Genome Report Requirements

1. *Title*: Include the organism and/or strain names (e.g. Genome Report: Whole genome sequence of two wild-derived Mus musculus domesticus inbred strains, LEWES/EiJ and ZALENDE/EiJ, with different diploid numbers.).
2. *Keywords*: Include the relevant organism and strain names.
3. *Abstract*: ~250 words. Concise summary of the results.
4. Introduction: No more than 500 words. The introduction should discuss the rationale for the WGS of the particular organism/strain.
5. *Methods & Materials:* Include the following (note: author may write additional subheadings as appropriate – the below points are not designed to be a list of complete subheadings, but rather, topics to be covered).
   * Organism/strain origin and derivation
   * Sequencing methods and preparation details
   * Data processing methods
6. *Results and Discussion*: Include a description of the genomes, coverage amount of genome sequenced, details of sequence variants ascertained, identifications of deletions, comparison of strains/genomes (if reporting WGS of multiple strains/organisms), and relevance of findings to overall organism/strain catalog.
7. *Data Availability Statement*
   * Data availability listing where to access all raw reads, processed data, BWTs, and other relevant data. The assembly should be uploaded to [NCBI](http://www.ncbi.nlm.nih.gov/) or [ENA](http://www.ebi.ac.uk/ena)
8. *Acknowledgments*
9. *Conflict of Interest*
10. *Funder Information*
11. *Literature Cited*
12. *Title*: Genome Report: Whole genome sequence of two synthetically-derived *Brassica napus* inbred strain, DaAe).
13. *Keywords*: Canola, Allotetraploid, Rapeseed, Hi-C, Long Read Sequencing, etc…
14. *Abstract:* 
    * Alignment to other genomes
    * Size
    * Genes
    * HE
15. Introduction:
    * Economical value of the plant
    * Prevalence in agriculture
    * Increase oil output
16. *Methods & Materials:*
    * Organism/strain origin and derivation
      1. DaAe Creation
    * Sequencing methods and preparation details
      1. Hi-C, PacBio, 10X
    * Data processing methods
      1. Metrics
      2. Alignments
      3. HE Analysis
17. *Results and Discussion*: Include a description of the genomes, coverage amount of genome sequenced, details of sequence variants ascertained, identifications of deletions, comparison of strains/genomes (if reporting WGS of multiple strains/organisms), and relevance of findings to overall organism/strain catalog.
18. *Data Availability Statement*
    * https://submit.ncbi.nlm.nih.gov/subs/wgs/SUB7298190/overview
19. *Acknowledgments*
20. *Conflict of Interest*
21. *Funder Information*
22. *Literature Cited*