# Product Description SALSA® MLPA® Probemix P325-A3 OCA2

To be used with the MLPA General Protocol.

**Version A3.** As compared to version A2, four reference probes have been replaced. For complete product history see page 7.

**Catalogue numbers:**
- **P325-025R:** SALSA MLPA Probemix P325 OCA2, 25 reactions.
- **P325-050R:** SALSA MLPA Probemix P325 OCA2, 50 reactions.
- **P325-100R:** SALSA MLPA Probemix P325 OCA2, 100 reactions.

To be used in combination with a SALSA MLPA reagent kit and Coffalyser.Net data analysis software. MLPA reagent kits are either provided with FAM or Cy5.0 dye-labelled PCR primer, suitable for Applied Biosystems and Beckman/SCIEX 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 P325 OCA2 is a **research use only (RUO)** assay for the detection of deletions or duplications in the *OCA2* and *TYR* genes, which are associated with oculocutaneous albinism.

Oculocutaneous albinism (OCA) is a group of autosomal recessive disorders characterised by hypopigmentation in the skin, hair and eyes due to disorders in the melanin biosynthesis. There are different types of OCA of which OCA type 1 and type 2 (OCA1 and OCA2) are the most common. Defects in the tyrosinase gene (*TYR*) and the oculocutaneous albinism gene (*OCA2*, formerly known as the *P* gene) are considered to be causes of OCA1 and OCA2, respectively. The protein encoded by the *OCA2* gene is the P protein, whereas the protein encoded by the *TYR* gene is tyrosinase. Tyrosinase is important during the initial steps of melanin production, while the P protein is a transporter protein.

The *OCA2* gene (24 exons) spans ~344 kb of genomic DNA and is located on 15q12-q13.1, 26 Mb from the p-telomere. The *TYR* gene (5 exons) spans ~118 kb of genomic DNA and is located on 11q14.3, 89 Mb from the p-telomere.

More information is available at https://www.ncbi.nlm.nih.gov/books/NBK1232/.

**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/

**Exon numbering:**
The *OCA2* exon numbering used in this P325-A3 OCA2 product description is the exon numbering from the RefSeq transcript NM_000275.3, which is identical to the NG_009846.1 sequence. The *TYR* exon numbering used in this P325-A3 OCA2 product description is the exon numbering from the RefSeq transcript NM_000372.5, which is identical to the NG_008748.1 sequence. The exon numbering and NM_ sequences

used have been retrieved on 10/2020. As changes to the NCBI database can occur after release of this product description, exon numbering may not be up-to-date.

**Probemix content:** The SALSA MLPA Probemix P325-A3 OCA2 contains 42 MLPA probes with amplification products between 130 and 472 nucleotides (nt). This includes 26 probes for the *OCA2* gene (one for each exon, except for exons 8 and 23, and four *OCA2* probes that detect intronic sequences) and five probes for the *TYR* gene (one for each exon, except exon 5, and one *TYR* probe that detects an intronic sequence). Four of the *OCA2* probes are present in or near the common 2.7-kb deletion area. In addition, 11 reference probes are included that detect autosomal chromosomal locations. Complete probe sequences and the identity of the genes detected by the reference probes are available online (www.mlpa.com).

This probemix contains nine quality control fragments generating amplification products between 64 and 105 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 nt and 96 nt fragment indicates incomplete denaturation) |
| 92 | Benchmark fragment |
| 100 | X-fragment (X chromosome specific) |
| 105 | Y-fragment (Y chromosome specific) |

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

**MLPA technique validation:** Internal validation of the MLPA technique using 16 DNA samples from healthy individuals is required, in particular when using MLPA for the first time, or when changing the sample handling procedure, DNA extraction method or instruments used. This validation experiment should result in a standard deviation ≤0.10 for all probes over the experiment.

**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:** A sufficient number (≥3) of reference samples should be included in each MLPA experiment for data normalisation. 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 oculocutaneous albinism. 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 Institute (https://catalog.coriell.org) and Leibniz Institute 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. Sample ID numbers NA08618 and NA09596 from the Coriell Institute have been tested with this P325-A3 probemix at MRC-Holland and can be used as positive control samples to detect a heterozygous duplication and a heterozygous deletion of the *TYR* gene, respectively. The quality of cell lines can change; therefore samples should be validated before use.

**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 each individual probe over all the reference samples should be ≤0.10 and the dosage quotient (DQ) of each individual reference probe 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 chromosomes or pseudo-autosomal regions:

| 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 (as described for *DMD* by 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 or flanking probes are unlikely to have any relation to the condition tested for.
- When running MLPA products, the capillary electrophoresis protocol may need optimization. False results can be obtained if one or more peaks are off-scale. For example, a duplication of one or more exons can be obscured when peaks are off-scale, resulting in a false negative result. The risk on off-scale peaks is higher when probemixes are used that contain a relatively low number of probes. Coffalyser.Net software warns for off-scale peaks while other software does not. If one or more peaks are off-scale, rerun the PCR products using either: lower injection voltage / injection time settings, or a reduced amount of sample by diluting PCR products.

**Limitations of the procedure:**

- In most populations, the major cause of genetic defects in the *OCA2* and *TYR* genes are small (point) mutations, most of which will not be detected by using SALSA MLPA Probemix P325 OCA2.
- 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.

***OCA2* and *TYR* mutation databases:** https://databases.lovd.nl/shared/genes/OCA2 and https://databases.lovd.nl/shared/genes/TYR. We strongly encourage users to deposit positive results in the Leiden Open Variation Database. Recommendations for the nomenclature to describe deletions/duplications of one or more exons can be found on http://varnomen.hgvs.org/.

Please report copy number changes detected by the reference probes, false positive results due to SNPs and unusual results (e.g., a duplication of *OCA2* exons 3 and 5 but not exon 4) to MRC-Holland: info@mlpa.com.

## Table 1. SALSA MLPA Probemix P325-A3 OCA2

| Length (nt) | SALSA MLPA probe | Chromosomal position (hg18)[a] | | |
|---|---|---|---|---|
| | | Reference | OCA2 | TYR |
| 64-105 | Control fragments – see table in probemix content section for more information | | | |
| 130 | Reference probe 19551-L26105 | 2p13 | | |
| 136 Ø # | **TYR** probe 14277-L15947 | | | **Intron 4** |
| 141 | **OCA2** probe 14278-L15948 | | **Exon 16** | |
| 148 | **OCA2** probe 14279-L15949 | | **Exon 3** | |
| 154 | **TYR** probe 14280-L16600 | | | **Exon 2** |
| 160 | **TYR** probe 14285-L15955 | | | **Exon 3** |
| 166 | **OCA2** probe 14281-L15951 | | **Exon 13** | |
| 172 | **OCA2** probe 14282-L16601 | | **Exon 6** | |
| 178 | **OCA2** probe 14283-L15953 | | **Exon 2** | |
| 184 * | Reference probe 21624-L30240 | 22q12 | | |
| 191 Ø + | **OCA2** probe 14284-L16595 | | **Intron 6** | |
| 200 | **OCA2** probe 14286-L16602 | | **Exon 24** | |
| 207 | **OCA2** probe 14287-L15957 | | **Exon 18** | |
| 214 | **OCA2** probe 14288-L15958 | | **Exon 4** | |
| 220 | **OCA2** probe 14289-L15959 | | **Exon 17** | |
| 226 Ø | **OCA2** probe 15003-L17557 | | **Intron 22** | |
| 232 + | **OCA2** probe 14291-L17801 | | **Exon 7** | |
| 238 | **OCA2** probe 14292-L18689 | | **Exon 10** | |
| 244 | **OCA2** probe 14293-L15963 | | **Exon 14** | |
| 250 | **OCA2** probe 14294-L15964 | | **Exon 15** | |
| 256 | **OCA2** probe 14295-L16479 | | **Exon 11** | |
| 260 Ø + | **OCA2** probe 14296-L15966 | | **Intron 7** | |
| 267 | Reference probe 14110-L15943 | 8p21 | | |
| 283 | **OCA2** probe 14297-L15967 | | **Exon 9** | |
| 292 | **OCA2** probe 14298-L15968 | | **Exon 12** | |
| 300 | **OCA2** probe 14299-L15969 | | **Exon 5** | |
| 313 | **TYR** probe 14300-L15970 | | | **Exon 1** |
| 328 | **OCA2** probe 14301-L15971 | | **Exon 19** | |
| 337 | Reference probe 01659-L01241 | 17p13 | | |
| 346 | **OCA2** probe 14302-L15972 | | **Exon 20** | |
| 355 | **TYR** probe 14303-L15973 | | | **Exon 4** |
| 366 * | Reference probe 14768-L29121 | 1q23 | | |
| 386 * | Reference probe 01794-L25919 | 13q14 | | |
| 400 | **OCA2** probe 14790-L01553 | | **Exon 22** | |
| 409 | Reference probe 10681-L11263 | 6p12 | | |
| 418 | **OCA2** probe 14307-L15977 | | **Exon 21** | |
| 427 | Reference probe 14406-L16088 | 12q13 | | |
| 436 | Reference probe 04720-L04138 | 7q21 | | |
| 445 | **OCA2** probe 02041-L03725 | | **Exon 1** | |
| 454 * | Reference probe 18691-L02476 | 5p15 | | |
| 463 Ø + | **OCA2** probe 14308-L15978 | | **Intron 6** | |
| 472 | Reference probe 12761-L13877 | 4q12 | | |

**a)** See above section on exon numbering for more information.

* New in version A3.
Ø Intron probe. Only included to help determine the extent of a deletion/duplication. Copy number alterations of only this probe are of unknown clinical significance.
+ This probe is present in or near the common 2.7-kb deletion area.
# This probe's specificity relies on a single nucleotide difference compared to a related gene or pseudogene. As a result, an apparent duplication of only this probe can be the result of a non-significant single nucleotide sequence change in the related gene or pseudogene.

## Table 2. P325-A3 probes arranged according to chromosomal location

Table 2a. *TYR* gene

| Length (nt) | SALSA MLPA probe | TYR exon[a] | Ligation site NM_000372.5 | Partial sequence[b] (24 nt adjacent to ligation site) | Distance to next probe |
|---|---|---|---|---|---|
| | | *start codon* | *80-82 (Exon 1)* | | |
| 313 | 14300-L15970 | Exon 1 | 19-20 | TAGTAGCTGGAA-AGAGAAATCTGT | 13.2 kb |
| 154 | 14280-L16600 | Exon 2 | 94 nt before exon 2 | CTCAGGAGAAGT-CTAACAACGATA | 37.2 kb |
| 160 | 14285-L15955 | Exon 3 | 296 nt after exon 3 | ATCCTGGTAGAA-GGTAAAGTATAC | 56.9 kb |
| 355 | 14303-L15973 | Exon 4 | 204 nt after exon 4 | ATTTTGCTTAAC-ATAGGCCATTTT | 9.4 kb |
| 136 Ø # | 14277-L15947 | Intron 4 | 633 nt before exon 5 | CCAGAGTGCGGA-CGCTCCAGGGTA | |
| | | *stop codon* | *1667-1669 (Exon 5)* | | |

Table 2b. *OCA2* gene

| Length (nt) | SALSA MLPA probe | OCA2 exon[a] | Ligation site NM_000275.3 | Partial sequence[b] (24 nt adjacent to ligation site) | Distance to next probe |
|---|---|---|---|---|---|
| | | *start codon* | *114-116 (Exon 2)* | | |
| 445 | 02041-L03725 | Exon 1 | 91-90 *reverse* | TGCACTTTACCT-GCGCACTTGCAG | 17.6 kb |
| 178 | 14283-L15953 | Exon 2 | 323-322 *reverse* | TTTGTGAGGAAT-GAAGCAAACTCC | 49.6 kb |
| 148 | 14279-L15949 | Exon 3 | 6 nt after exon 3 *reverse* | AGGGGGAAAATA-TCTCACCCTTTC | 4.0 kb |
| 214 | 14288-L15958 | Exon 4 | 7 nt before exon 4 *reverse* | GTGACCTGGAAA-GCAAGAGAGGTG | 3.2 kb |
| 300 | 14299-L15969 | Exon 5 | 643-642 *reverse* | TGACTTTCAGCC-ACTGCACACAGC | 2.4 kb |
| 172 | 14282-L16601 | Exon 6 | 722-721 *reverse* | AACAGCTGCCAG-AGCTTTCCTTGA | 0.8 kb |
| 463 Ø + | 14308-L15978 | Intron 6 | 747 nt after exon 6 | GCTGCCAGATTA-GATGCGCTTCCC | 1.2 kb |
| 191 Ø + | 14284-L16595 | Intron 6 | 1896 nt after exon 6 | CGACCTCTGCAT-TACTTCTCCAGG | 2.0 kb |
| 232 + | 14291-L17801 | Exon 7 | 5 nt before exon 7 *reverse* | TTCACGGCTCGG-AGAGTGTCAAGG | 1.2 kb |
| 260 Ø + | 14296-L15966 | Intron 7 | 1023 nt after exon 7 | TTGCATATTAAT-AACCCAGATTAA | 2.5 kb |
| 283 | 14297-L15967 | Exon 9 | 1090-1089 *reverse* | GGGTTTCTACAC-TTCCGCGGAGGT | 24.2 kb |
| 238 | 14292-L18689 | Exon 10 | 29 nt before exon 10 *reverse* | AAATTACCGCGT-TCCAGTGCACGA | 1.1 kb |
| 256 | 14295-L16479 | Exon 11 | 9 nt after exon 11 *reverse* | CACGGGGAGAGC-TGTAATTACCAT | 3.0 kb |
| 292 | 14298-L15968 | Exon 12 | 1352-1351 *reverse* | ATCATACCTACC-TTTACAGCACAA | 1.4 kb |
| 166 | 14281-L15951 | Exon 13 | 1403-1402 *reverse* | GCCGCGATGAGA-CAGAGCATGATG | 1.7 kb |
| 244 | 14293-L15963 | Exon 14 | 1543-1542 *reverse* | CAGCTCCTCCAA-TGTTTGTGAAGA | 16.6 kb |
| 250 | 14294-L15964 | Exon 15 | 2 nt before exon 15 *reverse* | AGTCCAGGCCCT-GGAAATAAACAA | 9.1 kb |
| 141 | 14278-L15948 | Exon 16 | 1764-1763 *reverse* | CCAGACGTGAAT-CTCGTGCTTCAG | 2.5 kb |
| 220 | 14289-L15959 | Exon 17 | 1922-1921 *reverse* | TTGGTCTCCCAA-TTTTTGTCCTCC | 3.4 kb |
| 207 | 14287-L15957 | Exon 18 | 1 nt after exon 18 *reverse* | AAATTAGACTCA-CCAAGATCAAGA | 25.6 kb |
| 328 | 14301-L15971 | Exon 19 | 2088-2087 *reverse* | TAGCAACCAGAT-GGCACCCAGAAT | 54.3 kb |
| 346 | 14302-L15972 | Exon 20 | 2219-2218 *reverse* | TCTCCAACATAT-TCTATTAAGTGG | 0.5 kb |
| 418 | 14307-L15977 | Exon 21 | 92 nt before exon 21 *reverse* | GCCCGAGGGTGT-TAGTCCTTCCTC | 19.9 kb |
| 400 | 14790-L01553 | Exon 22 | 2423-2424 | CCGCTCATGTAT-GCCCTGGCCTTC | 5.9 kb |
| 226 Ø | 15003-L17557 | Intron 22 | 450 nt before exon 23 *reverse* | CAACCAGGTGGA-ACCCCTTTCCTT | 90.3 kb |
| 200 | 14286-L16602 | Exon 24 | 2801-2800 *reverse* | TGGTGTTCCAAC-ATTCGCTTGAAT | |
| | | *stop codon* | *2628-2630 (Exon 24)* | | |

**a)** See above section on exon numbering for more information.

**b)** Only partial probe sequences are shown. Complete probe sequences are available at www.mlpa.com. Please notify us of any mistakes: info@mlpa.com.

Ø Intron probe. Only included to help determine the extent of a deletion/duplication. Copy number alterations of only this probe are of unknown clinical significance.
+ This probe is present in or near the common 2.7-kb deletion area.
# This probe's specificity relies on a single nucleotide difference compared to a related gene or pseudogene. As a result, an apparent duplication of only this probe can be the result of a non-significant single nucleotide sequence change in the related gene or pseudogene.

## Related SALSA MLPA probemixes

- P054 FOXL2-TWIST1. Contains probes for the *GPR143* (previously *OA1*) gene associated with X-linked ocular albinism.
- ME028 PWS/AS. Primary screening for Prader-Willi and Angelman Syndrome (copy number & methylation).

## 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.


## Selected publications using SALSA MLPA Probemix P325 OCA2


- Chuan Z et al. (2020). Mutation Analysis of 63 Northwest Chinese Probands with Oculocutaneous Albinism. *Curr Eye Res*. 1-4.
- Luo D et al. (2019). Molecular genetic study of 59 Chinese Oculocutaneous albinism families. *Eur J Med Genet*. 62:103709.
- Mauri L et al. (2014). SLC45A2 mutation frequency in Oculocutaneous Albinism Italian patients doesn't differ from other European studies. *Gene*. 533:398-402.
- Mauri L et al. (2017). Clinical evaluation and molecular screening of a large consecutive series of albino patients. *J Hum Genet*. 62:277-90.
- Norman CS et al. (2017). Identification of a functionally significant tri-allelic genotype in the Tyrosinase gene (TYR) causing hypomorphic oculocutaneous albinism (OCA1B). *Sci Rep*. 7:1-9.
- Rimoldi V et al. (2014). Functional characterization of two novel splicing mutations in the OCA2 gene associated with oculocutaneous albinism type II. *Gene*. 537:79-84.
- Straniero L et al. (2015). Two novel splicing mutations in the SLC45A2 gene cause Oculocutaneous Albinism Type IV by unmasking cryptic splice sites. *J Hum Genet*. 60:467–71.
- Wang Y et al. (2018). Identification of a Homozygous Missense Mutation in the TYR Gene in a Chinese Family with OCA1. *Curr Med Sci*. 38:932-936.


| **P325 Product history** | |
|---|---|
| *Version* | *Modification* |
| A3 | Four reference probes have been replaced. |
| A2 | One reference probe has been replaced. |
| A1 | First release. |

| **Implemented changes in the product description** |
|---|
| *Version A3-01 — 04 November 2020 (02P)*<br>- Product description rewritten and adapted to a new template.<br>- Product description adapted to a new product version (version number changed, changes in Table 1 and Table 2).<br>- Ligation sites of the probes targeting the *OCA2* and *TYR* genes updated according to new versions of the NM_ reference sequences.<br>- Warning added to Table 1 and Table 2 for probe specificity relying on a single nucleotide difference between target gene and related gene or pseudogene.<br>*Version 05 – 10 May 2017 (55)* |

- Product description adapted to a new product version (version number changed, lot number added, small changes in Table 1 and Table 2, new picture included).
- New reference added on page 1.
- Various minor textual changes.
- *Version 04 – 10 December 2015 (55)*
- Product description adapted to a new lot (lot number added, minor textual changes on page 1, new picture included).



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