Beckwith-Wiedemann Syndrome: \textit{H19} and \textit{LIT1} Methylation Panel

\textbf{Test Code:} BW  
\textbf{Turnaround time:} 3 weeks  
\textbf{CPT Codes:} 81401 x1

\section*{Condition Description}

Beckwith-Wiedemann syndrome (BWS) is a growth disorder. Clinical features commonly include: macrosomia (large body size), macroglossia (enlarged tongue), omphalocele, neonatal hypoglycemia, ear creases/pts, adrenocortical cyto-mergaly, and renal abnormalities (e.g., medullary dysplasia, nephrocalcinosis, medullary sponge kidney, and nephromegaly). Polyhydramnios may be identified during pregnancy. Infants with BWS have an approximately 20\% mortality rate, mainly caused by complications of prematurely, omphalocele, and/or hypoglycemia. Macroglossia and macrosomia are generally present at birth but may have postnatal onset. The growth rate slows around seven to eight years of age. Hemihyperplasia may affect segmental regions of the body or selected organs and tissues. In addition, individuals with BWS are at an increased risk of developing embryonal tumors (e.g., Wilms tumor, hepatoblastoma, neuroblastoma, rhabdomyosarcoma). Development and intelligence are typically unaffected, with the exception of mild speech delay in some individuals with severe macroglossia.

Defects in imprinted gene expression at 11p15 are associated with BWS \cite{1,2}. Greater than 70\% of cases are found to have alterations in DNA methylation at two distinct differentially methylated regions (DMRs) at 11p15. DMR1 is located within the telomeric domain (also known as ICR1) and controls the expression of two genes, \textit{IGF2} and \textit{H19}. DMR2 is located within the centromeric domain (also known as ICR2) and controls the expression of the \textit{KCNQ1}, \textit{CDKN1C}, \textit{SLC22A1L} and \textit{TSSC3} genes. Alterations in DNA methylation at either of these DMRs causes aberrant expression of these imprinted genes leading to Beckwith-Wiedemann syndrome.

BWS is typically sporadic, though inheritance has also been reported in an autosomal dominant pattern, due to other mutations. No single explanation can account for the phenotypic heterogeneity seen in patients with BWS. The recurrence risk due to methylation defects is estimated to be low.

\begin{itemize}
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\end{itemize}

\section*{Genes}
\textit{H19}, \textit{LIT1}

\section*{Indications}
This test is indicated for:
\begin{itemize}
\item Individuals with a clinical diagnosis of Beckwith-Wiedemann syndrome.
\item Individuals with isolated segmental hemihyperplasia.
\end{itemize}

\section*{Methodology}
Methylation-specific MLPA (MS-MLPA) is used to test for BWS. One advantage of MS-MLPA is that in addition to detecting DNA methylation abnormalities (epimutations), similar to Southern blot and quantitative methylation sensitive PCR, it also detects deletions and duplications (CNVs) of the 11p15 region. CNVs are estimated to be present in ~10\% of patients with BWS. The presence of a CNV can increase the recurrence risk from that of the general population up to a 50\% risk. Both methylation and CNVs will be reported from this analysis.

\section*{Detection}
Hypomethylation of DMR2 (LIT1 gene) is expected to detect up to 60-70\% of individuals with BWS. Hypermethylation of DMR1 (H19 gene) is expected to detect an additional 2-13\% of individuals with BWS. Therefore, the total detection rate for both DMR1 and DMR2 methylation analysis is estimated to be 62-83\%.

\section*{Reference Range}
For DMR1 (H19 gene), an increase in DNA methylation of greater than two standard deviations above the mean of normal is consistent with BWS. For DMR2 (LIT1 gene), a decrease in DNA methylation of greater than two standard deviations below the mean of normal is consistent with BWS. See Coffee et al. for explanation of reference range \cite{3}.

\section*{Specimen Requirements}
Submit only 1 of the following specimen types

\begin{itemize}
\item Type: DNA, Isolated
\end{itemize}

\begin{itemize}
\item Specimen Requirements: 
Microtainer
\end{itemize}
3µg
Isolation using the Perkin Elmer™ Chemagen™ Automated Extraction method or Qiagen™ Puregene kit for DNA extraction is recommended.

Specimen Collection and Shipping:
Refrigerate until time of shipment in 100 ng/µL in TE buffer. Ship sample at room temperature with overnight delivery.

Type: Whole Blood (EDTA)

Specimen Requirements:
EDTA (Purple Top)
Infants and Young Children (2 years of age to 10 years old): 3-5 ml
Older Children & Adults: 5-10 ml
Autopsy: 2-3 ml unclotted cord or cardiac blood

Specimen Collection and Shipping:
Ship sample at room temperature for receipt at EGL within 24 hours of collection. Do not refrigerate or freeze.

Related Tests

- Chromosome analysis (CA, CB) and array CGH (VA) are available for children with growth disorders and congenital anomalies with or without mental retardation.
- Methylation for DMR1 (H19 gene) or DMR2 (Lit1 gene) alone is available.