Award Form

This Award Form creates the Contract. It summarises the main features of the procurement and includes the Buyer and the Supplier's contact details.

1.	**Buyer**	Food Standards Agency (the Buyer) Its offices are on: Clive House 70 Petty France London, SW1H 9EX
2.	**Supplier**	Name: **Fera Science Ltd** Address: York Biotech Campus, Sand Hutton, York, North Yorkshire, YO41 1LZ
3.	**Contract**	This Contract between the Buyer and the Supplier is for the supply of Deliverables.
4.	**Contract Reference**	FS430676
5.	**Deliverables**	See Schedule 2 (Specification)
6.	**Start Date**	14th February 2021
7.	**End Date**	30th January 2024
8.	**Extension Period**	Up to 6 Months
9.	**Incorporated Terms** (together these documents form the 'the Contract')	The following documents are incorporated into the Contract. Where numbers are missing we are not using these Schedules. If the documents conflict, the following order of precedence applies: 1. This Award Form 2. Any Special Terms (see **Section 10 Special Terms** in this Award Form) 3. Core Terms (version 1.0) 4. Schedule 1 (Definitions) 5. Schedule 20 (Processing Data) 6. The following Schedules (in equal order of precedence): ● Schedule 2 (Specification)

		• Schedule 3 (Charges) • Schedule 4 (Tender) • Schedule 13 (Contract Management) • Schedule 16 (Security) • Schedule 20 (Processing Data) • Schedule 21 (Variation Form) • Schedule 22 (Insurance Requirements) • Schedule 27 (Key Subcontractors) • Schedule 32 (Background Checks)
10.	**Special Terms**	Not Used
11.	**Social Value Commitment**	Not Used
12.	**Commercially Sensitive Information**	Not applicable
13.	**Charges**	Details in Schedule 3 (Charges)
14.	**Reimbursable expenses**	Recoverable as set out in Schedule 3 (Charges)]
15.	**Payment Method**	All invoices must be sent, quoting a valid purchase order number (PO Number), to: Accounts-Payable.fsa@gov.sscl.com Within 10 Working Days of receipt of your countersigned copy of this letter, we will send you a unique PO Number. You must be in receipt of a valid PO Number before submitting an invoice. To avoid delay in payment it is important that the invoice is compliant and that it includes a valid PO Number, PO Number item number (if applicable) and the details (name and telephone number) of your Buyer contact (i.e. Contract Manager). Non-compliant invoices will be sent back to you, which may lead to a delay in payment.

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18	**Supplier**	Dr John Walshaw
		SW11 9LX

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Core Terms – Mid-tier

1. Definitions used in the contract

1.1 Interpret this Contract using Schedule 1 (Definitions).

2. How the contract works

2.1 If the Buyer decides to buy Deliverables under the Contract it must state its requirements using the Award Form). If allowed by the Regulations, the Buyer can:

- make changes to Award Form
- create new Schedules
- exclude optional template Schedules
- use Special Terms in the Award Form to add or change terms

2.2 The Contract:

- is between the Supplier and the Buyer
- includes Core Terms, Schedules and any other changes or items in the completed Award Form

2.3 The Supplier acknowledges it has all the information required to perform its obligations under the Contract before entering into it. When information is provided by the Buyer no warranty of its accuracy is given to the Supplier.

2.4 The Supplier won't be excused from any obligation, or be entitled to additional Costs or Charges because it failed to either:

- verify the accuracy of the Due Diligence Information
- properly perform its own adequate checks

2.5 The Buyer will not be liable for errors, omissions or misrepresentation of any information.

2.6 The Supplier warrants and represents that all statements made and documents submitted as part of the procurement of Deliverables are and remain true and accurate.

3. What needs to be delivered

3.1 All deliverables

3.1.1 The Supplier must provide Deliverables:

- that comply with the Specification, the Tender Response and the Contract
- using Good Industry Practice
- using its own policies, processes and internal quality control measures as long as they don't conflict with the Contract
- on the dates agreed
- that comply with Law

3.1.2 In the event that a level of warranty is not specified in the Award Form, the Supplier must provide Deliverables with a warranty of at least 90 days from Delivery against all obvious defects.

3.2 Goods clauses

3.2.1 All Goods delivered must be new, or as new if recycled, unused and of recent origin.

3.2.2 All manufacturer warranties covering the Goods must be assignable to the Buyer on request and for free.

3.2.3 The Supplier transfers ownership of the Goods on Delivery or payment for those Goods, whichever is earlier.

3.2.4 Risk in the Goods transfers to the Buyer on Delivery of the Goods, but remains with the Supplier if the Buyer notices damage following Delivery and lets the Supplier know within 3 Working Days of Delivery.

3.2.5 The Supplier warrants that it has full and unrestricted ownership of the Goods at the time of transfer of ownership.

3.2.6 The Supplier must deliver the Goods on the date and to the specified location during the Buyer's working hours.

3.2.7 The Supplier must provide sufficient packaging for the Goods to reach the point of Delivery safely and undamaged.

3.2.8 All deliveries must have a delivery note attached that specifies the order number, type and quantity of Goods.

3.2.9 The Supplier must provide all tools, information and instructions the Buyer needs to make use of the Goods.
3.2.10 The Supplier must indemnify the Buyer against the costs of any Recall of the Goods and give notice of actual or anticipated action about the Recall of the Goods.

3.2.11 The Buyer can cancel any order or part order of Goods which has not been Delivered. If the Buyer gives less than 14 days notice then it will pay the Supplier's reasonable and proven costs already incurred on the cancelled order as long as the Supplier takes all reasonable steps to minimise these costs.

3.2.12 The Supplier must at its own cost repair, replace, refund or substitute (at the Buyer's option and request) any Goods that the Buyer rejects because they don't conform with Clause 3. If the Supplier doesn't do this it will pay the Buyer's costs including repair or re-supply by a third party.

3.3 Services clauses

3.3.1 Late Delivery of the Services will be a Default of the Contract.

3.3.2 The Supplier must co-operate with the Buyer and third party suppliers on all aspects connected with the Delivery of the Services and ensure that Supplier Staff comply with any reasonable instructions of the Buyer or third party suppliers.

3.3.3 The Supplier must at its own risk and expense provide all Supplier Equipment required to Deliver the Services.

3.3.4 The Supplier must allocate sufficient resources and appropriate expertise to the Contract.

3.3.5 The Supplier must take all reasonable care to ensure performance does not disrupt the Buyer's operations, employees or other contractors.

3.3.6 The Supplier must ensure all Services, and anything used to Deliver the Services, are of good quality and free from defects.

3.3.7 The Buyer is entitled to withhold payment for partially or undelivered Services but doing so does not stop it from using its other rights under the Contract.

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5. The buyer's obligations to the supplier

5.1 If Supplier Non-Performance arises from a Buyer Cause:

- the Buyer cannot terminate the Contract under Clause 10.4.1
- the Supplier is entitled to reasonable and proven additional expenses and to relief from Delay Payments, liability and Deduction under this Contract
- the Supplier is entitled to additional time needed to make the Delivery
- the Supplier cannot suspend the ongoing supply of Deliverables

5.2 Clause 5.1 only applies if the Supplier:

- gives notice to the Buyer of the Buyer Cause within 10 Working Days of becoming aware
- demonstrates that the Supplier Non-Performance only happened because of the Buyer Cause
- mitigated the impact of the Buyer Cause

6. Record keeping and reporting

6.1 The Supplier must attend Progress Meetings with the Buyer and provide Progress Reports when specified in the Award Form.

6.2 The Supplier must keep and maintain full and accurate records and accounts in respect of the Contract for 7 years after the End Date and in accordance with the GDPR.

6.3 The Supplier must allow any Auditor access to their premises to verify all contract accounts and records of everything to do with the Contract and provide copies for an Audit.

6.4 The Supplier must provide information to the Auditor and reasonable co-operation at their request.

6.5 If the Supplier is not providing any of the Deliverables, or is unable to provide them, it must immediately:

- tell the Buyer and give reasons
- propose corrective action
- provide a deadline for completing the corrective action

7. Supplier staff

7.1 The Supplier Staff involved in the performance of the Contract must:

- be appropriately trained and qualified
- be vetted using Good Industry Practice
- comply with all conduct requirements when on the Buyer's Premises

7.2 Where the Buyer decides one of the Supplier's Staff is not suitable to work on the Contract, the Supplier must replace them with a suitably qualified alternative.

7.3 If requested, the Supplier must replace any person whose acts or omissions have caused the Supplier to breach Clause 27.

7.4 The Supplier must provide a list of Supplier Staff needing to access the Buyer's Premises and say why access is required.

7.5 The Supplier indemnifies the Buyer against all claims brought by any person employed by the Supplier caused by an act or omission of the Supplier or any Supplier Staff.

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9. Intellectual Property Rights (IPRs)

[redacted]

10.3 Ending the contract without a reason

[redacted]

[redacted]

10.4 When the Buyer can end the Contract

10.4.1 If any of the following events happen, the Buyer has the right to immediately terminate the Contract by issuing a Termination Notice to the Supplier:

- there's a Supplier Insolvency Event
- there's a Default that is not corrected in line with an accepted Rectification Plan
- the Buyer rejects a Rectification Plan or the Supplier does not provide it within 10 days of the request
- there's any material Default of the Contract
- there's any material Default of any Joint Controller Agreement relating to the Contract
- there's a Default of Clauses 2.6, 9, 14, 15, 27, 32 or Schedule 19 (Cyber Essentials) (where applicable) relating to the Contract
- there's a consistent repeated failure to meet the Service Levels in Schedule 10 (Service Levels)
- there's a Change of Control of the Supplier which isn't pre-approved by the Buyer in writing
- there's a Variation to the Contract which cannot be agreed using Clause 24 (Changing the contract) or resolved using Clause 34 (Resolving disputes)
- The Buyer discovers that the Supplier was in one of the situations in 57 (1) or 57(2) of the Regulations at the time the Contract was awarded
- the Court of Justice of the European Union uses Article 258 of the Treaty on the Functioning of the European Union (TFEU) to declare that the Contract should not have been awarded to the Supplier because of a serious breach of the TFEU or the Regulations
- the Supplier or its Affiliates embarrass or bring the Buyer into disrepute or diminish the public trust in them

10.4.2 If there is a Default, the Buyer can, without limiting its other rights, request that the Supplier provide a Rectification Plan.

10.4.3 When the Buyer receives a requested Rectification Plan it can either:

- reject the Rectification Plan or revised Rectification Plan, giving reasons
- accept the Rectification Plan or revised Rectification Plan (without limiting its rights) and the Supplier must immediately start work on the actions in the Rectification Plan at its own cost, unless agreed otherwise by the Parties

10.4.4 Where the Rectification Plan or revised Rectification Plan is rejected, the Buyer:

- must give reasonable grounds for its decision
- may request that the Supplier provides a revised Rectification Plan within 5 Working Days

10.4.5 If any of the events in 73 (1) (a) to (c) of the Regulations happen, the Buyer has the right to immediately terminate the Contract and Clause 10.5.2 to 10.5.7 applies.

10.5 What happens if the contract ends

Where the Buyer terminates the Contract under Clause 10.4.1 all of the following apply:

10.5.1 The Supplier is responsible for the Buyer's reasonable costs of procuring Replacement Deliverables for the rest of the Contract Period.

10.5.2 The Buyer's payment obligations under the terminated Contract stop immediately.

10.5.3 Accumulated rights of the Parties are not affected.

10.5.4 The Supplier must promptly delete or return the Government Data except where required to retain copies by law.

10.5.5 The Supplier must promptly return any of the Buyer's property provided under the terminated Contract.

10.5.6 The Supplier must, at no cost to the Buyer, co-operate fully in the handover and re-procurement (including to a Replacement Supplier).

10.5.7 The following Clauses survive the termination of the Contract: 3.2.10, 6, 7.2, 9, 11, 14, 15, 16, 17, 18, 34, 35 and any Clauses and Schedules which are expressly or by implication intended to continue.

10.6 When the supplier can end the contract

10.6.1 The Supplier can issue a Reminder Notice if the Buyer does not pay an undisputed invoice on time. The Supplier can terminate the Contract if the Buyer fails to

pay an undisputed invoiced sum due and worth over 10% of the total Contract Value within 30 days of the date of the Reminder Notice.

10.6.2 If a Supplier terminates the Contract under Clause 10.6.1:

- the Buyer must promptly pay all outstanding Charges incurred to the Supplier
- the Buyer must pay the Supplier reasonable committed and unavoidable Losses as long as the Supplier provides a fully itemised and costed schedule with evidence - the maximum value of this payment is limited to the total sum payable to the Supplier if the Contract had not been terminated
- Clauses 10.5.4 to 10.5.7 apply

10.7 When subcontracts can be ended

At the Buyer's request, the Supplier must terminate any Subcontracts in any of the following events:

- there is a Change of Control of a Subcontractor which isn't pre-approved by the Buyer in writing
- the acts or omissions of the Subcontractor have caused or materially contributed to a right of termination under Clause 10.4
- a Subcontractor or its Affiliates embarrasses or brings into disrepute or diminishes the public trust in the Buyer

10.8 Partially ending and suspending the contract

10.8.1 Where the Buyer has the right to terminate the Contract it can terminate or suspend (for any period), all or part of it. If the Buyer suspends the Contract it can provide the Deliverables itself or buy them from a third party.

10.8.2 The Buyer can only partially terminate or suspend the Contract if the remaining parts of that Contract can still be used to effectively deliver the intended purpose.

10.8.3 The Parties must agree any necessary Variation required by Clause 10.8 using the Variation Procedure, but the Supplier may not either:

- reject the Variation
- increase the Charges, except where the right to partial termination is under Clause 10.3

10.8.4 The Buyer can still use other rights available, or subsequently available to it if it acts on its rights under Clause 10.8.

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12. Obeying the law

12.1 The Supplier must use reasonable endeavours to comply with the provisions of Schedule 26 (Corporate Social Responsibility).

12.2 The Supplier indemnifies the Buyer against any costs resulting from any Default by the Supplier relating to any applicable Law.

12.3 The Supplier must appoint a Compliance Officer who must be responsible for ensuring that the Supplier complies with Law, Clause 12.1 and Clauses 27 to 32.

13. Insurance

The Supplier must, at its own cost, obtain and maintain the Required Insurances in Schedule 22 (Insurance Requirements).

14. Data protection

14.1 The Supplier must process Personal Data and ensure that Supplier Staff process Personal Data only in accordance with Schedule 20 (Processing Data).

14.2 The Supplier must not remove any ownership or security notices in or relating to the Government Data.

14.3 The Supplier must make accessible back-ups of all Government Data, stored in an agreed off-site location and send the Buyer copies every 6 Months.

14.4 The Supplier must ensure that any Supplier system holding any Government Data, including back-up data, is a secure system that complies with the Security Policy and any applicable Security Management Plan.

14.5 If at any time the Supplier suspects or has reason to believe that the Government Data provided under the Contract is corrupted, lost or sufficiently degraded, then the Supplier must notify the Buyer and immediately suggest remedial action.

14.6 If the Government Data is corrupted, lost or sufficiently degraded so as to be unusable the Buyer may either or both:

- tell the Supplier to restore or get restored Government Data as soon as practical but no later than 5 Working Days from the date that the Buyer receives notice, or the Supplier finds out about the issue, whichever is earlier
- restore the Government Data itself or using a third party

14.7 The Supplier must pay each Party's reasonable costs of complying with Clause 14.6 unless the Buyer is at fault.

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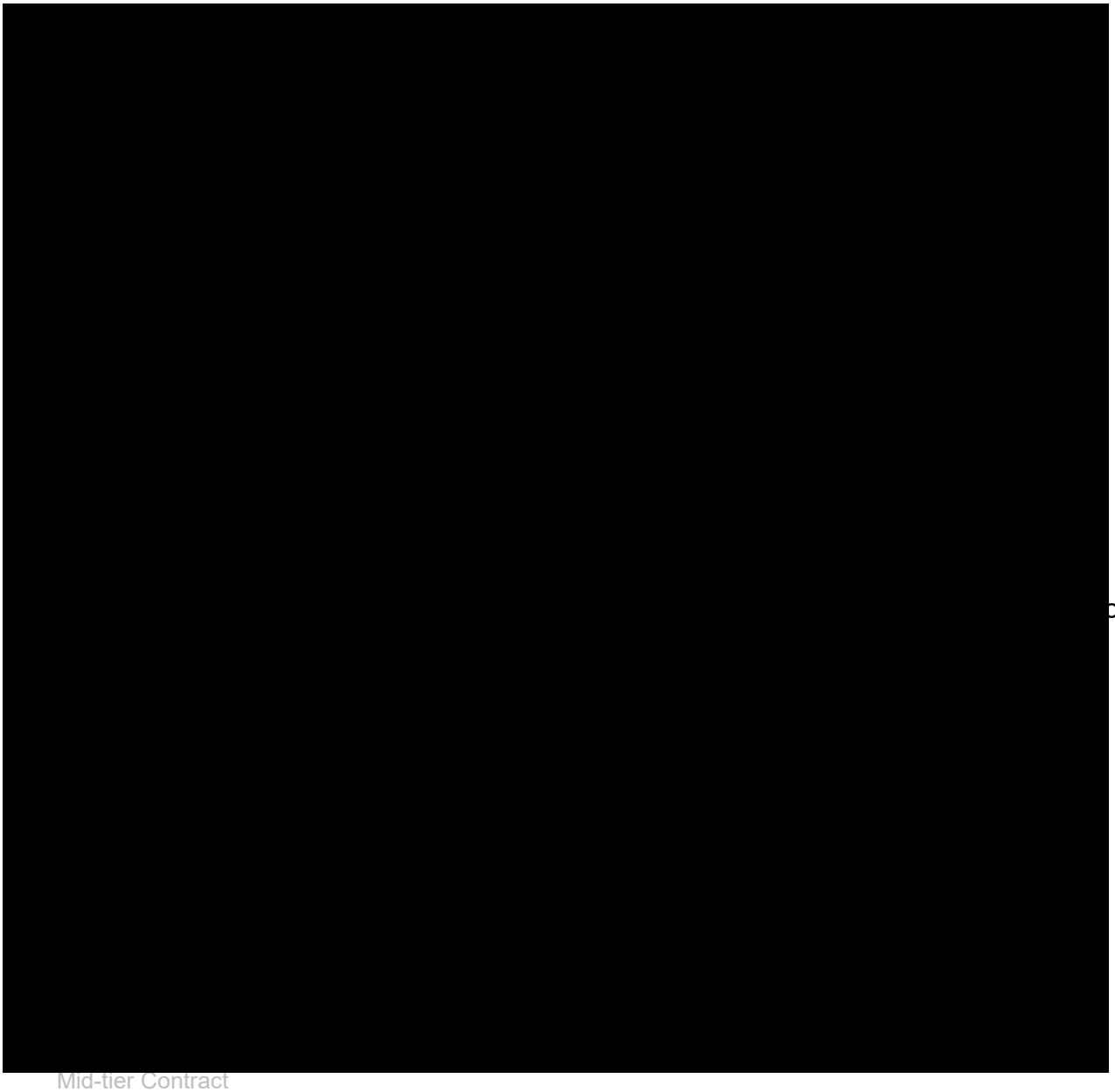

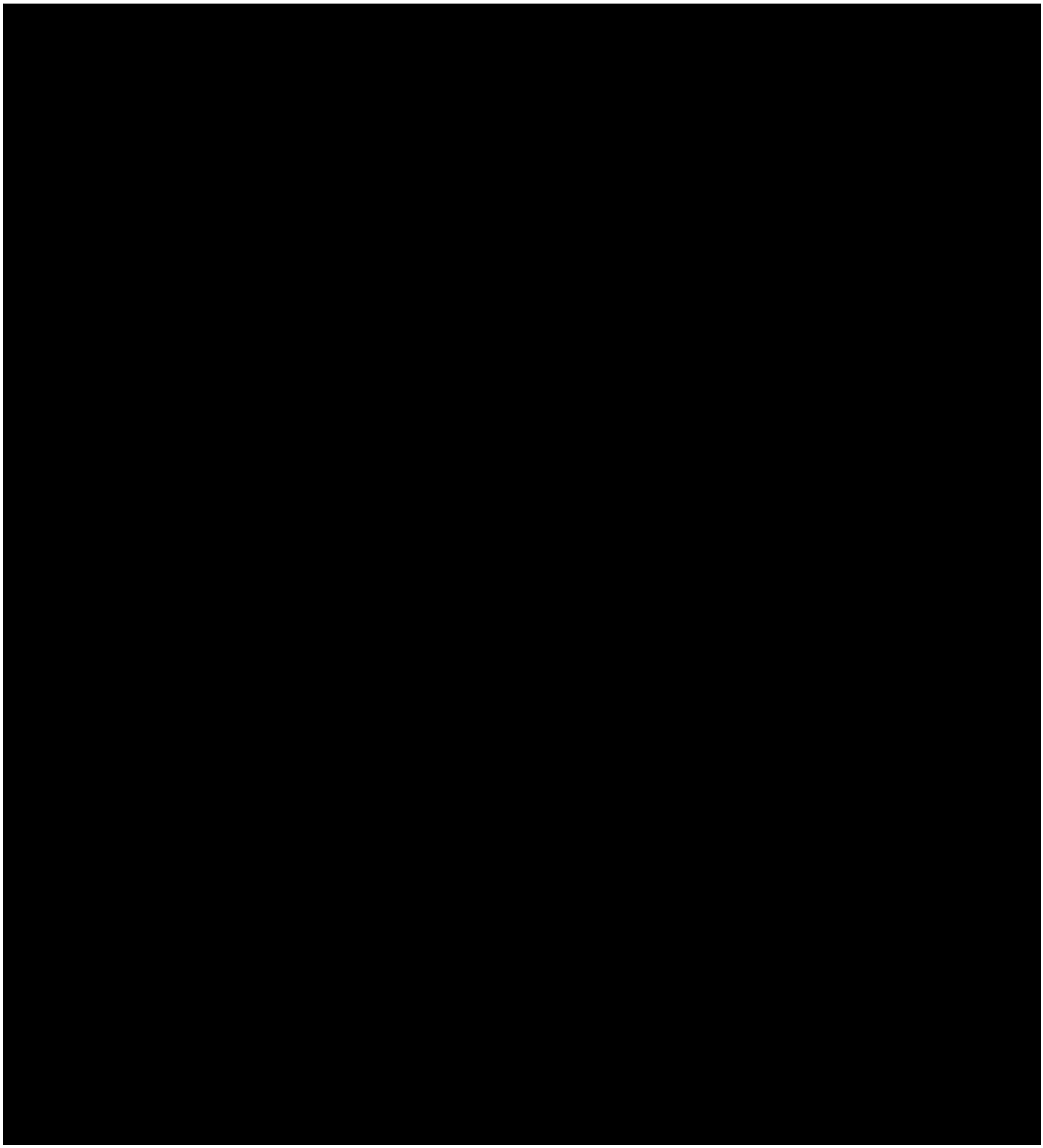

16. When you can share information

16.1 The Supplier must tell the Buyer within 48 hours if it receives a Request For Information.

16.2 Within the required timescales the Supplier must give the Buyer full co-operation and information needed so the Buyer can:

- publish the Transparency Information
- comply with any Freedom of Information Act (FOIA) request
- comply with any Environmental Information Regulations (EIR) request

16.3 The Buyer may talk to the Supplier to help it decide whether to publish information under Clause 16. However, the extent, content and format of the disclosure is the Buyer's decision, which does not need to be reasonable.

17. Invalid parts of the contract

If any part of the Contract is prohibited by Law or judged by a court to be unlawful, void or unenforceable, it must be read as if it was removed from that Contract as much as required and rendered ineffective as far as possible without affecting the rest of the Contract, whether it's valid or enforceable.

18. No other terms apply

The provisions incorporated into the Contract are the entire agreement between the Parties. The Contract replaces all previous statements and agreements whether written or oral. No other provisions apply.

19. Other people's rights in the Contract

No third parties may use the Contracts (Rights of Third Parties) Act (CRTPA) to enforce any term of the Contract unless stated (referring to CRTPA) in the Contract. This does not affect third party rights and remedies that exist independently from CRTPA.

20. Circumstances beyond your control

20.1 Any Party affected by a Force Majeure Event is excused from performing its obligations under the Contract while the inability to perform continues, if it both:

- provides a Force Majeure Notice to the other Party
- uses all reasonable measures practical to reduce the impact of the Force Majeure Event

20.2 Either party can partially or fully terminate the affected Contract if the provision of the Deliverables is materially affected by a Force Majeure Event which lasts for 90 days continuously.

20.3 Where a Party terminates under Clause 20.2:

- each party must cover its own Losses
- Clause 10.5.2 to 10.5.7 applies

21. Relationships created by the contract

The Contract does not create a partnership, joint venture or employment relationship. The Supplier must represent themselves accordingly and ensure others do so.

22. Giving up contract rights

A partial or full waiver or relaxation of the terms of the Contract is only valid if it is stated to be a waiver in writing to the other Party.

23. Transferring responsibilities

23.1 The Supplier cannot assign the Contract without the Buyer's written consent.

23.2 The Buyer can assign, novate or transfer its Contract or any part of it to any Crown Body, public or private sector body which performs the functions of the Buyer.

23.3 When the Buyer uses its rights under Clause 23.2 the Supplier must enter into a novation agreement in the form that the Buyer specifies.

23.4 The Supplier can terminate the Contract novated under Clause 23.2 to a private sector body that is experiencing an Insolvency Event.

23.5 The Supplier remains responsible for all acts and omissions of the Supplier Staff as if they were its own.

23.6 If the Buyer asks the Supplier for details about Subcontractors, the Supplier must provide details of Subcontractors at all levels of the supply chain including:

- their name
- the scope of their appointment
- the duration of their appointment

24. Changing the contract

24.1 Either Party can request a Variation to the Contract which is only effective if agreed in writing and signed by both Parties

24.2 The Supplier must provide an Impact Assessment either:

- with the Variation Form, where the Supplier requests the Variation
- within the time limits included in a Variation Form requested by the Buyer

24.3 If the Variation to the Contract cannot be agreed or resolved by the Parties, the Buyer can either:

- agree that the Contract continues without the Variation
- terminate the affected Contract, unless the Supplier has already provided part or all of the provision of the Deliverables, or where the Supplier can show evidence of substantial work being carried out to provide them
- refer the Dispute to be resolved using Clause 34 (Resolving Disputes)

24.4 The Buyer is not required to accept a Variation request made by the Supplier.

24.5 If there is a General Change in Law, the Supplier must bear the risk of the change and is not entitled to ask for an increase to the Charges.

24.6 If there is a Specific Change in Law or one is likely to happen during the Contract Period the Supplier must give the Buyer notice of the likely effects of the changes as soon as reasonably practical. They must also say if they think any Variation is needed either to the Deliverables, the Charges or the Contract and provide evidence:

- that the Supplier has kept costs as low as possible, including in Subcontractor costs
- of how it has affected the Supplier's costs

24.7 Any change in the Charges or relief from the Supplier's obligations because of a Specific Change in Law must be implemented using Clauses 24.1 to 24.4.

25. How to communicate about the contract

25.1 All notices under the Contract must be in writing and are considered effective on the Working Day of delivery as long as they're delivered before 5:00pm on a Working Day. Otherwise the notice is effective on the next Working Day. An email is effective when sent unless an error message is received.

25.2 Notices to the Buyer must be sent to the Buyer Authorised Representative's address or email address in the Award Form.

25.3 This Clause does not apply to the service of legal proceedings or any documents in any legal action, arbitration or dispute resolution.

27. Preventing fraud, bribery and corruption

27.1 The Supplier must not during any Contract Period:

- commit a Prohibited Act or any other criminal offence in the Regulations 57(1) and 57(2)

- do or allow anything which would cause the Buyer, including any of their employees, consultants, contractors, Subcontractors or agents to breach any of the Relevant Requirements or incur any liability under them

27.2 The Supplier must during the Contract Period:

- create, maintain and enforce adequate policies and procedures to ensure it complies with the Relevant Requirements to prevent a Prohibited Act and require its Subcontractors to do the same
- keep full records to show it has complied with its obligations under Clause 27 and give copies to the Buyer on request
- if required by the Buyer, within 20 Working Days of the Start Date of the Contract, and then annually, certify in writing to the Buyer, that they have complied with Clause 27, including compliance of Supplier Staff, and provide reasonable supporting evidence of this on request, including its policies and procedures

27.3 The Supplier must immediately notify the Buyer if it becomes aware of any breach of Clauses 27.1 or 27.2 or has any reason to think that it, or any of the Supplier Staff, has either:

- been investigated or prosecuted for an alleged Prohibited Act
- been debarred, suspended, proposed for suspension or debarment, or is otherwise ineligible to take part in procurement programmes or contracts because of a Prohibited Act by any government department or agency
- received a request or demand for any undue financial or other advantage of any kind related to the Contract
- suspected that any person or Party directly or indirectly related to the Contract has committed or attempted to commit a Prohibited Act

27.4 If the Supplier notifies the Buyer as required by Clause 27.3, the Supplier must respond promptly to their further enquiries, co-operate with any investigation and allow the Audit of any books, records and relevant documentation.

27.5 In any notice the Supplier gives under Clause 27.4 it must specify the:

- Prohibited Act
- identity of the Party who it thinks has committed the Prohibited Act
- action it has decided to take

28. Equality, diversity and human rights

28.1 The Supplier must follow all applicable equality Law when they perform their obligations under the Contract, including:

- protections against discrimination on the grounds of race, sex, gender reassignment, religion or belief, disability, sexual orientation, pregnancy, maternity, age or otherwise
- any other requirements and instructions which the Buyer reasonably imposes related to equality Law

28.2 The Supplier must take all necessary steps, and inform the Buyer of the steps taken, to prevent anything that is considered to be unlawful discrimination by any court or tribunal, or the Equality and Human Rights Commission (or any successor organisation) when working on the Contract.

29. Health and safety

29.1 The Supplier must perform its obligations meeting the requirements of:

- all applicable Law regarding health and safety
- the Buyer's current health and safety policy while at the Buyer's Premises, as provided to the Supplier

29.2 The Supplier must as soon as possible notify the other of any health and safety incidents or material hazards they're aware of at the Buyer Premises that relate to the performance of the Contract.

30. Environment

30.1 When working on Site the Supplier must perform its obligations under the Buyer's current Environmental Policy, which the Buyer must provide.

30.2 The Supplier must ensure that Supplier Staff are aware of the Buyer's Environmental Policy.

31. Tax

31.1 The Supplier must not breach any tax or social security obligations and must enter into a binding agreement to pay any late contributions due, including where applicable, any interest or any fines. The Buyer cannot terminate the Contract where the Supplier has not paid a minor tax or social security contribution.

31.2 Where the Charges payable under the Contract are or are likely to exceed £5 million at any point during the relevant Contract Period, and an Occasion of Tax Non-Compliance occurs, the Supplier must notify the Buyer of it within 5 Working Days including:

- the steps that the Supplier is taking to address the Occasion of Tax Non-Compliance and any mitigating factors that it considers relevant
- other information relating to the Occasion of Tax Non-Compliance that the Buyer may reasonably need

31.3 Where the Supplier or any Supplier Staff are liable to be taxed or to pay National Insurance contributions in the UK relating to payment received under the Contract, the Supplier must both:

- comply with the Income Tax (Earnings and Pensions) Act 2003 and all other statutes and regulations relating to income tax, the Social Security Contributions and Benefits Act 1992 (including IR35) and National Insurance contributions
- indemnify the Buyer against any Income Tax, National Insurance and social security contributions and any other liability, deduction, contribution, assessment or claim arising from or made during or after the Contract Period in connection with the provision of the Deliverables by the Supplier or any of the Supplier Staff

31.4 If any of the Supplier Staff are Workers who receive payment relating to the Deliverables, then the Supplier must ensure that its contract with the Worker contains the following requirements:

- the Buyer may, at any time during the Contract Period, request that the Worker provides information which demonstrates they comply with Clause 31.3, or why those requirements do not apply, the Buyer can specify the information the Worker must provide and the deadline for responding
- the Worker's contract may be terminated at the Buyer's request if the Worker fails to provide the information requested by the Buyer within the time specified by the Buyer
- the Worker's contract may be terminated at the Buyer's request if the Worker provides information which the Buyer considers isn't good enough to demonstrate how it complies with Clause 31.3 or confirms that the Worker is not complying with those requirements
- the Buyer may supply any information they receive from the Worker to HMRC for revenue collection and management

32. Conflict of interest

32.1 The Supplier must take action to ensure that neither the Supplier nor the Supplier Staff are placed in the position of an actual or potential Conflict of Interest.

32.2 The Supplier must promptly notify and provide details to the Buyer if a Conflict of Interest happens or is expected to happen.

32.3 The Buyer can terminate its Contract immediately by giving notice in writing to the Supplier or take any steps it thinks are necessary where there is or may be an actual or potential Conflict of Interest.

33. Reporting a breach of the contract

33.1 As soon as it is aware of it the Supplier and Supplier Staff must report to the Buyer any actual or suspected breach of:

- Law
- Clause 12.1
- Clauses 27 to 32

33.2 The Supplier must not retaliate against any of the Supplier Staff who in good faith reports a breach listed in Clause 33.1 to the Buyer or a Prescribed Person.

34. Resolving disputes

34.1 If there is a Dispute, the senior representatives of the Parties who have authority to settle the Dispute will, within 28 days of a written request from the other Party, meet in good faith to resolve the Dispute.

34.2 If the Dispute is not resolved at that meeting, the Parties can attempt to settle it by mediation using the Centre for Effective Dispute Resolution (CEDR) Model Mediation Procedure current at the time of the Dispute. If the Parties cannot agree on a mediator, the mediator will be nominated by CEDR. If either Party does not wish to use, or continue to use mediation, or mediation does not resolve the Dispute, the Dispute must be resolved using Clauses 34.3 to 34.5.

34.3 Unless the Buyer refers the Dispute to arbitration using Clause 34.4, the Parties irrevocably agree that the courts of England and Wales have the exclusive jurisdiction to:

- determine the Dispute
- grant interim remedies
- grant any other provisional or protective relief

34.4 The Supplier agrees that the Buyer has the exclusive right to refer any Dispute to be finally resolved by arbitration under the London Court of International Arbitration Rules current at the time of the Dispute. There will be only one arbitrator. The seat or legal place of the arbitration will be London and the proceedings will be in English.

34.5 The Buyer has the right to refer a Dispute to arbitration even if the Supplier has started or has attempted to start court proceedings under Clause 34.3, unless the Buyer has agreed to the court proceedings or participated in them. Even if court proceedings have started, the Parties must do everything necessary to ensure that the court proceedings are stayed in favour of any arbitration proceedings if they are started under Clause 34.4.

34.6 The Supplier cannot suspend the performance of the Contract during any Dispute.

35. Which law applies

This Contract and any issues arising out of, or connected to it, are governed by English law.

Schedule 1 (Definitions)

1.1 In the Contract, unless the context otherwise requires, capitalised expressions shall have the meanings set out in this Schedule 1 (Definitions) or the relevant Schedule in which that capitalised expression appears.

1.2 If a capitalised expression does not have an interpretation in this Schedule or any other Schedule, it shall, in the first instance, be interpreted in accordance with the common interpretation within the relevant market sector/industry where appropriate. Otherwise, it shall be interpreted in accordance with the dictionary meaning.

1.3 In the Contract, unless the context otherwise requires:

1.3.1 the singular includes the plural and vice versa;

1.3.2 reference to a gender includes the other gender and the neuter;

1.3.3 references to a person include an individual, company, body corporate, corporation, unincorporated association, firm, partnership or other legal entity or Crown Body;

1.3.4 a reference to any Law includes a reference to that Law as amended, extended, consolidated or re-enacted from time to time;

1.3.5 the words "including", "other", "in particular", "for example" and similar words shall not limit the generality of the preceding words and shall be construed as if they were immediately followed by the words "without limitation";

1.3.6 references to "writing" include typing, printing, lithography, photography, display on a screen, electronic and facsimile transmission and other modes of representing or reproducing words in a visible form, and expressions referring to writing shall be construed accordingly;

1.3.7 references to "representations" shall be construed as references to present facts, to "warranties" as references to present and future facts and to "undertakings" as references to obligations under the Contract;

1.3.8 references to "Clauses" and "Schedules" are, unless otherwise provided, references to the clauses and schedules of the Core Terms and references in any Schedule to parts, paragraphs, annexes and tables are, unless otherwise provided, references to the parts, paragraphs, annexes and tables of the Schedule in which these references appear;

1.3.9 references to "Paragraphs" are, unless otherwise provided, references to the paragraph of the appropriate Schedules unless otherwise provided; and

1.3.10 references to a series of Clauses or Paragraphs shall be inclusive of the clause numbers specified.

1.3.11 the headings in the Contract are for ease of reference only and shall not affect the interpretation or construction of the Contract; and

1.3.12 where the Buyer is a Crown Body it shall be treated as contracting with the Crown as a whole.

1.4 In the Contract, unless the context otherwise requires, the following words shall have the following meanings:

"Achieve"	in respect of a Test, to successfully pass such Test without any Test Issues and in respect of a Milestone, the issue of a Satisfaction Certificate in respect of that Milestone and "**Achieved**", "**Achieving**" and "**Achievement**" shall be construed accordingly;
"Affected Party"	the party seeking to claim relief in respect of a Force Majeure Event;
"Affiliates"	in relation to a body corporate, any other entity which directly or indirectly Controls, is Controlled by, or is under direct or indirect common Control of that body corporate from time to time;
"Annex"	extra information which supports a Schedule;
"Approval"	the prior written consent of the Buyer and "**Approve**" and "**Approved**" shall be construed accordingly;
"Audit"	the Buyer's right to: a) verify the accuracy of the Charges and any other amounts payable by the Buyer under a Contract (including proposed or actual variations to them in accordance with the Contract); b) verify the costs of the Supplier (including the costs of all Subcontractors and any third party suppliers) in connection with the provision of the Services; c) verify the Open Book Data; d) verify the Supplier's and each Subcontractor's compliance with the applicable Law; e) identify or investigate actual or suspected breach of Clauses 27 to 33 and/or Schedule 26 (Corporate Social Responsibility), impropriety or accounting mistakes or any breach or threatened breach of security and in these circumstances the Buyer shall have no obligation to inform the Supplier of the purpose or objective of its investigations; f) identify or investigate any circumstances which may impact upon the financial stability of the Supplier, any Guarantor, and/or any Subcontractors or their ability to provide the Deliverables;

	g) obtain such information as is necessary to fulfil the Buyer's obligations to supply information for parliamentary, ministerial, judicial or administrative purposes including the supply of information to the Comptroller and Auditor General; h) review any books of account and the internal contract management accounts kept by the Supplier in connection with the Contract; i) carry out the Buyer's internal and statutory audits and to prepare, examine and/or certify the Buyer's annual and interim reports and accounts; j) enable the National Audit Office to carry out an examination pursuant to Section 6(1) of the National Audit Act 1983 of the economy, efficiency and effectiveness with which the Buyer has used its resources. a)
"Auditor"	a) the Buyer's internal and external auditors; b) the Buyer's statutory or regulatory auditors; c) the Comptroller and Auditor General, their staff and/or any appointed representatives of the National Audit Office; d) HM Treasury or the Cabinet Office; e) any party formally appointed by the Buyer to carry out audit or similar review functions; and f) successors or assigns of any of the above;
"Buyer Cause"	any breach of the obligations of the Buyer or any other default, act, omission, negligence or statement of the Buyer, of its employees, servants, agents in connection with or in relation to the subject-matter of the Contract and in respect of which the Buyer is liable to the Supplier;
"BACS"	the Bankers' Automated Clearing Services, which is a scheme for the electronic processing of financial transactions within the United Kingdom;
"Beneficiary"	a Party having (or claiming to have) the benefit of an indemnity under this Contract;
"Buyer Assets"	the Buyer's infrastructure, data, software, materials, assets, equipment or other property owned by and/or licensed or leased to the Buyer and which is or may be used in connection with the provision of the Deliverables which remain the property of the Buyer throughout the term of the Contract;
"Buyer Authorised Representative"	the representative appointed by the Buyer from time to time in relation to the Contract initially identified in the Award Form;

"Buyer Premises"	premises owned, controlled or occupied by the Buyer which are made available for use by the Supplier or its Subcontractors for the provision of the Deliverables (or any of them);
"Contract"	the contract between the Buyer and the Supplier, which consists of the terms set out and referred to in the Award Form;
"Contract Period"	the Contract Period in respect of the Contract;
"Central Government Body"	a body listed in one of the following sub-categories of the Central Government classification of the Public Sector Classification Guide, as published and amended from time to time by the Office for National Statistics: a) Government Department; b) Non-Departmental Public Body or Assembly Sponsored Public Body (advisory, executive, or tribunal); c) Non-Ministerial Department; or d) Executive Agency;
"Change in Law"	any change in Law which impacts on the supply of the Deliverables and performance of the Contract which comes into force after the Start Date;
"Change of Control"	a change of control within the meaning of Section 450 of the Corporation Tax Act 2010;
"Charges"	b) the prices (exclusive of any applicable VAT), payable to the Supplier by the Buyer under the Contract, as set out in the Award Form, for the full and proper performance by the Supplier of its obligations under the Contract less any Deductions;
"Claim"	any claim which it appears that a Beneficiary is, or may become, entitled to indemnification under this Contract;
"Commercially Sensitive Information"	the Confidential Information listed in the Award Form (if any) comprising of commercially sensitive information relating to the Supplier, its IPR or its business or which the Supplier has indicated to the Buyer that, if disclosed by the Buyer, would cause the Supplier significant commercial disadvantage or material financial loss;
"Comparable Supply"	the supply of Deliverables to another Buyer of the Supplier that are the same or similar to the Deliverables;
"Compliance Officer"	the person(s) appointed by the Supplier who is responsible for ensuring that the Supplier complies with its legal obligations;
"Confidential Information"	means any information, however it is conveyed, that relates to the business, affairs, developments, trade secrets, Know-How, personnel and suppliers of the Buyer or the Supplier, including IPRs, together with information derived from the above, and any other information clearly designated as being confidential (whether or not

	it is marked as **"confidential"**) or which ought reasonably to be considered to be confidential;
"Conflict of Interest"	a conflict between the financial or personal duties of the Supplier or the Supplier Staff and the duties owed to the Buyer under the Contract, in the reasonable opinion of the Buyer;
"Contract"	c) the contract to be entered into between the Buyer and the Supplier for the provision of the Deliverables;
"Contracts Finder"	the Government's publishing portal for public sector procurement opportunities and contract data;
"Contract Period"	the term of the Contract from the earlier of the: a) applicable Start Date; or b) the Effective Date until the applicable End Date;
"Contract Value"	the higher of the actual or expected total Charges paid or payable under the Contract where all obligations are met by the Supplier;
"Contract Year"	a consecutive period of twelve (12) Months commencing on the Start Date or each anniversary thereof;
"Control"	control in either of the senses defined in sections 450 and 1124 of the Corporation Tax Act 2010 and "**Controlled**" shall be construed accordingly;
"Controller"	has the meaning given to it in the GDPR;
"Core Terms"	d) the Buyer's standard terms and conditions for common goods and services which comprise one part of the Contract the full title of

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"Crown Body"	the government of the United Kingdom (including the Northern Ireland Assembly and Executive Committee, the Scottish Government and the National Assembly for Wales), including, but not limited to, government ministers and government departments and particular bodies, persons, commissions or agencies from time to time carrying out functions on its behalf;
"CRTPA"	the Contract Rights of Third Parties Act 1999;
"Data Protection Impact Assessment	an assessment by the Controller of the impact of the envisaged Processing on the protection of Personal Data;

"Data Protection Legislation"	(i) the GDPR, the LED and any applicable national implementing Laws as amended from time to time (ii) the DPA 2018 to the extent that it relates to Processing of personal data and privacy; (iii) all applicable Law about the Processing of personal data and privacy;
"Data Protection Officer"	has the meaning given to it in the GDPR;
"Data Subject"	has the meaning given to it in the GDPR
"Data Subject Access Request"	a request made by, or on behalf of, a Data Subject in accordance with rights granted pursuant to the Data Protection Legislation to access their Personal Data;
"Deductions"	all Service Credits, Delay Payments (if applicable), or any other deduction which the Buyer is paid or is payable to the Buyer under the Contract;
"Default"	any breach of the obligations of the Supplier (including abandonment of the Contract in breach of its terms) or any other default (including material default), act, omission, negligence or statement of the Supplier, of its Subcontractors or any Supplier Staff howsoever arising in connection with or in relation to the subject-matter of the Contract and in respect of which the Supplier is liable to the Buyer;
"Delay Payments"	the amounts (if any) payable by the Supplier to the Buyer in respect of a delay in respect of a Milestone as specified in the Implementation Plan;
"Deliverables"	Goods and/or Services that may be ordered under the Contract including the Documentation;
"Delivery"	delivery of the relevant Deliverable or Milestone in accordance with the terms of the Contract as confirmed and accepted by the Buyer by the either (a) confirmation in writing to the Supplier; or (b) where Schedule 8 (Implementation Plan and Testing) is used issue by the Buyer of a Satisfaction Certificate. "**Deliver**" and "**Delivered**" shall be construed accordingly;
"Disaster"	the occurrence of one or more events which, either separately or cumulatively, mean that the Deliverables, or a material part thereof will be unavailable (or could reasonably be anticipated to be unavailable) for the period specified in the Award Form (for the purposes of this definition the **"Disaster Period"**);
"Disclosing Party"	the Party directly or indirectly providing Confidential Information to the other Party in accordance with Clause 15 (What you must keep confidential);

"Dispute"	any claim, dispute or difference arises out of or in connection with the Contract or in connection with the negotiation, existence, legal validity, enforceability or termination of the Contract, whether the alleged liability shall arise under English law or under the law of some other country and regardless of whether a particular cause of action may successfully be brought in the English courts;
"Dispute Resolution Procedure"	the dispute resolution procedure set out in Clause 34 (Resolving disputes);
"Documentation"	descriptions of the Services and Service Levels, technical specifications, user manuals, training manuals, operating manuals, process definitions and procedures, system environment descriptions and all such other documentation (whether in hardcopy or electronic form) is required to be supplied by the Supplier to the Buyer under the Contract as: a) would reasonably be required by a competent third party capable of Good Industry Practice contracted by the Buyer to develop, configure, build, deploy, run, maintain, upgrade and test the individual systems that provide the Deliverables b) is required by the Supplier in order to provide the Deliverables; and/or c) has been or shall be generated for the purpose of providing the Deliverables;
"DOTAS"	the Disclosure of Tax Avoidance Schemes rules which require a promoter of tax schemes to tell HMRC of any specified notifiable arrangements or proposals and to provide prescribed information on those arrangements or proposals within set time limits as contained in Part 7 of the Finance Act 2004 and in secondary legislation made under vires contained in Part 7 of the Finance Act 2004 and as extended to National Insurance Contributions;
"Due Diligence Information"	any information supplied to the Supplier by or on behalf of the Buyer prior to the Start Date;
"Effective Date"	the date on which the final Party has signed the Contract;
"EIR"	the Environmental Information Regulations 2004;
"Employment Regulations"	the Transfer of Undertakings (Protection of Employment) Regulations 2006 (SI 2006/246) as amended or replaced or any other Regulations implementing the European Council Directive 77/187/EEC;
"End Date"	the earlier of: a) the Expiry Date (as extended by any Extension Period exercised by the Buyer under Clause 10.2); or

	b) if the Contract is terminated before the date specified in (a) above, the date of termination of the Contract;
"Environmental Policy"	to conserve energy, water, wood, paper and other resources, reduce waste and phase out the use of ozone depleting substances and minimise the release of greenhouse gases, volatile organic compounds and other substances damaging to health and the environment, including any written environmental policy of the Buyer;
"Estimated Year 1 Charges	the anticipated total Charges payable by the Buyer in the first Contract Year specified in the Award Form;
"Estimated Yearly Charges"	means for the purposes of calculating each Party's annual liability under clause 11.2 : i) in the first Contract Year, the Estimated Year 1 Charges; or ii) in any subsequent Contract Years, the Charges paid or payable in the previous Contract Year; or e) f) iii) after the end of the Contract, the Charges paid or payable in the last Contract Year during the Contract Period; g)
"Equality and Human Rights Commission"	the UK Government body named as such as may be renamed or replaced by an equivalent body from time to time;
"Existing IPR"	any and all IPR that are owned by or licensed to either Party and which are or have been developed independently of the Contract (whether prior to the Start Date or otherwise);
"Expiry Date"	the date of the end of the Contract as stated in the Award Form;
"Extension Period"	such period or periods beyond which the Initial Period may be extended up to a maximum of the number of years in total specified in the Award Form;
"FOIA"	the Freedom of Information Act 2000 and any subordinate legislation made under that Act from time to time together with any guidance and/or codes of practice issued by the Information Commissioner or relevant Government department in relation to such legislation;
"Force Majeure Event"	any event, circumstance, matter or cause affecting the performance by either the Buyer or the Supplier of its obligations arising from: h) acts, events, omissions, happenings or non-happenings beyond the reasonable control of the Affected Party which prevent or

	materially delay the Affected Party from performing its obligations under a Contract; a) riots, civil commotion, war or armed conflict, acts of terrorism, nuclear, biological or chemical warfare; b) acts of a Crown Body, local government or regulatory bodies; c) fire, flood or any disaster; or d) an industrial dispute affecting a third party for which a substitute third party is not reasonably available but excluding: i) any industrial dispute relating to the Supplier, the Supplier Staff (including any subsets of them) or any other failure in the Supplier or the Subcontractor's supply chain; ii) any event, occurrence, circumstance, matter or cause which is attributable to the wilful act, neglect or failure to take reasonable precautions against it by the Party concerned; and iii) any failure of delay caused by a lack of funds;
"Force Majeure Notice"	a written notice served by the Affected Party on the other Party stating that the Affected Party believes that there is a Force Majeure Event;
"Award Form"	the document outlining the Incorporated Terms and crucial information required for the Contract, to be executed by the Supplier and the Buyer;
" Incorporated Terms"	the contractual terms applicable to the Contract specified in the Award Form;
" Special Terms"	any additional terms and conditions specified in the Award Form incorporated into the Contract;
" Tender Response"	the tender submitted by the Supplier to the Buyer and annexed to or referred to in Schedule 4 (Tender);
"GDPR"	the General Data Protection Regulation (Regulation (EU) 2016/679)
"General Anti-Abuse Rule"	a) the legislation in Part 5 of the Finance Act 2013 and; and b) any future legislation introduced into parliament to counteract tax advantages arising from abusive arrangements to avoid National Insurance contributions;
"General Change in Law"	a Change in Law where the change is of a general legislative nature (including taxation or duties of any sort affecting the Supplier) or which affects or relates to a Comparable Supply;
"Goods"	goods made available by the Supplier as specified in Schedule 2 (Specification) and in relation to a Contract as specified in the Award Form;
"Good Industry Practice"	standards, practices, methods and procedures conforming to the Law and the exercise of the degree of skill and care, diligence,

	prudence and foresight which would reasonably and ordinarily be expected from a skilled and experienced person or body engaged within the relevant industry or business sector;
"Government"	the government of the United Kingdom (including the Northern Ireland Assembly and Executive Committee, the Scottish Government and the National Assembly for Wales), including government ministers and government departments and other bodies, persons, commissions or agencies from time to time carrying out functions on its behalf;
"Government Data"	the data, text, drawings, diagrams, images or sounds (together with any database made up of any of these) which are embodied in any electronic, magnetic, optical or tangible media, including any of the Buyer's Confidential Information, and which: i) are supplied to the Supplier by or on behalf of the Buyer; or ii) the Supplier is required to generate, process, store or transmit pursuant to the Contract;
"Government Procurement Card"	the Government's preferred method of purchasing and payment for low value goods or services https://www.gov.uk/government/publications/government-procurement-card--2;
"Guarantor"	the person (if any) who has entered into a guarantee in the form set out in Schedule 23 (Guarantee) in relation to this Contract;
"Halifax Abuse Principle"	the principle explained in the CJEU Case C-255/02 Halifax and others;
"HMRC"	Her Majesty's Revenue and Customs;
"ICT Policy"	the Buyer's policy in respect of information and communications technology, referred to in the Award Form, which is in force as at the Start Date (a copy of which has been supplied to the Supplier), as updated from time to time in accordance with the Variation Procedure;
"Impact Assessment"	an assessment of the impact of a Variation request by the Buyer completed in good faith, including: a) details of the impact of the proposed Variation on the Deliverables and the Supplier's ability to meet its other obligations under the Contract; b) details of the cost of implementing the proposed Variation; c) details of the ongoing costs required by the proposed Variation when implemented, including any increase or decrease in the Charges (as applicable), any alteration in the resources and/or expenditure required by either Party and any alteration to the working practices of either Party;

	d) a timetable for the implementation, together with any proposals for the testing of the Variation; and e) such other information as the Buyer may reasonably request in (or in response to) the Variation request;
"Implementation Plan"	the plan for provision of the Deliverables set out in Schedule 8 (Implementation Plan and Testing) where that Schedule is used or otherwise as agreed between the Supplier and the Buyer;
"Indemnifier"	a Party from whom an indemnity is sought under this Contract;
"Independent Control"	where a Controller has provided Personal Data to another Party which is not a Processor or a Joint Controller because the recipient itself determines the purposes and means of Processing but does so separately from the Controller providing it with Personal Data and "**Independent Controller**" shall be construed accordingly;
"Indexation"	the adjustment of an amount or sum in accordance with the Award Form;
"Information"	has the meaning given under section 84 of the Freedom of Information Act 2000;
"Information Commissioner"	the UK's independent authority which deals with ensuring information relating to rights in the public interest and data privacy for individuals is met, whilst promoting openness by public bodies;
"Initial Period"	the initial term of the Contract specified in the Award Form;
"Insolvency Event"	a) in respect of a person: b) a proposal is made for a voluntary arrangement within Part I of the Insolvency Act 1986 or of any other composition scheme or arrangement with, or assignment for the benefit of, its creditors; or c) a shareholders' meeting is convened for the purpose of considering a resolution that it be wound up or a resolution for its winding-up is passed (other than as part of, and exclusively for the purpose of, a bona fide reconstruction or amalgamation); or d) a petition is presented for its winding up (which is not dismissed within fourteen (14) Working Days of its service) or an application is made for the appointment of a provisional liquidator or a creditors' meeting is convened pursuant to section 98 of the Insolvency Act 1986; or e) a receiver, administrative receiver or similar officer is appointed over the whole or any part of its business or assets; or f) an application order is made either for the appointment of an administrator or for an administration order, an administrator is appointed, or notice of intention to appoint an administrator is given; or

	g) it is or becomes insolvent within the meaning of section 123 of the Insolvency Act 1986; or h) being a "small company" within the meaning of section 382(3) of the Companies Act 2006, a moratorium comes into force pursuant to Schedule A1 of the Insolvency Act 1986; or i) where the person is an individual or partnership, any event analogous to those listed in limbs (a) to (g) (inclusive) occurs in relation to that individual or partnership; or j) any event analogous to those listed in limbs (a) to (h) (inclusive) occurs under the law of any other jurisdiction;
"Installation Works"	all works which the Supplier is to carry out at the beginning of the Contract Period to install the Goods in accordance with the Contract;
"Intellectual Property Rights" or "IPR"	a) copyright, rights related to or affording protection similar to copyright, rights in databases, patents and rights in inventions, semi-conductor topography rights, trade marks, rights in internet domain names and website addresses and other rights in trade or business names, goodwill, designs, Know-How, trade secrets and other rights in Confidential Information; b) applications for registration, and the right to apply for registration, for any of the rights listed at (a) that are capable of being registered in any country or jurisdiction; and c) all other rights having equivalent or similar effect in any country or jurisdiction;
"Invoicing Address"	the address to which the Supplier shall Invoice the Buyer as specified in the Award Form;
"IPR Claim"	any claim of infringement or alleged infringement (including the defence of such infringement or alleged infringement) of any IPR, used to provide the Deliverables or otherwise provided and/or licensed by the Supplier (or to which the Supplier has provided access) to the Buyer in the fulfilment of its obligations under the Contract;
"IR35"	the off-payroll rules requiring individuals who work through their company pay the same tax and National Insurance contributions as an employee which can be found online at: https://www.gov.uk/guidance/ir35-find-out-if-it-applies;
"Joint Controller Agreement"	the agreement (if any) entered into between the Buyer and the Supplier substantially in the form set out in Annex 2 of Schedule 20 (*Processing Data*);
"Joint Controllers"	where two or more Controllers jointly determine the purposes and means of Processing;
"Key Personnel"	the individuals (if any) identified as such in the Award Form;

"Key Sub-Contract"	each Sub-Contract with a Key Subcontractor;
"Key Subcontractor"	any Subcontractor: a) which is relied upon to deliver any work package within the Deliverables in their entirety; and/or b) which, in the opinion of the Buyer performs (or would perform if appointed) a critical role in the provision of all or any part of the Deliverables; and/or c) with a Sub-Contract with the Contract value which at the time of appointment exceeds (or would exceed if appointed) 10% of the aggregate Charges forecast to be payable under the Contract, and the Supplier shall list all such Key Subcontractors in section 29 of the Award Form;
"Know-How"	all ideas, concepts, schemes, information, knowledge, techniques, methodology, and anything else in the nature of know-how relating to the Deliverables but excluding know-how already in the other Party's possession before the applicable Start Date;
"Law"	any law, subordinate legislation within the meaning of Section 21(1) of the Interpretation Act 1978, bye-law, enforceable right within the meaning of Section 2 of the European Communities Act 1972, regulation, order, regulatory policy, mandatory guidance or code of practice, judgment of a relevant court of law, or directives or requirements with which the Supplier is bound to comply;
"LED"	i) Law Enforcement Directive (Directive (EU) 2016/680)
"Losses"	all losses, liabilities, damages, costs, expenses (including legal fees), disbursements, costs of investigation, litigation, settlement, judgment, interest and penalties whether arising in contract, tort (including negligence), breach of statutory duty, misrepresentation or otherwise and "**Loss**" shall be interpreted accordingly;
"Lots"	the number of lots specified in Schedule 2 (Specification), if applicable;
"Marketing Contact"	shall be the person identified in the Award Form;
"Milestone"	an event or task described in the Implementation Plan;
"Milestone Date"	the target date set out against the relevant Milestone in the Implementation Plan by which the Milestone must be Achieved;
"Month"	a calendar month and "**Monthly**" shall be interpreted accordingly;
"National Insurance"	contributions required by the National Insurance Contributions Regulations 2012 (SI 2012/1868) made under section 132A of the Social Security Administration Act 1992;

"New IPR"	a) IPR in items created by the Supplier (or by a third party on behalf of the Supplier) specifically for the purposes of the Contract and updates and amendments of these items including (but not limited to) database schema; and/or b) IPR in or arising as a result of the performance of the Supplier's obligations under the Contract and all updates and amendments to the same; but shall not include the Supplier's Existing IPR;
"Occasion of Tax Non – Compliance"	where: a) any tax return of the Supplier submitted to a Relevant Tax Authority on or after 1 October 2012 which is found on or after 1 April 2013 to be incorrect as a result of: i) a Relevant Tax Authority successfully challenging the Supplier under the General Anti-Abuse Rule or the Halifax Abuse Principle or under any tax rules or legislation in any jurisdiction that have an effect equivalent or similar to the General Anti-Abuse Rule or the Halifax Abuse Principle; ii) the failure of an avoidance scheme which the Supplier was involved in, and which was, or should have been, notified to a Relevant Tax Authority under the DOTAS or any equivalent or similar regime in any jurisdiction; and/or b) any tax return of the Supplier submitted to a Relevant Tax Authority on or after 1 October 2012 which gives rise, on or after 1 April 2013, to a criminal conviction in any jurisdiction for tax related offences which is not spent at the Start Date or to a civil penalty for fraud or evasion;

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"Parliament"	takes its natural meaning as interpreted within by Law;
"Party"	the Buyer or the Supplier and "**Parties**" shall mean both of them where the context permits;
"Personal Data"	has the meaning given to it in the GDPR;
"Personal Data Breach"	has the meaning given to it in the GDPR;
"Prescribed Person"	a legal adviser, an MP or an appropriate body which a whistle-blower may make a disclosure to as detailed in 'Whistleblowing: list of prescribed people and bodies', 24 November 2016, available online at: https://www.gov.uk/government/publications/blowing-the-whistle-list-of-prescribed-people-and-bodies--2/whistleblowing-list-of-prescribed-people-and-bodies;
"Progress Meeting"	a meeting between the Buyer Authorised Representative and the Supplier Authorised Representative;
"Progress Meeting Frequency"	the frequency at which the Supplier shall conduct a Progress Meeting in accordance with Clause 6.1 as specified in the Award Form;

"Progress Report"	a report provided by the Supplier indicating the steps taken to achieve Milestones or delivery dates;
"Progress Report Frequency"	the frequency at which the Supplier shall deliver Progress Reports in accordance with Clause 6.1 as specified in the Award Form;
"Prohibited Acts"	a) to directly or indirectly offer, promise or give any person working for or engaged by the Buyer or any other public body a financial or other advantage to: i) induce that person to perform improperly a relevant function or activity; or ii) reward that person for improper performance of a relevant function or activity; b) to directly or indirectly request, agree to receive or accept any financial or other advantage as an inducement or a reward for improper performance of a relevant function or activity in connection with the Contract; or c) committing any offence: i) under the Bribery Act 2010 (or any legislation repealed or revoked by such Act); or ii) under legislation or common law concerning fraudulent acts; or iii) defrauding, attempting to defraud or conspiring to defraud the Buyer or other public body; or d) any activity, practice or conduct which would constitute one of the offences listed under (c) above if such activity, practice or conduct had been carried out in the UK;
"Protective Measures"	technical and organisational measures which must take account of: j) a) the nature of the data to be protected k) b)harm that might result from Data Loss Event; l) c) state of technological development m) d) the cost of implementing any measures including but not limited to pseudonymising and encrypting Personal Data, ensuring confidentiality, integrity, availability and resilience of systems and services, ensuring that availability of and access to Personal Data can be restored in a timely manner after an incident, and regularly assessing and evaluating the effectiveness of the such measures adopted by it;
"Recall"	a request by the Supplier to return Goods to the Supplier or the manufacturer after the discovery of safety issues or defects (including defects in the IPR rights) that might endanger health or hinder performance;

"Recipient Party"	the Party which receives or obtains directly or indirectly Confidential Information;
"Rectification Plan"	the Supplier's plan (or revised plan) to rectify it's breach using the template in Schedule 25 (Rectification Plan Template) which shall include: a) full details of the Default that has occurred, including a root cause analysis; b) the actual or anticipated effect of the Default; and c) the steps which the Supplier proposes to take to rectify the Default (if applicable) and to prevent such Default from recurring, including timescales for such steps and for the rectification of the Default (where applicable);
"Rectification Plan Process"	the process set out in Clause 10.4.2 to 10.4.4 (Rectification Plan Process);
"Regulations"	the Public Contracts Regulations 2015 and/or the Public Contracts (Scotland) Regulations 2015 (as the context requires);
"Reimbursable Expenses"	the reasonable out of pocket travel and subsistence (for example, hotel and food) expenses, properly and necessarily incurred in the performance of the Services, calculated at the rates and in accordance with the Buyer's expenses policy current from time to time, but not including: a) travel expenses incurred as a result of Supplier Staff travelling to and from their usual place of work, or to and from the premises at which the Services are principally to be performed, unless the Buyer otherwise agrees in advance in writing; and b) subsistence expenses incurred by Supplier Staff whilst performing the Services at their usual place of work, or to and from the premises at which the Services are principally to be performed;
"the Buyer's Confidential Information"	c) all Personal Data and any information, however it is conveyed, that relates to the business, affairs, developments, property rights, trade secrets, Know-How and IPR of the Buyer (including all Buyer Existing IPR and New IPR); d) any other information clearly designated as being confidential (whether or not it is marked "confidential") or which ought reasonably be considered confidential which comes (or has come) to the Buyer's attention or into the Buyer's possession in connection with the Contract; and information derived from any of the above;
"Relevant Requirements"	all applicable Law relating to bribery, corruption and fraud, including the Bribery Act 2010 and any guidance issued by the Secretary of State pursuant to section 9 of the Bribery Act 2010;

"Relevant Tax Authority"	HMRC, or, if applicable, the tax authority in the jurisdiction in which the Supplier is established;
"Reminder Notice"	a notice sent in accordance with Clause 10.6 given by the Supplier to the Buyer providing notification that payment has not been received on time;
"Replacement Deliverables"	any deliverables which are substantially similar to any of the Deliverables and which the Buyer receives in substitution for any of the Deliverables , whether those goods are provided by the Buyer internally and/or by any third party;
"Replacement Subcontractor"	a Subcontractor of the Replacement Supplier to whom Transferring Supplier Employees will transfer on a Service Transfer Date (or any Subcontractor of any such Subcontractor);
"Replacement Supplier"	any third party provider of Replacement Deliverables appointed by or at the direction of the Buyer from time to time or where the Buyer is providing Replacement Deliverables for its own account, shall also include the Buyer;
"Request For Information"	a request for information or an apparent request relating to the Contract for the provision of the Deliverables or an apparent request for such information under the FOIA or the EIRs;
"Required Insurances"	the insurances required by Schedule 22 (Insurance Requirements);
"Satisfaction Certificate"	the certificate (materially in the form of the document contained in Annex 2 of Part B of Schedule 8 (Implementation Plan and Testing) or as agreed by the Parties where Schedule 8 is not used in this Contract) granted by the Buyer when the Supplier has Achieved a Milestone or a Test;
"Schedules"	any attachment to the Contract which contains important information specific to each aspect of buying and selling;
"Security Management Plan"	the Supplier's security management plan prepared pursuant to Schedule 16 (Security) (if applicable);
"Security Policy"	the Buyer's security policy, referred to in the Award Form, in force as at the Start Date (a copy of which has been supplied to the Supplier), as updated from time to time and notified to the Supplier;
"Serious Fraud Office"	the UK Government body named as such as may be renamed or replaced by an equivalent body from time to time;
"Service Levels"	any service levels applicable to the provision of the Deliverables under the Contract (which, where Schedule 10 (Service Levels) is used in this Contract, are specified in the Annex to Part A of such Schedule);
"Service Period"	has the meaning given to it in the Award Form;

"Services"	services made available by the Supplier as specified in Schedule 2 (Specification) and in relation to a Contract as specified in the Award Form;
"Service Transfer"	any transfer of the Deliverables (or any part of the Deliverables), for whatever reason, from the Supplier or any Subcontractor to a Replacement Supplier or a Replacement Subcontractor;
"Service Transfer Date"	the date of a Service Transfer;
"Sites"	any premises (including the Buyer Premises, the Supplier's premises or third party premises) from, to or at which: a) the Deliverables are (or are to be) provided; or b) the Supplier manages, organises or otherwise directs the provision or the use of the Deliverables; c) those premises at which any Supplier Equipment or any part of the Supplier System is located (where ICT Services are being provided)
"SME"	an enterprise falling within the category of micro, small and medium sized enterprises defined by the Commission Recommendation of 6 May 2003 concerning the definition of micro, small and medium enterprises;
"Special Terms"	any additional Clauses set out in the Award Form which shall form part of the respective Contract;
"Specific Change in Law"	a Change in Law that relates specifically to the business of the Buyer and which would not affect a Comparable Supply where the effect of that Specific Change in Law on the Deliverables is not reasonably foreseeable at the Start Date;
"Specification"	the specification set out in Schedule 2 (Specification), as may, in relation to the Contract, be supplemented by the Award Form;
"Standards"	any: a) standards published by BSI British Standards, the National Standards Body of the United Kingdom, the International Organisation for Standardisation or other reputable or equivalent bodies (and their successor bodies) that a skilled and experienced operator in the same type of industry or business sector as the Supplier would reasonably and ordinarily be expected to comply with; b) standards detailed in the specification in Schedule 2 (Specification); c) standards detailed by the Buyer in the Award Form or agreed between the Parties from time to time;

	d) relevant Government codes of practice and guidance applicable from time to time;
"Start Date"	the date specified on the Award Form;
"Storage Media"	the part of any device that is capable of storing and retrieving data;
"Sub-Contract"	any contract or agreement (or proposed contract or agreement), other than a Contract, pursuant to which a third party: a) provides the Deliverables (or any part of them); b) provides facilities or services necessary for the provision of the Deliverables (or any part of them); and/or c) is responsible for the management, direction or control of the provision of the Deliverables (or any part of them);
"Subcontractor"	any person other than the Supplier, who is a party to a Sub-Contract and the servants or agents of that person;
"Subprocessor"	any third Party appointed to process Personal Data on behalf of the Supplier related to the Contract;
"Supplier"	the person, firm or company identified in the Award Form;
"Supplier Assets"	all assets and rights used by the Supplier to provide the Deliverables in accordance with the Contract but excluding the Buyer Assets;
"Supplier Authorised Representative"	the representative appointed by the Supplier named in the Award Form, or later defined in a Contract;
"Supplier's Confidential Information"	a) any information, however it is conveyed, that relates to the business, affairs, developments, IPR of the Supplier (including the Supplier Existing IPR) trade secrets, Know-How, and/or personnel of the Supplier; b) any other information clearly designated as being confidential (whether or not it is marked as "confidential") or which ought reasonably to be considered to be confidential and which comes (or has come) to the Supplier's attention or into the Supplier's possession in connection with the Contract; c) Information derived from any of (a) and (b) above;
"Supplier's Contract Manager	the person identified in the Award Form appointed by the Supplier to oversee the operation of the Contract and any alternative person whom the Supplier intends to appoint to the role, provided that the Supplier informs the Buyer prior to the appointment;
"Supplier Equipment"	the Supplier's hardware, computer and telecoms devices, equipment, plant, materials and such other items supplied and used by the Supplier (but not hired, leased or loaned from the Buyer) in the performance of its obligations under this Contract;

"Supplier Non-Performance"	where the Supplier has failed to: a) Achieve a Milestone by its Milestone Date; b) provide the Goods and/or Services in accordance with the Service Levels ; and/or c) comply with an obligation under the Contract;

[redacted]

"Supplier Staff"	all directors, officers, employees, agents, consultants and contractors of the Supplier and/or of any Subcontractor engaged in the performance of the Supplier's obligations under the Contract;
"Supply Chain Information Report Template"	the document at Annex 1 of Schedule 18 Supply Chain Visibility;
"Supporting Documentation"	sufficient information in writing to enable the Buyer to reasonably assess whether the Charges, Reimbursable Expenses and other sums due from the Buyer under the Contract detailed in the information are properly payable;
"Termination Notice"	a written notice of termination given by one Party to the other, notifying the Party receiving the notice of the intention of the Party giving the notice to terminate the Contract on a specified date and setting out the grounds for termination;
"Test Issue"	any variance or non-conformity of the Deliverables or Deliverables from their requirements as set out in the Contract;
"Test Plan"	a plan: a) for the Testing of the Deliverables; and b) setting out other agreed criteria related to the achievement of Milestones;
"Tests and Testing"	any tests required to be carried out pursuant to the Contract as set out in the Test Plan or elsewhere in the Contract and "**Tested**" shall be construed accordingly;
"Third Party IPR"	Intellectual Property Rights owned by a third party which is or will be used by the Supplier for the purpose of providing the Deliverables;
"Transferring Supplier Employees"	those employees of the Supplier and/or the Supplier's Subcontractors to whom the Employment Regulations will apply on the Service Transfer Date;

"Transparency Information"	the Transparency Reports and the content of the Contract, including any changes to this Contract agreed from time to time, except for – n) (i) any information which is exempt from disclosure in accordance with the provisions of the FOIA, which shall be determined by the Buyer; and (ii) Commercially Sensitive Information;
"Transparency Reports"	the information relating to the Deliverables and performance pursuant to the Contract which the Supplier is required to provide to the Buyer in accordance with the reporting requirements in Schedule 6 (Transparency Reports);
"Variation"	has the meaning given to it in Clause 24 (Changing the contract);
"Variation Form"	the form set out in Schedule 21 (Variation Form);
"Variation Procedure"	the procedure set out in Clause 24 (Changing the contract);
"VAT"	value added tax in accordance with the provisions of the Value Added Tax Act 1994;
"VCSE"	a non-governmental organisation that is value-driven and which principally reinvests its surpluses to further social, environmental or cultural objectives;
"Worker"	any one of the Supplier Staff which the Buyer, in its reasonable opinion, considers is an individual to which Procurement Policy Note 08/15 (Tax Arrangements of Public Appointees) (https://www.gov.uk/government/publications/procurement-policy-note-0815-tax-arrangements-of-appointees) applies in respect of the Deliverables; and
"Working Day"	any day other than a Saturday or Sunday or public holiday in England and Wales unless specified otherwise by the Parties in the Award Form.
"Work Day"	7.5 Work Hours, whether or not such hours are worked consecutively and whether or not they are worked on the same day;
"Work Hours"	the hours spent by the Supplier Staff properly working on the provision of the Deliverables including time spent travelling (other than to and from the Supplier's offices, or to and from the Sites) but excluding lunch breaks;

Schedule 2 (Specification)

GENERAL INTRODUCTION

The Food Standards Agency is an independent Government department working across England, Wales and Northern Ireland to protect public health and consumers wider interest in food. We make sure food is safe and what it says it is.

- The Agency is committed to openness, transparency and equality of treatment to all suppliers. As well as these principles, for science projects the final project report will be published on the Food Standards Agency website (www.food.gov.uk). For science projects we will encourage contractors to publish their work in peer reviewed scientific publications wherever possible. Also, in line with the Government's Transparency Agenda which aims to encourage more open access to data held by government, the Agency is developing a policy on the release of underpinning data from all of its science- and evidence-gathering projects. Data should be made freely available in an accessible format, as fully and as promptly as possible. Consideration should be given to data management as new contracts are being negotiated. Resource implications for this should be taken into account. The mechanism for publishing underpinning data should allow the widest opportunity for to enable its re-use. Where possible, underpinning data should be included in the final project report. Where data are included in the final report in pdf format, they should also be published separately in a format that can be used for further analysis. Large data sets can be provided separately in an annex to the report, and published, where possible, alongside the final report online Where it is more appropriate to publish underpinning data in an existing database, archive, repository or other community resource, or for data to be saved in a specialist proprietary format, information will be provided on how the data can be accessed. There will be some circumstances where release of data may need to be restricted or anonymised for reasons of commercial and/or personal sensitivities.
- This project will enable the FSA to understand and subsequently protect public health from risks that may arise from the consumption of GM foods or feed and thus enable us to ensure that food is safe and what it says it is.
- Garnering bioinformatics expertise will enable us to support empowerment of consumers through improved expertise in GM risk assessment which will help ensure the public are able to make informed decisions on the foods they eat through greater choice of safe foods and a wider awareness of potential risks.

A. THE SPECIFICATION

Background

Following the end of the transition period, the UK will be responsible for the approval of regulated products. These are products that require a pre-market safety assessment and include genetically modified foods and feed.

Part of the legal requirement for applicants wishing to bring a food or feed containing genetically modified organisms to the UK market from January 2021, is to provide detailed information relating to the genes inserted/altered in the organism and the flanking areas of that region. These data need to be interrogated to identify potential genes of concern within the GM organism such as those for anti-microbial resistance. We wish to engage an external contractor with independent bioinformatic expertise in order to identify any risks associated with the GM event within the genome.

The Specification

Tenders are invited to carry out analysis of genomic data for applications to the UK under the UK regulations on genetically modified food and feed to be costed on a per-dossier basis. The requirements of European regulation (EC) No 1829/2003 of the European Parliament and of the Council of 22 September 2003 on genetically modified food and feed have been directly transcribed into UK law and will come into effect on the 1st January 2021. These and their associated EFSA guidance require an applicant wishing to place a novel GM food or feed product on to the market in the UK to provide the nucleic acid(s) sequences (SANGER and/or NGS) for the inserted gene(s) and flanking regions. The links to the relevant guidance for applicants can be found below. These will give an idea on the types of data the applicants will be submitting.

Technical note on the requirements for sequencing data (including specification of file types and requirements): https://www.efsa.europa.eu/en/efsajournal/pub/5345

Application guidance:
https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2013.3491

Renewal guidance:
https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/sp.efsa.2019.EN-1668

Draft microorganism guidance:
https://www.efsa.europa.eu/sites/default/files/consultation/consultation/consultation_EFSA-Statement-WGS-microorganisms.pdf

The contractor's role may include the following on a per application basis:

- Check the completeness of the sequencing data provided by the applicant

- Evaluate the analyses of SANGER and/or NGS sequence data for both 5’ and 3’ flanking regions at each insertion site, with the aim of identifying interruptions of known genes including:-
    - Evaluate the parameters of bioinformatic searches of the flanking sequences
    - Evaluation of the data sources and software tools used by the applicant
    - Independent analyses of raw sequence data for both 5’ and 3’ flanking regions at each insertion site
- Evaluation of the analyses of Open Reading Frames (ORFs) present within the insert and spanning the junction sites and possible similarity of putative polypeptides with known toxins and allergens including:-
    - Evaluation of the parameters of bioinformatic methods used for analyses of ORFs
    - Evaluation of the data sources and software tools used by the applicant
    - Independent analysis of ORFs
    - Independent analysis of similarity between derived amino acid sequences resulting from detected ORFs and known toxins and allergens
    - Preparation of an analysis of the sequence similarity between GM plant DNA and microbial DNA for an evaluation of the potential for horizontal transfer of the GM sequence

In their tender, the Supplier must be able to demonstrate the following:

- Extensive experience in producing, and assessing sequencing data generated both with Sanger and NGS technologies; experience in bioinformatics for the analyses of complex sequencing data and use of relevant software for such analyses; experience in understanding methodology and data in the fields of molecular and plant biology, such as GMOs. **A list of recently completed projects and an example of the type of report the supplier expects to deliver should be provided.**
- Ability to provide a team of at least 2 experts in Bioinformatics ideally along with molecular biology expertise including GM. **Detailed CV’s of the project team must be provided.**
- Ability and capacity to meet the strict timelines enshrined in legislation by which risk assessment of GM food and feed products must be completed. Checks per application should be complete and the report available within 3 weeks of receipt from the FSA or details of missing documentation supplied as soon as possible to enable the FSA to “stop the clock” on an assessment and request further data from the applicant
- Experience in preparing scientific publications and technical reports, and extensive and demonstrable experience in the evaluation and elaboration of bioinformatic analyses
- How the team will keep up to date with the newest analytical methods and approaches. Potentially through a professional science body linked to chartership or other means.

- Availability of adequate technical equipment, software and databases with security in place to ensure commercially sensitive data is not released to third parties and data backups are secure. **A signed statement to this effect must be provided**.
- A commitment to confidentiality and no conflicts of interest (to be agreed on a per application basis) that may impact their ability to make impartial judgements. **A signed statement to this effect must be provided.**
- Must be open to feedback and willing to adapt their approach accordingly.

Anticipated volumes

We currently anticipate around 10-15 per year including new applications and renewals but we ask that potential contractors demonstrate flexibility to handle a higher or lower volume if required.

Data protection

All data remains the property of the applicant and must be treated as sensitive data throughout. No distribution to third parties is permitted without the express permission of the applicant. The FSA will obtain permission from each applicant to share genomic data with the contractor.

'Please outline in your tender how you will comply with the GDPR, recognising the commissioning authority's role as the 'data controller' and the contractor's role as the 'data processor', and responding to the sections below. If successful you may also be asked to carry out a Privacy Impact Assessment (PIA), and a privacy notice may be required, which will be reviewed by the FSA data security team.

Data security

Please confirm in your tender that you have in place, or that you will have in place by contract award, the human and technical resources to perform the contract to ensure compliance with the General Data Protection Regulation and to ensure the protection of the rights of data subjects.

Please provide details of the technical facilities and measures (including systems and processes) you have in place, or will have in place by contract award, to ensure compliance with the General Data Protection Regulation and to ensure the protection of the rights of data subjects. Your response should include, but should not be limited to facilities and measures:

- to ensure ongoing confidentiality, integrity, availability and resilience of processing systems and services;
- to comply with the rights of data subjects in respect of receiving privacy information, and access, rectification, deletion and portability of personal data;
- to ensure that any consent-based processing meets standards of active, informed consent, and that such consents are recorded and auditable;
- to ensure legal safeguards are in place to legitimise transfers of personal data outside the EU (if such transfers will take place);

- to maintain records of personal data processing activities; and
- to regularly test, assess and evaluate the effectiveness of the above measures.'

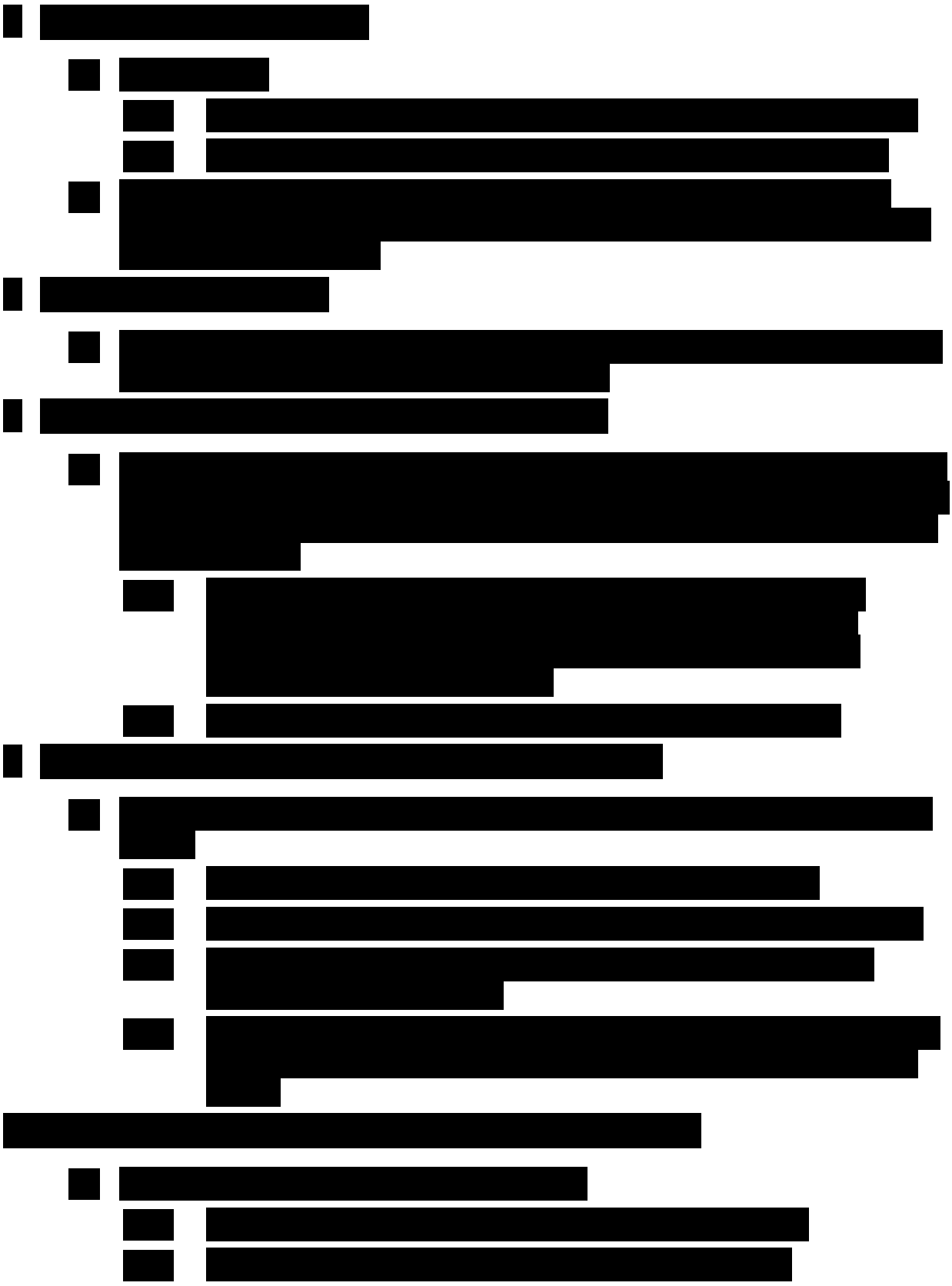
Dissemination and exploitation

We wish to receive the conclusions of the analyses in a report format which should be distributed to the FSA only and not to any third party or made public in any way. The contractor will not be permitted to use the data provided to them for any other purpose than that stated in this specification document.

Quality

Reports will be peer-reviewed by our Scientific Advisory Committee and feedback may be given. Amendments may be requested and we would request that the contractor takes any suggestions on board for future work.

Schedule 3 (Charges)



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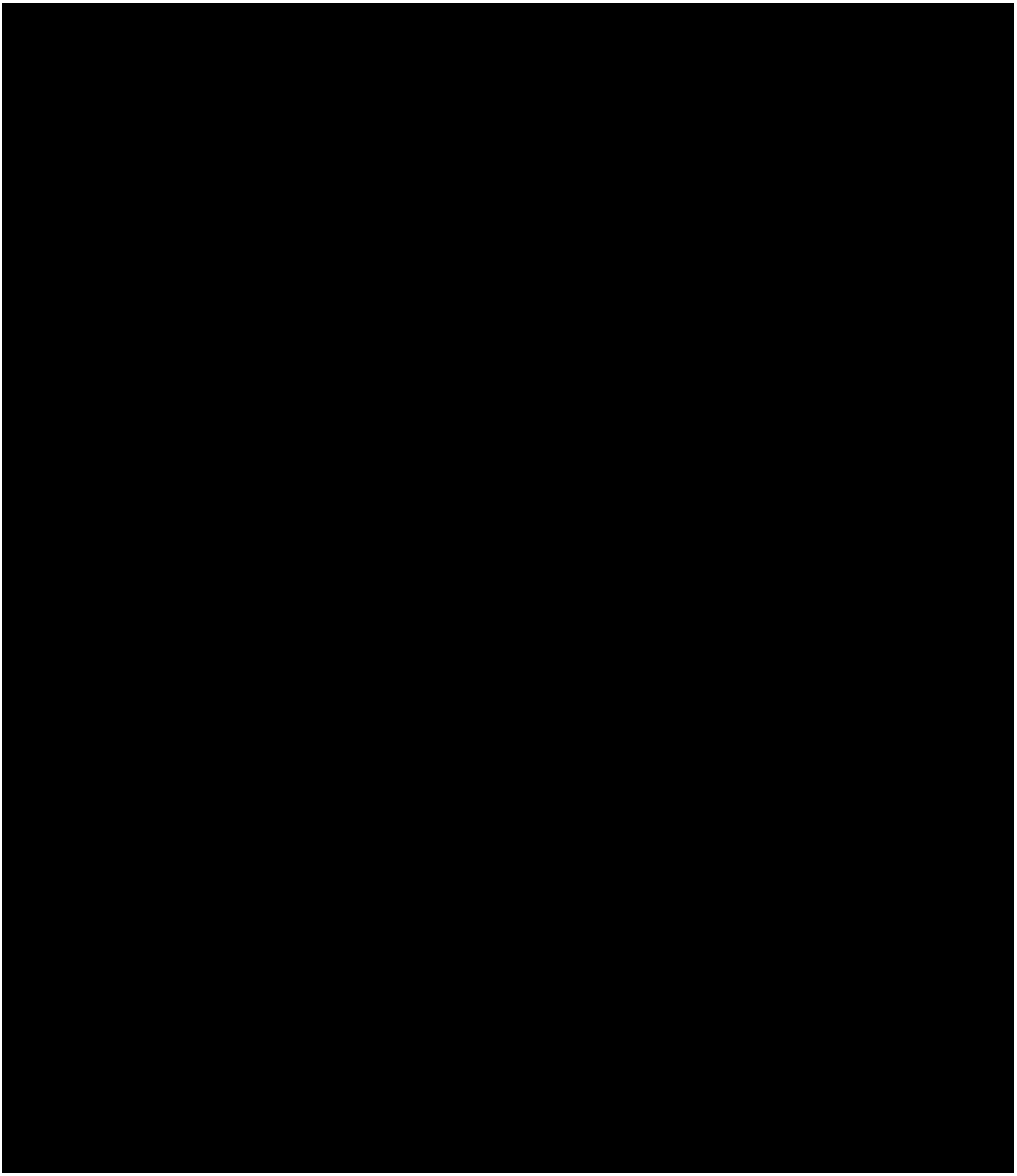
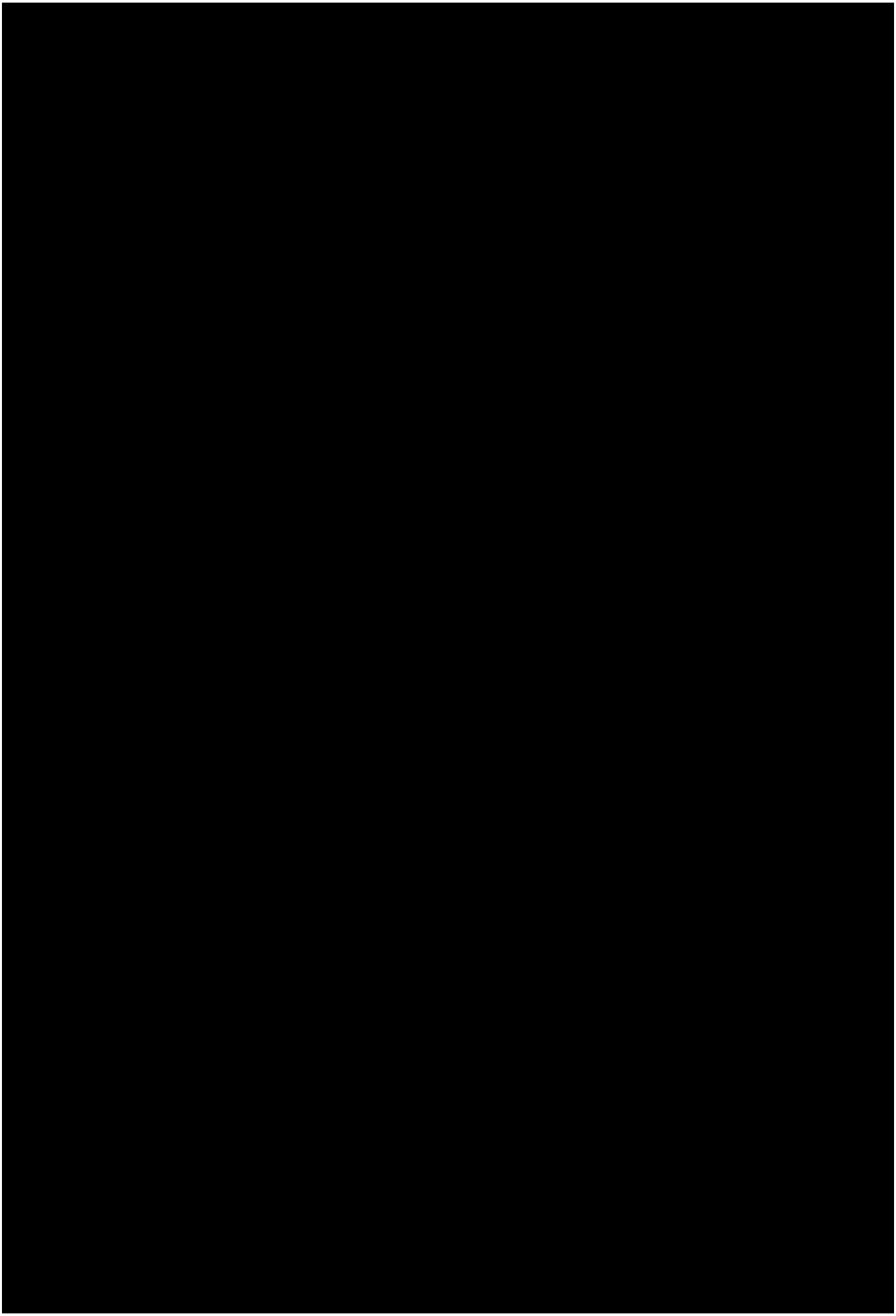
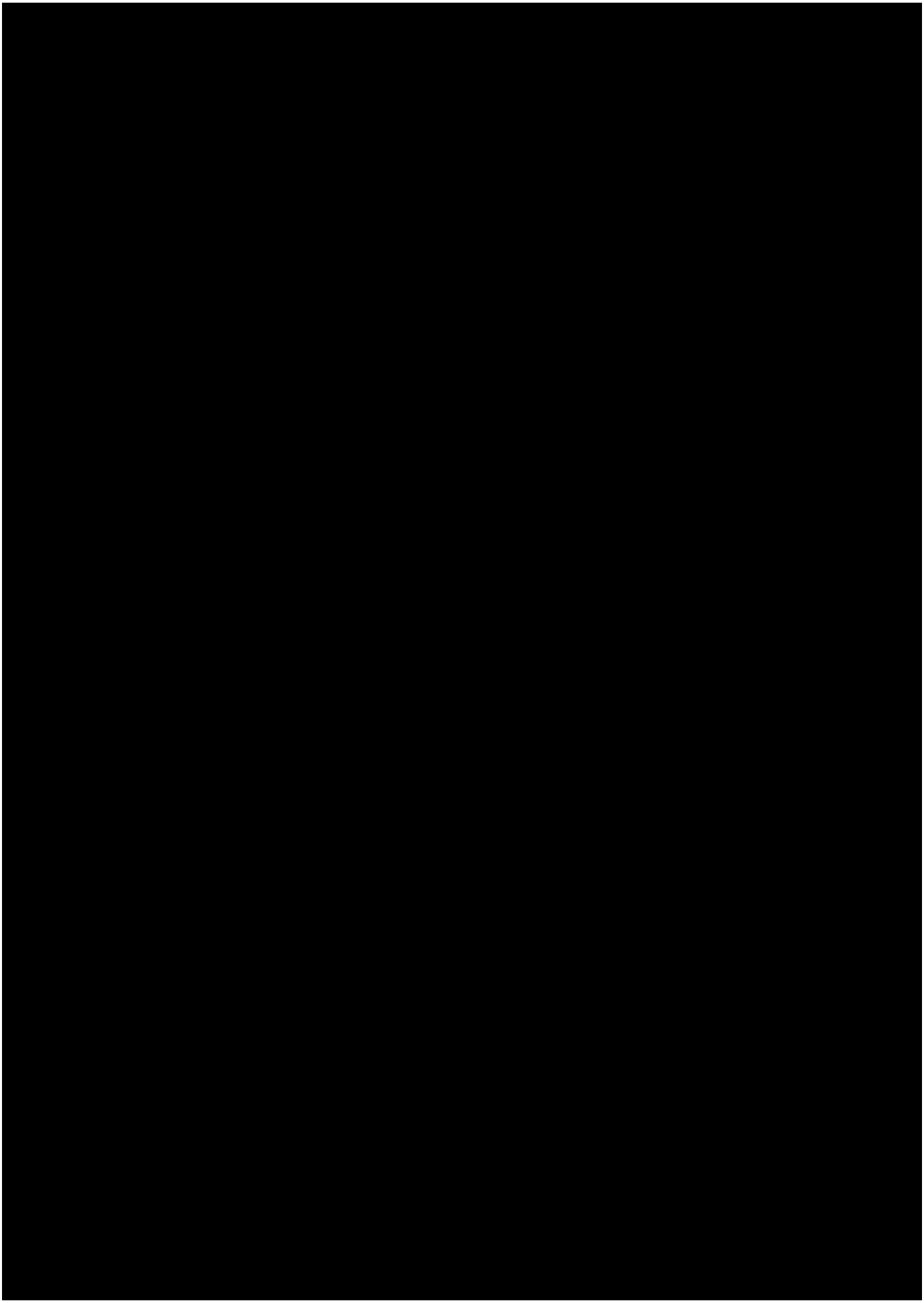
Total Project Costs	£7,305.62

Total Labour Costs	**£ 7,305.62**
* Total Overhead Costs (if not shown above)	

Schedule 4 (Tender)







Our assumption is that from the outset of the contract, requirements of Applicants for GMO authorisations will be in continuity with the current EU/EFSA specifications, with reference in particular to:

- Regulation (EU) No 503/2013 of 3rd April 2013 (referred to hereon in as "Reg. 503/2013")
  - https://eur-lex.europa.eu/eli/reg_impl/2013/503
- EFSA guidance on the submission of applications for authorisation of genetically modified plants under Regulation (EC) No 1829/2003 ("EFSA submission guidance")
  - https://doi.org/10.2903/j.efsa.2013.3491
- Administrative guidance on the submission of applications for renewal of authorisation of genetically modified food and feed under Articles 11 and 23 of Regulation (EC) No 1829/2003 ("EFSA renewal guidance")
  - https://doi.org/10.2903/sp.efsa.2019.EN-1668
- Guideline for the submission of DNA sequences derived from genetically modified organisms and associated annotations within the framework of Directive 2001/18/EC and Regulation (EC) No 1829/2003 ("EU sequence submission guideline")
  - https://gmo-crl.jrc.ec.europa.eu/doc/Guideline-Sequencing-Feb-2016-mod-April-2017.pdf
- Technical Note on the quality of DNA sequencing for the molecular characterisation of genetically modified plants [EFSA GMO Panel, 2018] ("EFSA Technical Note")
  - https://doi.org/10.2903/j.efsa.2018.5345
- Explanatory note on DNA sequence similarity searches in the context of the assessment of horizontal gene transfer from plants to microorganisms ("EFSA HGT Explanatory Note")
  - https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/sp.efsa.2017.EN-1273
  - (N.B. publisher-stated DOI URL appears to be currently broken: https://doi.org/10.2903/sp.efsa.2017.EN-1273)
- EFSA statement on the requirements for whole genome sequence analysis of microorganisms intentionally used in the food chain (DRAFT)
  - https://www.efsa.europa.eu/sites/default/files/consultation/consultation/consultation_EFSA-Statement-WGS-microorganisms.pdf

  A.
- including all associated Annex documents.

We will refer to particular sections of the above in the relevant sections of the following text, and also cite additional EFSA publications as appropriate.
We also recognize that regulatory details and guidance could potentially change during the course of the contract; causes of this may include technological advances such as the recognition of newer platforms as suitable standards for GMO characterisation, and we address some of this potential in this specification, regarding whole genome sequencing in particular.

Minimal information and analysis results that we expect to be provided (regarding biological sequences/bioinformatics)

Reg. 503/2013 specifies minimum requirements across the broad range of data and evidence that must be provided in an Application, including for DNA sequence data and analyses thereof (including arising matters such as translated protein sequence analysis). Within each domain of data it also specifies additional requirements which may be conditional upon the circumstances of the particular GMO.

Reg. 503/2013 provides the most specific definitions of biological sequence data and bioinformatics analyses required, in particular in subsections of section II of Annex II (Scientific requirements for the risk assessment of genetically modified food and feed), where we note especially the subsections on Molecular Characterisation. These include the formal specifications of which molecular sequence data and associated information must be provided and which DNA sequence data must be subjected to particular analyses (section II, 1.2); as well as pertinent sequence analysis directives regarding toxicology (II, 1.4) and allergenicity (II, 1.5).
We expand on those aspects below, but also note other information which is of direct relevance, listed in Reg. 503/2013 Annex I and described in more detail in Annex II, in the EU sequence submission guideline, in the EFSA Technical Note, and elsewhere.

Basic/general data
This includes some information which is straightforward but essential, such as precise identification of the recipient organism (to cultivar/breeding line/strain level; Reg. 503/2013 Annex II / II, 1.1.2), as in effect this specifies any reference genome sequence (and provides the context of sequences of closely-related cultivars which may be encountered in similarity searches, for example). The donor organism, if any, must also be identified in the same way.

The transformation procedure, including vectors used
Relating to Annex II / II , 1.2.1.1 - 1.2.1.2, the Applicants will describe the vector used in the transformation, including a description of all elements therein and their locations; and all other relevant information about the transformation methodology.

The source of DNA used for the transformation, included intended insertion sequences
Also mandatory is the complete sequence of the DNA which was intended to be inserted, along with a description of any relevant sequence similarities, such as relate to sequences of potential concern. (Annex II / II , 1.2.1.3).

The inserted (or deleted) DNA, and the adjacent food-organism genomic DNA (and analyses thereof)
We refer to the inserted DNA (associated with one insertion event) and the flanking 5' and 3' genomic sequences (of whatever length has been characterised in the Application,) collectively as the "integration site sequence" (in other contexts this is referred by different terms, e.g. "final sequence" in the EFSA Technical Note). Alternatively, some GMO events may intentionally be deletions of the food-organism DNA, rather than an insertion of foreign DNA, and for these the term "deletion site sequence" can be used interchangeably - this will also include food-organism genomic sequence flanking the site which will have been subject to analysis.

Expected accompanying details of the integration site sequence are as follows:

Expected numbers of integration sites or deletion sites
We expect there to be one integration site (or deletion) sequence per transformation event (we expect that this will usually be one) per specimen genome. There will usually be more than one specimen genome investigated. Overall, an Application will need to demonstrate genetic stability of the insert, which will often be in the context of a specimen from each of the first and last generation of a sequence of five generations (Reg. 503/2013 Annex II / II, 1.2.2.4). Potentially, some Application dossiers of a supplementary / resubmission nature may include data from only one specimen.
We expect the number and size of all inserts to be provided, irrespective of the methodology used to ascertain it, as per Annex II / II 1.2.2.2.

Flanking genomic sequences
There are no minimum length criteria for the flanking sequences, but the Applicants can be expected to have characterised sufficient sequence length for the genomic origin to be identified (rearrangements compared to the pre-transformed recipient genome are not uncommon, and this can have a bearing on the length of flanking sequence characterised).

Annotations
Detailed annotations of the integration site sequences, including both the inserted and flanking DNA, are an essential component of the Application (Annex II / II 1.2.2.2). This will include coordinates of all components of the integration sites, and how they relate to both the intended DNA to be inserted and the host-organism genome. All identified deletions at the site (in both insertion-based and deletion-based GMOs) should be identified. All open reading frame (ORF) sequences should be specified, using the broadest definition as per the Annex (i.e. all reading frames between two stop codons, irrespective of any start codons).

The full length of the integration site sequence should be accounted for. Various rearrangments and deletions, sometimes involving integration of other parts of the food-organism genome, have not been uncommon in GMOs, of both a research and commercial nature (Wilson et al 2006).

The annotations would therefore be expected to describe any modification of the originally intended gene sequence. This might include additional copies, perhaps partial in nature, perhaps in a tandem arrangement or separated by segments of the recipient genome.

The presence and nature of any gene(s) or other sequence not intended to have been inserted must also be described, irrespective of its origin. For example, additional segments of DNA between the identifiable genomic flanking region and the insert, must be annotated even if not identifiable (such "filler" DNA can span only a few base pairs in some cases, and in essence be unidentifiable).

Any other components of the transgenic or other constructs or plasmids involved in the transformation procedures, which have been inserted, should be annotated.

Such annotations also apply to the flanking regions of the host organism's genome, including specification of any identified rearrangements or deletions of the host genome in these regions. These might include translocations of other components of the genome.

Sequence comparison
Beyond those annotations, components of the integration site will have been analysed regarding similarity of the nucleotide sequence or polypeptide translation to potential sequences of concern including toxin and allergenic proteins - described in the next subsection. Other comparative sequence analyses will have been performed conditional upon the type of inserted gene. For example, miRNA and siRNA genes will require sequence search results to highlight or rule out the presence of any non-intended target sequences in the food-organism genome.
A sequence comparison analysis which will need to have been undertaken in the general case is for the purpose of qualitatively identifying risks of horizontal gene transfer (HGT), as specified in Reg. 503/2013 Annex II / II, 1.2.2.5; details of expected methodology are contained in EFSA HGT Explanatory Note, section 3.2.

The intended and potential polypeptide sequences encoded by the inserted DNA (and analyses thereof)
In many cases, the intended inserted DNA will include a protein-coding gene, whose gene product effects the trait. The Application will include the sequence of this protein and results of analyses as specified in Reg. 503/2013 Annex II / II, 1.4.1(b). These analyses consist of sequence similarity searches to determine whether the gene product is homologous to any proteins (from any organism) with a known function of relevance. These functions include directly detrimental (toxins)

but also those with metabolic and structural functions in the donor organism, since there may be implications of such proteins entering the food chain. These constitute a potential toxicity risk in that sense.

Reg. 503/2013 Annex II / II, 1.5.1(a) provides some detail on the sequence similarity searches which should be performed for identification of similarity to known allergenic proteins. This requires an analysis beyond solely a sequence similarity search using standard tools. The results of additional comparisons described in the same Annex section, regarding short oligopeptide sequences, may also have been provided.

As set out in Annex II / II 1.2.2.2 (f), molecular characterisation of the inserted DNA includes a careful consideration of all ORFs, notably with no minimum length limit. Potentially, an ORFs may extend into the genomic flanking sequence (either out-of-frame with respect to the inserted gene coding sequence and stop codon, or if the stop codon of the intended DNA was not inserted). A generally similar treatment as for the intended protein sequence should have been applied by the Applicants to these ORFs, notwithstanding that some may be too short to fulfil some of the criteria (e.g. those involving 80 amino acid sliding windows; Annex II / II, 1.5.1(a)).

We also note the requirement for sequence comparisons, for each integration site sequence, to be carried out with all sequences that have been determined, in any previously-submitted applications, which have been submitted for the same event's sequence (this EFSA/EURL GMFF requirement came into effect in 2016).

Raw DNA sequence data supporting the integration site sequences (and analyses thereof)

The DNA sequences described in the previous sections will be the result of one of several sequencing platforms, and the underlying raw data will be expected to have been provided as part of the Application.

The EFSA Technical Note on the quality of DNA sequencing for the molecular characterisation of genetically modified plants (referred to here as "the EFSA Technical Note") provides a clear specification of sequence data requirements. It is not prescriptive of sequencing technology or strategy, which is "at the discretion of the applicant" (Submission Guideline, Section 3). Minimal requirements in the Application dossier are a description of the sequencing technology used, the sequencing method (e.g. targeted sequencing, amplicon sequencing, primer-walking sequencing, whole genome sequencing). Details of the experimental design must be stated (Technical Note, Section 4; and EU sequence Submission Guideline, Section 3.1).

We refer to those referenced documents/Sections, but note here the minimal requirements for provision of the integration site sequence if PCR is used (a minimum of two PCR products per event site per specimen must be sequenced; our expectation is that the resulting sequences would be stated, and should be identical so that these would still constitute a single integration site sequence per event site per specimen ("per specimen" typically refers to the multi-generation aspect of the required evidence).

We also note the requirements for Sanger sequencing, which is that the integration site sequence must be sequenced on both the forward and reverse strands (given the above minimum of 2 PCR products, this will result in a minimum of 4 Sanger sequences).

For Next-Generation Sequencing (NGS), the Technical Note, Section 4.2.3 requires that numbers of reads is stated, and sequencing depth is reported and justified in terms of the sequencing technology used. Further, it must be a minimum of 40. This refers to average read depth, as specified by the formula in the same Tehchnical Note Section.

DNA sequence quality metrics
Base-calling procedures must be specified in detail, for any sequencing technology used.

For integration site sequences determined by NGS, the unassembled NGS reads must be provided. The EFSA Technical Note, Section 4, includes NGS reads which have already been quality-filtered and trimmed under the definition of "raw". All methodology for performing all QC must also be described in detail.

Standard sequence formats must be used for both Sanger- and NGS- sequences, as described in the EFSA Technical Note (FASTQ, with ABI also permitted for Sanger). Standard alignment file formats are also specified, including CLUSTAL, FASTA for Sanger and SAM/BAM, CRAM for NGS assemblies.

Different purposes of the DNA sequence data
In many cases, the procedure would have been targeted sequencing or amplification of the integration site(s), followed by sequencing using Sanger sequencing or a next-generation sequencing (NGS) approach.

Alternatively, the sequencing of the integration sites might have been achieved directly by NGS sequencing, involving a computational junction-site analysis of the read data (rather than a *de novo* genome assembly, which is generally a very complex process for eukaryote organisms, especially for higher plant genomes where it can be a huge undertaking). Briefly, this kind of approach involves discarding DNA sequence reads which match only the reference (non-GMO recipient) genome. Analysis of the junctions between the genome and the inserted DNA may be an end in itself (which should identify the number of integration sites). However, this approach also in principle enables assembly of the reads which wholly or partially match the expected transgenic DNA (or at least, fail to match the host genome), thus resulting in sequences of the insert(s) along with an amount of flanking genomic sequence in each case.

Transcriptomic sequence data (and analyses thereof)
We note here that Reg. 503/2013 Annex II / II, 1.2.2.3 states as mandatory that Applications shall include data on whether the inserted/modified sequence results in intended changes at the protein, RNA and/or metabolite level. While some sort of expression assays can therefore be expected as part of an Application, we do not anticipate transcriptomics sequence data / analyses to be submitted in every case. We expand elsewhereon the extent to which we would expect to review and report on transcriptomics data.

Additional data provided conditionally

Sequence data providing evidence for expression of inserted DNA (and wider expression data)
To evaluate expression of the intended gene(s) (Annex II / II, 1.2.2.3), protein expression might be assayed directly, and/or at the transcript level.

Thus, RNA-seq (transcriptomic) data might be provided in an Application. As also alluded to in that Annex section, where tissue-specific transgene expression is intended/expected due to the promoter sequences used, expression data from more than one tissue of the host organism will be expected.

For GMOs containing stacked events (i.e. multiple single-transformation events, arrived at by subsequent transformation or by crossing transformed lines), expression data will be provided from multiple lines according to Reg. 503/2013 Annex II / II, 1.2.2.3, to demonstrate "any differences" between the stacked GMO and corresponding single-event GMOs, or lack thereof; the assumed context is that differences between the two (or more) inserted genes are of the most concern here. Irrespective, stacked-event GMOs may well therefore be accompanied by the results of complex differential expression analyses.

In the context of miRNA or siRNA genes where an RNAi process is the basis of the new trait, this section of Annex II also refers to analysis to identify alternative target genes; we consider this as part of the genomic (insert/transgene) analysis.

Reference genome data
The provision of reference genome data also relates to some of the previous sections, in those cases where the expected analyses require this data.

Provision of a complete genome sequence of the recipient organism is not states as a requirement (Reg. 503/2013 Annex II / II, 1.1) and indeed, the determination of such a reference genome can be a huge undertaking even for large research consortia, for various crops and other plants.

Nonetheless, some kind of reference genome sequence (not necessarily of the same cultivar) may be available, and where this has been used in the analyses described in the Application, it must be precisely referenced, or potentially the sequence data provided. The same applies to any reference genomes which are currently available only in part.

Other reference sequence data
In their various analyses, the Applicants will have made use of a number of reference sequence databases. Some of these will be large and very general (e.g. NCBI Nucleotide collection), whereas others will be smaller and dedicated to particular types of data (e.g. vector sequences, toxin proteins, allergenic proteins, other function-orientated databases, particular bacterial genomes).

Any reference data which has been used by any of the analyses in the Application is also expected to be either referenced (e.g. publicly-accessible databases or records therein) or if not publicly-accessible, supplied.

Description of Applicants' methodology relating to sequence data analysis

The corresponding bioinformatics analyses (Technical Note, Section 4.2.4; EU sequence submission guideline 4), and choices of software, are at the discretion of the Applicant.

In all cases the bioinformatics software and reference data used must be clearly specified including version numbers of any 3rd-party software tools, database accessions of any referenced sequences, and the dates on which any online searches of databases were performed will also be expected.

These descriptions should be at a degree of detail such that the analyses would be repeatable.

As part of this expectation, either exact command lines used to run the software should be included as part of the documentation, or else all parameters used specified precisely.

Many of the standard, leading tools for performing the kinds of expected analysis are freely available without restriction, and the Fera bioinformaticians have a sound knowledge of their capabilities.

Proprietary software

Potentially, the Applicants' analyses may have been performed using proprietary tools. We note here that we will be in a position to comment on the suitability of the underlying methodologies as long as adequate documentation is directly available to us. At Fera, we do use commercial molecular biology/bioinformatics software for some purposes, so potentially we would have direct access to the necessary sources of information. We would in any case expect methodology used via any software platform to be thoroughly described by the Applicant.

Unpublished/in-house software
We note that the EFSA Technical Note on quality of DNA sequencing, Section 4.2.4 "Description of bioinformatic analysis" states:

"The applicant can choose any appropriate bioinformatics pipeline for the various analyses of NGS data sets; however, the methodology and tools used should be thoroughly described by the applicant. In particular for unpublished or in-house tools, a full description along with the scripts, source code and pipelines, inputs and outputs of each of the steps in the analysis, and other parameters used should be provided."

2. Our Report for a dossier

2a. Our review of data, methodology and results

The purposes of this section of the proposal are:

1) to indicate which aspects of an Application's presented sequence data, bioinformatics methodology and results thereof we will be commenting on in the provided Report, since a dossier may include many other sections which are not relevant to this;
2) to provide more details about how we will assess the data/methodology/results in those areas where the details are not specified in EU/EFSA regulations/guidelines.

Details of how the results of the review described below will be set out can be found in section ***2c. a proforma Report***.

When reviewing the data and methodology described in the Application dossier, a general principal is that this is defined by what is described in section ***1. Expected format and content.***

That in turn refers to specific requirements and guidelines in the EU/EFSA specifications, which in some cases are very detailed regarding bioinformatics parameters. In other aspects, these details are more open in those publications.

Here we thus address assessment of:

- Presence of dossier components and associated data files.

Regarding the content of the data:

- Sequencing data
- Sequence assembly methodology

and also considerations of various aspects of sequence comparison:
- General considerations for pairwise sequence comparison
- Sequence similarity searching
- Window-based approaches
- Analysis of protein and translated ORF sequences
- Assessing homology

and these types of NGS-bases analyses for specific goals:
- Junction read analysis
- Transcriptomics analysis.

Presence of dossier components and associated data files

The Fera Bioinformaticians will review the dossier in order to assess the components relevant to sequence analysis / bioinformatics. Assuming that the dossier adheres to the structure specified by Reg. 503/2013 Annex I / VII, then these components should be readily identifiable. The Fera Report will state which sections of the dossier the rest of the Report contents refer to. Normally, these will include subsections under the Molecular Characterisation and also Toxicology and Allergenicity sections, but this will be assessed in each Application dossier.

The Fera Bioinformaticians will check the data files provided, which should be in accordance with Annex 02 of the EU Sequences Submission Guideline ("Instructions to organise the sequencing information and data submitted in accordance to

the Guideline..."). There should be one "GM event" data folder for each insertion event in the GMO. The number of insert sequences will be stated in section 3.1 of Annex 01 ("Reporting Form") of the same the Guideline document.

The Annex 02 is very brief and relatively non-prescriptive, so considerable variability can be expected from one Application to another. We would recommend that Applicants should provide checksum files, created using a standard digest tool of their choice, such as MD5, SHA-1, SHA-256, etc. This will enable the completion of the download of all files to be verified.

Sense checks on the contents of the relevant data files will also be performed. This will ensure that these contain the expected content type and that other problems such as truncation of compressed files have not occured (such issues might occur at the Applicant end prior to checksum generation and submission).

Sequencing data

We will assess the Applicants' sequence data and their described approaches to its processing including quality-control and sequence assembly, with reference to the details in the previous section (***1. Expected format and content***) of this tender document, which in turn makes reference to both of:

- *The EFSA Technical Note on the quality of DNA sequencing for the molecular characterisation of genetically modified plants* (referred to here as "the EFSA Technical Note")
- the *Guideline for the submission of DNA sequences derived from genetically modified organisms and associated annotations within the framework of Directive 2001/18/EC and Regulation (EC) No 1829/2003* ("EU Sequence Submission Guideline").

Within the Fera team described in this proposal, we have very extensive experience in the analysis of sequence data from a number of platforms, including Sanger, Illumina and Oxford Nanopore Technologies. We have an in-depth understanding of the considerations involved in processing such data from its raw state onwards, for various purposes. These include genotyping, genome sequence assembly and analysis, transcriptomics and others.

Also while clear specifications are provided by the EFSA Technical Note and EU sequence submission guideline regarding some basic aspects of sequencing and assembly (such as depth coverage), others are left more open, for example threshold standards applied to basecall quality-score filtering, and some sequence data-processing methods which are necessarily platform-dependent. (Reporting of the quality-score statistics themselves is mandatory; Technical Note, Section 4.2.1). These are at the discretion of the Applicant. We will thus provide our opinion on any of these aspects as they arise.

Sequence assembly methodology

The *EFSA Technical Note on the quality of DNA sequencing for the molecular characterisation of genetically modified plants* is not prescriptive about the sequencing technology used or the methods to process the sequence data, which are at the discretion of the Applicant. (Technical Note, Section 4; Submission Guideline, Sections 3 and 4).

Within the Fera team we have extensive experience of assembly of sequence data from Sanger, Illumina and Nanopore platforms, including techniques such as hybrid assembly of Illumina and Nanopore reads. This includes sequencing of prokaryote and eukaryote organisms. We therefore have a sound hands-on knowledge of the relevant software tools, and how to evaluate assemblies and assembly methodology.

General considerations for pairwise sequence comparison

The most commonly used metric of the similarity of two nucleic acid or protein sequences is sequence identity (invariably expressed as a percentage). Since exact levels of sequence identity form some of the requirements of legislation (e.g. Reg. 503/2013 Annex II / II, 1.5.1(a)) and associated guidelines, it is appropriate to briefly discuss this metric in relation to the details which are required in the Application.

Percentage sequence identity (PID) is often quoted as if it is an immutable metric defining the difference/similarity of a pair of sequences, but this is not the case (other than in trivial cases where the sequences are completely identical, or where one is identical to a continuous segment of another).

PID is the percentage of positions in a pairwise sequence alignment at which the two sequences have an identical nucleotide (or amino acid). The exact nature of the alignment depends on how the alignment was created, which in turn depends on the parameters used in the alignment algorithm.

Normally, these parameters include substitution scores (from a matrix specifying how similar/different each pair of amino acids, or pair of nucleotides, is) and affine gap penalties (the penalty scores for introducing and extending gaps). The values of these parameters affect the details of the alignment, and thus the precise PID which results. For example, the use of very high gap penalties (which are appropriate for some kinds of analysis) can therefore result in fewer identical amino acids being aligned, with a resulting decrease in PID compared to the alignments resulting from other parameters.

<u>The significance of alignment parameters</u>
This is not merely an academic consideration, because even very small differences in PID (e.g. the difference between 34% and 35%) could make the difference between a transgenic protein being ruled as a clear negative, and a potential positive triggering further investigation, e.g. in comparison to the sequence of a known allergenic protein; Annex II / II, 1.5.1(a).

The difference between 95% and 94% is the difference between a 200 bp nucleotide sequence requiring mandatory reporting as a potential risk for HGT by homologous recombination, or not (EFSA Explanatory note on DNA sequence similarity searches in the context of the assessment of horizontal gene transfer from plants to microorganisms, section 3.2.4).

Therefore, all alignment parameters should ideally be stated by the Applicant, even if that is "default parameters" for a particular piece of software. We note that this is explicitly required by some guidelines (e.g. EFSA HGT Explanatory Note section 3.2.2 on Algorithms and parameters) but is not stated as a requirement in the other EU/EFSA documents. If these parameter statements are absent or are particularly unusual, then this will be flagged in our report.

Sequence similarity searching
The principal factor of concern is the sequence database, against which the query sequence is searched. We address this in the section on Reference Databases.

The similarity scoring matrix and gap penalty considerations (previous section) also apply to sequence similarity searching, where the search algorithm involves pairwise alignment of hits at some stage.

Commonly used heuristic search methods for large reference databases
The most commonly used sequence similarity search tool is BLAST (Camacho et al., 2009). This is a software package containing a number of programs for different purposes including nucleotide sequence searches and protein sequence searches (BlastN, BlastP, etc). This will be suitable for the Applicants' analyses which require a very large number of reference sequences to be searched, and is among the tools recommended by EFSA guidelines (e.g. EFSA Explanatory note on HGT, section 3.2.2).

Regarding the similarity scoring matrix and gap penalty considerations: the same requirements for stating parameters used apply (even if they are default, e.g. "default NCBI www BlastN search parameters"). Combinations of these parameter values are somewhat restricted in BLAST for reasons of statistical integrity, but can be varied to good purpose, e.g. changing the matrix to try to detect remote homologues. Default parameters will be suitable for most of the tasks which an Applicant will have completed, which in many (not all) cases involve the detection of highly similar sequences to a query.

Use of BLAST and other similarity search tools involves additional parameters and settings. Depending on the query sequences involved, it may be appropriate to perform multiple searches with differences in some other BLAST parameters. For example, low-complexity regions of query sequences can result in large numbers of non-homologous hits, whereas using settings to mask out such regions can aid in the identification of putative homologues, which can then be examined in their un-masked form in more detail. Other related aspects such as use of composition-based scoring are of less concern (default parameters, i.e. composition-based on by default, are usually the most suitable).

Care with short query sequences
Extra considerations can arise when using short sequences as queries with commonly used sequence similarity search tools such as BLAST.

For example, Reg. 503/2013 Annex II / II, 1.2.2.3 (e) requires where the inserted DNA has a silencing function by RNAi expression, potential 'off target' genes should be searched by in silico analysis. When searching for putative targets of genes which perform their function by RNAi (miRNA, siRNA genes), the relevant sequence motifs can be < 25 bp long, which can be problematic. Given that it is insufficient to search for exact sequence matches as potential miRNA/siRNA targets, database hits with mismatches and also small insertions must not be missed. For example, the BLAST algorithm for nucleotide searches by default uses a 'word' size that would generally be unsuitable for looking for (for example) matches to a 21 bp siRNA query motif (locations of exact words are indexed and then looked up as the starting point for the subsequent steps). Any potential targets which differ from such a motif by a single mismatch in the middle, would be missed. Instead, dedicated tools should be used (Sablok et al., 2019) .

BLAST searches using very short protein sequences can also be problematic.

Window-based approaches

Some of the requirements and guidelines in the EU/EFSA publications specify, for some searches, that all windows of a particular size must be analysed (e.g. for similarity of insert-gene protein sequences to allergenic proteins: "The calculation of PID shall be performed on a window of 80 amino acids with gaps so that inserted gaps are treated as mismatches."; Reg. 503/2013 Annex II / II, 1.5.1 (a)).

Using that as an example, simply analysing BLAST hit alignments (MSPs) of ≥ 80 amino acids length is insufficient, and may result in false negatives. To give an extreme example, two proteins of length ≥ 80 could be 100% identical over a span of 79 amino acids, but a BLAST search (or pairwise local alignment) may well return an alignment of length 79 (depending on the nature of the adjacent non-identical amino acids). A pairwise global alignment would often solve this, but would still require all windows of length 80 to be assessed, and an optimal global alignment does not guarantee that each length-80 segment of the query sequence is optimally aligned.

A solution is to identify any segment pair, of any length, where at least 28 positions are identical (this does require performing an alignment first, which could include performing a BlastP search with liberal search criteria). A matching

segment pair of any length ≥ 28 which contains identical amino acids at 28 positions is guaranteed to fulfil the 35% identity criteria over 80 amino acids, even if none of the other 52 positions match - as long as both protein sequences extend enough to achieve a length-80 segment.

Similar window-size considerations also apply for identification of possible homologous recombination sites, as specified in Section 3.2.4 of the EFSA GMO Panel Explanatory note on DNA sequence similarity searches, in the context of the assessment of horizontal gene transfer from plants to microorganisms.

Analysis of protein and translated ORF sequences

Determination of ORF sequences and their predicted polypeptides is trivial, but the required definition (between stop codons; not start-to-stop codons) must be observed.

Translated ORFs must then be used as queries for a number of searches. We note that Reg. 503/2013 Annex II / II 1.2.2.2 (f) states that there is no length limit for ORFs which require analysis, and that "bioinformatic analyses shall be conducted to investigate possible similarities with known toxins or allergens"; while also noting that Annex II / II 1.5.1 (a) states, "for assessing short peptidic fragments such as ORFs, a search for sequences of contiguous identical or chemically similar amino acid residue can be conducted. However, this search shall not be carried out routinely for the identification of potential linear IgE binding epitopes because of its poor sensitivity or specificity". Our interpretation is that it is appropriate to use short ORF translations in this way (but it is not necessary to analyse segments of the intended full-length protein sequence). Further, we note that previously, identical segments of 8 consecutive amino acids were used as a criterion for allergen comparisons (e.g.((EFSA), 2009)).

Assessing homology

Homology is explicitly stated in the requirements documents (e.g. Reg. 503/2013 Annex II / II 1.4.1 (b); "search for homology to proteins known to cause adverse effects, such as toxic proteins. [and others] ".

There are no absolute, definitive criteria for determining from sequence similarity whether two sequences' similarity is due to sharing a common ancestor (i.e. are homologues) or due to random chance (not homologues), and sequence identity can serve as a guide but is of limited use for very short sequences. Some degrees of sequence similarity are beyond question regarding homology, and some of the less clear cases can be soundly assessed to those with sufficient experience. Sequence similarity search tools (e.g. BLAST) provide useful statistics (E-values), but E-value cutoffs are themselves somewhat arbitrary, and also depend on the size of the database being searched. For potentially short sequences especially, it is difficult to be prescriptive.

Where it is possible to determine with statistical certainty that two genes or proteins are homologous, or likely to be, it is important to note the limitations of the conclusions that may be drawn from that. "Homology" means "common descent"; two homologous proteins do not necessarily have the same function; the only sound conclusion that can ever be drawn on the basis of homology alone is that two proteins have the same overall structure ("fold"), which can also differ in some of the structural details. Protein superfamilies exist consisting of numerous functional families which are all homologues (thus have the same fold) but which do not share functions between these homologous families. Many proteins are modular (multi-domain) and homology can occur over only one domain whereas a protein's toxigenic function (for example) may result from other domains. Homology (common descent) can sometimes be demonstrated for relatively short segments (smaller than normal "domains").

Therefore an inference of homology serves as no more than an indicator of further investigation that may be required, and it is possible that Application dossiers may include such analyses (e.g. to rule out consequences of concern that had arisen from a positive homology result), including *in silico* analyses. We have the expertise in the team to provide opinion on such analyses, but these are difficult to anticipate and require a case-by-case approach.

Junction read analysis

Regarding the integration site sequences, we note that "The final [integration site] sequence can be generated with a strategy and sequencing technology at the discretion of the applicant" (Section 3 of the EU sequence submission guideline). Often this will have been done by targetee sequencing, or by amplifying the sequence with PCR, which is then sequenced, potentially by an NGS platform.

Potentially, the Applicants may have performed a broader DNA sequencing exercise, for one or both of the following aims:

1. to determine the number of insertion events, or confirm the results of other assays performed for that purpose;
2. to determine the sequence of the integration site (insert + flanking regions) itself.

In either case, an approach involves whole genome shotgun sequencing. Such an approach is suggested by the Sections 1 and 5.2 of the EFSA Technical Note on the quality of DNA sequencing for the molecular characterisation of genetically modified plants (Panel)", 2018). A number of proofs of principle have been published, both with model plants and commercial crops (Kovalic et al., 2012, Schouten et al., 2017, Yang et al., 2013) . This method invariably involves a reference sequence of some kind, since *de novo* assembly of eukaryote organisms does, in general, require considerable time, effort and expertise, and a number of crop plants are among the largest and more complex organisms in terms of genomes. Thus, the sequence read data is "mapped" to the reference sequence, which is by far a more tractable problem.

This reference could be a recipient-organism genome sequence, as is the case in most of the published studies, or possibly just the expected insert-DNA.

In the context of a GMO regulatory Application, the expected transgenic DNA sequence will be known, which aids in the identification of pairs of sequence reads (normally, paired-end (PE) short reads would be used) which map to both reference genome and transgenic sequence. In practice, the approach of discarding read pairs which wholly map to the reference genome can also be adopted in order to identify **any** sizeable insertions relative to the reference, whether anticipated or not. (This potentially identifies any contaminant sequences.) There may be additional sequence segments originating from the host genome itself, which exhibit various splintering, rearrangement and deletion patterns, possibly scrambled with pieces of the transgene, resulting in segment sequences which confound the short read-mapping process. Further, additional sequences not found in the reference genome can simply be the result of the base cultivar for the GMO development being different to the sequenced cultivar. Clarity in the Application is therefore essential, concerning the cultivars/strains in question.

The analysis of such sequence data requires considerable care and expertise. For example (Yang et al., 2013) successfully identified inserts in two previously-characterised transgenic lines of rice, in an analysis including a reference genome. However, various false positives occurred which required analysis in order to identify them as artefacts. For example, one of the lines was a 2-event GMO, and inserts were correctly identified on the two chromosomes expected. However, other reads were mapped to no fewer than 10 other chromosomes, ultimately rejected by the researchers as false positives.

The potential does exist for "genome-blind" identification (without genome assembly) of the immediate flanking regions of an inserted DNA construct using whole genome shotgun (WGS) data, assuming the sequence of the insert is known. In principle this could identify whether multiple insertion events have occurred. This methodology would require paired-end (PE) reads (normal for WGS in any case) and involves the assembly of all those read pairs where one or both reads mapped wholly or partially to the insert-DNA sequence. Depending on the PE insert length, the sequence of flanking regions of several hundred bp can be determined.

Transcriptomics analysis

ANNEX II, Part II, Section 1.2.2.3 of Regulation (EU) No 503/2013 (https://eur-lex.europa.eu/eli/reg_impl/2013/503) is not especially prescriptive of the approaches that should be taken by the Applicants to assess expression of the insert(s), but this can be at the RNA level. It is anticipated that if transcriptomics data/analysis has been submitted, this will be focussed on the insert(s) transcripts, rather than on an assessment of general effects on the transcriptome in a large-scale differential expression analysis. General RNA-seq analysis is a complex, multi-stage procedure, involving characterisation of transcripts by assembly or reference-mapping techniques, consequent estimation of transcript frequencies, and then statistical assessment of differences between transcripts within samples and/or the more complex between-sample context.

We will be in a position to provide opinion on the general soundness of large-scale studies using RNA-seq, beyond simply methodology for evaluating the insert-gene transcripts. Normally, however, we would not be expecting to fully evaluate a whole-organism differential-expression (transcriptome-wide) study (e.g. comparing recipient non-GMO cultivar with GMO for all and any transcriptomic effects). This is therefore not stated as a deliverable. The potential exists if, agreed on a case-by-case basis, the FSA wished to direct the Team's time to this area. Within the team, we have experience of conducting full peer review of RNA-seq methodology. We also perform transcriptomics (RNA-seq) analysis at Fera for other projects (usually using Trinity (Grabherr et al., 2011) for the assembly/quantification).

2b. Independent analyses to be conducted at Fera

The analyses conducted at Fera are in two categories:

1) those which, in agreement with the FSA at the outset, we undertake to perform for each Application dossier, unless:
    a) the dossier-processing has been halted or concluded as a result of the supplied data causing a technical barrier to its being processed, e.g.
        i) the data files are not available, not clearly identified by the documentation, not readable, do not contain the stated data, or other technical reasons (in short, failure of the assessments described in **Presence of dossier components and associated data files**)
    b) the dossier-processing has been halted or concluded as a result of our identifying a potential concern from the regulatory point of view (any of the stated requirements are not met, whether this is inadequate annotation, file formats not meeting the requirements, lack of sufficient number of sequence reads/depth, the intended gene product being found to be similar to a protein of concern, etc)
    c) the dossier-processing has been halted or concluded as a result of any other directive from the FSA
2) strictly beyond-scope analyses: those which are not part of the deliverables for the project, but which we might perform on a case-by-case basis, if we deem them relevant and useful to performing the processing of a given dossier.

This section is also concluded by a description of the reference databases that we would be using.

A general aspect of our analyses is that they are informed by the technical principles described in section 2a above.

In the text below, "integration site sequence" should be read as "deletion site sequence" for those GMO events which involve deletion of a food-organism gene or other genomic element, instead of insertion of foreing DNA. In both cases, this includes some 5' and 3' flanking sequence from the food-organism genome.

1) We can undertake to perform and report on the following analyses for each Application dossier, unless not required as directed by the FSA.

Which of the analyses described below should be regarded as "routine" (i.e. applied to all dossiers unless otherwise directed for a particular dossier), and which are regarded by the FSA as not (normally) necessary, would be agreed at the outset of the contract.

Validation of Applicants' annotations of the integration site sequence using public sequence data

We will examine the Applicants' annotations (as per Reg. 503/2013 Annex II / II 1.2.2) and attempt to validate their annotations of each part of the integration site sequence, where possible. This will involve using the whole sequence as a Blast query, and also sequence segments defined by the annotation (e.g. the beginning and ending coordinates of the inserted gene, each other element, and the flanking regions) will be used as queries.

In practice, this will be largely automated, as it will involve automatically obtaining the coordinates of each feature and taking action using a pipeline, since the final sequence submitted in the Application will have all genetic elements annotated according to the INSDC Feature Table Definition Document (Guideline for the submission of DNA sequences, Section 5). This will also determine the appropriate search type to make for each sequence segment. For example, segments annotated as the CaMV 35S or other promoters will be searched against the UniVec database. Segments annotated as flanking genomic sequences will be searched versus the relevant genome sequence (if available). Some manual input may be required; for example, if the inserted gene is of bacterial origin, we would want to direct that search against the bacterial genome sequences (ideally, of the relevant species), which may require us to provide this information as input to the pipeline.

All elements will also be searched against the general nucleotide and protein sequence databases. These Blast searches can use stringent search parameters, since the goal is to identify the exact sequences, where they exist in the public resources.

The results of all automated searches will be inspected by the Fera bioinformaticians, and the outcomes of these searches reported.

Not all elements will necessarily exist in public resources, and we will in any case be referring to the Applicants' supplied information on the source of vector, source of inserted DNA (with reference to Reg. 503/2013 Annex II / II 1.2.2). Some sequences may be proprietary information, for example. These sequences are likely to be small in number, and would usually be automatically compared using pairwise alignment software.

Where unaccounted-for segments remain, we will not undertake exhaustive attempts to identify the origin of all nucleotides. We will make reasonable attempts to do so, depending on the number and lengths of such segments. With decreasing segment lengths below around 30 bp, false negatives using tools such as Blast become more likely for statistical reasons. Nonetheless, with single unknown segments, checks using standard methods against the reference genome are reasonable and may reveal the origin. For example, in the well-known MON810 transgenic maize, it was determined that a 45 bp segment formed partly from the end of a novel ORF (where the original stop codon was omitted from the insertion) and continuing through a new stop codon, was completely identical to part of the maize mitochondrial genome (Rosati et al., 2008) . We will report if any such searches have been necessary, and the outcomes. Potentially, the first-principles search (below) will achieve such identifications in any case.

The deliverable is as stated in Section 9 of the proforma report (see ***2c. a proforma Report***).

First-principles annotation of integration site sequence using public data

To support the validation and to flag up any unexpected matches to sequence data, we will also take a slightly different approach using a similar pipeline, where the initial segmentation of the full-length integration site sequence is determined by BLAST searches. Initially, the query sequence will be searched against UniVec, UniProt and the NCBI nt databases. Potentially this would identify all parts of the sequence, but it is likely (where matches to a particular segment dominate a hit list) that an iterative approach will be necessary, whereby already accounted-for segments are removed and the other segment(s) are then searched in the same way.

This ensures that any obvious matches which require continuity across different elements of the full-length query sequence (which are in contrast *a priori* segmented in the previous validation searches) will not be missed. It may also identify short segments which might be missing from the annotations (as assumed "unidentifiable").

The deliverable is as stated in Section 10 of the proforma report (see ***2c. a proforma Report***).

Determination of all ORF sequences in the entire integration site sequence

All ORFs, using the broadest definition (i.e. all sequences spanning the region between either two stop codons, or a stop codon and either end of the sequence) will be determined in all reading frames. This is trivial, and there are software tools

which perform this, e.g. the getorf program of the EMBOSS package (Rice et al., 2000). This tool will also provide translations as well as the ORF sequences themselves.

The deliverable is as stated in Section 12 of the proforma report (see ***2c. a proforma Report***).

Searches of putative polypeptide sequences

Many of the translated ORF sequences derived in the previous step will be used as queries for a number of searches. Some will be excluded by length; we propose that there is little to be gained from using polypeptides of fewer than 8 amino acids length, but we can be flexible.

We will also use, as a query, the sequence of the translation of the intended gene as stated by the Applicants, since this will not necessarily be the same as any of the above ORF-translations (because not all ORFs will begin with a start codon).

We propose that for any ORFs of between 8 and 15 amino acids length, pattern-match methods allowing no gaps will be used to search the relevant databases (this applies to allergen proteins). Any matches involving at least 8 consecutive identical positions will be reported.

For longer polypeptide sequences, BlastP will be used, notwithstanding that the allergen protein comparison requires special treatment, as described.

Search against toxin protein sequences

As per Reg. 503/2013 Annex II / II 1.4.1 (b), we will use the above as queries versus our proposed database of protein toxin sequences, in order to identify any cases of pattern-matches as described, or homology in the cases of the longer queries.

We refer to the section ***Assessing homology*** above in ***2a. Our review of data, methodology and results*** in which we discuss the identification of homology. We will report the best BlastP matches for each translated ORF query as long as it is better than a poor threshold (e.g. $E=10^{-3}$), for completeness. We will state whether those best matches should be considered as confidently indicating homology.

The deliverable is as stated in Section 13 of the proforma report (see ***2c. a proforma Report***).

Search against allergen protein sequences

We suggest that we would discuss with the FSA at the beginning of the contract regarding the interpretation of the currently stated EU/EFSA requirements regarding the necessity or not of searching for short oligopeptide sequence matches.

If it is agreed that this should be performed routinely, then the pattern-matching described above will serve the very short queries (reporting matches of 8 consecutive amino acids identity, or the otherwise agreed length). For longer queries which are still < 80 amino acids, these will be aligned against the allergen sequences and any instances of 8 (or the agreed number) of consecutive amino acids identity, reported.

For the longer queries, we refer to ***Window-based approaches*** in ***2a. Our review of data, methodology and results,*** for a brief description of methodology.

For completeness, we will report the best hit (as long as they are above the basic threshold) for each translated ORF sequence of ≥ 80 amino acids, irrespective of the outcome of the above.

The deliverable is as stated in Section 14 of the proforma report (see ***2c. a proforma Report***), notwithstanding that it may be agreed beforehand that the treatment of short ORF sequences is not required.

Search against bacterial sequences to identify potential homologous recombination risk sites

The context is that segments of the integration site sequence which are sufficiently long and exhibit sufficiently high sequence identity with segments of microbial genomes, may promote homologous recombination with the microbe and thus a route to horizontal gene transfer.

Details of the bioinformatics analysis required to assess this are contained in the EFSA HGT Explanatory Note, section 3.2. In short, the integration site sequence must be compared to the available genome sequence data of all microbes which might encounter the transgenic DNA as a consequence of it being in the food chain. All segments of at least 200 bp in length exhibiting at least 95% identity (PID) are deemed reportable (EFSA HGT Explanatory Note, section 3.2.4). All such segments can be expected to be found with a BLAST search even with stringent criteria.

We will perform a BlastN search using the entire integration site sequence as the query, against the prokaryote subsection of the in-house installation of the NCBI nt database.

All hit sequences need to be examined, because treating only those hit alignments (MSPs) as positives where the reported length is ≥ 200 bp and the reported sequence identity is ≥ 95%, risks false negatives occurring. For example, an MSP of 300 bp length might have sequence identity of 90%, while containing a 200 bp segment of ≥ 95% identity. While some MPS can be discarded on a mathematical basis of a too-low identity for any of the segments therein to meet the criteria, others will need to be analysed directly to check all the 200 bp windows.

Deliverable: We will report any positives in terms of unambiguous references (sequence database accessions) for the microbial sequences, the sequence coordinates therein relating to the match, and the corresponding coordinates in the query sequence. We will state any functional and taxonomic annotation that is attached to the hit microbial sequence.

The deliverable is as stated in Section 11 of the proforma report (see ***2c. a proforma Report***).

2) Bioinformatics analyses beyond the scope of normal dossier analysis

Regarding the clarification provided by the FSA during the Tender process (response of 7th Dec, 2020) we have noted that the emphasis will not be on re-running all the analyses carried out by the applicant but identifying potential areas for concern and ensuring the searches and analyses have been carried out correctly.

Therefore we would not routinely perform any analyses other than those in section (1) above. Thus, we would not be expecting to repeat assembly of the NGS reads of an integration site sequence, junction read analysis, analysis of transcriptomics reads, etc.

However, we do not rule out that we would perform additional analysis, if it were relevant to the assessment and tractable within the timeframe. For example, if a stated depth coverage associated with a supplied SAM/BAM file appeared implausible given the stated number of reads and length of the assembled sequence, a straightforward analysis of the file would confirm it.

References databases

The following is a description of the reference databases we propose to use for the Fera analyses of the Applicant data. We view the choice of databases as flexible; where the need for new types of analyses arise during the course of the contract, we will adapt the portfolio as necessary.
The reference databases fall into these categories:

- General sequence databases.
- Genome sequence databases.
- Broadly, function-specific databases.

In the above categories, we maintain the following databases in-house at Fera, for use on our servers.

General sequence databases

- The NCBI nucleotide collection ("nt" database).
    - This is a very large primary sequence database including GenBank (merged with its equivalents maintained at the European Bioinformatics Institute and the DNA Database of Japan) as well as the large NCBI RefSeq database, and sequences arising from the protein structures database (PDB). It is non-redundant; identical sequences have been combined into single database entries, with the original provenance records preserved.
- The NCBI non-redundant protein sequence database ("nr").
    - This consists of the translations of all coding sequences of GenBank, as well as the SwissProt database (a reviewed subsection of UniProt) and sequences from several other smaller databases including PDB.

Refer to (Sayers et al., 2020) for more information on these NCBI resources.

- UniProt (UniProt Consortium, 2018)
    - This is the principal primary database for protein sequences. It includes the curated SwissProt component of curator-reviewed protein sequences, as well as a much larger number of protein sequences arising from the automated translation of coding sequences in the primary nucleotide databases.

Potentially, due to their comprehensive nature, these databases could be used to complete a wide range of the analyses of relevance to the GMO Applications, but smaller dedicated databases are preferable for some purposes (see below). We note that the EFSA HGT Explanatory Note section 3.2.3 recommends the NCBI nucleotide database (or European equivalent, ENA).

We update our local copies of these databases several times a year. When necessary, we will interrogate the online versions, if there are issues with e.g. Applicant-annotated segments of an integration site sequence which cannot be found to match a database sequence. NCBI databases can be accessed programmatically.

Genome sequence databases

It is likely that some sequence similarity searches versus organism-specific genomic sequence data will be informative. This is likely to apply to various plant genomes as per the Applications, and bacterial (and potentially other microbes). The Applicants may provide genomic reference data for the food organism in question.

Currently, we have the sequences of more than 20 publicly-available crop-plant genomes installed on our servers at Fera, and will obtain other publicly-available genome sequences when required by the contract.

We currently have a local copy of the NCBI RefSeq genomes database, for bacterial species (> 180,000 genomes) (Li et al., 2020) .

Function-specific databases
Using function in a broad sense here, this includes:

- UniVec

This is a freely accessible NCBI database which includes vector sequences, but also sequences of other elements which are commonly used in cloning, such as adapters, linkers, primers. The current version contains more than 6,000 sequences. We also have the subset version (UniVec_Core) which is designed to minimize false-positive hits (> 3,100 sequences).
http://www.ncbi.nlm.nih.gov/tools/vecscreen/univec/

- COMPARE (the Comprehensive Protein Allergen Resource)

This is a freely accessible database, updated annually. We have the sequence data installed locally. The current version contains > 2,200 protein sequences. These can be regarded as high-quality data since the database records are reviewed by allergy experts.
https://comparedatabase.org/

- Antimicrobial resistance (AMR) gene sequence databases: MEGARes and DeepARG

These are freely available sequence databases of AMR gene (ARG) sequences. MEGARes(Lakin et al., 2017) is manually curated and contains > 7,000 sequences. The DeepARG database contains almost 13,000 sequences, and includes some entries compiled by deep-learning (software of the same name, (Arango-Argoty et al., 2018)). ARGs encode various types of AMR proteins, in terms of antibiotic-degraders/disposers, mutant drug targets, etc. In the GMO sequence analysis context, it should be sufficient to identify a protein sequence as an AMR gene generally, without the need to perform more detailed analysis (for example, determining whether a drug target protein has particular mutations which confer an AMR property on it). We therefore do not anticipate that more sophisticated databases will be required.

Further derivative databases proposed

We do not currently maintain a database of toxic protein sequences ideal for this project, and some previously available databases which would have been promising candidates are now defunct. However, searches against UniProt, especially the reviewed component (SwissProt) should serve this purpose. For example, the curation of SwissProt enables all sequences annotated as toxins to be easily identified, and indeed it is trivial to create a dedicated database for searching. The keyword 0800 meaning "toxin" currently returns almost 7,100 sequences, with a further 85,000 in the unreviewed section of UniProt. In the same way, the 0020 keyword ("allergen") returns 965 SwissProt sequences (a further single instance occurs in the unreviewed section).

2c. A proforma Report

The format of the report that would be delivered for each dossier is shown below.

This is the deliverable for Objective 1.

PROFORMA FERA REPORT OF BIOINFORMATICS EVALUATION OF A GMO APPLICATION DOSSIER

REFERENCE ID OF THIS REPORT:
(generated by Fera; always unique; it will include an iteration identifier; for example, if this report was evaluating a dossier which had been submitted in an earlier version containing a now-corrected error, this would be iteration 2; it will also include the Application Reference No. - see below)
[Numbered sections follow:]

1. IDENTIFICATION OF APPLICATION

Application Reference No. (supplied by FSA)
Name of Application Organisation
(assuming this is supplied by FSA and not anonymised)
Name of product (GMO): e.g. "NPO921 maize"
Number of GM insertion (or deletion) events: e.g. "1"

2. RELEVANT SECTIONS OF DOSSIER IDENTIFIED

(a) **Summary statement.** A brief statement summarising the **bioinformatics-relevant aspects** of the Application Dossier. E.g.:

"This is an Application for authorisation of NPO921 maize, in which there has been 1 insertion event. The dossier includes a molecular sequence characterisation of the various elements of the integration site sequence, which has been sequenced by the Sanger platform in specimens from two generations. The dossier describes comparisons of the sequence with databases of sequences of potential concern, including toxins, allergens, antimicrobial resistance genes, and includes a sequence-based assessment of the potential for HGT by homologous recombination with bacteria. They have used RNA-seq as a means of checking that the inserted gene transcript sequence is as expected in vegetative tissue, and to check that this transcript is absent in pollen samples."

(b) **Bioinformatics-relevant dossier sections.** A list of all sections of the Application text which **are relevant to the bioinformatics report**. We assume that the entire structure of the Application dossier will be as specified by regulations, here assuming that the specification will be identical to "PART VII: SUMMARY OF APPLICATIONS" of ANNEX I relating to Regulation (EU) No 503/2013 (https://eur-lex.europa.eu/eli/reg_impl/2013/503).

Example:

"The sections of the Application Dossier relevant to this bioinformatics evaluation have been identified as follows:
3.1 (Information relating the the genetic modification)
3.2 Information relating to the genetically modified plant, specifically:
3.2.2. Information on the nucleic acid(s) sequences actually inserted or deleted
3.2.3 Information on the expression of the insert
3.2.4 Genetic stability of the insert
3.2.6 (a) Any change to the ability of the genetically modified plant to transfer genetic material to bacteria

5.4.1 Search of homology of translated ORFs to proteins of potential concern (toxins and metabolic proteins)"
6.4.1 Assessment of similarity of translated ORFs to proteins of allergenic concern

(c) **Bioinformatics-relevant data.** A list of all sections of the submitted data files which **are relevant to the bioinformatics report** (sequence files, analysis results files, script files, associated READMEs etc). We assume that this structure will adhere to formal specifications, and would by default assume these would be as in "Annex 02. Instructions to organise the sequencing information and data..." of "Guideline for the submission of DNA sequences derived from genetically modified organisms and associated annotations within the framework of Directive 2001/18/EC and Regulation (EC) No 1829/2003" (EURL GMFF; https://gmo-crl.jrc.ec.europa.eu/doc/Guideline-Sequencing-Feb-2016-mod-April-2017.pdf). This list will make reference to major folders in the folder structure and may list some key filenames as appropriate, but will **not list all data files**.

3. SPECIAL EXEMPTIONS, CONSIDERATIONS OR CIRCUMSTANCES

Summary. This will be a statement (which could be "None apply.") describing any particular aspects of the GMO / Application which can be expected to change the normal considerations of the bioinformatics evaluation. These may point towards particular bioinformatics analyses which may be required, or which may make some normal evaluations unnecessary. E.g.:

"Relatively high sequence identity between the intended gene product and an allergen protein of livestock concern (toxin name) has previously been highlighted. Subsequently, the Applicants performed allergenicity studies which they submitted in Application XY0123."

In the event of there being sequence data for more than one generation, this will also include statements about the stated relationships between them (e.g. that the Dossier states that two integration site sequences have been determined for two different generations of a single-event GMO, and that these sequences are the same).

(a) **List of exemptions including reasons.**

E.g.: "We expect to find the previously-identified sequence identity with (allergen protein name). There will be no need to repeat earlier sliding-window analysis."

E.g.: "This is a stacked event GMO, involving two events. One of the event integration site sequences has previously been characterised in (*document reference*) for a single event GMO. As advised by the FSA, there is no requirement to comment on or reanalyse this event site (*site identifier*)."

4. SUMMARY OF THE REVIEW PROCESS

(a) List of review process steps we have completed. E.g.:

"Presence of relevant dossier sections.
Presence and sense of relevant data files.
Sequence data quality assessment.
Opinion on sequence assembly methodology.
Opinion on methodology of molecular sequence characterisation of integration site.
Opinion on methodology of ORF-translations' similarity to toxin proteins.
(etc)
Validation of molecular sequence characterisation of integration site.
Independent analysis of ORF-translations' similarity to toxin proteins.
(etc)"

(b) Statement of reason for termination of review process.

Example: "Normal completion."

Example: "Sequence data files referred to in Dossier section 3.2.2 are unreadable."

Example: "We identified that there is no description of an analysis of the integration site sequence regarding similarity to allergenic proteins. The FSA have confirmed that there is no reason that this should be absent."

5. PRESENCE AND SENSE OF DOSSIER SECTIONS AND DATA

(a) Dossier sections.

This will be a statement such as "All Dossier sections identified in Section 2(b) of this Report are present." or else a list of absent sections.

(b) Data files.

(i) **Data file presence.** This will be a statement indicating that "All data folders and files identified in Section 2(c) of this Report are present." or else a list of absent data files.

(ii) **Checksum results.** This will be a statement such as "No checksum files were provided"; or "Checksums were provided for all sequence data files and these were all validated"; or "failure of checksum validation for the following file occurred (file name)".

(iii) **Data file sense.** The relevant sequence data files, any database files, documentation files will be checked to ensure that these contain the expected content type. (For example, if a problem such as a truncated compressed file had occurred at the Applicant end prior to checksum generation and submission, this would not be picked up by (ii)).

(iv) **File list reference.** There will also be a statement referencing a list of all of the data files relevant to this report. This will reference part of the Dossier if it provides a suitable list, or else we will reference an APPENDIX to this Report.

6. SEQUENCE DATA QUALITY

This section reports on several measures of quality of the complete sequence of the integrations site(s) (which may result from sequence assembly). We will refer to the requirements stated in *The EFSA Technical Note on the quality of DNA sequencing for the molecular characterisation of genetically modified plants* and the *Guideline for the submission of DNA sequences derived from genetically modified organisms...* (EURL GMFF)" (see above). This relates to the forward+reverse nature and minimum number of Sanger sequences; and minimum average depth of NGS assemblies. If PCR has been used to generate the integration site DNA for sequencing, the minimum number of PCR products to be sequenced is also specified in those requirements.

Assuming that there is more than one sequence data set, there will be one such section for each event, numbered 6A, 6B, 6C etc. Each will reference the integration event and the location of the files in the submitted data tree.

(a) **Presence of data files.** This includes sequence and alignment/mapping files, as required by the *Technical Note* and the *Guideline.* These will be confirmed or otherwise commented on.

(b) **Statutory metrics.** This reports statutory metrics, pertinent to the platform concerned, for each sequence data set ("data set" could constitute as few as 4 Sanger reads), as described above.

(c) **Concerns arising.** This will be "None" or else will state the concerns. These concerns may also reference Section 7, if they impact on particular analyses described therein.

7. OPINION ON SEQUENCING, ASSEMBLY AND OTHER ANALYSES OF DNA SEQUENCE READ DATA.

This can include comments on whether relevant data has been included or not (e.g. SAM/BAM mapping / assembly files). The inclusion of some of those data types may not have been prescribed in the regulations.

This cannot be overly-prescriptive here because the kinds of analyses performed could be quite variable. We anticipate that (a) to (c) below will be common. Where present, will provide our opinion on:

(a) The sequencing itself

This refers to comments about the sequencing procedure itself, with reference especially to the issues described in Sections 2 and 3 of "Guideline for the submission of DNA sequences derived from genetically modified organisms... (EURL GMFF)" (see above). Example: "No concerns arise."

(b) Basic sequence data processing methodology

This essentially relates to standard quality procedures such as read-trimming and filtering.

(c) Sequence assembly methodology

Often this will refer to relatively short sequences (e.g. integration site sequences). If the GMO is microbial, then *de novo* assembly of the whole genome might be expected. We believe that *de novo* assembly of non-microbial (non-microfungal, etc) eukaryote genomes will be unusual. Assembly using a reference genome sequence (mapping of new NGS reads to it) may be more likely, and would be covered by (d).

(d) Sequence read mapping methodology

"Mapping" of DNA reads to reference data (of various kinds/lengths) is quite likely to arise as part of the Applicants' methodology.

(e) Junction read analysis methodology.

This methodology would be likely to involve aspects of (c) and (d). We would provide opinion on other aspects of the methodology particular to junction read analysis.

(f) Transcriptomics analysis methodology.

ANNEX II, Part II, Section 1.2.2.3 of Regulation (EU) No 503/2013 (https://eur-lex.europa.eu/eli/reg_impl/2013/503) is not especially prescriptive of the approaches that should be taken by the Applicants to assess expression of the insert(s), but this can be at the RNA level. It is anticipated that if transcriptomics data/analysis has been submitted, this will therefore be focussed on the insert(s) transcripts, rather than on an assessment of general effects on the transcriptome in a large-scale differential expression analysis.

The above sections will reference the sequencing data set concerned, as per the Applicants' labelling of these. Subsections numbered (i), (ii), etc will be used as necessary, with one subsection per data set. Some of the above sections (a), (b),... may refer collectively to the Application as a whole, if that is appropriate.

8. OPINION ON THE METHODOLOGY USED FOR ANALYSIS OF THE EVENT INTEGRATION SITE(S)

This regards the description of the Applicants' full molecular characterisation of the whole integration site(s) (or deletion site(s), in terms of annotating all elements therein and checking them for similarity to sequences of concern.
Each of the analyses must necessarily be reviewed on a case by case basis. For example, there will be no overarching section providing opinion on the reference databases used, sequence similarity search parameters, software tools, etc; since these may differ from one analysis to the next.
Numerous aspects of the below relate to definitions in ANNEX II, Part II, Section 1.2.2.3 of Regulation (EU) No 503/2013 (https://eur-lex.europa.eu/eli/reg_impl/2013/503).

(a) Opinion on methodology used to identify/annotate the elements of the integration site sequence.
(b) Opinion on methodology of analysis of integration site sequence(s) for potential sites of homologous recombination
(c) Opinion on methodology for determination of all ORF sequences and their translated polypeptide sequences.
(d) Opinion on methodology for assessing similarity of protein/translated ORF sequences with toxin proteins
(e) Opinion on methodology for assessing similarity of protein/translated ORF sequences with allergenic proteins
(f) Opinion on methodology for assessing similarity of protein/translated ORF sequences with other proteins
(g) Opinion on methodology for any other analyses of the integration site sequences. Numbered (i), (ii) etc.

9. INDEPENDENT ANALYSIS OF INTEGRATION SITE SEQUENCE FEATURES

If there is more than one event (integration site), there will be one such section for each event, numbered 9A, 9B, 9C etc. Each will identify the event as per the Applicants' labelling of these (see Annex02 of "Guideline for the submission of DNA sequences derived from ..." (EURL-GMFF)). Each Section 9 A, B, C... describes the results of performing our own analysis of the integration site sequence. This format will also apply where multiple integration site sequences have been supplied for multiple generations of single-event GMOs (i.e. the same site in two or more specimens). In those circumstances, statements will be included (below) regarding the similarity/identity between them.

(a) List of features

These will refer to the features annotated either EMBL, GenBank or ASN.1 format as required by Section 5. of the above "Guideline for the submission of DNA sequences..." document. It will also list by bp coordinates any segments which are unaccounted for in the features list. Note that the different sequence features annotated by the Applicant can overlap, and this will often be the case.
Where more than one generation's sequence data has been supplied, then the 9B (etc) version of this section will confirm that the feature list for this sequence is the same as for 9A, or else state the differences.

(b) Results of validation

i. **Results for first Feature.** E.g.:

"Feature '35S promoter from CaMV' (coordinates 1-328) of integration site sequence is 100% identical to bp 557-884 of UniVec: U28417.1 'Cloning vector p35S-GFP' and 100% identical to bp 3202-3529 of GenBank: MN991175.1 'Cloning vector pBOB11_C-Term, complete sequence' "
Normally, all 100%-identical matches will be stated in this way. If there are a large number of such matches, they will be visible in the APPENDIX TO SECTION 9, which will in any case contain sequence similarity search output (usually BLAST). If there are no exact matches, then at a minimum the best match from any database used will be stated. In this case, the extent of commentary on the difference will depend on the level of similarity and will be determined on a case-by-case basis.

ii. **Results for second Feature.** etc

Section (b) will be omitted for 9B (etc) sequences where the dossier has stated that the integration site sequence is identical to 9A (for multiple generations of the same GMO); or omitted for all those features which are stated as identical.

(c) Summary of validation

This will be a statement "all features validated" or else there will be a list of those features which could not be validated.

10. INDEPENDENT SEQUENCE SIMILARITY ANALYSIS OF INTEGRATION SITE

This describes the results of Fera's first-principles annotation of integration site sequence using public data. The nature of these results could be quite variable from one Dossier/event site to the next. The results may also inform Report Section 11. If there is more than one event (integration site), there will be one such section for each event, numbered 10A, 10B, 10C etc. Each will identify the event as per the Applicants' labelling of these.

(a) Overview of results.

This will include statements about the number of segments that could be accounted for, and the details of any parts of the integration site sequence which could not. Where multiple sections occur (10A, 10B,...) **and** the corresponding sequences have been stated in the Dossier as being identical (due to being the same site obtained from specimens from different generations), then the 10B (etc) version of this subsection will confirm that the sequences are the same, or if one is a subsequence of the other, or any other differences. If identical then no further analysis results will be present here.

(b) Results for each segment.

i. **Results for first segment.** This will state the bp coordinates of the integration site sequence, and the results in a similar manner to Report Section 9(b). Where long lists of matching hits occur, these will be listed in the APPENDIX TO SECTION 10. Again, this will include BLAST output files.

ii. **Results for second Feature.** etc

(c) **Summary of independent analysis.** This will explicitly state if any above results are cause for concern at any level.

11. INDEPENDENT ANALYSIS OF INTEGRATION SITE SEQUENCE(S) FOR POTENTIAL SITES OF HOMOLOGOUS RECOMBINATION (HR)

The results stated in Report Section 10 may already have highlighted similarities with microbial genomic sequences which need further scrutiny. Irrespective of this, we will have performed a sequence similarity search versus the genomic sequence databases of the microbes in question (our default assumption is that bacteria will suffice).
If there is more than one event (integration site), there will be one such section for each event, numbered 11A, 11B, 11C etc. Each will identify the event as per the Applicants' labelling of these.

(a) **Overall finding.** A statement as to whether any matching database segments ("MSPs" or "HSPs" in Blast terminology) of sufficient length / identity to be of concern directly (due to the MSP characteristics) have been found, and if not, the best match of any kind will be stated. Again, if there are multiple instances of the same event site sequence from different generations, where each each sequence is stated as identical, then for the 11B (etc) there will be a statement confirming that this is the case (or not), and if so, no further analyses will be presented.
(b) **List of sequences of concern.** (Database sequences and their MSP coordinates.) "Of concern" includes sequences which overall do not meet the MSP metrics, but which could contain segments within which do. This would exclude cases where it is mathematically impossible for the best (but still poor) hit to meet the criteria. Hits whose MSP metrics mean that they could be close to the criteria count as "of concern" (see below).
(c) **Results of analysis of all 200 bp segments obtained from the MSPs of concern**, regarding the sequence identity criteria (EFSA HGT Explanatory Note, section 3.2.4). All positives will be stated, as will all near positives (sequence identity falls only narrowly short).
(d) **Results of analysis of any near-positives.** These are the results of analysing any near-positive 200 bp segments (the bacterial segment aligned against the integration site sequence using a local Smith-Waterman alignment, e.g. EMBOSS 'water' using default parameters. Any segments which are positive by these alignments will be reported.
(e) **Summary of conclusions.** Essentially confirmation of whether the above amounts to a positive or negative result.

12. ORFS AND TRANSLATIONS OF ORFS IN THE INTEGRATION SITE SEQUENCE

If there is more than one event (integration site), there will be one such section for each event, numbered 12A, 12B, 12C etc. Each will identify the event as per the Applicants' labelling of these.

(a) Total number of ORFs (when referenced by other analyses, ORFs are identified by number 1 .. N) and the length of the longest ORF. E.g.: "286 ORFs; longest 2,514 bp."
(b) Length distribution of ORFs, e.g.:
"length 2514 bp (838 aa) 1
length 2472 bp (824 aa) 1
length 741 bp (247 aa) 1
length 636 bp (212 aa) 1
length 429 bp (143 aa) 1
length 321 bp (107 aa) 1
length 294 bp (98 aa) 1
length 288 bp (96 aa) 1
length 282 bp (94 aa) 1
length 252 bp (84 aa) 3
length 246 bp (82 aa) 1"
(etc)

The details of the sequences will be included in APPENDIX TO SECTION 12.
(c) Statement as to whether any of the translated ORF sequences are identical to the intended protein sequence stated in the Application dossier. (This may not be the case, since the ORFs are between-stop codon ORFs, not necessarily beginning with a start codon.)
(d) If multiple integration site sequences have been submitted **and** these represent the same site from different generations of the same GMO (i.e. will probably have been stated in the Application as being identical), then in the 12B (etc) version of this section, subsection (d) will confirm whether these event site sequences are the same, or otherwise if any differences cause there to be any differences in the ORFs; and if so, these differences will be stated (essentially, which are new ORFs to be analysed).

13. INDEPENDENT ANALYSIS OF PROTEIN/ORF SEQUENCES' SIMILARITY TO TOXIN PROTEINS

The intended protein sequence and all translated ORFs of at least 15 amino acids length will have been used as sequence similarity search queries in our analysis. (Though mindful of Regulation (EU) No 503/2013, ANNEX II, Part II section 1.2.2.2 (f), we have explained elsewhere in the Technical Specification that there is little to be achieved by using shorter queries for BlastP searches.)
If there is more than one event (integration site), there will be one such section for each event, numbered 13A, 13B, 13C etc. Each will identify the event as per the Applicants' labelling of these. If these multiple sites are stated as being the same site from different generations, then in 13B (etc) only translated ORFs (if any) specific to that site will be described here.

(a) Statement of total number of query sequences used e.g. "226 queries".

(b) Numbers of queries which have at least one match with an E-value lower than each point on a descending log-scale threshold, starting at 10^{-3} . E.g.:
   B. Number of queries with hit(s) of E ≤ 10^{-3} : 4
   C. Number of queries with hit(s) of E ≤ 10^{-4} : 0

(c) **Hits for further investigation.** All instances of queries (ORFs are identified by number; see Section 12) with at least 1 MSP of E ≤ 10^{-3} with a toxin-annotated protein sequence will be listed, along with information on the query length, the coverage of both the query and hit sequence, MSP sequence identity and other data deemed pertinent.
   i. **Results for query ORF #25 versus UniProt: B5U2W0 (VSP_BOMIG) aa 180-197**
      1. Details.
      2. Conclusion.
   ii. **Results for query ORF #102 versus UniProt: Q1JPL7 (PME18_ARATH) aa 320-345**
      1. Details.
      2. Conclusion.
   iii. **etc.**

(d) Summary as to whether any homology can be reasonably concluded (noting that a positive does not by any means necessarily imply the same function as the matching protein(s)).

14 . INDEPENDENT ANALYSIS OF PROTEIN/ORF SEQUENCES' SIMILARITY TO ALLERGENIC PROTEINS

If there is more than one event (integration site), there will be one such section for each event, numbered 14A, 14B, 14C etc. Each will identify the event as per the Applicants' labelling of these. If these multiple sites are stated as being the same site from different generations, then in 14B (etc) only translated ORFs (if any) specific to that site will be described here, and no further analyses presented if the sequences are confirmed as the same.

(a) Statement of total number of query sequences used which are ≥ 80 amino acids long ("long queries"), and total number of ORF query sequences used (between 15 and 79 amino acids long inclusive; "short queries").

(b) **Long-query hits for further investigation.** List of long queries and their database hit sequences which have at least one BlastP MSP of where at least 28 positions are identical (query and MSP coordinates will be stated).

(c) **Results of analysis of above long-query hits.** This will state the details of any positives, i.e. any cases of a segment of 80 amino acids where at least 28 (35%) positions are identical.

(d) **Short-query hits.** List of short queries and their database hit sequences which have at least one segment pair of 8 consecutive positions where the amino acids are identical.

(e) Summary of results. Essentially confirmation of whether the above amounts to a positive or negative result.

15. ADDITIONAL BIOINFORMATICS OBSERVATIONS

Any other detailed bioinformatics observations regarding analyses undertaken by the Applicants or the Fera team.
If for any reason there has been a need to perform any further bioinformatics analysis on the Fera side, this will be described here. It is also possible that various bioinformatics analyses beyond the statutory requirements have been performed and described in the Application dossier. If they are deemed to have relevance to this Report, that will be described here. It may be "None required".

16. BIOINFORMATICS SUMMARY STATEMENT

This will be written by the Dossier Lead Bioinformatician and will summarise the conclusions of the previous sections, and highlight any areas for concern, whether arising from problems with dossier/data content, the quality of the methodology, positives arising from the Applicants' or Fera teams analyses, etc. This will also include the bioinformatics perspective on any matters arising from a discussion of the results with the Dossier Lead GMO specialist.

17. GMO SPECIALIST STATEMENT

This statement by the Dossier Lead GMO Specialist will place the overall conclusions in the context of any other considerations surrounding this GMO, and the technology and molecular biology techniques which the Applicants have used. Also commentary on legislative issues, including the status of particular GMO events in question. For example, the current EU/ member state authorisation status of the GMO, which could have implications on its release to market in the EU.; the status of single-event's authorisation in relation to stacked-event GMOs may also have a bearing on which of the bioinformatics assessments would need to be performed, given a stacked-event dossier. Regarding other details, this section will include any commentary that may be required on elements in the integration site sequences. Similarly, perspective if appropriate on the particular matching genes or proteins which might have arisen in the bioinformatics results. This commentary may relate to the evidence supplied by the Applicants, or the results and opinions of the Fera bioinformaticians, or both. Any other relevant information will also be stated.

APPENDIX A.

This will contain the specification of the bioinformatics resources used by the Fera team when performing any analyses described: software, databases, with versions/dates/parameters used.

VARIOUS APPENDICES TO SECTIONS: AS MENTIONED IN THE ABOVE TEXT.

(Proforma ends)

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B. INNOVATION

Please provide details of any aspect of the proposed work which are considered innovative in design and/or application? E.g. Introduction of new or significant improved products, services, methods, processes, markets and forms of organization

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Strengthening the FSAs knowledge-base.
The Fera team for this proposal possesses a particularly strong combination of skills and expertise in bioinformatics and molecular biology applied to GMOs. The team has many years' experience in DNA sequencing, gene and protein sequence analysis, and the application of these techniques for genomic-based testing and detection.

The ongoing application of the team's expertise to the challenges of assessing applications for GMO authorisation, throughout the course of this proposed work, will strengthen the FSAs own knowledge-base in this area of bioinformatics and related molecular biology. We believe the Team will bring a fresh perspective to the implementing of best practices in the DNA and protein sequence analyses specified in the published regulations and guidelines.

We will draw upon our extensive knowledge of developments in the DNA sequencing field, in which Team members are currently engaged in innovative research, especially regarding long-read sequencing. The Fera team will continue to develop its own expertise in GMOs, being currently engaged in ongoing R&D in GMO testing and maintaing knowledge-exchange with international laboratories. Three members of the team (EJ, RB and SG) are representatives for Defra at the European Network of GMO Laboratories meetings.

In summary, the work will leave the FSA better placed in their future considerations of sequence-based methods in their approach to regulated food/feed products in general, and GMOs in particular.

3: THE PROJECT PLAN AND DELIVERABLES

A. THE PLAN

Please provide a detailed project plan including, the tasks and sub-tasks required to realise the objectives (detailed in Part 1). The tasks should be numbered in the same way as the objectives and should be clearly linked to each of the objectives. Please also attach a flow chart illustrating the proposed plan.

The Project Plan description consists of the following sections:

- Roles and processes
  - Overall contract
  - Each Application dossier
- Biocomputing resources
- Receipt and storage of materials from FSA

ROLES AND PROCESSES

Roles and duties

Roles refers to the **long-term roles** of the Fera project team members over the **duration of the 3-year project** constituting this contract.

Dossier-processing duties (usually abbreviated to "duties") here refers to the tasks for which each member of staff will be responsible, during the processing of a **single Application dossier**. It is likely that these will not always be the same for a team member for all dossiers, given the short turnaround time of 3 weeks, due to availability. For example, on occasions annual leave or unavoidable unplanned leave can be expected to prevent a team member from being assigned to their usual role, for a newly-received dossier.

Therefore when each new Application is received, dossier-processing duties will be assigned to members of the team.

Roles

"B1", "B2", "G1", "G2", "G3" represent different members of the team (two bioinformaticians and three GMO molecular biology specialists).
Fera staff assigned to these roles are:

B1	Dr John Walshaw	(JW)
B2	Sam McGreig	(SM)
G1	Dr Steven Bryce	(SB)
G2	Dr Rati Bell	(RB)
G3	Dr Eleanor Jones	(EJ)

Under exceptional circumstances such as long-term absence for any reason, these roles may be reassigned during the project. The FSA will be kept fully informed of any such developments. See Risks.

Bioinformatician 1 ("B1")

This role is lead bioinformatician during the 3-year contract, and also project manager. Responsibilities which are general to the project (not per-dossier specific) include:

- Managing the project overall, including ongoing communication with FSA representatives on a regular timetabled basis as well as timely additional communication when any special eventualities arise.
- Regular communication with all other members of the team.
- Ultimate decision-making within the team regarding the criteria by which the sequencing, sequence analysis and other bioinformatics submitted in Application dossiers are evaluated. This will also be in the context of discussions with Bioinformatician 2 (B2), and of GMO specialist advice received from the Fera team members as well as any steers from the FSA.
- This includes ultimate responsibility for the choice of any analysis methodology employed at Fera for our in-house validation of Application data, and responsibility for ensuring that such methodology is implemented and any technical problems resolved.
- Maintaining a knowledge of the GMO field where it is especially pertinent to molecular characterisation and associated sequencing technologies and bioinformatics. This will be under the guidance of the 3 GMO Specialists. This will also be discussed with B2.
- Maintaining a knowledge of all bioinformatics methodology and developments in sequencing platform technology which are relevant to analyses employed for evaluating GMOs. This will be done in close communication with B2.
- Providing all information on requirements, which B2 may need in order to deploy bioinformatics resources and perform analyses required for the specific goals of the project.
- Participation in the development, deployment and documentation of these bioinformatics resources, in tandem with Bioinformatician 2 (B2).
- When necessary, investigating and solving technical problems (with analysis pipelines, etc).
- Ongoing training of B2 regarding the particular aspects of report-writing and other dossier-processing aspects which are B1's particular responsibilities.

Bioinformatician 2 ("B2")

Responsibilities which are general to the project (not per-dossier specific) include:

- Regular communication with all other members of the Fera project team, most frequently with B1.
- Participation in some of the regular meetings with FSA representatives, as required.
- Ensuring that in any urgent circumstances which may arise, any relevant communications are made to the FSA, usually via a senior Fera team member but directly if circumstances dictate.
- In discussion with B1 and with the guidance of the 3 GMO Specialists, maintaining a knowledge of the GMO field where it is directly relevant to molecular characterisation/associated sequencing technologies and bioinformatics.
- Maintaining a knowledge of all bioinformatics methodology and developments in sequencing platform technology which are relevant to analysis for the purpose of evaluating GMOs. This will be done in close communication with B1.
- Discussing with B1 the requirements for deploying bioinformatics resources and performing analyses for the specific goals of the project.
- Taking a major role in the development and deployment of these bioinformatics resources, in tandem with B1. (Responsibility for ensuring availability for these resources ultimately lies with B1.)
- Under normal circumstances, being the point of first recourse for investigation of technical problems (such as software failure etc). (B1 will also be expected to contribute to this, and will also take ultimate project responsibility for ensuring availability of resources.)
- As the project progresses, developing knowledge with B1's guidance of the particular aspects of report-writing and other dossier-processing aspects which are B1's particular responsibilities.
- As the project progresses, potentially taking on the duties for some dossiers that would in the earlier stages be performed by B1.

GMO Specialist 1 ("G1")

This role is lead GMO specialist during the 3-year contract.

Responsibilities which are general to the project (not per-dossier specific) include:

- Fulfilling the role within the team of ultimate authority on molecular biology aspects of GMOs.
- Ultimate decision-making within the team regarding the criteria by which any molecular biology aspects of submitted dossiers should be evaluated, where this informs any of the bioinformatics analyses concerned in the project. This will be in the context of discussion with the team bioinformaticians, especially B1, and G2 and G3.
- Regular communication with all other members of the Fera project team.
- Ongoing communication with FSA representatives, attending a number of the regular timetabled meetings
- Timely additional communication with the FSA and B1 when any special eventualities arise.
- In ongoing consultation with B1 and B2, maintaining an appreciation of the capabilities and limitations of the various bioinformatics methodologies, where it is relevant to the GMO molecular biology considerations of this project.
- Providing advice to B1, B2 regarding possible strengths and shortcomings of bioinformatics methodologies being suggested for implementation, based on GMO molecular biology considerations.
- With some example dossiers, advising G2 and G3 regarding the particular aspects of report-writing and other dossier-processing aspects which are G1's particular responsibilities.
- Under normal circumstances, taking the lead role on the GMO specialist side in evaluating submitted dossiers, and writing summaries of the Fera reports.

GMO Specialist 2 and GMO Specialist 3 ("G2" and "G3").

These are essentially equivalent roles within the project, to support G1 and to be able to step into the principal GMO specialist role for a given dossier, when G1 is unavailable. In general, the roles will be similar to G1, but with less frequent activity.
Responsibilities which are general to the project (not per-dossier specific) include:

- Providing expertise regarding the criteria by which any molecular biology aspects of submitted dossiers should be evaluated, where this informs any of the bioinformatics analyses concerned in the project. This will be in the context of discussion with the team bioinformaticians, especially B1, and G1.
- Regular communication with all other members of the Fera project team.
- Ongoing communication with FSA representatives, attending some of the regular timetabled meetings when required.
- As the project progresses, developing knowledge with G1's guidance of the particular aspects of report-writing and other dossier-processing aspects which are G1's particular responsibilities.
- With guidance from B1 and B2, maintaining an appreciation of the capabilities and limitations of the various bioinformatics methodologies, where they are relevant to the GMO molecular biology considerations of this project.

Overall contract

The activities of the Fera project team throughout the contract is necessarily not limited to the 3-week delivery windows of each dossier. Other duties include regular communication with the FSA both at the beginning of the project (Objective 2) and throughout its 3-year duration (Objective 3). Implementation and maintenance of computational resources (Objective 4) is also an important component. The *average total* cost of processing one dossier, including these ongoing activities which contribute to the completion of dossiers, has been arrived at by taking these factors into account. The expected range of dossiers to be processed p.a., as indicated in the FSA Specification, has been used.

The total number of days p.a. to undertake Objectives 2-4 (i.e. outside the hours spent within the 3-week window for a dossier / spent specifically on that dossier) has been specified as 4 p.a. for each of B1 and B2, with respectively an additional 3 and 4 days p.a. for the first year of the project only. For G1 it is 1.5 days p.a. for each of the 3 years, and for G2 and G3 it is 1 day p.a. for each of the 3 years.

Establishment of technical and procedural aspects of the report preparation and delivery, in agreement with the FSA.

Objective 2 will be achieved by a project kick-off videoconference meeting of the Fera team with the FSA as soon as possible after the start date, followed up if necessary with a conference call ideally within 3 weeks (not necessarily involving the whole Fera team) to finalise any outstanding procedural or technical matters (see Objective 2.) Correspondence by email may also be sufficient following the kick-off meeting. Refer to *Section 5. Project Management* of this tender for further details, and *Section 3B. Deliverables.*

Ongoing review of technical and procedural aspects of the report preparation and delivery

Objective 3 will consist of quarterly review meetings supported by a quarterly review document. A larger annual review document will provide the basis of an annual review meeting. Refer to *Section 5. Project Management* of this tender for further details, and *Section 3B. Deliverables.*

Implementation of automated systems for conducting independent analyses of the GM event-site DNA where appropriate

Objective 4 will be achieved using the additional time assigned to B1 and B2 in the first year, with ongoing maintenance and improvement (e.g. new suitable databases, search software, etc) assigned to the annual allocated time. Implementation and maintenance includes all aspects of testing and documentation. Our projected completion milestone would be 3 months after the project commences, but this may be subject to the details agreed in Objective 2.

John Walshaw (B1) and Sam McGreig (B2) both have in-depth experience of implementing bioinformatics analysis pipelines involving 3rd-party software and in-house developed software. They routinely implement bioinformatics resources at Fera using robust, community-supported pipeline platforms including SnakeMake and NextFlow, and manage and use a large portfolio of bioinformatics tools maintained via Bioconda and by other means as necessary. They are both very experienced in script development.

Each Application dossier

Dossier-processing duties

These duties for **a particular dossier** will be assigned when it is received. Note that some team members will be assigned **more than one** duty; e.g. normally the Dossier Manager would also be either the Lead Bioinformatician or the Lead GMO Specialist. In some cases due to availability, duties that would normally be taken on by two team members may be carried out by one person (e.g. both bioinformatics duties).
In the event of unavoidable absence between the assignment of duties and report delivery, duties may need to be reassigned (e.g. if the Dossier Manager takes sick leave).

Dossier Manager
The Manager has responsibility for ensuring that the dossier is processed correctly, that the final report is delivered and that any other necessary communications to the FSA are made (e.g. early alerts of problems identified).

When available, this would normally be B1 (JW), but otherwise G1 (SB). If neither are available then this would be either G2 (RB) or G3 (EJ).

Dossier Lead Bioinformatician

- The Lead Bioinformatician is responsible for initial assessment of the dossier from the bioinformatics point of view, in order to identify which of the sections therein, and which of any accompanying data, require review by a bioinformatician. This is also agreed in consultation with the Lead GMO Specialist (see below).

- The Lead Bioinformatician is responsible for ensuring that the identified bioinformatics results and methodology presented in the dossier are assessed, and that any in-house analysis required is performed (but would not necessarily perform all of these tasks personally).

- The duties include performing the critical review of methodology and results. At a minimum, conclusions will be shared with the Support Bioinformation (when available), but would often involve discussions with the latter as part of forming the conclusions. For example, fine details of a number of particular software packages may be implicated, or an assessment of unpublished methodology. Many aspects may be clear-cut, however.

- If any pipeline analysis is performed (this will often be the case), the Lead Bioinformatician will also scrutinise the results. If any other analyses are performed, this may be done either as part of the Lead or Support Bioinformatician duties, to be determined on a case-by-case basis.

- The Lead Bioinformatician is also responsible for ensuring that the bioinformatics-related content of the report is available and delivered, and would normally supply most of this content.

- The Lead Bioinformatician is ultimately responsible for flagging any problematic issues with the dossier, arising from bioinformatics considerations, to the Dossier Manager (or if this is the same person, then to the FSA).

- Lead bioinformatician will also sign off on the final report.

When available, the Lead Bioinformatician would normally be B1 (JW), but otherwise B2 (SM). As the 3-year project progresses, we anticipate that B2 (SM) might on occasions take on this role even when B1 (JW) is available (who would for those dossiers take on the Support Bioinformatician role).

Dossier Lead GMO Specialist

- The Lead GMO Specialist is responsible for initial assessment of the dossier from the molecular biologists point of view, in order to identify any serious issues which arise.

- Otherwise, the Lead GMO Specialist will provide their opinion to the Lead Bioinformatician, regarding which parts of the dossier require review by a bioinformatician; they will also advise on any considerations which the team bioinformaticians should be aware of, particular to this dossier.

- The Lead GMO Specialist is also responsible for ensuring that the GMO content of the report is delivered, and would normally supply this content. Usually, this would be a summary section, but additional components might be provided in special cases.

- The Lead GMO Specialist is ultimately responsible for flagging any problematic issues with the dossier, arising from their molecular biology and wider knowledge of GMOs, to the Dossier Manager (or if this is the same person, then to the FSA).

When available, Lead GMO Specialist would normally be G1 (SB), but otherwise either G2 (RB) or G3 (EJ), depending on rotation considerations and availability.

Dossier Support Bioinformatician
(*These duties could be performed by the same team member who performs the Lead Bioinformatician duties, if dictated by availability.*)

- The Support Bioinformatician duties include checking for presence and basic correctness of those data files, scripts and other accompanying contents which have been identified as requiring assessment. These first-level checks

include locatability of the data, check-sum validation, sense checking (e.g. documentation files actually contain documentation text; numbers of sequencing data files are as described, etc).

- Second-level checks would include aspects such as checking average quality scores of NGS data files or coverage depth of assembled data.

- The Support Bioinformatician duties also include running the analysis pipelines for integration site sequences, and checking the results. If any other analyses are performed, this may be done either as part of the Lead or Support Bioinformatician duties, to be determined on a case-by-case basis.

- All results and the locations of any output data files will be clearly communicated to the Lead Bioinformatician (if that is a different team member). Any problematic features of any of the data or analysis results will also be communicated.

- The Support Bioinformatician duties also include contribution to the critical review of methodology and results.

At least in the earlier stages of the 3-year project, the Support Bioinformatician duties will be assigned to B2 (SM) if available, but otherwise to B1 (JW).

Dossier Support GMO specialist

- The Support GMO specialist will be briefed by the Lead GMO specialist regarding the dossier. This is so that they will be in a position to step into the Lead role for this dossier should the need arise due to unforseen circumstances, and also to ensure that they will maintain familiarity with the process, since they will be likely to be Lead on some future dossiers.
- Irrespective, they will contribute their expertise on matters arising from each dossier, to any other members of the team as necessary.

Process for a dossier

Normally, the FSA should direct communications announcing a new dossier to both B1 (John Walshaw) and G1 (Steven Bryce), but the FSA will be kept informed of any changes to this due to e.g. annual leave, in which case the FSA will be told in advance of the appropriate contacts within the team, should a new Dossier be sent.

1. The contacts within the Fera team receive the Dossier from FSA. The Fera contact(s) will acknowledge receipt of this communication.
2. The contacts within the Fera team will assign duties according to the procedures described in the previous section. This will take account of any significant amount of planned leave or other unavailability occurring in the next 3 weeks.
3. If any data files need to be downloaded via a separate route to that via which the Dossier was received, then this will be performed as soon as possible. If any problems (not solved by a repeat attempt) occur with this transfer, the FSA will be informed immediately by the Dossier Manager.
4. When all of the necessary files have been obtained, the Dossier Manager will confirm this to the FSA.
5. The FSA will be informed by the assigned Dossier Manager of the names of the Manager and the other Lead, as the principal and secondary points of contact. In the earlier stages of the 3-year project, we propose that a videoconference meeting/conference call between the two Leads at Fera and an FSA representative be held.
6. All other members of the Fera team will be alerted to the Dossier, unless they are ruled out of the 3-week window for unavailability reasons.
7. The Lead Bioinformatician and Lead GMO Specialist will briefly review the general nature of the GMO Application at the earliest opportunity.
8. If either realises there are significant concerns at this stage (this could just be a requirement for clarification of some kind), they will confer and if the problem is agreed, the FSA will be informed as soon as possible.
9. Assuming that the process is not terminated by the preceding step, the two Leads will inform each other of the time by which they expect to have more fully reviewed the Dossier.
10. The reading of the Dossier by both Leads is part of the quality-control. It decreases the risk of incorrect interpretation of the Application such that the Bionformatics side would not analyse the correct number of integration site sequences (for example). E.g. for multiple-event GMOs where the need to analyse one sequence may be rendered unnecessary by a previous Application; but see (13) below. Additionally, the reading by the Lead GMO Specialist increases the chances of other anomalies being detected, which may not have been noted until now.
11. After reviewing the Dossier, the Lead GMO Specialist will brief the assigned Support GMO Specialist. On a case-by-case basis, the Support GMO Specialist will review that part (or possibly whole) of the Dossier where any particular concerns or other matters arise. Any new matters of relevance to the bioinformatics review will be communicated to the Lead Bioinformatician.
12. The Lead Bioinformatician will review the Dossier with the principal initial aims of identifying the relevant sections of the dossier regarding the bioinformatics evaluation (which will include all information concerning the number of event sites which need in practice to be evaluated, as well as the descriptions of the bioinformatics analyses/results); and identifying the associated data.

13. Once that has been done, then unless it has been previously clarified, the Dossier Manager would inform the FSA of all of the data sets (e.g. data for one event site; NGS short read data set; etc) and associated text in the Dossier, which are to be reviewed at Fera.
14. Assuming that no advice to the contrary is received from the FSA, the next step is to validate the required data files in terms of presence; expected checksums (if any were provided to check); and basic sense (regarding content-type, etc). Normally, these are Support Bioinformatician duties - which may have been assigned to the Lead Bioinformatician, depending on availability of other staff; or will have been assigned to the other bioinformatician in the team. "Required" files includes any files which are statutory requirements, irrespective of whether they would normally be the subject of analysis at Fera.
15. If there are any failures/absences of required files, then the failure will be confirmed by the other bioinformatician (if available) before making the Dossier Manager aware. The latter will ensure that the FSA are informed as soon as possible.
16. Where there have been failures of checksum validation, reasonable attempts will be made to obtain the problem file(s) again, assuming that it is possible for the Fera side to initiate this transfer. A repeat checksum failure will be reported immediately by the Dossier Manager to the FSA and no further attempts repeated.
17. If no such problems have arisen, the bioinformatician(s) is/are in a position to proceed with
    a) reviewing the stated attributes and quality of the sequencing data;
    b) reviewing all of the relevant methodology;
    c) performing integration site sequence analysis.
18. As stated in the definitions of the duties of the Lead and Support Bioinformatician for the Dossier (above), both bioinformaticians (unless there is only one for this Dossier) would contribute to the review processes, and division of labour would be decided on a case-by-case basis. The details and volume to review could vary somewhat between Dossiers.
19. That would also be informed by the normal situation regarding running the pipeline analyses, i.e. the Support Bioinformatician would be performing this.
20. Problems arising: All of the above evaluations (a,b,c) could potentially raise an issue at any point.
21. Such issues could be serious: e.g. a particular mandatory analysis might not have been performed by the Applicants, or might clearly have been performed incorrectly; or much less clear cut :e.g. the reviewer might find the details of the methodology unorthodox, at a level which should merely be mentioned in the final Report.
22. If there are two bioinformaticians assigned to the Dossier and the Support Bioinformatician discovers an issue, they will report it to the Lead Bioinformatician. For the not-clear cut cases, it will be for the Lead to decide whether it is of sufficient concern to alert the FSA straight away (via the Dossier manager).
23. During this process, whenever an issue is judged by the Lead Bioinformatician to be of sufficient concern to be potentially informed by the expertise of the GMO experts, this will be relayed to the Lead GMO Specialist. Especially during the earlier stages of the 3-year project, it will be seen as good practice for the Lead Bioinformatician to keep the Lead GMO Specialist informed of progress reasonably frequently in any case. Meetings to discuss any issues will take place if necessary.
24. Whenever an issue is reported to the FSA (at an earlier stage than the normal submission of a completed Report), the FSA will provide advice as to whether the Fera team should proceed with the remaining review/analyses, or whether to conclude the review and proceed to Report-writing. The latter option would accelerate the pausing of the wider risk assessment (i.e. beyond bioinformatics) of the GMO Application.
25. Prior to writing the Report, the two Leads will confer to brief each other of any of their findings not yet communicated.
26. The Lead Bioinformatician will ensure that the Report is then compiled as specified in the Proforma example, writing much of the content but potentially delegating some sections to the Support Bioinformatician. The Lead Bioinformatician will write Section 16, Bioinformatics Summary Statement.
27. The draft-stage Report would normally be passed to the Support Bioinformatician for review (if a separate member of the team has been assigned to this duty).
28. This draft-stage Report will then be passed to the Lead GMO Specialist, who will review it and add Section 17, GMO Specialist Statement. This may also be reviewed by the Support GMO Specialist, depending on the outcome of the previous discussions.
29. The completed Report will be checked by the Dossier Manager before it is delivered to the FSA.

Average time per team member per dossier

The following summarises the average **time** spent by the named team members on dossier-specific activities, i.e. within the 3-week window for specific dossiers, rather than the additional time specified in the ***Overall Contract*** section, above. (As explained there, the average **cost** to Fera for processing each dossier over the 3 years factors in that time required for the ongoing communications and development.)

Per-dossier activity, not including the project-specifict time (see Overall Contract section, above).	estimated **average days** per person per activity **per dossier**				
	JW	SM	SB	EJ	RB
reading submission, including description of data and methodology	0.3	0.2	0.4	0.05	0.05
ensuring data is present and correct, and all other aspects documented clearly	0.1	0.35			
running auto-analyses and sense-checking results		0.35			
running any additional analyses (could include Applicant's own scripts etc)	0.1	0.3			
bioinfo troubleshooting overhead (could include bespoke Applicant scripts)	0.1	0.3			
reviewing GM issues relating to sequence data/analysis			0.8	0.01	0.01
Meetings regarding bioinformatics data, analyses, results, any troubleshooting	0.25	0.25			
Meetings between lead bioinformatician and lead GM specialist, post initial review of Application, and after bioinfo analysis is complete; also at final stage of report-writing	0.4	0.1	0.5	0.13	0.13
meetings/correspondence with FSA	0.3	0.05	0.3	0.01	0.01
writing contributions to report	0.7	0.25	0.5	0.05	0.05
TOTAL	2.25	2.15	2.5	0.25	0.25

BIOCOMPUTING RESOURCES

This describes the resources available on-site at Fera. All of these are accessible remotely by all Team members, e.g. when working from home.

The resources available to Fera bioinformaticians include multiple Linux servers. The principal servers consist of two which each have 144 dual-threaded cores and 0.5 Tb RAM, while two additional servers have 80 dual-threaded cores and the same amount of RAM. We also have several other lower-specificaton servers (example spec: 32 cores, 100 Gb RAM). Even these less powerful servers would be suitable for performing the low-throughput (very low numbers of query sequences) analyses described in this proposal. In the event that we would need to perform more computationally demanding analyses for any reason, the principal servers are ample resources to perform these in tractable time (recent real example: mapping of 63 million short reads of plant genomic DNA to a ~ 400 Mbase reference genome took 65 minutes on one of these servers).

Additionally, Fera has a VMWare platform which hosts a number of virtual Linux machines. These VMs are more modest, but suitable for the low-throughput bioinformatics analyses.

Local storage devices (i.e. for each server) range from 2 Tb to 5 Tb for the four principal servers. Shared storage volumes are much larger (22 Tb per volume), with one currently networked to these servers with others ready configured to be deployed as soon as needed.

All the above machines are on a 4 hour support contract. In event of hardware failure requiring replacement of parts/whole servers, these are expected to be present on-site the following day at the latest. All machines are additionally on a double-redundant battery backup system. In the event of a serious software issue at the operating system (OS) level, OS-rebuilding by Fera staff would be completed inside 1 day, which would potentially require subsequent re-installation of applications software (since the existing versions may not work with the OS modifications).

RECEIPT AND STORAGE OF MATERIALS FROM FSA

Our assumption is that we would receive the dossier and associated materials from FSA, and that the data (of the format defined in Annex 02 of the EU Sequences Submission Guideline) would be provided via secure FTP, HTTPS, with the details of transfer to be advised by the FSA.

The FSA has indicated (formal response of 7th Dec 2020) that NGS data sets will be expected in most of the Applications. We anticipate that these may include short-read data which was subsequently used by the Applicants to assemble the integration site sequences, and possibly short-read data for other purposes. Potentially, there will be whole genome shotgun data sets, which may have been the basis of junction read analysis. We would not normally be performing analyses on these as such, but (unless directed by the FSA) we may need to determine basic metrics such as mean quality scores, numbers of reads, etc and thus we would need to store the data for the duration of the dossier-processing. We estimate that in the largest cases, such data sets would occupy no more than several Tb of storage, for which we have capacity.

To take an extreme hypothetical example, the wheat genome is 17 Gbases in size. 100 x coverage reads, i.e. 1.7 Tbases, would amount to approximately 2 Tb of compressed sequence data. If this were provided for two specimens (e.g. first and last generation) this would still amount to < 5 Tb.

We have noted the possibility of transcriptomic data sets as a means of satisfying the requirements of Reg. 503/2013 Annex II / II 1.2.2.3, although this is by no means expected in every case. Notwithstanding potential variability in numbers of specimens, replicate samples, etc, these data sets would not be of a significantly greater size than the above. We expect the size of dataset to be far smaller in the majority of applications.

Following completion of a Report, we will retain the data for a length of time agreed with the FSA at the contract outset. This will be short (we suggest 3 weeks) and will serve the purpose of avoiding the need to reacquire the data should a short-term enquiry arise for any reason from or via the FSA We would not under normal circumstances be performing any re-checking of the data after the Report is delivered, however. After the retention time has elapsed, we will delete the data.

B. DELIVERABLES

Please outline the proposed project milestones and deliverables. Please provide a timetable of key dates or significant events for the project (for example fieldwork dates, dates for provision of research materials, draft and final reporting). Deliverables must be linked to the objectives.
For larger or more complex projects please insert as many deliverables /milestones as required.
Each deliverable should be:

i. no more 100 characters in length
ii. self-explanatory
iii. cross referenced with objective numbers i.e. deliverables for Objective 1 01/01, 01/02 Objective 2 02/01, 02/02 etc

Please insert additional rows to the table below as required.

A final deliverable pertaining to a retention fee of 20 % of the total value of the prosed work will automatically be calculated on the financial template.

DELIVERABLE NUMBER OR MILESTONE IN ORDER OF EXPECTED ACHIEVEMENT	TARGET DATE	TITLE OF DELIVERABLEOR MILESTONE
1.	VARIABLE	(DELIV.)FOR EACH DOSSIER:EVALUATION REPORT AS DESCRIBED. DELIVERY WITHIN 3 WKS OF RECEIPT(OBJ. 1)

2.	**04/02/2021**	**(MILESTONE) KICK-OFF MEETING. (OBJECTIVE 2)**
3.	**30/04/2021**	**(DELIVERABLE) QUARTERLY REPORT Y1.1 (OBJECTIVE 3)**
4.	**07/05/2021**	**(MILESTONE) QUARTERLY REVIEW MEETING Y1.1 (OBJECTIVE 3)**
5.	**02/07/2021**	**(MILESTONE) PIPELINE FOR AUTOMATION OF INDEPENDENT ANALYSES, VERSION 1.0 (OBJECTIVE 4)**
6.	**30/07/2021**	**(DELIVERABLE) QUARTERLY REPORT Y1.2 (OBJECTIVE 3)**
7.	**04/08/2021**	**(MILESTONE) QUARTERLY REVIEW MEETING Y1.2 (OBJECTIVE 3)**
8.	**29/10/2021**	**(DELIVERABLE) QUARTERLY REPORT Y1.3 (OBJECTIVE 3)**
9.	**05/11/2021**	**(MILESTONE) QUARTERLY REVIEW MEETING Y1.3 (OBJECTIVE 3)**
10.	**28/01/2022**	**(DELIVERABLE) ANNUAL REPORT Y1 (OBJECTIVE 3)**
11.	**04/02/2022**	**(MILESTONE) ANNUAL REVIEW MEETING Y1 (OBJECTIVE 3)**
12.	**29/04/2022**	**(DELIVERABLE) QUARTERLY REPORT Y2.1 (OBJECTIVE 3)**
13.	**06/05/2022**	**(MILESTONE) QUARTERLY REVIEW MEETING Y2.1 (OBJECTIVE 3)**
14.	**29/07/2022**	**(DELIVERABLE) QUARTERLY REPORT Y2.2 (OBJECTIVE 3)**
15.	**05/08/2022**	**(MILESTONE) QUARTERLY REVIEW MEETING Y2.2 (OBJECTIVE 3)**
16.	**28/10/2022**	**(DELIVERABLE) QUARTERLY REPORT Y2.3 (OBJECTIVE 3)**
17.	**04/11/2022**	**(MILESTONE) QUARTERLY REVIEW MEETING Y2.3 (OBJECTIVE 3)**
18.	**31/01/2023**	**(DELIVERABLE) ANNUAL REPORT Y2 (OBJECTIVE 3)**
19.	**03/02/2023**	**(MILESTONE) ANNUAL REVIEW MEETING Y2 (OBJECTIVE 3)**
20.	**28/04/2023**	**(DELIVERABLE) QUARTERLY REPORT Y3.1 (OBJECTIVE 3)**
21.	**05/05/2023**	**(MILESTONE) QUARTERLY REVIEW MEETING Y3.1 (OBJECTIVE 3)**
22.	**28/07/2023**	**(DELIVERABLE) QUARTERLY REPORT Y3.2 (OBJECTIVE 3)**
23.	**04/08/2023**	**(MILESTONE) QUARTERLY REVIEW MEETING Y3.2 (OBJECTIVE 3)**
24.	**31/10/2023**	**(DELIVERABLE) QUARTERLY REPORT Y3.3 (OBJECTIVE 3)**
25.	**03/11/2023**	**(MILESTONE) QUARTERLY REVIEW MEETING Y3.3 (OBJECTIVE 3)**
26.	**22/01/2024**	**(DELIVERABLE) ANNUAL REPORT Y3 (OBJECTIVE 3)**
27.	**29/01/2024**	**(MILESTONE) ANNUAL REVIEW MEETING Y3 (OBJECTIVE 3)**

4: ORGANISATIONAL EXPERIENCE, EXPERTISE and STAFF EFFORT

D. PARTICIPATING ORGANISATIONS' PAST PERFORMANCE

Please provide evidence of up to three similar projects that the project lead applicant and/or members of the project team are currently undertaking or have recently completed. Please include:

- The start date (and if applicable) the end date of the project/(s)
- Name of the client who commissioned the project?
- Details of any collaborative partners and their contribution
- The value
- A brief description of the work carried out.
- How the example(s) demonstrate the relevant skills and/or expertise.
- What skills the team used to ensure the project (s) were successfully delivered.

Project title & value	Start date & end date	Client	Collaborative partners	Description of work	Relevant skills/expertise to ensure success
Characterising GM events using next-generation sequencing Value: £18,925	January 2020 to March 2020	Defra	n/a	Use of a recently developed genome walking and long-read sequencing approach to characterise GM event insertion sites in transgenic plants	Bioinformatic identification and characterisation of GM event insertion sites
Burden of Antimicrobial Resistance Genes in Selected Ready-to-Eat Foods Value: £348,356	February 2019 to February 2021	FSA	HallMark Veterinary & Compliance Services	Project uses a metagenomic approach to detect AMR genes in a variety of Ready-to-eat foods, and will use this data to estimate the dietary burden of AMR genes from RTE foods.	Bioinformatic analyses for detection of genes of interest (in this case AMR genes), identification of colocalised genes (i.e. understanding the genomic context of those genes), and taxonomic identification of metagenomes .
GM Long Term Service Agreement Value: c.£50-60,000 p.a. (variable).	2015 - present	Defra	n/a	Routine testing of GM samples to accredited standards, forensic advice, statistical advice on aspects of GM testing, attendance at annual meeting of the European Network of GMO Laboratories, development and validation of GMO detection methods as requested. Preparedness to provide an analytical service in the event of an	Maintenance of scientific knowledge and expertise of GM technologies and GMOs. Statistical expertise relating to GM sampling and detection.

				emergency scenario	

E. NAMED STAFF MEMBERS AND DETAILS OF THEIR SPECIALISM AND EXPERTISE

For each participating organisation on the project team please list:- the names and grades of all staff who will work on the project together with details of their specialism and expertise, their role in the project and details of up to 4 of their most recent, relevant published peer reviewed papers (where applicable). If new staff will be hired to deliver the project, please detail their grade, area/(s) of specialism and their role in the project team.

Lead Applicant	Fera Science Ltd

Named staff members, details of specialism and expertise.

Bioinformatic Analyses

Dr John Walshaw

John Walshaw is Senior Bioinformatician at Fera Science Ltd, where he is leading the ongoing development of Fera's bioinformatics capability. His role includes establishment of best practices in data analysis and management of bioinformatics data and software systems. Concerned with DNA sequence data, especially from high-throughput platforms, he is based in a team researching and developing detection and surveillance protocols, broadly in the agri-food and environmental monitoring fields. Approaches include genomics, metabarcoding, metagenomics, genotyping and transcriptomics. Dr Walshaw has extensive research and development experience in both high-throughput and detailed "low-throughput" protein and gene sequence analysis, and associated bioinformatics resource management, programming, algorithm development and pipeline implementation. He has more than 10 years of line-management experience.

Mr Sam McGreig

Sam McGreig is a Bioinformatician at Fera Science Ltd. He is mainly involved in the analysis of amplicon, whole genome, metagenome and RNA-Seq data generated by both Illumina and Nanopore High Throughput sequencing technologies. He has previously worked on the detection and identification of transgenic insertion sites from Nanopore sequence data.

Molecular Biology and GM Expertise

Dr Steven Bryce

Steve Bryce is a molecular biology science leader in the Plant Protection Programme at Fera and manager for the 'Molecular Technology Unit'; a suite of dedicated laboratories for the application of molecular biology methods in diagnostic testing and research. His role includes advice, method development and validation for GMO detection methods for Defra and the APHA GM inspectorate. Additionally, he directly oversees the delivery of services for detection and identification of GMOs in food, feedstuffs, seed and unauthorised environmental releases, for both statutory and commercial purposes.

Dr Rati Bell

Rati is a Molecular Biologist at Fera Science Ltd. She is interested in transforming R&D processes into validated, fit-for-purpose applications and products for high throughput service delivery. Rati is a member of the Molecular Technology Unit where she has delivered molecular diagnostic testing of samples for plant and animal health. She has led successful completion of the EURL-GMFF proficiency testing rounds for the last two years. Rati has also contributed to maintaining ISO 17025 accreditation for GMO testing and plant health.

Dr Eleanor Jones

Dr Jones is a Senior Molecular Geneticist at Fera Science Ltd. She works on the development and interpretation of DNA-based detection methods for GM, Plant Health and the environment. Her particular skills of relevance to this contract are the uses of DNA sequencing (particularly Sanger sequencing) data, scientific analytical skills and writing scientific reports. She has worked within the Detection and Surveillance Technologies team for six years. Dr Jones provides expert scientific advice on aspects relating to GM for APHA's GM Inspectorate under Defra's Long Term Service Agreement.

F. STAFF EFFORT

In the table below, please detail the staff time to be spent on the project (for every person named in section above) and their role in delivering the proposal If new staff will be hired in order to deliver the project please include their grade, name and the staff effort required.

Name and Role of Person where known/ Role of person to be recruited	Working hours per staff member on this project
Dr John Walshaw, project manager / bioinformatician (1)	19.05 (average per dossier)
Mr Sam McGreig, bioinformatician (2)	18.83 (average per dossier)
Dr Steven Bryce, lead GMO molecular biology specialist	19.50 (average per dossier)
Dr Rati Bell, GMO molecular biology specialist (2)	2.40 (average per dossier)
Dr Eleanor Jones, GMO molecular biology specialist (3)	2.40 (average per dossier)
Total staff effort	62.18 (average per doc

5: PROJECT MANAGEMENT

Please fully describe how the project will be managed to ensure that objectives and deliverables will be achieved on time and on budget. Please describe how different organisations/staff will interact to deliver the desired outcomes.
Highlight any in-house or external accreditation for the project management system and how this relates to this project.

Project management is recognised as an important aspect of Fera's work. Fera has designated this a key competence and provides ongoing training and development of project management skills for its staff. The Project Management System applied across Fera is based on Prince 2™ methodology and complies with ISO 9001 standards. This supports best practice and continuous improvement thus enabling delivery of a high quality and cost-effective service to our customer. Fera uses proprietary software (Retain International) to draw up resourcing plans for delivery staff, and progress against them is measured using the timesheet system. Individuals and teams are managed by dedicated Active Managers.

This project will be closely managed by John Walshaw who will be the project manager (PM) with overall responsibility for the delivery of the contract. Individual applications will be project managed by John Walshaw or by Steven Bryce/Rati Bell, who will have overall responsibility for the delivery of the individual applications to specification, to time and to the required quality standard. They will be supported by Fera's Project Management Team and Finance Team, who will monitor and support the smooth running of the overall contract and the individual applications to ensure milestones and budgets are met and invoices are issued on time.

For the overall contract, John Walshaw and other expert staff as necessary will liaise closely with the FSA Project Officer.
To monitor contract delivery, Fera proposes:

- Brief monthly progress meetings to summarise activities relating to individual applications, supported by short monthly review notes;
- Quarterly review meetings, supported by a quarterly review document which tracks numbers of individual applications and their progress, details of any complaints received and progress on responses to complaints, any other issues arising;
- Annual review meetings to discuss the Annual Review document, which will include an overview of all applications received in year and their compliance to the agreed timelines, financial costs, details of any complaints and their resolution, summary of Fera's Accreditation and proficiency test reports for that year.

Our preference is for these meetings to take place or via teleconference to reduce environmental impact and covid-19 risk (while still relevant).

To monitor delivery on individual applications, Fera propose:

- A short inception meeting at the start of an application, with the FSA and / or Applicant, as necessary;
- A wash up meeting at the end of the application process to deliver the final application report, data etc to the FSA and close down the application.

The frequency and nature of these meetings will be subject to revision once Fera and the FSA are more familiar with the application process. Fera proposes to hold these meetings via teleconference.

Should any immediate issues arise with either the individual applications or the overall contract, John Walshaw or the application lead will act quickly and take appropriate remedial action involving the FSA Project officer in any decisions where appropriate.

Fera has the in-house support of dedicated specialists in Information Management, Intellectual Property, Law, Copyright and Health and Safety. John Walshaw will assess and address any issues that may arise concerning these matters.

6. RISK MANAGEMENT

In the table provided, please identify all relevant risks in delivering this project on time and to budget. Briefly outline what steps will be taken to minimise these risks and how they will be managed by the project team.
Please add more lines as required

Identified risk	Likelihood of risk (high, medium, low)	Impact of Risk (high, medium, low)	Risk management strategy
Staff loss or absence	**Medium**	**Low**	Fera's staff resource management system (Retain) has been checked to ensure that they are available during the project life. However, should these staff become unexpectedly unavailable (e.g. through illness), this tool would be used for mitigation to identify alternative experienced scientists and colleagues who would be able to deliver this project. A number of scientists with appropriate expertise have been identified in this proposal, and the potential for distributing work among them has been described in the body of the tender. If necessary there are other Molecular Biology staff at Fera with Bioinformatics experience who could be trained to implement some of the bioinformatics processes.
Loss of data through IT failure	**Low**	**Medium**	All data are automatically backed up daily onto Fera servers; key documents are stored in a central secure project folder.
Breach of data protection	**Low**	**Low**	Fera uses a secure data transfer portal which has been used for numerous other commercially sensitive projects. This is maintained by our on-site IT team. Fera is fully compliant with the new GDPR regulations having previously completed a four-month project.
Incorrect submission from Applicant	**Low**	**Low**	Fera will identify missing aspects of the application early on in the process, allowing the applicant time to rapidly rectify this. If the missing aspect causes a long delay, then Fera in consultation with the FSA would pause the application timeline, or reject the application.
Covid-19 impact on delivery	**Low**	**Low**	It is highly unlikely that covid-19 developments or restrictions will impact on delivery of this work, as all work in the project is desk based, and all staff are capable of performing that work from home.
Fera reports do not align with EFSA reports on parallel applications	**Low**	**Medium**	Agree with FSA to discuss and resolve any differences with the EFSA following publication of reports.
Too many applications received at one time	**Medium**	**High**	Agree with FSA on trigger level of number of dossiers where an extended turnaround time would be required.

7. QUALITY MANAGEMENT

A. QUALITY MANAGEMENT

Please provide details of the measures that will be taken to manage and assure the quality of work. You should upload your Quality Assurance policy in the supporting documents section of your application.

This should include information on the quality assurance (QA) systems, , which have been implemented or are planned, and should be appropriate to the work concerned. All QA systems and procedures should be clear and auditable, and may include compliance with internationally accepted quality standards specified in the ITT e.g. ISO 9001 and ISO17025.

Specific to science projects and where relevant, applicants must indicate whether they would comply with the Joint Code of Practice for Research (JCoPR). If applicants do not already fully comply with the JCoPR please provide a statement to this effect to provide an explanation of how these requirements will be met. The FSA reserves the right to audit projects against the code and other quality standards

The lead principal investigator is responsible for all work carried out in the project; (including work supplied by sub-contractors) and should therefore ensure that the project is carried out in accordance with the Joint Code of Practice

This project will be conducted under the ISO 9001 accreditation held by Fera Science Ltd.

Fera Science Ltd has a comprehensive and robust system of policies and procedures which underpins its high-quality delivery and international reputation for scientific excellence. These systems are regularly subject to internal and external audits to ensure consistency of service.

Fera has gained Certification by Lloyds Quality Assurance for compliance to ISO 9001: 2015. The scope of activities covered by the certification includes the provision of scientific services in the areas of agriculture, food and the environment to Government and non-Government customers worldwide. Research carried out by Fera is implemented to meet the requirements of the Defra/FSA Joint Code of Practice for Research.

The quality standards of this specific work will be ensured by frequent meetings among the project team. As highlighted in section 3A, meetings will take place among the project bioinformaticians, to decide on appropriate analyses and troubleshoot any problems; among the GMO experts to review any pertinent GM issues which might impact the project; and among all project members to review the initial review of the dossier.

B. ETHICS

Please identify the key ethical issues for this project and how these will be managed. Please respond to any issues raised in the Specification document
Please describe the ethical issues of any involvement of people, human samples, animal research or personal data in this part. In addition, please describe the ethical review and governance arrangements that would apply to the work done.

Applicants are reminded that, where appropriate, the need to obtain clearance for the proposed project from their local ethics committee. This is the responsibility of the project Lead Applicant. However, if a sub-contractor requires such clearance the project Lead Applicant should ensure that all relevant procedures have been followed. If there are no ethical issues please state this

No ethical issues around the involvement of human or animal subjects or samples exist in this project. Issues around personal data are addressed in section 7C, Data Protection. The remaining ethical Issue identified in this tender is that of conflict of interest, with the Specification requiring “A commitment to confidentiality and no conflicts of interest (to be agreed on a per application basis) that may impact their ability to make impartial judgements. A signed statement to this effect must be provided.” Fera does not currently undertake work developing GMOs for food/feed use or provide services to assist companies developing GMOs, so it is not anticipated that there will be any conflicts of interest. Nonetheless we happily commit that during the Kick-off Meeting for each dossier this will be discussed, and any conflicts of interests will be identified and resolved, and if necessary Fera will recuse itself from the dossier. A signed statement to this effect is attached.

C. DATA PROTECTION

Please identify any specific data protection issues for this project and how these will be managed. Please respond to any specific issues raised in the Specification document.
Please note that the successful Applicant will be expected to comply with the Data Protection Act (DPA) 1998 and ensure that any information collected, processed and transferred on behalf of the FSA, will be held and transferred securely.

In this part please provide details of the practices and systems which are in place for handling data securely including transmission between the field and head office and then to the FSA. Plans for how data will be deposited (i.e. within a community or institutional database/archive) and/or procedures for the destruction of physical and system data should also be included in this part (this is particularly relevant for survey data and personal data collected from clinical research trials). The project Lead Applicant will be responsible for ensuring that they and any sub-contractor who processes or handles information on behalf of the FSA are conducted securely.

Electronic applications and associated data will be accessed via a secure website and the measures used to ensure the security of this data are described below (see Data Security). Hard-copy applications will be stored in secure lockable cupboards and will only be available to those staff who require access to them.

Fera will ensure compliance with Articles 30 and 31 (EC) No 1829/2003 by updating our procedures and processes to account for this data processing. Our privacy notice will be updated to ensure that there is transparency for the data subjects.

Data security

Fera will take all reasonable technical and organisational precautions to prevent the loss, misuse or alteration of the personal data. In order to do this, we have currently implemented the following measures:

- Fera holds a Public Services Network ("PSN") compliance certificate which demonstrates that our security arrangements, policies and controls are sufficiently rigorous to allow us to interact with the PSN and those connected to it;
- Fera limits access to personal data so that it is only seen by those who need access;
- any personal data which is taken offsite is encrypted and Fera uses pseudonymisation/anonymisation, where appropriate, when transferring/sharing data. Any personal data transferred by Fera will be transmitted via Fera's Secure Data Transfer facility or use of encryption technology;
- when engaging sub-processors, we are fully compliant with Article 28(2) GDPR;
- all credit and debit card details are stored in compliance with the Payment Card Industry Data Security Standards (PCI-DSS);
- Fera staff receive annual training in both 'Data Protection Awareness' and 'Cyber and Information Security Awareness';
- when personal data is no longer needed, it is removed from our servers and will be retained in our backup system for a maximum of two years (unless otherwise instructed by the client);
- data protection is administered within Fera by the Information Governance Officer and we additionally have a Data Protection Officer (DPO) who is located within Capita Group.

Among others, Fera complies with the following processes in order to ensure compliance with both data protection and data security:

- Capita Plc Business Continuity Standard;
- Capita Plc Cyber and Information Security Policy;
- Capita Plc Security Standard: Acceptable Use;
- Capita Plc Security Standard: Data Security;
- Capita Plc Security Standard: Information Technology;
- Capita Plc Security Standard: Physical Security;

- Fera Data Protection Policy;
- Fera Data Retention Policy;
- Fera Data Protection by Design and Default;
- Fera Data Transfers Outside the EEA;
- Fera Sharing Personal Data with Third Parties Procedure.

Rights of data subjects: to comply with the rights of data subjects, Fera will amend its privacy notice and this will be provided to data subjects at the time of data collection. This privacy notice will inform data subjects of their rights with respect to any data which Fera processes about them and how to exercise these rights. Fera has a

procedure in place to respond to such requests and there is also a separate procedure for Subject Access Requests (SARs).

Legal basis for processing: Fera will liaise with the FSA regarding the legal basis for processing the data. It is not expected that consent will be used in this instance. However, if this changes, Fera has relevant guidance documentation in place to ensure that the processing complies with GDPR.

Data transfers: as a result of delivering this project, Fera does not expect to make restricted transfers of personal data outside the EU. However, if this does occur, Fera will ensure that legal safeguards are in place prior to any data being transferred.

Records of data processing: to meet our obligations under Article 30 (1) GDPR, Fera maintains an Information Asset Register (IAR) of all its processing activities as both a controller and a processor. This is regularly updated by Fera's Information Governance Officer (IGO).

Fera has a number of processes in place to ensure that its data protection and data security processes/procedures are tested/complied with.

- Fera's data protection and data security processes/procedures are made available to all staff. These processes and procedures are regularly reviewed and, where necessary, improved. To ensure that these policies and procedures are being adhered to, all staff are annually trained in both data protection and data security;
- when undertaking any new data processing, Fera undertakes an analysis of the risks presented.by the processing. This analysis will determine which measures need to be put in place;
- to ensure that data can be restored in the event of an incident, we have an appropriate backup process. Our backups are stored on encrypted disk arrays with weekly and monthly encrypted copies made to tape which are stored off-premise and rotated accordingly;
- we ensure that any data processors we use also implement appropriate technical and organisational measures;
- Fera has up-to-date anti-virus software in place and conducts regular Penetration Testing. If any issues are discovered as a result of this, they are resolved as soon as possible.

- we ensure that any data processors we use also implement appropriate technical and organisational measures;

- Fera has up-to-date anti-virus software in place and conducts regular Penetration Testing. If any issues are discovered as a result of this, they are resolved as soon as possible.

GDPR Statement

No specific data protection issues have been identified for this project. The data to be collected is not expected to identify any living individuals and will therefore not be caught by the Regulations. However, any personal data which may be exchanged as a result of carrying out this project will be managed as set out below.

Fera has embedded a series of policies and procedures throughout the organisation to achieve compliance with the applicable data protection legislation, including the Data Protection Act 2018 and the General Data Protection Regulation (EU) 2016/679 ("GDPR"). Where Fera is a data Processor, personal data will be processed on the documented instructions of the data Controller. To meet our obligations under Article 30 (1) GDPR, Fera's Information Governance Officer (IGO) maintains an Information Asset Register (IAR) which details Fera's data processing activities. Fera additionally has documented procedures for:

personal data breaches;
Subject Access Requests;
Data Protection Impact Assessments.

System data will be stored on our secure network which is PSN (Public Services Network) compliant: https://www.gov.uk/guidance/public-services-network-psn-compliance. Any system personal data transferred by Fera will be transmitted via Fera's Secure Data Transfer/use of encryption. When it is no longer needed, it will be removed from our servers and will be retained in our backup system for a maximum of two years.

When in use, any hard-copy personal data generated will be stored securely and will only be accessed by those who need to access it. If any hard-copy personal data is transferred, it will be done so by use of secure courier/in person. When it is no longer needed, hard-copy personal data is destroyed by use of our secure document destruction service or returned to the data Controller.

D. SUSTAINABILITY

The Food Standards Agency is committed to improving sustainability in the management of operations. Procurement looks to its suppliers to help achieve this goal. You will need to demonstrate your approach to sustainability, in particular how you will apply it to this project taking into account economic, environmental and social aspects. This will be considered as part of our selection process and you must upload your organisations sustainability policies into the eligibility criteria in Bravo.
Please state what(if any) environmental certification you hold or briefly describe your current Environmental Management System (EMS)

Fera and our parent company Capita take sustainability seriously and follow a robust environmental policy that includes challenging targets. In the five years prior to establishing Fera Science Limited, The Food and Environment Research Agency reduced water use by 50%, reduced gas consumption by 30% (equivalent to 1428t CO_2) and electricity use by 28%. A project to replace half of the main chillers in the site saved 172t CO_2 and insulation of the exposed pipework in the greenhouses reduced emissions by 85t CO_2 annually. Fera's previous Sustainable Development Action Plan was one of a very few to be awarded the green star. With the formation of Fera Science Limited, the site was retained by Defra and Fera became one of several tenants and therefore unable to provide representative reporting on current metrics.

As part of Capita Group which is predominantly a service business, Capita's direct environmental impacts are not broad; but the scale of the business means our impacts need to be managed carefully. Almost all Capita employees are office-based meaning that our environmental impacts are those associated with normal modern office facilities.

The Capita focus is on our main Group-wide environmental impacts:

- Minimising energy use at our sites
- Reducing business travel
- Managing our resource use and waste management.

Our environmental management system, Certified by BSI to ISO 14001 standard, allows us to monitor and manage our impacts and continually improve performance in these areas. Our environmental policy sets out our commitment to complying with the relevant environmental legislation and board level responsibilities.

We have reported our carbon footprint since 2005 and in 2015, our carbon emissions were 124,329 tonnes CO_2eq representing a year-on-year decrease of 11% (2014: 139,672 CO_2eq). This decrease was down to a dramatic reduction in business travel emissions of 28% achieved by an 82% reduction in air, a 45% reduction in rail and a 12% reduction in car emissions, partly as a result of our 'smarter working' initiative.

In 2010, we set ourselves a target to reduce the carbon intensity of our offices by 4.5% per year. In 2015, although our carbon emissions for scopes 1 and 2 increased to 88,280 CO_2eq (2014: 84,103 CO_2eq) due to the growth of our international operations, our carbon intensity actually decreased from 15.1 to 19.2.

Also attached with this tender are copies of Fera's Environmental Policy and Manual, and Capita's Environmental Policy and Policy Statement.

Within this project we will comply fully with these policies. For example, we propose that as many meetings as practicable be held online (e.g. via Microsoft Teams). This project will involve no laboratory work, so disposable reagents are not an issue. However, as much project documentation as possible will be digital only, reducing the amount of paper waste generated in this project.

E. DISSEMINATION AND EXPLOITATION (Science Projects Only)

Where applicable please indicate how you intend to disseminate the results of this project, including written and verbal communication routes if appropriate. Applicants are advised to think carefully about how their research aligns with the FSA strategy, what is the impact that their research has on public health/ consumers and decide how the results can best be communicated to the relevant and appropriate people and organisations in as cost-effective manner as possible. Please provide as much detail as possible on what will be delivered. Any costs associated with this must be documented in the Financial Template.

The applicant should describe plans for the dissemination of the results for the project team as a whole and for individual participants. Details should include anticipated numbers of publications in refereed journals, articles in trade journals etc., presentations or demonstrations to the scientific community, trade organisations and internal reports or publications. Plans to make any information and/or reports available on the internet with the FSA's

permission are also useful, however, this does not remove the requirement for Tenderers to think how best to target the output to relevant groups. If a final report is part of the requirement, please make sure, as part of the executive summary, that aims and results are clear to the general audience and that the impact of the research on public health/consumers and it's alignment to FSA priorities is clearly stated. Please note that permission to publish or to present findings from work supported by the FSA must be sought in advance from the relevant FSA Project Officer. The financial support of the FSA must also be acknowledged. Please indicate whether any Intellectual Property (IP) may be generated by this project and how this could be exploited. Please be aware the FSA retains all rights to the intellectual property generated by any contract and where appropriate may exploit the IP generated for the benefit of public health. In this part Applicants should demonstrate the credibility of the partnership for exploitation of the results and explain the partnership's policy in respect of securing patents or granting licenses for the technology (if applicable). It should deal with any possible agreements between the partners to extend their co-operation in the exploitation phase and with relevant agreements with companies, in particular users, external to the partnership
Not applicable to this tender.

Schedule 13 (Contract Management)

1. Definitions

1.1 In this Schedule, the following words shall have the following meanings and they shall supplement Schedule 1 (Definitions):

"Project Manager"	the manager appointed in accordance with paragraph 2.1 of this Schedule;

2. Project Management

2.1 The Supplier and the Buyer shall each appoint a Project Manager for the purposes of this Contract through whom the provision of the Services and the Deliverables shall be managed day-to-day.

2.2 The Parties shall ensure that appropriate resource is made available on a regular basis such that the aims, objectives and specific provisions of this Contract can be fully realised.

3. Role of the Supplier Project Manager

3.1 The Supplier Project Manager shall be:

3.1.1 the primary point of contact to receive communication from the Buyer and will also be the person primarily responsible for providing information to the Buyer;

3.1.2 able to delegate his position to another person at the Supplier but must inform the Buyer before proceeding with the delegation and it will be delegated person's responsibility to fulfil the Project Manager's responsibilities and obligations;

3.1.3 able to cancel any delegation and recommence the position himself; and

3.1.4 replaced only after the Buyer has received notification of the proposed change.

3.2 The Buyer may provide revised instructions to the Supplier's Project Manager in regards to the Contract and it will be the Supplier Project Manager's responsibility to ensure the information is provided to the Supplier and the actions implemented.

3.3 Receipt of communication from the Supplier Project Manager by the Buyer does not absolve the Supplier from its responsibilities, obligations or liabilities under the Contract.

4. Contract Risk Management

4.1 Both Parties shall pro-actively manage risks attributed to them under the terms of this Contract.

4.2 The Supplier shall develop, operate, maintain and amend, as agreed with the Buyer, processes for:

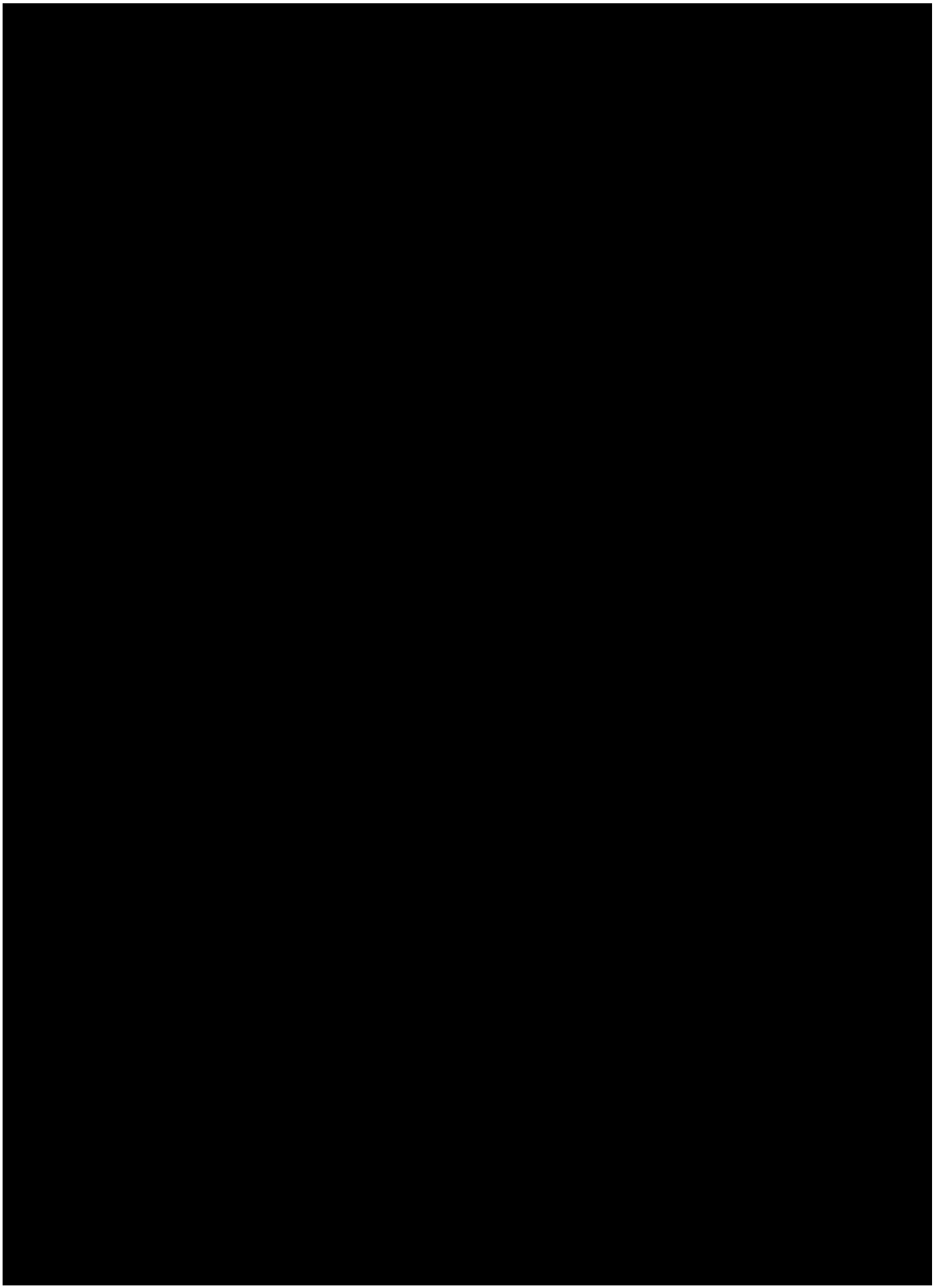
4.2.1 the identification and management of risks;

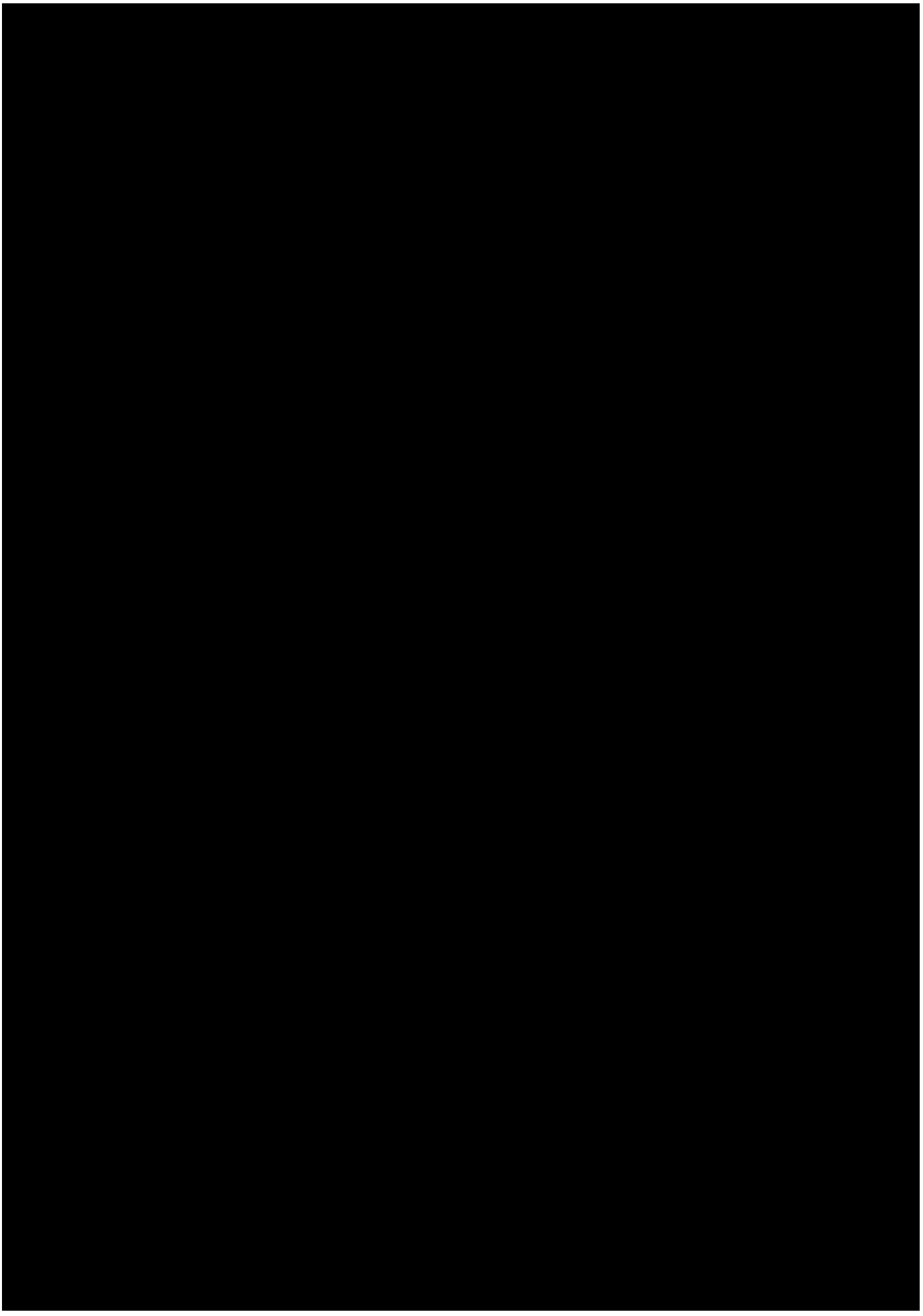
4.2.2 the identification and management of issues; and

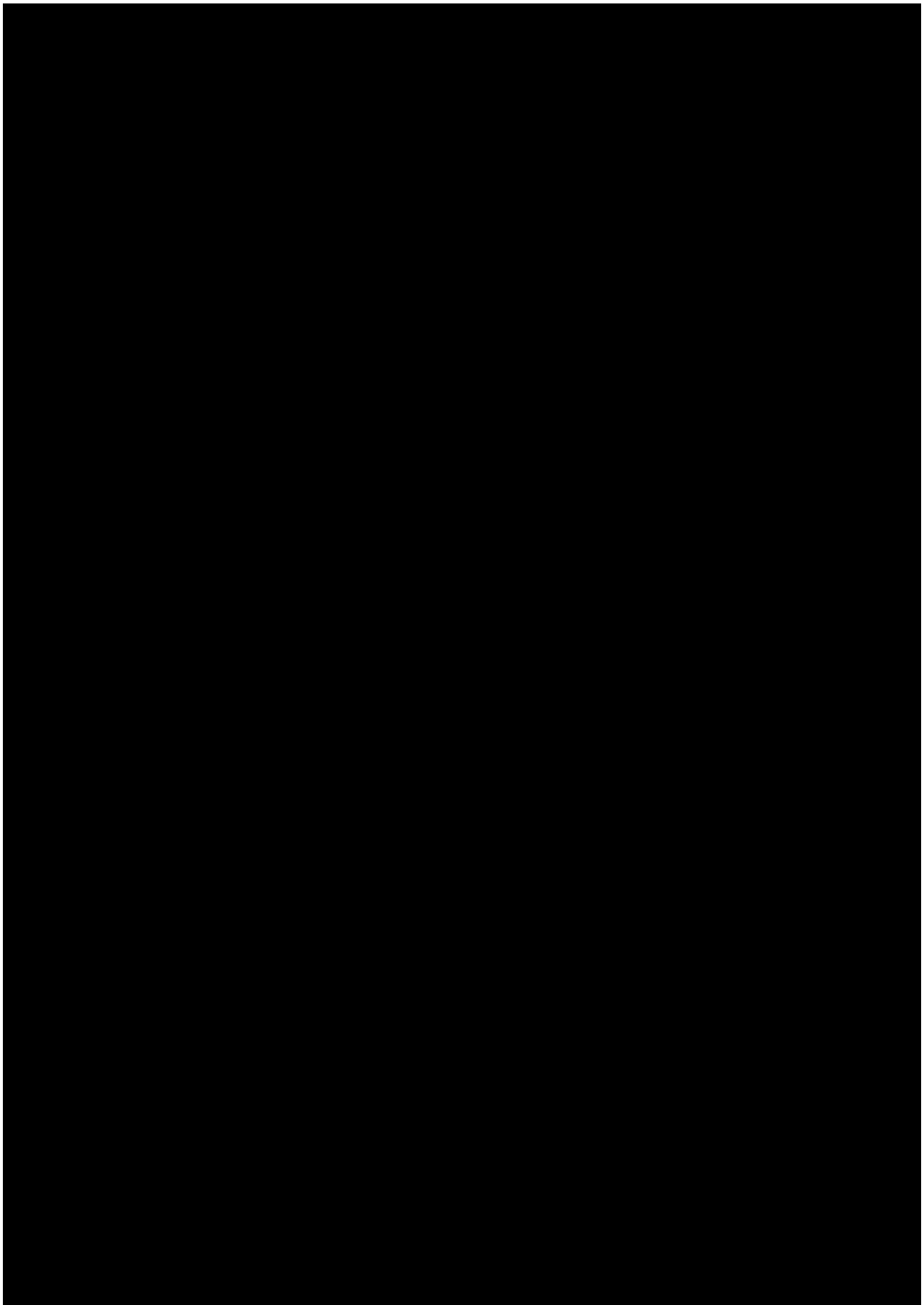
4.2.3 monitoring and controlling project plans.

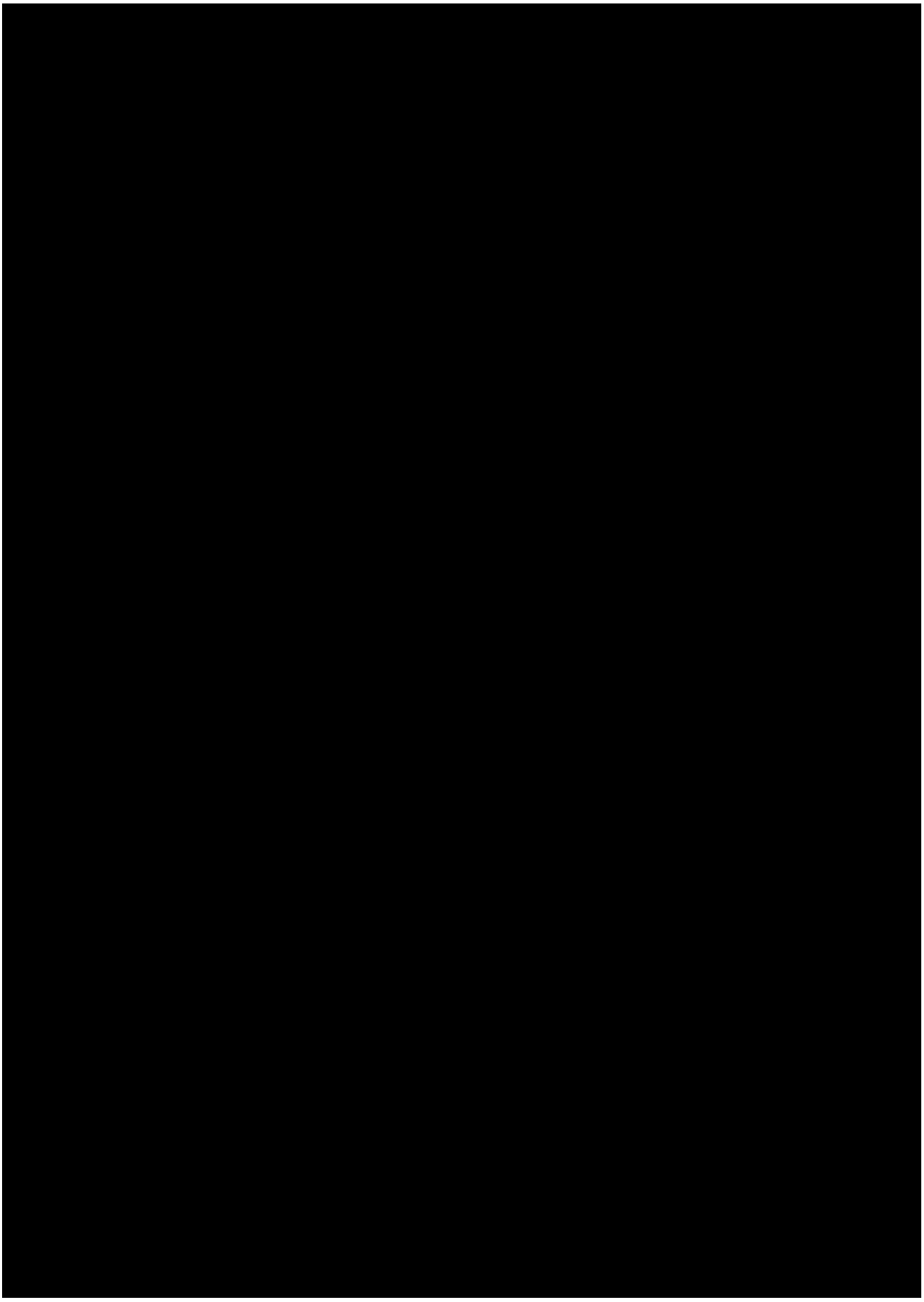
4.3 The Supplier allows the Buyer to inspect at any time within working hours the accounts and records which the Supplier is required to keep.

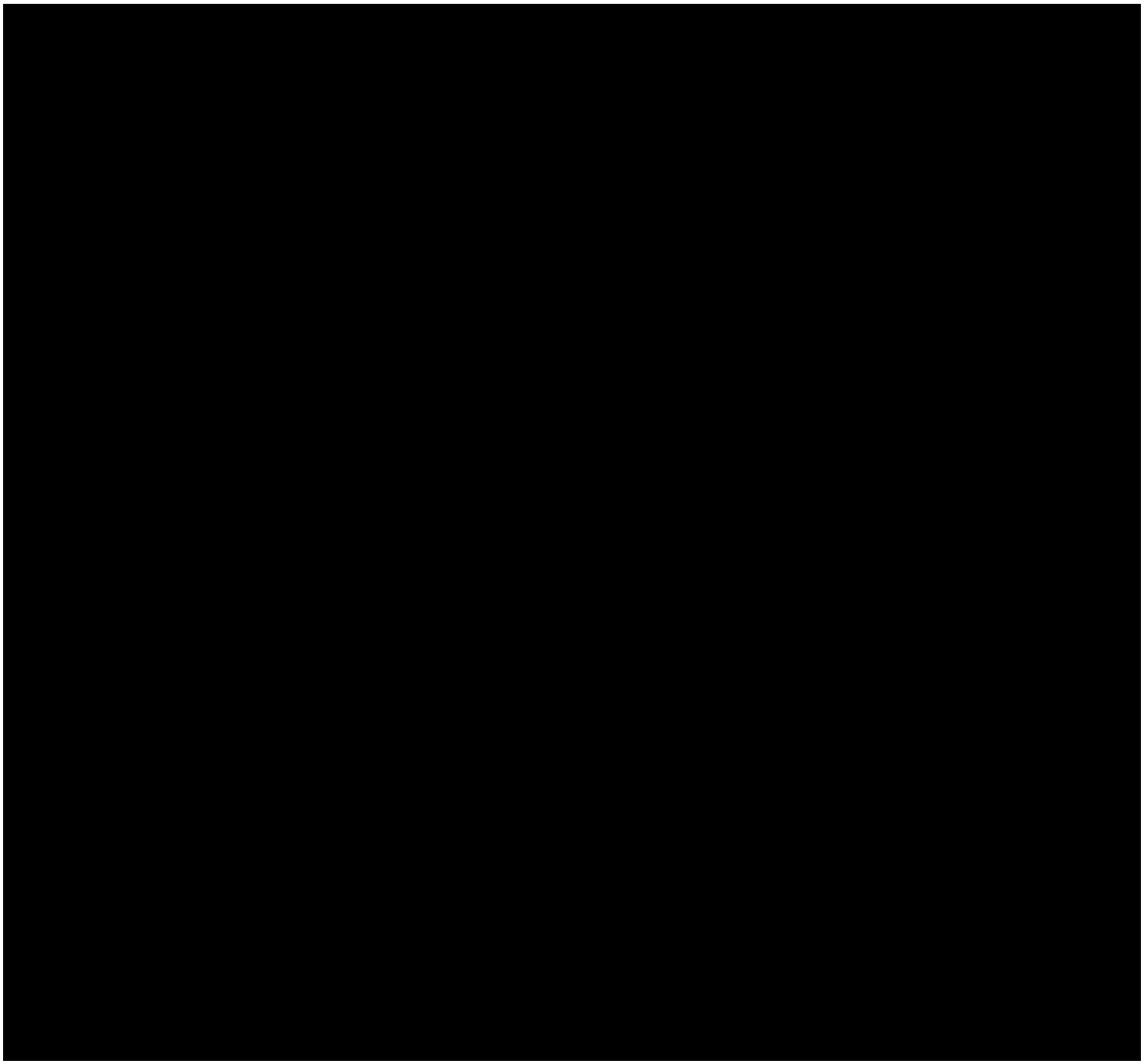
4.4 The Supplier will maintain a risk register of the risks relating to the Contract which the Buyer and the Supplier have identified.











Schedule 20 (Processing Data)

Status of the Controller

1. The Parties acknowledge that for the purposes of the Data Protection Legislation, the nature of the activity carried out by each of them in relation to their respective obligations under a Contract dictates the status of each party under the DPA. A Party may act as:

(a) "Controller" in respect of the other Party who is "Processor";

(b) "Processor" in respect of the other Party who is "Controller";

(c) "Joint Controller" with the other Party;

(d) "Independent Controller" of the Personal Data where the other Party is also "Controller",

in respect of certain Personal Data under a Contract and shall specify in Annex 1 *(Processing Personal Data)* which scenario they think shall apply in each situation.

Where one Party is Controller and the other Party its Processor

2. Where a Party is a Processor, the only Processing that it is authorised to do is listed in Annex 1 *(Processing Personal Data*) by the Controller.

3. The Processor shall notify the Controller immediately if it considers that any of the Controller's instructions infringe the Data Protection Legislation.

4. The Processor shall provide all reasonable assistance to the Controller in the preparation of any Data Protection Impact Assessment prior to commencing any Processing. Such assistance may, at the discretion of the Controller, include:

(a) a systematic description of the envisaged Processing and the purpose of the Processing;

(b) an assessment of the necessity and proportionality of the Processing in relation to the Services;

(c) an assessment of the risks to the rights and freedoms of Data Subjects; and

(d) the measures envisaged to address the risks, including safeguards, security measures and mechanisms to ensure the protection of Personal Data.

5. The Processor shall, in relation to any Personal Data Processed in connection with its obligations under the Contract:

(a) Process that Personal Data only in accordance with Annex 1 *(Processing Personal Data*), unless the Processor is required to do otherwise by Law. If it is

so required the Processor shall notify the Controller before Processing the Personal Data unless prohibited by Law;

(b) ensure that it has in place Protective Measures, including in the case of the Supplier the measures set out in Clause 14.3 of the Core Terms*,* which the Controller may reasonably reject (but failure to reject shall not amount to approval by the Controller of the adequacy of the Protective Measures) having taken account of the:

(i) nature of the data to be protected;

(ii) harm that might result from a Personal Data Breach;

(iii) state of technological development; and

(iv) cost of implementing any measures;

(c) ensure that :

(i) the Processor Personnel do not Process Personal Data except in accordance with the Contract (and in particular Annex 1 *(Processing Personal Data*));

(ii) it takes all reasonable steps to ensure the reliability and integrity of any Processor Personnel who have access to the Personal Data and ensure that they:

(A) are aware of and comply with the Processor's duties under this Schedule 20, Clauses 14 (*Data protection*), 15 (*What you must keep confidential*) and 16 (*When you can share information*);

(B) are subject to appropriate confidentiality undertakings with the Processor or any Subprocessor;

(C) are informed of the confidential nature of the Personal Data and do not publish, disclose or divulge any of the Personal Data to any third party unless directed in writing to do so by the Controller or as otherwise permitted by the Contract; and

(D) have undergone adequate training in the use, care, protection and handling of Personal Data;

(d) not transfer Personal Data outside of the EU unless the prior written consent of the Controller has been obtained and the following conditions are fulfilled:

(i) the Controller or the Processor has provided appropriate safeguards in relation to the transfer (whether in accordance with GDPR Article 46 or LED Article 37) as determined by the Controller;

(ii) the Data Subject has enforceable rights and effective legal remedies;

(iii) the Processor complies with its obligations under the Data Protection Legislation by providing an adequate level of protection to any Personal Data that is transferred (or, if it is not so bound, uses its best endeavours to assist the Controller in meeting its obligations); and

(iv) the Processor complies with any reasonable instructions notified to it in advance by the Controller with respect to the Processing of the Personal Data; and

(e) at the written direction of the Controller, delete or return Personal Data (and any copies of it) to the Controller on termination of the Contract unless the Processor is required by Law to retain the Personal Data.

6. Subject to paragraph 7 of this Schedule 20, the Processor shall notify the Controller immediately if in relation to it Processing Personal Data under or in connection with the Contract it:

(a) receives a Data Subject Access Request (or purported Data Subject Access Request);

(b) receives a request to rectify, block or erase any Personal Data;

(c) receives any other request, complaint or communication relating to either Party's obligations under the Data Protection Legislation;

(d) receives any communication from the Information Commissioner or any other regulatory authority in connection with Personal Data Processed under the Contract;

(e) receives a request from any third Party for disclosure of Personal Data where compliance with such request is required or purported to be required by Law; or

(f) becomes aware of a Personal Data Breach.

7. The Processor's obligation to notify under paragraph 6 of this Schedule 20 shall include the provision of further information to the Controller, as details become available.

8. Taking into account the nature of the Processing, the Processor shall provide the Controller with assistance in relation to either Party's obligations under Data Protection Legislation and any complaint, communication or request made under paragraph 6 of this Schedule 20 (and insofar as possible within the timescales reasonably required by the Controller) including by immediately providing:

(a) the Controller with full details and copies of the complaint, communication or request;

(b) such assistance as is reasonably requested by the Controller to enable it to comply with a Data Subject Access Request within the relevant timescales set out in the Data Protection Legislation;

(c) the Controller, at its request, with any Personal Data it holds in relation to a Data Subject;

(d) assistance as requested by the Controller following any Personal Data Breach; and/or

(e) assistance as requested by the Controller with respect to any request from the Information Commissioner's Office, or any consultation by the Controller with the Information Commissioner's Office.

9. The Processor shall maintain complete and accurate records and information to demonstrate its compliance with this Schedule 20. This requirement does not apply where the Processor employs fewer than 250 staff, unless:

(a) the Controller determines that the Processing is not occasional;

(b) the Controller determines the Processing includes special categories of data as referred to in Article 9(1) of the GDPR or Personal Data relating to criminal convictions and offences referred to in Article 10 of the GDPR; or

(c) the Controller determines that the Processing is likely to result in a risk to the rights and freedoms of Data Subjects.

10. The Processor shall allow for audits of its Data Processing activity by the Controller or the Controller's designated auditor.

11. The Parties shall designate a Data Protection Officer if required by the Data Protection Legislation.

12. Before allowing any Subprocessor to Process any Personal Data related to the Contract, the Processor must:

(a) notify the Controller in writing of the intended Subprocessor and Processing;

(b) obtain the written consent of the Controller;

(c) enter into a written agreement with the Subprocessor which give effect to the terms set out in this Schedule 20 such that they apply to the Subprocessor; and

(d) provide the Controller with such information regarding the Subprocessor as the Controller may reasonably require.

13. The Processor shall remain fully liable for all acts or omissions of any of its Subprocessors.

14. The Buyer may, at any time on not less than 30 Working Days' notice, revise this Schedule 20 by replacing it with any applicable controller to processor standard clauses or similar terms forming part of an applicable certification scheme (which shall apply when incorporated by attachment to the Contract).

15. The Parties agree to take account of any guidance issued by the Information Commissioner's Office. The Buyer may on not less than 30 Working Days' notice to the Supplier amend the Contract to ensure that it complies with any guidance issued by the Information Commissioner's Office.

Where the Parties are Joint Controllers of Personal Data

16. In the event that the Parties are Joint Controllers in respect of Personal Data under the Contract, the Parties shall implement paragraphs that are necessary to comply with GDPR Article 26 based on the terms set out in Annex 2 to this Schedule 20 (*Processing Data*).

Independent Controllers of Personal Data

17. With respect to Personal Data provided by one Party to another Party for which each Party acts as Controller but which is not under the Joint Control of the Parties, each Party undertakes to comply with the applicable Data Protection Legislation in respect of their Processing of such Personal Data as Controller.

18. Each Party shall Process the Personal Data in compliance with its obligations under the Data Protection Legislation and not do anything to cause the other Party to be in breach of it.

19. Where a Party has provided Personal Data to the other Party in accordance with paragraph 7 of this Schedule 20 above, the recipient of the Personal Data will provide all such relevant documents and information relating to its data protection policies and procedures as the other Party may reasonably require.

20. The Parties shall be responsible for their own compliance with Articles 13 and 14 GDPR in respect of the Processing of Personal Data for the purposes of the Contract.

21. The Parties shall only provide Personal Data to each other:

(a) to the extent necessary to perform their respective obligations under the Contract;

(b) in compliance with the Data Protection Legislation (including by ensuring all required data privacy information has been given to affected Data Subjects to meet the requirements of Articles 13 and 14 of the GDPR); and

(c) where it has recorded it in Annex 1 *(Processing Personal Data).*

22. Taking into account the state of the art, the costs of implementation and the nature, scope, context and purposes of Processing as well as the risk of varying likelihood and severity for the rights and freedoms of natural persons, each Party shall, with respect to its Processing of Personal Data as Independent Controller, implement and maintain appropriate technical and organisational measures to ensure a level of security appropriate to that risk, including, as appropriate, the measures referred to in Article 32(1)(a), (b), (c) and (d) of the GDPR, and the measures shall, at a minimum, comply with the requirements of the Data Protection Legislation, including Article 32 of the GDPR.

23. A Party Processing Personal Data for the purposes of the Contract shall maintain a record of its Processing activities in accordance with Article 30 GDPR and shall make the record available to the other Party upon reasonable request.

24. Where a Party receives a request by any Data Subject to exercise any of their rights under the Data Protection Legislation in relation to the Personal Data provided to it by the other Party pursuant to the Contract **("Request Recipient")**:

(a) the other Party shall provide any information and/or assistance as reasonably requested by the Request Recipient to help it respond to the request or correspondence, at the cost of the Request Recipient; or

(b) where the request or correspondence is directed to the other Party and/or relates to that other Party's Processing of the Personal Data, the Request Recipient will:

(i) promptly, and in any event within five (5) Working Days of receipt of the request or correspondence, inform the other Party that it has received the same and shall forward such request or correspondence to the other Party; and

(ii) provide any information and/or assistance as reasonably requested by the other Party to help it respond to the request or correspondence in the timeframes specified by Data Protection Legislation.

25. Each Party shall promptly notify the other Party upon it becoming aware of any Personal Data Breach relating to Personal Data provided by the other Party pursuant to the Contract and shall:

(a) do all such things as reasonably necessary to assist the other Party in mitigating the effects of the Personal Data Breach;

(b) implement any measures necessary to restore the security of any compromised Personal Data;

(c) work with the other Party to make any required notifications to the Information Commissioner's Office and affected Data Subjects in accordance with the Data Protection Legislation (including the timeframes set out therein); and

(d) not do anything which may damage the reputation of the other Party or that Party's relationship with the relevant Data Subjects, save as required by Law.

26. Personal Data provided by one Party to the other Party may be used exclusively to exercise rights and obligations under the Contract as specified in Annex 1 *(Processing Personal Data).*

27. Personal Data shall not be retained or processed for longer than is necessary to perform each Party's respective obligations under the Contract which is specified in Annex 1 *(Processing Personal Data)*.

28. Notwithstanding the general application of paragraphs 2 to 15 of this Schedule 20 to Personal Data, where the Supplier is required to exercise its regulatory and/or legal obligations in respect of Personal Data, it shall act as an Independent Controller of Personal Data in accordance with paragraphs16 to 27 of this Schedule 20.

Annex 1 - Processing Personal Data

This Annex shall be completed by the Controller, who may take account of the view of the Processors, however the final decision as to the content of this Annex shall be with the Buyer at its absolute discretion.

1.1 The Processor shall comply with any further written instructions with respect to Processing by the Controller.
1.2 Any such further instructions shall be incorporated into this Annex.

Description	Details
Identity of Controller for each Category of Personal Data	**The Buyer is Controller and the Supplier is Processor** The Parties acknowledge that in accordance with paragraph 2 to paragraph 15 and for the purposes of the Data Protection Legislation, the Buyer is the Controller and the Supplier is the Processor of the following Personal Data: ● No specific personal data has been identified as required to be processed.
Duration of the Processing	The duration of the Contract
Nature and purposes of the Processing	
Type of Personal Data	
Categories of Data Subject	

Plan for return and destruction of the data once the Processing is complete UNLESS requirement under Union or Member State law to preserve that type of data	

Schedule 21 (Variation Form)

This form is to be used in order to change a contract in accordance with Clause 24 of the Core Terms (Changing the Contract)

Contract Details		
This variation is between:	**[**Buyer**]** (**"the Buyer"**) And **[insert** name of Supplier**]** (**"the Supplier"**)	
Contract name:	**[insert** name of contract to be changed] **("the Contract")**	
Contract reference number:	**[insert** contract reference number]	
Details of Proposed Variation		
Variation initiated by:	**[delete** as applicable: Buyer/Supplier]	
Variation number:	**[insert** variation number]	
Date variation is raised:	**[insert** date]	
Proposed variation		
Reason for the variation:	**[insert** reason]	
An Impact Assessment shall be provided within:	**[insert** number] days	
Impact of Variation		
Likely impact of the proposed variation:	**[Supplier to insert** assessment of impact]	
Outcome of Variation		
Contract variation:	This Contract detailed above is varied as follows: • **[Buyer to insert** original Clauses or Paragraphs to be varied and the changed clause]	
Financial variation:	Original Contract Value:	£ **[insert** amount]
	Additional cost due to variation:	£ **[insert** amount]
	New Contract value:	£ **[insert** amount]

1. This Variation must be agreed and signed by both Parties to the Contract and shall only be effective from the date it is signed by the Buyer

2. Words and expressions in this Variation shall have the meanings given to them in the Contract.

3. The Contract, including any previous Variations, shall remain effective and unaltered except as amended by this Variation.

Signed by an authorised signatory for and on behalf of the Buyer

Signature .....

Date .....

Name (in Capitals) .....

Address .....

.....

Signed by an authorised signatory to sign for and on behalf of the Supplier

Signature .....

Date .....

Name (in Capitals) .....

Address .....

Schedule 22 (Insurance Requirements)

1. The insurance you need to have

1.1 The Supplier shall take out and maintain or procure the taking out and maintenance of the insurances as set out in the Annex to this Schedule and any other insurances as may be required by applicable Law (together the "**Insurances**"). The Supplier shall ensure that each of the Insurances is effective no later than

the Start Date in respect of those Insurances set out in the Annex to this Schedule and those required by applicable Law; and

1.2 The Insurances shall be:

1.2.1 maintained in accordance with Good Industry Practice;

1.2.2 (so far as is reasonably practicable) on terms no less favourable than those generally available to a prudent contractor in respect of risks insured in the international insurance market from time to time;

1.2.3 taken out and maintained with insurers of good financial standing and good repute in the international insurance market; and

1.2.4 maintained for at least six (6) years after the End Date.

2. How to manage the insurance

2.1 Without limiting the other provisions of this Contract, the Supplier shall:

2.1.1 take or procure the taking of all reasonable risk management and risk control measures in relation to Deliverables as it would be reasonable to expect of a prudent contractor acting in accordance with Good Industry Practice, including the investigation and reports of relevant claims to insurers;

2.1.2 promptly notify the insurers in writing of any relevant material fact under any Insurances of which the Supplier is or becomes aware; and

2.1.3 hold all policies in respect of the Insurances and cause any insurance broker effecting the Insurances to hold any insurance slips and other evidence of placing cover representing any of the Insurances to which it is a party.

3. What happens if you aren't insured

3.1 The Supplier shall not take any action or fail to take any action or (insofar as is reasonably within its power) permit anything to occur in relation to it which would entitle any insurer to refuse to pay any claim under any of the Insurances.

3.2 Where the Supplier has failed to purchase or maintain any of the Insurances in full force and effect, the Buyer may elect (but shall not be obliged) following written notice to the Supplier to purchase the relevant Insurances and recover the reasonable premium and other reasonable costs incurred in connection therewith as a debt due from the Supplier.

4. Evidence of insurance you must provide

4.1 The Supplier shall upon the Start Date and within 15 Working Days after the renewal of each of the Insurances, provide evidence, in a form satisfactory to the Buyer, that the Insurances are in force and effect and meet in full the requirements of this Schedule.

5. Making sure you are insured to the required amount

5.1 The Supplier shall ensure that any Insurances which are stated to have a minimum limit "in the aggregate" are maintained at all times for the minimum limit of indemnity specified in this Contract and if any claims are made which do not relate to this Contract then the Supplier shall notify the Buyer and provide details of its proposed solution for maintaining the minimum limit of indemnity.

6. Cancelled Insurance

6.1 The Supplier shall notify the Buyer in writing at least five (5) Working Days prior to the cancellation, suspension, termination or non-renewal of any of the Insurances.

6.2 The Supplier shall ensure that nothing is done which would entitle the relevant insurer to cancel, rescind or suspend any insurance or cover, or to treat any insurance, cover or claim as voided in whole or part. The Supplier shall use all reasonable endeavours to notify the Buyer (subject to third party confidentiality obligations) as soon as practicable when it becomes aware of any relevant fact, circumstance or matter which has caused, or is reasonably likely to provide grounds to, the relevant insurer to give notice to cancel, rescind, suspend or void any insurance, or any cover or claim under any insurance in whole or in part.

7. Insurance claims

7.1 The Supplier shall promptly notify to insurers any matter arising from, or in relation to, the Deliverables, or the Contract for which it may be entitled to claim under any of the Insurances. In the event that the Buyer receives a claim relating to or arising out of the Contract or the Deliverables, the Supplier shall co-operate with the Buyer and assist it in dealing with such claims including without limitation providing information and documentation in a timely manner.

7.2 Except where the Buyer is the claimant party, the Supplier shall give the Buyer notice within twenty (20) Working Days after any insurance claim in excess of 10% of the sum required to be insured pursuant to Paragraph 5.1 relating to or arising out of the provision of the Deliverables or this Contract on any of the Insurances or which, but for the application of the applicable policy excess, would be made on any of the Insurances and (if required by the Buyer) full details of the incident giving rise to the claim.

7.3 Where any Insurance requires payment of a premium, the Supplier shall be liable for and shall promptly pay such premium.

7.4 Where any Insurance is subject to an excess or deductible below which the indemnity from insurers is excluded, the Supplier shall be liable for such excess

or deductible. The Supplier shall not be entitled to recover from the Buyer any sum paid by way of excess or deductible under the Insurances whether under the terms of this Contract or otherwise.

[redacted]

[redacted]

[redacted]

[redacted]

[redacted]

[redacted]

[redacted]

[redacted]

[redacted]

Schedule 27 (Key Subcontractors)

Not Applicable

Schedule 32 (Background Checks)

Not Applicable