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**Genomics facility request form**

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| Name |  |
| Group |  |
| Dept |  |
| email |  |

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| Brief description of your project |
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| --- | --- |
| Have you got low input material? |  |
| Which library type is required? | DNA | RNA |
| If submitting RNA samples, how do you prefer to have them depleted of ribosomal RNA? | PolyA isolation | RiboZero depletion |
| How many samples? |  |
| ERCC spike-ins required (for RNA)? |  |
| Run type for sequencing? | SE50 | PE150 |
| How many lanes on a HiSeq 4000? |  |
| Species |  |
| If you are submitting human samples, have you got ethical consent? |  |
| Who is doing the bioinformatic analysis? (contact email for when data become available) |  |
| Grant code, if available |  |

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| --- | --- |
| How was the DNA/RNA prepared? |  |
| How was the material quantified? |  |
| Have you done a DNAse digest (for RNA) / RNAse digest (for DNA)? |  |
| In what volume is the sample supplied? |  |
| Will you need to keep the libraries and any leftover material? (Please arrange a handover when project completed!) |  |

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| Any extra information? |
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