



Fapas® – GM Proficiency Test Report GeMMU126

GM Events in 100% Soya Flour

May-July 2025

PARTICIPANT LABORATORY NUMBER

Participants can log in to Fapas® SecureWeb at any time to obtain their laboratory number for this proficiency test.

Laboratory numbers are displayed in SecureWeb next to the download link for this report and are therefore fully confidential to each laboratory.

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SUMMARY

1. The test materials for Fapas® – GM proficiency test GeMMU126 were dispatched in May 2025. Each participant received a 100% soya flour test material to be analysed for GM soya events. Participants also had the option of submitting results for genetic elements; 35S promoter (p35S), nopaline synthase terminator (tNOS) and any other elements detected.
2. Qualitative results for this proficiency test are summarised as follows:

analyte	consensus	number of satisfactory results / number of results agreeing with consensus	total number of results	satisfactory results / results agreeing with consensus, %
35S Promoter	detected	30	30	100
NOS Terminator	detected	27	27	100
FMV	not detected	22	22	100
Cry1AbAc	not detected	9	9	100
PAT	not detected	18	18	100
Roundup Ready® (40-3-2) Soya	detected	26	26	100
MON89788 Soya	not detected	23	23	100

3. An assigned value (x_a) was determined for Roundup Ready® (40-3-2) Soya, and in conjunction with the standard deviation for proficiency (σ_p) was used to calculate a z-score for each result.
4. Quantitative results for this proficiency test are summarised as follows:

analyte	assigned value, x_a	units	number of scores, $ z \leq 2$	total number of scores	% $ z \leq 2$
Roundup Ready® (40-3-2) Soya	1.2	% w/w	16	18	89

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1. INTRODUCTION

1.1. Proficiency Testing

Proficiency testing aims to provide an independent assessment of the competence of participating laboratories. Together with the use of validated methods, proficiency testing is an essential element of laboratory quality assurance.

Further details of the Fapas® – GM proficiency testing scheme are available in our protocols [7, 8].

2. TEST MATERIAL

2.1. Preparation

Preparation of the samples for this proficiency test was sub-contracted to a laboratory meeting the quality requirements of the scheme's accreditation [3].

Test materials were prepared by milling and blending a quantity of 100% Roundup Ready® (40-3-2) soya flour and a quantity of non-GM soya flour. The ingredients were mixed to produce a homogeneous test material.

Samples were stored at +4°C until dispatch.

2.2. Homogeneity Testing and Stability

To test for homogeneity, randomly selected test materials were analysed in duplicate. Testing was sub-contracted to a laboratory meeting the quality requirements of the scheme's accreditation [3].

These data showed sufficient homogeneity and were not included in the subsequent calculation of the assigned value.

Fapas® proficiency test materials are prepared such that they are known to be sufficiently stable for the duration of the test, inclusive of transportation [7]. No further specific stability testing was required for this proficiency test.

2.3. Dispatch

The start date was 16 May 2025. Test materials were sent to 32 participants.

3. RESULTS

Participants were able to report their data qualitatively (indicating whether the genetic element analysed for and/or GM event was 'detected' or 'not detected') and semi-quantitatively or quantitatively, expressing results as a percentage (%) present in the test material provided, using any appropriate method, along with their relevant limits of detection and quantification.

Quantitative data for GM events in Fapas® – GM proficiency tests may be expressed either on a weight basis, i.e. w/w of the total soya/maize present and/or, on a genome basis, i.e. relative to the number of haploid genomes present in the test material.

Results were submitted by 32 participants (100%) before the closing date for this test, 03 July 2025.

Each participant was given a laboratory number, assigned in order of receipt of results. The reported qualitative results are given in Table 1-3, whilst the quantitative results are given in Tables 4-6.

Details regarding any other elements detected and/or quantified are given in Table 2 and Table 5.

Participants' comments are given in Table 7.

The analytical methods used by each participant are summarised in APPENDIX I.

4. QUALITATIVE ANALYSIS OF DATA

Sourcing uncontaminated material for GM testing is increasingly difficult. It is only for GM events knowingly added to the matrix during test material preparation that it can confidently be assumed that the participants' consensus will be 'detected'. For all other events the possibility of trace contamination means that the expected result will be 'not known'. Qualitative results are therefore evaluated against the consensus and then may be expressed as either Agreeing or Disagreeing with the consensus; in this case either result could be deemed as valid. In addition, where a test material is known to be positive with respect to GM contamination, results may be expressed as Satisfactory or Not Satisfactory.

The GM event Roundup Ready® (40-3-2) soya contains the 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) gene, under regulation of the 35S promoter (p35S) and nopaline synthase terminator (tNOS) [9].

Consequently, it can be concluded that p35S and tNOS were deliberately added during the preparation of the test material GeMMU126.

Qualitative data are tabulated in the report and are denoted as 'S' for satisfactory or 'NS' for not satisfactory for GM events deliberately added during preparation, or annotated as 'A' for agrees or 'D' for disagrees for GM events not deliberately added, after comparison of the result with the consensus.

The number and percentage of satisfactory evaluations and evaluations agreeing with the consensus are given in Table 8.

5. STATISTICAL EVALUATION OF RESULTS

The results submitted by participants were statistically analysed in order to provide an assigned value for each GM event. The assigned values were then used in combination with the standard deviation for proficiency, σ_p , to calculate a z-score [10] for each result. The procedure is detailed in the relevant protocols [7, 8].

Further background on the procedure followed can be found in the IUPAC International Harmonised Protocol for the Proficiency Testing of Analytical Chemistry Laboratories [11].

5.1. Calculation of the Assigned Value, x_a

The assigned value, x_a , for each GM event was derived from the consensus of the results submitted by participants.

The procedure used to derive this consensus involved:

- i) exclusion, if present, of any non numerical results i.e. qualitative or semi-quantitative results or results reported as zero,
- ii) a $\log_{10}$ transformation of submitted results to obtain a normal distribution [12, 13, 14],

- iii) exclusion, if present, of any results that were approximately 10, 100 or 1000 × greater or smaller than the majority of submitted results (as these were considered to be reporting errors).

For Roundup Ready® (40-3-2) Soya, the median was chosen as the assigned value due to the low number of data points.

It was not possible to derive an assigned value or issue z-scores for each of the other quantitative analytes as there were insufficient results.

The assigned value for each of the analytes is shown in Table 9.

5.2. Standard Deviation for Proficiency, σ_p

The standard deviation for proficiency, σ_p , was set at a value that reflects best practice for the analyses in question.

For each GM event, σ_p was calculated using fitness-for-purpose criteria derived from recent Fapas® – GM data, in discussion with the Fapas® Advisory Committee.

The values for σ_p used to calculate z-scores from the reported results of this test are given in Table 9.

5.3. Individual z-Scores

Participants' z-scores were calculated as:

$$z = \frac{(x - x_a)}{\sigma_p}$$

where x = the participant's reported result,
 x_a = the assigned value, see Table 9,
 and σ_p = the standard deviation for proficiency, see Table 9.

Participants' z-scores are given in Table 6 and shown as a histogram in Figure 1. It is possible for the z-scores published in this report to differ slightly from the z-score that can be calculated using the formula given above. These differences arise from the necessary rounding of the actual assigned value and standard deviation for proficiency prior to their publication in Table 9.

The number and percentage of z-scores in the range $-2 \leq z \leq 2$ are given in Table 10.

6. INTERPRETATION OF SCORES

In normal circumstances, over time, about 95% of z-scores will lie in the range $-2 \leq z \leq 2$. Occasional scores in the range $2 < |z| < 3$ are to be expected, at a rate of 1 in 20. Whether or not such scores are of importance can only be decided by considering them in the context of the other scores obtained by that laboratory.

Scores where $|z| > 3$ are to be expected at a rate of about 1 in 300. Given this rarity, such z-scores very strongly indicate that the result is not fit-for-purpose and almost certainly requires investigation.

The consideration of a set or sequence of z-scores over time provides more useful information than a single z-score. Examples of suitable methods of comparison are provided in the IUPAC International Harmonised Protocol for the Proficiency Testing of Analytical Chemistry Laboratories [11].

7. REFERENCES

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Table 1: Qualitative Results and Assessments for p35S, tNOS and FMV

laboratory number	analyte								
	35S Promoter consensus: 100% detected (positive) (expected result: detected)			NOS Terminator consensus: 100% detected (positive) (expected result: detected)			FMV consensus: 100% not detected (negative) (expected result: not known)		
	result	Limit of Detection, (LoD)	assessment	result	Limit of Detection, (LoD)	assessment	result	Limit of Detection, (LoD)	assessment
001	Detected	0.1%	S	Detected	0.1%	S	Not Detected	0.1%	A
002	Detected	0.1%	S	Detected	0.1%	S	Not Detected	0.1%	A
003	Detected		S	Detected		S			
004	Detected	0.01	S	Detected	0.01	S	Not Detected	0.01	A
005	Detected	0.01	S						
006	Detected		S	Detected		S	Not Detected		A
007	Detected	0.1%	S	Detected	0.1%	S	Not Detected	0.1%	A
008	Detected	0.01	S	Detected	0.01	S	Not Detected		A
009	Detected	0.01%	S	Detected	0.01%	S	Not Detected	0.01%	A
010									
011	Detected		S						

LoD = limit of detection

A = agrees with consensus

S = satisfactory

D = disagrees with consensus

NS = not satisfactory

Table 1 (continued): Qualitative Results and Assessments for p35S, tNOS and FMV

laboratory number	analyte								
	35S Promoter consensus: 100% detected (positive) (expected result: detected)			NOS Terminator consensus: 100% detected (positive) (expected result: detected)			FMV consensus: 100% not detected (negative) (expected result: not known)		
	result	Limit of Detection, (LoD)	assessment	result	Limit of Detection, (LoD)	assessment	result	Limit of Detection, (LoD)	assessment
012	Detected	0.01	S	Detected	0.01	S	Not Detected	0.01	A
013	Detected	20 copies	S	Detected	20 copies	S	Not Detected	20 copies	A
014	Detected	10copies	S	Detected	10copies	S	Not Detected	10copies	A
015	Detected	0.01	S	Detected	0.01	S			
016	Detected	0.025	S	Detected	0.025	S	Not Detected	0.025	A
017	Detected	0.025	S	Detected	0.025	S	Not Detected	0.025	A
018									
019	Detected	0.1	S	Detected	0.1	S	Not Detected	0.1	A
020	Detected		S	Detected		S	Not Detected		A
021	Detected		S	Detected		S	Not Detected		A
022	Detected		S	Detected		S	Not Detected		A

LoD = limit of detection

A = agrees with consensus

D = disagrees with consensus

S = satisfactory

NS = not satisfactory

Table 1 (continued): Qualitative Results and Assessments for p35S, tNOS and FMV

laboratory number	analyte								
	35S Promoter consensus: 100% detected (positive) (expected result: detected)			NOS Terminator consensus: 100% detected (positive) (expected result: detected)			FMV consensus: 100% not detected (negative) (expected result: not known)		
	result	Limit of Detection, (LoD)	assessment	result	Limit of Detection, (LoD)	assessment	result	Limit of Detection, (LoD)	assessment
023	Detected	0.01	S	Detected	0.01	S	Not Detected	0.01	A
024	Detected	0.1%	S	Detected	0.1%	S	Not Detected	0.1%	A
025	Detected	0.1%	S						
026	Detected		S	Detected		S			
027	Detected	0.05	S	Detected	0.05	S			
028	Detected	0.01%	S	Detected	0.01%	S	Not Detected	0.01%	A
029	Detected	0.01	S	Detected	0.01	S	Not Detected	0.01	A
030	Detected		S	Detected		S	Not Detected		A
031	Detected	0.1%	S	Detected	0.1%	S	Not Detected	0.1%	A
032	Detected	0.01%	S	Detected	0.01%	S			

LoD = limit of detection

A = agrees with consensus

S = satisfactory

D = disagrees with consensus

NS = not satisfactory

Table 2: Qualitative Results and Assessments for Cry1AbAc, PAT and Other Elements

laboratory number	analyte								
	Cry1AbAc consensus: 100% not detected (negative) (expected result: not known)			PAT consensus: 100% not detected (negative) (expected result: not known)			Other Element Detected		
	result	Limit of Detection, (LoD)	assessment	result	Limit of Detection, (LoD)	assessment	result	Limit of Detection, (LoD)	assessment
001				Not Detected	0.1%	A			
002				Not Detected	0.1%	A			
003				Not Detected		A			
004	Not Detected	0.01	A	Not Detected	0.01	A			
005				Not Detected	0.01	A			
006									
007									
008	Not Detected		A	Not Detected		A			
009				Not Detected	0.01%	A			
010									
011									

LoD = limit of detection

A = agrees with consensus

S = satisfactory

D = disagrees with consensus

NS = not satisfactory

Table 2 (continued): Qualitative Results and Assessments for Cry1AbAc, PAT and Other Elements

laboratory number	analyte								
	Cry1AbAc consensus: 100% not detected (negative) (expected result: not known)			PAT consensus: 100% not detected (negative) (expected result: not known)			Other Element Detected		
	result	Limit of Detection, (LoD)	assessment	result	Limit of Detection, (LoD)	assessment	result	Limit of Detection, (LoD)	assessment
012	Not Detected	0.01	A	Not Detected	0.01	A			
013				Not Detected	20 copies	A			
014									
015									
016	Not Detected	0.025	A	Not Detected	0.025	A			
017									
018									
019				Not Detected	0.1	A	Detected	cp4epsps	
020									
021	Not Detected		A	Not Detected		A	Detected CP4- epsps	CP4-epsps	
022	Not Detected		A	Not Detected		A			

LoD = limit of detection

A = agrees with consensus

S = satisfactory

D = disagrees with consensus

NS = not satisfactory

Table 2 (continued): Qualitative Results and Assessments for Cry1AbAc, PAT and Other Elements

laboratory number	analyte								
	Cry1AbAc consensus: 100% not detected (negative) (expected result: not known)			PAT consensus: 100% not detected (negative) (expected result: not known)			Other Element Detected		
	result	Limit of Detection, (LoD)	assessment	result	Limit of Detection, (LoD)	assessment	result	Limit of Detection, (LoD)	assessment
023				Not Detected	0.01	A	DAS44406 - Not Detected	0.01	
024	Not Detected	0.1%	A	Not Detected	0.1%	A			
025									
026									
027				Not Detected	0.05	A			
028	Not Detected	0.01%	A	Not Detected	0.01%	A			
029	Not Detected	0.01	A	Not Detected	0.01	A			
030									
031									
032									

LoD = limit of detection

A = agrees with consensus

S = satisfactory

D = disagrees with consensus

NS = not satisfactory

Table 3: Qualitative Results and Assessments for Roundup Ready® (40-3-2) Soya and MON89788 Soya

laboratory number	analyte					
	Roundup Ready® (40-3-2) Soya consensus: 100% detected (positive) (expected result: detected)			MON89788 Soya consensus: 100% not detected (negative) (expected result: not known)		
	result	Limit of Detection, (LoD)	assessment	result	Limit of Detection, (LoD)	assessment
001	Detected	0.1%	S	Not Detected		A
002						
003	Detected	0.05	S	Not Detected	0.05	A
004	Detected	0.01	S	Not Detected	0.01	A
005	Detected	0.01	S	Not Detected	0.01	A
006						
007						
008	Detected	0.01	S	Not Detected		A
009	Detected	0.01%	S	Not Detected	0.01%	A
010	Detected		S	Not Detected		A
011	Detected	0.1%	S			

LoD = limit of detection

A = agrees with consensus

S = satisfactory

D = disagrees with consensus

NS = not satisfactory

Table 3 (continued): Qualitative Results and Assessments for Roundup Ready® (40-3-2) Soya and MON89788 Soya

laboratory number	analyte					
	Roundup Ready® (40-3-2) Soya consensus: 100% detected (positive) (expected result: detected)			MON89788 Soya consensus: 100% not detected (negative) (expected result: not known)		
	result	Limit of Detection, (LoD)	assessment	result	Limit of Detection, (LoD)	assessment
012	Detected	0.01	S	Not Detected	0.01	A
013	Detected	20 copies	S	Not Detected	20 copies	A
014	Detected	%0.045	S	Not Detected	%0.045	A
015	Detected	0.01	S	Not Detected	0.01	A
016	Detected	0.025	S	Not Detected	0.025	A
017	Detected	0.01	S	Not Detected	0.01	A
018	Detected		S			
019	Detected	0.1	S	Not Detected	0.05	A
020	Detected		S	Not Detected		A
021	Detected		S	Not Detected		A
022						

LoD = limit of detection

A = agrees with consensus

S = satisfactory

D = disagrees with consensus

NS = not satisfactory

Table 3 (continued): Qualitative Results and Assessments for Roundup Ready® (40-3-2) Soya and MON89788 Soya

laboratory number	analyte					
	Roundup Ready® (40-3-2) Soya consensus: 100% detected (positive) (expected result: detected)			MON89788 Soya consensus: 100% not detected (negative) (expected result: not known)		
	result	Limit of Detection, (LoD)	assessment	result	Limit of Detection, (LoD)	assessment
023	Detected	0.01	S	Not Detected	0.01	A
024	Detected	0.1%	S	Not Detected	0.1%	A
025	Detected	0.5%	S	Not Detected	0.1	A
026	Detected		S	Not Detected		A
027	Detected	0.05	S	Not Detected	0.05	A
028						
029	Detected	0.01	S	Not Detected	0.01	A
030	Detected	0.045	S	Not Detected	0.045	A
031	Detected	0.1%	S			
032						

LoD = limit of detection

A = agrees with consensus

S = satisfactory

D = disagrees with consensus

NS = not satisfactory

Table 4: Qualitative Results and Assessments for p35S, tNOS and FMV

laboratory number	analyte								
	35S Promoter assigned value: not set			NOS Terminator assigned value: not set			FMV assigned value: not set		
	result, %	Limit of Quantification, (LoQ)	z-score	result, %	Limit of Quantification, (LoQ)	z-score	result, %	Limit of Quantification, (LoQ)	z-score
001									
002									
003									
004									
005									
006									
007									
008	1.5	0.1		1.4	0.1				
009									
010									
011									

LoQ = limit of quantification

no assigned value or z-scores issued, see Section 5.1

Table 4 (continued): Qualitative Results and Assessments for p35S, tNOS and FMV

laboratory number	analyte								
	35S Promoter assigned value: not set			NOS Terminator assigned value: not set			FMV assigned value: not set		
	result, %	Limit of Quantification, (LoQ)	z-score	result, %	Limit of Quantification, (LoQ)	z-score	result, %	Limit of Quantification, (LoQ)	z-score
012									
013									
014									
015	1.1	0.1		0.8	0.1				
016									
017	2.18	0.1							
018									
019									
020									
021									
022									

LoQ = limit of quantification

no assigned value or z-scores issued, see Section 5.1

Table 4 (continued): Qualitative Results and Assessments for p35S, tNOS and FMV

laboratory number	analyte								
	35S Promoter assigned value: not set			NOS Terminator assigned value: not set			FMV assigned value: not set		
	result, %	Limit of Quantification, (LoQ)	z-score	result, %	Limit of Quantification, (LoQ)	z-score	result, %	Limit of Quantification, (LoQ)	z-score
023	1.57	0.05		1.52	0.05				
024									
025									
026									
027	0.60	0.1							
028	<0.1	0.1%		<0.1	0.1%		Not Detected	0.1%	
029									
030									
031									
032	0.50	0.1%		>1.0	Relative				

LoQ = limit of quantification

no assigned value or z-scores issued, see Section 5.1

Table 5: Qualitative Results and Assessments for Cry1AbAc, PAT and Other Elements

laboratory number	analyte								
	Cry1AbAc assigned value: not set			PAT assigned value: not set			Other Element assigned value: no data		
	result, %	Limit of Quantification, (LoQ)	z-score	result, %	Limit of Quantification, (LoQ)	z-score	result	Limit of Quantification, (LoQ)	z-score
001									
002									
003									
004									
005				0.00	0.1				
006									
007									
008									
009									
010									
011									

LoQ = limit of quantification

no assigned value or z-scores issued, see Section 5.1

Table 5 (continued): Qualitative Results and Assessments for Cry1AbAc, PAT and Other Elements

laboratory number	analyte								
	Cry1AbAc assigned value: not set			PAT assigned value: not set			Other Element assigned value: no data		
	result, %	Limit of Quantification, (LoQ)	z-score	result, %	Limit of Quantification, (LoQ)	z-score	result	Limit of Quantification, (LoQ)	z-score
012									
013									
014									
015									
016									
017									
018									
019									
020									
021									
022									

LoQ = limit of quantification

no assigned value or z-scores issued, see Section 5.1

Table 5 (continued): Qualitative Results and Assessments for Cry1AbAc, PAT and Other Elements

laboratory number	analyte								
	Cry1AbAc assigned value: not set			PAT assigned value: not set			Other Element assigned value: no data		
	result, %	Limit of Quantification, (LoQ)	z-score	result, %	Limit of Quantification, (LoQ)	z-score	result	Limit of Quantification, (LoQ)	z-score
023									
024									
025									
026									
027									
028	Not Detected	0.1%		Not Detected	0.1%				
029									
030									
031									
032									

LoQ = limit of quantification

no assigned value or z-scores issued, see Section 5.1

Table 6: Qualitative Results and Assessments for Roundup Ready® (40-3-2) Soya and MON89788 Soya

laboratory number	analyte					
	Roundup Ready® (40-3-2) Soya assigned value: 1.2 % w/w			MON89788 Soya assigned value: not set		
	result	Limit of Quantification, (LoQ)	z-score	result, % w/w	Limit of Quantification, (LoQ)	z-score
001						
002						
003						
004	1.95	0.1	1.5			
005	2.30	0.05	2.0	0.00	0.05	
006						
007						
008	1.5	0.1	0.8			
009						
010	0.43		-2.9	0		
011	1.348	0.1%	0.5			

LoQ = limit of quantification

z-scores outside $|z| > 2$ are shown in **bold**, see Section 6

Table 6 (continued): Qualitative Results and Assessments for Roundup Ready® (40-3-2) Soya and MON89788 Soya

laboratory number	analyte					
	Roundup Ready® (40-3-2) Soya assigned value: 1.2 % w/w			MON89788 Soya assigned value: not set		
	result	Limit of Quantification, (LoQ)	z-score	result, % w/w	Limit of Quantification, (LoQ)	z-score
012	0.72	0.05	-1.4			
013	1.28	0.05%	0.3			
014	0.99	%0.09	-0.4			
015	1.1	0.1	-0.1	nd	0.1	
016	1.88	0.05	1.4			
017	2.08	0.1	1.7			
018						
019	0.87	0.09	-0.8	Not Detected	0.1	
020	0.9		-0.7			
021	0.51		-2.4			
022	1.8	0.09	1.3			

LoQ = limit of quantification

z-scores outside $|z| > 2$ are shown in **bold**, see Section 6

Table 6 (continued): Qualitative Results and Assessments for Roundup Ready® (40-3-2) Soya and MON89788 Soya

laboratory number	analyte					
	Roundup Ready® (40-3-2) Soya assigned value: 1.2 % w/w			MON89788 Soya assigned value: not set		
	result	Limit of Quantification, (LoQ)	z-score	result, % w/w	Limit of Quantification, (LoQ)	z-score
023						
024	1.21	0.1%	0.1			
025						
026						
027	0.60	0.1	-1.9	0.00	0.1	
028						
029	>2	0.1				
030	0.92	0.09	-0.7			
031						
032						

LoQ = limit of quantification

z-scores outside $|z| > 2$ are shown in **bold**, see Section 6

Table 7: Participants' Comments

laboratory number	comments
001	Foodproof GMO screening Lyokit 1 & Lyokit 2 (BIOTECON)
004	30% uncertainty
005	Endogenous genes(Le1)is very low. The soya flour appeared to have been heat treated.
007	Employ ID :65879 - 65904 - 65529
021	Elements not detected include: ctp2/CP4-epsps and T-E9.
025	Nucleic acid concentration measurement device (NanoDrop1000, NanoSpec) and thermal cycler (9700, SimpliAmp validation.
029	Our accredited quantification range is 0.1%-2%, so for the assay Roundup Ready (40-3-2) soya we can just say >2%.

comments are as submitted by participants but some may have been edited to maintain participant anonymity

Table 8: Number and Percentage of Satisfactory Results and Results Agreeing with the Consensus

analyte	consensus	number of satisfactory results / number of results agreeing with consensus	total number of results	satisfactory results / results agreeing with consensus, %
35S Promoter	detected	30	30	100
NOS Terminator	detected	27	27	100
FMV	not detected	22	22	100
Cry1AbAc	not detected	9	9	100
PAT	not detected	18	18	100
Roundup Ready® (40-3-2) Soya	detected	26	26	100
MON89788 Soya	not detected	23	23	100

Table 9: Assigned Values and Standard Deviations for Proficiency

analyte	data points, n	assigned value, x_a	units	uncertainty, u	standard deviation for proficiency, σ_p
Roundup Ready® (40-3-2) Soya	18	1.2	% w/w	0.1	GM FIXED 0.15

Table 10: Number and Percentage of z-Scores where $|z| \leq 2$

analyte	number of scores where $ z \leq 2$	total number of scores	% $ z \leq 2$
Roundup Ready [®] (40-3-2) Soya	16	18	89

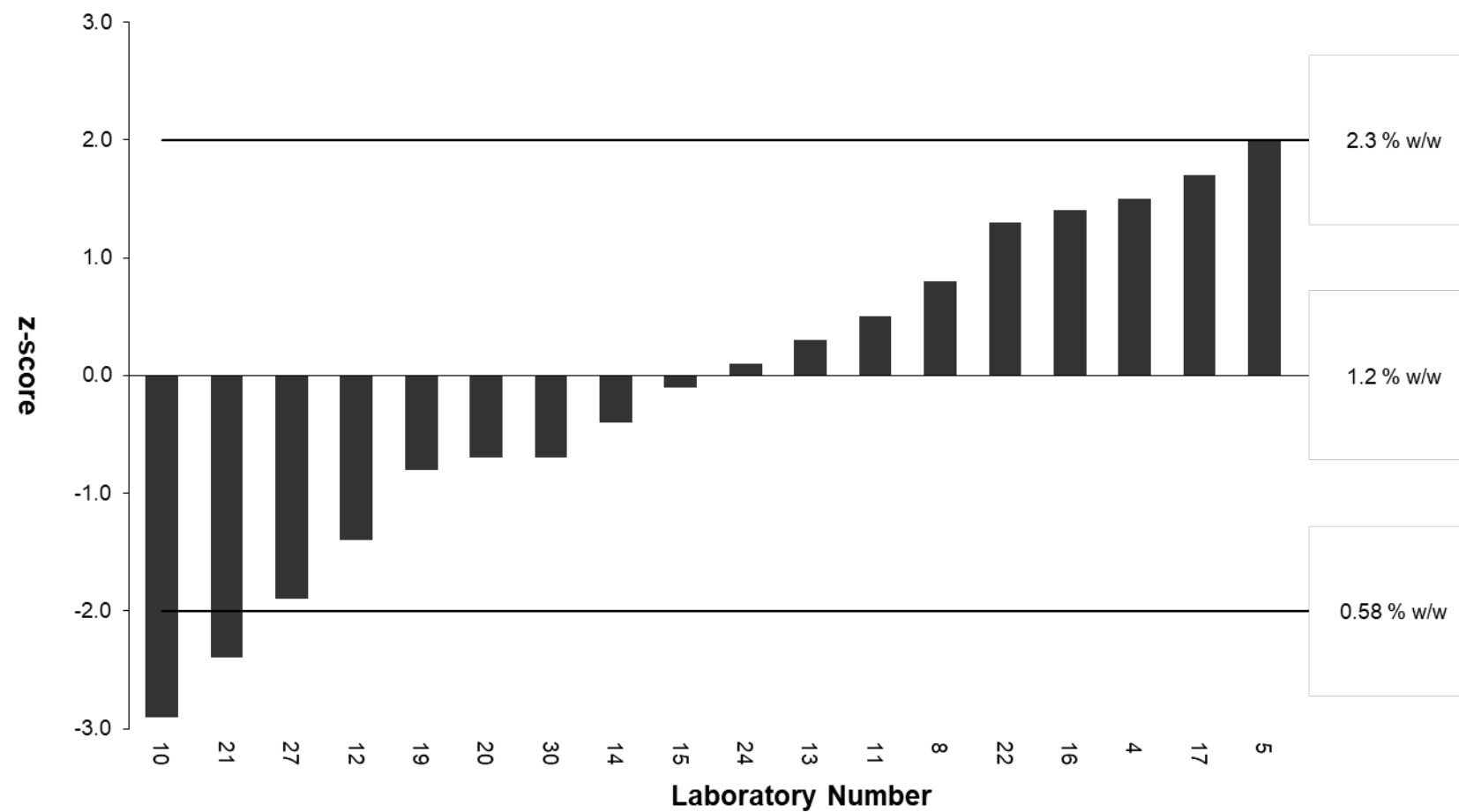


Figure 1: z-Scores for Roundup Ready® (40-3-2) Soya

APPENDIX I: Analytical Methods Used by Participants

Methods are tabulated according to the information supplied by participants, but some responses may have been combined or edited for clarity. Text that appears as unreadable symbols are derived from entries made using non-Western characters.

GM Qualitative (All TMs)

Does your lab have an externally recognised Quality System?	laboratory number
---	-------------------

no	011 013
yes	001 002 004 005 006 007 010 012 016 017 018 019 020 025 027 028 029 031 032

If 'yes' is the external recognition:	laboratory number
---------------------------------------	-------------------

ISO 9000 series certification	010 017 028
GLP	005
ISO 17025 accreditation	001 002 004 005 007 012 016 017 018 019 020 025 027 028 029 031 032

If you selected 'ISO 17025 accreditation' is the particular method used for the analysis of this analyte covered by your ISO 17025 accreditation?	laboratory number
---	-------------------

no	005 011 020 031
yes	001 002 004 007 012 017 018 019 025 027 028 029 032

Reference	laboratory number
2012	025
AFNOR	032
Compendium of validated GMO Detection Methods. Assembled by the Molecular Biology and Genomics Unit MBG of the Institute for Health and Consumer Protection IHCP, nominated European Union Reference Laboratory for Genetically modified Food And Feed EURL-GMF	017
ISO 2005 ISO 21569:2005 8	028
JRC	004
Manufacturer's Instructions	001
NA	002
validated in house method	018
DNA	011

Number of Replicate DNA Extractions from Test Material	laboratory number
1	001
2	002 005 007 016 017 018 019 025 027 028
3	010
4	020
5	011

Sample Weight per Replicate (g)	laboratory number
<0.1	002 011 012 018
≥0.1 - <0.5	001 007 016 017 019 020 028 032
≥0.5 - <1	010
≥1 - <1.5	005 025

DNA Extraction Kit	laboratory number
Machery Nagel Nucleospin	019
Qiagen DNeasy plant maxi kit	025
Qiagen DNeasy plant mini kit	010
Qiagen QIAquick	012
Conventional method- CTAB method	028
CTAB	016
DNeasy Mericon Food kit	017
Foodproof® sample preparation kit III	020
GM-Quicker4	005
Gold Standard Diagnostics Genespin	032
Invsorb Spin Plant Mini Kit	002
Kogene DNA Extraction from Food and Feed Kit	007
Our Preparation reagent	011
Promega maxwell kit	004
Tianlong	018

Extraction Buffers Used?	laboratory number
supplied with kit	001 002 005 007 010 017 018 019 020 025
CTAB	004 011 012 016 028

DNA Clean-up	laboratory number
Ethanol precipitation	007 010 011 012 025 028
none	002 017 018 019 020 032
DNAway	005

Method of Measurement of DNA	laboratory number
UV Spectrophotometer (Optical Density)	002 005 010 012 016 017 018 019 025 027
none	001 004 007
Fluorimetry	011
nanodrop	020 032
Nanospectrophotometer	028

Amount of DNA (ng)	laboratory number
≥40 - <60	010 016
≥80 - <100	012
≥100 - <150	017 019
≥150 - <200	032
≥200 - <250	005
≥250 - <300	018 025 028
≥400 - <500	020
≥500	002
not known	004 011

Dilution of DNA Used in PCR	laboratory number
undiluted	011 020 032
1:1	018
1:2	017
1:5 - 1:9	001 005 012 019 028
1:11 - 1:49	002 025
not known	004 010

Qualitative : PCR Method	laboratory number
Conventional Monoplex PCR	018 019 025
Monoplex Real Time PCR	005 011 016 017 025 027
Multiplex Real Time PCR	001 002 004 007 010 012 020 028 032

Qualitative Gel PCR: Number of Replicate Analyses per DNA Extraction	laboratory number
1	025
2	019
3	010

Qualitative Gel PCR: Number of PCR Cycles	laboratory number
40	010 025
45	019
50	001

Qualitative Real Time PCR: Number of Replicate Analyses per DNA Extraction**laboratory number**

1	001 025 027
2	002 005 007 011 016 017 019 020 032
3	010 028

Qualitative Real Time PCR: Number of PCR Cycles**laboratory number**

40	010
45	002 005 007 011 016 017 019 025 027 028 032
50	020

Qualitative : Amplicon Detection Instrumentation**laboratory number**

Light Cycler	010 027
Rotorgene	019
ABI StepOne PLUS	025
ABI7500	005
Biorad- CFX 96	028
Biorad CFX96 Real Time PCR System	002
QS7 / NGS	012
Quant studio 5	007 011
QuantStudio 6 Pro Real-time PCR	017

Qualitative : Amplicon Detection Technology**laboratory number**

Taqman (fret) probe	005 007 010 011 012 016 017 020 025 027 028
FAM- BHQ1	019

Positive Controls Used	laboratory number
AOCS 0906- B2, ERM-BF410, ERM-BF422b	028
CRM	007
Internal control sample	025
MON 89034 CRM	032
MRC	017
plasmids	005
Supplied with Kit	002
Using positive controls in the case of quantitative test	011
with Kit	020
Yes	018 019

Negative Controls Used	laboratory number
reagent / extraction blank	001 004 007 012 016 018 019 025 027 028
water blank	011 016 019 020 028
ColE1/TE	005
Cotton DNA	017
Kit NTC	032
Supplied with Kit	002
none	010

Did You Use a Target Specific or Screening Only Method?	laboratory number
Target Specific	002 007 011 018 019 025 028
Screening	001 004 005 020 032
both	012 016 017

Target DNA Sequences for Screening Method	laboratory number
35S promoter	001 002 005 007 011 016 017 019 020 028 032
NOS terminator	001 002 007 016 017 019 020 028 032
ABII	032
bar, FMV	020
FMV	007
FMV, pat, Plant	002
pFMV	017
pFMV, pat, bar,CTP2-CP4EPSPS	001
pFMV, PAT, cp4epsps	019

Amplicon Size (base pairs) - Screening Method	laboratory number
101bp	005
78	017
Not applicable	028

Target DNA Sequences for Soya	laboratory number
121bp	025
280	018
Le1	005
LEC	017
lectin	019
Lectin gene	028

Amplicon Size (base pairs) - Endogenous gene for Soya	laboratory number
118	019
118bp	005 025
200	018
74	017
Not applicable	028

Target DNA Sequences for Roundup Ready Soya**laboratory number**

35S promoter	001 011 017
35S terminator	020
CTP -> EPSPS	001
Lectin	012 017
NOS terminator	001 017 020
RR Soya specific	004 005 012 017 019 020 025

Amplicon Size (base pairs) - GM event gene for Roundup Ready Soya**laboratory number**

121bp	005 025
171	017
280	018
84	019
Not applicable	028

Target DNA Sequences for Maize**laboratory number**

ADH	004
-----	-----

Amplicon Size (base pairs) - Endogenous gene for Maize**laboratory number**

Not applicable	028
----------------	-----

Target DNA Sequences for Bt176 Maize**laboratory number**

Bt176 specific	004
----------------	-----

Amplicon Size (base pairs) - GM event gene for Bt176 Maize**laboratory number**

Not applicable	028
----------------	-----

Target DNA Sequences for Bt11 Maize**laboratory number**

Bt11 specific	004
---------------	-----

Amplicon Size (base pairs) - GM event gene for Bt11 Maize	laboratory number
Not applicable	028
Target DNA Sequences for MON810 Maize	laboratory number
MON810 specific	004
Amplicon Size (base pairs) - GM event gene for MON810 Maize	laboratory number
Not applicable	028
Target DNA Sequences for GA21 Maize	laboratory number
GA21 specific	004
Amplicon Size (base pairs) - GM event gene for GA21 Maize	laboratory number
Not applicable	028
Target DNA Sequences for NK603 Maize	laboratory number
NK603 specific	004
Amplicon Size (base pairs) - GM event gene for NK603 Maize	laboratory number
Not applicable	028
Target DNA Sequences for TC1507 Maize	laboratory number
TC1507 specific	004
Amplicon Size (base pairs) - GM event gene for TC1507 Maize	laboratory number
Not applicable	028

Target DNA Sequences for MON863 Maize	laboratory number
---------------------------------------	-------------------

MON863 specific	004
-----------------	-----

Amplicon Size (base pairs) - GM event gene for MON863 Maize	laboratory number
---	-------------------

Not applicable	028
----------------	-----

Target DNA Sequences for MIR604 Maize	laboratory number
---------------------------------------	-------------------

MIR604 specific	004
-----------------	-----

Amplicon Size (base pairs) - GM event gene for MIR604 Maize	laboratory number
---	-------------------

Not applicable	028
----------------	-----

Target DNA Sequences for MON88017 Maize	laboratory number
---	-------------------

MON88017 specific	004
-------------------	-----

Amplicon Size (base pairs) - GM event gene for MON88017 Maize	laboratory number
---	-------------------

Not applicable	028
----------------	-----

Source of Reference Materials for Roundup Ready Soya	laboratory number
--	-------------------

ERM-BF410 Series (RRS)	012 017 018 019
------------------------	-----------------

plasmids	005
----------	-----

GM Quantitative (All TMs)

Does your lab have an externally recognised Quality System?	laboratory number
---	-------------------

no	011 025
----	---------

yes	005 010 012 016 017 019 020 027 028
-----	-------------------------------------

If 'no' what in-house quality systems are in place?	laboratory number
---	-------------------

According to qualitative test.	025
--------------------------------	-----

If 'yes' is the external recognition:	laboratory number
---------------------------------------	-------------------

ISO 9000 series certification	010 017 028
GLP	005
ISO 17025 accreditation	005 012 016 017 019 020 027 028

If you selected 'ISO 17025 accreditation' is the particular method used for the analysis of this analyte covered by your ISO 17025 accreditation?	laboratory number
---	-------------------

no	005 011 020
yes	012 016 017 019 027 028

Reference	laboratory number
-----------	-------------------

Compendium of validated GMO Detection Methods Assembled by the Molecular Biology and Genomics Unit MBG of the Institute for Health and Consumer Protection IHCP, nominated European Union Reference Laboratory for Genetically modified Food And Feed EURL-GMFF	017
ISO 2005 ISO 21570:2005 12	028
DNA	011

Number of Replicate DNA Extractions from Test Material	laboratory number
--	-------------------

2	012 016 017 019 028
3	010
5	011

Sample Weight per Replicate (g)	laboratory number
---------------------------------	-------------------

<0.1	011 012
≥0.1 - <0.5	010 016 017 019 020 028
≥1 - <1.5	005

DNA Extraction Kit	laboratory number
Machery Nagel Nucleospin	019
Qiagen DNeasy plant mini kit	010
Qiagen QIAquick	012
Conventional- CTAB method	028
DNeasy Mericon Food	017
Foodproof® sample preparation kit III	020
GM-Quicker4	005
Our Preparation reagent	011

Extraction Buffers Used?	laboratory number
supplied with kit	005 010 017 019 020
CTAB	011 012 016 028

DNA Clean-up	laboratory number
Ethanol precipitation	010 011 012 028
none	017 019 020
DNAway	005

Method of Measurement of DNA	laboratory number
UV Spectrophotometer (Optical Density)	005 010 012 016 017 019 027
Fluorimetry	011
nanodrop	020
Nanospectrophotometer	028

Amount of DNA (ng)	laboratory number
≥40 - <60	010 016
≥80 - <100	012
≥100 - <150	017 019
≥200 - <250	005
≥250 - <300	028
≥400 - <500	020
not known	011

Dilution of DNA Used in PCR	laboratory number
undiluted	011 020
1:2	017
1:4	019
1:5 - 1:9	005 012 028
1:10	016
not known	010

Quantitative : PCR Method	laboratory number
Monoplex Real Time PCR	005 011 016 017 019 020 027
Multiplex Real Time PCR	010 012 028

Quantitative Real Time PCR: Number of Replicate Analyses per DNA Extraction	laboratory number
2	011 012 016 017 019 020 027
3	005 010 028

Quantitative Real Time PCR: Number of PCR Cycles	laboratory number
40	010 016
45	005 011 017 019 020 027 028
50	012

Quantitative : Amplicon Detection Instrumentation	laboratory number
Light Cycler	010 027
Rotorgene	019
ABI7500	005
Biorad CFX 96	028
ddPCR	012
QuantStudio 6 Pro Real-timePCR	017

Quantitative : Amplicon Detection Technology	laboratory number
SYBR Green	012
Taqman (fret) probe	005 010 011 017 020 027 028
AABI	016
Method of Quantification	laboratory number
Copy Number Standard Curve Using Plasmid Dilution Series from One Standard	005 010
Percentage (%) Standard Curve Using Dilution Series from One Standard	017 020 028
Percentage (%) Standard Curve Using Range of Percentage Standards	011
digital droplet PCR	012
Percentage Standards Used	laboratory number
10; 1; 0.1	019
100	017
100%	028
500000,50000,5000,500,50 Copies	020
yes	011
Target DNA Sequences for Soya	laboratory number
Le1	005
LEC	017
lectin	019
Lectin gene	028
RRS	011
Amplicon Size (base pairs) – Endogenous gene for Soya	laboratory number
118bp	005
74	017 019
Not Applicable	028

Target DNA Sequences for Roundup Ready Soya	laboratory number
---	-------------------

35S promoter	017
Lectin	012 017
RR Soya specific	005 012 017 019 020

Amplicon Size (base pairs) - GM event gene for Roundup Ready Soya	laboratory number
---	-------------------

121bp	005
171	017
84	019
Not Applicable	028

Target DNA Sequences for Maize	laboratory number
--------------------------------	-------------------

Zein	012
------	-----

Amplicon Size (base pairs) - GM event gene for Bt176 Maize	laboratory number
--	-------------------

Not Applicable	028
----------------	-----

Amplicon Size (base pairs) - GM event gene for Bt11 Maize	laboratory number
---	-------------------

Not Applicable	028
----------------	-----

Amplicon Size (base pairs) - GM event gene for MON810 Maize	laboratory number
---	-------------------

Not Applicable	028
----------------	-----

Amplicon Size (base pairs) - GM event gene for GA21 Maize	laboratory number
---	-------------------

Not Applicable	028
----------------	-----

**Amplicon Size (base pairs) - GM event
gene for NK603 Maize****laboratory number**

Not Applicable

028

**Amplicon Size (base pairs) - GM event
gene for TC1507 Maize****laboratory number**

Not Applicable

028

**Amplicon Size (base pairs) - GM event
gene for MON863 Maize****laboratory number**

Not Applicable

028

**Amplicon Size (base pairs) - GM event
gene for MIR604 Maize****laboratory number**

Not Applicable

028

**Amplicon Size (base pairs) - GM event
gene for MON88017 Maize****laboratory number**

Not Applicable

028

**Source of Reference Materials for Roundup
Ready Soya****laboratory number**

ERM-BF410 Series (RRS)

017 019

plasmids

005

**Did you calculate the analytical
uncertainty of your results?****laboratory number**

no

005 011 020 028

yes

017 019

If yes, please state the analyte(s) and relevant uncertainty(s). laboratory number

35S Y MON 40-3-2= 8.6 %

017

50 %

019

Not Applicable

028

Is this uncertainty

laboratory number

an expanded uncertainty

017 019

If it was an expanded uncertainty, what coverage factor was applied?

laboratory number

2

019

K=2

017

Not Applicable

028

APPENDIX II: Fapas® SecureWeb, Protocol and Contact Details

1. Fapas® SECUREWEB

Access to the secure area of our website is only available to participants in our proficiency tests. Please contact us if you require a UserID and Password. Fapas® SecureWeb allows participants to:

- Obtain their laboratory numbers for the proficiency tests in which they have participated.
- View the results they submitted in past and current proficiency tests.
- Submit their results and methods for current tests.
- Review future tests they have ordered.
- Order proficiency tests, reference materials and quality control materials.
- Freely download copies of reports (PDF file), of proficiency tests in which they have participated.
- View charts of their z-scores obtained in previous Fapas® – Food Chemistry proficiency tests.

2. PROTOCOL

The Protocols [7, 8] set out how Fapas® – GM is organised. Copies can be downloaded from our website.

3. CONTACT DETAILS

This report was prepared and authorised on behalf of Fapas® by Sri Sumathi (Round Coordinator). Participants with any comments or concerns about this proficiency test should contact:

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