

Annex 01: Reporting Form

Form for the submission of DNA sequences and associated annotations to the European Union Reference Laboratory for GM Food and Feed or EFSA, according to appropriate existing EU legislation

1.		Genetically modified organism (GMO) general information
		<p>Name:</p> <p>Unique identifier:</p> <p>EFSA application code (if available):</p> <p>EURL GMFF application code (if available):</p> <p>This form is used for the submission of</p>
2.		Material and sample requirements
2.1		I confirm that the accompanying dossier provides information about the sample source.
2.2		<p>The material (e.g. leaves, roots, seeds) from which the DNA was extracted is clearly identified and it is:</p> <p><i>Please check the box and specify</i></p>
2.3		I confirm that all reported sequences have been obtained from the same sample.
2.4		<p>A full report on the sample has been attached to this document.</p> <p>It includes the description of the GM event, the material used, the number of individuals used/pooled and their origin, the protocol for DNA extraction, the overall strategy to obtain the DNA fragments used for sequencing.</p> <p><i>Please check the box and specify the report file name below</i></p>
2.5		I confirm that a sample used for the sequencing will be made available if requested.
2.6		<p><i>[In case of stacks]</i></p> <p>I confirm that all reported sequences for all stacked events have been obtained from the same sample extracted from the same material.</p>

3.		Sequencing requirements
3.1		I confirm that the number of inserts is <i>Please check the box and give a number</i>
3.2		I confirm that the used sequencing technology is <i>Please check the box and specify</i>
3.3		I confirm that the used sequencing method (or a combination of) was: <i>Please check the box and choose at least one</i> Primer walking Amplicon sequencing Whole genome sequencing Other, please specify:
3.4		<i>[ONLY In case the sequencing required the amplification of the template with a Polymerase Chain Reaction (PCR)]</i> I confirm that the final sequences have been generated from at least two independent PCR products. The exact number is <i>Please check the box and give a number</i>
3.5		I confirm that genomic flanking regions of each insert have been sequenced and are provided according to the guideline.
3.6a		<i>[ONLY for Sanger-based sequencing]</i> I confirm that the sequence has been produced by bi-directional sequencing (i.e. each base has been sequenced on the forward and reverse strand) and in at least two independent PCR amplicons. The individual generated sequences are included in the following format <i>Please check the box and specify</i>
3.6b		<i>[ONLY for NGS]</i> <i>For sequences generated with NGS, please indicate the NGS technology used (or a combination of):</i> Roche 454 Illumina Ion Torrent PacBio Other, please specify: The average obtained sequencing depth of each insert and flanking region (the number of times each base of the produced sequence has been sequenced) is I confirm that the raw NGS reads generated are included in FASTQ format, already filtered and eventually trimmed of the used adapters. <i>Please check the box and specify</i>
3.7		A full report on the sequencing strategy and the details of the experimental procedures has been attached to this document. It includes the description of the technology used, the sequencing method of the sequence generation, and the details

		<p>of the experimental design.</p> <p><i>Please check the box and specify the report file name below</i></p>
4.		Bioinformatics analyses
4.1		<p>A full report on the conducted Bioinformatics analyses has been attached to this document.</p> <p>It provides a detailed description of used software and tools, including their names, versions, options and parameters used. In case of analyses made by an ad-hoc developed software, its description is also reported. Moreover, the details of the base-calling procedure are reported, including the software tools (name and version), options and parameters used.</p> <p><i>Please check the box and specify the report file name below</i></p>
4.2		<p><i>[ONLY in case of re-sequencing]:</i></p> <p>I confirm that the sequence of each GM event contained in the application has been compared with all sequences of the event in question that were previously submitted after July 2016 to the European Commission, EFSA or the EURL GMFF. All differences found between any of the versions are reported.</p>
4.3a		<p><i>[ONLY for Sanger-based sequencing]</i></p> <p>I confirm that the sequences are provided in ABI or FASTQ format.</p> <p>The format of the alignment of Sanger sequences is</p> <p><i>Please check the box and specify</i></p>
4.3b		<p><i>[ONLY for NGS]</i></p> <p>I confirm that raw NGS-reads are provided in FASTQ format, already filtered, and trimmed of the used adapters. The software and parameters used for the filtering and trimming are described.</p> <p>The format of the alignment of assembled reads is</p> <p><i>Please check the box and specify</i></p>
4.4		<p><i>[optional]</i></p> <p>An additional ACE file has been included</p>
4.5		<p><i>[optional]</i></p> <p>I confirm that a taxon-specific reference gene sequence taken from a public database and used for the detection method assay, the relevant references to the source database and record are provided in the dossier.</p>

5		Sequence submission format
5.1		<p>I confirm that the final event sequence(s) of the GMO is/are provided as electronic ASCII text file(s) in the following format(s):</p> <p><i>Please check the box and choose at least one</i></p> <p>NCBI's Sequin (ASN.1)</p> <p>EMBL</p> <p>GenBank</p>
5.2		<p>I confirm that each final sequence is reported in one different file. In total, the submission consists of files.</p> <p><i>Please check the box and give a number</i></p>
5.3		<p>I confirm that the provided sequence files are annotated according to the INSDC Feature Table Definition Document.</p>
5.4		<p><i>[Optional]</i></p> <p>I confirm that a taxon-specific reference gene is included in the submission and the full sequence of the species-specific target and its GenBank accession number have been submitted in the same format as the final sequence.</p>

PLACE

DATE

NAME, SURNAME
CONTACT DETAILS

SIGNATURE