

## Russell-Silver Syndrome: *H19* Methylation

**Test Code:** RT

**Turnaround time:** 3 weeks

**CPT Codes:** 81401 x1

### Condition Description

Russell-Silver syndrome (RSS) is a disorder of growth characterized by intrauterine growth retardation with postnatal growth deficiency. Many patients have diminished subcutaneous fat and may experience hypoglycemia during infancy. Short stature typically presents between 2 and 10 years and is proportional. Bone age may be delayed. Serum growth hormone levels are typically normal and patients generally have normal growth velocity. Limb length asymmetry is common, and isolated relative hemiasymmetry, due to underdevelopment of the affected side, is reported. Children may be at risk for motor delays and learning disabilities, however typically do not have mental retardation. Other symptoms include gastrointestinal and genitourinary dysfunction. Gastroesophageal reflux is most common; however, esophagitis and food aversions are also reported. Many patients are considered failure to thrive. Congenital genitourinary disorders have been reported. Additional features include fifth finger clinodactyly, brachydactyly, and multiple cafe au lait spots. Suggested criteria for diagnosis include the following:

- IUGR with birth weight 2SD below the mean
- Postnatal growth 2SD below the mean for length
- Proportional short stature with preservation of occipitofrontal head circumference
- Facial features include prominent forehead, small triangular face, and narrow chin
- Limb, body, or facial asymmetry
- Additional features that can be diagnostically helpful include fifth finger clinodactyly, brachydactyly, cafe au lait spots, and arm span less than height

RSS is a heterogenous disorder that may represent a clinical spectrum rather than a discrete clinical entity. The occurrence of RSS is thought to be sporadic in most cases, and is seen in all racial and ethnic groups. Defects in gene expression are associated with RSS. It is estimated that between 20-35% of RSS are due to hypomethylation of the differentially methylated region (DMR1) at the *H19* gene (located on chromosome 11p15). The recurrence risk of RSS due to hypomethylation of *H19* is estimated to be very low. Approximately 10% of RSS is due to maternal uniparental disomy (UPD) for chromosome 7. Some forms of RSS are inherited in autosomal dominant or autosomal recessive patterns, for which genes have not been identified. No single explanation can account for the phenotypic heterogeneity seen in patients with RSS.

#### References:

1. Price, S.M.; Stanhope, R.; Garrett, C.; Preece, M.A.; Trembath, R.C.: The spectrum of Silver-Russell syndrome: a clinical and molecular genetic study and new diagnostic criteria. *J. Med. Genet.* 36: 837-842, 1999.
2. Gicquel, C.; Rossignol, S.; Cabrol, S.; Houang, M.; Steunou, V.; Barbu, V.; Danton, F.; Thibaud, N.; Le Merrer, M.; Burglen, L.; Bertrand, A.M.; Netchine, I.; Le Bouc, Y. Epimutation of the telomeric imprinting center region on chromosome 11p15 in Silver-Russell syndrome. *Nature Genet.* 37: 1003-1007, 2005.
3. Eggermann, T.; Schonherr, N.; Meyer, E.; Obermann, C.; Mavany, M.; Eggermann, K.; Ranke, M. B.; Wollmann, H. A.: Epigenetic mutations in 11p15 in Silver-Russell syndrome are restricted to the telomeric imprinting domain. (Letter) *J. Med. Genet.* 43: 615-616, 2006.

### Genes

#### [H19](#)

### Indications

This test is indicated for:

- Individuals with a clinical diagnosis of RSS.
- Individuals with limb asymmetry combined with prenatal and postnatal growth delay.

### Methodology

Methylation-specific MLPA (MS-MLPA) is used to test for hypomethylation of DMR1 at 11p15 for RSS. One advantage of MS-MLPA is that it not only detects DNA methylation abnormalities (epimutations), similar to Southern blot and quantitative methylation sensitive PCR, but it will also detect deletions and duplications (CNVs) of the 11p15 region. 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.

### Detection

Hypomethylation of *H19* is expected to detect up to 35% of individuals with a clinical diagnosis of SRS.

### Reference Range

Normal methylation range of *H19* was determined by quantifying DNA methylation in a cohort of normal individuals (see Coffee et al. *Genet Med.* 8:628-634 2006). The mean methylation index (MI, or the amount of methylated DMR1 DNA divided by methylated and unmethylated DMR1 DNA) was 0.49 with a standard deviation of 0.08, resulting in normal MI range of 0.33-0.65 (mean 2 standard deviations).

### Specimen Requirements

**Submit only 1 of the following specimen types**

**Type: DNA, Isolated****Specimen Requirements:**

Microtainer

3µg

Isolation using the Perkin Elmer™ Chemagen™ 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 &amp; 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 72 hours of collection. Do not freeze.

**Related Tests**

- Standard Chromosome Analysis (Test Codes: CA, CB) and EmArray Cyto (Test Code: VA) are available for children with growth and developmental delay.