED TISSUE
0112U	INFECTIOUS AGENT DETECTION AND IDENTIFICATION, TARGETED SEQUENCE ANALYSIS (16S AND 18S RRNA GENES) WITH DRUGRESISTANCE GENE
0113U	ONCOLOGY (PROSTATE), MEASUREMENT OF PCA3 AND TMPRSS2-ERG IN URINE AND PSA IN SERUM FOLLOWING PROSTATIC MASSAGE, BY RNA AMPLIFICATION AND FLUORESCENCEBASED DETECTION, ALGORITHM REPORTED AS RISK SCORE
0114U	GASTROENTEROLOGY (BARRETT'S ESOPHAGUS), VIM AND CCNA1 METHYLATION ANALYSIS, ESOPHAGEAL CELLS, ALGORITHM REPORTED AS LIKELIHOOD FOR BARRETT'S ESOPHAGUS
0118U	TRANSPLANTATION MEDICINE, QUANTIFICATION OF DONOR-DERIVED CELL-FREE DNA USING WHOLE GENOME NEXT-GENERATION SEQUENCING, PLASMA, REPORTED AS PERCENTAGE OF DONORDERIVED CELL-FREE DNA IN THE TOTAL CELL-FREE DNA
0120U	ONCOLOGY (B-CELL LYMPHOMA CLASSIFICATION), MRNA, GENE EXPRESSION PROFILING BY FLUORESCENT PROBE HYBRIDIZATION OF 58 GENES (45 CONTENT AND 13 HOUSEKEEPING GENES), FORMALIN-FIXED PARAFFIN-EMBEDDED TISSUE, ALGORITHM REPORTED AS LIKELIHOOD FOR PRIMARY MEDIASTINAL B-CELL LYMPHOMA (PMBCL) AND DIFFUSE LARGE B-CELL LYMPHOMA (DLBCL) WITH CELL OF ORIGIN SUBTYPING IN THE LATTER
0129U	HEREDITARY BREAST CANCER-RELATED DISORDERS (EG, HEREDITARY BREAST CANCER, HEREDITARY OVARIAN CANCER, HEREDITARY ENDOMETRIAL CANCER), GENOMIC SEQUENCE ANALYSIS AND DELETION/DUPLICATION ANALYSIS PANEL (ATM, BRCA1, BRCA2, CDH1, CHEK2, PALB2, PTEN, AND TP53)
0130U	HEREDITARY COLON CANCER DISORDERS (EG, LYNCH SYNDROME, PTEN HAMARTOMA SYNDROME, COWDEN SYNDROME, FAMILIAL ADENOMATOSIS POLYPOSIS), TARGETED MRNA SEQUENCE ANALYSIS PANEL (APC, CDH1, CHEK2, MLH1, MSH2, MSH6, MUTYH, PMS2, PTEN, AND TP53) (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
0131U	HEREDITARY BREAST CANCER-RELATED DISORDERS (EG, HEREDITARY BREAST CANCER, HEREDITARY OVARIAN CANCER, HEREDITARY ENDOMETRIAL CANCER), TARGETED MRNA SEQUENCE ANALYSIS PANEL (13 GENES) (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
0132U	HEREDITARY OVARIAN CANCER-RELATED DISORDERS (EG, HEREDITARY BREAST CANCER, HEREDITARY OVARIAN CANCER, HEREDITARY ENDOMETRIAL CANCER), TARGETED MRNA SEQUENCE ANALYSIS PANEL (17 GENES) (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
0133U	HEREDITARY PROSTATE CANCER-RELATED DISORDERS, TARGETED MRNA SEQUENCE ANALYSIS PANEL (11 GENES) (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
0134U	HEREDITARY PAN CANCER (EG, HEREDITARY BREAST AND OVARIAN CANCER, HEREDITARY ENDOMETRIAL CANCER, HEREDITARY COLORECTAL CANCER), TARGETED MRNA SEQUENCE

	ANALYSIS PANEL (18 GENES) (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
0135U	HEREDITARY GYNECOLOGICAL CANCER (EG, HEREDITARY BREAST AND OVARIAN CANCER, HEREDITARY ENDOMETRIAL CANCER, HEREDITARY COLORECTAL CANCER), TARGETED MRNA SEQUENCE ANALYSIS PANEL (12 GENES) (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
0136U	ATM (ATAXIA TELANGIECTASIA MUTATED) (EG, ATAXIA TELANGIECTASIA) MRNA SEQUENCE ANALYSIS (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
0137U	PALB2 (PARTNER AND LOCALIZER OF BRCA2) (EG, BREAST AND PANCREATIC CANCER) MRNA SEQUENCE ANALYSIS (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
0138U	BRCA1 (BRCA1, DNA REPAIR ASSOCIATED), BRCA2 (BRCA2, DNA REPAIR ASSOCIATED) (EG, HEREDITARY BREAST AND OVARIAN CANCER) MRNA SEQUENCE ANALYSIS (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
0140U	INFECTIOUS DISEASE (FUNGI), FUNGAL PATHOGEN IDENTIFICATION, DNA (15 FUNGAL TARGETS), BLOOD CULTURE, AMPLIFIED PROBE TECHNIQUE, EACH TARGET REPORTED AS DETECTED OR NOT DETECTED
0141U	INFECTIOUS DISEASE (BACTERIA AND FUNGI), GRAM-POSITIVE ORGANISM IDENTIFICATION AND DRUG RESISTANCE ELEMENT DETECTION, DNA (20 GRAM-POSITIVE BACTERIAL TARGETS, 4 RESISTANCE GENES, 1 PAN GRAM-NEGATIVE BACTERIAL TARGET, 1 PAN CANDIDA TARGET), BLOOD CULTURE, AMPLIFIED PROBE TECHNIQUE, EACH TARGET REPORTED AS DETECTED OR NOT DETECTED
0142U	INFECTIOUS DISEASE (BACTERIA AND FUNGI), GRAM-NEGATIVE BACTERIAL IDENTIFICATION AND DRUG RESISTANCE ELEMENT DETECTION, DNA (21 GRAM-NEGATIVE BACTERIAL TARGETS, 6 RESISTANCE GENES, 1 PAN GRAM-POSITIVE BACTERIAL TARGET, 1 PAN CANDIDA TARGET), AMPLIFIED PROBE TECHNIQUE, EACH TARGET REPORTED AS DETECTED OR NOT DETECTED
0152U	INFECTIOUS DISEASE (BACTERIA, FUNGI, PARASITES, AND DNA VIRUSES), MICROBIAL CELL-FREE DNA, PLASMA, UNTARGETED NEXT-GENERATION SEQUENCING, REPORT FOR SIGNIFICANT POSITIVE PATHOGENS
0153U	ONCOLOGY (BREAST), MRNA, GENE EXPRESSION PROFILING BY NEXT-GENERATION SEQUENCING OF 101 GENES, UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED TISSUE, ALGORITHM REPORTED AS A TRIPLE NEGATIVE BREAST CANCER CLINICAL SUBTYPE(S) WITH INFORMATION ON IMMUNE CELL INVOLVEMENT
0154U	ONCOLOGY (UROTHELIAL CANCER), RNA,ANALYSIS BY REAL-TIME RT-PCR OF THE FGFR3 (FIBROBLAST GROWTH FACTOR RECEPTOR 3) GENE ANALYSIS (IE, P.R248C [C.742C>T], P.S249C [C.746C>G], P.G370C [C.1108G>T], P.Y373C [C.1118A>G], FGFR3-TACC3V1, AND FGFR3-TACC3V3) UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED UROTHELIAL CANCER TUMOR TISSUE, REPORTED AS FGFR GENE ALTERATION STATUS
0155U	ONCOLOGY (BREAST CANCER), DNA, PIK3CA (PHOSPHATIDYLINOSITOL-4,5BISPHOSPHATE 3-KINASE, CATALYTIC SUBUNIT ALPHA) (EG, BREAST CANCER) GENE ANALYSIS (IE, P.C420R, P.E542K, P.E545A, P.E545D [G.1635G>T ONLY], P.E545G,

	P.E545K, P.Q546E, P.Q546R, P.H1047L, P.H1047R, P.H1047Y), UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED BREAST TUMOR TISSUE, REPORTED AS PIK3CA GENE MUTATION STATUS
0156U	COPY NUMBER (EG, INTELLECTUAL DISABILITY, DYSMORPHOLOGY), SEQUENCE ANALYSIS
0157U	APC (APC REGULATOR OF WNT SIGNALING PATHWAY) (EG, FAMILIAL ADENOMATOSIS POLYPOSIS [FAP]) MRNA SEQUENCE ANALYSIS (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
0158U	MLH1 (MUTL HOMOLOG 1) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) MRNA SEQUENCE ANALYSIS (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
0159U	MSH2 (MUTS HOMOLOG 2) (EG, HEREDITARY COLON CANCER, LYNCH SYNDROME) MRNA SEQUENCE ANALYSIS (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
0160U	MSH6 (MUTS HOMOLOG 6) (EG, HEREDITARY COLON CANCER, LYNCH SYNDROME) MRNA SEQUENCE ANALYSIS (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
0161U	PMS2 (PMS1 HOMOLOG 2, MISMATCH REPAIR SYSTEM COMPONENT) (EG, HEREDITARY NONPOLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) MRNA SEQUENCE ANALYSIS (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
0162U	HEREDITARY COLON CANCER (LYNCH SYNDROME), TARGETED MRNA SEQUENCE ANALYSIS PANEL (MLH1, MSH2, MSH6, PMS2) (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
0169U	NUDT15 (NUDIX HYDROLASE 15) AND TPMT (THIOPURINE S-METHYLTRANSFERASE) (EG, DRUG METABOLISM) GENE ANALYSIS, COMMON VARIANTS
0170U	NEUROLOGY (AUTISM SPECTRUM DISORDER [ASD]), RNA, NEXT-GENERATION SEQUENCING, SALIVA, ALGORITHMIC ANALYSIS, AND RESULTS REPORTED AS PREDICTIVE PROBABILITY OF ASD DIAGNOSIS
0171U	TARGETED GENOMIC SEQUENCE ANALYSIS PANEL, ACUTE MYELOID LEUKEMIA, MYELODYSPLASTIC SYNDROME, AND MYELOPROLIFERATIVE NEOPLASMS, DNA ANALYSIS, 23 GENES, INTERROGATION FOR SEQUENCE VARIANTS, REARRANGEMENTS AND MINIMAL RESIDUAL DISEASE, REPORTED AS PRESENCE/ABSENCE
0172U	ONCOLOGY (SOLID TUMOR AS INDICATED BY THE LABEL), SOMATIC MUTATION ANALYSIS OF BRCA1 (BRCA1, DNA REPAIR ASSOCIATED), BRCA2 (BRCA2, DNA REPAIR ASSOCIATED) AND ANALYSIS OF HOMOLOGOUS RECOMBINATION DEFICIENCY PATHWAYS, DNA, FORMALIN-FIXED PARAFFIN-EMBEDDED TISSUE, ALGORITHM QUANTIFYING TUMOR GENOMIC INSTABILITY SCORE
0173U	PSYCHIATRY (IE, DEPRESSION, ANXIETY), GENOMIC ANALYSIS PANEL, INCLUDES VARIANT ANALYSIS OF 14 GENES
0175U	PSYCHIATRY (EG, DEPRESSION, ANXIETY), GENOMIC ANALYSIS PANEL, VARIANT ANALYSIS OF 15 GENES
0177U	ONCOLOGY (BREAST CANCER), DNA, PIK3CA (PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE 3-KINASE CATALYTIC SUBUNIT ALPHA) GENE ANALYSIS OF 11 GENE VARIANTS UTILIZING PLASMA, REPORTED AS PIK3CA GENE MUTATION STATUS

0179U	ONCOLOGY (NON-SMALL CELL LUNG CANCER), CELL-FREE DNA, TARGETED SEQUENCE ANALYSIS OF 23 GENES (SINGLE NUCLEOTIDE VARIATIONS, INSERTIONS AND DELETIONS, FUSIONS WITHOUT PRIOR KNOWLEDGE OF PARTNER/BREAKPOINT, COPY NUMBER VARIATIONS), WITH REPORT OF SIGNIFICANT MUTATION(S)
0180U	RED CELL ANTIGEN (ABO BLOOD GROUP) GENOTYPING (ABO), GENE ANALYSIS SANGER/CHAIN TERMINATION/CONVENTIONAL SEQUENCING, ABO (ABO, ALPHA 1-3-N-ACETYLGALACTOSAMINYLTRANSFERASE AND ALPHA 1-3-GALACTOSYLTRANSFERASE) GENE, INCLUDING SUBTYPING, 7 EXONS
0181U	RED CELL ANTIGEN (COLTON BLOOD GROUP) GENOTYPING (CO), GENE ANALYSIS, AQP1 (AQUAPORIN 1 [COLTON BLOOD GROUP]) EXON 1
0182U	RED CELL ANTIGEN (CROMER BLOOD GROUP) GENOTYPING (CROM), GENE ANALYSIS, CD55 (CD55 MOLECULE [CROMER BLOOD GROUP]) EXONS 1-10
0183U	RED CELL ANTIGEN (DIEGO BLOOD GROUP) GENOTYPING (DI), GENE ANALYSIS, SLC4A1 (SOLUTE CARRIER FAMILY 4 MEMBER 1 [DIEGO BLOOD GROUP]) EXON 19
0184U	RED CELL ANTIGEN (DOMBROCK BLOOD GROUP) GENOTYPING (DO), GENE ANALYSIS, ART4 (ADP-RIBOSYLTRANSFERASE 4 [DOMBROCK BLOOD GROUP]) EXON 2
0185U	RED CELL ANTIGEN (H BLOOD GROUP) GENOTYPING (FUT1), GENE ANALYSIS, FUT1 (FUCOSYLTRANSFERASE 1 [H BLOOD GROUP]) EXON 4
0186U	RED CELL ANTIGEN (H BLOOD GROUP) GENOTYPING (FUT2), GENE ANALYSIS, FUT2 (FUCOSYLTRANSFERASE 2) EXON 2
0187U	RED CELL ANTIGEN (DUFFY BLOOD GROUP) GENOTYPING (FY), GENE ANALYSIS, ACKR1 (ATYPICAL CHEMOKINE RECEPTOR 1 [DUFFY BLOOD GROUP]) EXONS 1-2
0188U	RED CELL ANTIGEN (GERBICH BLOOD GROUP) GENOTYPING (GE), GENE ANALYSIS, GYPC (GLYCOPHORIN C [GERBICH BLOOD GROUP]) EXONS 1-4
0189U	RED CELL ANTIGEN (MNS BLOOD GROUP) GENOTYPING (GYPA), GENE ANALYSIS, GYPA (GLYCOPHORIN A [MNS BLOOD GROUP]) INTRONS 1, 5, EXON 2
0190U	RED CELL ANTIGEN (MNS BLOOD GROUP) GENOTYPING (GYPB), GENE ANALYSIS, GYPB (GLYCOPHORIN B [MNS BLOOD GROUP]) INTRONS 1, 5, PSEUDOEXON 3
0191U	RED CELL ANTIGEN (INDIAN BLOOD GROUP) GENOTYPING (IN), GENE ANALYSIS, CD44 (CD44 MOLECULE [INDIAN BLOOD GROUP]) EXONS 2, 3, 6
0192U	RED CELL ANTIGEN (KIDD BLOOD GROUP) GENOTYPING (JK), GENE ANALYSIS, SLC14A1 (SOLUTE CARRIER FAMILY 14 MEMBER 1 [KIDD BLOOD GROUP]) GENE PROMOTER, EXON 9
0193U	RED CELL ANTIGEN (JR BLOOD GROUP) GENOTYPING (JR), GENE ANALYSIS, ABCG2 (ATP BINDING CASSETTE SUBFAMILY G MEMBER 2 [JUNIOR BLOOD GROUP]) EXONS 2-26
0194U	RED CELL ANTIGEN (KELL BLOOD GROUP) GENOTYPING (KEL), GENE ANALYSIS, KEL (KELL METALLO-ENDOPEPTIDASE [KELL BLOOD GROUP]) EXON 8

0195U	KLF1 (KRUPPEL-LIKE FACTOR 1), TARGETED SEQUENCING (IE, EXON 13)
0196U	RED CELL ANTIGEN (LUTHERAN BLOOD GROUP) GENOTYPING (LU), GENE ANALYSIS, BCAM (BASAL CELL ADHESION MOLECULE [LUTHERAN BLOOD GROUP]) EXON 3
0197U	RED CELL ANTIGEN (LANDSTEINER-WIENER BLOOD GROUP) GENOTYPING (LW), GENE ANALYSIS, ICAM4 (INTERCELLULAR ADHESION MOLECULE 4 [LANDSTEINER-WIENER BLOOD GROUP]) EXON 1
0198U	RED CELL ANTIGEN (RH BLOOD GROUP) GENOTYPING (RHD AND RHCE), GENE ANALYSIS SANGER/CHAIN TERMINATION/CONVENTIONAL SEQUENCING, RHD (RH BLOOD GROUP D ANTIGEN) EXONS 1-10 AND RHCE (RH BLOOD GROUP CCEE ANTIGENS) EXON 5
0199U	RED CELL ANTIGEN (SCIANNA BLOOD GROUP) GENOTYPING (SC), GENE ANALYSIS, ERMAP (ERYTHROBLAST MEMBRANE ASSOCIATED PROTEIN [SCIANNA BLOOD GROUP]) EXONS 4, 12
0200U	RED CELL ANTIGEN (KX BLOOD GROUP) GENOTYPING (XK), GENE ANALYSIS, XK (X-LINKED KX BLOOD GROUP) EXONS 1-3
0201U	RED CELL ANTIGEN (YT BLOOD GROUP) GENOTYPING (YT), GENE ANALYSIS, ACHE (ACETYLCHOLINESTERASE [CARTWRIGHT BLOOD GROUP]) EXON 2
0203U	AUTOIMMUNE (INFLAMMATORY BOWEL DISEASE), MRNA, GENE EXPRESSION PROFILING BY QUANTITATIVE RT-PCR, 17 GENES (15 TARGET AND 2 REFERENCE GENES), WHOLE BLOOD, REPORTED AS A CONTINUOUS RISK SCORE AND CLASSIFICATION OF INFLAMMATORY BOWEL DISEASE AGGRESSIVENESS
0204U	ONCOLOGY (THYROID), MRNA, GENE EXPRESSION ANALYSIS OF 593 GENES (INCLUDING BRAF, RAS, RET, PAX8, AND NTRK) FOR SEQUENCE VARIANTS AND REARRANGEMENTS, UTILIZING FINE NEEDLE ASPIRATE, REPORTED AS DETECTED OR NOT DETECTED
0205U	OPHTHALMOLOGY (AGE-RELATED MACULAR DEGENERATION), ANALYSIS OF 3 GENE VARIANTS (2 CFH GENE, 1 ARMS2 GENE), USING PCR AND MALDI-TOF, BUCCAL SWAB, REPORTED AS POSITIVE OR NEGATIVE FOR NEOVASCULAR AGE-RELATED MACULAR-DEGENERATION RISK ASSOCIATED WITH ZINC SUPPLEMENTS
0209U	CYTOGENOMIC CONSTITUTIONAL (GENOME-WIDE) ANALYSIS, INTERROGATION OF GENOMIC REGIONS FOR COPY NUMBER, STRUCTURAL CHANGES AND AREAS OF HOMOZYGOSITY FOR CHROMOSOMAL ABNORMALITIES
0211U	ONCOLOGY (PAN-TUMOR), DNA AND RNA BY NEXT-GENERATION SEQUENCING, UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED TISSUE, INTERPRETATIVE REPORT FOR SINGLE NUCLEOTIDE VARIANTS, COPY NUMBER ALTERATIONS, TUMOR MUTATIONAL BURDEN, AND MICROSATELLITE INSTABILITY, WITH THERAPY ASSOCIATION
0212U	RARE DISEASES (CONSTITUTIONAL/HERITABLE DISORDERS), WHOLE GENOME AND MITOCHONDRIAL DNA SEQUENCE ANALYSIS, INCLUDING SMALL SEQUENCE CHANGES, DELETIONS, DUPLICATIONS, SHORT TANDEM REPEAT GENE EXPANSIONS, AND VARIANTS IN NON-UNIQUELY MAPPABLE REGIONS, BLOOD OR SALIVA, IDENTIFICATION AND CATEGORIZATION OF GENETIC VARIANTS, PROBAND

0213U	RARE DISEASES (CONSTITUTIONAL/HERITABLE DISORDERS), WHOLE GENOME AND MITOCHONDRIAL DNA SEQUENCE ANALYSIS, INCLUDING SMALL SEQUENCE CHANGES, DELETIONS, DUPLICATIONS, SHORT TANDEM REPEAT GENE EXPANSIONS, AND VARIANTS IN NON-UNIQUELY MAPPABLE REGIONS, BLOOD OR SALIVA, IDENTIFICATION AND CATEGORIZATION OF GENETIC VARIANTS, EACH COMPARATOR GENOME (EG, PARENT, SIBLING)
0214U	RARE DISEASES (CONSTITUTIONAL/HERITABLE DISORDERS), WHOLE EXOME AND MITOCHONDRIAL DNA SEQUENCE ANALYSIS, INCLUDING SMALL SEQUENCE CHANGES, DELETIONS, DUPLICATIONS, SHORT TANDEM REPEAT GENE EXPANSIONS, AND VARIANTS IN NON-UNIQUELY MAPPABLE REGIONS, BLOOD OR SALIVA, IDENTIFICATION AND CATEGORIZATION OF GENETIC VARIANTS, PROBAND
0215U	RARE DISEASES (CONSTITUTIONAL/HERITABLE DISORDERS), WHOLE EXOME AND MITOCHONDRIAL DNA SEQUENCE ANALYSIS, INCLUDING SMALL SEQUENCE CHANGES, DELETIONS, DUPLICATIONS, SHORT TANDEM REPEAT GENE EXPANSIONS, AND VARIANTS IN NON-UNIQUELY MAPPABLE REGIONS, BLOOD OR SALIVA, IDENTIFICATION AND CATEGORIZATION OF GENETIC VARIANTS, EACH COMPARATOR EXOME (EG, PARENT, SIBLING)
0216U	NEUROLOGY (INHERITED ATAXIAS), GENOMIC DNA SEQUENCE ANALYSIS OF 12 COMMON GENES INCLUDING SMALL SEQUENCE CHANGES, DELETIONS, DUPLICATIONS, SHORT TANDEM REPEAT GENE EXPANSIONS, AND VARIANTS IN NON-UNIQUELY MAPPABLE REGIONS, BLOOD OR SALIVA, IDENTIFICATION AND CATEGORIZATION OF GENETIC VARIANTS
0217U	NEUROLOGY (INHERITED ATAXIAS), GENOMIC DNA SEQUENCE ANALYSIS OF 51 GENES INCLUDING SMALL SEQUENCE CHANGES, DELETIONS, DUPLICATIONS, SHORT TANDEM REPEAT GENE EXPANSIONS, AND VARIANTS IN NON-UNIQUELY MAPPABLE REGIONS, BLOOD OR SALIVA, IDENTIFICATION AND CATEGORIZATION OF GENETIC VARIANTS
0218U	NEUROLOGY (MUSCULAR DYSTROPHY), DMD GENE SEQUENCE ANALYSIS, INCLUDING SMALL SEQUENCE CHANGES, DELETIONS, DUPLICATIONS, AND VARIANTS IN NON-UNIQUELY MAPPABLE REGIONS, BLOOD OR SALIVA, IDENTIFICATION AND CHARACTERIZATION OF GENETIC VARIANTS
0219U	INFECTIOUS AGENT (HUMAN IMMUNODEFICIENCY VIRUS), TARGETED VIRAL NEXT-GENERATION SEQUENCE ANALYSIS (IE, PROTEASE [PR], REVERSE TRANSCRIPTASE [RT], INTEGRASE [INT]), ALGORITHM REPORTED AS PREDICTION OF ANTIVIRAL DRUG SUSCEPTIBILITY
0221U	RED CELL ANTIGEN (ABO BLOOD GROUP) GENOTYPING (ABO), GENE ANALYSIS, NEXT-GENERATION SEQUENCING, ABO (ABO, ALPHA 1-3-N-ACETYLGALACTOSAMINYLTRANSFERASE AND ALPHA 1-3-GALACTOSYLTRANSFERASE) GENE
0222U	RED CELL ANTIGEN (RH BLOOD GROUP) GENOTYPING (RHD AND RHCE), GENE ANALYSIS, NEXT-GENERATION SEQUENCING, RH PROXIMAL PROMOTER, EXONS 1-10, PORTIONS OF INTRONS 2-3
0227U	DRUG ASSAY, PRESUMPTIVE, 30 OR MORE DRUGS OR METABOLITES, URINE, LIQUID CHROMATOGRAPHY WITH TANDEM MASS SPECTROMETRY (LC-MS/MS) USING MULTIPLE REACTION

	MONITORING (MRM), WITH DRUG OR METABOLITE DESCRIPTION, INCLUDES SAMPLE VALIDATION
0229U	BCAT1 (BRANCHED CHAIN AMINO ACID TRANSAMINASE 1) AND IKZF1 (IKAROS FAMILY ZINC FINGER 1) (EG, COLORECTAL CANCER) PROMOTER METHYLATION ANALYSIS
0230U	AR (ANDROGEN RECEPTOR) (EG, SPINAL AND BULBAR MUSCULAR ATROPHY, KENNEDY DISEASE, X CHROMOSOME INACTIVATION), FULL SEQUENCE ANALYSIS, INCLUDING SMALL SEQUENCE CHANGES IN EXONIC AND INTRONIC REGIONS, DELETIONS, DUPLICATIONS, SHORT TANDEM REPEAT (STR) EXPANSIONS, MOBILE ELEMENT INSERTIONS, AND VARIANTS IN NON-UNIQUELY MAPPABLE REGIONS
0231U	CACNA1A (CALCIUM VOLTAGE-GATED CHANNEL SUBUNIT ALPHA 1A) (EG, SPINOCEREBELLAR ATAXIA), FULL GENE ANALYSIS, INCLUDING SMALL SEQUENCE CHANGES IN EXONIC AND INTRONIC REGIONS, DELETIONS, DUPLICATIONS, SHORT TANDEM REPEAT (STR) GENE EXPANSIONS, MOBILE ELEMENT INSERTIONS, AND VARIANTS IN NON-UNIQUELY MAPPABLE REGIONS
0232U	CSTB (CYSTATIN B) (EG, PROGRESSIVE MYOCLONIC EPILEPSY TYPE 1A, UNVERRICHT-LUNDBORG DISEASE), FULL GENE ANALYSIS, INCLUDING SMALL SEQUENCE CHANGES IN EXONIC AND INTRONIC REGIONS, DELETIONS, DUPLICATIONS, SHORT TANDEM REPEAT (STR) EXPANSIONS, MOBILE ELEMENT INSERTIONS, AND VARIANTS IN NON-UNIQUELY MAPPABLE REGIONS
0233U	FXN (FRATAXIN) (EG, FRIEDREICH ATAXIA), GENE ANALYSIS, INCLUDING SMALL SEQUENCE CHANGES IN EXONIC AND INTRONIC REGIONS, DELETIONS, DUPLICATIONS, SHORT TANDEM REPEAT (STR) EXPANSIONS, MOBILE ELEMENT INSERTIONS, AND VARIANTS IN NON-UNIQUELY MAPPABLE REGIONS
0234U	MECP2 (METHYL CPG BINDING PROTEIN 2) (EG, RETT SYNDROME), FULL GENE ANALYSIS, INCLUDING SMALL SEQUENCE CHANGES IN EXONIC AND INTRONIC REGIONS, DELETIONS, DUPLICATIONS, MOBILE ELEMENT INSERTIONS, AND VARIANTS IN NON-UNIQUELY MAPPABLE REGIONS
0235U	PTEN (PHOSPHATASE AND TENSIN HOMOLOG) (EG, COWDEN SYNDROME, PTEN HAMARTOMA TUMOR SYNDROME), FULL GENE ANALYSIS, INCLUDING SMALL SEQUENCE CHANGES IN EXONIC AND INTRONIC REGIONS, DELETIONS, DUPLICATIONS, MOBILE ELEMENT INSERTIONS, AND VARIANTS IN NON-UNIQUELY MAPPABLE REGIONS
0236U	SMN1 (SURVIVAL OF MOTOR NEURON 1, TELOMERIC) AND SMN2 (SURVIVAL OF MOTOR NEURON 2, CENTROMERIC) (EG, SPINAL MUSCULAR ATROPHY) FULL GENE ANALYSIS, INCLUDING SMALL SEQUENCE CHANGES IN EXONIC AND INTRONIC REGIONS, DUPLICATIONS AND DELETIONS, AND MOBILE ELEMENT INSERTIONS
0237U	CARDIAC ION CHANNELOPATHIES (EG, BRUGADA SYNDROME, LONG QT SYNDROME, SHORT QT SYNDROME, CATECHOLAMINERGIC POLYMORPHIC VENTRICULAR TACHYCARDIA), GENOMIC SEQUENCE ANALYSIS PANEL INCLUDING ANK2, CASQ2, CAV3, KCNE1, KCNE2, KCNH2, KCNJ2, KCNQ1, RYR2, AND SCN5A, INCLUDING SMALL SEQUENCE CHANGES IN EXONIC AND INTRONIC REGIONS, DELETIONS, DUPLICATIONS, MOBILE

	ELEMENT INSERTIONS, AND VARIANTS IN NON-UNIQUELY MAPPABLE REGIONS
0238U	ONCOLOGY (LYNCH SYNDROME), GENOMIC DNA SEQUENCE ANALYSIS OF MLH1, MSH2, MSH6, PMS2, AND EPCAM, INCLUDING SMALL SEQUENCE CHANGES IN EXONIC AND INTRONIC REGIONS, DELETIONS, DUPLICATIONS, MOBILE ELEMENT INSERTIONS, AND VARIANTS IN NON-UNIQUELY MAPPABLE REGIONS
0239U	TARGETED GENOMIC SEQUENCE ANALYSIS PANEL, SOLID ORGAN NEOPLASM, CELL-FREE DNA, ANALYSIS OF 311 OR MORE GENES, INTERROGATION FOR SEQUENCE VARIANTS, INCLUDING SUBSTITUTIONS, INSERTIONS, DELETIONS, SELECT REARRANGEMENTS, AND COPY NUMBER VARIATIONS
0242U	TARGETED GENOMIC SEQUENCE ANALYSIS PANEL, SOLID ORGAN NEOPLASM, CELL-FREE CIRCULATING DNA ANALYSIS OF 55-74 GENES, INTERROGATION FOR SEQUENCE VARIANTS, GENE COPY NUMBER AMPLIFICATIONS, AND GENE REARRANGEMENTS
0244U	ONCOLOGY (SOLID ORGAN), DNA, COMPREHENSIVE GENOMIC PROFILING, 257 GENES, INTERROGATION FOR SINGLE-NUCLEOTIDE VARIANTS, INSERTIONS/DELETIONS, COPY NUMBER ALTERATIONS, GENE REARRANGEMENTS, TUMOR-MUTATIONAL BURDEN AND MICROSATELLITE INSTABILITY, UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED TUMOR TISSUE
0245U	ONCOLOGY (THYROID), MUTATION ANALYSIS OF 10 GENES AND 37 RNA FUSIONS AND EXPRESSION OF 4 MRNA MARKERS USING NEXT-GENERATION SEQUENCING, FINE NEEDLE ASPIRATE, REPORT INCLUDES ASSOCIATED RISK OF MALIGNANCY EXPRESSED AS A PERCENTAGE
0246U	RED BLOOD CELL ANTIGEN TYPING, DNA, GENOTYPING OF AT LEAST 16 BLOOD GROUPS WITH PHENOTYPE PREDICTION OF AT LEAST 51 RED BLOOD CELL ANTIGENS
0250U	ONCOLOGY (SOLID ORGAN NEOPLASM), TARGETED GENOMIC SEQUENCE DNA ANALYSIS OF 505 GENES, INTERROGATION FOR SOMATIC ALTERATIONS (SNVS [SINGLE NUCLEOTIDE VARIANT], SMALL INSERTIONS AND DELETIONS, ONE AMPLIFICATION, AND FOUR TRANSLOCATIONS), MICROSATELLITE INSTABILITY AND TUMOR-MUTATION BURDEN
0252U	FETAL ANEUPLOIDY SHORT TANDEM-REPEAT COMPARATIVE ANALYSIS, FETAL DNA FROM PRODUCTS OF CONCEPTION, REPORTED AS NORMAL (EUPLOIDY), MONOSOMY, TRISOMY, OR PARTIAL DELETION/DUPLICATIONS, MOSAICISM, AND SEGMENTAL ANEUPLOIDY
0253U	REPRODUCTIVE MEDICINE (ENDOMETRIAL RECEPTIVITY ANALYSIS), RNA GENE EXPRESSION PROFILE, 238 GENES BY NEXT-GENERATION SEQUENCING, ENDOMETRIAL TISSUE, PREDICTIVE ALGORITHM REPORTED AS ENDOMETRIAL WINDOW OF IMPLANTATION (EG, PRE-RECEPTIVE, RECEPTIVE, POST-RECEPTIVE)
0254U	REPRODUCTIVE MEDICINE (PREIMPLANTATION GENETIC ASSESSMENT), ANALYSIS OF 24 CHROMOSOMES USING EMBRYONIC DNA GENOMIC SEQUENCE ANALYSIS FOR ANEUPLOIDY, AND A MITOCHONDRIAL DNA SCORE IN EUPLOID EMBRYOS, RESULTS REPORTED AS NORMAL (EUPLOIDY), MONOSOMY, TRISOMY, OR PARTIAL DELETION/DUPLICATIONS, MOSAICISM, AND SEGMENTAL ANEUPLOIDY, PER EMBRYO TESTED

0258U	AUTOIMMUNE (PSORIASIS), MRNA, NEXTGENERATION SEQUENCING, GENE EXPRESSION PROFILING OF 50-100 GENES, SKIN-SURFACE COLLECTION USING ADHESIVE PATCH, ALGORITHM REPORTED AS LIKELIHOOD OF RESPONSE TO PSORIASIS BIOLOGICS
0260U	RARE DISEASES (CONSTITUTIONAL/HERITABLE DISORDERS), IDENTIFICATION OF COPY NUMBER VARIATIONS, INVERSIONS, INSERTIONS, TRANSLOCATIONS, AND OTHER STRUCTURAL VARIANTS BY OPTICAL GENOME MAPPING
0262U	ONCOLOGY (SOLID TUMOR), GENE EXPRESSION PROFILING BY REAL-TIME RT-PCR OF 7 GENE PATHWAYS (ER, AR, PI3K, MAPK, HH, TGFB, NOTCH), FORMALIN-FIXED PARAFFINEMBEDDED (FFPE), ALGORITHM REPORTED AS GENE PATHWAY ACTIVITY SCORE
0264U	RARE DISEASES (CONSTITUTIONAL/HERITABLE DISORDERS), IDENTIFICATION OF COPY NUMBER VARIATIONS, INVERSIONS, INSERTIONS, TRANSLOCATIONS, AND OTHER STRUCTURAL VARIANTS BY OPTICAL GENOME MAPPING
0265U	RARE CONSTITUTIONAL AND OTHER HERITABLE DISORDERS, WHOLE GENOME AND MITOCHONDRIAL DNA SEQUENCE ANALYSIS, BLOOD, FROZEN AND FORMALIN-FIXED PARAFFINEMBEDDED (FFPE) TISSUE, SALIVA, BUCCAL SWABS OR CELL LINES, IDENTIFICATION OF SINGLE NUCLEOTIDE AND COPY NUMBER VARIANTS
0266U	UNEXPLAINED CONSTITUTIONAL OR OTHER HERITABLE DISORDERS OR SYNDROMES, TISSUESPECIFIC GENE EXPRESSION BY WHOLETRANSCRIPTOME AND NEXT-GENERATION SEQUENCING, BLOOD, FORMALIN-FIXED PARAFFINEMBEDDED (FFPE) TISSUE OR FRESH FROZEN TISSUE, REPORTED AS PRESENCE OR ABSENCE OF SPLICING OR EXPRESSION CHANGES
0267U	RARE CONSTITUTIONAL AND OTHER HERITABLE DISORDERS, IDENTIFICATION OF COPY NUMBER VARIATIONS, INVERSIONS, INSERTIONS, TRANSLOCATIONS, AND OTHER STRUCTURAL VARIANTS BY OPTICAL GENOME MAPPING AND WHOLE GENOME SEQUENCING
0268U	HEMATOLOGY (ATYPICAL HEMOLYTIC UREMIC SYNDROME [AHUS]), GENOMIC SEQUENCE ANALYSIS OF 15 GENES, BLOOD, BUCCAL SWAB, OR AMNIOTIC FLUID
0269U	HEMATOLOGY (AUTOSOMAL DOMINANT CONGENITAL THROMBOCYTOPENIA), GENOMIC SEQUENCE ANALYSIS OF 14 GENES, BLOOD, BUCCAL SWAB, OR AMNIOTIC FLUID
0270U	HEMATOLOGY (CONGENITAL COAGULATION DISORDERS), GENOMIC SEQUENCE ANALYSIS OF 20 GENES, BLOOD, BUCCAL SWAB, OR AMNIOTIC FLUID
0271U	HEMATOLOGY (CONGENITAL NEUTROPENIA), GENOMIC SEQUENCE ANALYSIS OF 23 GENES, BLOOD, BUCCAL SWAB, OR AMNIOTIC FLUID
0272U	HEMATOLOGY (GENETIC BLEEDING DISORDERS), GENOMIC SEQUENCE ANALYSIS OF 51 GENES, BLOOD, BUCCAL SWAB, OR AMNIOTIC FLUID, COMPREHENSIVE
0273U	HEMATOLOGY (GENETIC HYPERFIBRINOLYSIS, DELAYED BLEEDING), GENOMIC SEQUENCE ANALYSIS OF 8 GENES (F13A1, F13B, FGA, FGB, FGG, SERPINA1, SERPINE1, SERPINF2, PLAU), BLOOD, BUCCAL SWAB, OR AMNIOTIC FLUID
0274U	HEMATOLOGY (GENETIC PLATELET DISORDERS), GENOMIC SEQUENCE ANALYSIS OF 43 GENES, BLOOD, BUCCAL SWAB, OR AMNIOTIC FLUID

0276U	HEMATOLOGY (INHERITED THROMBOCYTOPENIA), GENOMIC SEQUENCE ANALYSIS OF 42 GENES, BLOOD, BUCCAL SWAB, OR AMNIOTIC FLUID
0277U	HEMATOLOGY (GENETIC PLATELET FUNCTION DISORDER), GENOMIC SEQUENCE ANALYSIS OF 31 GENES, BLOOD, BUCCAL SWAB, OR AMNIOTIC FLUID
0278U	HEMATOLOGY (GENETIC THROMBOSIS), GENOMIC SEQUENCE ANALYSIS OF 12 GENES, BLOOD, BUCCAL SWAB, OR AMNIOTIC FLUID
0282U	RED BLOOD CELL ANTIGEN TYPING, DNA, GENOTYPING OF 12 BLOOD GROUP SYSTEM GENES TO PREDICT 44 RED BLOOD CELL ANTIGEN PHENOTYPES
0285U	ONCOLOGY, RESPONSE TO RADIATION, CELL-FREE DNA, QUANTITATIVE BRANCHED CHAIN DNA AMPLIFICATION, PLASMA, REPORTED AS A RADIATION TOXICITY SCORE
0286U	CEP72 (CENTROSOMAL PROTEIN, 72-KDA), NUDT15 (NUDIX HYDROLASE 15) AND TPMT (THIOPURINE S-METHYLTRANSFERASE) (EG, DRUG METABOLISM) GENE ANALYSIS, COMMON VARIANTS
0287U	ONCOLOGY (THYROID), DNA AND MRNA, NEXT-GENERATION SEQUENCING ANALYSIS OF 112 GENES, FINE NEEDLE ASPIRATE OR FORMALIN-FIXED PARAFFIN-EMBEDDED (FFPE) TISSUE, ALGORITHMIC PREDICTION OF CANCER RECURRENCE, REPORTED AS A CATEGORICAL RISK RESULT (LOW, INTERMEDIATE, HIGH)
0288U	ONCOLOGY (LUNG), MRNA, QUANTITATIVE PCR ANALYSIS OF 11 GENES (BAG1, BRCA1, CDC6, CDK2AP1, ERBB3, FUT3, IL11, LCK, RND3, SH3BGR, WNT3A) AND 3 REFERENCE GENES (ESD, TBP, YAP1), FORMALIN-FIXED PARAFFIN-EMBEDDED (FFPE) TUMOR TISSUE, ALGORITHMIC INTERPRETATION REPORTED AS A RECURRENCE RISK SCORE
0289U	NEUROLOGY (ALZHEIMER DISEASE), MRNA, GENE EXPRESSION PROFILING BY RNA SEQUENCING OF 24 GENES, WHOLE BLOOD, ALGORITHM REPORTED AS PREDICTIVE RISK SCORE
0290U	PAIN MANAGEMENT, MRNA, GENE EXPRESSION PROFILING BY RNA SEQUENCING OF 36 GENES, WHOLE BLOOD, ALGORITHM REPORTED AS PREDICTIVE RISK SCORE
0291U	PSYCHIATRY (MOOD DISORDERS), MRNA, GENE EXPRESSION PROFILING BY RNA SEQUENCING 144 GENES, WHOLE BLOOD, ALGORITHM REPORTED AS PREDICTIVE RISK SCORE
0292U	PSYCHIATRY (STRESS DISORDERS), MRNA, GENE EXPRESSION PROFILING BY RNA SEQUENCING OF 72 GENES, WHOLE BLOOD, ALGORITHM REPORTED AS PREDICTIVE RISK SCORE
0293U	PSYCHIATRY (SUICIDAL IDEATION), MRNA, GENE EXPRESSION PROFILING BY RNA SEQUENCING OF 54 GENES, WHOLE BLOOD, ALGORITHM REPORTED AS PREDICTIVE RISK SCORE
0294U	LONGEVITY AND MORTALITY RISK, MRNA, GENE EXPRESSION PROFILING BY RNA SEQUENCING OF 18 GENES, WHOLE BLOOD, ALGORITHM REPORTED AS PREDICTIVE RISK SCORE
0296U	ONCOLOGY (ORAL AND/OR OROPHARYNGEAL CANCER), GENE EXPRESSION PROFILING BY RNA SEQUENCING OF AT LEAST 20 MOLECULAR FEATURES (EG, HUMAN AND/OR MICROBIAL MRNA), SALIVA, ALGORITHM REPORTED AS POSITIVE OR NEGATIVE FOR SIGNATURE ASSOCIATED WITH MALIGNANCY

0297U	ONCOLOGY (PAN TUMOR), WHOLE GENOME SEQUENCING OF PAIRED MALIGNANT AND NORMAL DNA SPECIMENS, FRESH OR FORMALIN-FIXED PARAFFIN-EMBEDDED (FFPE) TISSUE, BLOOD OR BONE MARROW, COMPARATIVE SEQUENCE ANALYSES AND VARIANT IDENTIFICATION
0298U	ONCOLOGY (PAN TUMOR), WHOLE TRANSCRIPTOME SEQUENCING OF PAIRED MALIGNANT AND NORMAL RNA SPECIMENS, FRESH OR FORMALIN-FIXED PARAFFIN-EMBEDDED (FFPE) TISSUE, BLOOD OR BONE MARROW, COMPARATIVE SEQUENCE ANALYSES AND EXPRESSION LEVEL AND CHIMERIC TRANSCRIPT IDENTIFICATION
0299U	ONCOLOGY (PAN TUMOR), WHOLE GENOME OPTICAL GENOME MAPPING OF PAIRED MALIGNANT AND NORMAL DNA SPECIMENS, FRESH FROZEN TISSUE, BLOOD, OR BONE MARROW, COMPARATIVE STRUCTURAL VARIANT IDENTIFICATION
0300U	ONCOLOGY (PAN TUMOR), WHOLE GENOME SEQUENCING AND OPTICAL GENOME MAPPING OF PAIRED MALIGNANT AND NORMAL DNA SPECIMENS, FRESH TISSUE, BLOOD, OR BONE MARROW, COMPARATIVE SEQUENCE ANALYSES AND VARIANT IDENTIFICATION
0301U	INFECTIOUS AGENT DETECTION BY NUCLEIC ACID (DNA OR RNA), BARTONELLA HENSELAE AND BARTONELLA QUINTANA, DROPLET DIGITAL PCR (DDPCR)
0302U	INFECTIOUS AGENT DETECTION BY NUCLEIC ACID (DNA OR RNA), BARTONELLA HENSELAE AND BARTONELLA QUINTANA, DROPLET DIGITAL PCR (DDPCR); FOLLOWING LIQUID ENRICHMENT
0313U	ONCOLOGY (PANCREAS), DNA AND MRNA NEXT-GENERATION SEQUENCING ANALYSIS OF 74 GENES AND ANALYSIS OF CEA (CEACAM5) GENE EXPRESSION, PANCREATIC CYST FLUID, ALGORITHM REPORTED AS A CATEGORICAL RESULT (IE, NEGATIVE, LOW PROBABILITY OF NEOPLASIA OR POSITIVE, HIGH PROBABILITY OF NEOPLASIA)
0314U	ONCOLOGY (CUTANEOUS MELANOMA), MRNA GENE EXPRESSION PROFILING BY RT-PCR OF 35 GENES (32 CONTENT AND 3 HOUSEKEEPING), UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED (FFPE) TISSUE, ALGORITHM REPORTED AS A CATEGORICAL RESULT (IE, BENIGN, INTERMEDIATE, MALIGNANT)
0315U	ONCOLOGY (CUTANEOUS SQUAMOUS CELL CARCINOMA), MRNA GENE EXPRESSION PROFILING BY RT-PCR OF 40 GENES (34 CONTENT AND 6 HOUSEKEEPING), UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED (FFPE) TISSUE, ALGORITHM REPORTED AS A CATEGORICAL RISK RESULT (IE, CLASS 1, CLASS 2A, CLASS 2B)
0332U	ONCOLOGY (PAN-TUMOR), GENETIC PROFILING OF 8 DNA-REGULATORY (EPIGENETIC) MARKERS BY QUANTITATIVE POLYMERASE CHAIN REACTION (QPCR), WHOLE BLOOD, REPORTED AS A HIGH OR LOW PROBABILITY OF RESPONDING TO IMMUNE CHECKPOINT-INHIBITOR THERAPY
0333U	ONCOLOGY (LIVER), SURVEILLANCE FOR HEPATOCELLULAR CARCINOMA (HCC) IN HIGHRISK PATIENTS, ANALYSIS OF METHYLATION PATTERNS ON CIRCULATING CELL-FREE DNA (CFDNA) PLUS MEASUREMENT OF SERUM OF AFP/AFP-L3 AND ONCOPROTEIN DES-GAMMACARBOXY-PROTHROMBIN (DCP), ALGORITHM REPORTED AS NORMAL OR ABNORMAL RESULT
0335U	RARE DISEASES (CONSTITUTIONAL/HERITABLE DISORDERS), WHOLE GENOME SEQUENCE ANALYSIS, INCLUDING SMALL

	SEQUENCE CHANGES, COPY NUMBER VARIANTS, DELETIONS, DUPLICATIONS, MOBILE ELEMENT INSERTIONS, UNIPARENTAL DISOMY (UPD), INVERSIONS, ANEUPLOIDY, MITOCHONDRIAL GENOME SEQUENCE ANALYSIS WITH HETEROPLASMY AND LARGE DELETIONS, SHORT TANDEM REPEAT (STR) GENE EXPANSIONS, FETAL SAMPLE, IDENTIFICATION AND CATEGORIZATION OF GENETIC VARIANTS
0336U	RARE DISEASES (CONSTITUTIONAL/HERITABLE DISORDERS), WHOLE GENOME SEQUENCE ANALYSIS, INCLUDING SMALL SEQUENCE CHANGES, COPY NUMBER VARIANTS, DELETIONS, DUPLICATIONS, MOBILE ELEMENT INSERTIONS, UNIPARENTAL DISOMY (UPD), INVERSIONS, ANEUPLOIDY, MITOCHONDRIAL GENOME SEQUENCE ANALYSIS WITH HETEROPLASMY AND LARGE DELETIONS, SHORT TANDEM REPEAT (STR) GENE EXPANSIONS, BLOOD OR SALIVA, IDENTIFICATION AND CATEGORIZATION OF GENETIC VARIANTS, EACH COMPARATOR GENOME (EG, PARENT)
0340U	ONCOLOGY (PAN-CANCER), ANALYSIS OF MINIMAL RESIDUAL DISEASE (MRD) FROM PLASMA, WITH ASSAYS PERSONALIZED TO EACH PATIENT BASED ON PRIOR NEXT-GENERATION SEQUENCING OF THE PATIENT'S TUMOR AND GERMLINE DNA, REPORTED AS ABSENCE OR PRESENCE OF MRD, WITH DISEASE-BURDEN CORRELATION, IF APPROPRIATE
0341U	FETAL ANEUPLOIDY DNA SEQUENCING COMPARATIVE ANALYSIS, FETAL DNA FROM PRODUCTS OF CONCEPTION, REPORTED AS NORMAL (EUPLOIDY), MONOSOMY, TRISOMY, OR PARTIAL DELETION/DUPLICATION, MOSAICISM, AND SEGMENTAL ANEUPLOID
81105	HUMAN PLATELET ANTIGEN 1 GENOTYPING (HPA-1), ITGB3 (INTEGRIN, BETA 3 [PLATELET GLYCOPROTEIN IIIA], ANTIGEN CD61 [GPIIIA]) (EG, NEONATAL ALLOIMMUNE THROMBOCYTOPENIA [NAIT], POST-TRANSFUSION PURPURA), GENE ANALYSIS, COMMON VARIANT, HPA-1A/B (L33P)
81106	HUMAN PLATELET ANTIGEN 2 GENOTYPING (HPA-2), GP1BA (GLYCOPROTEIN IB [PLATELET], ALPHA POLYPEPTIDE [GPIBA]) (EG, NEONATAL ALLOIMMUNE THROMBOCYTOPENIA [NAIT], POST-TRANSFUSION PURPURA), GENE ANALYSIS, COMMON VARIANT, HPA-2A/B (T145M)
81107	HUMAN PLATELET ANTIGEN 3 GENOTYPING (HPA-3), ITGA2B (INTEGRIN, ALPHA 2B [PLATELET GLYCOPROTEIN IIB OF IIB/IIIA COMPLEX], ANTIGEN CD41 [GPIIB]) (EG, NEONATAL ALLOIMMUNE THROMBOCYTOPENIA [NAIT], POST-TRANSFUSION PURPURA), GENE ANALYSIS, COMMON VARIANT, HPA-3A/B (I843S)
81108	HUMAN PLATELET ANTIGEN 4 GENOTYPING (HPA-4), ITGB3 (INTEGRIN, BETA 3 [PLATELET GLYCOPROTEIN IIIA], ANTIGEN CD61 [GPIIIA]) (EG, NEONATAL ALLOIMMUNE THROMBOCYTOPENIA [NAIT], POST-TRANSFUSION PURPURA), GENE ANALYSIS, COMMON VARIANT, HPA-4A/B (R143Q)
81109	HUMAN PLATELET ANTIGEN 5 GENOTYPING (HPA-5), ITGA2 (INTEGRIN, ALPHA 2 [CD49B, ALPHA 2 SUBUNIT OF VLA-2 RECEPTOR] [GPIA]) (EG, NEONATAL ALLOIMMUNE THROMBOCYTOPENIA [NAIT], POST-TRANSFUSION PURPURA), GENE ANALYSIS, COMMON VARIANT (EG, HPA-5A/B [K505E])
81110	HUMAN PLATELET ANTIGEN 6 GENOTYPING (HPA-6W), ITGB3 (INTEGRIN, BETA 3 [PLATELET GLYCOPROTEIN IIIA, ANTIGEN CD61]

	[GPIIIA]) (EG, NEONATAL ALLOIMMUNE THROMBOCYTOPENIA [NAIT], POST-TRANSFUSION PURPURA), GENE ANALYSIS, COMMON VARIANT, HPA-6A/B (R489Q)
81111	HUMAN PLATELET ANTIGEN 9 GENOTYPING (HPA-9W), ITGA2B (INTEGRIN, ALPHA 2B [PLATELET GLYCOPROTEIN IIB OF IIB/IIIA COMPLEX, ANTIGEN CD41] [GPIIB]) (EG, NEONATAL ALLOIMMUNE THROMBOCYTOPENIA [NAIT], POST-TRANSFUSION PURPURA), GENE ANALYSIS, COMMON VARIANT, HPA-9A/B (V837M)
81112	HUMAN PLATELET ANTIGEN 15 GENOTYPING (HPA-15), CD109 (CD109 MOLECULE) (EG, NEONATAL ALLOIMMUNE THROMBOCYTOPENIA [NAIT], POST-TRANSFUSION PURPURA), GENE ANALYSIS, COMMON VARIANT, HPA-15A/B (S682Y)
81120	IDH1 (ISOCITRATE DEHYDROGENASE 1 [NADP+], SOLUBLE) (EG, GLIOMA), COMMON VARIANTS (EG, R132H, R132C)
81121	IDH2 (ISOCITRATE DEHYDROGENASE 2 [NADP+], MITOCHONDRIAL) (EG, GLIOMA), COMMON VARIANTS (EG, R140W, R172M)
81161	DMD (DYSTROPHIN) (EG, DUCHENNE/BECKER MUSCULAR DYSTROPHY) DELETION ANALYSIS, AND DUPLICATION ANALYSIS, IF PERFORMED
81162	BRCA1 (BRCA1, DNA REPAIR ASSOCIATED), BRCA2 (BRCA2, DNA REPAIR ASSOCIATED) (EG, HEREDITARY BREAST AND OVARIAN CANCER) GENE ANALYSIS; FULL SEQUENCE ANALYSIS AND FULL DUPLICATION/DELETION ANALYSIS (IE, DETECTION OF LARGE GENE REARRANGEMENTS)
81163	BRCA1 (BRCA1, DNA REPAIR ASSOCIATED), BRCA2 (BRCA2, DNA REPAIR ASSOCIATED) (EG, HEREDITARY BREAST AND OVARIAN CANCER) GENE ANALYSIS; FULL SEQUENCE ANALYSIS
81164	BRCA1 (BRCA1, DNA REPAIR ASSOCIATED), BRCA2 (BRCA2, DNA REPAIR ASSOCIATED) (EG, HEREDITARY BREAST AND OVARIAN CANCER) GENE ANALYSIS; FULL DUPLICATION/DELETION ANALYSIS (IE, DETECTION OF LARGE GENE REARRANGEMENTS)
81165	BRCA1 (BRCA1, DNA REPAIR ASSOCIATED) (EG, HEREDITARY BREAST AND OVARIAN CANCER) GENE ANALYSIS; FULL SEQUENCE ANALYSIS
81166	BRCA1 (BRCA1, DNA REPAIR ASSOCIATED) (EG, HEREDITARY BREAST AND OVARIAN CANCER) GENE ANALYSIS; FULL DUPLICATION/DELETION ANALYSIS (IE, DETECTION OF LARGE GENE REARRANGEMENTS)
81167	BRCA2 (BRCA2, DNA REPAIR ASSOCIATED) (EG, HEREDITARY BREAST AND OVARIAN CANCER) GENE ANALYSIS; FULL DUPLICATION/DELETION ANALYSIS (IE, DETECTION OF LARGE GENE REARRANGEMENTS)
81168	CCND1/IGH (T(11;14)) (EG, MANTLE CELL LYMPHOMA) TRANSLOCATION ANALYSIS, MAJOR BREAKPOINT, QUALITATIVE AND QUANTITATIVE, IF PERFORMED
81170	ABL1 (ABL PROTO-ONCOGENE 1, NON-RECEPTOR TYROSINE KINASE) (EG, ACQUIRED IMATINIB TYROSINE KINASE INHIBITOR RESISTANCE), GENE ANALYSIS, VARIANTS IN THE KINASE DOMAIN
81171	AFF2 (AF4/FMR2 FAMILY, MEMBER 2 [FMR2]) (EG, FRAGILE X MENTAL RETARDATION 2 [FRAXE]) GENE ANALYSIS; EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81172	AFF2 (AF4/FMR2 FAMILY, MEMBER 2 [FMR2]) (EG, FRAGILE X MENTAL RETARDATION 2 [FRAXE]) GENE ANALYSIS;

	CHARACTERIZATION OF ALLELES (EG, EXPANDED SIZE AND METHYLATION STATUS)
81173	AR (ANDROGEN RECEPTOR) (EG, SPINAL AND BULBAR MUSCULAR ATROPHY, KENNEDY DISEASE, X CHROMOSOME INACTIVATION) GENE ANALYSIS; FULL GENE SEQUENCE
81174	AR (ANDROGEN RECEPTOR) (EG, SPINAL AND BULBAR MUSCULAR ATROPHY, KENNEDY DISEASE, X CHROMOSOME INACTIVATION) GENE ANALYSIS; KNOWN FAMILIAL VARIANT
81175	ASXL1 (ADDITIONAL SEX COMBS LIKE 1, TRANSCRIPTIONAL REGULATOR) (EG, MYELODYSPLASTIC SYNDROME, MYELOPROLIFERATIVE NEOPLASMS, CHRONIC MYELOMONOCYTIC LEUKEMIA), GENE ANALYSIS; FULL GENE SEQUENCE
81176	ASXL1 (ADDITIONAL SEX COMBS LIKE 1, TRANSCRIPTIONAL REGULATOR) (EG, MYELODYSPLASTIC SYNDROME, MYELOPROLIFERATIVE NEOPLASMS, CHRONIC MYELOMONOCYTIC LEUKEMIA), GENE ANALYSIS; TARGETED SEQUENCE ANALYSIS (EG, EXON 12)
81177	ATN1 (ATROPHIN 1) (EG, DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY) GENE ANALYSIS, EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81178	ATXN1 (ATAXIN 1) (EG, SPINOCEREBELLAR ATAXIA) GENE ANALYSIS, EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81179	ATXN2 (ATAXIN 2) (EG, SPINOCEREBELLAR ATAXIA) GENE ANALYSIS, EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81180	ATXN3 (ATAXIN 3) (EG, SPINOCEREBELLAR ATAXIA, MACHADO-JOSEPH DISEASE) GENE ANALYSIS, EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81181	ATXN7 (ATAXIN 7) (EG, SPINOCEREBELLAR ATAXIA) GENE ANALYSIS, EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81182	ATXN8OS (ATXN8 OPPOSITE STRAND [NON-PROTEIN CODING]) (EG, SPINOCEREBELLAR ATAXIA) GENE ANALYSIS, EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81183	ATXN10 (ATAXIN 10) (EG, SPINOCEREBELLAR ATAXIA) GENE ANALYSIS, EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81184	CACNA1A (CALCIUM VOLTAGE-GATED CHANNEL SUBUNIT ALPHA1 A) (EG, SPINOCEREBELLAR ATAXIA) GENE ANALYSIS; EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81185	CACNA1A (CALCIUM VOLTAGE-GATED CHANNEL SUBUNIT ALPHA1 A) (EG, SPINOCEREBELLAR ATAXIA) GENE ANALYSIS; FULL GENE SEQUENCE
81186	CACNA1A (CALCIUM VOLTAGE-GATED CHANNEL SUBUNIT ALPHA1 A) (EG, SPINOCEREBELLAR ATAXIA) GENE ANALYSIS; KNOWN FAMILIAL VARIANT
81187	CNBP (CCHC-TYPE ZINC FINGER NUCLEIC ACID BINDING PROTEIN) (EG, MYOTONIC DYSTROPHY TYPE 2) GENE ANALYSIS, EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81188	CSTB (CYSTATIN B) (EG, UNVERRICHT-LUNDBORG DISEASE) GENE ANALYSIS; EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES

81189	CSTB (CYSTATIN B) (EG, UNVERRICHT-LUNDBORG DISEASE) GENE ANALYSIS; FULL GENE SEQUENCE
81190	CSTB (CYSTATIN B) (EG, UNVERRICHT-LUNDBORG DISEASE) GENE ANALYSIS; KNOWN FAMILIAL VARIANT(S)
81191	NTRK1 (NEUROTROPHIC RECEPTOR TYROSINE KINASE 1) (EG, SOLID TUMORS) TRANSLOCATION ANALYSIS
81192	NTRK2 (NEUROTROPHIC RECEPTOR TYROSINE KINASE 2) (EG, SOLID TUMORS) TRANSLOCATION ANALYSIS
81193	NTRK3 (NEUROTROPHIC RECEPTOR TYROSINE KINASE 3) (EG, SOLID TUMORS) TRANSLOCATION ANALYSIS
81194	NTRK (NEUROTROPHIC RECEPTOR TYROSINE KINASE 1, 2, AND 3) (EG, SOLID TUMORS) TRANSLOCATION ANALYSIS
81200	ASPA (ASPARTOACYLASE) (EG, CANAVAN DISEASE) GENE ANALYSIS, COMMON VARIANTS (EG, E285A, Y231X)
81201	APC (ADENOMATOUS POLYPOSIS COLI) (EG, FAMILIAL ADENOMATOSIS POLYPOSIS [FAP], ATTENUATED FAP) GENE ANALYSIS; FULL GENE SEQUENCE
81202	APC (ADENOMATOUS POLYPOSIS COLI) (EG, FAMILIAL ADENOMATOSIS POLYPOSIS [FAP], ATTENUATED FAP) GENE ANALYSIS; KNOWN FAMILIAL VARIANTS
81203	APC (ADENOMATOUS POLYPOSIS COLI) (EG, FAMILIAL ADENOMATOSIS POLYPOSIS [FAP], ATTENUATED FAP) GENE ANALYSIS; DUPLICATION/DELETION VARIANTS
81204	AR (ANDROGEN RECEPTOR) (EG, SPINAL AND BULBAR MUSCULAR ATROPHY, KENNEDY DISEASE, X CHROMOSOME INACTIVATION) GENE ANALYSIS; CHARACTERIZATION OF ALLELES (EG, EXPANDED SIZE OR METHYLATION STATUS)
81205	BCKDHB (BRANCHED-CHAIN KETO ACID DEHYDROGENASE E1, BETA POLYPEPTIDE) (EG, MAPLE SYRUP URINE DISEASE) GENE ANALYSIS, COMMON VARIANTS (EG, R183P, G278S, E422X)
81206	BCR/ABL1 (T(9;22)) (EG, CHRONIC MYELOGENOUS LEUKEMIA) TRANSLOCATION ANALYSIS; MAJOR BREAKPOINT, QUALITATIVE OR QUANTITATIVE
81207	BCR/ABL1 (T(9;22)) (EG, CHRONIC MYELOGENOUS LEUKEMIA) TRANSLOCATION ANALYSIS; MINOR BREAKPOINT, QUALITATIVE OR QUANTITATIVE
81208	BCR/ABL1 (T(9;22)) (EG, CHRONIC MYELOGENOUS LEUKEMIA) TRANSLOCATION ANALYSIS; OTHER BREAKPOINT, QUALITATIVE OR QUANTITATIVE
81209	BLM (BLOOM SYNDROME, RECQ HELICASE-LIKE) (EG, BLOOM SYNDROME) GENE ANALYSIS, 2281DEL6INS7 VARIANT
81210	BRAF (B-RAF PROTO-ONCOGENE, SERINE/THREONINE KINASE) (EG, COLON CANCER, MELANOMA), GENE ANALYSIS, V600 VARIANT(S)
81212	BRCA1 (BRCA1, DNA REPAIR ASSOCIATED), BRCA2 (BRCA2, DNA REPAIR ASSOCIATED) (EG, HEREDITARY BREAST AND OVARIAN CANCER) GENE ANALYSIS; 185DELAG, 5385INSC, 6174DELT VARIANTS
81215	BRCA1 (BRCA1, DNA REPAIR ASSOCIATED) (EG, HEREDITARY BREAST AND OVARIAN CANCER) GENE ANALYSIS; KNOWN FAMILIAL VARIANT
81216	BRCA2 (BRCA2, DNA REPAIR ASSOCIATED) (EG, HEREDITARY BREAST AND OVARIAN CANCER) GENE ANALYSIS; FULL SEQUENCE ANALYSIS

81217	BRCA2 (BRCA2, DNA REPAIR ASSOCIATED) (EG, HEREDITARY BREAST AND OVARIAN CANCER) GENE ANALYSIS; KNOWN FAMILIAL VARIANT
81218	CEBPA (CCAAT/ENHANCER BINDING PROTEIN [C/EBP], ALPHA) (EG, ACUTE MYELOID LEUKEMIA), GENE ANALYSIS, FULL GENE SEQUENCE
81219	CALR (CALRETICULIN) (EG, MYELOPROLIFERATIVE DISORDERS), GENE ANALYSIS, COMMON VARIANTS IN EXON 9
81220	CFTR (CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR) (EG, CYSTIC FIBROSIS) GENE ANALYSIS; COMMON VARIANTS (EG, ACMG/ACOG GUIDELINES)
81221	CFTR (CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR) (EG, CYSTIC FIBROSIS) GENE ANALYSIS; KNOWN FAMILIAL VARIANTS
81222	CFTR (CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR) (EG, CYSTIC FIBROSIS) GENE ANALYSIS; DUPLICATION/DELETION VARIANTS
81223	CFTR (CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR) (EG, CYSTIC FIBROSIS) GENE ANALYSIS; FULL GENE SEQUENCE
81224	CFTR (CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR) (EG, CYSTIC FIBROSIS) GENE ANALYSIS; INTRON 8 POLY-T ANALYSIS (EG, MALE INFERTILITY)
81225	CYP2C19 (CYTOCHROME P450, FAMILY 2, SUBFAMILY C, POLYPEPTIDE 19) (EG, DRUG METABOLISM), GENE ANALYSIS, COMMON VARIANTS (EG, *2, *3, *4, *8, *17)
81226	CYP2D6 (CYTOCHROME P450, FAMILY 2, SUBFAMILY D, POLYPEPTIDE 6) (EG, DRUG METABOLISM), GENE ANALYSIS, COMMON VARIANTS (EG, *2, *3, *4, *5, *6, *9, *10, *17, *19, *29, *35, *41, *1XN, *2XN, *4XN)
81227	CYP2C9 (CYTOCHROME P450, FAMILY 2, SUBFAMILY C, POLYPEPTIDE 9) (EG, DRUG METABOLISM), GENE ANALYSIS, COMMON VARIANTS (EG, *2, *3, *5, *6)
81228	CYTOGENOMIC (GENOME-WIDE) ANALYSIS FOR CONSTITUTIONAL CHROMOSOMAL ABNORMALITIES; INTERROGATION OF GENOMIC REGIONS FOR COPY NUMBER VARIANTS, COMPARATIVE GENOMIC HYBRIDIZATION [CGH] MICROARRAY ANALYSIS
81229	CYTOGENOMIC (GENOME-WIDE) ANALYSIS FOR CONSTITUTIONAL CHROMOSOMAL ABNORMALITIES; INTERROGATION OF GENOMIC REGIONS FOR COPY NUMBER AND SINGLE NUCLEOTIDE POLYMORPHISM (SNP) VARIANTS, COMPARATIVE GENOMIC HYBRIDIZATION (CGH) MICROARRAY ANALYSIS
81230	CYP3A4 (CYTOCHROME P450 FAMILY 3 SUBFAMILY A MEMBER 4) (EG, DRUG METABOLISM), GENE ANALYSIS, COMMON VARIANT(S) (EG, *2, *22)
81231	CYP3A5 (CYTOCHROME P450 FAMILY 3 SUBFAMILY A MEMBER 5) (EG, DRUG METABOLISM), GENE ANALYSIS, COMMON VARIANTS (EG, *2, *3, *4, *5, *6, *7)
81232	DPYD (DIHYDROPYRIMIDINE DEHYDROGENASE) (EG, 5-FLUOROURACIL/5-FU AND CAPECITABINE DRUG METABOLISM), GENE ANALYSIS, COMMON VARIANT(S) (EG, *2A, *4, *5, *6)

81233	BTK (BRUTON'S TYROSINE KINASE) (EG, CHRONIC LYMPHOCYTIC LEUKEMIA) GENE ANALYSIS, COMMON VARIANTS (EG, C481S, C481R, C481F)
81234	DMPK (DM1 PROTEIN KINASE) (EG, MYOTONIC DYSTROPHY TYPE 1) GENE ANALYSIS; EVALUATION TO DETECT ABNORMAL (EXPANDED) ALLELES
81235	EGFR (EPIDERMAL GROWTH FACTOR RECEPTOR) (EG, NON-SMALL CELL LUNG CANCER) GENE ANALYSIS, COMMON VARIANTS (EG, EXON 19 LREA DELETION, L858R, T790M, G719A, G719S, L861Q)
81236	EZH2 (ENHANCER OF ZESTE 2 POLYCOMB REPRESSIVE COMPLEX 2 SUBUNIT) (EG, MYELODYSPLASTIC SYNDROME, MYELOPROLIFERATIVE NEOPLASMS) GENE ANALYSIS, FULL GENE SEQUENCE
81237	EZH2 (ENHANCER OF ZESTE 2 POLYCOMB REPRESSIVE COMPLEX 2 SUBUNIT) (EG, DIFFUSE LARGE B-CELL LYMPHOMA) GENE ANALYSIS, COMMON VARIANT(S) (EG, CODON 646)
81238	F9 (COAGULATION FACTOR IX) (EG, HEMOPHILIA B), FULL GENE SEQUENCE
81239	DMPK (DM1 PROTEIN KINASE) (EG, MYOTONIC DYSTROPHY TYPE 1) GENE ANALYSIS; CHARACTERIZATION OF ALLELES (EG, EXPANDED SIZE)
81240	F2 (PROTHROMBIN, COAGULATION FACTOR II) (EG, HEREDITARY HYPERCOAGULABILITY) GENE ANALYSIS, 20210G>A VARIANT
81241	F5 (COAGULATION FACTOR V) (EG, HEREDITARY HYPERCOAGULABILITY) GENE ANALYSIS, LEIDEN VARIANT
81242	FANCC (FANCONI ANEMIA, COMPLEMENTATION GROUP C) (EG, FANCONI ANEMIA, TYPE C) GENE ANALYSIS, COMMON VARIANT (EG, IVS4+4A>T)
81243	FMR1 (FRAGILE X MENTAL RETARDATION 1) (EG, FRAGILE X MENTAL RETARDATION) GENE ANALYSIS; EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81244	FMR1 (FRAGILE X MENTAL RETARDATION 1) (EG, FRAGILE X MENTAL RETARDATION) GENE ANALYSIS; CHARACTERIZATION OF ALLELES (EG, EXPANDED SIZE AND PROMOTER METHYLATION STATUS)
81245	FLT3 (FMS-RELATED TYROSINE KINASE 3) (EG, ACUTE MYELOID LEUKEMIA), GENE ANALYSIS; INTERNAL TANDEM DUPLICATION (ITD) VARIANTS (IE, EXONS 14, 15)
81246	FLT3 (FMS-RELATED TYROSINE KINASE 3) (EG, ACUTE MYELOID LEUKEMIA), GENE ANALYSIS; TYROSINE KINASE DOMAIN (TKD) VARIANTS (EG, D835, I836)
81247	G6PD (GLUCOSE-6-PHOSPHATE DEHYDROGENASE) (EG, HEMOLYTIC ANEMIA, JAUNDICE), GENE ANALYSIS; COMMON VARIANT(S) (EG, A, A-)
81248	G6PD (GLUCOSE-6-PHOSPHATE DEHYDROGENASE) (EG, HEMOLYTIC ANEMIA, JAUNDICE), GENE ANALYSIS; KNOWN FAMILIAL VARIANT(S)
81249	G6PD (GLUCOSE-6-PHOSPHATE DEHYDROGENASE) (EG, HEMOLYTIC ANEMIA, JAUNDICE), GENE ANALYSIS; FULL GENE SEQUENCE
81250	G6PC (GLUCOSE-6-PHOSPHATASE, CATALYTIC SUBUNIT) (EG, GLYCOGEN STORAGE DISEASE, TYPE 1A, VON GIERKE DISEASE) GENE ANALYSIS, COMMON VARIANTS (EG, R83C, Q347X)

81251	GBA (GLUCOSIDASE, BETA, ACID) (EG, GAUCHER DISEASE) GENE ANALYSIS, COMMON VARIANTS (EG, N370S, 84GG, L444P, IVS2+1G>A)
81252	GJB2 (GAP JUNCTION PROTEIN, BETA 2, 26KDA, CONNEXIN 26) (EG, NONSYNDROMIC HEARING LOSS) GENE ANALYSIS; FULL GENE SEQUENCE
81253	GJB2 (GAP JUNCTION PROTEIN, BETA 2, 26KDA, CONNEXIN 26) (EG, NONSYNDROMIC HEARING LOSS) GENE ANALYSIS; KNOWN FAMILIAL VARIANTS
81254	GJB6 (GAP JUNCTION PROTEIN, BETA 6, 30KDA, CONNEXIN 30) (EG, NONSYNDROMIC HEARING LOSS) GENE ANALYSIS, COMMON VARIANTS (EG, 309KB [DEL(GJB6-D13S1830)] AND 232KB [DEL(GJB6-D13S1854)])
81255	HEXA (HEXOSAMINIDASE A [ALPHA POLYPEPTIDE]) (EG, TAY-SACHS DISEASE) GENE ANALYSIS, COMMON VARIANTS (EG, 1278INSTATC, 1421+1G>C, G269S)
81256	HFE (HEMOCHROMATOSIS) (EG, HEREDITARY HEMOCHROMATOSIS) GENE ANALYSIS, COMMON VARIANTS (EG, C282Y, H63D)
81257	HBA1/HBA2 (ALPHA GLOBIN 1 AND ALPHA GLOBIN 2) (EG, ALPHA THALASSEMIA, HB BART HYDROPS FETALIS SYNDROME, HBH DISEASE), GENE ANALYSIS; COMMON DELETIONS OR VARIANT (EG, SOUTHEAST ASIAN, THAI, FILIPINO, MEDITERRANEAN, ALPHA3.7, ALPHA4.2, ALPHA20.5, CONSTANT SPRING)
81258	HBA1/HBA2 (ALPHA GLOBIN 1 AND ALPHA GLOBIN 2) (EG, ALPHA THALASSEMIA, HB BART HYDROPS FETALIS SYNDROME, HBH DISEASE), GENE ANALYSIS; KNOWN FAMILIAL VARIANT
81259	HBA1/HBA2 (ALPHA GLOBIN 1 AND ALPHA GLOBIN 2) (EG, ALPHA THALASSEMIA, HB BART HYDROPS FETALIS SYNDROME, HBH DISEASE), GENE ANALYSIS; FULL GENE SEQUENCE
81260	IKBKAP (INHIBITOR OF KAPPA LIGHT POLYPEPTIDE GENE ENHANCER IN B-CELLS, KINASE COMPLEX-ASSOCIATED PROTEIN) (EG, FAMILIAL DYSAUTONOMIA) GENE ANALYSIS, COMMON VARIANTS (EG, 2507+6T>C, R696P)
81261	IGH@ (IMMUNOGLOBULIN HEAVY CHAIN LOCUS) (EG, LEUKEMIAS AND LYMPHOMAS, B-CELL), GENE REARRANGEMENT ANALYSIS TO DETECT ABNORMAL CLONAL POPULATION(S); AMPLIFIED METHODOLOGY (EG, POLYMERASE CHAIN REACTION)
81262	IGH@ (IMMUNOGLOBULIN HEAVY CHAIN LOCUS) (EG, LEUKEMIAS AND LYMPHOMAS, B-CELL), GENE REARRANGEMENT ANALYSIS TO DETECT ABNORMAL CLONAL POPULATION(S); DIRECT PROBE METHODOLOGY (EG, SOUTHERN BLOT)
81263	IGH@ (IMMUNOGLOBULIN HEAVY CHAIN LOCUS) (EG, LEUKEMIA AND LYMPHOMA, B-CELL), VARIABLE REGION SOMATIC MUTATION ANALYSIS
81264	IGK@ (IMMUNOGLOBULIN KAPPA LIGHT CHAIN LOCUS) (EG, LEUKEMIA AND LYMPHOMA, B-CELL), GENE REARRANGEMENT ANALYSIS, EVALUATION TO DETECT ABNORMAL CLONAL POPULATION(S)
81265	COMPARATIVE ANALYSIS USING SHORT TANDEM REPEAT (STR) MARKERS; PATIENT AND COMPARATIVE SPECIMEN (EG, PRE-TRANSPLANT RECIPIENT AND DONOR GERMLINE TESTING, POST-TRANSPLANT NON-HEMATOPOIETIC RECIPIENT GERMLINE [EG, BUCCAL SWAB OR OTHER GERMLINE TISSUE SAMPLE] AND DONOR

	TESTING, TWIN ZYGOSITY TESTING, OR MATERNAL CELL CONTAMINATION OF FETAL CELLS)
81266	COMPARATIVE ANALYSIS USING SHORT TANDEM REPEAT (STR) MARKERS; EACH ADDITIONAL SPECIMEN (EG, ADDITIONAL CORD BLOOD DONOR, ADDITIONAL FETAL SAMPLES FROM DIFFERENT CULTURES, OR ADDITIONAL ZYGOSITY IN MULTIPLE BIRTH PREGNANCIES) (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
81267	CHIMERISM (ENGRAFTMENT) ANALYSIS, POST TRANSPLANTATION SPECIMEN (EG, HEMATOPOIETIC STEM CELL), INCLUDES COMPARISON TO PREVIOUSLY PERFORMED BASELINE ANALYSES; WITHOUT CELL SELECTION
81268	CHIMERISM (ENGRAFTMENT) ANALYSIS, POST TRANSPLANTATION SPECIMEN (EG, HEMATOPOIETIC STEM CELL), INCLUDES COMPARISON TO PREVIOUSLY PERFORMED BASELINE ANALYSES; WITH CELL SELECTION (EG, CD3, CD33), EACH CELL TYPE
81269	HBA1/HBA2 (ALPHA GLOBIN 1 AND ALPHA GLOBIN 2) (EG, ALPHA THALASSEMIA, HB BART HYDROPS FETALIS SYNDROME, HBH DISEASE), GENE ANALYSIS; DUPLICATION/DELETION VARIANTS
81270	JAK2 (JANUS KINASE 2) (EG, MYELOPROLIFERATIVE DISORDER) GENE ANALYSIS, P.VAL617PHE (V617F) VARIANT
81271	HTT (HUNTINGTIN) (EG, HUNTINGTON DISEASE) GENE ANALYSIS; EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81272	KIT (V-KIT HARDY-ZUCKERMAN 4 FELINE SARCOMA VIRAL ONCOGENE HOMOLOG) (EG, GASTROINTESTINAL STROMAL TUMOR [GIST], ACUTE MYELOID LEUKEMIA, MELANOMA), GENE ANALYSIS, TARGETED SEQUENCE ANALYSIS (EG, EXONS 8, 11, 13, 17, 18)
81273	KIT (V-KIT HARDY-ZUCKERMAN 4 FELINE SARCOMA VIRAL ONCOGENE HOMOLOG) (EG, MASTOCYTOSIS), GENE ANALYSIS, D816 VARIANT(S)
81274	HTT (HUNTINGTIN) (EG, HUNTINGTON DISEASE) GENE ANALYSIS; CHARACTERIZATION OF ALLELES (EG, EXPANDED SIZE)
81275	KRAS (KIRSTEN RAT SARCOMA VIRAL ONCOGENE HOMOLOG) (EG, CARCINOMA) GENE ANALYSIS; VARIANTS IN EXON 2 (EG, CODONS 12 AND 13)
81276	KRAS (KIRSTEN RAT SARCOMA VIRAL ONCOGENE HOMOLOG) (EG, CARCINOMA) GENE ANALYSIS; ADDITIONAL VARIANT(S) (EG, CODON 61, CODON 146)
81277	CYTOGENOMIC NEOPLASIA (GENOME-WIDE) MICROARRAY ANALYSIS, INTERROGATION OF GENOMIC REGIONS FOR COPY NUMBER AND LOSS-OF-HETEROZYGOSITY VARIANTS FOR CHROMOSOMAL ABNORMALITIES
81278	IGH@/BCL2 (T(14;18)) (EG, FOLLICULAR LYMPHOMA) TRANSLOCATION ANALYSIS, MAJOR BREAKPOINT REGION (MBR) AND MINOR CLUSTER REGION (MCR) BREAKPOINTS, QUALITATIVE OR QUANTITATIVE
81279	JAK2 (JANUS KINASE 2) (EG, MYELOPROLIFERATIVE DISORDER) TARGETED SEQUENCE ANALYSIS (EG, EXONS 12 AND 13)
81283	IFNL3 (INTERFERON, LAMBDA 3) (EG, DRUG RESPONSE), GENE ANALYSIS, RS12979860 VARIANT
81284	FXN (FRATAXIN) (EG, FRIEDREICH ATAXIA) GENE ANALYSIS; EVALUATION TO DETECT ABNORMAL (EXPANDED) ALLELES

81285	FXN (FRATAXIN) (EG, FRIEDREICH ATAXIA) GENE ANALYSIS; CHARACTERIZATION OF ALLELES (EG, EXPANDED SIZE)
81286	FXN (FRATAXIN) (EG, FRIEDREICH ATAXIA) GENE ANALYSIS; FULL GENE SEQUENCE
81287	MGMT (O-6-METHYLGUANINE-DNA METHYLTRANSFERASE) (EG, GLIOBLASTOMA MULTIFORME) PROMOTER METHYLATION ANALYSIS
81288	MLH1 (MUTL HOMOLOG 1, COLON CANCER, NONPOLYPOSIS TYPE 2) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; PROMOTER METHYLATION ANALYSIS
81289	FXN (FRATAXIN) (EG, FRIEDREICH ATAXIA) GENE ANALYSIS; KNOWN FAMILIAL VARIANT(S)
81290	MCOLN1 (MUCOLIPIN 1) (EG, MUCOLIPIDOSIS, TYPE IV) GENE ANALYSIS, COMMON VARIANTS (EG, IVS3-2A>G, DEL6.4KB)
81291	MTHFR (5,10-METHYLENETETRAHYDROFOLATE REDUCTASE) (EG, HEREDITARY HYPERCOAGULABILITY) GENE ANALYSIS, COMMON VARIANTS (EG, 677T, 1298C)
81292	MLH1 (MUTL HOMOLOG 1, COLON CANCER, NONPOLYPOSIS TYPE 2) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; FULL SEQUENCE ANALYSIS
81293	MLH1 (MUTL HOMOLOG 1, COLON CANCER, NONPOLYPOSIS TYPE 2) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; KNOWN FAMILIAL VARIANTS
81294	MLH1 (MUTL HOMOLOG 1, COLON CANCER, NONPOLYPOSIS TYPE 2) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; DUPLICATION/DELETION VARIANTS
81295	MSH2 (MUTS HOMOLOG 2, COLON CANCER, NONPOLYPOSIS TYPE 1) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; FULL SEQUENCE ANALYSIS
81296	MSH2 (MUTS HOMOLOG 2, COLON CANCER, NONPOLYPOSIS TYPE 1) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; KNOWN FAMILIAL VARIANTS
81297	MSH2 (MUTS HOMOLOG 2, COLON CANCER, NONPOLYPOSIS TYPE 1) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; DUPLICATION/DELETION VARIANTS
81298	MSH6 (MUTS HOMOLOG 6 [E. COLI]) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; FULL SEQUENCE ANALYSIS
81299	MSH6 (MUTS HOMOLOG 6 [E. COLI]) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; KNOWN FAMILIAL VARIANTS
81300	MSH6 (MUTS HOMOLOG 6 [E. COLI]) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; DUPLICATION/DELETION VARIANTS
81301	MICROSATELLITE INSTABILITY ANALYSIS (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) OF MARKERS FOR MISMATCH REPAIR DEFICIENCY (EG, BAT25, BAT26), INCLUDES COMPARISON OF NEOPLASTIC AND NORMAL TISSUE, IF PERFORMED
81302	MECP2 (METHYL CPG BINDING PROTEIN 2) (EG, RETT SYNDROME) GENE ANALYSIS; FULL SEQUENCE ANALYSIS
81303	MECP2 (METHYL CPG BINDING PROTEIN 2) (EG, RETT SYNDROME) GENE ANALYSIS; KNOWN FAMILIAL VARIANT

81304	MECP2 (METHYL CPG BINDING PROTEIN 2) (EG, RETT SYNDROME) GENE ANALYSIS; DUPLICATION/DELETION VARIANTS
81305	MYD88 (MYELOID DIFFERENTIATION PRIMARY RESPONSE 88) (EG, WALDENSTROM'S MACROGLOBULINEMIA, LYMPHOPLASMACYTIC LEUKEMIA) GENE ANALYSIS, P.LEU265PRO (L265P) VARIANT
81306	NUDT15 (NUDIX HYDROLASE 15) (EG, DRUG METABOLISM) GENE ANALYSIS, COMMON VARIANT(S) (EG, *2, *3, *4, *5, *6)
81307	PALB2 (PARTNER AND LOCALIZER OF BRCA2) (EG, BREAST AND PANCREATIC CANCER) GENE ANALYSIS; FULL GENE SEQUENCE
81308	PALB2 (PARTNER AND LOCALIZER OF BRCA2) (EG, BREAST AND PANCREATIC CANCER) GENE ANALYSIS; KNOWN FAMILIAL VARIANT
81309	PIK3CA (PHOSPHATIDYLINOSITOL-4, 5-BIPHOSPHATE 3-KINASE, CATALYTIC SUBUNIT ALPHA) (EG, COLORECTAL AND BREAST CANCER) GENE ANALYSIS, TARGETED SEQUENCE ANALYSIS (EG, EXONS 7, 9, 20)
81310	NPM1 (NUCLEOPHOSMIN) (EG, ACUTE MYELOID LEUKEMIA) GENE ANALYSIS, EXON 12 VARIANTS
81311	NRAS (NEUROBLASTOMA RAS VIRAL [V-RAS] ONCOGENE HOMOLOG) (EG, COLORECTAL CARCINOMA), GENE ANALYSIS, VARIANTS IN EXON 2 (EG, CODONS 12 AND 13) AND EXON 3 (EG, CODON 61)
81312	PABPN1 (POLY[A] BINDING PROTEIN NUCLEAR 1) (EG, OCULOPHARYNGEAL MUSCULAR DYSTROPHY) GENE ANALYSIS, EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81313	PCA3/KLK3 (PROSTATE CANCER ANTIGEN 3 [NON-PROTEIN CODING]/KALLIKREIN-RELATED PEPTIDASE 3 [PROSTATE SPECIFIC ANTIGEN]) RATIO (EG, PROSTATE CANCER)
81314	PDGFRA (PLATELET-DERIVED GROWTH FACTOR RECEPTOR, ALPHA POLYPEPTIDE) (EG, GASTROINTESTINAL STROMAL TUMOR [GIST]), GENE ANALYSIS, TARGETED SEQUENCE ANALYSIS (EG, EXONS 12, 18)
81315	PML/RARALPHA, (T(15;17)), (PROMYELOCYTIC LEUKEMIA/RETINOIC ACID RECEPTOR ALPHA) (EG, PROMYELOCYTIC LEUKEMIA) TRANSLOCATION ANALYSIS; COMMON BREAKPOINTS (EG, INTRON 3 AND INTRON 6), QUALITATIVE OR QUANTITATIVE
81316	PML/RARALPHA, (T(15;17)), (PROMYELOCYTIC LEUKEMIA/RETINOIC ACID RECEPTOR ALPHA) (EG, PROMYELOCYTIC LEUKEMIA) TRANSLOCATION ANALYSIS; SINGLE BREAKPOINT (EG, INTRON 3, INTRON 6 OR EXON 6), QUALITATIVE OR QUANTITATIVE
81317	PMS2 (POSTMEIOTIC SEGREGATION INCREASED 2 [S. CEREVISIAE]) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; FULL SEQUENCE ANALYSIS
81318	PMS2 (POSTMEIOTIC SEGREGATION INCREASED 2 [S. CEREVISIAE]) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; KNOWN FAMILIAL VARIANTS
81319	PMS2 (POSTMEIOTIC SEGREGATION INCREASED 2 [S. CEREVISIAE]) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; DUPLICATION/DELETION VARIANTS
81320	PLCG2 (PHOSPHOLIPASE C GAMMA 2) (EG, CHRONIC LYMPHOCYTIC LEUKEMIA) GENE ANALYSIS, COMMON VARIANTS (EG, R665W, S707F, L845F)

81321	PTEN (PHOSPHATASE AND TENSIN HOMOLOG) (EG, COWDEN SYNDROME, PTEN HAMARTOMA TUMOR SYNDROME) GENE ANALYSIS; FULL SEQUENCE ANALYSIS
81322	PTEN (PHOSPHATASE AND TENSIN HOMOLOG) (EG, COWDEN SYNDROME, PTEN HAMARTOMA TUMOR SYNDROME) GENE ANALYSIS; KNOWN FAMILIAL VARIANT
81323	PTEN (PHOSPHATASE AND TENSIN HOMOLOG) (EG, COWDEN SYNDROME, PTEN HAMARTOMA TUMOR SYNDROME) GENE ANALYSIS; DUPLICATION/DELETION VARIANT
81324	PMP22 (PERIPHERAL MYELIN PROTEIN 22) (EG, CHARCOT-MARIE-TOOTH, HEREDITARY NEUROPATHY WITH LIABILITY TO PRESSURE PALSIES) GENE ANALYSIS; DUPLICATION/DELETION ANALYSIS
81325	PMP22 (PERIPHERAL MYELIN PROTEIN 22) (EG, CHARCOT-MARIE-TOOTH, HEREDITARY NEUROPATHY WITH LIABILITY TO PRESSURE PALSIES) GENE ANALYSIS; FULL SEQUENCE ANALYSIS
81326	PMP22 (PERIPHERAL MYELIN PROTEIN 22) (EG, CHARCOT-MARIE-TOOTH, HEREDITARY NEUROPATHY WITH LIABILITY TO PRESSURE PALSIES) GENE ANALYSIS; KNOWN FAMILIAL VARIANT
81327	SEPT9 (SEPTIN9) (EG, COLORECTAL CANCER) PROMOTER METHYLATION ANALYSIS
81328	SLCO1B1 (SOLUTE CARRIER ORGANIC ANION TRANSPORTER FAMILY, MEMBER 1B1) (EG, ADVERSE DRUG REACTION), GENE ANALYSIS, COMMON VARIANT(S) (EG, *5)
81329	SMN1 (SURVIVAL OF MOTOR NEURON 1, TELOMERIC) (EG, SPINAL MUSCULAR ATROPHY) GENE ANALYSIS; DOSAGE/DELETION ANALYSIS (EG, CARRIER TESTING), INCLUDES SMN2 (SURVIVAL OF MOTOR NEURON 2, CENTROMERIC) ANALYSIS, IF PERFORMED
81330	SMPD1(SPHINGOMYELIN PHOSPHODIESTERASE 1, ACID LYSOSOMAL) (EG, NIEMANN-PICK DISEASE, TYPE A) GENE ANALYSIS, COMMON VARIANTS (EG, R496L, L302P, FSP330)
81331	SNRPN/UBE3A (SMALL NUCLEAR RIBONUCLEOPROTEIN POLYPEPTIDE N AND UBIQUITIN PROTEIN LIGASE E3A) (EG, PRADER-WILLI SYNDROME AND/OR ANGELMAN SYNDROME), METHYLATION ANALYSIS
81332	SERPINA1 (SERPIN PEPTIDASE INHIBITOR, CLADE A, ALPHA-1 ANTIPROTEINASE, ANTITRYPSIN, MEMBER 1) (EG, ALPHA-1-ANTITRYPSIN DEFICIENCY), GENE ANALYSIS, COMMON VARIANTS (EG, *S AND *Z)
81333	TGFBI (TRANSFORMING GROWTH FACTOR BETA-INDUCED) (EG, CORNEAL DYSTROPHY) GENE ANALYSIS, COMMON VARIANTS (EG, R124H, R124C, R124L, R555W, R555Q)
81334	RUNX1 (RUNT RELATED TRANSCRIPTION FACTOR 1) (EG, ACUTE MYELOID LEUKEMIA, FAMILIAL PLATELET DISORDER WITH ASSOCIATED MYELOID MALIGNANCY) GENE ANALYSIS, TARGETED SEQUENCE ANALYSIS (EG, EXONS 3-8)
81335	TPMT (THIOPURINE S-METHYLTRANSFERASE) (EG, DRUG METABOLISM), GENE ANALYSIS, COMMON VARIANTS (EG, *2, *3)
81336	SMN1 (SURVIVAL OF MOTOR NEURON 1, TELOMERIC) (EG, SPINAL MUSCULAR ATROPHY) GENE ANALYSIS; FULL GENE SEQUENCE
81337	SMN1 (SURVIVAL OF MOTOR NEURON 1, TELOMERIC) (EG, SPINAL MUSCULAR ATROPHY) GENE ANALYSIS; KNOWN FAMILIAL SEQUENCE VARIANT(S)

81338	MPL (MPL PROTO-ONCOGENE, THROMBOPOIETIN RECEPTOR) (EG, MYELOPROLIFERATIVE DISORDER) GENE ANALYSIS; COMMON VARIANTS (EG, W515A, W515K, W515L, W515R)
81339	MPL (MPL PROTO-ONCOGENE, THROMBOPOIETIN RECEPTOR) (EG, MYELOPROLIFERATIVE DISORDER) GENE ANALYSIS; SEQUENCE ANALYSIS, EXON 10
81340	TRB@ (T CELL ANTIGEN RECEPTOR, BETA) (EG, LEUKEMIA AND LYMPHOMA), GENE REARRANGEMENT ANALYSIS TO DETECT ABNORMAL CLONAL POPULATION(S); USING AMPLIFICATION METHODOLOGY (EG, POLYMERASE CHAIN REACTION)
81341	TRB@ (T CELL ANTIGEN RECEPTOR, BETA) (EG, LEUKEMIA AND LYMPHOMA), GENE REARRANGEMENT ANALYSIS TO DETECT ABNORMAL CLONAL POPULATION(S); USING DIRECT PROBE METHODOLOGY (EG, SOUTHERN BLOT)
81342	TRG@ (T CELL ANTIGEN RECEPTOR, GAMMA) (EG, LEUKEMIA AND LYMPHOMA), GENE REARRANGEMENT ANALYSIS, EVALUATION TO DETECT ABNORMAL CLONAL POPULATION(S)
81343	PPP2R2B (PROTEIN PHOSPHATASE 2 REGULATORY SUBUNIT BBETA) (EG, SPINOCEREBELLAR ATAXIA) GENE ANALYSIS, EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81344	TBP (TATA BOX BINDING PROTEIN) (EG, SPINOCEREBELLAR ATAXIA) GENE ANALYSIS, EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81345	TERT (TELOMERASE REVERSE TRANSCRIPTASE) (EG, THYROID CARCINOMA, GLIOBLASTOMA MULTIFORME) GENE ANALYSIS, TARGETED SEQUENCE ANALYSIS (EG, PROMOTER REGION)
81346	TYMS (THYMIDYLATE SYNTHETASE) (EG, 5-FLUOROURACIL/5-FU DRUG METABOLISM), GENE ANALYSIS, COMMON VARIANT(S) (EG, TANDEM REPEAT VARIANT)
81347	SF3B1 (SPLICING FACTOR [3B] SUBUNIT B1) (EG, MYELODYSPLASTIC SYNDROME/ACUTE MYELOID LEUKEMIA) GENE ANALYSIS, COMMON VARIANTS (EG, A672T, E622D, L833F, R625C, R625L)
81348	SRSF2 (SERINE AND ARGININE-RICH SPLICING FACTOR 2) (EG, MYELODYSPLASTIC SYNDROME, ACUTE MYELOID LEUKEMIA) GENE ANALYSIS, COMMON VARIANTS (EG, P95H, P95L)
81349	CYTOGENOMIC (GENOME-WIDE) ANALYSIS FOR CONSTITUTIONAL CHROMOSOMAL ABNORMALITIES; INTERROGATION OF GENOMIC REGIONS FOR COPY NUMBER AND LOSS-OF-HETEROZYGOSITY VARIANTS, LOW-PASS SEQUENCING ANALYSIS
81350	UGT1A1 (UDP GLUCURONOSYLTRANSFERASE 1 FAMILY, POLYPEPTIDE A1) (EG, DRUG METABOLISM, HEREDITARY UNCONJUGATED HYPERBILIRUBINEMIA [GILBERT SYNDROME]) GENE ANALYSIS, COMMON VARIANTS (EG, *28, *36, *37)
81351	TP53 (TUMOR PROTEIN 53) (EG, LI-FRAUMENI SYNDROME) GENE ANALYSIS; FULL GENE SEQUENCE
81352	TP53 (TUMOR PROTEIN 53) (EG, LI-FRAUMENI SYNDROME) GENE ANALYSIS; TARGETED SEQUENCE ANALYSIS (EG, 4 ONCOLOGY)
81353	TP53 (TUMOR PROTEIN 53) (EG, LI-FRAUMENI SYNDROME) GENE ANALYSIS; KNOWN FAMILIAL VARIANT
81355	VKORC1 (VITAMIN K EPOXIDE REDUCTASE COMPLEX, SUBUNIT 1) (EG, WARFARIN METABOLISM), GENE ANALYSIS, COMMON VARIANT(S) (EG, -1639G>A, C.173+1000C>T)

81357	U2AF1 (U2 SMALL NUCLEAR RNA AUXILIARY FACTOR 1) (EG, MYELODYSPLASTIC SYNDROME, ACUTE MYELOID LEUKEMIA) GENE ANALYSIS, COMMON VARIANTS (EG, S34F, S34Y, Q157R, Q157P)
81360	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)
81361	HBB (HEMOGLOBIN, SUBUNIT BETA) (EG, SICKLE CELL ANEMIA, BETA THALASSEMIA, HEMOGLOBINOPATHY); COMMON VARIANT(S) (EG, HBS, HBC, HBE)
81362	HBB (HEMOGLOBIN, SUBUNIT BETA) (EG, SICKLE CELL ANEMIA, BETA THALASSEMIA, HEMOGLOBINOPATHY); KNOWN FAMILIAL VARIANT(S)
81363	HBB (HEMOGLOBIN, SUBUNIT BETA) (EG, SICKLE CELL ANEMIA, BETA THALASSEMIA, HEMOGLOBINOPATHY); DUPLICATION/DELETION VARIANT(S)
81364	HBB (HEMOGLOBIN, SUBUNIT BETA) (EG, SICKLE CELL ANEMIA, BETA THALASSEMIA, HEMOGLOBINOPATHY); FULL GENE SEQUENCE
81370	HLA CLASS I AND II TYPING, LOW RESOLUTION (EG, ANTIGEN EQUIVALENTS); HLA-A, -B, -C, -DRB1/3/4/5, AND -DQB1
81371	HLA CLASS I AND II TYPING, LOW RESOLUTION (EG, ANTIGEN EQUIVALENTS); HLA-A, -B, AND -DRB1 (EG, VERIFICATION TYPING)
81372	HLA CLASS I TYPING, LOW RESOLUTION (EG, ANTIGEN EQUIVALENTS); COMPLETE (IE, HLA-A, -B, AND -C)
81373	HLA CLASS I TYPING, LOW RESOLUTION (EG, ANTIGEN EQUIVALENTS); ONE LOCUS (EG, HLA-A, -B, OR -C), EACH
81374	HLA CLASS I TYPING, LOW RESOLUTION (EG, ANTIGEN EQUIVALENTS); ONE ANTIGEN EQUIVALENT (EG, B*27), EACH
81375	HLA CLASS II TYPING, LOW RESOLUTION (EG, ANTIGEN EQUIVALENTS); HLA-DRB1/3/4/5 AND -DQB1
81376	HLA CLASS II TYPING, LOW RESOLUTION (EG, ANTIGEN EQUIVALENTS); ONE LOCUS (EG, HLA-DRB1, -DRB3/4/5, -DQB1, -DQA1, -DPB1, OR -DPA1), EACH
81377	HLA CLASS II TYPING, LOW RESOLUTION (EG, ANTIGEN EQUIVALENTS); ONE ANTIGEN EQUIVALENT, EACH
81378	HLA CLASS I AND II TYPING, HIGH RESOLUTION (IE, ALLELES OR ALLELE GROUPS), HLA-A, -B, -C, AND -DRB1
81379	HLA CLASS I TYPING, HIGH RESOLUTION (IE, ALLELES OR ALLELE GROUPS); COMPLETE (IE, HLA-A, -B, AND -C)
81380	HLA CLASS I TYPING, HIGH RESOLUTION (IE, ALLELES OR ALLELE GROUPS); ONE LOCUS (EG, HLA-A, -B, OR -C), EACH
81381	HLA CLASS I TYPING, HIGH RESOLUTION (IE, ALLELES OR ALLELE GROUPS); ONE ALLELE OR ALLELE GROUP (EG, B*57:01P), EACH
81382	HLA CLASS II TYPING, HIGH RESOLUTION (IE, ALLELES OR ALLELE GROUPS); ONE LOCUS (EG, HLA-DRB1, -DRB3/4/5, -DQB1, -DQA1, -DPB1, OR -DPA1), EACH
81383	HLA CLASS II TYPING, HIGH RESOLUTION (IE, ALLELES OR ALLELE GROUPS); ONE ALLELE OR ALLELE GROUP (EG, HLA-DQB1*06:02P), EACH
81400	MOLECULAR PATHOLOGY PROCEDURE, LEVEL 1 (EG, IDENTIFICATION OF SINGLE GERMLINE VARIANT [EG, SNP] BY

	TECHNIQUES SUCH AS RESTRICTION ENZYME DIGESTION OR MELT CURVE ANALYSIS)
81401	MOLECULAR PATHOLOGY PROCEDURE, LEVEL 2 (EG, 2-10 SNPS, 1 METHYLATED VARIANT, OR 1 SOMATIC VARIANT [TYPICALLY USING NONSEQUENCING TARGET VARIANT ANALYSIS], OR DETECTION OF A DYNAMIC MUTATION DISORDER/TRIPLET REPEAT)
81402	MOLECULAR PATHOLOGY PROCEDURE, LEVEL 3 (EG, >10 SNPS, 2-10 METHYLATED VARIANTS, OR 2-10 SOMATIC VARIANTS [TYPICALLY USING NON-SEQUENCING TARGET VARIANT ANALYSIS], IMMUNOGLOBULIN AND T-CELL RECEPTOR GENE REARRANGEMENTS, DUPLICATION/DELETION VARIANTS OF 1 EXON, LOSS OF HETEROZYGOSITY [LOH], UNIPARENTAL DISOMY [UPD])
81403	MOLECULAR PATHOLOGY PROCEDURE, LEVEL 4 (EG, ANALYSIS OF SINGLE EXON BY DNA SEQUENCE ANALYSIS, ANALYSIS OF >10 AMPLICONS USING MULTIPLEX PCR IN 2 OR MORE INDEPENDENT REACTIONS, MUTATION SCANNING OR DUPLICATION/DELETION VARIANTS OF 2-5 EXONS)
81404	MOLECULAR PATHOLOGY PROCEDURE, LEVEL 5 (EG, ANALYSIS OF 2-5 EXONS BY DNA SEQUENCE ANALYSIS, MUTATION SCANNING OR DUPLICATION/DELETION VARIANTS OF 6-10 EXONS, OR CHARACTERIZATION OF A DYNAMIC MUTATION DISORDER/TRIPLET REPEAT BY SOUTHERN BLOT ANALYSIS) UGT1A1 (UDP GLUCURONOSYLTRANSFERASE 1 FAMILY, POLYPEPTIDE A1) (EG, HEREDITARY UNCONJUGATED HYPERBILIRUBINEMIA [CRIGLER-NAJJAR SYNDROME]) FULL GENE SEQUENCE
81405	MOLECULAR PATHOLOGY PROCEDURE, LEVEL 6 (EG, ANALYSIS OF 6-10 EXONS BY DNA SEQUENCE ANALYSIS, MUTATION SCANNING OR DUPLICATION/DELETION VARIANTS OF 11-25 EXONS, REGIONALLY TARGETED CYTOGENOMIC ARRAY ANALYSIS)
81406	MOLECULAR PATHOLOGY PROCEDURE, LEVEL 7 (EG, ANALYSIS OF 11-25 EXONS BY DNA SEQUENCE ANALYSIS, MUTATION SCANNING OR DUPLICATION/DELETION VARIANTS OF 26-50 EXONS, CYTOGENOMIC ARRAY ANALYSIS FOR NEOPLASIA)
81407	MOLECULAR PATHOLOGY PROCEDURE, LEVEL 8 (EG, ANALYSIS OF 26-50 EXONS BY DNA SEQUENCE ANALYSIS, MUTATION SCANNING OR DUPLICATION/DELETION VARIANTS OF >50 EXONS, SEQUENCE ANALYSIS OF MULTIPLE GENES ON ONE PLATFORM) APOB (APOLIPOPROTEIN B) (EG, FAMILIAL HYPERCHOLESTEROLEMIA TYPE B) FULL GENE SEQUENCE
81408	MOLECULAR PATHOLOGY PROCEDURE, LEVEL 9 (EG, ANALYSIS OF >50 EXONS IN A SINGLE GENE BY DNA SEQUENCE ANALYSIS)
81410	AORTIC DYSFUNCTION OR DILATION (EG, MARFAN SYNDROME, LOEYS DIETZ SYNDROME, EHLER DANLOS SYNDROME TYPE IV, ARTERIAL TORTUOSITY SYNDROME); GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 9 GENES, INCLUDING FBN1, TGFBR1, TGFBR2, COL3A1, MYH11, ACTA2, SLC2A10, SMAD3, AND MYLK
81411	AORTIC DYSFUNCTION OR DILATION (EG, MARFAN SYNDROME, LOEYS DIETZ SYNDROME, EHLER DANLOS SYNDROME TYPE IV, ARTERIAL TORTUOSITY SYNDROME); DUPLICATION/DELETION ANALYSIS PANEL, MUST INCLUDE ANALYSES FOR TGFBR1, TGFBR2, MYH11, AND COL3A1
81412	ASHKENAZI JEWISH ASSOCIATED DISORDERS (EG, BLOOM SYNDROME, CANAVAN DISEASE, CYSTIC FIBROSIS, FAMILIAL

	DYSAUTONOMIA, FANCONI ANEMIA GROUP C, GAUCHER DISEASE, TAY-SACHS DISEASE), GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 9 GENES, INCLUDING ASPA, BLM, CFTR, FANCC, GBA, HEXA, IKBKAP, MCOLN1, AND SMPD1
81413	CARDIAC ION CHANNELOPATHIES (EG, BRUGADA SYNDROME, LONG QT SYNDROME, SHORT QT SYNDROME, CATECHOLAMINERGIC POLYMORPHIC VENTRICULAR TACHYCARDIA); GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 10 GENES, INCLUDING ANK2, CASQ2, CAV3, KCNE1, KCNE2, KCNH2, KCNJ2, KCNQ1, RYR2, AND SCN5A
81414	CARDIAC ION CHANNELOPATHIES (EG, BRUGADA SYNDROME, LONG QT SYNDROME, SHORT QT SYNDROME, CATECHOLAMINERGIC POLYMORPHIC VENTRICULAR TACHYCARDIA); DUPLICATION/DELETION GENE ANALYSIS PANEL, MUST INCLUDE ANALYSIS OF AT LEAST 2 GENES, INCLUDING KCNH2 AND KCNQ1
81415	EXOME (EG, UNEXPLAINED CONSTITUTIONAL OR HERITABLE DISORDER OR SYNDROME); SEQUENCE ANALYSIS
81416	EXOME (EG, UNEXPLAINED CONSTITUTIONAL OR HERITABLE DISORDER OR SYNDROME); SEQUENCE ANALYSIS, EACH COMPARATOR EXOME (EG, PARENTS, SIBLINGS) (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
81417	EXOME (EG, UNEXPLAINED CONSTITUTIONAL OR HERITABLE DISORDER OR SYNDROME); RE-EVALUATION OF PREVIOUSLY OBTAINED EXOME SEQUENCE (EG, UPDATED KNOWLEDGE OR UNRELATED CONDITION/SYNDROME)
81419	EPILEPSY GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE ANALYSES FOR ALDH7A1, CACNA1A, CDKL5, CHD2, GABRG2, GRIN2A, KCNQ2, MECP2, PCDH19, POLG, PRRT2, SCN1A, SCN1B, SCN2A, SCN8A, SLC2A1, SLC9A6, STXBP1, SYNGAP1, TCF4, TPP1, TSC1, TSC2, AND ZEB2
81420	FETAL CHROMOSOMAL ANEUPLOIDY (EG, TRISOMY 21, MONOSOMY X) GENOMIC SEQUENCE ANALYSIS PANEL, CIRCULATING CELL-FREE FETAL DNA IN MATERNAL BLOOD, MUST INCLUDE ANALYSIS OF CHROMOSOMES 13, 18, AND 21
81422	FETAL CHROMOSOMAL MICRODELETION(S) GENOMIC SEQUENCE ANALYSIS (EG, DIGEORGE SYNDROME, CRI-DU-CHAT SYNDROME), CIRCULATING CELL-FREE FETAL DNA IN MATERNAL BLOOD
81425	GENOME (EG, UNEXPLAINED CONSTITUTIONAL OR HERITABLE DISORDER OR SYNDROME); SEQUENCE ANALYSIS
81426	GENOME (EG, UNEXPLAINED CONSTITUTIONAL OR HERITABLE DISORDER OR SYNDROME); SEQUENCE ANALYSIS, EACH COMPARATOR GENOME (EG, PARENTS, SIBLINGS) (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
81427	GENOME (EG, UNEXPLAINED CONSTITUTIONAL OR HERITABLE DISORDER OR SYNDROME); RE-EVALUATION OF PREVIOUSLY OBTAINED GENOME SEQUENCE (EG, UPDATED KNOWLEDGE OR UNRELATED CONDITION/SYNDROME)
81430	HEARING LOSS (EG, NONSYNDROMIC HEARING LOSS, USHER SYNDROME, PENDRED SYNDROME); GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 60 GENES, INCLUDING CDH23, CLRN1, GJB2, GPR98, MTRNR1, MYO7A, MYO15A,

	PCDH15, OTOF, SLC26A4, TMC1, TMPRSS3, USH1C, USH1G, USH2A, AND WFS1
81431	HEARING LOSS (EG, NONSYNDROMIC HEARING LOSS, USHER SYNDROME, PENDRED SYNDROME); DUPLICATION/DELETION ANALYSIS PANEL, MUST INCLUDE COPY NUMBER ANALYSES FOR STRC AND DFNB1 DELETIONS IN GJB2 AND GJB6 GENES
81432	HEREDITARY BREAST CANCER-RELATED DISORDERS (EG, HEREDITARY BREAST CANCER, HEREDITARY OVARIAN CANCER, HEREDITARY ENDOMETRIAL CANCER); GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 10 GENES, ALWAYS INCLUDING BRCA1, BRCA2, CDH1, MLH1, MSH2, MSH6, PALB2, PTEN, STK11, AND TP53
81433	HEREDITARY BREAST CANCER-RELATED DISORDERS (EG, HEREDITARY BREAST CANCER, HEREDITARY OVARIAN CANCER, HEREDITARY ENDOMETRIAL CANCER); DUPLICATION/DELETION ANALYSIS PANEL, MUST INCLUDE ANALYSES FOR BRCA1, BRCA2, MLH1, MSH2, AND STK11
81434	HEREDITARY RETINAL DISORDERS (EG, RETINITIS PIGMENTOSA, LEBER CONGENITAL AMAUROSIS, CONE-ROD DYSTROPHY), GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 15 GENES, INCLUDING ABCA4, CNGA1, CRB1, EYS, PDE6A, PDE6B, PRPF31, PRPH2, RDH12, RHO, RP1, RP2, RPE65, RPGR, AND USH2A
81435	HEREDITARY COLON CANCER DISORDERS (EG, LYNCH SYNDROME, PTEN HAMARTOMA SYNDROME, COWDEN SYNDROME, FAMILIAL ADENOMATOSIS POLYPOSIS); GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 10 GENES, INCLUDING APC, BMPR1A, CDH1, MLH1, MSH2, MSH6, MUTYH, PTEN, SMAD4, AND STK11
81436	HEREDITARY COLON CANCER DISORDERS (EG, LYNCH SYNDROME, PTEN HAMARTOMA SYNDROME, COWDEN SYNDROME, FAMILIAL ADENOMATOSIS POLYPOSIS); DUPLICATION/DELETION ANALYSIS PANEL, MUST INCLUDE ANALYSIS OF AT LEAST 5 GENES, INCLUDING MLH1, MSH2, EPCAM, SMAD4, AND STK11
81437	HEREDITARY NEUROENDOCRINE TUMOR DISORDERS (EG, MEDULLARY THYROID CARCINOMA, PARATHYROID CARCINOMA, MALIGNANT PHEOCHROMOCYTOMA OR PARAGANGLIOMA); GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 6 GENES, INCLUDING MAX, SDHB, SDHC, SDHD, TMEM127, AND VHL
81438	HEREDITARY NEUROENDOCRINE TUMOR DISORDERS (EG, MEDULLARY THYROID CARCINOMA, PARATHYROID CARCINOMA, MALIGNANT PHEOCHROMOCYTOMA OR PARAGANGLIOMA); DUPLICATION/DELETION ANALYSIS PANEL, MUST INCLUDE ANALYSES FOR SDHB, SDHC, SDHD, AND VHL
81439	HEREDITARY CARDIOMYOPATHY (EG, HYPERTROPHIC CARDIOMYOPATHY, DILATED CARDIOMYOPATHY, ARRHYTHMOGENIC RIGHT VENTRICULAR CARDIOMYOPATHY), GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 5 CARDIOMYOPATHY-RELATED GENES (EG, DSG2, MYBPC3, MYH7, PKP2, TTN)
81440	NUCLEAR ENCODED MITOCHONDRIAL GENES (EG, NEUROLOGIC OR MYOPATHIC PHENOTYPES), GENOMIC SEQUENCE PANEL, MUST INCLUDE ANALYSIS OF AT LEAST 100 GENES, INCLUDING BCS1L,

	C10ORF2, COQ2, COX10, DGUOK, MPV17, OPA1, PDSS2, POLG, POLG2, RRM2B, SCO1, SCO2, SLC25A4, SUCLA2, SUCLG1, TAZ, TK2, AND TYMP
81442	NOONAN SPECTRUM DISORDERS (EG, NOONAN SYNDROME, CARDIO-FACIO-CUTANEOUS SYNDROME, COSTELLO SYNDROME, LEOPARD SYNDROME, NOONAN-LIKE SYNDROME), GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 12 GENES, INCLUDING BRAF, CBL, HRAS, KRAS, MAP2K1, MAP2K2, NRAS, PTPN11, RAF1, RIT1, SHOC2, AND SOS1
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)
81445	TARGETED GENOMIC SEQUENCE ANALYSIS PANEL, SOLID ORGAN NEOPLASM, DNA ANALYSIS, AND RNA ANALYSIS WHEN PERFORMED, 5-50 GENES (EG, ALK, BRAF, CDKN2A, EGFR, ERBB2, KIT, KRAS, NRAS, MET, PDGFRA, PDGFRB, PGR, PIK3CA, PTEN, RET), INTERROGATION FOR SEQUENCE VARIANTS AND COPY NUMBER VARIANTS OR REARRANGEMENTS, IF PERFORMED
81448	HEREDITARY PERIPHERAL NEUROPATHIES (EG, CHARCOT-MARIE-TOOTH, SPASTIC PARAPLEGIA), GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 5 PERIPHERAL NEUROPATHY-RELATED GENES (EG, BSCL2, GJB1, MFN2, MPZ, REEP1, SPAST, SPG11, SPTLC1)
81450	TARGETED GENOMIC SEQUENCE ANALYSIS PANEL, HEMATOLYMPHOID NEOPLASM OR DISORDER, DNA ANALYSIS, AND RNA ANALYSIS WHEN PERFORMED, 5-50 GENES (EG, BRAF, CEBPA, DNMT3A, EZH2, FLT3, IDH1, IDH2, JAK2, KRAS, KIT, MLL, NRAS, NPM1, NOTCH1), INTERROGATION FOR SEQUENCE VARIANTS, AND COPY NUMBER VARIANTS OR REARRANGEMENTS, OR ISOFORM EXPRESSION OR MRNA EXPRESSION LEVELS, IF PERFORMED
81455	TARGETED GENOMIC SEQUENCE ANALYSIS PANEL, SOLID ORGAN OR HEMATOLYMPHOID NEOPLASM, DNA ANALYSIS, AND RNA ANALYSIS WHEN PERFORMED, 51 OR GREATER GENES (EG, ALK, BRAF, CDKN2A, CEBPA, DNMT3A, EGFR, ERBB2, EZH2, FLT3, IDH1, IDH2, JAK2, KIT, KRAS, MLL, NPM1, NRAS, MET, NOTCH1, PDGFRA, PDGFRB, PGR, PIK3CA, PTEN, RET), INTERROGATION FOR SEQUENCE VARIANTS AND COPY NUMBER VARIANTS OR REARRANGEMENTS, IF PERFORMED
81460	WHOLE MITOCHONDRIAL GENOME (EG, LEIGH SYNDROME, MITOCHONDRIAL ENCEPHALOMYOPATHY, LACTIC ACIDOSIS, AND STROKE-LIKE EPISODES [MELAS], MYOCLONIC EPILEPSY WITH RAGGED-RED FIBERS [MERFF], NEUROPATHY, ATAXIA, AND RETINITIS PIGMENTOSA [NARP], LEBER HEREDITARY OPTIC NEUROPATHY [LHON]), GENOMIC SEQUENCE, MUST INCLUDE SEQUENCE ANALYSIS OF ENTIRE MITOCHONDRIAL GENOME WITH HETEROPLASMY DETECTION
81465	WHOLE MITOCHONDRIAL GENOME LARGE DELETION ANALYSIS PANEL (EG, KEARNS-SAYRE SYNDROME, CHRONIC PROGRESSIVE

	EXTERNAL OPHTHALMOPLEGIA), INCLUDING HETEROPLASMY DETECTION, IF PERFORMED
81470	X-LINKED INTELLECTUAL DISABILITY (XLID) (EG, SYNDROMIC AND NON-SYNDROMIC XLID); GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 60 GENES, INCLUDING ARX, ATRX, CDKL5, FGD1, FMR1, HUWE1, IL1RAPL, KDM5C, L1CAM, MECP2, MED12, MID1, OCRL, RPS6KA3, AND SLC16A2
81471	X-LINKED INTELLECTUAL DISABILITY (XLID) (EG, SYNDROMIC AND NON-SYNDROMIC XLID); DUPLICATION/DELETION GENE ANALYSIS, MUST INCLUDE ANALYSIS OF AT LEAST 60 GENES, INCLUDING ARX, ATRX, CDKL5, FGD1, FMR1, HUWE1, IL1RAPL, KDM5C, L1CAM, MECP2, MED12, MID1, OCRL, RPS6KA3, AND SLC16A2
81479	UNLISTED MOLECULAR PATHOLOGY PROCEDURE
81490	AUTOIMMUNE (RHEUMATOID ARTHRITIS), ANALYSIS OF 12 BIOMARKERS USING IMMUNOASSAYS, UTILIZING SERUM, PROGNOSTIC ALGORITHM REPORTED AS A DISEASE ACTIVITY SCORE
81493	CORONARY ARTERY DISEASE, MRNA, GENE EXPRESSION PROFILING BY REAL-TIME RT-PCR OF 23 GENES, UTILIZING WHOLE PERIPHERAL BLOOD, ALGORITHM REPORTED AS A RISK SCORE
81500	ONCOLOGY (OVARIAN), BIOCHEMICAL ASSAYS OF TWO PROTEINS (CA-125 AND HE4), UTILIZING SERUM, WITH MENOPAUSAL STATUS, ALGORITHM REPORTED AS A RISK SCORE
81503	ONCOLOGY (OVARIAN), BIOCHEMICAL ASSAYS OF FIVE PROTEINS (CA-125, APOLIPOPROTEIN A1, BETA-2 MICROGLOBULIN, TRANSFERRIN, AND PRE-ALBUMIN), UTILIZING SERUM, ALGORITHM REPORTED AS A RISK SCORE
81504	ONCOLOGY (TISSUE OF ORIGIN), MICROARRAY GENE EXPRESSION PROFILING OF > 2000 GENES, UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED TISSUE, ALGORITHM REPORTED AS TISSUE SIMILARITY SCORES
81506	ENDOCRINOLOGY (TYPE 2 DIABETES), BIOCHEMICAL ASSAYS OF SEVEN ANALYTES (GLUCOSE, HBA1C, INSULIN, HS-CRP, ADIPONECTIN, FERRITIN, INTERLEUKIN 2-RECEPTOR ALPHA), UTILIZING SERUM OR PLASMA, ALGORITHM REPORTING A RISK SCORE
81507	FETAL ANEUPLOIDY (TRISOMY 21, 18, AND 13) DNA SEQUENCE ANALYSIS OF SELECTED REGIONS USING MATERNAL PLASMA, ALGORITHM REPORTED AS A RISK SCORE FOR EACH TRISOMY
81508	FETAL CONGENITAL ABNORMALITIES, BIOCHEMICAL ASSAYS OF TWO PROTEINS (PAPP-A, HCG [ANY FORM]), UTILIZING MATERNAL SERUM, ALGORITHM REPORTED AS A RISK SCORE
81509	FETAL CONGENITAL ABNORMALITIES, BIOCHEMICAL ASSAYS OF THREE PROTEINS (PAPP-A, HCG [ANY FORM], DIA), UTILIZING MATERNAL SERUM, ALGORITHM REPORTED AS A RISK SCORE
81510	FETAL CONGENITAL ABNORMALITIES, BIOCHEMICAL ASSAYS OF THREE ANALYTES (AFP, UE3, HCG [ANY FORM]), UTILIZING MATERNAL SERUM, ALGORITHM REPORTED AS A RISK SCORE
81511	FETAL CONGENITAL ABNORMALITIES, BIOCHEMICAL ASSAYS OF FOUR ANALYTES (AFP, UE3, HCG [ANY FORM], DIA) UTILIZING MATERNAL SERUM, ALGORITHM REPORTED AS A RISK SCORE (MAY INCLUDE ADDITIONAL RESULTS FROM PREVIOUS BIOCHEMICAL TESTING)

81512	FETAL CONGENITAL ABNORMALITIES, BIOCHEMICAL ASSAYS OF FIVE ANALYTES (AFP, UE3, TOTAL HCG, HYPERGLYCOSYLATED HCG, DIA) UTILIZING MATERNAL SERUM, ALGORITHM REPORTED AS A RISK SCORE
81513	INFECTIOUS DISEASE, BACTERIAL VAGINOSIS, QUANTITATIVE REAL-TIME AMPLIFICATION OF RNA MARKERS FOR ATOPOBIUM VAGINAE, GARDNERELLA VAGINALIS, AND LACTOBACILLUS SPECIES, UTILIZING VAGINAL-FLUID SPECIMENS, ALGORITHM REPORTED AS A POSITIVE OR NEGATIVE RESULT FOR BACTERIAL VAGINOSIS
81514	INFECTIOUS DISEASE, BACTERIAL VAGINOSIS AND VAGINITIS, QUANTITATIVE REAL-TIME AMPLIFICATION OF DNA MARKERS FOR GARDNERELLA VAGINALIS, ATOPOBIUM VAGINAE, MEGASPHAERA TYPE 1, BACTERIAL VAGINOSIS ASSOCIATED BACTERIA-2 (BVAB-2), AND LACTOBACILLUS SPECIES (L. CRISPATUS AND L. JENSENII), UTILIZING VAGINAL-FLUID SPECIMENS, ALGORITHM REPORTED AS A POSITIVE OR NEGATIVE FOR HIGH LIKELIHOOD OF BACTERIAL VAGINOSIS, INCLUDES SEPARATE DETECTION OF TRICHOMONAS VAGINALIS AND/OR CANDIDA SPECIES (C. ALBICANS, C. TROPICALIS, C. PARAPSILOSIS, C. DUBLINIENSIS), CANDIDA GLABRATA, CANDIDA KRUSEI, WHEN REPORTED
81518	ONCOLOGY (BREAST), MRNA, GENE EXPRESSION PROFILING BY REAL-TIME RT-PCR OF 11 GENES (7 CONTENT AND 4 HOUSEKEEPING), UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED TISSUE, ALGORITHMS REPORTED AS PERCENTAGE RISK FOR METASTATIC RECURRENCE AND LIKELIHOOD OF BENEFIT FROM EXTENDED ENDOCRINE THERAPY
81519	ONCOLOGY (BREAST), MRNA, GENE EXPRESSION PROFILING BY REAL-TIME RT-PCR OF 21 GENES, UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED TISSUE, ALGORITHM REPORTED AS RECURRENCE SCORE
81520	ONCOLOGY (BREAST), MRNA GENE EXPRESSION PROFILING BY HYBRID CAPTURE OF 58 GENES (50 CONTENT AND 8 HOUSEKEEPING), UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED TISSUE, ALGORITHM REPORTED AS A RECURRENCE RISK SCORE
81521	ONCOLOGY (BREAST), MRNA, MICROARRAY GENE EXPRESSION PROFILING OF 70 CONTENT GENES AND 465 HOUSEKEEPING GENES, UTILIZING FRESH FROZEN OR FORMALIN-FIXED PARAFFIN-EMBEDDED TISSUE, ALGORITHM REPORTED AS INDEX RELATED TO RISK OF DISTANT METASTASIS
81522	ONCOLOGY (BREAST), MRNA, GENE EXPRESSION PROFILING BY RT-PCR OF 12 GENES (8 CONTENT AND 4 HOUSEKEEPING), UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED TISSUE, ALGORITHM REPORTED AS RECURRENCE RISK SCORE
81523	ONCOLOGY (BREAST), MRNA, NEXT-GENERATION SEQUENCING GENE EXPRESSION PROFILING OF 70 CONTENT GENES AND 31 HOUSEKEEPING GENES, UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED TISSUE, ALGORITHM REPORTED AS INDEX RELATED TO RISK TO DISTANT METASTASIS
81525	ONCOLOGY (COLON), MRNA, GENE EXPRESSION PROFILING BY REAL-TIME RT-PCR OF 12 GENES (7 CONTENT AND 5 HOUSEKEEPING), UTILIZING FORMALIN-FIXED PARAFFIN-

	EMBEDDED TISSUE, ALGORITHM REPORTED AS A RECURRENCE SCORE
81528	ONCOLOGY (COLORECTAL) SCREENING, QUANTITATIVE REAL-TIME TARGET AND SIGNAL AMPLIFICATION OF 10 DNA MARKERS (KRAS MUTATIONS, PROMOTER METHYLATION OF NDRG4 AND BMP3) AND FECAL HEMOGLOBIN, UTILIZING STOOL, ALGORITHM REPORTED AS A POSITIVE OR NEGATIVE RESULT
81529	ONCOLOGY (CUTANEOUS MELANOMA), MRNA, GENE EXPRESSION PROFILING BY REAL-TIME RT-PCR OF 31 GENES (28 CONTENT AND 3 HOUSEKEEPING), UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED TISSUE, ALGORITHM REPORTED AS RECURRENCE RISK, INCLUDING LIKELIHOOD OF SENTINEL LYMPH NODE METASTASIS
81535	ONCOLOGY (GYNECOLOGIC), LIVE TUMOR CELL CULTURE AND CHEMOTHERAPEUTIC RESPONSE BY DAPI STAIN AND MORPHOLOGY, PREDICTIVE ALGORITHM REPORTED AS A DRUG RESPONSE SCORE; FIRST SINGLE DRUG OR DRUG COMBINATION
81536	ONCOLOGY (GYNECOLOGIC), LIVE TUMOR CELL CULTURE AND CHEMOTHERAPEUTIC RESPONSE BY DAPI STAIN AND MORPHOLOGY, PREDICTIVE ALGORITHM REPORTED AS A DRUG RESPONSE SCORE; EACH ADDITIONAL SINGLE DRUG OR DRUG COMBINATION (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
81538	ONCOLOGY (LUNG), MASS SPECTROMETRIC 8-PROTEIN SIGNATURE, INCLUDING AMYLOID A, UTILIZING SERUM, PROGNOSTIC AND PREDICTIVE ALGORITHM REPORTED AS GOOD VERSUS POOR OVERALL SURVIVAL
81539	ONCOLOGY (HIGH-GRADE PROSTATE CANCER), BIOCHEMICAL ASSAY OF FOUR PROTEINS (TOTAL PSA, FREE PSA, INTACT PSA, AND HUMAN KALLIKREIN-2 [HK2]), UTILIZING PLASMA OR SERUM, PROGNOSTIC ALGORITHM REPORTED AS A PROBABILITY SCORE
81540	ONCOLOGY (TUMOR OF UNKNOWN ORIGIN), MRNA, GENE EXPRESSION PROFILING BY REAL-TIME RT-PCR OF 92 GENES (87 CONTENT AND 5 HOUSEKEEPING) TO CLASSIFY TUMOR INTO MAIN CANCER TYPE AND SUBTYPE, UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED TISSUE, ALGORITHM REPORTED AS A PROBABILITY OF A PREDICTED MAIN CANCER TYPE AND SUBTYPE
81541	ONCOLOGY (PROSTATE), MRNA GENE EXPRESSION PROFILING BY REAL-TIME RT-PCR OF 46 GENES (31 CONTENT AND 15 HOUSEKEEPING), UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED TISSUE, ALGORITHM REPORTED AS A DISEASE-SPECIFIC MORTALITY RISK SCORE
81542	ONCOLOGY (PROSTATE), MRNA, MICROARRAY GENE EXPRESSION PROFILING OF 22 CONTENT GENES, UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED TISSUE, ALGORITHM REPORTED AS METASTASIS RISK SCORE
81546	ONCOLOGY (THYROID), MRNA, GENE EXPRESSION ANALYSIS OF 10,196 GENES, UTILIZING FINE NEEDLE ASPIRATE, ALGORITHM REPORTED AS A CATEGORICAL RESULT (EG, BENIGN OR SUSPICIOUS)
81551	ONCOLOGY (PROSTATE), PROMOTER METHYLATION PROFILING BY REAL-TIME PCR OF 3 GENES (GSTP1, APC, RASSF1), UTILIZING FORMALIN-FIXED PARAFFIN-EMBEDDED TISSUE, ALGORITHM REPORTED AS A LIKELIHOOD OF PROSTATE CANCER DETECTION ON REPEAT BIOPSY

81552	ONCOLOGY (UVEAL MELANOMA), MRNA, GENE EXPRESSION PROFILING BY REAL-TIME RT-PCR OF 15 GENES (12 CONTENT AND 3 HOUSEKEEPING), UTILIZING FINE NEEDLE ASPIRATE OR FORMALIN-FIXED PARAFFIN-EMBEDDED TISSUE, ALGORITHM REPORTED AS RISK OF METASTASIS
81554	PULMONARY DISEASE (IDIOPATHIC PULMONARY FIBROSIS [IPF]), MRNA, GENE EXPRESSION ANALYSIS OF 190 GENES, UTILIZING TRANSBRONCHIAL BIOPSIES, DIAGNOSTIC ALGORITHM REPORTED AS CATEGORICAL RESULT (EG, POSITIVE OR NEGATIVE FOR HIGH PROBABILITY OF USUAL INTERSTITIAL PNEUMONIA [UIP])
81595	CARDIOLOGY (HEART TRANSPLANT), MRNA, GENE EXPRESSION PROFILING BY REAL-TIME QUANTITATIVE PCR OF 20 GENES (11 CONTENT AND 9 HOUSEKEEPING), UTILIZING SUBFRACTION OF PERIPHERAL BLOOD, ALGORITHM REPORTED AS A REJECTION RISK SCORE
81596	INFECTIOUS DISEASE, CHRONIC HEPATITIS C VIRUS (HCV) INFECTION, SIX BIOCHEMICAL ASSAYS (ALT, A2-MACROGLOBULIN, APOLIPOPROTEIN A-1, TOTAL BILIRUBIN, GGT, AND HAPTOGLOBIN) UTILIZING SERUM, PROGNOSTIC ALGORITHM REPORTED AS SCORES FOR FIBROSIS AND NECROINFLAMMATORY ACTIVITY IN LIVER
81599	UNLISTED MULTIANALYTE ASSAY WITH ALGORITHMIC ANALYSIS
G0452	MOLECULAR PATHOLOGY PROCEDURE; PHYSICIAN INTERPRETATION AND REPORT

ICD-10 Codes That Are Covered

It is the provider's responsibility to select codes carried out to the highest level of specificity and selected from the ICD-10-CM code book appropriate to the year in which the service is rendered for the claim(s) submitted.

Revision History Information

Revision History Date	Revision History Number	Revision History Explanation
10/01/2022	R6	Article revised and published on 10/06/2022 effective for dates of service on and after 10/01/2022 to reflect the October Quarterly HCPCS/CPT Code updates. The following CPT codes have been added to the Article: 0332U, 0333U, 0335U, 0336U, 0340U, and 0341U to 'Group 1 codes". The following CPT codes have been deleted and therefore have been removed from the article: 0012U, 0013U, 0014U, and 0056U from the 'Group 1 Codes'. The following CPT codes have had either a long descriptor or short descriptor change. Depending on which descriptor was changed there may not be any change in how the code displays: 0229U, 0262U, 0276U, 0296U.
07/01/2022	R5	Article revised and published on 08/04/2022 effective for dates of service on and after 07/01/2022 to reflect the July quarterly CPT/HCPCS code updates. The following CPT codes had short description changes. Depending on which

		description is used in this article, there may not be any change in how the code displays in the document: 0016M and 0229U.
04/01/2022	R4	Article revised and published on 05/05/2022 effective for dates of service on and after 04/01/2022 to reflect the April Quarterly CPT/HCPCS Update. The following CPT codes have been added to the 'CPT/HCPCS Codes' section for 'Group 1 Codes': 0313U, 0314U and 0315U. The following CPT code has been deleted from the 'CPT/HCPCS Codes' section for 'Group 1 Codes': 0097U. For the following CPT code either the short description and/or the long description was changed. Depending on which description is used in this article, there may not be any change in how the code displays: 0022U in the 'CPT/HCPCS Codes' section for 'Group 1 Codes'.
01/01/2022	R3	Article revised and published on 01/20/2022 effective for dates of service on and after 01/01/2022 to reflect the Annual HCPCS/CPT Code Updates. The following CPT codes have been added to the 'CPT/HCPCS Codes' section for 'Group 1 Codes': 81349, 81523, 0285U, 0286U, 0287U, 0288U, 0289U, 0290U, 0291U, 0292U, 0293U, 0294U, 0296U, 0297U, 0298U, 0299U, 0300U, 0301U, and 0302U. The following CPT code has been deleted from the 'CPT/HCPCS Codes' section for 'Group 1 Codes' and therefore has been removed from the article: 0208U. For the following CPT codes either the short description and/or the long description was changed. Depending on which description is used in this article, there may not be any change in how the code displays: 0016M, 0090U, 0154U, 0155U, 0177U, 0180U, 0193U, 0200U, 0205U, 0216U, 0221U, 0244U, 0258U, 0262U, 0265U, 0266U, 0276U, 81194, 81228, 81229, and 81405 in the 'CPT/HCPCS Codes' section for 'Group 1 Codes'.
12/30/2021	R2	Article revised and published on 12/30/2021. Documentation requirement #5 has been revised. Information regarding the requirement for a relationship between the ordering/referring practitioner and the patient has been added to the text of the article and a separate documentation requirement, #6, was created to address using the test results in the management of the patient. The following CPT codes have been removed from the Group 1 CPT Codes: 0115U, 0151U, 0202U, 0223U, 0225U, 0240U, and 0241U.
11/08/2021	R1	Article revised and published on November 4, 2021 effective for dates of service on and after November 8, 2021. The instructions for reporting CPT code 81479 have been clarified, multiple CPT codes that did not represent molecular pathology services have been deleted and the following CPT codes have been added in response to the October 2021 Quarterly HCPCS Update: 0258U, 0260U, 0262U, 0264U, 0265U, 0266U, 0267U, 0268U, 0269U, 0270U, 0271U, 0272U, 0273U, 0274U, 0276U, 0277U, 0278U, and 0282U.