

# **GMOQuant**

## **Duplex (LR)**

### **35S/ AgroBorder II Soy**

**Test kit for the quantification of  
CaMV 35S promoter and  
AgroBorder II soy DNA**

Cat. No. 5125222301, -10, -50

GMOQuant Duplex (LR) 35S/AgroBorder II Soy ID2666

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**Eurofins GeneScan Technologies GmbH**

Engesser Str. 4  
79108 Freiburg, Germany  
Phone: + 49-(0)761-5038-100  
Fax: + 49-(0)761-5038-111  
kits@eurofins.com  
www.eurofins.com/kits

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Test kits, their components and instructions for use are subject to alterations. They are intended for research purposes only.

# GMOQuant Duplex (L R) 35S/AgroBorder II Soy

**Kit for the quantification of the CaMV 35S Promoter and AgroBorder II DNA with soy DNA (Ie1) reference PCR**

## 1 INTRODUCTION AND TEST PRINCIPLE

The Kit provides materials for the simultaneous detection and the quantitative measurement of the 35S promoter, a regulatory DNA element derived from the Cauliflower Mosaic Virus (CaMV), and the AgroBorder II modification in DNA extracted from soybean samples or products with soy content.

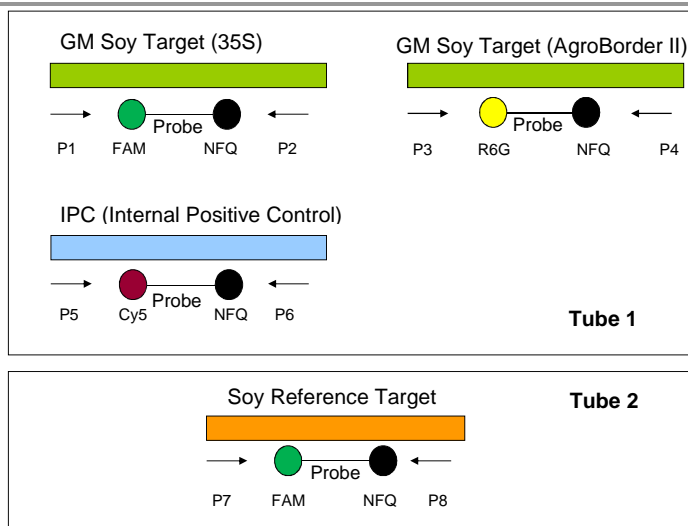
DNA amplification and detection methods take advantage of the relative stability of the DNA, which resists the processing steps which are used in food and feed production. DNA can be detected and quantified with high sensitivity and precision. The procedure follows the basic principles of the real-time PCR amplification method and of relative quantification using the standard curve method.

The relative content of DNA carrying one of the two GMO targets (35S/AgroBorder II) in the soybean fraction of a sample can be determined (quantitative approach).

The quantification results reflect the 35S as well as the AgroBorder II content in relation to the soybean-specific reference system lectin1 (Ie1), as copy/copy ratio.

For quantitative measurement, three standard curves are generated, one for the 35S system, one (in the same PCR reaction) for the AgroBorder II system, and the third one for the soy reference system.

The GMOQuant Duplex 35S/AgroBorder II can also be used in a qualitative approach to simultaneously detect the Cauliflower Mosaic Virus 35S promoter and AgroBorder II soy together with an internal positive control in a triplex PCR – please request the separate manual for setup and evaluation in case at [kits@eurofins.com](mailto:kits@eurofins.com).



FAM™ is the fluorescent reporter dye attached to the probes for the 35S promoter and the soy reference (Ie1) detection systems. R6G is the fluorescent reporter dye attached to the probe for the AgroBorder II. The internal positive control uses Cy5® as reporter dye. The quenchers are non-fluorescent quenchers. AgroBorder II, 35S and the IPC are amplified simultaneously in the same PCR reaction vessel (triplex PCR).

For each standard curve, four calibration points are determined with the calibration DNA standards included in the kit. The sample DNA is compared to the calibration curves and copy numbers are deducted. Subsequently the percentage of GMO in the unknown DNA samples is calculated as ratio of the amount of the single GMO targets to the soy DNA content (35S/soy ref; AgroBorder II/soy ref).

The kit uses the following dyes:

- FAM™ (Reporter dye 35S and soy reference)
- R6G (Reporter dye AgroBorder II)
- Cy5® (Reporter dye IPC- required for the qualitative assay)
- ROX™ (Normalizer)

Non-fluorescent quenchers (NFQ) are used as a quencher.

The ROX concentration of this kit is laid out for PCR real-time machines requiring a low ROX level, like e.g. the 7500 from Applied Biosystems or the Agilent Mx3000P™/ Mx3005P™.

### 1.1 Important remarks for the 35S and AgroBorder II quantification

The 35S screen system and the AgroBorder II screen system are highly economical tools for a semi-quantitative GMO screening in food and feed. The 35S promoter and the AgroBorder II modification is an element of the genetic modification in different GMO varieties of soy and also other species.

It is important to make sure that the sample does not contain other GMO sources (species) than soy, because 35S promoter DNA and AgroBorder II DNA from GMO of other species may contribute to the quantification result and corrupt the result (i.e. when GM corn interferes with the quantification).

Samples, mainly from *Brassica* species, which are infected with the cauliflower mosaic virus, will also show deviating 35S quantification results, because the 35S of the natural virus will be added to potential GMO sources.

The AgroBorder II modification is commonly found in soybeans from Monsanto, e.g. MON89788, MON87701, MON87705, MON87769 and MON87708, which may contain different copy numbers of the AgroBorder II

modification, e.g. MON87705 soy contains two copies of the AgroBorder II sequences. AgroBorder II sequences are also found in Ti plasmids of *Agrobacterium tumefaciens*. Analysis of samples consisting of plant tissue naturally infected with tumor inducing *Agrobacterium tumefaciens* bacteria may produce positive results for the AgroBorder II-specific PCR system.

However, even when the sample contains only soy as possible GMO source, there are still different GM soy varieties in question, which may contain different copy numbers of the 35S promoter (see table 1) and AgroBorder II modification (see above).

**For this reason it is very important to keep in mind that the quantification results achieved with this kit cannot be more than semi-quantitative with regard to the 35S and AgroBorder II result.**

GM Soy	Copy no. of the p35S per haploid genome
Roundup Ready™ Soy, GTS 40-3-2	1
Dupont Soy, G94-1, G94-6, G94-19 and G168	1 or more
LibertyLink™ Soy, A5547-127	1
LibertyLink™ Soy, A2704-12,	2
LibertyLink™ Soy, GU262	2
LibertyLink™ Soy, A2704-21 and A5547-35	1 or more
LibertyLink™ Soy, W62 and W98	unknown
AgroBorder II	0
DP-304523-1	0
DP-356043-5	0
CV127	0

Table 1: CaMV 35S promoter copies in different GM soy lines. (No responsibility is taken for this information.)

## 2 REAGENTS

The GMOQuant Duplex IPC (LR) 35S/AgroBorder II Soy kit contains following reagents: Store all reagents light protected at -20°C.

- BasicMix 35S / AgroBorder II:** GS-P-26.009 • EFGi2x QNTP(NR) 2U (**STRIPED RED AND WHITE CAPS**) PCR reaction mix, dNTPs, hot-start polymerase, buffer; 1 tube for 48 reactions each (625 µL), # -01: 1 x 625 µL, # -10: 10 x 625 µL, # -50: 50 x 625 µL
- OligoMix 35S / AgroBorder II:** OligoMix QN RT IPC (LR/HR+) GS-P-07.108 • 35S/ABII incl. primers, probe, dNTPs, 1 tube for 48 reactions each (375 µL) (**RED CAPS**) # -01: 1 x 375 µL, # -10: 10 x 375 µL, # -50: 50 x 375 µL
- BasicMix / Soy Lectin:** GS-P-26.008 EFG 2x QN TP (NR) 1U (**STRIPED GREEN AND WHITE CAPS**) PCR reaction mix, dNTPs, hot-start polymerase, buffer; 1 tube for 48 reactions each (625 µL), # -01: 1 x 625 µL, # -10: 10 x 625 µL, # -50: 50 x 625 µL

4. **OligoMix / Soy Lectin:** OligoMix QN RT(LR/HR+), GS-P-25.010 • Soybean Lectin1• incl. primers, probe, dNTPs, 1 tubes for 48 reactions each (375 µL) (**GREEN CAPS**) # -01: 1 x 375 µL, # -10: 10 x 375 µL, # -50: 50 x 375 µL

5. **Calibration Standards 1-5** for soy reference / lectin1 and GM soy (35S/AgroBorder II): # -01: 5 x 65 µL, # -10: 10 x 5 x 65 µL, # -50: 25 x 5 x 65 µL

Use #1-4 for soy reference/lectin1 (#1: WHITE CAP, #2-4 STRIPED VIOLET CAPS)

Use #2-5 for GM soy (35S/AgroBorder II) (plasmid pGSE672) (#2-4 STRIPED VIOLET CAPS, #5: VIOLET CAP)

MATERIAL	Copy Number Soy Ref/Rxn	Copy Number 35S and AgroBorder II each/Rxn
Standard 1	100,000	
Standard 2	12,500	12,500
Standard 3	1,563	1,563
Standard 4	195	195
Standard 5		49

*Shown are the assigned target copy numbers per 5 µL of the calibration standards.*

6. **Quantification control:**

1% GM Soy (35S/AgroBorder II) control DNA, made from 1% (w/w) RR-Soy (ERM-BF410e) and 1% (w/w) MON89788 soy (AOCS 0906B) (CLEAR CAP) # -01: 65 µL, # -10: 10 x 65 µL, # -50: 25 x 65 µL

**2.1 Materials Required But Not Supplied**

- Optical plates and optical seals
- Precision pipette (for 5 µL and 20 µL)
- Vortex mixer
- Centrifuge (1,500 x g, preferably refrigerated)
- Centrifuge for 96-well plates (preferably refrigerated)
- Applied Biosystems® 7500 SDS, ABI7500 Fast, Agilent MX3000P™, MX3005P™, AriaMx™, CFX96 Touch™ or LC480 instrument with required filter sets.

**3 RECOMMENDATIONS AND WORKING PRECAUTIONS**

For DNA extraction use only molecular-biology grade reagents and sterile-filtrated, deionised water (DNA-free) and 0,1 x TE buffer for DNA dilutions (Tris-HCl pH = 8,0; c = 1 mmol/L; EDTA pH = 8,0 c = 0,1 mmol/L):

Maintain separate working areas for DNA preparation, reaction setup, amplifications and reaction product analyses. Never transfer amplified products into the reaction setup, or extraction area. Use filter-plugged pipette tips in order to avoid possible cross-contamination. Use only powder-free gloves and change them frequently during the process. Clean lab-benches and equipment periodically with a DNA destroying reagent. To obtain reliable quantification results all pipettes have to be checked regularly for precision and if necessary have to be calibrated.

## 4 PROCEDURAL NOTES

A thorough understanding of this package insert is necessary for successful use of the product. Reliable results will only be obtained by using precise laboratory techniques and accurately following the package insert. The standard curves must be included in each quantification run.

Do not mix various lots of any kit component within an individual run. Do not use any component beyond the expiration date shown on its label.

After removing reagents from the refrigerator, allow them to thaw slowly and mix them by vortexing and briefly centrifuge before use.

Thaw only the amounts of reagents needed for the run. If smaller volumes are needed, aliquot reagents at the first use. Standards and positive controls should be mixed by vortexing and briefly centrifuged before use.

Prepare only the amount of MasterMix needed; unused mixed MasterMix cannot be stored!

## 5 TEST PROCEDURE

### 5.1 General Description

Different assay formats are possible: For one laboratory sample either one DNA extraction with two or more PCR-replicates or two parallel (“A” and “B”) DNA-extractions (e.g. as recommended by certain national and international standards) may be analysed. Different numbers of replicates analysed per DNA sample (e.g. triplicates in case of only one DNA sample) may be chosen. The mean value of several replicates will yield increased precision of the analysis. Furthermore, different ways to check sample DNAs for inhibitory effects may be applied – e.g. with analysis of the DNA in two defined dilutions. This can either be done in a preceding monitor run or, according to the user’s preference, it can also be done in the quantitation run without prior monitor run.

The proceedings described are made for the following format and assumption:

#### DNA - Test-Samples

Two independent DNA extracts yielding an “A” and a “B” sample DNA are taken. Each DNA is analysed in two different defined concentrations (dilution 1 (dil.1) and

dilution 2 (dil.2)). For example, each DNA could be analysed undiluted (dil. 1) and a known dilution like e.g. a fivefold dilution with water or TE (dil. 2). Each DNA dilution is analysed by a single determination (no replicates).

#### Calibration curves

Four concentrations per target are analysed in duplicate each.

#### NTC

Two reactions per target

#### Quantification control

Two reactions of a 1% RRS/ 1% MON89788 DNA

### 5.2 Sample DNA

Absolute DNA amount and purity (meaning: free of PCR inhibiting substances) affect overall sensitivity as well as accuracy of the analysis. Low DNA amount subjected to analysis results in poor LOD and LOQ with regard to the specific test sample. Insufficiently pure DNA displaying inhibitory effects increase inaccuracy or even lead to totally biased results.

It is recommended to use approx. 100 ng DNA of the species of interest per undiluted reaction. The

concentration of DNA should be adjusted accordingly prior to the set-up of the reactions. DNA amount can be determined prior to analysis by one of the following methods:

- Real Time PCR monitor run (preferred method)
- Fluorimetric or spectrophotometric or other physical measurements, e.g. gel electrophoresis may be applied. Especially the spectrophotometric methods can suffer significant errors due to interfering DNA impurities or partial DNA denaturation / degradation. When analysing matrices which are well-known with regard to extraction yield and purity, DNA measurement may be omitted.

### 5.3 Plate Setup

Calculate the number of reactions and amount of equivalent master mix reagents before thawing the reagents.

- Just thaw as much OligoMix and BasicMix as needed.
- The MasterMixes are prepared of the pre-made reagents ready for direct use after mixing of the two components.
- The composed MasterMixes can be stored up to 4 hours in the refrigerator, but must not be used after this period.

Quantitative analyses require at least the following reactions:

Reaction Type		Sample Number per run			
		1		9	
		GMO Rxns	Soy Ref. Rxns	GMO Rxns	Soy Ref. Rxns
Sample DNA Two Extracts in 2 Dilutions	DNA #1A (dil.1)	1	1	9	9
	DNA #1A (dil.2)	1	1	9	9
	DNA #1B (dil.1)	1	1	9	9
	DNA #1B (dil.2)	1	1	9	9
Calibration Standards	GMO STND (2)	8	-	8	-
	Soy Ref. STND	-	8	-	8
Controls	No Template Control (NTC)	2	2	2	2
	Quantification Control	2	2	2	2
Pipetting aberation	(Additional)	1	1	2	2
	Number of Rxns	17	17	50	50
	<b>Total MM volume</b>	<b>340 µL</b>	<b>340 µL</b>	<b>1 mL</b>	<b>1 mL</b>
	BasicMix (12,5 µL/rxn)	212,5 µL	212,5 µL	625 µL or 1 tube	625 µL or 1 tube
	OligoMix (7,5 µL/rxn)	127,5 µL	127,5 µL	375 µL or 1 tube	375 µL or 1 tube

The following plate document shows the distribution of reactions used for quantitative analysis of 9 samples.

	1	2	3	4	5	6	7	8	9	10	11	12
A	St1	St1	St2	St2	St3	St3	St4	St4	NTC	NTC	NTC	NTC
B	St2	St2	St3	St3	St4	St4	St5	St5	1%	1%	1%	1%
C	1a	1b	1a	1b	1a D	1b D	1a D	1b D	2a	2b	2a	2b
D	2a D	2b D	2a D	2b D	3a	3b	3a	3b	3a D	3b D	3a D	3b D
E	4a	4b	4a	4b	4a D	4b D	4a D	4b D	5a	5b	5a	5b
F	5a D	5b D	5a D	5b D	6a	6b	6a	6b	6a D	6b D	6a D	6b D
G	7a	7b	7a	7b	7a D	7b D	7a D	7b D	8a	8b	8a	8b
H	8a D	8b D	8a D	8b D	9a	9b	9a	9b	9a D	9b D	9a D	9b D

Plate layout for 9 samples: green: Species ref. MasterMix; orange: GM MasterMix; NTC = no template control; St = Standard (row A: Species ref. standards, row B: GM standards); a and b = duplicates of sample; D = Dilution of sample

48 reactions are needed for each system (GM = 35S / AgroBorder II MasterMix; Species Ref. = soy MasterMix). Thirty-six of these reactions in each system will analyse 9 test samples (#01 to #09), where DNA-extracts a and b are tested at two dilution levels. The remaining 12 reactions in each system analyse the 4 calibration standards (Stnd 1 to Stnd 4 or Stnd 2 to 5, respectively) in duplicate, two no template controls in duplicate and two quantitation controls (1%).

MasterMixes should be mixed by vortexing and briefly centrifuged before use.

1. Add 20 µL of the MasterMix into appropriate tubes or wells of the plate according to the programmed plate document.
2. Add 5 µL of DNA solution (Standards, Controls or Unknowns) to the inner side of the tube or well.
3. Carefully close the plate with optical seal.
4. Centrifuge plate carefully at low speed.
5. Place plate into the thermal block of the instrument and start the run.

#### 5.4 Programming of Plate Documents

Before starting the practical work, program the plate document. For general and more detailed instructions please refer to the user guide of the instrument and respective software version. For description of the instrument programming please refer to the user manual of the respective instrument and software version and to our Application Notes for use of our kits on your cycler ([www.euofins.com/kits](http://www.euofins.com/kits)).

For the plate template, you may use our templates for ABI 7500 (Fast), CFX96 Touch™ and Agilent Mx3000P™/ Mx3005P™, Agilent AriaMx™ and LC480 (send an e-mail mentioning your cycler model to [kits@euofins.com](mailto:kits@euofins.com) to receive a copy) or program your own template with the following settings.

If you wish to use the Eurofins GeneScan Technologies evaluation sheet with automated data import, please use the detector/assay names given below.

The IPC (internal positive control) is only required for the qualitative approach (e.g.: as confirmation for the existence of the GMO in the dynamic range of the reaction.) Please request the separate manual for setup and evaluation in case at [kits@euofins.com](mailto:kits@euofins.com).



ABI 7500 (7500 Fast)

System	Detector	Reporter	Quencher
35S	7108a	FAM™	NONE
ABII	7108b	VIC™	NONE
IPC	7108i	Cy5®	NONE
Lectin	7108s	FAM™	NONE
Passive reference:		ROX™	

AriaMx™

System	Detector	Reporter
35S	7108a	FAM™
ABII	7108b	HEX™
IPC	7108i	Cy5®
Lectin	7108s	FAM™

Agilent Mx3005P™ (3000P™)

System	Detector	Reporter
35S	7108a	FAM™/SYBR® Green I
ABII	7108b	HEX™/JOE™/VIC™
IPC	7108i	Cy5®
Lectin	7108s	FAM™/SYBR® Green
Passive reference:		ROX™

Bio-Rad CFX96 Touch™

System	Detector	Reporter
35S	7108a	FAM™
ABII	7108b	VIC™
IPC	7108i	Cy5®
Lectin	7108s	FAM™

A reference dye is not used

The fluorescence signals are scanned in the following order: (1) ROX™, (2) FAM™, (3) HEX™, (4) Cy5®

Roche LC480

Color compensation for FAM, R6G and Cy5 is performed according to the manual. FAM signal is collected using the FAM detector. The R6G signal is measured in the HEX/VIC/Yellow555 channel.

Ramp rate is set to 4.4 for heating and 2.2 for cooling. Reference dye is not used for normalisation.

The PCR temperature profile is:

Temperature	Time
95°C	10 min
95°C	15 sec
60°C	90 sec

} 45 cycles

ABI 7500 Fast

PCR is performed in "Standard 7500" run mode.

**6 RESULTS**

**6.1 Calculation of quantitative results**

Ct values obtained for the four calibration standards with the lectin as well as the 35S and AgroBorder II PCR systems are used to calculate three calibration curves, one for the soybean-specific reference system, one for the 35S system and one for the AgroBorder II detection system by linear regression of Ct values versus log [copy numbers].

The resulting linear regression equations are subsequently used to calculate the copy numbers of the target sequences in the unknown samples from the experimentally determined Ct values.

The relative amount of 35S and AgroBorder II soybean respectively in each sample is calculated by dividing the copy number of 35S and AgroBorder II by the copy number determined with the soybean-specific reference system in the same volume of the same dilution of the same sample in order to obtain the relative GM ratio (%).

Then, the ratios of GM soy/soy reference can be compared and averaged among all replicates of a sample.

A sample of known GMO concentration (DNA containing 1% RRS and 1% MON 89788 from certified reference material) is included in the analysis, this sample serves as a control for the calibration and the quantification process and should not show a deviation of more than 30% from the expected result.

Quantification of the relative number of copies of each target DNA can be done e.g. with the standard curve function of the ABI 7500 SDS software. However, our recommendation is to export the Ct values from the cycler's software to a local spreadsheet (e.g. Microsoft Excel™) with subsequent standard curve calculation, because this saves individual programming of plates (Slightly different results may be obtained with both ways due to rounding errors). The following section gives a short protocol for data analysis of quantitative runs.

## 6.2 Evaluation

Refer to your cycler's manual for details. An evaluation (Excel™) sheet can be requested at kits@eurofins.com.

### Threshold:

- **ABI 7500 (Fast), Agilent Mx3000P™ /Mx3005P™ , Agilent AriaMx™**

The threshold should be placed in the region of exponential amplification across all of the amplification plots. This region is depicted in the log view of the amplification plots as the portion of the plot which is linear. The threshold line should neither be placed in the plateau phase nor in the initial linear phase of amplification.

- **Roche LC 480:** No threshold settings
- **Bio-rad CFX96 Touch™:** Auto calculated threshold can be used

### Baseline:

- **ABI 7500/7500 Fast:** Set manually, 3-15
- **Agilent Mx3000P™/Mx3005P™:** Adaptive
- **Agilent AriaMx™:** Adaptive baseline correction can be used
- **Bio-Rad CFX96 Touch™:** Baseline Subtracted Curve Fit, Auto calculated
- **Roche LC480**  
To obtain CP values use 'Abs Quant / 2<sup>nd</sup> Derivate Max' Analysis and high Confidence settings. To obtain Endpoint fluorescence values use the Endpoint Genotyping Analysis mode.

## 6.3 Interpretation of Results

### 6.3.1 Unit of Measurement

The overall unit of measurement is copy number ratio because the calibration standards are made from plasmid DNA with a 35S: AgroBorder II: Lectin1 ratio of 1:1:1. The quantification results reflect the 35S / AgroBorder II soy to lectin ratio as copy / copy ratio.

### 6.3.2 Calculation of the final result

The relative amount of GM (35S or AgroBorder II) containing DNA in each sample is calculated as the ratio of the copy numbers of GM (35S or AgroBorder II) DNA quantity divided by the soy reference DNA quantity (in copy numbers).



Use a spread sheet table to calculate the GM Soy DNA content in percent. An Excel™ evaluation table is available on request.

Sample Name	GM target	Soy Ref. copy number	Relative GM Content	Mean GM Content
#1/A dil.1	680	70652	0.96 %	1.02 %
#1/B dil.1	644	55241	1.17 %	
#1/A dil.2	136	15902	0.86 %	
#1/B dil.2	156	14420	1.08 %	

The example above shows a relative GM soy DNA content for the quantification control, calculated using the procedure above. Two DNA extracts were prepared in parallel from the material and two dilutions of these DNA extracts were analysed. The mean 35S or AgroBorder II DNA content as well as the corresponding standard deviation is calculated from the four individual results obtained with the DNA sample dilutions.

### 6.3.3 Parameters and Acceptance criteria

These criteria have to be fulfilled:

- Correlation coefficient of regression line ( $R^2$ )  $\geq 0.98$
- The average value of the slope of the standard curves should be approximately in the range of  $-3.1 \geq \text{slope} \geq -3.6$ , corresponding to amplification efficiencies of 90% to 110%.  
( $\text{Efficiency} [\%] = [10^{(-1/\text{slope})} - 1] \times 100$ )
- Deviation of quantification result of quantification control (prepared from certified reference material - CRM) from expected result +/- 30%
- No template controls (NTC) show no amplification

### 6.3.4 Asymmetric target situation

All samples containing more than 4.000 copies per reaction of GM 1 and positive for GM 2 have to be repeated in the GM 2 simplex quantification system, and vice versa.

### 6.3.5 Homogeneity

If independently extracted DNAs show significant deviations between "A" and "B", this may be due to sample material non-homogeneity (if differences in the quantification results) or to non-uniformities in the DNA-

extraction efficiency (if differences in the determined copy numbers). If the two quantification results and/or DNA copy numbers for the species reference system show significant differences, repeat DNA extraction and homogenise sample more thoroughly.

### 6.3.6 Inhibition Control with Sample Dilution

At least two dilutions of the DNA test sample should be used to detect inhibitory effects. As inhibition control the experimentally determined dilution factors in the species specific as well as in the GMO specific systems are calculated using the following equation:

$$\text{Dilution factor} = \frac{\text{Copy number}_{\text{undiluted sample}}}{\text{Copy number}_{\text{diluted sample}}}$$

The calculated dilution factor is then compared with the dilution of the sample. Deviation of +/- 20% can be accepted.

Deviation from calculated dilution factor to actual dilution factor:

Dilution of sample	Acceptable calculated dilution factor
1:5	1:4 to 1:6
1:10	1:8 to 1:12
1:20	1:16 to 1:24

If deviations occur, samples can be accepted after case to case evaluation. But deviation of quantification of duplicates should not be greater than -50% to + 100%. For greater deviations, the analysis has to be repeated.

## 7 PRODUCT WARRANTIES AND SATISFACTION GUARANTEE

Eurofins GeneScan Technologies GmbH (“GeneScan”) warrants the products manufactured by it will be free of defects in materials and workmanship when used in accordance with the applicable instructions for a period equal to or shorter of one year from the date of shipment of the product(s) or the expiration date marked on the product packaging under the storage conditions, recommended in the instructions and/or on the package. Application protocols published by GeneScan are intended to be only guidelines for the buyers of the products. Each buyer is expected to validate the applicability of each application protocol to his individual application. GeneScan makes no other warranty, expressed or implied. There is no warranty of merchantability or fitness for a particular purpose. GeneScan’s sole obligation with the respect to the foregoing warranties shall be, at its option, to either replace or to refund the purchase price of the product(s) or part thereof that proves defective in materials or workmanship within the warranty period, provided the customer notifies GeneScan promptly of any such defect.

GeneScan shall not be liable for any direct, indirect or consequential damages resulting from economic loss or property damages sustained by buyer or any customer from the use of the product(s). A copy of Eurofins GeneScan Technologies GmbH terms and conditions can be obtained on request, and is also provided in our price lists.

## 8 PRODUCT USE LIMITATIONS

This Eurofins GeneScan Technologies GMOQuant Kit is developed, designed, and sold for research purposes only. It is not to be used for diagnostic purposes or analysis of food and feed unless expressly cleared for that purpose by the appropriate regulatory authorities in the country of use. All due care and attention should be exercised in the handling of many of the materials described in this text.

## 9 TECHNICAL SERVICE

If you have any questions or experience any difficulties regarding this kit or Eurofins GeneScan Technologies products in general, please do not hesitate to contact us.

For technical assistance and more information please contact the Eurofins GeneScan Technologies Technical Service Department or your local distributor.