



EpiSign V3 List of disorders and genes.

Unique Multi-locus Epigenetic Signatures

Imprinting Abnormalities

Angelman syndrome

Beckwith-Wiedemann syndrome

Diabetes Mellitus, transient neonatal 1

Fragile X syndrome

Kagami-Ogata syndrome

Mulchandani-Bhoj-Conlin syndrome

Prader-Willi syndrome

Pseudohypoparathyroidism, Type 1A-1C

Russell-Silver syndrome 1

Russell-Silver syndrome 2

Temple syndrome

Related Region or Gene(s)

15q11.2 methylation abnormality

11p15 imprinting abnormality

PLAGL1 imprinting abnormality

FMR1 methylation abnormality

MEG3 imprinting abnormality

20q11-q13 imprinting abnormality involving
GNAS complex locus

15q11.2 methylation abnormality

20q13.32 imprinting abnormality involving
GNAS complex locus

11p15 imprinting abnormality

UPD 7 imprinting abnormality

MEG3 imprinting abnormality

Conditions with Strong Signatures

7q11.23 duplication
AD Cerebellar Ataxia, Deafness, Narcolepsy (ADCADN)
Alpha-thalassemia X-linked Intellectual Disability
BAFopathy 1: including Coffin-Siris syndrome & Nicolaides-Baraitser ¹
BAFopathy 2: Coffin-Siris syndrome 1 & 2
Beck-Fahrner syndrome ^{3,4}
Blepharophimosis Intellectual Disability SMARCA2 syndrome
CHARGE syndrome
Coffin-Siris syndrome-4
Cornelia de Lange syndrome ²
Down syndrome
Dystonia-28
Epileptic Encephalopathy, childhood-onset
Floating-Harbor syndrome
Gabriele-de Vries syndrome
Helsmoortel-Van der Aa syndrome
Hunter-McAlpine syndrome

Intellectual development disorder with seizures and language delay
Intellectual Disability, X-linked syndromic, Claes-Jensen type ³
Intellectual Disability, X-linked syndromic, Nascimento-type
Kabuki syndrome 1 & 2
KDM2B-related syndrome
Kleefstra syndrome
Koolen-De Vries syndrome
Luscan-Lumish syndrome
Menke-Hennekam syndrome 1 & 2 (IDR4 domain only)
Myopathy, lactic acidosis, and sideroblastic anemia-2
Phelan-McDermid syndrome
PRC2 complex disorders: Weaver & Cohen-Gibson syndromes
Rahman syndrome
Rubinstein-Taybi syndrome 1
Rubinstein-Taybi syndrome 2
Sotos syndrome 1
Velocardiofacial syndrome
Wiedemann-Steiner syndrome
Williams-Beuren syndrome
Wolf-Hirschhorn syndrome

Related Region or Gene(s)

7q11.23 duplication (Chr7:72,745,0470-74,138,460)
DNMT1
ATRX
ARID1A, *ARID1B*, *SMARCB1*, *SMARCA4*, *SMARCA2*
ARID1A (c.6133-c.6254), *ARID1B* (c.6133-c.6254)
TET3
SMARCA2
CHD7
SMARCA4 (c.2656)
NIPBL, *RAD21*, *SMC3*, *SMC1A*
Trisomy 21
KMT2B
CHD2
SRCAP
YY1
ADNP
5q35.2q35.3 duplication
(Chr5:175,728,979-177,047,793) involving *NSD1*
SETD1B
KDM5C
UBE2A
KDM6A, *KMT2D*
KDM2B
EHMT1
KANSL1
SETD2
CREBBP (c.5563-5614), *EP300* (c.5471-5495)
YARS2
22q13.3 deletion (Chr22:45,277,036-51,244,566)
EZH2, *EED*
HIST1H1E
CREBBP
EP300
NSD1
22q11.2 deletion (Chr22: 16,888,899-21,915,509)
KMT2A
7q11.23 deletion (Chr7:72,744,455-74,142,510)
4p16.3 deletion (Chr4:331,568-2,010,962)
involving *NSD2*

■ Genes/conditions listed in blue are new signatures for EpiSign version 3.

Conditions with Moderate Signatures

Arboleda-Tham syndrome

Austism, susceptibility to, 18

Borjeson-Forsman-Lehmann syndrome

Coffin-Siris syndrome 9

Genitopatellar syndrome

Immunodeficiency-centromeric instability-facial anomalies syndrome, type 1

Immunodeficiency-centromeric instability-facial anomalies syndrome, types 2-4

Intellectual Developmental Disorder, autosomal dominant 65

Intellectual Developmental Disorder, X-linked, syndromic, Armfield type

Intellectual Disability, autosomal dominant 23

Intellectual Disability, autosomal dominant 51 ³

Intellectual Disability, X-linked 93 ³

Intellectual Disability, X-linked 97

Renpenning syndrome

SBBYS syndrome

Snyder-Robinson syndrome

Tatton-Brown-Rahman syndrome

Related Region or Gene(s)

KAT6A

CHD8

PHF6

SOX11

KAT6B

DNMT3B

CDCA7, ZBTB24, HELLS

KDM4B

FAM50A

SETD5

KMT5B

BRWD3

ZNF711

PQBP1

KAT6B

SMS

DNMT3A

¹Patients with variants in other BAFopathy genes may be detected, but this finding has not been confirmed.

²*HDAC8* for males may also be detected, but this finding has not been confirmed.

³Healthy carriers and those with incomplete penetrance are detectable.

⁴Patients with biallelic variants are distinguishable from those with monoallelic variants.

Note: All coordinates are based on human genome build hg19.

Disclaimer: *Some conditions/genes have been classified as having more moderate signatures based on signature strength, small cohort size, or types of mutations.* Females tested for X-linked conditions may have a moderate signature or a potentially false negative result. As with many clinical tests, uncertain results are possible. Please note that a normal result does not rule out the possibility that the patient is affected with one of these conditions. In some case, specific follow-up testing may be suggested to confirm or rule out a diagnosis.