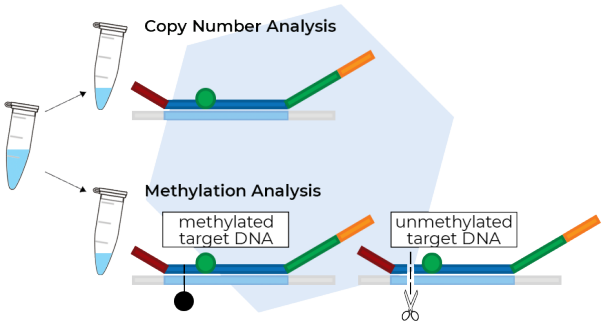
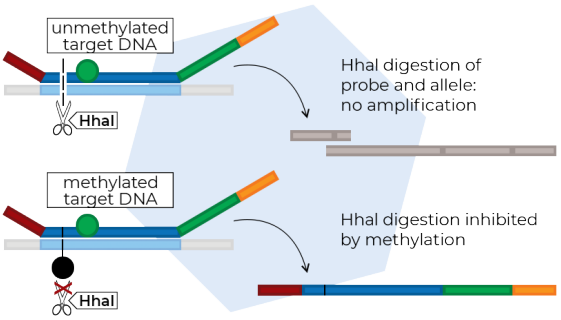
Methylation-Specific MLPA
Bisulfite-free methylation analysis

Methylation-Specific MLPA (MS-MLPA) is a variant of the SALSA® MLPA® technique, the gold standard in copy number determination. Combining MLPA with the methylation-sensitive endonuclease HhaI allows for the detection of both DNA copy number and methylation status. With MS-MLPA, simultaneous semi-quantitative methylation profiling of multiple targets is accomplished easily and without bisulfite treatment.

The Principle of MS-MLPA

MLPA probes hybridise to their target sequences on the sample DNA. The MLPA reaction is then split into two: a reaction for copy number analysis, and a reaction for methylation analysis, to which the methylation-sensitive HhaI restriction enzyme is added. HhaI digests the *unmethylated* DNA-probe complexes .





Digested MLPA probes lose the binding site for the fluorescent PCR primer and hence do not generate a signal. In contrast, DNA-probe complexes in which the DNA target is *methylated* are protected from HhaI digestion and *do* generate a signal. By comparing the copy number and the methylation reaction, the average methylation status can be calculated for the sample and target of interest.

Methylation-Specific Probemixes for Tumour Profiling

SALSA MLPA Probemix	Application
ME001 Tumour suppressor mix	Methylation profiling for 25 tumour suppressor genes.
ME011 Mismatch Repair Genes	*MLH1* methylation, *BRAF* p.V600E point mutation and associated Lynch syndrome genome changes profiling.
ME012 MGMT-IDH-TERT	Targeted glioma profiling including *MGMT* methylation and *IDH1/2* mutation detection.
ME024 9p21 CDKN2A/2B region	Cell cycle regulator profiling on 9p21 region associated with multiple tumour types including melanoma.
ME042 CIMP	CpG Island Methylator Phenotype profiling (CIMP).
P047 RB1	*RB1* promoter and imprinted locus methylation profiling, and *RB1* gene single exon level copy number detection.
ME053 BRCA1-BRCA2-RAD51C	Targeted methylation profiling of *BRCA1*, *BRCA2* and *RAD51C* promoter regions in germline or somatic DNA.

Methylation-Specific Probemixes for Imprinting Disorders

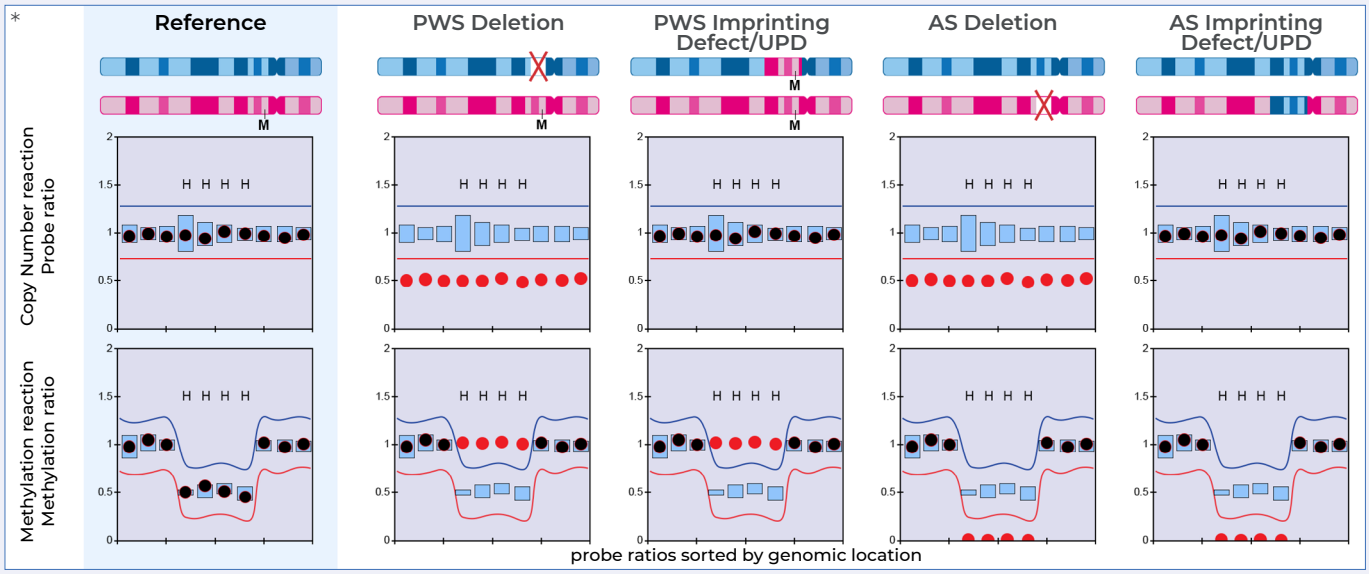
SALSA MLPA Probemix	Application
ME028 Prader-Willi/Angelman	Imprinting disorder profiling for Prader-Willi, Angelman and 15q11 duplication syndromes.
ME029 FMR1/AFF2	Fragile X syndrome associated promoter methylation profiling for male samples.
ME030 BWS/RSS	Imprinting disorder profiling for Beckwith-Wiedemann and Russell-Silver syndromes.
ME031 GNAS	Imprinting disorder profiling for Albright hereditary osteodystrophy and pseudohypoparathyroidism.
ME032 UPD7-UPD14	Imprinting disorder profiling for UPD7, RSS, UPD14 (Temple & Kagami-Ogata syndromes).
ME033 TNDM	Imprinting disorder profiling for Transient Neonatal Diabetes Mellitus (TNDM).
ME034 Multi-locus Imprinting	Multilocus imprinting disturbance profiling; distinguishing maternal from paternal triploidies.

Application Highlight: Imprinting Disorders

MS-MLPA is used worldwide to assess methylation status in imprinting disorders such as Prader-Willi/Angelman and Beckwith-Wiedemann/Russell-Silver syndromes. These syndromes can be caused not only by genomic alterations, but also by imprinting defects such as those caused by uniparental disomy (UPD). MS-MLPA examines both genomic and epigenomic aspects in one simple test.

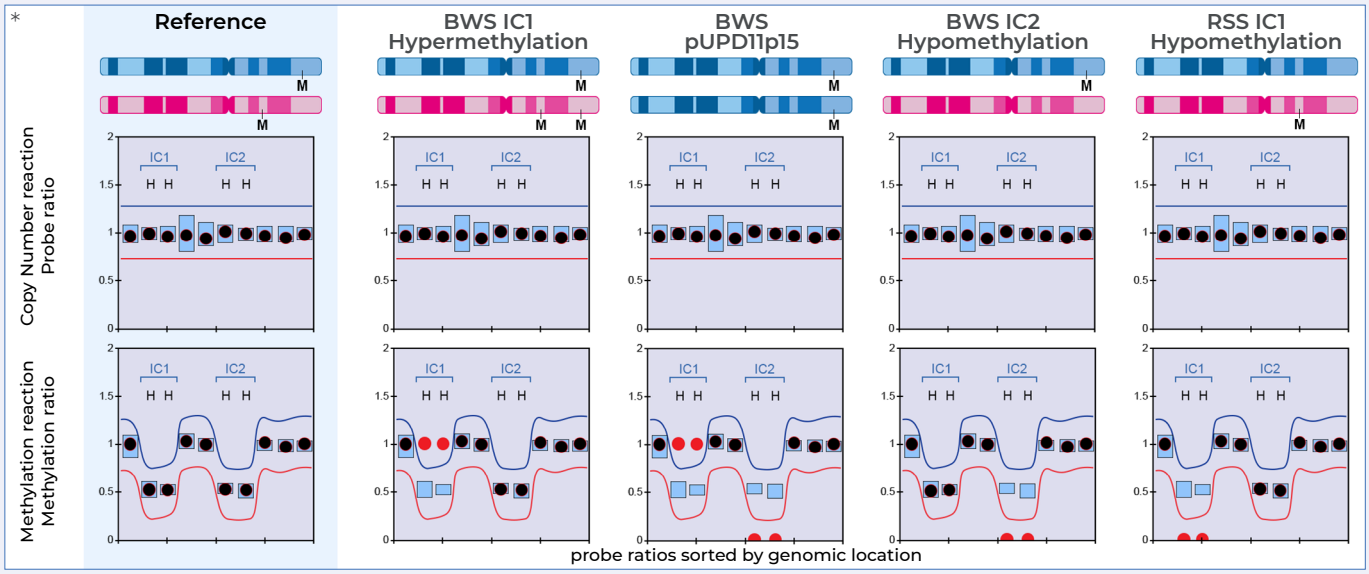
Prader-Willi and Angelman syndromes - analysis by ME028 PWS/AS

SALSA® MLPA® Probemix ME028 Prader-Willi/Angelman contains over 40 probes for copy number quantification of the 15q11 region critical for Prader-Willi and Angelman syndromes. In addition, five methylation-sensitive probes enable the methylation profiling of this same region.



Beckwith-Wiedemann and Russell-Silver syndromes - analysis by ME030 BWS/RSS

SALSA® MLPA® Probemix ME030 BWS/RSS contains over 40 probes used for copy number quantification of the 11p15 region that is critical for Beckwith-Wiedemann and Russell-Silver syndromes. In addition, eight methylation-sensitive probes enable the methylation profiling of the H19DMR/IC1 and KvDMR/IC2 domains in this same region.



* *Images are a simplified representation and do not show all probes.*
M *Targeted methylation site*
H *Target probe with an HhaI site*

Normal probe ratio distribution based on reference samples
Probe Ratio - not aberrant
Probe Ratio - aberrant

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