**Sample Information**

1. Species
2. Sample Name
3. Alternate Names
4. Sample ID
5. Sex
6. Age
7. Date of death
8. Hours postmortem that the sample was collected
9. Cause of death
10. Possible other health conditions
11. Source
12. Ethnicity/subspecies/admixture

**RNA-Seq Information**

1. RNA-seq flow cell number
2. Run ID
3. Flow-cell ID
4. Machine ID
5. Run number
6. Run date
7. Sequencing location
8. Sequence encoding
9. Lane number on the flow cell
10. Multiplexing mix
11. Samples in the multiplexing mixes

**RNA-seq and processing information (note: there is some overlap with the previous section)**

1. Individual
2. Tissue
3. RNA concentration
4. RNA extraction date
5. RIN score
6. Library ID
7. Library concentration
8. Library fragments size (bp)
9. Library preparation date
10. Multiplexing index ID / Multiplexing index sequence
11. In multiplexing mix number 1
12. In multiplexing mix number 2
13. In multiplexing mix number 3
14. In multiplexing mix number 4
15. Total number of reads sequenced
16. Percentage of bp trimmed (adaptors)
17. Number of reads shorter than 20bp removed
18. Minimum read length after trimming
19. Maximum read length after trimming
20. Total number of reads processed in TopHat
21. Total number of mapped reads
22. Total number of unmapped reads
23. Percentage of mapped reads
24. Percentage of mapped reads overlapping a junction
25. Number of junctions
26. Number of reads mapped on orthologous exons
27. Number of orthologous exons with at least 1 mapped read
28. Number of orthologous genes with at least 1 mapped read

**BS-seq flow cell layout**

1. BS-seq flow cell
2. Run ID
3. Flow cell ID
4. Machine ID
5. Run number
6. Run date
7. Sequencing location
8. Sequence encoding
9. Lane
10. Condition
11. Multiplexing index ID
12. Read length
13. DNA concentration (ng/uL)
14. Library fragments size (bp)
15. Library concentration (ng/uL)
16. Library preparation date

**BS-seq and processing information**

1. Number of sequenced reads
2. Number of reads after trimming
3. Percentage of reads removed after trimming
4. Number of mapped reads
5. Mapping efficiency
6. Number of reads after deduplication
7. Percentage of duplication
8. Number 5’ nucleotides ignored for methylation extraction
9. Number of CpG sites covered
10. Percentage of methylation in CpG context
11. Percentage of methylation in non-CpG context
12. Number of reads mapped to lambda phage genome
13. Coverage on lambda phage DNA
14. Conversion efficiency of lambda phage DNA
15. Number of reads used for methylation extraction
16. Number of CpG sites with at least 1X coverage
17. Number of CpG sites with at least 2X coverage
18. Number of CpG sites with at least 4X coverage
19. Mean coverage at orthologous CpG sites
20. Proportion of orthologous CpG sites with low methylation
21. Proportion of orthologous CpG sites with intermediation methylation
22. Proportion of orthologous CpG sites with high methylation
23. Mean methylation level at orthologous CpG sites

***The following variables from the above list were tested as potential confounders with tissue and species (our biological variables of interest) with gene expression information. The first 5 are “sanity check” variables (because we know what the pattern should be with PCs).***

1. Sample ID
2. Sample name
3. Species
4. Tissue
5. Individual
6. RNA extraction date
7. Multiplexing index sequence
8. Multiplexing mixes code
9. Sequenced at UCGF or not
10. Total number of reads sequenced
11. Percentage of bp trimmed (adaptors)
12. Number of reads shorter than 20bp removed
13. Maximum read length after trimming
14. Total number of reads processed in TopHat
15. Total number of mapped reads
16. Percentage of mapped reads overlapping a junction
17. Number of junctions
18. Number of reads mapped on orthologous exons
19. Number of orthologous exons with at least 1 mapped read
20. Number of orthologous genes with at least 1 mapped read
21. RNA concentration
22. RIN score
23. Library concentration
24. Library fragments size

***The following variables from the above list were tested as potential confounders with tissue and species (our biological variables of interest) with methylation information.***

1. Number of reads used for methylation extraction
2. Number of CpG sites with at least 1X coverage
3. Number of CpG sites with at least 2X coverage
4. Number of CpG sites with at least 4X coverage
5. Mean coverage at orthologous CpG sites
6. Proportion of orthologous CpG sites with low methylation
7. Proportion of orthologous CpG sites with intermediation methylation
8. Proportion of orthologous CpG sites with high methylation
9. Mean methylation level at orthologous CpG sites
10. Number of sequenced reads
11. Number of reads after trimming
12. Number of mapped reads
13. Number of reads after deduplication
14. Number of 5’ nt ignored for methylation extraction (averaged over technical replicates)
15. Percentage of methylation in non-CpG context (averaged over technical replicates)
16. Number of reads mapped to the lambda phage genome (averaged over technical replicates)
17. Coverage on the lambda phage genome (averaged over technical replicates)
18. Conversion efficiency of lambda phage DNA (averaged over technical replicates)
19. Read length (averaged over technical replicates)
20. DNA concentration (averaged over technical replicates)
21. Library fragments size (averaged over technical replicates)
22. Library concentration (averaged over technical replicates)
23. Number of libraries
24. Flowcell
25. Library preparation date
26. Multiplexing index ID
27. Machine ID
28. Sequencing location
29. Sequence encoding