

JRC GMO web applications

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Joint Research Centre (JRC), EURL GMFF

GMO Analysis and New Genomic Techniques 14-16 March 2023 Berlin

European Commission - JRC



The Joint Research Centre provides independent, evidence-based knowledge and science, supporting EU policies to positively impact society.



Legal Mandates

- Under [Regulation \(EC\) No 1829/2003](#)
- Under [Regulation \(EU\) 2017/625](#)



Regulation (EC) No 1829/2003

- Validation of methods
- Control samples
- Disputes between Member States

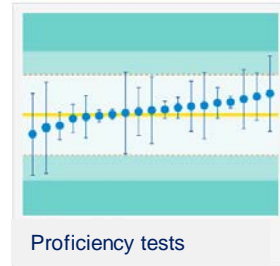


Regulation (EU) 2017/625

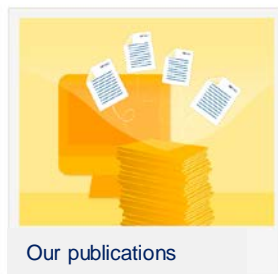
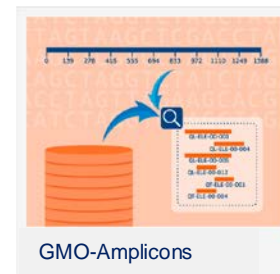
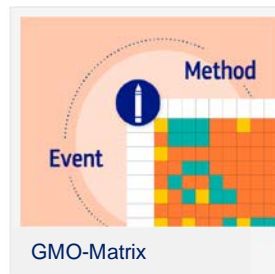
- EU Reference Methods
- Proficiency Tests (PT)
- Training for NRLs
- CRMs
- Unauthorized GMOs

EURL GMFF Activities

What we do

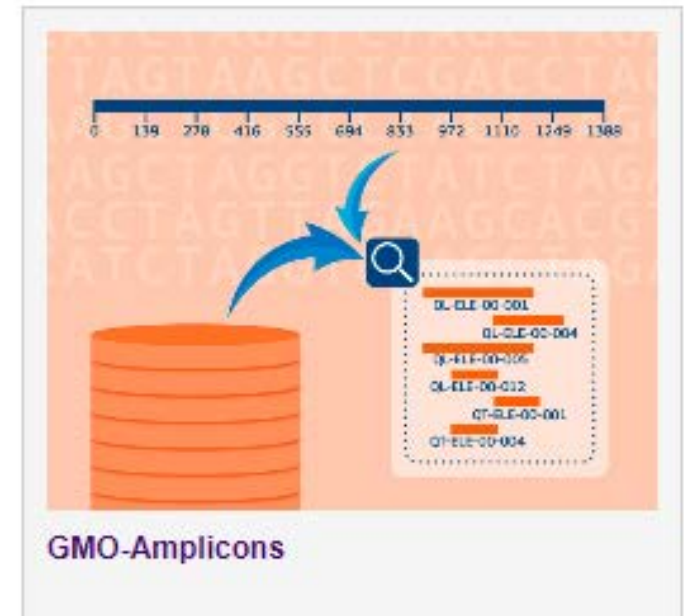
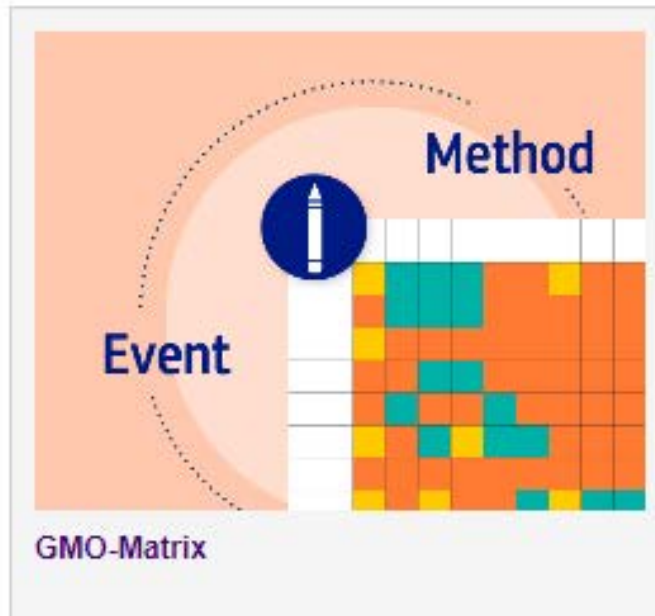


Tools



Other information

EURL GMFF WEB Applications



GMOMETHODS database

Perform your search by keyword, select a GMO unique identifier or click a link in the section below.

keyword Search or by GMO unique identifier:

Quantitative methods

- GMO specific
 - Event specific
 - Cotton
 - Maize
 - Oilseed rape
 - Papaya
 - Potato
 - Rice
 - Soybean
 - Sugar beet
 - Construct specific
 - Element specific
 - CaMV 35S promoter (CaMV P-35S)
 - Synthetic cry1A(b) gene (cry1A(b))
 - Phosphinothricin N-acetyltransferase gene (pat)
- Taxon specific
 - Species-specific methods
 - Validated independently
 - Validated in combination

Qualitative methods

- GMO specific
 - Event specific
 - Carnation
 - E. coli
 - Maize
 - Oilseed rape
 - Papaya
 - Rice
 - Construct specific
 - Element specific
 - CaMV 35S promoter/terminator (CaMV P-35S, CaMV T-35S)
 - CP4-EPSPS gene (CP4-EPSPS)
 - Cry1A genes (Cr1Ab/Ac, Cry1A(b), Cry1Ac)
 - Figwort Mosaic Virus 35S promoter (P-FMV)
 - Neomycin phosphotransferase II gene (nptII)
 - Nopaline synthase promoter/terminator (P-nos, T-nos)
 - Phosphinothricin N-acetyltransferase gene (bar, pat)
 - tE9 terminator (tE9)
- Taxon specific
 - Species-specific methods
 - Validated independently
 - Validated in combination
 - Plant-specific methods


<https://gmo-crl.jrc.ec.europa.eu/gmomethods/>

Criteria for inclusion into GMOMETHODS

Methods are:

- Validated in collaborative studies according to int'l standards
- Validated in single laboratory for legal purposes
- In line with ENGL Method Performance Requirements (MPR)

GMOMETHODS database



GMOMETHODS: EU DATABASE OF REFERENCE METHODS

Quantitative PCR method for detection of maize event MON 95379 (EURL GMFF, 2022)

Event specific **Maize** Last updated 20/12/2022

1. GENERAL INFORMATION

Target genetic element 3' integration border region (IBR) between the insert of maize event MON 95379 and the maize host genome

Assay Simplex

Detection Chemistry TaqMan®

Compendium Reference QT-EVE-ZM-033

2. VALIDATION DATA

Collaborative trial coordinator	JRC
Test material applied in collaborative trial	DNA
Materials used for calibration/controls	Genomic DNA extracted from non-GM and GM maize event MON95379 ground seeds and grains

Tested GM Events


Event Name	Unique Identifier	Species
MON95379	MON-95379-3	<i>Zea mays</i>

Collaborative Trial Description

The participants received twenty blinded test samples representing five GM levels, namely 10 %, 5 %, 1 %, 0.45 % and 0.06 % of maize event MON95379 DNA in non-GM maize DNA. In addition the laboratories received five calibration samples, reaction reagents, primers and probes for the maize high mobility group (*hmg*) reference gene and for the event MON95379 specific system. Four replicates for each GM level were analysed in two runs with both the reference and the transgenic specific system.

Method Performance

LOD Relative	not assessed	LOD Absolute	≤ 5 HGE
LOQ Relative	≤0.085 %	LOQ Absolute	not reported



Values determined in the collaborative trial

	Test Level				
	0.06	0.45	1	5	10
Mean Value (%)	0.06	0.46	1	5.1	10
RSDr (%)	15%	12%	7.6%	13%	3.9%
RSDR (%)	17%	15%	11%	15%	6.1%
Bias (%)	6.9	2.4	4.0	1.9	1.2

Unit of Measurement Test Level % GMO copy N./genome copy N.

	GMO Target	Taxon Target
Mean Slope	-3.4	-3.5
Mean PCR Efficiency %	97	95
Mean R2	1.00	1.00

Comment

The LOD absolute and LOQ relative values (expressed as copy number ratio of GM material to non-GM haploid genomes) were provided by the method developer and determined in 250 ng and 160 ng respectively of total maize DNA per reaction.


3. REFERENCES

European Union Reference Laboratory for GM Food and Feed (EURL GMFF), Joint Research Centre (JRC), European Commission. Event-specific Method for the Quantification of Maize MON 95379 Using Real-time PCR - Validation Report. 2022. JRC130976. Online Publication <https://gmo-crl.jrc.ec.europa.eu/summaries/EURL-VL-06-20-VR.pdf>

4. PRIMERS AND PROBES SEQUENCES

GM-target(s) 3' integration border region (IBR) between the insert of maize event MON 95379 and the maize host genome

Primer Forward	5'-CCAAGAAGAAGCATTGGCAAAC-3'
Target element	insert
Primer Reverse	5'-GGCACAGGCACGCCTCTG-3'
Target element	3'-host genome
Amplicon length	87 bp
Probe	5'-FAM-ATGGGTATTATGGGTAGGCACATGGGAATATAG-TAMRA-3'



Taxon-target(s) high-mobility-group (*hmg*) gene

Primer Forward	5'-TTGGACTAGAAATCTCGTCTGA-3'
Target element	<i>hmg</i>
Primer Reverse	5'-GCTACATAGGGAGCCTGTCTCT-3'
Target element	<i>hmg</i>
Amplicon length	79 bp
Probe	5'-FAM-CAATCCACACAAACGACGCGTA-TAMRA-3'

5. PCR REACTIONS SETUP

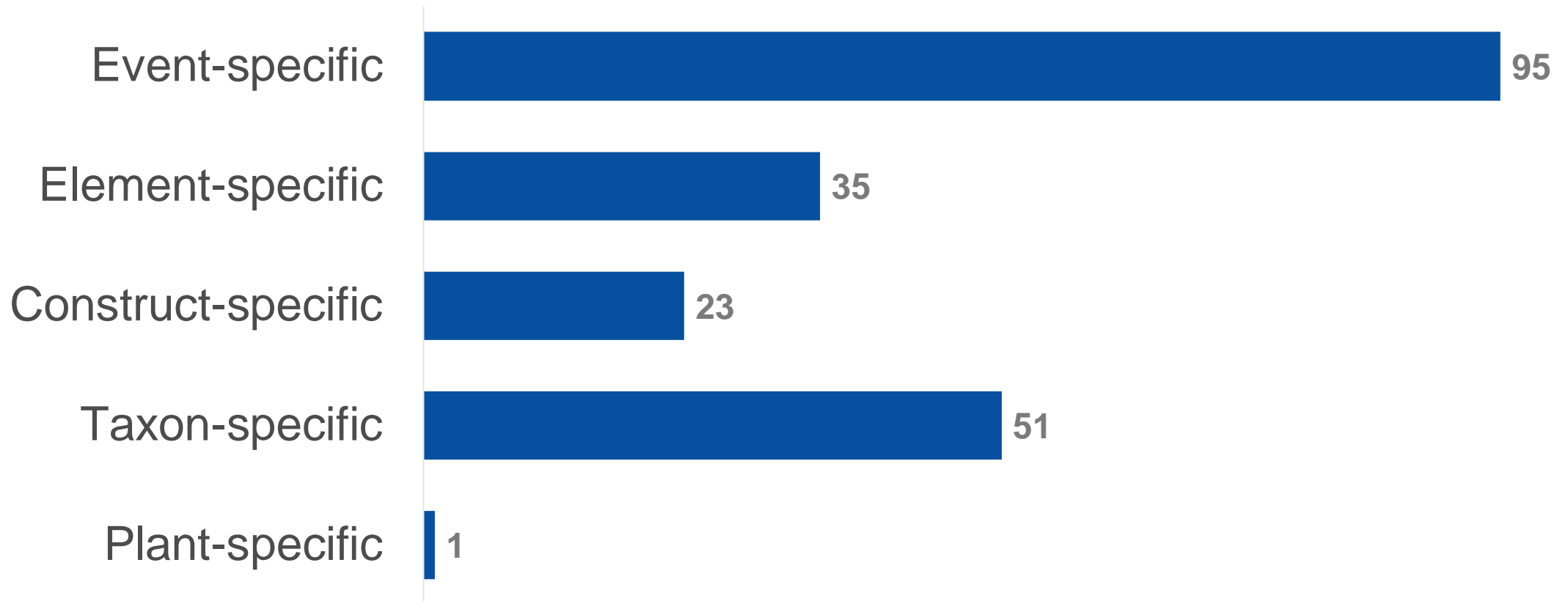
GM-target(s)	Taxon-target(s)		
Reagent	Final Concentration	Reagent	Final Concentration
TaqMan Universal PCR Master Mix (2x)	1x	TaqMan Universal PCR Master Mix (2x)	1x
Primer Fw	0.40 µmol/L	Primer Fw	0.30 µmol/L
Primer Rev	0.40 µmol/L	Primer Rev	0.30 µmol/L
Probe	0.20 µmol/L	Probe	0.16 µmol/L
Nuclease-free water	#	Nuclease-free water	#
Template DNA	4 µL	Template DNA	4 µL
Final volume	25 µL	Final volume	25 µL

6. AMPLIFICATION CONDITIONS

GM-target(s) and taxon-target(s)

Stage	Temperature	Time	NoCycles
Decontamination (UNG)	50°C	120"	1
Activation/Initial Denaturation	95°C	600"	1
Denaturation	95°C	15"	
Annealing & Extension	60°C	60"	
Denaturing, Annealing & Extension			45

GMOMETHODS content



In silico PCR predictions for GMOs detection

GMO-Matrix

Assembles two-dimensional matrices (chosen GMO events vs chosen GMO methods) to visualise the analytical coverage of the methods and identify potential gaps in the users screening approach.

Authorised events	QL-ELE-00-012 (C&M V P-355)	QT CON 00-206 (GTP-eEPSPS)	QL-ELE 00-013 (T-nen)	QL-ELE 00-026 (bar)	QL-ELE 00-025 (pat)
11-001425 Cotton (ACS-GH001-3)	2	0	2	2	0
MON 1415 Cotton (MON 01445-2)	2	0	2	0	0
MON 15047 Cotton (MON-15085-7)	2	0	2	0	0
MON 531 Cotton (MON-02531-6)	2	0	2	0	0
MON 88913 Cotton (MON-88913-8)	2	0	0	0	0
010014 Cotton (ECS-GH002-5)	0	2	0	0	0
GHB119 Cotton (BCS-GH005-6)	1	0	2	2	0
T304-40 Cotton (ECS-GH004-7)	2	0	2	2	0
GHB311 Cotton (BCS-GH11-4)	0	2	0	0	0

GMO-Event finder

Allows identification of potential GMO(s) present in a sample based on a set of detection methods defined by the user and the obtained positive and negative experimental results.

GMO-Event finder

- 1) Select taxon(s)
By taxon:
- 2) Select positive method(s)
Event search:
Detection method:
Current count:
- 3) Select negative method(s)
Event search:
Detection method:
Current count:
- 4) Select maximum number of events

Please select at least one method

For an example request: Events positive for GHB119 and T304, but negative for bar

GMO-Screen

Provides a general screening proposal and a screening specific for EU authorised GMOs with a web-based tool to interpret the results. The tool may also be applied to a ready-to-use, multi-target screening device developed by the JRC known as the Pre-Spotted Plate (PSP).

Pre-spotted plates

The PSP consists of 96 wells (8x12) and contains specific primers for genotyping authorised GMOs and qualified panels of non-qualified reference GMOs (including the reference GMOs). The detection method is based on the presence of a specific marker.

- 1) Select the results of taxon-specific methods
Taxon:
Method:
Event search:
Detection method:
Current count:
- 2) Select the results of element-specific methods
Taxon:
Method:
Event search:
Detection method:
Current count:
- 3) Select the results of event-specific methods
Taxon:
Method:
Event search:
Detection method:
Current count:

JRC-GMO-Matrix

GMO-Matrix

1) Select GMO(s)

By taxon(s)

× Cotton (Gossypium hirsutum)

Specific GMO(s)

2) Select legal status

Regulation (EC) No 1829/2003

Directive 2001/18/EC

- Authorised events
- Events in authorised stacks
- Pending events
- Expired events
- Withdrawn events
- Unauthorised events

- Authorised events
- Pending events

3) Select method(s)

Event-specific

Construct-specific

Element-specific

× bar (QL-ELE-00-014)
 × CaMV P-35S (QT-ELE-00-001)
 × pat (QT-ELE-00-002) × T-nos (QL-ELE-00-007)

Show

Cancel

Export as CSV

CaMV P-35S (QT-ELE-00-001)

pat (QT-ELE-00-002)

bar (QL-ELE-00-014)

Authorised events

GHB119 Cotton (BCS-GH005-8) **A**

2

0

2

GHB614 Cotton (BCS-GH002-5) **A**

0

0

0

GHB811 Cotton (BCS-GH811-4) **A**

0

0

0

LLCotton25 Cotton (ACS-GH001-3) **A**

2

0

2

MON 1445 Cotton (MON-01445-2) **A**

1

0

0

MON 15947 Cotton (MON-15985-7) * **A**

2

0

0

MON 531 Cotton (MON-00531-6) **A**

2

0

0

MON 88913 Cotton (MON-88913-8) **A**

0

0

0

T304-40 Cotton (BCS-GH004-7) **A**

2

0

2

Events in authorised stacks

281-24-236 Cotton (DAS-24236-5) **S**

0

2

0

3006-210-23 Cotton (DAS-21023-5) **S**

0

2

0

Pending events

COT102 Cotton (SYN-IR102-7) **P**

0

0

0

DAS-81910-7 Cotton (DAS-81910-7) **P**

0

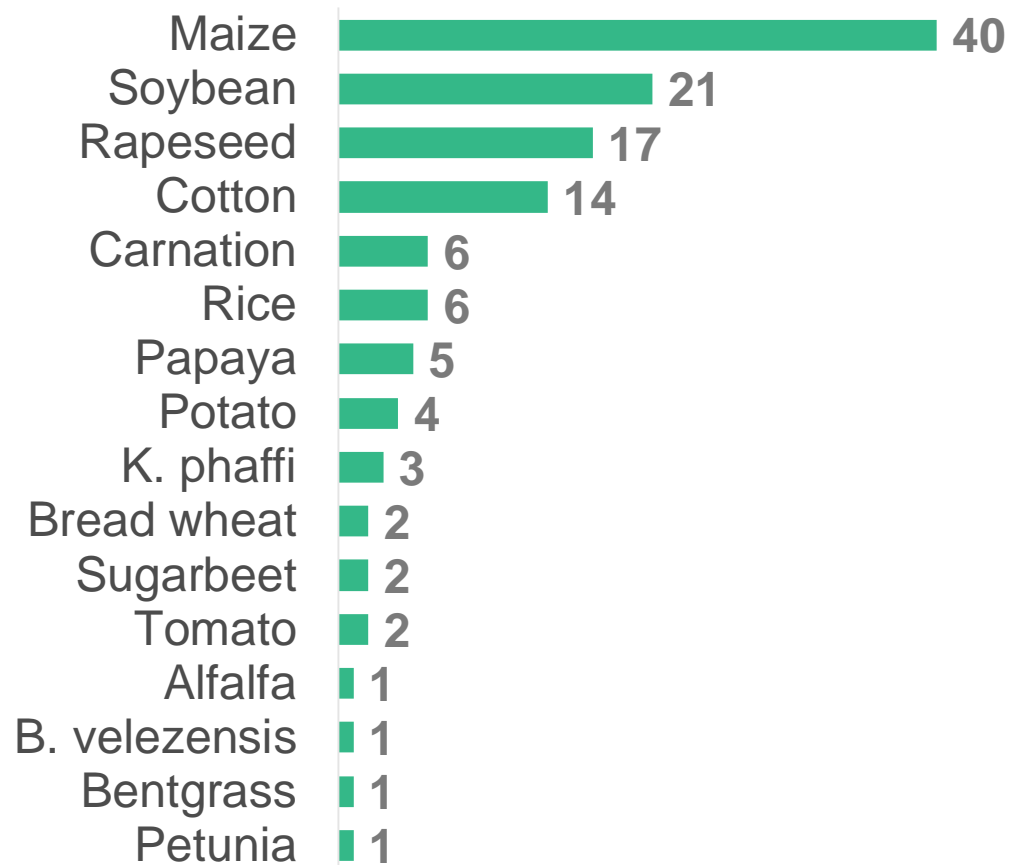
2

0

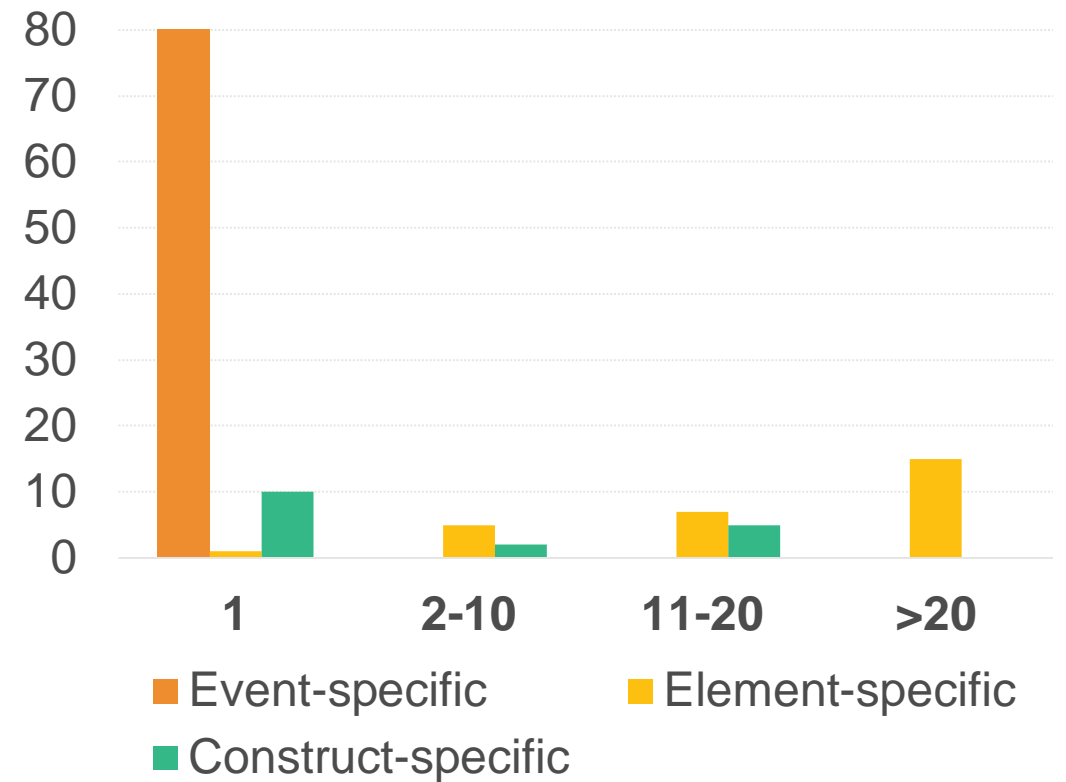
<https://gmo-crl.jrc.ec.europa.eu/jrcgmomatrix/>

JRC-GMO-Matrix

Number of GM events



Targeted GMOs/method



JRC GMO-Event finder

GMO-Event finder

1) Select taxon(s)

By taxon(s)

× Cotton (Gossypium hirsutum)

2) Select positive method(s)

Event-specific

Construct-specific

Element-specific

× bar (QL-ELE-00-022)

× CaMV P-35S (QL-ELE-00-001)

× T-nos (QL-ELE-00-011)

3) Select negative method(s)

Event-specific

Construct-specific

Element-specific

× pat (QT-ELE-00-002)

4) Select maximum number of events

1 2 3

Show

Cancel

JRC GMO-Event finder

Single events

	pat (QT-ELE-00-002)	bar (QL-ELE-00-022)	CaMV P-35S (QL-ELE-00-001)	T-nas (QL-ELE-00-011)
GHB119 Cotton (BCS-GH005-8) A	0	2	1	2
LLCotton25 Cotton (ACS-GH001-3) A	0	2	2	2
MON 88701 Cotton (MON-88701-3) U	0	2	2	2
T304-40 Cotton (BCS-GH004-7) A	0	2	2	2

Legend:

- 0 No amplification predicted
- 1 Amplification predicted, imperfect annealing*
- 2 Amplification predicted, perfect annealing

* Up to a maximum of 2 gaps and 2 mismatches for each primer

JRC GMO-Event finder

Other possible events

The results above show the event(s) which are sufficient to explain the selected pattern of results. Other GM event(s), as long that they would test negative for the methods for which a negative result was obtained, could potentially also be present in the tested sample. These include:

	pat (QT-ELE-00-002)	bar (QL-ELE-00-022)	CaMV P-35S (QL-ELE-00-001)	T-nos (QL-ELE-00-011)
COT102 Cotton (SYN-IR102-7) P	0	0	0	2
GHB614 Cotton (BCS-GH002-5) A	0	0	0	0
GHB811 Cotton (BCS-GH811-4) A	0	0	0	0
MON 1445 Cotton (MON-01445-2) A	0	0	1	2
MON 15947 Cotton (MON-15985-7) A	0	0	2	2
MON 531 Cotton (MON-00531-6) A	0	0	2	2
MON 88913 Cotton (MON-88913-8) A	0	0	0	0

GMO-Screen

GMO-Screen

1) Select screening strategy


- Screening for authorised GMOs
- General screening
- Prespotted plates

2) Select taxon(s)

By taxon(s)

* Cotton (Gossypium hirsutum)

3) Select legal status

Regulation (EC) No 1829/2003 

Directive 2001/18/EC 

- | | |
|---|--|
| <input checked="" type="checkbox"/> Authorised events | <input type="checkbox"/> Authorised events |
| <input checked="" type="checkbox"/> Events in authorised stacks | <input type="checkbox"/> Pending events |
| <input checked="" type="checkbox"/> Pending events | |
| <input checked="" type="checkbox"/> Expired events | |
| <input checked="" type="checkbox"/> Withdrawn events | |
| <input checked="" type="checkbox"/> Unauthorised events | |










CaMV P-35S (QT-ELE-00-004)

T-nos (QL-ELE-00-013)

pat (QT-ELE-00-002)

OTP-mEPSPS (QT-CON-00-008)



Authorised events

GHB119 Cotton (BCS-GH005-8) 	1	2	0	0
GHB614 Cotton (BCS-GH002-5) 	0	0	0	2
GHB811 Cotton (BCS-GH811-4) 	0	0	0	2
LLCotton25 Cotton (ACS-GH001-3) 	2	2	0	0
MON 1445 Cotton (MON-01445-2) 	2	2	0	0
MON 15947 Cotton (MON-15985-7) * 	2	2	0	0
MON 531 Cotton (MON-00531-6) 	2	2	0	0
MON 88913 Cotton (MON-88913-8) 	2	0	0	0
T304-40 Cotton (BCS-GH004-7) 	2	2	0	0

Events in authorised stacks

281-24-236 Cotton (DAS-24236-5) 	0	0	2	0
3006-210-23 Cotton (DAS-21023-5) 	0	0	2	0

Pending events

COT102 Cotton (SYN-IR102-7) 	0	2	0	0
DAS-81910-7 Cotton (DAS-81910-7) 	0	0	2	0

GMO-Screen

Screening for authorised GMOs

The JRC provides screening proposals with element-, construct- and event-specific methods for identifying authorised GM events. This decision-support system is designed for interpreting the positive (+), negative (-) and inconclusive/unavailable (?) results of the tests. Leave the result as unavailable (?) for the methods that you didn't use in your screening.

Select the results of element and construct-specific methods

Target	GMOMETHODS Reference	Result
CaMV P-35S	QT-ELE-00-004	<input type="radio"/> + <input type="radio"/> - <input type="radio"/> ?
OTP-mEPSPS	QT-CON-00-008	<input type="radio"/> + <input type="radio"/> - <input type="radio"/> ?
pat	QT-ELE-00-002	<input type="radio"/> + <input type="radio"/> - <input type="radio"/> ?
T-Nos	QL-ELE-00-013	<input type="radio"/> + <input type="radio"/> - <input type="radio"/> ?

Show

Cancel

GMO-Screen

The following single events match the selected pattern and the selected species (cotton). One or more may thus be present in the sample:

Single events

	CaMV P-35S (QT-ELE-00-004)	T-nos (QL-ELE-00-013)	pat (QT-ELE-00-002)	OTP-mEPSPS (QT-CON-00-008)
GHB119 Cotton (BCS-GH005-8) A	1	2	0	0
LLCotton25 Cotton (ACS-GH001-3) A	2	2	0	0
MON 1445 Cotton (MON-01445-2) A	2	2	0	0
MON 15947 Cotton (MON-15985-7) A	2	2	0	0
MON 531 Cotton (MON-00531-6) A	2	2	0	0
MON 88701 Cotton (MON-88701-3) U	2	2	0	0
T304-40 Cotton (BCS-GH004-7) A	2	2	0	0

Legend:

0 No amplification predicted

1 Amplification predicted, imperfect annealing*

2 Amplification predicted, perfect annealing

* Up to a maximum of 2 gaps and 2 mismatches for each primer

GMO-Screen

Other possible events

The results above show the event(s) which are sufficient to explain the selected pattern of results. Other GM event(s), as long that they would test negative for the methods for which a negative result was obtained, could potentially also be present in the tested sample. These include:

	CaMV P-35S (QT-ELE-00-004)	T-nos (QL-ELE-00-013)	pat (QT-ELE-00-002)	OTP-mEPSPS (QT-CON-00-008)
COT102 Cotton (SYN-IR102-7) P	0	2	0	0
MON 88913 Cotton (MON-88913-8) A	2	0	0	0

Legend:

- 0 No amplification predicted
- 1 Amplification predicted, imperfect annealing*
- 2 Amplification predicted, perfect annealing

* Up to a maximum of 2 gaps and 2 mismatches for each primer

GMO-Screen

GMO-Screen

1) Select screening strategy

- Screening for authorised GMOs
- General screening
- Prespotted plates

2) Select taxon(s)

By taxon(s)

× All taxons















3) Select legal status

Regulation (EC) No 1829/2003 

Directive 2001/18/EC 

- | | |
|---|--|
| <input checked="" type="checkbox"/> Authorised events | <input type="checkbox"/> Authorised events |
| <input checked="" type="checkbox"/> Events in authorised stacks | <input type="checkbox"/> Pending events |
| <input checked="" type="checkbox"/> Pending events | |
| <input checked="" type="checkbox"/> Expired events | |
| <input checked="" type="checkbox"/> Withdrawn events | |
| <input checked="" type="checkbox"/> Unauthorised events | |

Authorised events

1507 Maize (DAS-01507-1) 	1	0	2	0
305423 Soybean (DP-305423-1) 	0	0	0	0
40-3-2 Soybean (MON-04032-6) 	2	2	0	0
4114 Maize (DP-004114-3) 	2	0	2	0
5307 Maize (SYN-05307-1) 	0	2	0	0
59122 Maize (DAS-59122-7) 	2	0	2	0
73496 Rapeseed (DP-073496-4) 	0	0	0	0
A2704-12 Soybean (ACS-GM005-3) 	2	0	2	0
A5547-127 Soybean (ACS-GM006-4) 	2	0	2	0
Bt11 Maize (SYN-BT011-1) 	2	2	2	0
CV127 Soybean (BPS-CV127-9) 	0	0	0	0
DAS-40278-9 Maize (DAS-40278-9) 	0	0	0	0
DAS-44406-6 Soybean (DAS-44406-6) 	0	0	2	0
DAS-68416-4 Soybean (DAS-68416-4) 	0	0	2	0

GMO-Screen

1) Select the results of taxon-specific methods

Target	GMOMETHODS Reference	Result
AdhC (cotton)	QT-TAX-GH-019	+ - ?
hmg (maize)	QT-TAX-ZM-002	+ - ?
FatA(A) (rapeseed)	QT-TAX-BN-001	+ - ?
Le1 (soybean)	QT-TAX-GM-002	+ - ?
anthocyanidin synthase (carnation)	QL-TAX-DC-001	+ - ?
chymopapain (papaya)	QT-TAX-CP-001	+ - ?
gs (sugarbeet)	QT-TAX-BV-013	+ - ?
LAT52 (tomato)	QT-TAX-SL-002	+ - ?
lectin (pea)	QL-TAX-PS-001	+ - ?
pld (rice)	QT-TAX-OS-017	+ - ?
stearoyl-acyl carrier protein desaturase (flax)	QL-TAX-LU-001	+ - ?
ugp (potato)	QT-TAX-ST-010	+ - ?

2) Select the results of element and construct-specific methods

Target	GMOMETHODS Reference	Result
bar	QL-ELE-00-014	+ - ?
CaMV P-35S	QT-ELE-00-001	+ - ?
CaMV P-35S	QT-ELE-00-004	+ - ?
cry1Ab/Ac	QL-ELE-00-016	+ - ?
CTP2-CP4epsps	QL-CON-00-008	+ - ?
nptII	QL-ELE-00-002	+ - ?
OTP-mEPSPS	QT-CON-00-008	+ - ?
pat	QT-ELE-00-002	+ - ?
P-FMV	QL-ELE-00-015	+ - ?
P-Nos	QL-ELE-00-008	+ - ?
t-E9	QL-ELE-00-024	+ - ?
T-Nos	QL-ELE-00-013	+ - ?

3) Select the results of event-specific methods

Target	GMOMETHODS Reference	Result
305423 (soybean)	QT-EVE-GM-008	+ - ?
73496 (rapeseed)	QT-EVE-BN-009	+ - ?
CV127 (soybean)	QT-EVE-GM-011	+ - ?
DAS40278 (maize)	QT-EVE-ZM-004	+ - ?
MON 94100 (rapeseed)	QT-EVE-BN-014	+ - ?

Show

Cancel

GMO-Screen

The following single events match the selected pattern. One or more may thus be present in the sample:

Single events

	CaMV P-35S (QT-ELE-00-004)	CaMV P-35S (QT-ELE-00-001)	T-nos (QL-ELE-00-013)	pat (QT-ELE-00-002)	bar (QL-ELE-00-014)	tE9 (QL-ELE-00-024)	CTP2-CP4 EPSPS (QL-CON-00-008)	P-nos (QL-ELE-00-008)	nptII (QL-00-008)
1345-4 Tomato U	2	2	2	0	0	0	0	2	
16-0-1 Papaya U	2	2	2	0	0	0	0	2	
18-2-4 Papaya U	2	2	2	0	0	0	0	2	
55-1 Rainbow Papaya (CUH-CP551-8) U	2	2	2	0	0	0	0	2	
Huanong No.1 Papaya U	2	2	2	0	0	0	0	2	
X17-2 Papaya (UFL-X17CP-9) U	2	2	2	0	0	0	0	2	

GMO-Screen

Other possible events

The results above show the event(s) which are sufficient to explain the selected pattern of results. Other GM event(s), as long that they would test negative for the methods for which a negative result was obtained, could potentially also be present in the tested sample. These include:

	CaMV P-35S (QT- ELE-00-004)	CaMV P-35S (QT- ELE-00-001)	T-nos (QL-ELE- 00-013)	pat (QT-ELE-00- 002)	bar (QL-ELE-00- 014)	tE9 (QL-ELE-00- 024)	CTP2-CP4 EPSPS (QL-CON- 00-008)	P-nos (QL-ELE- 00-008)	nptII (QL-ELE-00- 002)
GM Bacillus velezensis U	0	0	0	0	0	0	0	0	0
KK179 Alfalfa (MON-00179-5) U	0	0	2	0	0	0	0	0	0
MxY0541 - Insert 1 U	0	0	0	0	0	0	0	0	0
MxY0541 - Insert 2 U	0	0	0	0	0	0	0	0	0
MxY0541 - Insert 3 U	0	0	0	0	0	0	0	0	0
Purple Tomato U	0	0	0	0	0	0	0	2	2
RL01-17 Petunia U	2	1	0	0	0	0	0	2	2

Pre-Spotted-Plates (PSPs)

JRC screening PSPs with methods:

- taxon-specific
- element-specific
- construct-specific
- event-specific for authorised soybean and maize events

Pre-spotted plates

The JRC provides pre-spotted plates with element- and construct- specific methods for performing screening analysis and pre-spotted plates with event-specific methods for identifying soybean and maize authorised events. This decision-support system is designed for interpreting the positive (+), negative (-) and inconclusive (?) results of the tests.

1) Select the results of taxon-specific methods

Target	GMOMETHODS Reference	Result
hmg (maize)	QT-TAX-ZM-002	+ - ?
Le1 (soy)	QT-TAX-GM-002	+ - ?
cruA (rapeseed)	QT-TAX-BN-012	+ - ?
sah7 (cotton)	QT-TAX-GH-016	+ - ?
ugp (potato)	QT-TAX-ST-010	+ - ?
pld (rice)	QT-TAX-OS-017	+ - ?
gs (sugarbeet)	QT-TAX-BV-013	+ - ?

2) Select the results of element-specific methods

Target	GMOMETHODS Reference	Result
p35S	QT-ELE-00-004	+ - ?
tNos	QL-ELE-00-013	+ - ?
CTP2-CP4EPS	QL-CON-00-008	+ - ?
pat	QT-ELE-00-002	+ - ?
bar	QL-ELE-00-014	+ - ?
cry1Ab/Ac	QL-ELE-00-016	+ - ?

3) Select the results of event-specific methods

Target	GMOMETHODS Reference	Result
DAS40278 (maize)	QT-EVE-ZM-004	+ - ?
CV127 (soybean)	QT-EVE-GM-011	+ - ?
DP-305423 (soybean)	QT-EVE-GM-008	+ - ?

Show Cancel

JRC GMO-Amplicons

Amplicon finder

Query public sequence databases for specific amplicons using selected EU reference methods.

Target finder

Examine potential amplicons on specific target sequences from public databanks.

Amplicon finder

1) Select detection method(s)

Note: if more than one method is selected, only records that produce amplicons with all those methods will be shown

Event-specific	<input type="text" value="QT-EVE-BN-002 (Ms8)"/>
Construct-specific	<input type="text"/>
Element-specific	<input type="text"/>
Taxon-specific	<input type="text"/>

2) Optionally select also negative method(s)

Note: If you select methods here, records that produce amplicons with any of those methods will be removed

3) Select database(s)

- nt GenBank nt section (NCBI)
- embreltgn ENA transgenic data class division (EMBL-EBI)
- embrelpat ENA patent data class division (EMBL-EBI)
- nrnl1 Non-redundant patent nucleotide database level-1 (EMBL-EBI)

4) Select the maximum number of gaps/mismatches

Gaps:

Mismatches:

<input type="button" value="Submit"/>	<input type="button" value="Cancel"/>
---------------------------------------	---------------------------------------

JRC GMO-Amplicons

Results : 14 amplicons

Restrict to taxon(s):

Restrict

View 14 unique records

Record ID	Database	Record description	Record length	Taxon	Method	Amplicon size	Match details
AR275289.1	emblrepat	Sequence 18 from patent US 6506963.	537 bp	unidentified	QT-EVE-BN-002	130 bp	View
AR275309.1	emblrepat	Sequence 38 from patent US 6506963.	522 bp	unidentified	QT-EVE-BN-002	130 bp	View
AR321700.1	emblrepat	Sequence 18 from patent US 6563026.	537 bp	unidentified	QT-EVE-BN-002	130 bp	View
AR321720.1	emblrepat	Sequence 38 from patent US 6563026.	522 bp	unidentified	QT-EVE-BN-002	130 bp	View
AX172457.1	emblrepat	Sequence 18 from Patent WO0141558.	537 bp	synthetic construct	QT-EVE-BN-002	130 bp	View
AX172477.1	emblrepat	Sequence 38 from Patent WO0141558.	522 bp	synthetic construct	QT-EVE-BN-002	130 bp	View
GV638084.1	emblrepat	Sequence 18 from patent US 7659095.	537 bp	unidentified	QT-EVE-BN-002	130 bp	View

In silico PCR predictions in public databases

<https://gmo-crl.jrc.ec.europa.eu/jrcgmoamplicons/>

JRC GMO-Amplicons

Match details

Record ID: AR275289.1
Database: emblrelpat [Go to original record](#)
Description: Sequence 18 from patent US 6506963.
Taxon: *unidentified*
Original size: 537 bp
Patents: US6506963 (lens, espacenet)

Method: QT-EVE-BN-002 [Go to GMOMETHODS record](#)

[View in JRC GMO-Matrix](#)

Description: Quantitative PCR method for detection of oilseed rape event Ms8 (Mazzara et al., 2007).

Target: Ms8

[View other 13 matches for this method](#)

Predicted amplification details:

Mismatches	Gaps	From	To	Strand	Amplicon size
0	0	79	208	+	130 bp

Amplicon: 130 bp

```
1      gttagaaaaa gtaaacaatt aatatagcog gctattttgtg taaaaatccc
51     taatataatc gacggatccc cggaattcc gggggaagct tagatccatg
101    gatttgttat gataacaaa aacaccctcc
```

[View other 13 matches with an identical amplicon](#)

Primers and probe alignment:

Primer/Probe	% Identity	Length	Mismatches	Gaps	From	To	Score
primerA	100.0	31 bp	0	0	1	31	8.34e-15
primerB	100.0	20 bp	0	0	130	111	6.57e-09
probe	100.0	28 bp	0	0	52	79	3.42e-13

JRC GMO-Amplicons

Target finder

Insert sequence accession number

Record ID:

Show

Cancel

Record ID: AR275289.1

Description: Sequence 18 from patent US 6506963.

Length: 537 bp

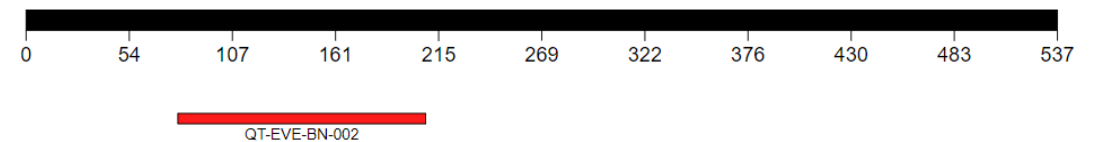
Found in databases: embrelpat

Found in the following 1 patent: US6506963 (lens, espacenet)

1 amplicon

[View all records targeted by these methods](#)

[View these methods in JRC GMO-Matrix](#)



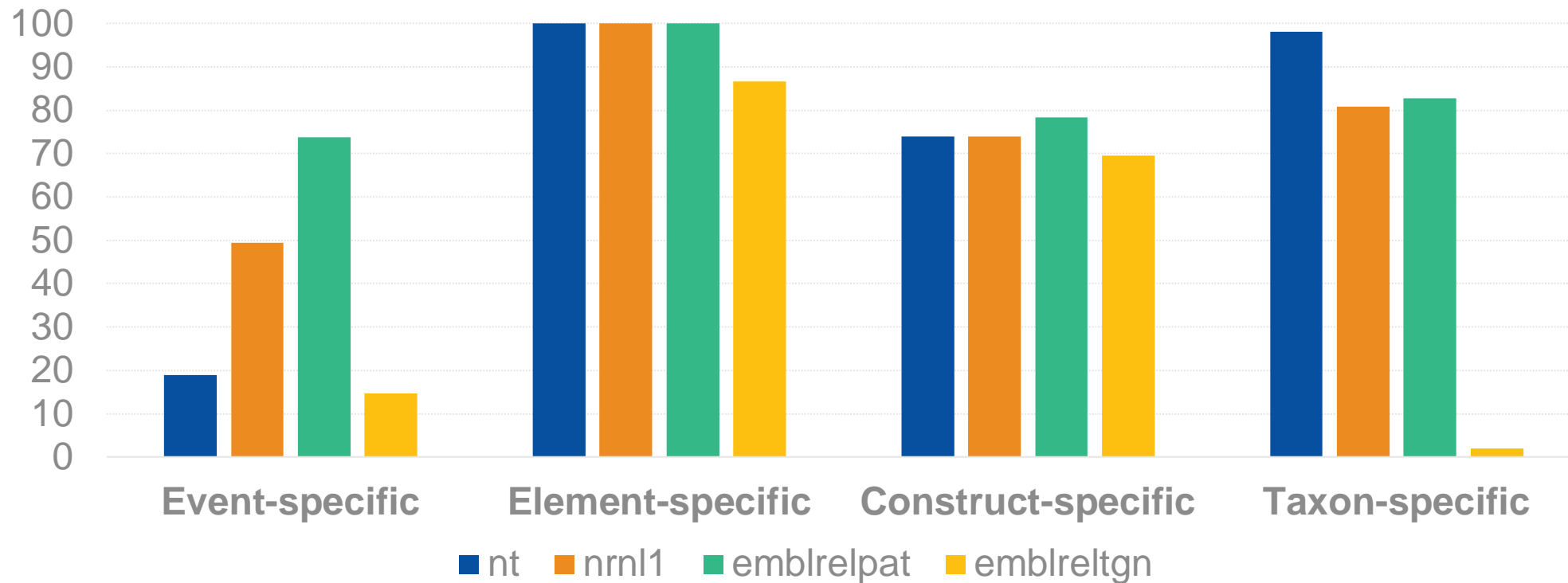
Legend

- Event-specific method
- Element-specific method
- Construct-specific method
- Taxon-specific method

Record ID	Database	Record description	Record length	Taxon	Method	Amplicon size	Match details
AR275289.1	embrelpat	Sequence 18 from patent US 6506963.	537 bp	unidentified	QT-EVE-BN-002	130 bp	View

JRC GMO-AMPLICONS

% methods in JRC db with targets in public databases



Conclusions

GMOMETHODS and the other EURL GMFF web applications

Ensure:

- Analyses on accurate sequences
- Consistent/reproducible results
- Updated information
- Comprehensive bioinformatics suite

Facilitate:

- Confidence in results
- Harmonisation of GMO analysis
- Trade and consumer trust
- Official controls

European Union Reference Laboratory for Genetically Modified Food and Feed (EURL GMFF)

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Feedback is welcomed !

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[Yes](#)[No](#)

Acknowledgements

Benny Kusters (DG SANTE)

for collaborating on the data exchange between the GMO Register and the JRC GMO-Matrix application.

DG JRC

IT consultant [Moreno Colaiacovo](#) for the latest development on the JRC web applications. [Mauro Petrillo](#) and [Alexandre Angers](#) for the first development of the tools. [Enrico Ben](#) for the IT support.

[Veronique Vanherck](#) for graphical assistance.

[EURL GMFF](#) colleagues for feedback and support.

Keep in touch

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Thank you



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