Product Description SALSA® MLPA® Probemix P116-B2 SGC

To be used with the MLPA General Protocol.

Version B2. As compared to version B1, one reference probe has been replaced and several probe lengths have been adjusted. For complete product history see page 8.

Catalogue numbers:
- **P116-025R:** SALSA MLPA Probemix P116 SGC, 25 reactions.
- **P116-050R:** SALSA MLPA Probemix P116 SGC, 50 reactions.
- **P116-100R:** SALSA MLPA Probemix P116 SGC, 100 reactions.

To be used in combination with a SALSA MLPA reagent kit, available for various number of reactions. MLPA reagent kits are either provided with FAM or Cy5.0 dye-labelled PCR primer, suitable for Applied Biosystems and Beckman capillary sequencers, respectively (see www.mlpa.com).

Certificate of Analysis: Information regarding storage conditions, quality tests, and a sample electropherogram from the current sales lot is available at www.mlpa.com.

Precautions and warnings: For professional use only. Always consult the most recent product description AND the MLPA General Protocol before use: www.mlpa.com. It is the responsibility of the user to be aware of the latest scientific knowledge of the application before drawing any conclusions from findings generated with this product.

General Information: The SALSA MLPA Probemix P116 SGC is a **research use only (RUO)** assay for the detection of deletions or duplications in the *SGCA*, *SGCB*, *SGCD*, *SGCG* and *FKRP* genes, which are associated with Limb-Girdle Muscular Dystrophy. This Probemix can also be used to detect the presence of the *FKRP* L276I point mutation.

Limb-Girdle Muscular Dystrophy (LGMD) is characterised by loss of muscle bulk and strength in patients. The distal muscles are affected late in LGMD, if affected at all. LGMD is typically an inherited disorder, though it may be inherited as a dominant, recessive or X-linked genetic defect. The muscle cells of patients with LGMD cannot properly form the proteins needed for normal muscle function. Defects of different proteins are involved in LGMD, each related to a specific type of muscular dystrophy.

Autosomal recessive LGMD is a genetically heterogeneous disorder. Of the many genes that can result in this disorder, the following genes are present in the P116 SGC probemix:

Gene	Number of exons	Number of probes	Length	Location	LGMD type
SGCA	10 exons	11¬	9.9 kb	17q21	LGMD2D
SGCB	6 exons	6	17.6 kb	4q12	LGMD2E
SGCD	9 exons	9	441.0 kb	5q33	LGMD2F
SGCG	8 exons	8	144.2 kb	13q12	LGMD2C
FKRP	4 exons	5§	12.5 kb	19q13	LGMD2I

¬ This includes a flanking probe located downstream of the *SGCA* gene.
§ This includes a probe specific for the *FKRP* L276I mutation. This probe will only generate a signal when the mutation is present.

More information is available at https://www.ncbi.nlm.nih.gov/books/NBK1408/

This SALSA MLPA Probemix is not CE/FDA registered for use in diagnostic procedures. Purchase of this product includes a limited license for research purposes.

Gene structure and Transcript variants:
Entrez Gene shows transcript variants of each gene: http://www.ncbi.nlm.nih.gov/sites/entrez?db=gene
For NM_ mRNA reference sequences: http://www.ncbi.nlm.nih.gov/sites/entrez?db=nucleotide
Locus Reference Genomic (LRG) database: http://www.lrg-sequence.org/

Probemix content: The SALSA MLPA Probemix P116-B2 SGC contains 48 MLPA probes with amplification products between 130 and 492 nt. This includes one probe specific for the *FKRP* L276I mutation which will only generate a signal when the mutations is present. In addition, nine reference probes are included and detect nine different autosomal chromosomal locations. Complete probe sequences and the identity of the genes detected by the reference probes is available online (www.mlpa.com).

This Probemix contains nine quality control fragments generating amplification products between 64 and 121 nt: four DNA Quantity Fragments (Q-fragments), two DNA Denaturation Fragments (D-fragments), one benchmark fragment, and one chromosome X and one chromosome Y-specific fragment (see table below). More information on how to interpret observations on these control fragments can be found in the MLPA General Protocol and online at www.mlpa.com.

Length (nt)	Name
64-70-76-82	Q-fragments (Only visible with <100 ng sample DNA)
88-96	D-fragments (Low signal of 88 or 96 fragment indicates incomplete denaturation)
92	Benchmark fragment
100	X-fragment (X chromosome specific)
105	Y-fragment (Y chromosome specific)

No DNA controls results in only five major peaks shorter than 121 nucleotides (nt): four Q-fragments at 64, 70, 76 and 82 nt, and one 19 nt peak corresponding to the unused portion of the fluorescent PCR primer. Non-specific peaks longer than 121 nt AND with a height >25% of the median of the four Q-fragments should not be observed. Note: peaks below this 25% threshold are not expected to affect MLPA reactions when sufficient amount of sample DNA (50-200 ng) is used.

MLPA technique: The principles of the MLPA technique (Schouten et al. 2002) are described in the MLPA General Protocol (www.mlpa.com).

Required specimens: Extracted DNA, free from impurities known to affect MLPA reactions. For more information please refer to the section on DNA sample treatment found in the MLPA General Protocol.

Reference samples: All samples tested, including reference DNA samples, should be derived from the same tissue type, handled using the same procedure, and prepared using the same DNA extraction method when possible. Reference samples should be derived from unrelated individuals who are from families without a history of LGMD. More information regarding the selection and use of reference samples can be found in the MLPA General Protocol.

Positive control DNA samples: MRC-Holland cannot provide positive DNA samples. Inclusion of a positive sample in each experiment is recommended. Coriell Biobank (https://catalog.coriell.org) and DSMZ (https://www.dsmz.de/home.html) have a diverse collection of biological resources which may be used as a positive control DNA sample in your MLPA experiments. The quality of cell lines can change, therefore samples should be validated before use.

SALSA Binning DNA SD030: The SD030 Binning DNA provided with this Probemix can be used as Binning DNA sample for binning of the *FKRP* L276I mutation-specific probe (FKPR probe 11373-L13479). SD030 Binning DNA is a mixture of genomic DNA from healthy individuals and plasmid DNA that contains the target sequence detected by the above mentioned probe. Inclusion of one reaction with 5 µl SD030 Binning DNA in initial MLPA experiments is essential as it can be used to aid in data binning of the peak pattern using Coffalyser.Net software. Furthermore, Binning DNA should be included in the experiment whenever changes have been applied to the set-up of the capillary electrophoresis device (e.g. when capillaries have been renewed). Binning DNA should never be used as a reference sample in the MLPA data analysis, neither should it be used in quantification of mutation signal, as for this purpose true mutation positive patient

samples or cell lines should be used. It is strongly advised to use DNA sample and reference DNA samples extracted with the same method and derived from the same source of tissue. For further details, please consult the SD030 Binning DNA product description provided. **This product is for research use only (RUO).**

Data analysis: Coffalyser.Net software should be used for data analysis in combination with the appropriate lot-specific MLPA Coffalyser sheet. For both, the latest version should be used. Coffalyser.Net software is freely downloadable at www.mlpa.com. Use of other non-proprietary software may lead to inconclusive or false results. For more details on MLPA quality control and data analysis, including normalisation, see the Coffalyser.Net Reference Manual.

Interpretation of results: The standard deviation of all probes in the reference samples should be <0.10 and the dosage quotient (DQ) of the reference probes in the patient samples should be between 0.80 and 1.20. When these criteria are fulfilled, the following cut-off values for the DQ of the probes can be used to interpret MLPA results for autosomal or pseudo-autosomal chromosomes:

Copy Number status	Dosage quotient
Normal	0.80 < DQ < 1.20
Homozygous deletion	DQ = 0
Heterozygous deletion	0.40 < DQ < 0.65
Heterozygous duplication	1.30 < DQ < 1.65
Heterozygous triplication/ Homozygous duplication	1.75 < DQ < 2.15
Ambiguous copy number	All other values

- Arranging probes according to chromosomal location facilitates interpretation of the results and may reveal more subtle changes such as those observed in mosaic cases. Analysis of parental samples may be necessary for correct interpretation of complex results.
- False positive results: Please note that abnormalities detected by a single probe (or multiple consecutive probes) still have a considerable chance of being a false positive result. Incomplete DNA denaturation (e.g. due to salt contamination) can lead to a decreased probe signal, in particular for probes located in or near a GC-rich region. The use of an additional purification step or an alternative DNA extraction method may resolve such cases. Additionally, contamination of DNA samples with cDNA or PCR amplicons of individual exons can lead to an increased probe signal (Varga et al. 2012). Analysis of an independently collected secondary DNA sample can exclude these kinds of contamination artefacts.
- Normal copy number variation in healthy individuals is described in the database of genomic variants: http://dgv.tcag.ca/dgv/app/home. Users should always consult the latest update of the database and scientific literature when interpreting their findings.
- Not all abnormalities detected by MLPA are pathogenic. In some genes, intragenic deletions are known that result in very mild or no disease (Schwartz et al. 2007). For many genes, more than one transcript variant exists. Copy number changes of exons that are not present in all transcript variants may not have clinical significance. Duplications that include the first or last exon of a gene (e.g. exons 1-3) might not result in inactivation of that gene copy.
- Copy number changes detected by reference probes are unlikely to have any relation to the condition tested for.

Limitations of the procedure:

- In most populations, the major cause of genetic defects in the LGMD-related genes are small (point) mutations, most of which will not be detected by using SALSA® MLPA® Probemix P116 SGC.
- MLPA cannot detect any changes that lie outside the target sequence of the probes and will not detect copy number neutral inversions or translocations. Even when MLPA did not detect any aberrations, the possibility remains that biological changes in that gene or chromosomal region *do* exist but remain undetected.
- Sequence changes (e.g. SNPs, point mutations, small indels) in the target sequence detected by a probe can cause false positive results. Mutations/SNPs (even when >20 nt from the probe ligation site) can reduce the probe signal by preventing ligation of the probe oligonucleotides or by destabilising the binding of a probe oligonucleotide to the sample DNA.

Confirmation of results: Copy number changes detected by only a single probe always require confirmation by another method. An apparent deletion detected by a single probe can be due to e.g. a mutation/polymorphism that prevents ligation or destabilises the binding of probe oligonucleotides to the DNA sample. Sequence analysis can establish whether mutations or polymorphisms are present in the probe target sequence. The finding of a heterozygous mutation or polymorphism indicates that two different alleles of the sequence are present in the sample DNA and that a false positive MLPA result was obtained.

Copy number changes detected by more than one consecutive probe should be confirmed by another independent technique such as long range PCR, qPCR, array CGH or Southern blotting, whenever possible. Deletions/duplications of more than 50 kb in length can often be confirmed by FISH.

Please report copy number changes detected by the reference probes, false positive results due to SNPs and unusual results (e.g., a duplication of *SGCA* exons 6 and 8 but not exon 7) to MRC-Holland: info@mlpa.com.

Table 1. SALSA MLPA Probemix P116-B2 SGC

Length (nt)	SALSA MLPA probe	Chromosomal position (hg18)					
		reference	*SGCA*	*SGCB*	*SGCD*	*SGCG*	*FKRP*
64-105	Control fragments – see table in probemix content section for more information						
130	Reference probe 00797-L13645	5q31					
136	**SGCA probe** 11367-L12092		**Exon 8**				
142	**SGCG probe** 03387-L02780					**Exon 1**	
148	**SGCA probe** 03372-L02765		**Exon 2**				
154	Reference probe 15163-L16938	3q27					
160	**SGCB probe** 04611-L02767			**Exon 3**			
172	**SGCA probe** 03373-L13241		**Exon 9**				
178	**SGCG probe** 03388-L20658					**Exon 2**	
184	**SGCB probe** 03375-L20659			**Exon 5**			
190	**SGCB probe** 11368-L12093			**Exon 6**			
196 «	**SGCB probe** 17268-L20690			**Exon 1**			
202	**SGCD probe** 03376-L12512				**Exon 1**		
208	**SGCD probe** 11369-L12094				**Exon 2**		
214	Reference probe 08940-L09035	11p15					
222 «	**FKRP probe** 11370-L20320						**Exon 2**
228	**SGCG probe** 03390-L02783					**Exon 4**	
232	**SGCD probe** 11371-L13242				**Exon 8**		
238	**SGCD probe** 03377-L02770				**Exon 3**		
245	Reference probe 08677-L08689	13q32					
252	**SGCA probe** 11372-L12899		**Exon 6**				
259 § «	**FKRP probe** 11373-L13479						**L276I mut**
265	**SGCG probe** 03391-L12902					**Exon 5**	
274	**SGCD probe** 03378-L02771				**Exon 4**		
280 ¥	**SGCD probe** 21678-L31529				**Exon 6**		
285	Reference probe 05387-L21105	12p11					
292	**SGCA probe** 11374-L12099		**Exon 1**				
301 ±	**SGCG probe** 03392-L02785					**Exon 6**	
310	**SGCD probe** 03379-L02772				**Exon 5**		
320	**SGCA probe** 11375-L12901		**Exon 4**				
328	Reference probe 09571-L10025	22q13					
337	**SGCG probe** 03393-L13243					**Exon 7**	
343	**SGCB probe** 11376-L12101			**Exon 2**			
355	**SGCA probe** 11377-L12102		**Exon 5**				
362 ¬	**COL1A1 probe** 07983-L07764		**Downstream**				
373	**SGCG probe** 03394-L02787					**Exon 8**	
381	**SGCD probe** 03380-L04677				**Exon 7**		
388	**SGCD probe** 03381-L04694				**Exon 9**		
396	**SGCA probe** 11378-L20660		**Exon 10**				
403	Reference probe 04960-L20661	1p22					
409 «	**FKRP probe** 11379-L12104						**Exon 3**
418 «	**FKRP probe** 11380-L12105						**Exon 4**
427	**SGCA probe** 11381-L12106		**Exon 7**				
432 ¥	**SGCB probe** 21891-L12107			**Exon 4**			
445	Reference probe 10370-L09644	6q27					
454	**SGCA probe** 11383-L12108		**Exon 3**				
471 «	**FKRP probe** 11384-L21239						**Exon 1**
481	**SGCG probe** 11620-L20322					**Exon 3**	
492 *	Reference probe 18547-L24044	9q34					

* New in version B2 (from lot B2-1218 onwards).

¥ Changed in version B2 (from lot B2-1218 onwards). Small change in length, no change in sequence detected.

§ Mutation-specific probe. This probe will only generate a signal when the L276I mutation is present. It has been tested on artificial DNA **but not on positive human samples!**

« Probe located in or near a GC-rich region. A low signal can be caused by salt contamination in the DNA sample leading to incomplete DNA denaturation, especially of GC-rich regions.

¬ Flanking probe. Included to help determine the extent of a deletion/duplication. Copy number alterations of only the flanking or reference probes are unlikely to be related to the condition tested.

± SNP rs114160429 mutation could influence the probe signal. In case of apparent deletions, it is recommended to sequence the region targeted by this probe.

Table 2. P116 probes arranged according to chromosomal location

Table 2a. *SGCA*

Length (nt)	SALSA MLPA probe	*SGCA* exon	Ligation site NM_000023.2	Partial sequence (24 nt adjacent to ligation site)	Distance to next probe
		start codon	*37-39 (exon 1)*		
292	11374-L12099	Exon 1	60-61	CTCTTCTGGACT-CCTCTCCTCGTG	1.4 kb
148	03372-L02765	Exon 2	155-156	TGTGCACACCTT-GGACCATGAGAC	0.3 kb
454	11383-L12108	Exon 3	323-324	TGCCACCCCAGA-AGATCGTGGGCT	0.3 kb
320	11375-L12901	Exon 4	377-378	GGACAGCTTTGA-TACCACTCGGCA	0.5 kb
355	11377-L12102	Exon 5	492-493	CTGCCCTCAACA-CCTGCCAGCCGC	0.8 kb
252	11372-L12899	Exon 6	739-740	CTTGCTACGACA-CCTTGGCACCCC	1.1 kb
427	11381-L12106	Exon 7	902-903	CTTCTTGGTGGA-TGCTCTGGTCAC	0.4 kb
136	11367-L12092	Exon 8	1011-1012	AGAGACCTGGCT-ACCTCCGAGTGA	4.7 kb
172	03373-L13241	Exon 9	1129-1130	CCATGTTCAATG-TGCACACAGGTG	0.4 kb
396	11378-L20660	Exon 10	1239-1238, reverse	GAGAAGGGAGGA-TGAAGTCAGGGC	9.3 kb
		stop codon	*1198-1200 (exon 9)*		
362 ¬	07983-L07764	*COL1A1*		AAGACACAGGAA-ACAATGTATTGT	

¬ Flanking probe. Included to help determine the extent of a deletion/duplication. Copy number alterations of only the flanking or reference probes are unlikely to be related to the condition tested.

Note: The exon numbering used in this P116-B2 SGC product description is the exon numbering from the RefSeq transcript NM_000023.2, which is identical to the LRG_203 sequence. The exon numbering and NM sequence used is from 12/2018, but can be changed (e.g. by NCBI) after the release of the product description. Please notify us of any mistakes: info@mlpa.com.

Table 2b. *SGCB*

Length (nt)	SALSA MLPA probe	*SGCB* exon	Ligation site NM_000232.4	Partial sequence (24 nt adjacent to ligation site)	Distance to next probe
		start codon	*61-63 (exon 1)*		
196 «	17268-L20690	Exon 1	163 nt before exon 1, reverse	GGCGCGTTGTAT-TGCACAGGGGCC	5.0 kb
343	11376-L12101	Exon 2	200-201	ATACATTCCGAT-TGATGAAGATCG	3.8 kb
160	04611-L02767	Exon 3	396-397	CGATTTAAGCAA-GTATCTGACATG	0.9 kb
432 ¥	21891-L12107	Exon 4	533-534	TGTAGAAAACAA-CAAAACTTCTAT	0.9 kb
184	03375-L20659	Exon 5	764-765	TGTATTCATTAT-GGGCAAAACCAT	4.0 kb
190	11368-L12093	Exon 6	948-949	GGGACGCTCTTC-AAGGTGCAAGTA	
		stop codon	*1015-1017 (exon 6)*		

¥ Changed in version B2 (from lot B2-1218 onwards). Small change in length, no change in sequence detected.
« Probe located in or near a GC-rich region. A low signal can be caused by salt contamination in the DNA sample leading to incomplete DNA denaturation, especially of GC-rich regions.

Note: The exon numbering used in this P116-B2 SGC product description is the exon numbering from the RefSeq transcript NM_000232.4, which is identical to the LRG_204 sequence. The exon numbering and NM sequence used is from 12/2018, but can be changed (e.g. by NCBI) after the release of the product description. Please notify us of any mistakes: info@mlpa.com.

Table 2c. *SGCD*

Length (nt)	SALSA MLPA probe	*SGCD* exon	Ligation site NM_000337.5	Partial sequence (24 nt adjacent to ligation site)	Distance to next probe
		start codon	*520-522 (exon 2)*		
202	03376-L12512	Exon 1	349-350	CTGACTGGGGCA-GCTTCTGAGCGC	2.5 kb
208	11369-L12094	Exon 2	1 nt after exon 2	AGGTGGAGATGG-TGAGTAATTCCC	15.0 kb
238	03377-L02770	Exon 3	564-565	AGCACCATGCCT-GGCTCTGTGGGG	164.2 kb
274	03378-L02771	Exon 4	804-805	AAAGAAATCCAG-TCCCGACCAGTA	80.6 kb
310	03379-L02772	Exon 5	846-847	TCTGCCAGAAAT-GTTACAGTGAAC	5.7 kb

Length (nt)	SALSA MLPA probe	*SGCD* exon	Ligation site NM_000337.5	Partial sequence (24 nt adjacent to ligation site)	Distance to next probe
280 ¥	21678-L31529	Exon 6	986-985, reverse	CTACTACCACTT-CATTATTGTCTG	52.5 kb
381	03380-L04677	Exon 7	1053-1054	CCTAAATCTATA-GAAACACCTAAT	110.2 kb
232	11371-L13242	Exon 8	1166-1167	AGAAGCTGGCAA-TATGGAAGCCAC	1.6 kb
388	03381-L04694	Exon 9	1302-1303	CAGAAGGTCTTC-GAGATCTGCGTC	
		stop codon	*1390-1392 (exon 9)*		

¥ Changed in version B2 (from lot B2-1218 onwards). Small change in length, no change in sequence detected.

Note: The exon numbering used in this P116-B2 SGC product description is the exon numbering from the RefSeq transcript NM_000337.5, which is identical to the LRG_205 sequence. The exon numbering and NM sequence used is from 12/2018 but can be changed (e.g. by NCBI) after the release of the product description. Please notify us of any mistakes: info@mlpa.com.

Table 2d. *SGCG*

Length (nt)	SALSA MLPA probe	*SGCG* exon	Ligation site NM_000231.2	Partial sequence (24 nt adjacent to ligation site)	Distance to next probe
		start codon	*156-158 (exon 2)*		
142	03387-L02780	Exon 1	109-110	TGGTAGAGCTCG-GGCCAGCTGTAG	22.8 kb
178	03388-L20658	Exon 2	273-274	TCTACTTGTTTG-TTCTTCTTTTAC	30.9 kb
481	11620-L20322	Exon 3	404-405	TTGGAAGGGGAA-TCAGAATTTTTA	16.0 kb
228	03390-L02783	Exon 4	497-498	GTGACTGTAAAT-GCGCGCAACTCA	28.7 kb
265	03391-L12902	Exon 5	588-589	AGATCAACTCCA-ACGACGGCAAGC	16.0 kb
301 ±	03392-L02785	Exon 6	689-690	TTTGAACATTCA-GTGGAGACACCC	25.2 kb
337	03393-L13243	Exon 7	763-764	GAGTCTAAGCAT-GGATGCCCCAAG	3.7 kb
373	03394-L02787	Exon 8	898-899	ACCCAAGCTGGT-GCAGGGGACGTG	
		stop codon	*1029-1031 (exon 8)*		

± SNP rs114160429 mutation could influence the probe signal. In case of apparent deletions, it is recommended to sequence the region targeted by this probe.

Note: The exon numbering used in this P116-B2 SGC product description is the exon numbering from the RefSeq transcript NM_000231.2, which is identical to the LRG_207 sequence. The exon numbering and NM sequence used is from 12/2018 but can be changed (e.g. by NCBI) after the release of the product description. Please notify us of any mistakes: info@mlpa.com.

Table 2e. *FKRP*

Length (nt)	SALSA MLPA probe	*FKRP* exon	Ligation site NM_024301.4	Partial sequence (24 nt adjacent to ligation site)	Distance to next probe
		start codon	*298-300 (exon 4)*		
471 «	11384-L21239	Exon 1	127 nt after exon 1	TCGTGCTGGATA-AAGTGCAGGATC	1.8 kb
222 «	11370-L20320	Exon 2	82-83	TGCCCTCCTGGA-ACTCCCCCAGCC	0.5 kb
409 «	11379-L12104	Exon 3	139-138, reverse	CTGGGTCTGAGT-TGCGATTTGGCC	7.7 kb
259 § «	11373-L13479	Exon 4	1123-1122, reverse; L276I mutation	CCAGCTCACTAT-GCGGATGCCCAG	0.9 kb
418 «	11380-L12105	Exon 4	1992-1993	CCAGATTTATCA-AATGGTCATGCC	
		stop codon	*1783-1785 (exon 4)*		

« Probe located in or near a GC-rich region. A low signal can be caused by salt contamination in the DNA sample leading to incomplete DNA denaturation, especially of GC-rich regions.
§ Mutation-specific probe. This probe will only generate a signal when the L276I mutation is present. It has been tested on artificial DNA **but not on positive human samples**!

Note: The exon numbering used in this P116-B2 SGC product description is the exon numbering from the RefSeq transcript NM_024301.4, which is identical to the LRG_761 sequence. The exon numbering and NM sequence used is from 12/2018 but can be changed (e.g. by NCBI) after the release of the product description. Please notify us of any mistakes: info@mlpa.com.

Related SALSA MLPA probemixes

- P268 DYSF: Contains probes for *DYSF* involved in LGMD2B.
- P176 CAPN3: Contains probes for *CAPN3* involved in LGMD2A.
- P061 Lissencephaly: Contains probes for *POMT1* and *POMGNT1* involved in LGMD2K and LGMD2O.
- P436 ANO5: Contains probes for *ANO5*, involved in LGMD2L.
- P048 LMNA/MYOT: Contains probes for *LMNA*, *MYOT* and *CAV3*.

References

- Schouten JP et al. (2002). Relative quantification of 40 nucleic acid sequences by multiplex ligation-dependent probe amplification. *Nucleic Acids Res.* 30:e57.
- Schwartz M et al. (2007). Deletion of exon 16 of the dystrophin gene is not associated with disease. *Hum Mutat.* 28:205.
- Varga RE et al. (2012). MLPA-based evidence for sequence gain: pitfalls in confirmation and necessity for exclusion of false positives. *Anal Biochem.* 421:799-801.

P116 Product history	
Version	*Modification*
B2	*One reference probe has been replaced and several probe lengths have been adjusted.*
B1	*One extra probe each for SGCB, SGCD and FKRP have been included. Five reference probes and the 88 nt and 96 nt control fragments have been replaced.*
A1	*First release.*

Implemented changes in the product description
Version B2-01 10 January 2019 (01P) - Product description restructured and adapted to a new template. - Product description adapted to a new product version (version number changed, changes in Table 1 and Table 2, new picture included). *Version 08 – 22 July 2015 (54)* - Product description adapted to a new lot (lot number added, new pictures included). - Various textual changes.

More information: www.mlpa.com; www.mlpa.eu	
	MRC-Holland bv; Willem Schoutenstraat 1 1057 DL, Amsterdam, The Netherlands
E-mail	info@mlpa.com (information & technical questions); order@mlpa.com (orders)
Phone	+31 888 657 200