

WHOLE EXOME AND WHOLE GENOME SEQUENCING

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[Instructions for Use](#) ⓘ

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COVERAGE RATIONALE

Whole Exome Sequencing (WES)

Whole Exome Sequencing (WES) is proven and medically necessary for the following:

- Diagnosing or evaluating a genetic disorder when the results are expected to directly influence medical management and clinical outcomes and **all** of the following criteria are met:
 - Clinical presentation is nonspecific and does not fit a well-defined syndrome for which a specific or targeted gene test is available. If a specific genetic syndrome is suspected, a single gene or targeted gene panel should be performed prior to determining if WES is necessary; and
 - WES is ordered by a board-certified medical geneticist, neonatologist, neurologist, or developmental and behavioral pediatrician; and
 - **One** of the following:
 - Clinical and/or family history strongly suggest a genetic cause for which a specific clinical diagnosis cannot be made with any clinically available targeted genetic tests; or
 - There is a clinical diagnosis of a genetic condition that can be caused by multiple genes and WES is a more practical approach to identifying the underlying genetic cause than are individual tests of multiple genes; or
 - There is likely a genetic disorder and multiple targeted gene tests have failed to identify the underlying cause
- Comparator (e.g., parents or siblings) WES for evaluating a genetic disorder when the above criteria have been met and WES is performed concurrently or has been previously performed on the individual

Due to insufficient evidence of efficacy, WES is unproven and not medically necessary for all other indications, including but not limited to the following:

- Evaluation of fetal demise
- Molecular profiling of tumors for the diagnosis, prognosis or management of cancer
- [Preimplantation Genetic Testing](#) (PGT) in embryos
- Prenatal genetic diagnosis or screening
- Screening and evaluating disorders in individuals when the above criteria are not met

Whole Genome Sequencing (WGS)

Whole Genome Sequencing (WGS) is unproven and not medically necessary for screening and evaluating any genetic disorder due to insufficient evidence of efficacy.

DOCUMENTATION REQUIREMENTS

Benefit coverage for health services is determined by the member specific benefit plan document and applicable laws that may require coverage for a specific service. The documentation requirements outlined below are used to assess

whether the member meets the clinical criteria for coverage but do not guarantee coverage of the service requested.

CPT Codes*	Required Clinical Information
Whole Exome and Whole Genome Sequencing	
0012U, 0013U, 0014U, 0036U, 0094U, 81415, 81416, 81417, 81425, 81426, 81427	<p>Medical notes documenting all of the following:</p> <ul style="list-style-type: none"> • Personal history of the condition, if applicable, including age at diagnosis • Complete family history (usually three-generation pedigree) relevant to condition being tested • Genetic testing results of family member, if applicable, and reason for testing • Ethnicity/ancestry (e.g., Ashkenazi Jewish), if reason for testing • Any prior genetic testing results • How clinical management will be impacted based on results of genetic testing • Genetic counseling (if available)

*For code descriptions, see the [Applicable Codes](#) section.

DEFINITIONS

Comparator: A DNA sequence that is used to compare to the individual's DNA sequence. This may be a parent or sibling of the individual, or non-cancerous tissue that is being compared to the individual's tumor tissue (Thun et al., 2017).

Next Generation Sequencing (NGS): New sequencing techniques that can quickly analyze multiple sections of DNA at the same time. Older forms of sequencing could only analyze one section of DNA at once.

Preimplantation Genetic Testing (PGT): A test performed to analyze the DNA from oocytes or embryos for human leukocyte antigen (HLA)-typing or for determining genetic abnormalities. These include:

- PGT-A: For aneuploidy screening (formerly PGS)
 - PGT-M: For monogenic/single gene defects (formerly single-gene PGD)
 - PGT-SR: For chromosomal structural rearrangements (formerly chromosomal PGD)
- (Zegers-Hochschild et al., 2017)

Variant of Unknown Significance (VUS): A variation in a genetic sequence that has an unknown association with disease. It may also be called an unclassified variant.

Whole Exome Sequencing (WES): About 1% of a person's DNA makes protein. These protein making sections are called exons. All the exons together are called the exome. WES is a DNA analysis technique that looks at all of the exons in a person at one time, rather than gene by gene (U.S. National Library of Medicine, What are whole exome sequencing and whole genome sequencing? 2018).

Whole Genome Sequencing (WGS): WGS determines the sequence of all of the DNA in a person, which includes the protein making (coding) as well as non-coding DNA elements (U.S. National Library of Medicine, What are whole exome sequencing and whole genome sequencing? 2018).

APPLICABLE CODES

The following list(s) of procedure and/or diagnosis codes is provided for reference purposes only and may not be all inclusive. Listing of a code in this policy does not imply that the service described by the code is a covered or non-covered health service. Benefit coverage for health services is determined by the member specific benefit plan document and applicable laws that may require coverage for a specific service. The inclusion of a code does not imply any right to reimbursement or guarantee claim payment. Other Policies and Coverage Determination Guidelines may apply.

CPT Code	Description
0012U	Germline disorders, gene rearrangement detection by whole genome next-generation sequencing, DNA, whole blood, report of specific gene rearrangement(s)
0013U	Oncology (solid organ neoplasia), gene rearrangement detection by whole genome next-generation sequencing, DNA, fresh or frozen tissue or cells, report of specific gene rearrangement(s)
0014U	Hematology (hematolymphoid neoplasia), gene rearrangement detection by whole genome next-generation sequencing, DNA, whole blood or bone marrow, report of specific gene rearrangement(s)

CPT Code	Description
0036U	Exome (i.e., somatic mutations), paired formalin-fixed paraffin-embedded tumor tissue and normal specimen, sequence analyses
0094U	Genome (e.g., unexplained constitutional or heritable disorder or syndrome), rapid sequence analysis
81415	Exome (e.g., unexplained constitutional or heritable disorder or syndrome); sequence analysis
81416	Exome (e.g., unexplained constitutional or heritable disorder or syndrome); sequence analysis, each comparator exome (e.g., parents, siblings) (List separately in addition to code for primary procedure)
81417	Exome (e.g., unexplained constitutional or heritable disorder or syndrome); re-evaluation of previously obtained exome sequence (e.g., updated knowledge or unrelated condition/syndrome)
81425	Genome (e.g., unexplained constitutional or heritable disorder or syndrome); sequence analysis
81426	Genome (e.g., unexplained constitutional or heritable disorder or syndrome); sequence analysis, each comparator genome (e.g., parents, siblings) (List separately in addition to code for primary procedure)
81427	Genome (e.g., unexplained constitutional or heritable disorder or syndrome); re-evaluation of previously obtained genome sequence (e.g., updated knowledge or unrelated condition/syndrome)

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DESCRIPTION OF SERVICES

Genetic counseling is strongly recommended prior to Whole Exome Sequencing (WES) in order to inform persons being tested about the advantages and limitations of the test as applied to their unique situation.

Whole Genome Sequencing (WGS) and Whole Exome Sequencing (WES) are increasingly clinically available due to significant advances in DNA sequencing technology over the last several years (Taber et al., 2014). WES refers to the sequence determination of the exome. The exome is the portion of an individual's genome that encodes protein (also known as exons). Approximately 1% of the genome is comprised of exons, which is about 30 million base pairs (Bertier, et al., 2016) and between 20,000-25,000 genes (U.S. National Library of Medicine, What is a gene? 2018).

Most known disease causing variants are found in the exons, and by sequencing them all simultaneously, a more efficient analysis can be completed than by sequencing each individual gene alone (Bertier et al., 2016). There is much that is unknown, however, and to date only 3,911 genes that are known to harbor one or more disease causing mutations have been identified (Online Mendelian Inheritance in Man, 2018). WES results in long lists of genetic variants, and the success of this technology is dependent on how consistently and accurately labs can identify disease causing mutations (Richards et al., 2015).

WGS determines the order of all the nucleotides in an individual's DNA and can determine variations in any part of the genome (U.S. Library of Medicine, What are whole exome sequencing and whole genome sequencing? 2018). As with WES, WGS results in long lists of unknown variants, and the methodology and databases available to interpret WGS are the same as WES, and focuses primarily on the exons (Richards et al., 2015; Landrum et al., 2015).

CLINICAL EVIDENCE

Whole Exome Sequencing

Pediatric (Non-Cancer)

The BabySeq project is a pilot randomized trial within the Newborn Sequencing in Genomic Medicine and Public Health (NSIGHT) study. NSIGHT is an NIH-funded consortium of four research programs designed to address questions and concerns about implementing routine WES into newborn care. Ceyhan-Birsoy et al. (2019) reports on their experience with the first 159 newborns analyzed in the BabySeq project, of which 127 were healthy newborns and 32 were ill and in the NICU. Fifteen newborns (ten healthy, five from the NICU) were found to be at risk for childhood onset diseases, none of which were anticipated from the known clinical or family histories. Five of these were in genes with a high penetrance rate, and included non-syndromic hearing loss, glomuvenous malformations, KBG syndrome, biotinidase deficiency, and congenital adrenal hyperplasia due to 21-hydroxylase deficiency. Eleven genetic variants found in this sub-group were associated with moderate penetrance genetic disorders and were disclosed because of the possibility of early intervention. Examples included hypertrophic cardiomyopathy, aortic stenosis, atypical hemolytic-uremic

syndrome, type I cystinuria and G6PD deficiency. Eighty-five newborns were found to have risks for adult-onset diseases, such as *BRCA* related cancer or Lynch syndrome. Only three newborns' parents chose to learn about the adult onset disease risks. One hundred and forty of the newborns were found to be carriers of at least one autosomal recessive disorder. Pharmacogenetic test results were also returned, and were limited to three genes felt by the BabySeq project to have the highest level of evidence for informing drug prescribing in the pediatric population; *DPYD*, *TPMT* and *G6PD*. Eight newborns had variants in these genes that could impact future care should the need for fluoropyrimidines or thiopurines arise. The infant with G6PD Deficiency was reported in the childhood onset disease section, as symptoms can be triggered by factors other than medications. Testing of parents was required and helpful in resolving results in thirteen cases. The authors concluded that this pilot study suggests that newborn WES may provide useful information beyond that currently available with routine newborn screening.

Ambry Genetics, a genetic testing lab in California, described their retrospective experience of WES on 66 neonatal patients who were referred to their laboratory for testing due to clinical findings at birth suggestive of a genetic disease (Powis et al., 2018). Additional samples on parents or other family members were also sent when available. Rapid turnaround time requests had verbal results provided before Sanger sequencing confirmation, but all positive findings were verified with Sanger sequencing regardless. Secondary findings were available per ACMG guidelines when requested. The average turnaround time from test to report for the rapid analysis was 8 days, and with Sanger confirmation, 15 days. For non-rapid testing, the average turnaround time was 72 days. Over half of the patients reported no prenatal genetic testing, and 26 had a chromosome microarray and 4 had a post-natal single gene test or gene panel, but all were reported negative. Thirty two patients had significant results from WES (48.5%). Fourteen had positive results in well characterized genes, eleven had likely positive results in well characterized genes, and six had VUS or uncertain gene/phenotype correlation in well characterized genes. One patient had a positive result in a novel candidate gene finding. Forty eight patients consented to receiving secondary findings, and one patient was found to have a mutation in the low density lipoprotein receptor *LDLR* gene. Changes in clinical management were reported by the authors on only one case; a male infant with low Apgar scores, limited spontaneous movement, and a fractured humerus. He tested negative for chromosome abnormalities, myotonic dystrophy, and spinal muscular atrophy. He had a complex family history.

Stark et al. (2018) explored the clinical utility of rapid whole exome sequencing (rWES) in acutely ill pediatric patients who were suspected to have a genetic disorder. Testing was performed on individual patients and did not include parents or other family members. A total of 40 patients met the enrollment criteria at two participating pediatric tertiary care centers in Melbourne, Australia between April 2016 and September 2017. Potential candidates were reviewed by a panel of study investigators, and a minimum of two medical geneticists had to agree that rWES was appropriate in order to enroll a patient. A phenotype driven list of candidate genes for prioritized analysis had to be provided by each clinician for their patient. Information on how the rWES impacted care was obtained from the patient's clinician. rWES provided a diagnosis in 21 (53%) of patients with a median time to diagnosis of 16 days. Most patients received the diagnosis during the hospital admission. rWES did better than biochemical testing for these patients. In one case, the diagnosis of aromatic L-amino acid decarboxylase (AADC) deficiency was made in 14 days with rWES, enabling immediate treatment, but it took 10 weeks for the biochemical results to be returned from the interstate lab. Additionally, rWES diagnosed short-chain enoyl-CoA hydratase (ECHS1) deficiency in a patient whose diagnostic urine pattern was obscured due to acute ketosis and acidosis. Only when the patient was stable and retested because of the rWES results did the urine metabolic screening become clear. Clinical management changed in 12 of the patients, and included lifesaving treatment for a patient with a riboflavin transporter defect who was ventilation dependent, but was treated once the diagnosis was received and was discharged home shortly after. The authors noted that to successfully implement this program, it was necessary to develop a multi-disciplinary "rapid team" and create a whole system approach in order to overcome early barriers, such as delays in referral, patient assessments by the genetics team, complexities in patient genetic counseling, samples not clearly identified as "rapid," and the concern that time pressures impacting the quality of data analysis. The authors conclude that rWES is very promising and that developing the capability to deliver in pediatric and other settings requires substantial investment to optimize test performance and equity of access.

Trujillano et al. (2017) reported on the results of WES performed on 1000 consecutive cases with suspected Mendelian disorders from 54 countries (78.5% Middle East, 10.6% Europe, and 10.9% from rest of the world) referred for diagnostic WES between January 2014 and January 2016. Patients ranged between 1 month and 59 years, 92.4% were 15 years or younger, with 14.1% younger than 1 year and 39.4% 1–5 years of age. The cohort also included 23 prenatal cases (2.3%). Notably, 45.3% of the cases were from consanguineous families and 38.1% presented family history of the disease. Most cases (82.7%) were analyzed with a trio design (parents and index). They identified pathogenic or likely pathogenic variants in 307 families (30.7%). In further 253 families (25.3%) a variant of unknown significance, possibly explaining the clinical symptoms of the index patient was identified. WES enabled timely diagnosing of genetic diseases, validation of causality of specific genetic disorders of *PTPN23*, *KCTD3*, *SCN3A*, *PPOX*, *FRMPD4*, and *SCN1B*, and setting dual diagnoses by detecting two causative variants in distinct genes in the same patient. There was a better diagnostic yield in consanguineous families, in severe and in syndromic phenotypes.

Based on these results, the authors recommend WES as a first-line diagnostic in all cases without a clear differential diagnosis.

Tan et al. (2017) conducted a prospective analysis of the utility of WES on consecutive patients presenting at the Victorian Clinical Genetics Services at the Royal Children's Hospital, Melbourne, Australia in 2015. These patients were older than 2 years of age and were suspected of having a monogenic disorder. The children had not previously had diagnostic testing, such as a single gene or gene panel test, but may have had a non-diagnostic microarray. All participants underwent WES with a phenotype driven data analysis. Of 61 children assessed, 44 underwent WES. A diagnosis was achieved in 23 by sequencing the child alone. The diagnosis was unanticipated in 8 children, and altered clinical management in 6. The range of ages was 2-18 years old. The average length of "diagnostic odyssey" was 6 years, and prior to WES the average number of clinical tests was 19, with 4 genetics consults and 4 consults with other specialists. Fifty nine children had undergone general anesthesia in order to perform a diagnostic test. The authors hypothesize that WES at the first indication of a genetic disorder would have reduced the number of tests and interventions, and provided an overall cost savings.

Visser et al. (2017) of the Radboud University Medical Center in the Netherlands studied 150 consecutive patients presenting in the neurology clinic with non-acute neurological symptoms that were suspected to have a genetic origin, and compared the traditional work-up and testing paradigm to the use of WES. Both were conducted in parallel. The typical clinical approach gave a diagnostic yield of about 7%, whereas WES gave a diagnostic yield of about 29%. The authors highlighted the need for genetic counseling and tailored consent regarding incidental findings.

Tarailo-Graovac et al. (2016) combined deep clinical phenotyping (the comprehensive characterization of the discrete components of a patient's clinical and biochemical phenotype) with WES analysis through a semiautomated bioinformatics pipeline in consecutively enrolled patients with intellectual developmental disorder and unexplained metabolic phenotypes. WES was performed on samples obtained from 47 probands. Of these patients, 6 were excluded, including 1 who withdrew from the study. The remaining 41 probands had been born to predominantly nonconsanguineous parents of European descent. In 37 probands, the investigators identified variants in 2 genes newly implicated in disease, 9 candidate genes, 22 known genes with newly identified phenotypes, and 9 genes with expected phenotypes; in most of the genes, the variants were classified as either pathogenic or probably pathogenic. Complex phenotypes of patients in five families were explained by coexisting monogenic conditions. A diagnosis was obtained in 28 of 41 probands (68%) who were evaluated. A test of a targeted intervention was performed in 18 patients (44%). The authors concluded that deep phenotyping and WES in 41 probands with intellectual developmental disorder and unexplained metabolic abnormalities led to a diagnosis in 68%, the identification of 11 candidate genes newly implicated in neurometabolic disease, and a change in treatment beyond genetic counseling in 44%.

Stark et al. (2016) prospectively evaluated the diagnostic and clinical utility of singleton WES as a first-tier test in infants with suspected monogenic disease at a single pediatric tertiary center. This occurred in parallel with standard investigations, including single- or multigene panel sequencing when clinically indicated. The diagnosis rate, clinical utility, and impact on management of singleton WES were evaluated. Of 80 enrolled infants, 46 received a molecular genetic diagnosis through singleton WES (57.5%) compared with 11 (13.75%) who underwent standard investigations in the same patient group. Clinical management changed following exome diagnosis in 15 of 46 diagnosed participants (32.6%). Twelve relatives received a genetic diagnosis following cascade testing, and 28 couples were identified as being at high risk of recurrence in future pregnancies. The authors concluded that this prospective study provides strong evidence for increased diagnostic and clinical utility of singleton WES as a first-tier sequencing test for infants with a suspected monogenic disorder. Singleton WES outperformed standard care in terms of diagnosis rate and the benefits of a diagnosis, namely, impact on management of the child and clarification of reproductive risks for the extended family in a timely manner.

Retterer et al. (2015) reported the diagnostic yield of WES in 3,040 consecutive cases at a single clinical laboratory. WES was performed for many different clinical indications and included the proband plus two or more family members in 76% of cases. The overall diagnostic yield of WES was 28.8%. The diagnostic yield was 23.6% in proband-only cases and 31.0% when three family members were analyzed. The highest yield was for patients who had disorders involving hearing (55%, N = 11), vision (47%, N = 60), the skeletal muscle system (40%, N = 43), the skeletal system (39%, N = 54), multiple congenital anomalies (36%, N = 729), skin (32%, N = 31), the central nervous system (31%, N = 1,082), and the cardiovascular system (28%, N = 54). Of 2,091 cases in which secondary findings were analyzed for 56 American College of Medical Genetics and Genomics-recommended genes, 6.2% (N = 129) had reportable pathogenic variants. In addition to cases with a definitive diagnosis, in 24.2% of cases a candidate gene was reported that may later be reclassified as being associated with a definitive diagnosis. According to the authors, analysis of trios significantly improves the diagnostic yield compared with proband-only testing for genetically heterogeneous disorders and facilitates identification of novel candidate genes.

Valencia et al. (2015) performed a retrospective review of the first 40 clinical cases to determine the performance characteristics of WES in a pediatric setting by describing patient cohort, calculating the diagnostic yield, and detailing the patients for whom clinical management was altered. Of these, genetic defects were identified in 12 (30%) patients, of which 47% of the mutations were previously unreported in the literature. Among the 12 patients with positive findings, seven had autosomal dominant disease and five had autosomal recessive disease. Ninety percent of the cohort opted to receive secondary findings and of those, secondary medical actionable results were returned in three cases. The diagnostic workup included a significant number of genetic tests with microarray and single-gene sequencing being the most popular tests. Genetic diagnosis from WES led to altered patient medical management in positive cases. The authors concluded that this review demonstrates the clinical utility of WES by establishing the clinical diagnostic rate and its impact on medical management in a large pediatric center. The cost-effectiveness of WES was demonstrated by ending the diagnostic odyssey in positive cases. According to the authors, in some cases it may be most cost-effective to directly perform WES.

Farwell et al. (2015) provided the results from the first 500 probands referred to a clinical laboratory for diagnostic exome sequencing. Family-based exome sequencing included WES followed by family inheritance-based model filtering, comprehensive medical review, familial cosegregation analysis, and analysis of novel genes. A positive or likely positive result in a characterized gene was identified in 30% of patients (152/500). A novel gene finding was identified in 7.5% of patients (31/416). The highest diagnostic rates were observed among patients with ataxia, multiple congenital anomalies, and epilepsy (44, 36, and 35%, respectively). Twenty-three percent of positive findings were within genes characterized within the past 2 years. The diagnostic rate was significantly higher among families undergoing a trio (37%) as compared with a singleton (21%) whole-exome testing strategy. According to the authors, data demonstrate the utility of family-based exome sequencing and analysis to obtain the highest reported detection rate in an unselected clinical cohort, illustrating the utility of diagnostic exome sequencing as a transformative technology for the molecular diagnosis of genetic disease.

Yang et al. (2014) performed clinical whole-exome sequencing and reported (1) the rate of molecular diagnosis among phenotypic groups, (2) the spectrum of genetic alterations contributing to disease, and (3) the prevalence of medically actionable incidental findings such as FBN1 mutations causing Marfan syndrome. This was an observational study of 2000 consecutive patients with clinical WES analyzed between June 2012 and August 2014. WES tests were performed at a clinical genetics laboratory in the United States. Results were reported by clinical molecular geneticists certified by the American Board of Medical Genetics and Genomics. Tests were ordered by the patient's physician. The patients were primarily pediatric (1756 [88%]; mean age, 6 years; 888 females [44%], 1101 males [55%], and 11 fetuses [1% gender unknown]), demonstrating diverse clinical manifestations most often including nervous system dysfunction such as developmental delay. A molecular diagnosis was reported for 504 patients (25.2%) with 58% of the diagnostic mutations not previously reported. Molecular diagnosis rates for each phenotypic category were 143/526 for the neurological group, 282/1147 for the neurological plus other organ systems group, 30/83 for the specific neurological group, and 49/244 for the non-neurological group. The Mendelian disease patterns of the 527 molecular diagnoses included 280 (53.1%) autosomal dominant, 181 (34.3%) autosomal recessive (including 5 with uniparental disomy), 65 (12.3%) X-linked, and 1 (0.2%) mitochondrial. Of 504 patients with a molecular diagnosis, 23 (4.6%) had blended phenotypes resulting from 2 single gene defects. About 30% of the positive cases harbored mutations in disease genes reported since 2011. There were 95 medically actionable incidental findings in genes unrelated to the phenotype but with immediate implications for management in 92 patients (4.6%), including 59 patients (3%) with mutations in genes recommended for reporting by the American College of Medical Genetics and Genomics. The authors concluded that WES provided a potential molecular diagnosis for 25% of a large cohort of patients referred for evaluation of suspected genetic conditions, including detection of rare genetic events and new mutations contributing to disease. According to the authors, the yield of WES may offer advantages over traditional molecular diagnostic approaches in certain patients.

Lee et al. (2014) reported on initial clinical indications for clinical exome sequencing (CES) referrals and molecular diagnostic rates for different indications and for different test types. Clinical exome sequencing was performed on 814 consecutive patients with undiagnosed, suspected genetic conditions between January 2012 and August 2014. Clinical exome sequencing was conducted as trio-CES (both parents and their affected child sequenced simultaneously) to effectively detect de novo and compound heterozygous variants or as proband-CES (only the affected individual sequenced) when parental samples were not available. Of the 814 cases, the overall molecular diagnosis rate was 26%. The molecular diagnosis rate for trio-CES was 31% and 22% for proband-CES. In cases of developmental delay in children (<5 years, n = 138), the molecular diagnosis rate was 41% for trio-CES cases and 9% for proband-CES cases. The significantly higher diagnostic yield of trio-CES was due to the identification of de novo and compound heterozygous variants. The authors concluded that in this sample of patients with undiagnosed, suspected genetic conditions, trio-CES was associated with higher molecular diagnostic yield than proband-CES or traditional molecular diagnostic methods.

Nambot et al. (2018) reported on the effectiveness of regularly re-analyzing WES over a period of three years to address ongoing advances in bioinformatics approaches and updates to the medical literature. In a retrospective

approach, the authors re-examined 416 WES tests that had been conducted in their clinic between June 2013 and June 2016. In the initial testing phase, 104 tests resulted in a diagnosis giving a diagnostic yield of 25%. There were 156 tests in the first two years of the study that did not provide a diagnosis or conclusive results and were reanalyzed. From this cohort, 24 new diagnoses were made with a yield of 15%. Half of the new diagnosis resulted from new information appearing in the literature, and bioinformatic pipeline updates resulting in reconsideration of misclassified variants and an improved ability to detect copy number variants. The other cases were resolved through collaboration with data sharing consortiums like the Matchmaker Exchange project, which uses case data to help researchers identify patients carrying variants in the same gene. The final overall yield of WES for this cohort, combining the initial results with the reanalysis, was 27.9%.

The Clinical Sequencing Exploratory Research Consortium (CSER) studied variant assessment between nine labs performing exome analysis and applying the ACMG and AMP sequence variant interpretation guidelines, and found that intra-lab concordance was 79%, but inter-lab concordance was only 34%. After consensus efforts, 70% concordance was achieved between labs, reflecting the continued subjectivity. Five percent of the discordant interpretations would impact clinical care (Green et al., 2016). In addition, because all genes are being analyzed simultaneously, an unexpected or incidental finding may be identified in the analysis that was outside of the clinical indication for the test (Richards et al., 2015). Novel variants may be discovered for the first time in the context of clinical care. Laboratories that perform WES are in the unique position of requiring detailed clinical information to interpret results and that may occasionally include testing of biological relatives (Richards et al., 2015).

WES may result in false positives due to the difficulty in reading CG rich regions, and poor coverage depth (Meienberg et al., 2016). A comparison of standard next generation sequencing (NGS) techniques and WES demonstrated that >98% of pathogenic variants are covered at depth adequate for detection (LaDuca et al., 2017).

For these reasons, it is critical that the ordering physician has specialty training and experience with these technologies and is prepared to work with the laboratory and interpret the results of such testing for their patient (Taber et al., 2014; Richards, et al., 2015; ACMG, 2012).

Pediatric (Cancer)

Zhang et al. (2015) studied the prevalence of cancer pre-disposition germline mutations in children and adolescents with cancer in 1,120 patients under the age of 20. Whole exomes were sequenced in 456 patients and whole genomes were sequenced in 595, or both in 69. Results were analyzed in 565 genes, including 60 that are associated with autosomal dominant cancer syndromes. Genetic variant pathogenicity was determined by a team of experts who relied on peer reviewed literature, cancer and locus specific databases, computational predictions, and second hits identified in the participant tumor genome. This same variant calling approach was used to analyze data on 966 controls from the 1000 Genomes Projects who were not known to have cancer and data from 733 children from an autism study. Overall, germline mutations were found in 95 children with cancer (8.5%), as compared to only 1.1% of 1000 Genome Project and 0.6% of autism study controls. The mutations were most commonly found in TP53, APC, BRCA2, NF1, PMS2, RB1 and RUNX3. Eighteen patients also have variants in tumor suppressor genes. Of the 58 patients who had family history information available and a mutation in a predisposing dominant cancer gene, 40% had a significant family history of cancer.

The results of the German pilot study called 'Individualized Therapy for Relapsed Malignancies in Childhood' (INFORM) was reported on by Worst et al. in 2016. This was a precision medicine study utilizing tumor and blood whole-exome, low-coverage whole-genome, and RNA sequencing, complemented with methylation and expression microarray analyses. The goal was to identify individualized therapies for children and adolescents diagnosed with a high risk relapsed/refractory cancer. Fifty-seven patients from 20 centers were prospectively tested, and diagnoses included sarcomas (n = 25), brain tumors (n = 23), and other (n = 9).

Parsons et al. (2016) conducted a study to determine the prevalence of somatic and germline mutations in children with solid tumors. From August 2012 through June 2014, children with newly diagnosed and previously untreated central nervous system (CNS) and non-CNS solid tumors were prospectively enrolled in the study at a large academic children's hospital. Blood and tumor samples underwent whole exome sequencing (WES) in a certified clinical laboratory with genetic results categorized by clinical relevance. A total of 150 children participated, with a mean age of 7 years, with 80 boys and 70 girls. Tumor samples were available for WES in 121 patients. In this group, somatic mutations with established clinical utility were found in 4 patients, and mutations with possible clinical utility were found in 29. CTNNB1 had the most mutations, followed by KIT, TSC2, BRAF, KRAS, and NRAS. Diagnostic germline mutations related to the child's clinical presentation was found in 150 patients and included 13 dominant mutations in known cancer susceptibility genes, including TP53, VHL, and BRCA1. One recessive liver disorder with liver cancer was identified in TJP2 and one renal cancer, CLCN5. Incidental findings were found in 8 patients. Nearly all patients (98%) had variants of unknown significance in known cancer genes, drug response genes, and genes known to be associated with recessive disorders.

The clinical impact of molecular profiling on pediatric tumors in children with refractory cancer was studied by Østrup et al. (2018) based on experiences in 2015 at the Center for Genomic Medicine, Rigshospitalet (Copenhagen, Denmark). Forty six tumor samples, two bone marrow aspirates, three cerebral spinal fluid samples, and one archived tumor DNA from 48 children were analyzed by WES, RNA sequencing, transcriptome arrays, and single nucleotide polymorphism (SNP) arrays for mutation burden and to determine if actionable results could be found. Twenty patients had extracranial solid tumors and 25 had CNS tumors. Three patients were diagnosed with a hematological malignancy. Eleven of the 25 CNS tumors underwent additional DNA methylation profiling to obtain a second opinion on the diagnosis. At the time of the study, six patients were deceased. In 33 patients, actionable findings were identified which included 18 findings that helped make a final diagnosis, and 22 that allowed identification of potential treatment targets. Eleven findings had both a diagnostic and a treatment impact. Nine of the 33 findings were already known by prior histopathology tests. The highest yield for actionable findings was from WES (39%), followed by SNP array (37%) and RNA sequencing (21%). Clinical interventions based on these results were implemented in 11 of 44 patients, including 8 patients who received therapy based on the molecular profile. Six patients experienced direct benefit with improved response or stable disease. Four received compassionate use therapy. The authors commented that although 60% of the reports that went back to clinicians contained actionable findings, the clinicians encountered barriers to obtaining available or approved treatments which limited the utility of the advanced diagnostics. There are clinical trials available based on advanced molecular profiling, but the authors note that not all facilities have the infrastructure in place to provide comprehensive molecular profiling.

WES Prenatal

Lord et al. (2019) reported on a prospective cohort study involving 34 fetal medicine units in England and Scotland. WES was used to evaluate the presence or absence of causative genetic variants in fetuses with structural anomalies identified on ultrasound after 11 weeks gestation. Women were included if they chose invasive testing, karyotyping or chromosome microarray testing was negative for aneuploidy or other copy number variants, and the father consented to being tested as well to enable a trio analysis. The study took place between October 2014 and June 2017, and clinical outcomes were collected until March 2018. In all, 610 fetuses and 1202 parent samples were tested. A diagnostic result was found in 52 (8.5%), and a VUS with potential clinical usefulness was found in 24 (3.9%). In 143 fetuses with multisystem anomalies, the diagnostic yield was 15.4%, in those with cardiac anomalies it was 11.1%, and 15.4% in those with skeletal anomalies. The lowest diagnostic yield was in those with an isolated nuchal thickness (3.2%). Although WES improved the identification of genetic disorders in fetuses with structural anomalies, the authors conclude that careful consideration should be given to which cases are selected.

The clinical utility of fetal exome sequencing was retrospectively reviewed by Normand et al. (2018) for 146 consecutive fetal exomes performed at the Baylor Genetics clinical diagnostic laboratory. Patients were included if reported between 2012 and 2017, where the fetal sample was derived from an amniocentesis, chorionic villi sampling (CVS), or a cordocentesis, or was a product of conception and the fetus had a confirmed anomaly on imaging or autopsy. A molecular diagnosis was found in 46 (32%) of fetuses. The number anomalies that were noted in the fetus was correlated with the likelihood of a genetic diagnosis. Excluding tissue culture time, the average turn-around time for a report was 14 days. The diagnostic rate did not differ between those with a contributing family history and a spontaneous case. Medical management changes were available in 14 cases. In four cases, medical management was altered by altering the neonatal care pregnancy termination plans. The remaining ten cases resulted in altered reproductive planning for the future, such as choosing preimplantation genetic diagnosis. The authors concluded that more research is needed overall on the clinical utility of fetal exome testing, but select cases may be appropriate for WES under the guidance of an experience multi-disciplinary team.

A prospective analysis was undertaken by Petrovski et al. (2019) at Columbia University Carmen and John Thain Center for Prenatal Pediatrics in New York. Between April 2015 and April 2017, 517 pregnancies with structural abnormalities identified by ultrasound were offered the opportunity to participate in a clinical utility study of trio WES. Eligible participants had a negative fetal karyotype or chromosome microarray. Overall a total of 234 trios consented and had good quality samples and completed testing. The diagnostic yield was 10% (24 pregnancies). There were also 46 pregnancies with variants that were likely pathogenic, but there was insufficient evidence to consider the result truly pathogenic. Nine of the twenty four pregnancies with a diagnosis were found to have a diagnosis that impacted future reproductive counseling. At the time of publication, two carrier couples had sought CVS in a subsequent pregnancy, and one is seeking preimplantation diagnosis. One family that had a suspected likely pathogenic variant had a second affected pregnancy before enough information was available in the medical literature to call the variant pathogenic, highlighting the difficult balance between over and under reporting VUS. The authors concluded that fetal exome analysis is feasible, but is complex and requires the collaboration of a multidisciplinary team.

Fu et al. (2017) did sequential analysis involving karyotype, chromosome microarray (CMA), and then WES in a cohort of 3949 structurally abnormal fetuses. Eighteen percent (720) fetuses had an abnormal karyotype. CMA analysis was performed on those with a normal karyotype (1680) and 8% (168) had a pathogenic copy number variant. Of those with a normal karyotype and CMA analysis, 196 underwent WES, and 47 (24%) had a pathogenic variant identified

that could potentially explain the phenotype; additionally, the incidence of variants of unknown significance (VUS) and secondary findings was 12% and 6%, respectively.

Aarabi et al. (2018) conducted a study of the utility of WES in prenatal cases with structural birth defects. Twenty fetuses with structural abnormalities with normal karyotype and chromosome microarray results underwent WES, as did their parents. Initial results using only prenatal ultrasound findings did not identify any pathogenic or likely pathogenic variants. WES results were later re-evaluated utilizing prenatal and post-natal phenotypes. Inclusion of the post-natal phenotypes results in identifying pathogenic variants in 20% of cases including *PORCN* gene in a fetus with split-hand/foot malformation, as well as reportable variants of uncertain significance in fetuses with postnatal muscle weakness and Adams-Oliver syndrome. In one patient, post-natal magnetic resonance imaging (MRI) identified the presence of holoprosencephaly. The case was referred for Sanger sequencing of related genes, and a 47 bp deletion was found in *ZIC2* that was missed by WES. The authors suggest that incomplete fetal phenotyping limits the utility of WES, and that if prenatal WES is undertaken, re-analysis of the data with additional postnatal phenotype information can be useful. Further studies are needed to establish the clinical validity and clinical utility of WES in this setting.

WES Adult (Non-Cancer)

Groopman et al. (2019) studied the utility of WES in 3315 patients from two independent study cohorts with chronic kidney disease. A Study to Evaluate the Use of Rosuvastatin in Subjects on Regular Hemodialysis: An Assessment of Survival and Cardiovascular Events (AURORA) contributed 1128 patients, and 2773 patients came from a Columbia University Medical Center (CUMC) on end-stage renal disease who were recruited from 280 medical centers in 25 nations. For patients in the AURORA cohort, only broad categories and diagnostic codes for major clinical features were available, and detail clinical information from the EHR was available for the CUMC cohort. Most participants were over 21 years of age (92%) and of European ancestry (65%). WES provided a diagnostic result in 307 (9.3%) patients of 66 different genetic disorders. Diagnoses were found in all clinical categories, including congenital or cystic disease, and idiopathic nephropathies. Of those with a genetic diagnosis, 34 patients (1.6%) had medically actionable findings that included a change in renal management or referral to a subspecialty clinic.

The use of WES in the diagnostic workup of individuals with an idiopathic bleeding tendency was studied by Saes et al. (2019). A total of 87 patients at a mean age of 41 with a bleeding diathesis were analyzed the Tosetto BAT score and standard diagnostic tests and divided into three groups; increased BAT with normal lab results (Group A), abnormal platelet count (Group B), or abnormal lab results without a definitive diagnosis (Group C). Patients were counseled by a clinical geneticist and consented to either a bleeding disorder gene panel only, or WES. All patients underwent WES, and for the targeted panel group, an *in silico* panel was applied to select only known thrombosis and hemostasis genes. In the target panel analysis, fifteen patients (17%) were found to have a pathogenic variant in the targeted panel. Group A had the highest incidence of cases solved (24%), Group B had a 5% diagnostic yield, and Group C came in at 4%. Exome analysis was performed in 54 of the 80 unsolved cases. WES identified three VUS in candidate genes.

As part of the North Carolina Clinical Genomic Evaluation by Next-Generation Exome Sequencing Study (NCGENES), Haskell et al. (2018) used WES to determine a genetic diagnosis in 93 patients with NMD. Patients were categorized into three groups based on clinical findings; primarily neuropathy, primarily myopathy, or complex. After DNA extraction and WES, variants were filtered through three different gene lists in order to compare diagnostic yield between different lists. A neuropathy list of 199 genes implicated in neuropathy phenotypes, a myopathy list of 181 genes, and a list of 482 genes implicated in NMD were used. Variants were then categorized using the American College of Medical Genetics and Genomics (ACMG) standards on pathogenicity. The overall diagnostic yield of WES for pathogenic or likely pathogenic variants was 12.9%, and each gene list gave a different diagnostic yield. In some cases, family testing was performed to determine gene segregation and verify pathogenicity. The authors found that in patients with a clear neuropathy or myopathy, WES had the same diagnostic yield as the broader diagnostic test list. In patients with a complex phenotype, the broader list had the best diagnostic yield (9%) when compared to the neuropathy (4.9%) or myopathy (0%) diagnostic lists. Many of these patients had undergone muscle biopsy (42%), nerve conduction studies or electromyograms (86%), and genetic testing previously (68% overall and 20% had a multi-gene panel) and a definitive diagnosis had not been reached. The participant's biopsy, electrodiagnostic testing, and prior genetic results were reviewed by three independent specialist reviewers who categorized the testing as informative or non-informative in the context of WES results. Sixty-three percent of the prior testing was considered informative, meaning that it correlated with the pathogenic variant identified in WES as a neuropathy, myopathy, or a complex disorder. In two cases, WES identified molecular diagnoses that directly impacted medical treatment. One patient had been clinically diagnosed with a chronic inflammatory demyelinating polyneuropathy, but WES demonstrated that the genetic diagnosis of Spastic Ataxia of Charlevoix-Saguenay, so unnecessary immunotherapy was avoided. The second patient had been thought to have a hereditary spastic paraplegia, but the genetic diagnosis was confirmed as a form of dopa-responsive dystonia, and after dopa therapy was started, she regained the ability to walk without assistance. The authors concluded that introducing genome-scale sequencing into the clinical workflow earlier may shorten the diagnostic odyssey, minimize invasive testing, and provide potential opportunities for clinical and investigational therapeutics for patients with NMD.

Bardakjian et al. (2018) studied adult patients with neurological disorders who had been recommended to have genetic testing to determine the diagnostic yield of, and patient interest in, different types of tests in a real world clinical setting. All patients were seen at a university based speciality or neurogenetics clinic between January 2016 and April 2017 and were identified retrospectively through the electronic medical system. Overall, 377 patients were evaluated. The primary clinical indications for diagnostic genetic testing included ataxia, epilepsy, hereditary spastic paraparesis, leukodystrophy, memory loss, movement disorders, neuromuscular disease, and predictive testing due to a family history of disease, such as Huntington Disease. Genetic testing recommendations took place in a speciality clinic for 182 patients and 195 in the neurogenetics clinic. Eighty percent of patients had genetic testing completed. For those who chose not to have testing, 71 declined testing after genetic counseling, and 3 wanted to have testing, but it was not performed due to lack of insurance coverage. The highest rate of choosing not to test was in the category of patients referred for predictive testing for Huntington Disease. Age was not found to be a factor in accepting or declining testing. The overall diagnostic rate was 32% in the 303 people who completed testing. The yield was highest (50%) in targeted testing, where one or two genes were selected for testing based on clinical findings (n=89). This category is followed by array comparative genome hybridization (aCGH) (45%) in 7 patients, followed by multigene panels (25%) in 155 patients, and exome testing (25%) in 52 patients. The authors reported that for individuals being worked up for dystonia, the use of a panel test reduced the total cost of the diagnostic process by 30% by eliminating unnecessary tests like MRIs, and reduced the time to diagnosis by 75%. In addition, the use of panel tests and WES increased the number of variants of uncertain significance (VUS). Using family segregation testing, de-identified genetic data sharing through commercial platforms or academic consortia, the authors reduced the number of reportable VUS by one third, but acknowledged this required the involvement of an expert clinician with the training and knowledge to resolve VUS.

The diagnostic utility of WES in adults with chronic kidney disease (CKD) was evaluated by Lata et al. (2018). Ninety-two individuals who were referred for analysis and workup due to CKD of unknown etiology or due to familial nephropathy or hypertension underwent WES. Overall a diagnosis was found in 24% of patients, including in 9 patients with CKD of unknown etiology. One BRCA2 mutation was found as an incidental finding, and the individual was diagnosed with breast cancer in a follow up appointment. Clinical management was altered in patients with a positive result and included a change in targeted surveillance, initiation of family screening to guide transplant donor selection, and changes in therapy.

Posey et al. (2016) performed a retrospective analysis of consecutive WES reports for adults from a diagnostic laboratory. Phenotype composition was determined using Human Phenotype Ontology terms. Molecular diagnoses were reported for 17.5% (85/486) of adults, lower than a primarily pediatric population (25.2%; $p=0.0003$); the diagnostic rate was higher (23.9%) in those 18–30 years of age compared to patients over 30 years (10.4%; $p=0.0001$). Dual Mendelian diagnoses contributed to 7% of diagnoses, revealing blended phenotypes. Diagnoses were more frequent among individuals with abnormalities of the nervous system, skeletal system, head/neck, and growth. Diagnostic rate was independent of family history information, and de novo mutations contributed to 61.4% of autosomal dominant diagnoses. This early WES experience in adults demonstrates molecular diagnoses in a substantial proportion of patients, informing clinical management, recurrence risk and recommendations for relatives. A positive family history was not predictive, consistent with molecular diagnoses often revealed by de novo events, informing the Mendelian basis of genetic disease in adults. Additional studies in WES sequencing are needed to validate its clinical utility.

WES Adult-Cancer

The Victorian Comprehensive Cancer Centre Alliance explored the feasibility of WES on solid tumor specimens that were proven to be malignant on biopsy in a pilot study (Lee et al., 2018). The study took place between March 2014 and March 2015, and 23 patients opted in for tumor WES. Targeted panel testing focusing on mutations in known hotspots for somatic mutations was performed. Fifteen samples passed the quality criteria for testing, and WES and targeted testing were successful on all samples. Of samples submitted, 65% success was achieved on formalin-fixed paraffin-embedded (FFPE) and 20% on fresh frozen (FF). A multi-disciplinary tumor board team reviewed the clinical relevance of identified variants and determined if they were actionable. WES identified somatic variants in 73% of cases, and targeted testing only found 53%. Clinical management changes were taken in 53% of cases that included referring patients to the familial cancer clinic, and considering new therapies.

Nicolson et al. (2018) used WES to identify the genetic variants found in follicular thyroid cancer (FTC). They analyzed 39 tumors that were classified by subtype; 12 were minimally invasive (miFTC), 17 were encapsulated angioinvasive (eaFTC), and 10 were widely invasive (wiFTC). Samples were collected between 2002 and 2013. All samples were reviewed by a minimum of two independent pathologists to histopathological confirmation using the World Health Organization (WHO) 2017 guidelines. Hurthle cells were included, although differentiated by the WHO 2017 guidelines, because both Hurthle and conventional FTCs can exhibit invasive behavior. Samples underwent exome sequencing for a minimum 20X coverage, copy number variation analysis, and 13 of the samples were able to be tested for three common gene fusions found in FTC: *PAX8-PPARY*, *RET-PTC1*, and *RET-PTC3*. Matched normal samples were collected

from adjacent normal tissue or from white blood cell DNA. SciClone was used to detect clonal populations of tumor cells in each sample. Age, gender, tumor size (by largest diameter), and American Joint Committee on Cancer (AJCC) stage (7th and 8th editions), and genetic test results were assessed for association with invasive status. Most patients were female (67%) and the mean age was 55 years old. The medial tumor diameter was 3.6 cm and 92% had Stage I or Stage II disease. After surgery, patients were followed for disease progression for a median 5.8 years. The overall recurrence and disease progression rate was 15%. Overall, mutations in the RAS gene family were found in 20% of samples. TSHR mutations were identified in 4 tumors. *DICER1*, *EIF1AX*, *KDM5C*, *NF1*, *PRDM1*, *PTEN*, and *TP53* were recurrently mutated in 2 samples each. The range of mutation burden in the tumors ranged from 1-44 variants per tumor. There were no statistically significant differences in mutation burden between subtypes. There were 55 germline variants found in potential cancer-associated genes, but none had been previously catalogued as a thyroid susceptibility gene. In general, the FTCs in this study had a general copy number gain. The most common gains were of 5q, 7p, and 12q. In the 13 samples that underwent fusion gene analysis, 1 was found to have the *PAX8-PPARY* fusion. When results were analyzed in the context of outcome, the total mutation burden, cancer driver burden, FTC driver burden and AJCC stage were all associated with worse prognosis. The authors' statistical analysis suggests that the genetic profile may be a strong prognostic factor independent of histopathology. More research is needed to determine if similar results could be obtained on less invasive biopsy specimens.

Patients with metastatic and treatment-resistant cancer were prospectively enrolled at a single academic center for paired metastatic tumor and normal tissue WES during a 19-month period (Beltran et al., 2015). A comprehensive computational pipeline was used to detect point mutations, indels, and copy number alterations. Mutations were categorized as category 1, 2, or 3 on the basis of level of potential action; clinical reports were generated and discussed in precision tumor board. Patients (n=97, with 154 tumor pairs) were observed for 7 to 25 months for correlation of molecular information with clinical response. Results showed that more than 90% of patients harbored actionable or biologically informative alterations, although treatment was guided by the information in only 5% of cases. This study highlights opportunities for future clinical trials regarding whole-exome sequencing in precision medicine.

Malhotra et al. (2014) evaluated whether there is evidence that WES improves outcomes for patients with cancer. Published evidence was evaluated using a methodology that combines the analytical validity, clinical validity, clinical utility and ethical, legal, and social implications (ACCE) model for genetic test evaluations with internationally accepted health technology assessment methodology. WES has been conducted most extensively (seven studies to date) in breast cancer patients, with fewer studies of other types of cancers (e.g., leukemia, prostate cancer, and ovarian cancer). Studies evaluating somatic alterations showed high intratumor and inter-tumor heterogeneity. In addition, both novel and previously implicated variants were identified. However, only three studies have shown potential for clinical utility of WES; whereby, variants identified through WES may determine response to drug treatment. The authors concluded that despite evidence for clinical validity of WES in cancers, clinical utility is very limited and needs to be further evaluated in large clinical studies.

In a breast cancer study, follow-up analyses showed enrichment of GATA3 variants (identified by WES) in samples showing a decline in Ki-67 levels, which is a marker for response to aromatase inhibitor treatment. This association suggests that presence of GATA3 variants may be a predictive marker to identify individuals who will respond to treatment with aromatase inhibitors (Ellis et al., 2012). A second study showed that somatic hypervariation detected through WES not only was a predictive factor for determining platinum-based chemotherapy response in ovarian cancer treatment, but was also statistically significantly associated with longer overall survival and progression-free survival (Sohn et al., 2012). Another WES study by Tzoneva et al. (2013) identified NT5C2 variants that were associated with AML relapse even when receiving treatment, and early relapse compared to late relapse, suggesting NT5C2 may be a potential marker to identify individuals who may experience AML relapse despite chemotherapy treatment. While these 3 studies suggest potential for clinical utility, they need to be validated in larger clinical studies.

Whole Genome Sequencing (WGS)

Although WGS has the potential to identify causal variants for a wide variety of conditions that may be missed with other technologies, as well as to identify predictive biomarkers, the information derived from WGS has not yet been translated into improved outcomes and changed medical management. Further studies are needed to establish the clinical utility of WGS.

WGS-Pediatric (Non-Cancer)

Children admitted to the pediatric intensive care unit are typically critically ill and require rapid clinical response. To determine if first tier WGS could impact patient outcomes, French et al. (2019) explored the clinical utility of trio WGS in 195 families who had a child in the pediatric intensive care unit (PICU) or neonatal intensive care unit (NICU) suspected of having a genetic disease, or were referred to the study because of a suspected genetic diagnosis. A total of 567 samples were analyzed between the probands and family members, and a definitive diagnosis was found in 21% of cases. The average turn-around time from blood sample to report was three weeks. The phenotypic description of the child was not well aligned with the final genetic diagnosis in many cases, suggesting that phenotype

should not drive the use of WGS in evaluating children in the PICU or NICU. In those receiving a genetic diagnosis, clinical management was changed in 65% of cases, and for those in the NICU cohort, management changed in 83%.

Scocchia et al. (2019) studied the use of WGS as a first tier test at a resource limited dysmorphology clinic in northern Mexico as part of a collaboration between the Illumina iHope Program and the Foundation for the Children of the Californias and Hospital Infantil de Las Californias. Sixty children who were being followed as suspected of having a genetic diagnosis that was unresolved after expert clinical examination were tested with WGS. Ordering clinicians completed a survey that queried their change in management resulting from WGS results. Clinically relevant results were found in 68.3% (41) of patients. Nearly half were copy number variants or chromosomal abnormalities (20), including a mosaic trisomy. WGS results produced a new clinical diagnosis in 33 cases, and confirmed a clinical diagnosis in eight. Clinicians reported a change in clinical management in 20 (48%) of cases, which included referrals to specialists not previously considered, for imaging, or functional testing. Muscle biopsy was avoided in three cases, and one patient was transferred to palliative care after a diagnosis of neuronal ceroid lipofuscinosis. In cases where no molecular diagnosis was found, clinicians reported that this information was helpful to the care of six patients by narrowing down the differential diagnosis, or expediting additional clinical workup, such as a muscle biopsy. One patient was enrolled in a clinical trial based on the identification of an interesting VUS. Additional studies are needed, but this suggests that WGS may be beneficial as a first tier analysis in children suspected of having a genetic diagnosis.

Clark et al. (2019) described the analytical validity and clinical validity of an approach to rapid whole genome sequencing utilizing a platform designed for rapid, population scale sequencing using automated phenotyping and interpretation tools to make a provisional diagnosis. Conventional rapid WGS (rWGS) relies on preparing purified DNA from blood, DNA quality review, normalization of DNA concentration, preparation of the sequencing library, and library quality assessment. This platform instead relies on manually preparing libraries directly from blood samples or dried blood spots using microbeads with appropriate chromosomal segments (transposons). This method proved to be faster and less labor intensive. In four timed runs, the mean time to prepare the library was two hours and 45 minutes, as compared to ten hours by conventional methods. In the conventional approach, after preparation, samples were sequenced with the HiSeq 2500 sequencer in rapid run mode, with one sample processed per instrument, taking an average of 25 hours. In the modified approach, rWGS was performed on the NovaSeq6000 and S1 flow cell, as this instrument is faster with automated washing after a run. In four timed trials, sequencing took a mean of 15 hours and 32 minutes and yielded 404-537 Gb per flow cell, enough for two or three 40x genome sequences. Analysis of the sequence data was performed utilizing Dynamic Read Analysis for GENomics (DRAGEN), software that was optimized for speed, sensitivity and accuracy. Alignment and variant calling took a median of 1 hour, and is similar to standard methods. Structural variants were not included. Analysis of relevant variants is typically achieved through filtering based on patient phenotype, and typically this is done by manual input of the patient's clinical features. Which features to select can be subjective and biased, and often incomplete. The team developed a natural language processing algorithm to extract clinical features from unstructured text in the EHR, and optimized the algorithm from the training set used by Rady Hospital on 16 children with genomic disease, and enriched with text used to identify children with orphan diseases. This included mapping 60% of Human Phenotype Ontology (HPO) terms and 75.4% of Orphanet Rare Disease HPO terms to SNOMED CT by lexical and logical methods and then manually verifying them. This set was then tested on a group of 10 children who had genome sequencing for genetic disease diagnosis to determine if the automated phenotype extraction from the EHR was reliable. A detailed manual review of the EHR was compared to the output of the algorithm, and the sensitivity was found to be 80%. To determine the clinical validity of this approach, the algorithm was compared in 101 children who had WGS where the phenotype to use for analysis was selected by a clinical expert. The algorithm identified 27 fold more phenotypic features than the expert manual selection, and four fold more than if Online Mendelian Inheritance of Man (OMIM) terms alone were used. The process described was tested retrospectively in 95 children who had already had prior manual expert interpretation, and a second manual expert interpretation and the automated process were compared. The new manual expert interpretation was concordant with the prior results in 93 children, with two children being issued new reports with new revised diagnoses. The automated approach was concordant with the new manual review in 99% of cases, and with the prior manual review in 97% of cases. This process was tested prospectively in seven seriously ill infants in the NICU. The median time from blood sample to diagnosis for 19 hours and 56 minutes, compared with the standard testing time of 48 hours and 23 minutes. Three patients received a genetic diagnosis, confirmed by the standard method and Sanger sequencing. One patient's diagnosis was 16 hours earlier and another 27 hours earlier than the conventional approach resulting in earlier and more confident treatments than would have otherwise been considered.

In order to analyze the application of WES and WGS as a routine diagnostic tool for patients, Smith et al. (2019) undertook a scoping review of the literature, following the Preferred Reporting Items for Systematic review and Meta-analysis (PRISMA) method of reporting observational studies. The timeframe from which they drew from the literature was 2009 to 2017, and focused on diagnostic WES or WGS for infant and pediatric patients. A total of 171 articles were found, of which 131 were case reports, 40 were aggregate analysis and 4 were focused on a cost-effectiveness objective. The only metric consistently reported across all studies was diagnostic yield, and that varied broadly by

clinical category and test type. In aggregate it was 33.2%. The authors concluded that multi-disciplinary research that focuses on consistency in outcome measurement is needed to demonstrate clinical utility.

Genetic hearing loss is heterogeneous and often difficult to diagnose. Sheppard et al. (2018) examined the clinical utility of WES on a cohort of 43 probands with hearing loss, and compared the diagnostic yield with a common hearing loss genetic tests in a sub-group of 32 patients. WES focused the analysis on 247 genes associated with hearing loss, and targeted sequencing was up to the ordering clinician. Four patients had a four gene panel, 19 had a 70 gene panel, and five had single gene testing. Twenty-four had a chromosome microarray performed, and a number of patients had more than one targeted test. Overall the diagnostic yield was 37.2% for WES, compared to 15.8% of the common hearing loss genetic tests.

The clinical utility of rapid WGS in the pediatric intensive care unit (PICU) was the subject of a study by Mestek-Boukhibar et al. (2018). They set up a multi-disciplinary team to identify patients at a tertiary NHS tertiary children's hospital with a 23-bed multidisciplinary PICU and a 20-bed pediatric cardiac intensive care unit (CICU). Patients were considered for inclusion that were considered critically ill but death was not imminent, had parents available for testing, and had a suspected heterogeneous monogenic disease with possible treatment available. An initial ten trios were used as a training set for the rapid sequencing and bioinformatics approach from which the team learned and revised the process for further optimization. A final 14 trios went through the finalized process. Overall, a primary molecular diagnosis was found in ten of 24 trios (42%). The shortest time to complete the full workflow, which included patient identification, informed consent, sample collection, and testing, was 5 days. There was impact on clinical management was significant for three patients. One child had a ruptured spleen and child protection concerns had been raised, but WGS identified Ehler-Danlos syndrome which explained the phenotype. Another child with renal failure had a pathogenic variant in the *WT1* gene, resulting in bilateral nephrectomy to prevent the development of Wilms tumors. The third child was diagnosed with Sotos syndrome, and had an atypical presentation that in other situations may not have been diagnosed for some time. The early diagnosis allowed for early endocrine management of the disease. In addition, one child who did not have a primary molecular diagnosis was found to have a homozygous *BCHE* mutation that conveys a risk of apnea with certain anesthesia. This altered the medical management as the child had to undergo several surgical procedures. The authors noted that traditional, targeted testing for these individuals may not have been done due to atypical presentations, or the results could have taken as long as 8 weeks. It was highlighted that this process required close and rapid communication with the clinical team, lab, and computational systems, and required optimization and revision of standard processes to meet the aggressive timeline.

Clark et al. (2018) conducted a meta-analysis comparing the diagnostic and clinical utility of WGS, WES and chromosome microarray (CMA) in children suspected of having genetic disease. An analysis of the literature from January 2011 to August 2017 was conducted following the Preferred Reporting Items for Systematic review and Meta-analysis (PRISMA) and Meta-analysis Of Observational Studies in Epidemiology (MOOSE) guidelines. Thirty seven studies of 20,068 children were included. Overall, the diagnostic utility of WES and WGS was greater than CMA. In studies from only 2017, the diagnostic utility of WGS was greater than CMA. Among studies featuring in co-hort comparisons, the diagnostic utility of WES was greater than CMA. The diagnostic utility between WGS and WES was not significantly different. In studies with in-cohort comparisons of WGS and WES, there was a greater chance of achieving a diagnosis when a trio was available than singleton testing, and with in-hospital interpretation versus a reference lab interpretation. In this study, clinical utility was defined as a change in clinical management. Cases where the only change was reproductive planning, or a change in genetic counseling, were excluded. The clinical utility of WES was greater, but not statistically significant, than CMA. However, WGS was higher for clinical utility than CMA, and met statistical significance ($p < 0.0001$). The authors identified several limitations with the meta-analysis, such as the heterogeneity of the pooled data, taking diagnostic rates at face value, and that only one study met the highest level of evidence criteria for clinical interventions. Overall, they concluded that more randomized, well designed and controlled clinical studies are needed but WES and WGS could be considered over CMA for a first-tier test in a child suspected of having a genetic diagnosis.

Over a two year period at the Hospital for Sick Children in Toronto, Canada, 103 patients eighteen years old or younger were prospectively recruited into a study that compared the standard of care targeted genetic testing approach with whole genome sequencing (WGS) (Lionel et al., 2018). Patients were identified from pediatric subspecialty clinics as likely to have a genetic disease, and about half were purposely recruited from outside the Clinical Genetics clinic. Eligibility criteria included that their disease was well characterized clinically and was likely genetically heterogeneous, the standard of care at the time was to diagnose through targeted genetic testing, the targeted genetic testing included multiple genes, and the existing multigene test had incomplete sensitivity. Both parents had to be available for testing as well, if needed to resolve complex results. In the standard approach, the average number of conventional genetic tests needed for a diagnosis across the cohort was 3, covering an average of 19 genes. The single most common test was chromosome microarray, which revealed a VUS in 6 participants and no diagnostic variants. Outside of molecular genetic testing, a number of participants had chromosome studies, chromosome breakage studies, X-inactivation studies, fluorescent *in situ* hybridization for mosaic trisomy, and PCR for triplet repeat

expansion analysis. None of these tests resulted in a diagnosis. WGS identified diagnostic variants in 41% of individuals, compared to conventional genetic testing that identified a diagnosis for only 24%. All diagnoses made with the standard genetic testing approach were found by WGS, and the additional 18 diagnoses made with WGS included structural and non-exon variants that would not be detectable by traditional methods or whole exome sequencing. The authors concluded that early use of WGS in this cohort would have shortened the diagnostic odyssey, the number of office visits, and eliminated a number of laboratory tests. They also noted that this study was underpowered and used research, not clinically validated, WGS and WES methodologies and further studies and development are needed to ensure that clinically validated WGS is available on a broad scale.

Petrikin et al. (2018) conducted a partially blinded randomized control trial on the clinical utility of rapid whole genome sequencing (rWGS) in neonatal intensive care unit/pediatric intensive care unit patients from October 2014 to June 2016. Eligible patients were <4 months old and had illnesses suggestive of a genetic disease, but were of unknown etiology. The studied intervention was trio rWGS, meaning WGS testing was completed in about 2 days, and was performed on the infant and parents. rWGS results were confirmed by another testing method prior to clinical reporting unless a situation arose where life-threatening progression was likely. There were 129 infants in the study period that were potential candidates, and 65 (50%) were ultimately enrolled. Thirty-two infants were randomized to rWGS plus standard genetic testing, and the remaining 33 had standard genetic testing alone. Standard genetic testing was defined as any genetic test considered standard of care, and therefore available to order through the electronic medical record. During the study period, non-rapid WGS became available, and was considered a standard test. The baseline characteristics of the infants in both groups were similar. The most common indications were congenital anomalies and neurological disorders. In the control group, only 6% of the infants had cardiovascular findings compared to the rWGS group (28%), and this may have impacted the likelihood of genetic disease. Other than newborn screening, the average age at first test order was 14 days. In those that had standard genetic testing, a diagnosis was identified by the test in 23% (7) of test cases, and 24% (8) of controls. The diagnostic rate by type of test included 6% by chromosome microarray, 18% by targeted panel testing, 33% by WES, and 13% by methylation testing. In this group, it is noted that rWGS would not identify 33%, or five of fifteen diagnoses, as four were structural variants and one was a change in DNA methylation not identifiable at the time of this study by rWGS. The median time from test order to diagnosis was 64 days. In the test group, rWGS identified a diagnosis in 31% (10) cases, with a median time to diagnosis of 14 days, which included confirmatory testing. After un-blinding the randomization after 10 days of enrollment, it was requested by participating physicians to allow 7 of the 33 controls to participate in rWGS. It was declined for two patients as they were not acutely ill and about to be discharged. The remaining 5 had rWGS, and 2 received a diagnosis by rWGS that was later confirmed by standard genetic testing that was already being performed. Overall, infants receiving trio rWGS had a higher rate of diagnosis and shorter time to diagnosis than infants receiving standard tests alone. The ability of this study to understand the clinical utility of rWGS was hampered by the cross-over requests after 10 days of enrollment un-blinding, and the increasing availability of targeted panel tests, WES and WGS during the study period as standard tests, which ultimately caused the study to end early. The authors concluded that rWGS trended toward earlier diagnosis in the NICU, prior to discharge, but more studies are needed to determine if a shorter time to diagnosis improves clinical utility, outcomes, or healthcare utilization.

In another view of rWGS in acutely ill infants, Farnaes et al. (2018) provides a retrospective review of inpatients from July 2016 to March 2017. A total of 42 families received rWGS plus standard of care genetic testing for the purpose of diagnosing genetic disorders. Trio testing was performed on 29 cases, 1 quad (parents plus two affected children), 9 duos (mother-infant) and three infants only. The majority of infants in the study were Hispanic/Latino (59%), and were in a neonatal intensive care unit (NICU), pediatric intensive care unit (PICU) or cardiovascular care unit (71%), on respiratory support (76%), and inotropic support (40%). The most common clinical indication was multiple congenital anomalies (29%). There was little consanguinity (2%). In examining the standard genetic testing results, the authors note that 4 infants received a diagnosis from these results. The most common standard test was chromosome microarray, but routine chromosome analysis, fluorescent *in situ* hybridization, and various biochemical tests were also utilized. One infant had a change in care as a result of the diagnosis. rWGS provided a diagnosis in 18 infants. All findings were confirmed through standard genetic tests. Thirteen children had a change in care as a result which included starting new medications (5), discontinuing medications (2), surgical procedures were changed (4). Palliative care was planned for one infant. Overall, the authors concluded that the availability of the rWGS results allowed changes in care that prevented morbidities in 11 of the infants and significant risk reduction in acute mortality in 1 from a medication change. In summary, the authors found that the diagnostic sensitivity in this cohort was 43% for rWGS and 10% for standard genetic testing, and concluded that rWGS may benefit acutely ill inpatient infants as a first tier test, but further studies are needed.

Bowling et al. (2017) report results of WES or WGS on 371 individuals with developmental delay or intellectual disabilities enrolled in the Clinical Sequencing Exploratory Research (CSER) consortium (WES for 127 and WGS for 244) A total of 284 participating families were enrolled with both biological parents and 35 affected individuals had one parent included. Mean age of study participants was 11 years and 58% were male. Affected individuals displayed symptoms described by 333 unique Human Phenotype Ontology terms with over 90% of individuals displaying

intellectual disability, 69% with speech delay, 45% with seizures, and 20% with microcephaly or macrocephaly; 18% had an abnormal brain magnetic resonance imaging (MRI) result and 81% had been subjected to prior genetic testing. Pathogenic or likely pathogenic variants were found in 100 individuals (27%), with variants of uncertain significance in an additional 42 (11%). The pathogenic or likely pathogenic identification rate was not significantly different between WES or WGS ($p = 0.30$) for single nucleotide variants or small insertions or deletions; although WGS can also identify copy number variants.

In a prospective study, Stavropoulos et al. (2016) utilized WGS and comprehensive medical annotation (CMA) to assess 100 patients referred to a pediatric genetics service, and compared the diagnostic yield versus standard genetic testing. WGS identified genetic variants meeting clinical diagnostic criteria in 34% of cases, representing a fourfold increase in diagnostic rate over CMA alone and more than twofold increase in CMA plus targeted gene sequencing. WGS identified all rare clinically significant CNVs that were detected by CMA. In 26 patients, WGS revealed indel and missense mutations presenting in a dominant (63%) or a recessive (37%) manner. The investigators found four subjects with mutations in at least two genes associated with distinct genetic disorders, including two cases harboring a pathogenic CNV and SNV. In the authors' opinion, when considering medically actionable secondary findings in addition to primary WGS findings, 38% of patients would benefit from genetic counselling. While promising, additional studies of WGS as a primary test in comparison to conventional genetic testing and WES are needed.

Bodian et al. (2016) assessed the potential of WGS to replicate and augment results from conventional blood-based newborn screening (NBS). Research-generated WGS data from an ancestrally diverse cohort of 1,696 infants and both parents of each infant were analyzed for variants in 163 genes involved in disorders included or under discussion for inclusion in US NBS programs. WGS results were compared with results from state NBS and related follow-up testing. NBS genes are generally well covered by WGS. There is a median of one (range: 0-6) database-annotated pathogenic variant in the NBS genes per infant. Results of WGS and NBS in detecting 28 state-screened disorders and four hemoglobin traits were concordant for 88.6% of true positives ($n = 35$) and 98.9% of true negatives ($n = 45,757$). Of the five infants affected with a state-screened disorder, WGS identified two whereas NBS detected four. WGS yielded fewer false positives than NBS (0.037 vs. 0.17%) but more results of uncertain significance (0.90 vs. 0.013%). The authors concluded that WGS may help rule in and rule out NBS disorders, pinpoint molecular diagnoses, and detect conditions not amenable to current NBS assays. There is a need for additional studies that compare WGS with traditional NBS methods and evaluate the change in patient management resulting from WGS for newborn screening.

Taylor et al. (2015) conducted a study to assess factors influencing the success of WGS to obtain a genetic diagnosis across a broad range of clinical conditions with no previously identified causal mutation. They sequenced 217 individuals from 156 independent cases or families across a broad spectrum of disorders in which previous screening had identified no pathogenic variants. The investigators quantified the number of candidate variants identified using different strategies for variant calling, filtering, annotation and prioritization. They found that jointly calling variants across samples, filtering against both local and external databases, deploying multiple annotation tools and using familial transmission above biological plausibility contributed to accuracy. Overall, the investigators identified disease-causing variants in 21% of cases, with the proportion increasing to 34% (23/68) for Mendelian disorders and 57% (8/14) in family trios. They also discovered 32 potentially clinically actionable variants in 18 genes unrelated to the referral disorder, although only 4 were ultimately considered reportable. According to the investigators, their results demonstrate the value of genome sequencing for but also highlight many outstanding challenges, including the challenges of interpreting unrelated variants.

Willig et al. (2015) performed a retrospective comparison of rapid whole-genome sequencing (STATseq) and standard genetic testing in a case series from the neonatal and pediatric intensive care units (NICU and PICU) of a large children's hospital. The participants were families with an infant younger than 4 months with an acute illness of suspected genetic cause. The intervention was STATseq of trios (both parents and their affected infant). The main measures were the diagnostic rate, time to diagnosis, and rate of change in management after standard genetic testing and STATseq. Twenty (57%) of 35 infants were diagnosed with a genetic disease by use of STATseq and three (9%) of 32 by use of standard genetic testing. Median time to genome analysis was 5 days (range 3-153) and median time to STATseq report was 23 days. Thirteen (65%) of 20 STATseq diagnoses were associated with de-novo mutations. Impact on clinical management was noted in 13 (65%) of 20 infants with a STATseq diagnosis, four (20%) had diagnoses that led to a clinical intervention and six (30%) were started on palliative care. The 120-day mortality was 57% (12 of 21) in infants with a genetic diagnosis. According to the authors, in selected acutely ill infants, STATseq had a high rate of diagnosis of genetic disorders. The authors indicated that while having a genetic diagnosis altered the management of infants in the NICU or PICU in this single institution; additional studies with a higher patient population are needed to validate the clinical utility of WGS in this patient population.

Soden et al. (2014) reported on one hundred families with 119 children affected by neurodevelopmental disorders (NDD) who had WGS, WES, or WES followed by WGS of parent-child trios, with the sequencing approach guided by acuity of illness. Forty-five percent received molecular diagnoses. An accelerated sequencing modality, rapid WGS,

yielded diagnoses in 73% of families with acutely ill children (11 of 15). Forty percent of families with children with nonacute NDD, followed in ambulatory care clinics (34 of 85), received diagnoses: 33 by WES and 1 by staged WES then WGS. A change in clinical care or impression of the pathophysiology was reported in 49% of newly diagnosed families. According to the authors, if WES or WGS had been performed at symptom onset, genomic diagnoses may have been made 77 months earlier. It is suggested that initial diagnostic evaluation of children with NDD should include trio WGS or WES, with extension of accelerated sequencing modalities to high-acuity patients. According to the authors, this study had several limitations. It was retrospective and lacked a control group. Clinical data were collected principally through chart review, which may have led to under- or overestimates of changes in clinical management. The authors did not ascertain information about long-term consequences of diagnosis, such as the impact of genetic counseling. Comparisons of costs of genomic and conventional diagnostic testing excluded associated costs of testing, such as outpatient visits, and may have included tests that would nevertheless have been performed, irrespective of diagnosis. The acuity-based approach to expedited WGS and non-expedited WES was a patient care-driven approach and was not designed to facilitate direct comparisons between the two methods.

A significant limitation of WGS is that the functional implications of variants outside the exons are relatively unknown (Klein and Foroud, 2017). To date, only a small number of research articles have addressed the clinical utility of WGS. Recently several small studies have addressed the analytical validity of WGS as compared to WES, and found that WGS may provide more uniform coverage than WES, may more accurately detect a small number of variants compared to WES, and be better at identifying copy number variants (Belkadi et al., 2015; Meienberg et al., 2016). However, due to the data complexity, processing time and interpretation time is much greater for WGS than for other NGS approaches (Klein and Foroud, 2017).

WGS-Other (Non-Cancer)

Alfares et al. (2018) examined the clinical utility of whole genome sequencing compare to re-analysis of whole exome sequencing. All cases that underwent CAP accredited CLIA lab WES and WGS in the genetics clinic of King Abdulaziz Medical City between 2013-2017 were examined, regardless of phenotype. WES was performed on either an Illumina NextSeq or HiSeq, or on an Ion Proton system. The average coverage depth was 95X. WGS was performed on a HiSeq 4000. The average coverage depth was 30X. Variant call files (VCF) were obtained for each case, and raw data analysis was performed in cases where the final results showed discrepancies. Discrepancies were classified into three categories; due to the time interval between tests, new discoveries could explain the discrepancy, intronic or large copy number variants may not have been seen due to WES limitations, and finally, the type of sequencing system could have created the discrepancy. Overall, 154 patients were included in the study and had negative comparative genome array results, and had negative or inconclusive WES results. Most were male (56%), pediatric (91%) and consanguineous (70%). Forty six were eventually excluded because WGS results were incomplete, additional testing was required, or WES VCF were not available from prior testing. The remaining 108 patients had complete clinical information and final WES and WGS results available. Of these, 10 patients had positive WGS results with prior negative WES results, and 5 had inconclusive results. The remaining 93 had negative WGS results. The average time between WES testing and WGS testing was only 5 months, and in that time no new clinical information was collected on the 10 positive WGS patients. However, in 3 cases, variants were found in WES, but not reported, because the data that demonstrated their pathogenicity was published after the initial WES was completed. In addition, four cases that had WES performed by the Ion Proton system missed variants that were anticipated to be found by WES. Original raw data files were not available from this lab to determine if the variants were present but filtered out, or if the genes were not adequately covered. Additional WES analysis using the Illumina system in these patients detected these four variants. Overall, only 3 cases were positive by WGS that were completely unidentifiable by WES. The authors concluded that in the final 108 patients, if they had re-analyzed the original WES data, they would have identified 30% of the positive cases, and that WGS only achieved a 7% higher detection rate. It was concluded that for this population re-analysis of WES data before, or in lieu of WGS, may have better clinical utility. Limitations of this study include the small sample size and the high rate of consanguinity, which may have resulted in a disproportionate number of positives on the initial WES test, which could in general limit the utility of WGS in the study population.

Another study that reviewed the utility of WES and WGS was conducted by Carss et al. (2017). The authors studied a cohort of 722 individuals with inherited retinal disease (IRD) who had WES (n=72), WGS (n=605) or both (n=45) as part of the NIHR-BioResource Rare Diseases research study. The diagnoses included in the cohort included retinitis pigmentosa (n = 311), retinal dystrophy (n = 101), cone-rod dystrophy (n = 53), Stargardt disease (n = 45), macular dystrophy (n = 37), and Usher syndrome (n = 37). In the 117 individuals who had WES, 59 (50%) had pathogenic variants identified. Forty five individuals with a negative WES had subsequent WGS, and an additional 14 pathogenic variants were found. In three of these, the variant location was absent from the WES hybrid capture kit. Three individuals had large copy number variants that could not be called by WES, and three others had variants that were found in the WES results, but the quality was poor and they were not called. In the remaining 5 individuals, the variants were also found in WES, but the mode of inheritance was unexpected so WGS was used to exclude other possible causes of the disease. The detection rate varied by phenotype, ranging from 84% in individuals with Usher syndrome to 29% in those with cone dystrophy. Ethnicity also impacted the detection rate. Only 30% of individuals

with African ancestry had cases solved, compared to 55% of European ancestry or 57% of South Asian ancestry. The authors further reviewed benefits of WGS. They noted that 3 individuals had pathogenic, non-coding variants that would not be detected by WES. They compared the IRD genes that were high or low in GC content in their WGS data set to the same genes in the WES ExAC database and concluded that the WGS dataset had consistent coverage whereas the WES data did not. They also noted that in their data set, WGS was better at detecting synonymous variants and variants in regulatory regions compared to WES. Overall the detection rate for WGS was 56% in this cohort. Factors that may influence this study compare to others is the technology used, phenotype screening and phenotypes used. They observed that the subset of people tested who had no prescreening had a higher pathogenic call rate, suggesting that the cohort may have been enriched for difficult cases, and the detection rate for WGS could be higher if used as a first line test. The authors noted that their WES coverage rate was 43X, compared to the >80X recommended for a commercial lab, and that might have influenced the results.

Ellingford et al. (2016) compared the use of next generation gene targeted next generation sequencing (NGS) with WGS in a nested cohort of 46 (of 562) people with inherited retinal disease (IRD). Targeted sequencing and WGS were found to have a similar sensitivity and specificity, but WGS identified an additional 14 clinically relevant variants. If applied to the whole cohort of 562, the authors hypothesized that WGS would provide an overall 29% (95% confidence interval, 15-45) uplift in diagnostic yield. They also noted, however, that creating a more targeted NGS panel would have a similar result.

Cirino et al. (2014) examined the validity of WGS in 41 patients with hypertrophic cardiomyopathy (HCM) who had undergone a HCM targeted next generation sequencing panel test. Twenty of the participants had pathogenic variants identified by targeted sequencing, and WGS detected 19 of them. Three additional variants were found in genes associated with HCM, but these genes are not typically included in HCM targeted sequencing panels. Additionally 84 secondary (incidental) findings were uncovered. The authors concluded that WGS may provide advantages in being able to interrogate more genes, and give the opportunity for re-analysis over time, but noted that expertise in genomic interpretation is required to incorporate into care.

Dewey et al. (2014) conducted a pilot study to determine the resources required to identify and interpret clinically relevant genetic variation using WGS technologies and to evaluate clinical action prompted by WGS findings. An exploratory study of WGS was conducted in 12 adult participants at Stanford University Medical Center between November 2011 and March 2012. A multidisciplinary team reviewed all potentially reportable genetic findings. Five physicians proposed initial clinical follow-up based on the genetic findings. Depending on sequencing platform, 10% to 19% of inherited disease genes were not covered to accepted standards for single nucleotide variant discovery. Genotype concordance was high for previously described single nucleotide genetic variants (99%-100%) but low for small insertion/deletion variants (53%-59%). Curation of 90 to 127 genetic variants in each participant required a median of 54 minutes per genetic variant, resulted in moderate classification agreement between professionals, and reclassified 69% of genetic variants cataloged as disease causing in mutation databases to variants of uncertain or lesser significance. Two to 6 personal disease-risk findings were discovered in each participant, including 1 frameshift deletion in the BRCA1 gene implicated in hereditary breast and ovarian cancer. Physician review of sequencing findings prompted consideration of a median of 1 to 3 initial diagnostic tests and referrals per participant, with fair interrater agreement about the suitability of WGS findings for clinical follow-up. The authors concluded that in this exploratory study of 12 volunteer adults, the use of WGS was associated with incomplete coverage of inherited disease genes, low reproducibility of detection of genetic variation with the highest potential clinical effects, and uncertainty about clinically reportable findings.

Additional peer-reviewed literature on WGS consists primarily of case reports and small case series (Willig et al., 2015; Yuen et al., 2015; Jiang et al., 2013). The limited clinical experience with WGS causes gaps in interpreting variants of uncertain significance or other incidental findings. As a result, the benefits and risks of WGS testing are poorly defined and the role of WGS in the clinical setting has not yet been established.

WGS-Cancer

One hundred and eighty four consecutive patients with cancer were recruited into a study examining the clinical utility of WGS at the Oxford University Hospitals Foundation Trust's Genomics Medicine Center as part of the 100,000 Genomes Project. All patients were undergoing surgical resection, and tissue samples collected from adjacent region tissue blocks were prepared as both fresh frozen (FF) and formalin-fixed, paraffin-embedded (FFPE). Peripheral blood was obtained as a comparator as well. A significant number of samples were lost due to poor quality; 87 had a poor FF sample, and 30 had poor FFPE results. Another 15 patients were excluded at other quality control steps. In the end, a total of 52 cancer patients had a usable trio of sample sets that included ten breast, 12 colorectal, seven endometrial, four prostate, 14 renal, and five thoracic cancers. The quality and quantity of DNA between FF and FFPE was evaluated for these 52 patients, and it was noted that FFPE typically had short, denatured DNA, and resulting sequence data revealed non-uniform coverage. Different results were found between FF and FFPE samples in terms of somatic SNVs and indels detected. There was relatively high agreement in regions that sequence reliably, but lower concordance in regions of complexity, and there were also differences found between different variant software used

(Shimmer vs Stelka). Some of the variability in results were the result of tumor and sampling heterogeneity between FF and FFPE tissues. When considering the possibility of FFPE introducing variation, it was noted that if considering all SNVs and indels and all cancer genes in the COSMIC cancer gene database, FFPE did have more mutations than FF. However, when considering only the most clinically relevant types of mutations, such as exonic and missense, >99% of genes were not more mutation in FFPE than FF samples. Overall, 73 variants in 207 samples in 46 relevant genes were identified, and verified through conformational testing using a different technology. The sensitivity of FF and FFPE were 86% and 82% respectively (Robbe et al., 2018).

Laskin et al. (2015) performed whole genome sequencing on the tumors of 100 individuals with incurable cancer, including 38 with refractory breast cancer, in the Personalized OncoGenomics (POG) study. Testing was completed in 78 patients. Of these, 55 patients received results that were considered "actionable" by a multi-disciplinary team. Twenty three patients received treatment that was driven by WGS results. Turnaround time was a challenge, and at the beginning of the study, results took >80 days to complete. By the end of the study, the results were completed in 50 days. The authors reported that there were limited treatment options available based on results, including even when considering available clinical trials.

Professional Societies

American College of Obstetricians and Gynecologists (ACOG)

In the Committee Opinion 682 (2016), ACOG states that "the routine use of whole-genome or whole-exome sequencing for prenatal diagnosis is not recommended outside of the context of clinical trials until sufficient peer-reviewed data and validation studies are published."

American Academy of Neurology (AAN)/American Association of Neuromuscular and Electrodiagnostic Medicine (AANEM)

The AAN and AANEM have indicated that there is low level evidence to consider WES or WGS in selected individuals with congenital muscular dystrophy in who a genetic variation has not been identified through standard testing approaches. Individuals with congenital muscular dystrophy that do not have causative genetic variations identified through routine methods can be considered for WES or WGS when those technologies are clinically available. Evidence Level C (Kang et al., 2015).

American Society of Human Genetics (ASHG)

ASHG (Botkin et al., 2015) makes the following recommendations pertaining to the genetic testing of children and adolescents:

- Diagnostic testing:
 - Pharmacogenetic testing in children may be appropriate in the context of clear evidence of clinical utility.
 - Genetic testing should be limited to single gene or targeted gene panels based on the patient's clinical presentation when appropriate. When WGS is performed, it is ethically acceptable to limit the analysis to a limited number of genes of interest.
 - Genome-scale sequencing is appropriate when prior, more limited genetic testing has failed to identify a causative variant. Genome-scale sequencing may be appropriate as an initial genetic test under certain circumstances.

American College of Medical Genetics and Genomics (ACMG)/Association for Molecular Pathology (AMP)

ACMG and AMP released guidance to laboratories in 2015 on how to evaluate variations found through next generation sequencing (NGS), including WES and WGS. They also highlighted the responsibility of the ordering provider in the process, stating "due to the complexity of genetic testing, optimal results are best realized when the referring healthcare provider and the clinical laboratory work collaboratively in the testing process".

The guidelines highlight that healthcare providers need to be prepared to provide detailed information on other lab tests performed, clinical evaluations and testing, and patient phenotype. They need to understand that some results returned, such as "variants of unknown significance," may not be actionable, or the clinical implication may be unknown for pathogenic mutations. Testing of additional family members may be required to interpret the test results of the patient. Finally, as new data emerges, the interpretation of a variant may change over time and the healthcare provider must be prepared to monitor and manage changing interpretations. As highlighted by ACMG and AMP, "variant analysis is at present imperfect and the variant category reported does not imply 100% certainty."

American College of Medical Genetics and Genomics (ACMG)

In 2016, the ACMG released an updated policy statement on recommendations for reporting of secondary findings in clinical exome and genome sequencing. Four new genes were added to the list of recommended secondary findings, along with the elimination of one of the earlier genes from the 2013 list. The new, updated secondary findings list includes 59 medically actionable genes recommended for return in clinical genomic sequencing (Kalia et al., 2016).

The ACMG Board of Directors (2012) published a policy statement regarding use of genomic testing that recommends that WGS/WES should be considered in the clinical diagnostic assessment of a phenotypically affected individual when:

- The phenotype or family history data strongly implicate a genetic etiology, but the phenotype does not correspond with a specific disorder for which a genetic test targeting a specific gene is available on a clinical basis.
- A patient presents with a defined genetic disorder that demonstrates a high degree of genetic heterogeneity, making WES or WGS analysis of multiple genes simultaneously a more practical approach.
 - A patient presents with a likely genetic disorder, but specific genetic tests available for that phenotype have failed to arrive at a diagnosis.
 - A fetus with a likely genetic disorder in which specific genetic tests, including targeted sequencing tests, available for that phenotype have failed to arrive at a diagnosis.
 - WGS/WES should not be used at this time as an approach to prenatal screening.
 - WGS/WES should not be used as a first-tier approach for newborn screening.

International Society of Prenatal Diagnosis (ISPD), the Society of Maternal Fetal Medicine (SMFM) and the Perinatal Quality Foundation (PQF) (2018)

In this joint position statement, the ISPD, SMFM and PQF note that routine diagnostic sequencing of the fetus cannot be supported due to insufficient validation data. It is recommended that a research setting where testing is offered on a case by case basis is the best current approach. However, there are some limited scenarios where testing may be beneficial:

- A current pregnancy with a single major anomaly or the multiple anomalies suggesting of a genetic etiology
- Chromosome microarray is negative
- A maternal and/or paternal history of a previous pregnancy with similar anomalies with no diagnosis
- A family history of recurrent stillbirths of unknown etiology

There is no indication for testing in the absence of fetal anomalies.

U.S. FOOD AND DRUG ADMINISTRATION (FDA)

Laboratories that perform genetic tests are regulated under the Clinical Laboratory Improvement Amendments (CLIA) Act of 1988. More information is available at:

<https://www.fda.gov/medicaldevices/deviceregulationandguidance/ivdregulatoryassistance/ucm124105.htm>.

(Accessed May 29, 2019)

No FDA-approved tests for WES or WGS are available at this time.

CENTERS FOR MEDICARE AND MEDICAID SERVICES (CMS)

Medicare does not have a National Coverage Determination (NCD) specifically addressing Whole Exome Sequencing (WES) and Whole Genome Sequencing (WGS) testing. Local Coverage Determinations (LCDs) exist; refer to the LCDs for [Biomarkers for Oncology](#), [Biomarkers Overview](#), [MoIDX: Molecular Diagnostic Tests \(MDT\)](#), [Molecular Diagnostic Tests \(MDT\)](#) and [Molecular Pathology Procedures](#).

(Accessed June 7, 2019)

REFERENCES

Aarabi M, Sniezek O, Jiang H, et al. Importance of complete phenotyping in prenatal whole exome sequencing. *Hum Genet.* 2018 Feb;137(2):175-181.

Alfares A, Aloraini T, Subaie LA, et al. Whole-genome sequencing offers additional but limited clinical utility compared with reanalysis of whole-exome sequencing. *Genet Med.* 2018 Nov;20(11):1328-1333.

American College of Medical Genetics and Genomics (ACMG) Board of Directors. Policy statement. Points to consider in the clinical application of genomic sequencing. May 2012. Available at: <https://www.acmg.net/PDFLibrary/Genomic-Sequencing-Clinical-Application.pdf>. Accessed June 28, 2019.

American College of Obstetricians and Gynecologists (ACOG). Committee on Genetics and the Society for Maternal-Fetal Medicine. Committee Opinion No. 682. Microarrays and next-generation sequencing technology: the use of advanced genetic diagnostic tools in obstetrics and gynecology. *Obstet Gynecol* 128(6): 1462-1463.

Bardakjian TM, Helbig I, Quinn C, et al. Genetic test utilization and diagnostic yield in adult patients with neurological disorders. *Neurogenetics.* 2018 May;19(2):105-110.

Belkadi A, Bolze A, Itan Y, et al. Whole-genome sequencing is more powerful than whole-exome sequencing for detecting exome variants. *Proc Natl Acad Sci USA.* 2015 Apr 28;112(17):5473-8.

Beltran H, Eng K, Mosquera JM, et al. Whole-exome sequencing of metastatic cancer and biomarkers of treatment response. *JAMA Oncol.* 2015 Jul; 1(4):466-74.

Bertier G, Héту M, Joly Y. Unsolved challenges of clinical whole-exome sequencing: a systematic literature review of end-users' views. *BMC Medical Genomics*. 2016 Aug 11;9(1):52.

Bodian DL, Klein E, Iyer RK, et al. Utility of whole-genome sequencing for detection of newborn screening disorders in a population cohort of 1,696 neonates. *Genet Med*. 2016 Mar;18(3):221-30.

Botkin JR, Belmont JW, Berg JS, et al. Points to Consider: Ethical, legal, and psychosocial implications of genetic testing in children and adolescents. *Am J Hum Genet*. 2015 Jul 2;97(1):6-21.

Bowling KM, Thompson ML, Amaral MD, et al. Genomic diagnosis for children with intellectual disability and/or developmental delay. *Genome Med*. 2017 May 30;9(1):43.

Carss KJ, Arno G, Erwood M, et al. Comprehensive rare variant analysis via whole-genome sequencing to determine the molecular pathology of inherited retinal disease. *Am J Hum Genet*. 2017 Jan 5;100(1):75-90.

Ceyhan-Birsoy O, Murry JB, Machini K, et al. Interpretation of genomic sequencing results in healthy and ill newborns: results from the BabySeq Project. *Am J Hum Genet*. 2019 Jan 3;104(1):76-93.

Cirino AL, Lakdawala NK, McDonough B, et al. A comparison of whole genome sequencing to multigene panel testing in hypertrophic cardiomyopathy patients. *Circ Cardiovasc Genet*. 2017 Oct;10(5).

Clark MM, Hildreth A, Batalov S, et al. Diagnosis of genetic diseases in seriously ill children by rapid whole-genome sequencing and automated phenotyping and interpretation. *Sci Transl Med*. 2019 Apr 24;11(489).

Clark MM, Stark Z, Farnaes L, et al. Meta-analysis of the diagnostic and clinical utility of genome and exome sequencing and chromosomal microarray in children with suspected genetic diseases. *NPJ Genom Med*. 2018 Jul 9;3:16.

Dewey FE, Grove ME, Pan C, et al. Clinical interpretation and implications of whole-genome sequencing. *JAMA*. 2014 Mar 12;311(10):1035-45.

Ellingford JM, Barton S, Bhaskar S, et al. Whole genome sequencing increases molecular diagnostic yield compared with current diagnostic testing for inherited retinal disease. *Ophthalmology*. 2016 May;123(5):1143-50.

Ellis MJ, Ding L, Shen D, et al. Whole-genome analysis informs breast cancer response to aromatase inhibition. *Nature*. 2012 Jun 10;486(7403):353-60.

Farnaes L, Hildreth A, Sweeney NM, et al. Rapid whole-genome sequencing decreases infant morbidity and cost of hospitalization. *NPJ Genom Med*. 2018 Apr 4;3:10.

Farwell KD, Shahmirzadi L, El-Khechen D, et al. Enhanced utility of family-centered diagnostic exome sequencing with inheritance model-based analysis: results from 500 unselected families with undiagnosed genetic conditions. *Genet Med*. 2015 Jul;17(7):578-86.

French CE, Delon I, Dolling H, et al. Whole genome sequencing reveals that genetic conditions are frequent in intensively ill children. *Intensive Care Med*. 2019 May;45(5):627-636.

Fu F, Li R, Li Y, et al. Whole exome sequencing as a diagnostic adjunct to clinical testing in fetuses with structural abnormalities. *Ultrasound Obstet Gynecol*. 2018 Apr;51(4):493-502.

Groopman EE, Marasa M, Cameron-Christie S, et al. Diagnostic utility of exome sequencing for kidney disease. *N Engl J Med*. 2019 Jan 10;380(2):142-151.

Green RC, Berg JS, Grody WW, et al.; American College of Medical Genetics and Genomics. ACMG recommendations for reporting of incidental findings in clinical exome and genome sequencing. *Genet Med*. 2013 Jul;15(7):565-74.

Green RC, Goddard KAB, Jarvik GP, et al. Clinical Sequencing Exploratory Research Consortium: accelerating evidence-based practice of genomic medicine. *Am J Hum Genet*. 2016 Jun 2;98(6):1051-1066.

Haskell GT, Adams MC, Fan Z, et al. Diagnostic utility of exome sequencing in the evaluation of neuromuscular disorders. *Neurol Genet*. 2018 Feb 1;4(1):e212.

International Society for Prenatal Diagnosis, Society for Maternal and Fetal Medicine, Perinatal Quality Foundation. Joint position statement from the International Society for Prenatal Diagnosis (ISPD), the Society for Maternal Fetal Medicine (SMFM), and the perinatal Quality Foundation (PQF) on the use of genome-wide sequencing for fetal diagnosis. *Prenat Diagn*. 2018 Jan; 38(1): 6- 9.

Jiang YH, Yuen RK, Jin X, et al. Detection of clinically relevant genetic variants in autism spectrum disorder by whole genome sequencing. *Am J Hum Genet*. 2013 Aug 8;93(2):249-63.

Kalia SS, Adelman K, Bale SJ et al. Recommendations for reporting of secondary findings in clinical exome and genome sequencing, 2016 update (ACMG SF v2.0): a policy statement of the American College of Medical Genetics and Genomics. *Genet Med*. 2017 Feb;19(2):249-255.

Kang PB, Morrison L, Iannaccone ST, et al.; Guideline Development Subcommittee of the American Academy of Neurology and the Practice Issues Review Panel of the American Association of Neuromuscular & Electrodiagnostic

Medicine. Evidence-based guideline summary: evaluation, diagnosis, and management of congenital muscular dystrophy: Report of the Guideline Development Subcommittee of the American Academy of Neurology and the Practice Issues Review Panel of the American Association of Neuromuscular & Electrodiagnostic Medicine. *Neurology*. 2015 Mar 31;84(13):1369-78.

Klein CJ, Foroud TM. Neurology individualized medicine: when to use next-generation sequencing panels. *Mayo Clin Proc*. 2017 Feb;92(2):292-305.

LaDuca H, Farwell KD, Vuong H, et al. Exome sequencing covers >98% of mutations identified on targeted next generation sequencing panels. *PLoS One*. 2017 Feb 2;12(2):e0170843.

Landrum MJ, Lee JM, Benson M, et al. ClinVar: public archive of interpretations of clinically relevant variants. *Nucleic Acids Res*. 2016 Jan 4;44(D1):D862-8.

Laskin J, Jones S, Aparicio S, et al. Lessons learned from the application of whole-genome analysis to the treatment of patients with advanced cancers. *Cold Spring Harb Mol Case Stud*. 2015 Oct;1(1):a000570.

Lata S, Marasa M, Li Y, et al. Whole-exome sequencing in adults with chronic kidney disease: a pilot study. *Ann Intern Med*. 2018 Jan 16;168(2):100-109.

Lee B, Tran B, Hsu AL, et al. Exploring the feasibility and utility of exome-scale tumour sequencing in a clinical setting. *Intern Med J*. 2018 Jul;48(7):786-794.

Lee H, Deignan JL, Dorrani N, et al. Clinical exome sequencing for genetic identification of rare Mendelian disorders. *JAMA*. 2014 Nov 12;312(18):1880-7.

Lionel AC, Costain G, Monfared N, et al. Improved diagnostic yield compared with targeted gene sequencing panels suggests a role for whole-genome sequencing as a first-tier genetic test. *Genet Med*. 2018 Apr;20(4):435-443.

Lord J, McMullan DJ, Eberhardt RY, et al.; Prenatal Assessment of Genomes and Exomes Consortium. Prenatal exome sequencing analysis in fetal structural anomalies detected by ultrasonography (PAGE): a cohort study. *Lancet*. 2019 Feb 23;393(10173):747-757.

Malhotra A, Levine S, Allingham-Hawkins D. Whole exome sequencing for cancer – is there evidence of clinical utility? *Advances in Genomics and Genetics* 2014 Aug 22;4 115–128.

Meienberg J, Bruggmann R, Oexle K, et al. Clinical sequencing: is WGS the better WES? *Hum Genet*. 2016 Mar;135(3):359-62.

Mestek-Boukhibar L, Clement E, Jones WD, et al. Rapid Paediatric Sequencing (RaPS): comprehensive real-life workflow for rapid diagnosis of critically ill children. *J Med Genet*. 2018 Nov;55(11):721-728.

Nambot S, Thevenon J, Kuentz P, et al.; Orphanomix Physicians' Group. Clinical whole-exome sequencing for the diagnosis of rare disorders with congenital anomalies and/or intellectual disability: substantial interest of prospective annual reanalysis. *Genet Med*. 2018 Jun;20(6):645-654.

Nicolson NG, Murtha TD, Dong W, et al. Comprehensive genetic analysis of follicular thyroid carcinoma predicts prognosis independent of histology. *J Clin Endocrinol Metab*. 2018 Jul 1;103(7):2640-2650.

Normand EA, Braxton A, Nassef S, et al. Clinical exome sequencing for fetuses with ultrasound abnormalities and a suspected Mendelian disorder. *Genome Med*. 2018 Sep 28;10(1):74.

Online Mendelian Inheritance in Man, OMIM[®]. McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University (Baltimore, MD). May 2018. Available at: www.omim.org/statistics/geneMap. Accessed May 29, 2019.

Østrup O, Nysom K, Scheie D, et al. Importance of comprehensive molecular profiling for clinical outcome in children with recurrent cancer. *Front Pediatr*. 2018 Apr 20;6:114.

Parsons DW, Roy A, Yang Y, et al. Diagnostic yield of clinical tumor and germline whole-exome sequencing for children with solid tumors. *JAMA Oncol*. 2016 May 1;2(5):616-624.

Petrikin JE, Cakici JA, Clark MM, et al. The NSIGHT1-randomized controlled trial: rapid whole-genome sequencing for accelerated etiologic diagnosis in critically ill infants. *NPJ Genom Med*. 2018 Feb 9;3:6.

Petrovski S, Aggarwal V, Giordano JL, et al. Whole-exome sequencing in the evaluation of fetal structural anomalies: a prospective cohort study. *Lancet*. 2019 Feb 23;393(10173):758-767.

Powis Z, Farwell Hagman KD, Speare V, et al. Exome sequencing in neonates: diagnostic rates, characteristics, and time to diagnosis. *Genet Med*. 2018 Nov;20(11):1468-1471.

Posey JE, Rosenfeld JA, James RA, et al. Molecular diagnostic experience of whole-exome sequencing in adult patients. *Genet Med*. 2016 Jul; 18(7):678-85.

Retterer K, Juusola J, Cho MT, et al. Clinical application of whole-exome sequencing across clinical indications. *Genet Med*. 2016 Jul;18(7):696-704.

Richards S, Aziz N, Bale S, et al.; ACMG Laboratory Quality Assurance Committee. Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. *Genet Med*. 2015 May;17(5):405-24.

Robbe P, Popitsch N, Knight SJL et al.; 100,000 Genomes Project. Clinical whole-genome sequencing from routine formalin-fixed, paraffin-embedded specimens: pilot study for the 100,000 Genomes Project. *Genet Med*. 2018 Oct;20(10):1196-1205.

Sawyer SL, Hartley T, Dymont DA, et al. The Finding Of Rare Disease GENes (FORGE) Canada project. Utility of whole exome sequencing for those near the end of the diagnostic odyssey: time to address gaps in care. *Clin Genet*. 2016 Mar;89(3):275-84.

Saes JL, Simons A, de Munnik SA, et al. Whole exome sequencing in the diagnostic workup of patients with a bleeding diathesis. *Haemophilia*. 2019 Jan;25(1):127-135.

Scocchia A, Wigby KM, Masser-Frye D, et al. Clinical whole genome sequencing as a first-tier test at a resource-limited dysmorphology clinic in Mexico. *NPJ Genom Med*. 2019 Feb 14;4:5.

S, Biswas S, Li MH, et al. Utility and limitations of exome sequencing as a genetic diagnostic tool for children with hearing loss. *Genet Med*. 2018 Dec;20(12):1663-1676.

Soden SE, Saunders CJ, Willig LK, et al. Effectiveness of exome and genome sequencing guided by acuity of illness for diagnosis of neurodevelopmental disorders. *Sci Transl Med*. 2014 Dec 3;6(265):265ra168.

Sohn I, Jung WY, Sung CO. Somatic hypermutation and outcomes of platinum based chemotherapy in patients with high grade serous ovarian cancer. *Gynecol Oncol*. 2012 Jul;126(1):103-8.

Smith HS, Swint JM, Lalani SR, et al. Clinical application of genome and exome sequencing as a diagnostic tool for pediatric patients: a scoping review of the literature. *Genet Med*. 2019 Jan;21(1):3-16.

Stark Z, Lunke S, Brett GR, et al.; Melbourne Genomics Health Alliance. Meeting the challenges of implementing rapid genomic testing in acute pediatric care. *Genet Med*. 2018 Dec;20(12):1554-1563.

Stark Z, Tan TY, Chong B, et al. A prospective evaluation of whole-exome sequencing as a first-tier molecular test in infants with suspected monogenic disorders. *Genet Med*. 2016 Nov;18(11):1090-1096.

Stavropoulos DJ, Merico D, Jobling R, et al. Whole genome sequencing expands diagnostic utility and improves clinical management in pediatric medicine. *NPJ Genom Med*. 2016 Jan 13;1. pii:15012.

Taber JM, Klein WM, Ferrer RA, et al. Dispositional optimism and perceived risk interact to predict intentions to learn genome sequencing results. *Health Psychol*. 2015 Jul;34(7):718-28.

Tan TY, Dillon OJ, Stark Z, et al. Diagnostic impact and cost-effectiveness of whole-exome sequencing for ambulant children with suspected monogenic conditions. *JAMA Pediatr*. 2017 Sep 1;171(9):855-862.

Tarailo-Graovac M, Shyr C, Ross CJ, et al. Exome sequencing and the management of neurometabolic disorders. *N Engl J Med*. 2016 Jun 9;374(23):2246-55.

Taylor JC, Martin HC, Lise S, et al. Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. *Nat Genet*. 2015 Jul;47(7):717-726.

Thun M, Linet MS, Cerhan JR, et al. *Cancer Epidemiology and Prevention*. 4th Edition. New York, NY. Oxford University Press, 2017.

Trujillano D, Bertoli-Avella AM, Kandaswamy KK, et al. Clinical exome sequencing: results from 2819 samples reflecting 1000 families. *Eur J Hum Genet*. 2017 Feb;25(2):176-182.

Tzoneva G, Perez-Garcia A, Carpenter Z, et al. Activating mutations in the NT5C2 nucleotidase gene drive chemotherapy resistance in relapsed ALL. *Nat Med*. 2013 Mar;19(3):368-71.

U.S. National Library of Medicine. What are whole exome sequencing and whole genome sequencing? Genetics Home Reference. May 2018. Available at: <https://ghr.nlm.nih.gov/primer/genomicresearch/sequencing>. Accessed May 29, 2019.

U.S. National Library of Medicine. What is a gene? Genetics Home Reference. May 2018. Available at: <https://ghr.nlm.nih.gov/primer/basics/gene>. Accessed May 29, 2019.

Valencia CA, Husami A, Holle J, et al. Clinical impact and cost-effectiveness of whole exome sequencing as a diagnostic tool: a pediatric center's experience. *Front Pediatr*. 2015 Aug 3;3:67.

Vissers LELM, van Nimwegen KJM, Schieving JH, et al. A clinical utility study of exome sequencing versus conventional genetic testing in pediatric neurology. *Genet Med*. 2017 Sep;19(9):1055-1063.

Willig LK, Petrikin JE, Smith LD, et al. Whole-genome sequencing for identification of Mendelian disorders in critically ill infants: a retrospective analysis of diagnostic and clinical findings. *Lancet Respir Med*. 2015 May;3(5):377-87.

Worst BC, van Tilburg CM, Balasubramanian GP, et al. Next-generation personalised medicine for high-risk paediatric cancer patients - The INFORM pilot study. *Eur J Cancer*. 2016 Sep;65:91-101.

Yang Y, Muzny DM, Xia F, et al. Molecular findings among patients referred for clinical whole-exome sequencing. *JAMA*. 2014 Nov 12;312(18):1870-9.

Yuen RK, Thiruvahindrapuram B, Merico D, et al. Whole-genome sequencing of quartet families with autism spectrum disorder. *Nat Med*. 2015 Feb;21(2):185-91.

Zegers-Hochschild F, Adamson GD, Dyer S, et al. The International glossary on infertility and fertility care, 2017. *Fertil Steril*. 2017 Sep;108(3):393-406.

Zhang, J, Walsh MF, Wu G, et al. Germline mutations in predisposition genes in pediatric cancer. *N Engl J Med*. 2015 Dec 10;373(24):2336-2346.

POLICY HISTORY/REVISION INFORMATION

Date	Action/Description
09/01/2019	<p>Related Policies</p> <ul style="list-style-type: none"> Added reference link to the Medical Policy titled <i>Preimplantation Genetic Testing</i> <p>Coverage Rationale</p> <ul style="list-style-type: none"> Simplified content Revised coverage criteria for Whole Exome Sequencing (WES); replaced criterion requiring: <ul style="list-style-type: none"> "<i>The clinical presentation or clinical and family history strongly suggest a genetic cause for which a specific clinical diagnosis cannot be made with any clinically available targeted genetic tests</i>" with "<i>clinical and/or family history strongly suggest a genetic cause for which a specific clinical diagnosis cannot be made with any clinically available targeted genetic tests</i>" "<i>There is a clinical diagnosis of a genetic condition where there is significant genetic heterogeneity and WES is a more practical approach to identifying the underlying genetic cause than are individual tests of multiple genes</i>" with "<i>there is a clinical diagnosis of a genetic condition that can be caused by multiple genes and WES is a more practical approach to identifying the underlying genetic cause than are individual tests of multiple genes</i>" <p>Supporting Information</p> <ul style="list-style-type: none"> Updated <i>Description of Services, Clinical Evidence, CMS, and References</i> sections to reflect the most current information Archived previous policy version 2019T0589F

INSTRUCTIONS FOR USE

This Medical Policy provides assistance in interpreting UnitedHealthcare standard benefit plans. When deciding coverage, the member specific benefit plan document must be referenced as the terms of the member specific benefit plan may differ from the standard plan. In the event of a conflict, the member specific benefit plan document governs. Before using this policy, please check the member specific benefit plan document and any applicable federal or state mandates. UnitedHealthcare reserves the right to modify its Policies and Guidelines as necessary. This Medical Policy is provided for informational purposes. It does not constitute medical advice.

This Medical Policy may also be applied to Medicare Advantage plans in certain instances. In the absence of a Medicare National Coverage Determination (NCD), Local Coverage Determination (LCD), or other Medicare coverage guidance, CMS allows a Medicare Advantage Organization (MAO) to create its own coverage determinations, using objective evidence-based rationale relying on authoritative evidence ([Medicare IOM Pub. No. 100-16, Ch. 4, §90.5](#)).

UnitedHealthcare may also use tools developed by third parties, such as the MCG™ Care Guidelines, to assist us in administering health benefits. UnitedHealthcare Medical Policies are intended to be used in connection with the independent professional medical judgment of a qualified health care provider and do not constitute the practice of medicine or medical advice.