Question: Can USDA confirm the species represented in the 110 tissue samples? The Statement of Work references research involving goats, sheep, and rodents, but the species for the samples to be sequenced are not explicitly stated. If multiple species are anticipated during the contract period, please provide an estimated breakdown.

Answer: We do not know the number or ratios, because the animal experiments have not started yet. Tentatively 40 lambs (sheep) and 70 rodents.

Question: Regarding the tissue samples from goats, sheep, and rodents: Will any of these contain parasites? If so, what specific protocols have been implemented to ensure the tissues are safe for handling?

Answer: Yes. The tissues are stored in TRIzol

Question: What is the biosafety level (BSL) associated with these tissue samples?

Answer: BSL2

Question: What specific type(s) of tissue will you be sending?

Answer: Intestine

Question: What is the expected amount or volume of tissue per sample?

Answer: Sufficient for >100 ug of total RNA (or ~2 cm in length of the intestine)

Question: You mentioned "providing digital gene expression signature profiles with full data analysis." Could you clarify if standard differential gene expression analysis is sufficient, or if you require any specific downstream analysis beyond that?

Answer: Standard gene expression analysis is sufficient (must include software version and parameters used, raw count table, FPKM table, DEG results and annotation), but the raw sequence data will need to be deposited to NCBI SRA wit PI's permission.

Question: Will your project require strand-specific information?

Answer: Yes

Question: Do you plan to send the samples altogether in one batch? If they will be split up, how many batches should we expect, and how many samples will be in each?

Answer: Up to two batches. The number of samples in each batch may vary.

Question: What type of RNA pre-processing is required for your project (e.g., poly-A selection or rRNA depletion)?

Answer: rRNA depletion is required.