Appendix

Table 1. Conditions Only Available as Targeted Episignature Analysis by Request

*Reduced sensitivity and/or specificity may be observed.

Conditions	Related regions/genes
Coffin-Siris syndrome 12*	BICRA*
Desanto-Shinawi syndrome	WAC
Developmental delay with or without dysmorphic facies and autism	TRRAP (only for variants p.960-p.1159)
Diamond-Blackfan anemia 1*	RPS19*
Diamond-Blackfan anemia 5*	RPL35A*
Fetal Valproate syndrome	Not applicable
Hypercholesterolemia, familial, 1	LDLR
Sensitivity against other hereditary hypercholesterolemia disorders has not been evaluated.	Both monoallelic and biallelic cases are detected.
Hypermethioninemia with deficiency of S-adenosylhomocysteine hydrolase	AHCY
Intellectual developmental disorder with dysmorphic facies and behavioral abnormalities	FBXO11
Intellectual developmental disorder, autosomal dominant 57	TLK2
Intellectual developmental disorder, X-linked 112*	ZMYM3* (male cases only)
Intellectual developmental disorder, X-linked syndromic, Siderius type	PHF8 (male cases only)
KMT2C-related syndrome*	KMT2C*
Neurodevelopmental-craniofacial syndrome with variable renal and cardiac abnormalities	ZMYM2
Neurofibromatosis, type 1*	NF1*
NOTCH1 associated syndrome*	NOTCH1*
PHF12-related syndrome	PHF12
Recurrent constellations of embryonic malformations	Not applicable
Includes cases with phenotypic presentation of OAV, OAVV, VACTERL and VATER.	
Schuurs-Hoeijmakers syndrome*	PACS1*
SETD1A-related syndrome	SETD1A
Tessadori-Bicknell-van Haaften neurodevelopmental syndrome 1, 3 and 4	H4C3, H4C4, H4C5, H4C9

Table 2. Complete Episignature Analysis I: Fragile X Syndrome and Imprinting Disorders

Conditions	Related regions/genes
Angelman syndrome (AS)	15q11.2-q13 (SNRPN promoter, SNURF)
The SNRPN promoter is sensitive but not specific for AS and only report	ed with a positive result for SNURF.
Prader-Willi syndrome (PWS)	15q11.2-q13 (SNRPN promoter, SNURF)
The SNRPN promoter is sensitive but not specific for PWS and only repo	rted with a positive result for SNURF.
Beckwith-Wiedemann syndrome	11p15.5 (IC1 and IC2)
Silver Russel syndrome 1 & 2	11p15.5 (IC1 and IC2), 7q32.2
Diabetes mellitus, transient neonatal 1	6q24 (PLAGL1)
Fragile X syndrome	FMR1 promoter
Kagami-Ogata syndrome	14q32 (MEG3 promoter)
Mulchandani-Bhoj-Conlin syndrome	20q11-q13 (GNAS)
Multi-locus imprinting disturbances	All EpiSign imprinting regions
Only positive sites will be reported.	
Pseudohypoparathyroidism IA & IB	20q11-q13 (GNAS)
Temple syndrome	14q32 (MEG3 promoter)

Table 3. Complete Episignature Analysis II: Single Gene and Chromosomal Disorders

*Reduced sensitivity may be observed. All genomic coordinates are provided in accordance with GRCh37/hg19.

Conditions	Related Regions/Genes	
Alpha-thalassemia/Impaired intellectual development syndrome, X-linked	ATRX (male cases only)	
Arboleda-Tham syndrome*	KAT6A*	
ARID1A duplication-related syndrome*	ARID1A dup* (Chr1: 26,964,202-27,099,490)	
CNVs overlapping or expanding this region may also be detected.		
BAFopathies: Coffin-Siris syndrome (CSS) 1-4 & Nicolaides-Baraitser syndromes	ARID1A, ARID1B, SMARCB1, SMARCA4, SMARCA2	
•Coffin-Siris syndrome 1*	ARID1B*	
Coffin-Siris syndrome 2*	ARID1A*	
•Coffin-Siris syndrome 3*	SMARCB1*	
•Coffin-Siris syndrome 4*	SMARCA4*	
Nicolaides-Baraitser syndrome*	SMARCA2*	
 Secondary signatures must also be positive for BAFopathy. Patients with other BAFopathy genes may be detected, but not confirmed. 		
BAFopathies: Coffin-Siris syndrome 1 & 2 (only for variants near c.6200)	ARID1A, ARID1B (near c.6200 in both genes)	

No separate episignature due to small cohort size, however these samples cluster se Coffin-Siris syndrome 6	ARID2
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Beck-Fahrner syndrome	TET3
Healthy carriers and those with incomplete penetrance are detectable. Patients with biallelic v	SMARCA2
Blepharophimosis-impaired intellectual development syndrome	SMARCAZ
Börjeson-Forssman-Lehmann, Chung-Jansen and White Kernohan syndromes	PHIP, PHF6, DDB1
(CHU_BFL_WHI)	20156*/
Börjeson-Forssman-Lehmann syndrome*	PHF6* (male cases only)
•Chung-Jansen syndrome*	PHIP*
•White-Kernohan syndrome*	DDB1*
Secondary signatures must also be positive for CHU_BFL_WHI. Provided to the description of the second state of the secon	
Branchial arch abnormalities, choanal atresia, athelia, hearing loss, and	KMT2D* (only for variants within p.3400-p.3700)
hypothyroidism syndrome*	DAIA 474 *
Cerebellar ataxia, deafness, and narcolepsy, autosomal dominant*	DNMT1*
CHARGE syndrome	CHD7
Chromosome 1p36 deletion syndrome*	1p36 del* (Chr1: 1,019,753-2,867,961)
CNVs overlapping or expanding this region may also be detected.	
Chromosome 19p13.13 deletion syndrome	19p13.13p13.2 del (Chr19: 13,201,983-13,213,144)
CNVs overlapping or expanding this region may also be detected. Only for CNVs. NFI.	
Chromosome Xp11.22 duplication syndrome*	Xp11.22 dup* (ChrX: 53,559,057-53,654,518)
CNVs overlapping or expanding this region may also be detected. Male cases only.	TDIDAG
Clark-Baraitser syndrome	TRIP12
Congenital heart defects, dysmorphic facial features, and Intellectual DD*	CDK13*, CCNK*
Cornelia de Lange syndromes (CdLs) 1-4	NIPBL, RAD21, SMC3, SMC1A
 Cornelia de Lange syndrome 1* 	NIPBL*
 Cornelia de Lange syndrome 2* 	SMC1A*
 Cornelia de Lange syndrome 3* 	SMC3*
 Cornelia de Lange syndrome 4* 	RAD21*
Male CdLS5 patients (HDAC8 mutations) may be detected, but not confirmed. •	
DEGCAGS syndrome	ZNF699
Heterozygotes have been shown to not match the episignature.	
Developmental and epileptic encephalopathy 54	HNRNPU
Developmental and epileptic encephalopathy 94	CHD2
Developmental delay with variable intellectual disability and dysmorphic facies*	JARID2*
Diets-Jongmans syndrome	KDM3B
Down syndrome	Trisomy 21
Dystonia 28, childhood-onset	KMT2B
Fanconi anemia	FANCA, FANCC, FANCD2, FANCG, FANCI, FANCL
Heterozygotes have been shown to not match the episignature. Patients with other	
Floating Harbour syndrome	SRCAP
Gabriele-de Vries syndrome*	YY1*
Genitopatellar syndrome (GTPTS)* and Ohdo syndrome, SBBYSS variant*	KAT6B*
Since GTPTS and SBBYSS are both caused by variants in KAT6B, it is recommended to	request both episianatures for VUS assessment.
Hao-Fountain syndrome	USP7
Helsmoortel-van der Aa syndrome Central episignature	ADNP (only for variants within c.2054-c.2340)
Helsmoortel-van der Aa syndrome_Terminal episignature	ADNP (outside of c.2054-c.2340)
Hunter McAlpine craniosynostosis syndrome	5q35 dup involving NSD1 (Chr5:175839681-176904798)
CNVs overlapping or expanding this region may also be detected.	3433 dup involving N3D1 (Cili3.173639661-176904796)
Immunodeficiency-centromeric instability-facial anomalies syndrome 1*	DNMT3B*
Immunodeficiency-centromeric instability-facial anomalies syndrome 2-4*	CDCA7*, ZBTB24*, HELLS*
Intellectual developmental disorder (IDD) with autism and macrocephaly*	CHD8*
IDD with dysmorphic facies, speech delay, and T-cell abnormalities*	BCL11B*
IDD with microcephaly and with or without ocular malformations or	SOX11*
hypogonadotropic hypogonadism*	
Intellectual developmental disorder with seizures and language delay	SETD1B
Intellectual developmental disorder, autosomal dominant 7	DYRK1A
Intellectual developmental disorder, autosomal dominant 21	CTCF
IDD, autosomal dominant 23; KBGS syndrome (KBGS_MRD23)	SETD5, ANKRD11
•IDD, autosomal dominant 23 (MRD23)*	SETD5*
•KBG syndrome*	ANKRD11*
 Secondary signatures must also be positive for KBGS_MRD23. 	
Intellectual developmental disorder, autosomal dominant 51*	KMT5B*
· · · · · · · · · · · · · · · · · · ·	
Healthy carriers and those with incomplete penetrance are detectable.	
Healthy carriers and those with incomplete penetrance are detectable. Intellectual developmental disorder, X-linked 93*	BRWD3*

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Intellectual developmental disorder, X-linked 97*	ZNF711*
Intellectual developmental disorder, X-linked syndromic, Nascimento type*	UBE2A* (male cases only)
Intellectual developmental disorder, X-linked, syndromic, Snyder-Robinson type*	SMS*
Intellectual developmental disorder, X-linked, syndromic, Armfield type*	FAM50A* (male cases only)
Intellectual developmental disorder, X-linked, syndromic, Claes-Jensen type	KDM5C
Healthy carriers and those with incomplete penetrance are detectable. Heterozygotes	, , , , ,
Kabuki syndrome 1 & 2	KMT2D, KDM6A
•Kabuki syndrome 1*	KMT2D*
•Kabuki syndrome 2*	KDM6A*
•Secondary signatures must also be positive for Kabuki syndrome 1 &2.	
KDM2B-related syndrome	KDM2B
Kleefstra syndrome 1	EHMT1
Klinefelter syndrome	ChrX duplication; 47,XXY
XXX and XYY cases may also be detected.	
Koolen de Vreis syndrome	KANSL1
Luscan-Lumish syndrome	SETD2
Menke-Hennekam syndrome 1 & 2	CREBBP, EP300
Only for domain ID4. MKHK1 & MKHK2 exhibit a shared ID4 domain episignature and	therefore cannot be distinguished. Other domains of MKHK1/2
are not available.	
Mowat-Wilson syndrome	ZEB2
MSL2-related syndrome*	MSL2*
Neurodevelopmental disorder with dysmorphic facies and behavioral abnormalities	SRSF1
Neurodevelopmental disorder with hypotonia, stereotypic hand movements, and	MEF2C
impaired language	WIEI 2C
Neuroocular syndrome*	PRR12*
Healthy carriers and those with incomplete penetrance are detectable.	
NSD2 duplication-related syndrome	NSD2 dup (Chr4: 1,832,733-1,975,031)
CNVs overlapping or expanding this region may also be detected.	
Phelan-McDermid syndrome	22q13.3 del (Chr22: 49,238,268-50,248,907)
CNVs overlapping or expanding this region may also be detected. Only for CNVs. SHAP	NK3 sequence variants do not match the episignature.
Pitt-Hopkins syndrome	TCF4
Potocki-Lupski syndrome*	17p11.2 dup* (Chr17:16,779,412-20,231,379)
CNVs overlapping or expanding this region may also be detected.	
PRC2 complex disorders (Weaver and Cohen-Gibson syndromes)	EZH2, EED
Shared episignature between PRC2 complex syndromes WVS & COGIS. Imagawa-Matsumoto s	syndrome cases with variants in SUZ12 have also been detected.
Rahman syndrome	H1-4
Renpenning syndrome*	PQBP1* (male cases only)
Rubinstein-Taybi syndrome 1 and 2 (RSTS 1&2)	CREBBP, EP300
•Rubinstein-Taybi syndrome 1	CREBBP
•Rubinstein-Taybi syndrome 2	EP300
 Secondary signatures must also be positive for RSTS 1 &2. 	
Sifrim-Hitz-Weiss syndrome	CHD4
SLC32A1-related syndrome*	SLC32A1*
Smith-Magenis syndrome	17p11.2 del (Chr17: 17,322,913-18,515,769)
CNVs overlapping or expanding this region may also be detected. Only for CNVs. RAI1	I sequence variants do not match the episignature.
Sotos syndrome	NSD1
Tatton-Brown-Rahman syndrome*	DNMT3A*
Turner syndrome	ChrX deletion; 45,X
Velocardiofacial syndromeEpisignature Analysis by Methylation Array Appendix	22 44 2 1 1/01 22 12 12 12 12 12 12 12 12 12 12 12 12
Table	22q11.2 del (Chr22: 19,510,547-20,285,090)
CNVs overlapping or expanding these regions may be detected.	
CNVs overlapping or expanding these regions may be detected. White-Sutton syndrome	POGZ
	POGZ ZC4H2* (male cases only)
White-Sutton syndrome	
White-Sutton syndrome Wieacker-Wolff syndrome* Wiedemann-Steiner syndrome	ZC4H2* (male cases only) KMT2A
White-Sutton syndrome Wieacker-Wolff syndrome* Wiedemann-Steiner syndrome Williams-Beuren region duplication syndrome	ZC4H2* (male cases only)
White-Sutton syndrome Wieacker-Wolff syndrome* Wiedemann-Steiner syndrome	ZC4H2* (male cases only) KMT2A 7q11.23 dup (Chr7: 73,953,518-74,138,459)
White-Sutton syndrome Wieacker-Wolff syndrome* Wiedemann-Steiner syndrome Williams-Beuren region duplication syndrome CNVs overlapping or expanding this region may also be detected. Williams-Beuren syndrome	ZC4H2* (male cases only) KMT2A
White-Sutton syndrome Wieacker-Wolff syndrome* Wiedemann-Steiner syndrome Williams-Beuren region duplication syndrome CNVs overlapping or expanding this region may also be detected.	ZC4H2* (male cases only) KMT2A 7q11.23 dup (Chr7: 73,953,518-74,138,459)
White-Sutton syndrome Wieacker-Wolff syndrome* Wiedemann-Steiner syndrome Williams-Beuren region duplication syndrome CNVs overlapping or expanding this region may also be detected. Williams-Beuren syndrome CNVs overlapping or expanding 7q11.23 may also be detected. Witteveen-Kolk syndrome*	ZC4H2* (male cases only) KMT2A 7q11.23 dup (Chr7: 73,953,518-74,138,459) 7q11.23 deletion SIN3A*
White-Sutton syndrome Wieacker-Wolff syndrome* Wiedemann-Steiner syndrome Williams-Beuren region duplication syndrome CNVs overlapping or expanding this region may also be detected. Williams-Beuren syndrome CNVs overlapping or expanding 7q11.23 may also be detected.	ZC4H2* (male cases only) KMT2A 7q11.23 dup (Chr7: 73,953,518-74,138,459) 7q11.23 deletion SIN3A* 4p16.3 del involving NSD2 (Chr4: 679,715-2,169,001)