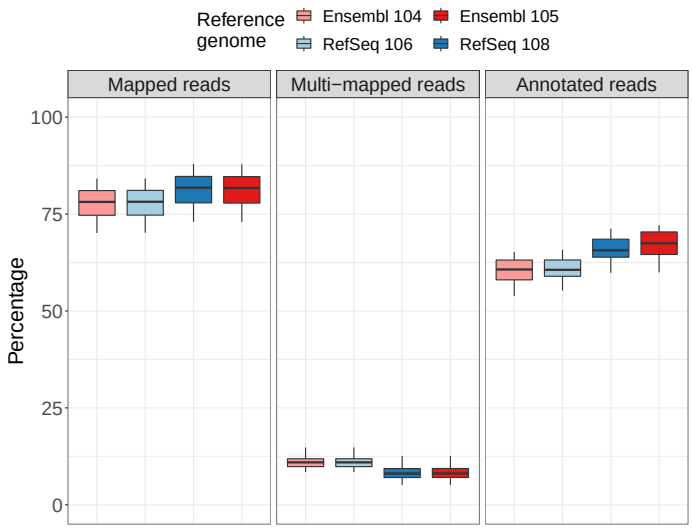
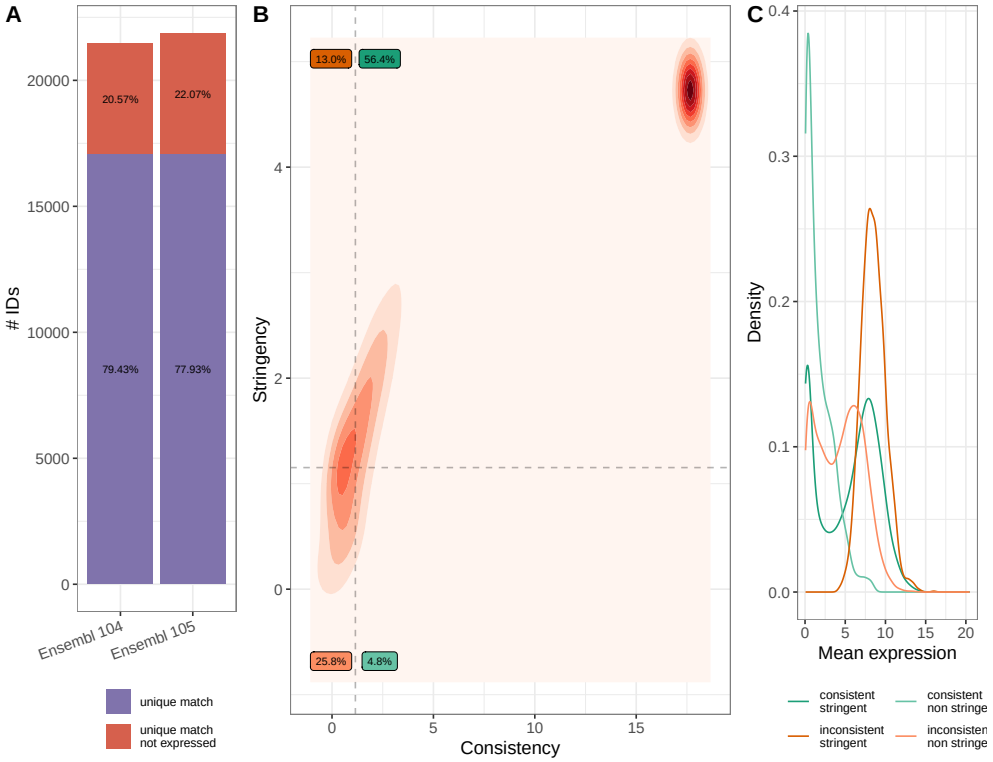
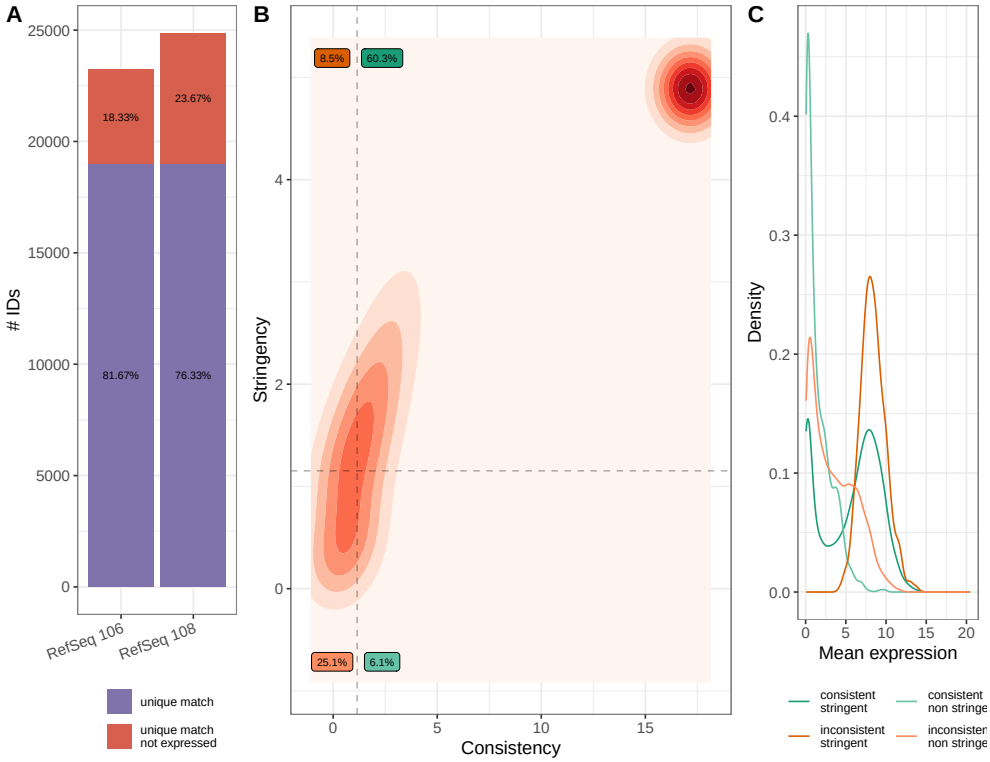


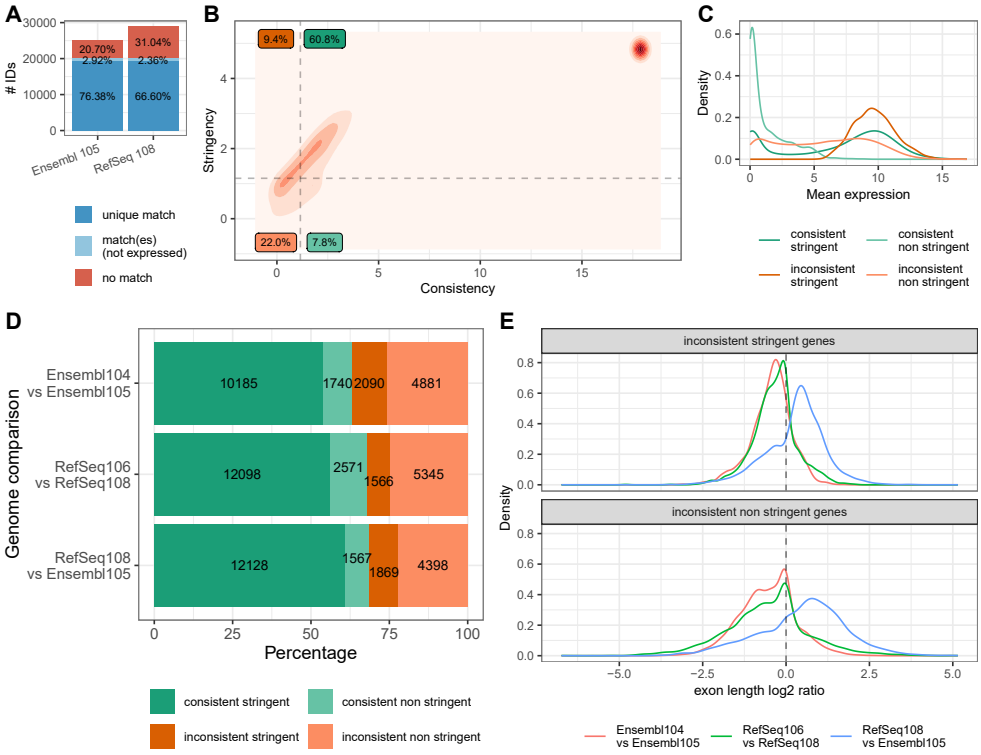
Supplementary fig. 1 Read mapping statistics with respect to *Rattus norvegicus* reference genomes for the GSE140420 dataset. The raw sequencing reads of all the samples of GSE179101 dataset were trimmed for adpaters and quality before being aligned against *Rattus norvegicus* reference genomes and assigned to annotations.



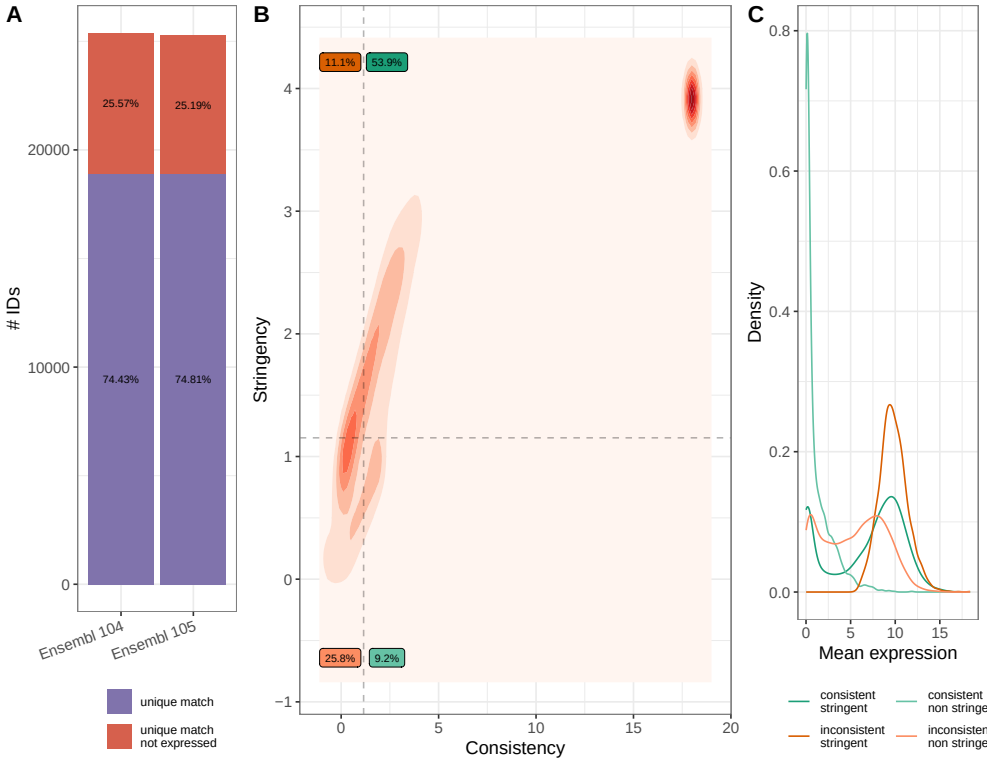
Supplementary fig. 2 Consistency and stringency of Ensembl 104 and Ensembl 105 *Rattus norvegicus* reference genomes for the analysis of GSE179101 dataset. A: gene identifier matching, B: consistency and stringency for all expressed genes in both matrices, C: distribution of mean expression of all the genes expressed in the matrix generated with Ensembl 105 genome.



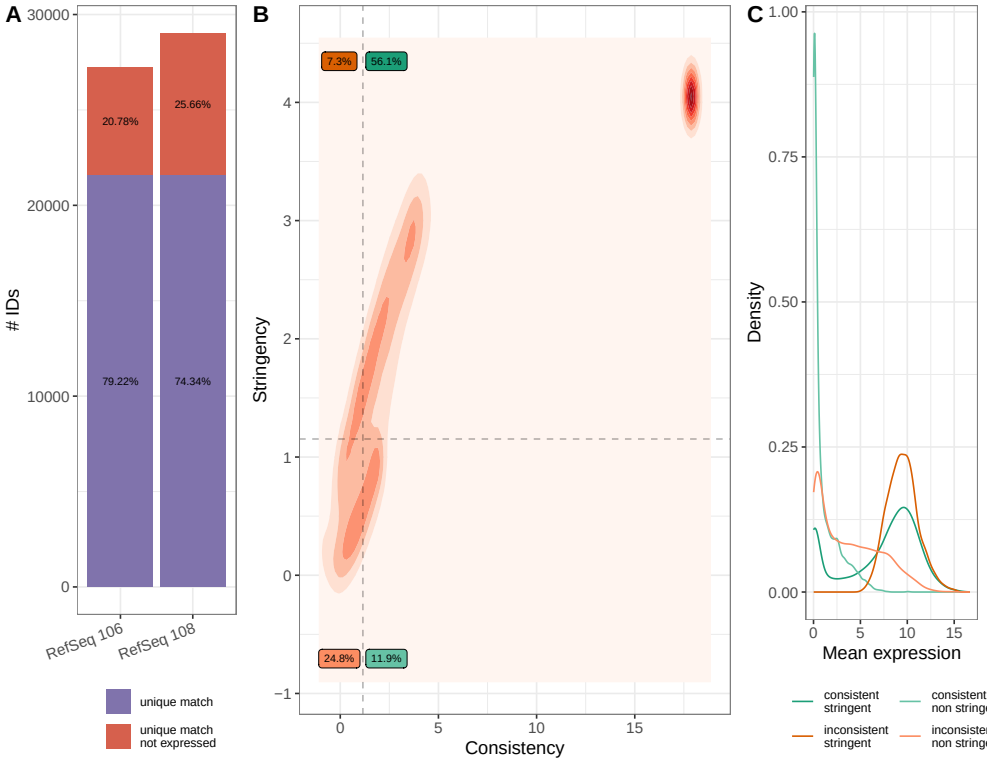
Supplementary fig. 3 Consistency and stringency of RefSeq 106 and RefSeq 108 *Rattus norvegicus* reference genomes for the analysis of GSE179101 dataset. A: gene identifier matching, B: consistency and stringency for all expressed genes in both matrices, C: distribution of mean expression of all the genes expressed in the matrix generated with Ensembl 105 genome.



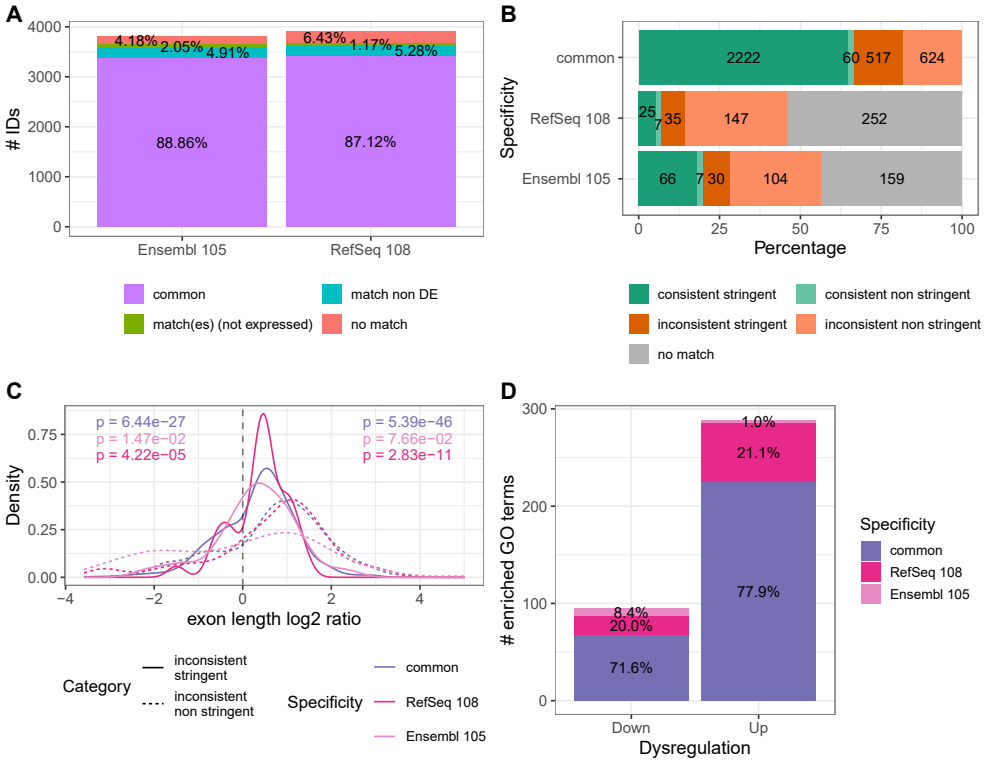
Supplementary fig. 4 Consistency and stringency of *Rattus norvegicus* reference genomes for the analysis of GSE140420 dataset. A: gene identifier matching, genes with multiple matches and genes whose match is not expressed were gathered in the same category, B: consistency and stringency for all expressed genes in both matrices, C: distribution of mean expression of all the genes expressed in the matrix generated with Ensembl 105 genome, D: gene counts per category defined by consistency and stringency for pairwise genome comparison, E: distribution of cumulative exon length ratio in the annotations of two reference genomes for inconsistent genes.



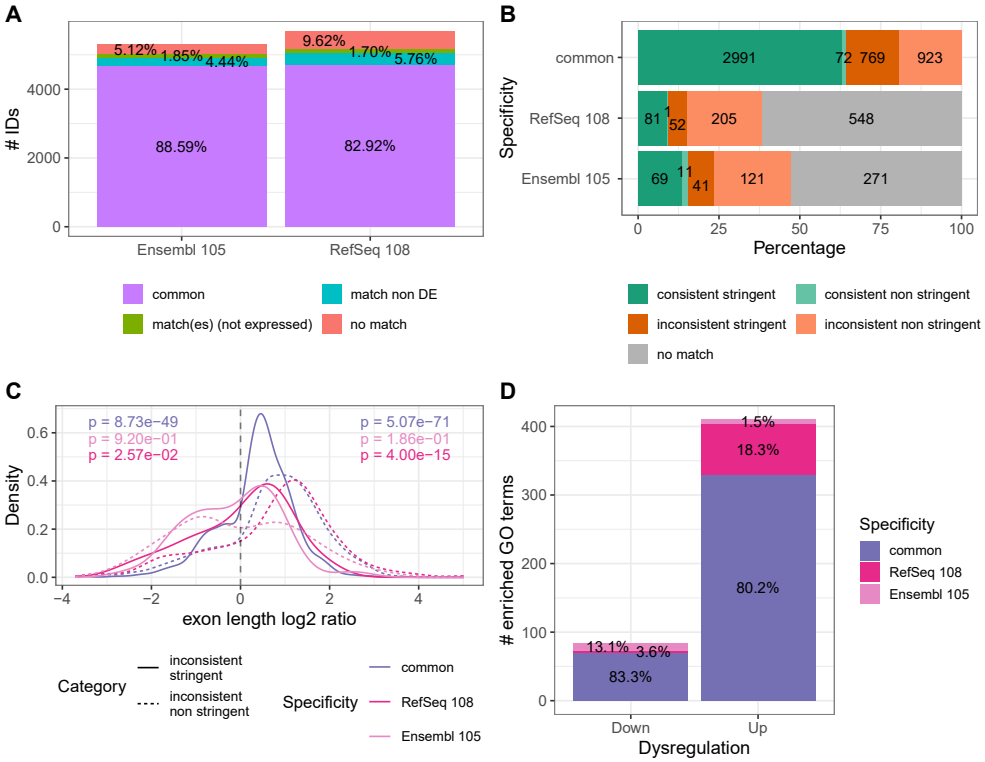
Supplementary fig. 5 Consistency and stringency of Ensembl 104 and Ensembl 105 *Rattus norvegicus* reference genomes for the analysis of GSE140420 dataset. A: gene identifier matching, B: consistency and stringency for all expressed genes in both matrices, C: distribution of mean expression of all the genes expressed in the matrix generated with Ensembl 105 genome.



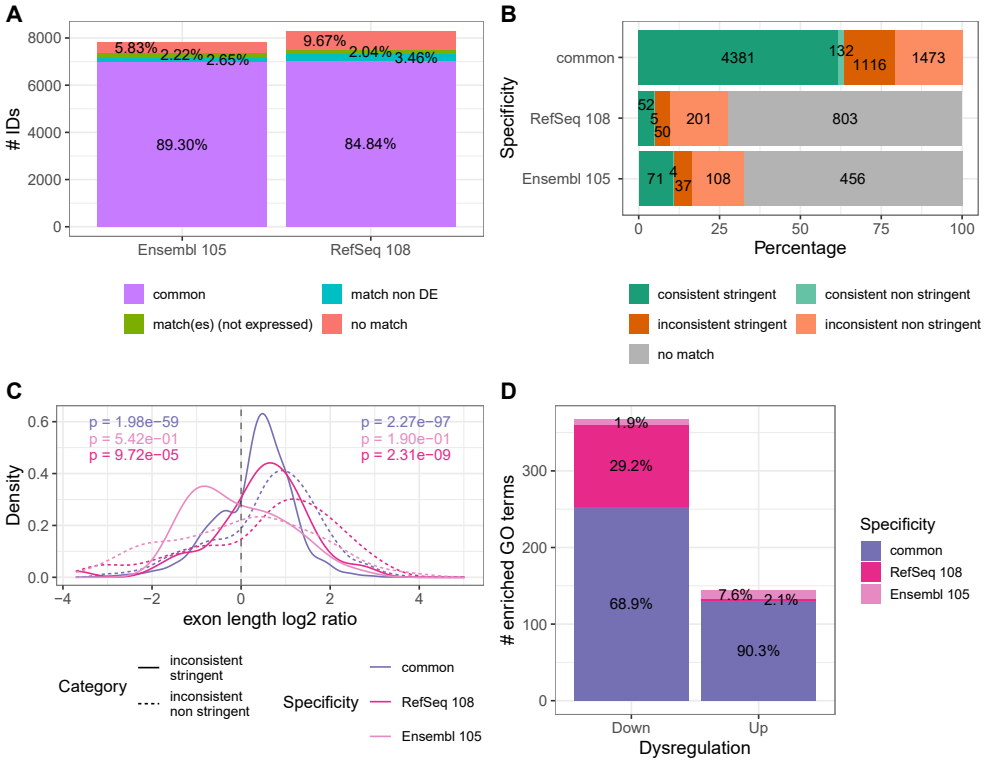
Supplementary fig. 6 Consistency and stringency of NCBI RefSeq 106 and NCBI RefSeq 108 *Rattus norvegicus* reference genomes for the analysis of GSE140420 dataset. A: gene identifier matching, B: consistency and stringency for all expressed genes in both matrices, C: distribution of mean expression of all the genes expressed in the matrix generated with RefSeq 108 genome.



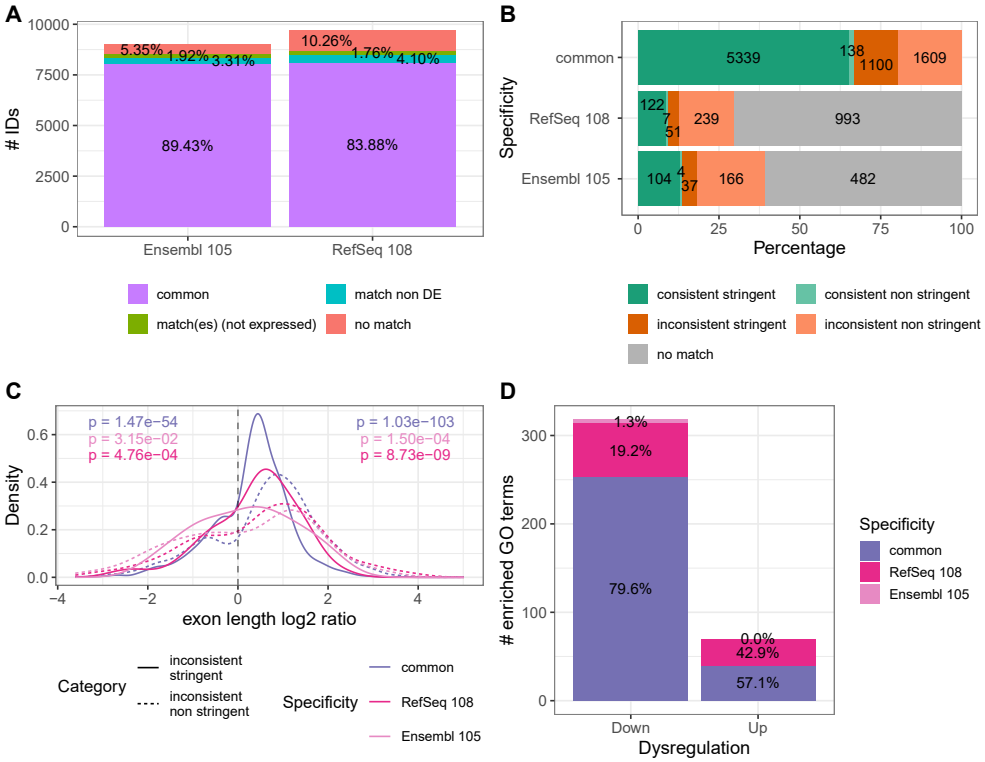
Supplementary fig. 7 Impact of *Rattus norvegicus* reference genomes on the comparison of CA2 subregion to other subregions. Samples of the CA1, CA2, CA3 and DG subregions from the GSE179101 dataset were used for the differenrial expression anlalysis. A: gene identifier matching, genes with multiple matches and genes whose match is not expressed were gathered in the same category, B: differentially expressed (DE) gene counts per category defined by consistency and stringency, C: distribution of cumulative exon length ratio in the annotations of the two reference genomes for inconsistent DE genes, p-values of one-sided Wilcoxon signed-rank tests for paired difference in exon length where the alternative is a greater exon length in RefSeq 108 annotations are displayed per specificity and for inconsistent stringent genes (left) and inconsistent non stringent genes (right). D: enriched Gene Ontology term counts among down-regulated and upregulated genes.



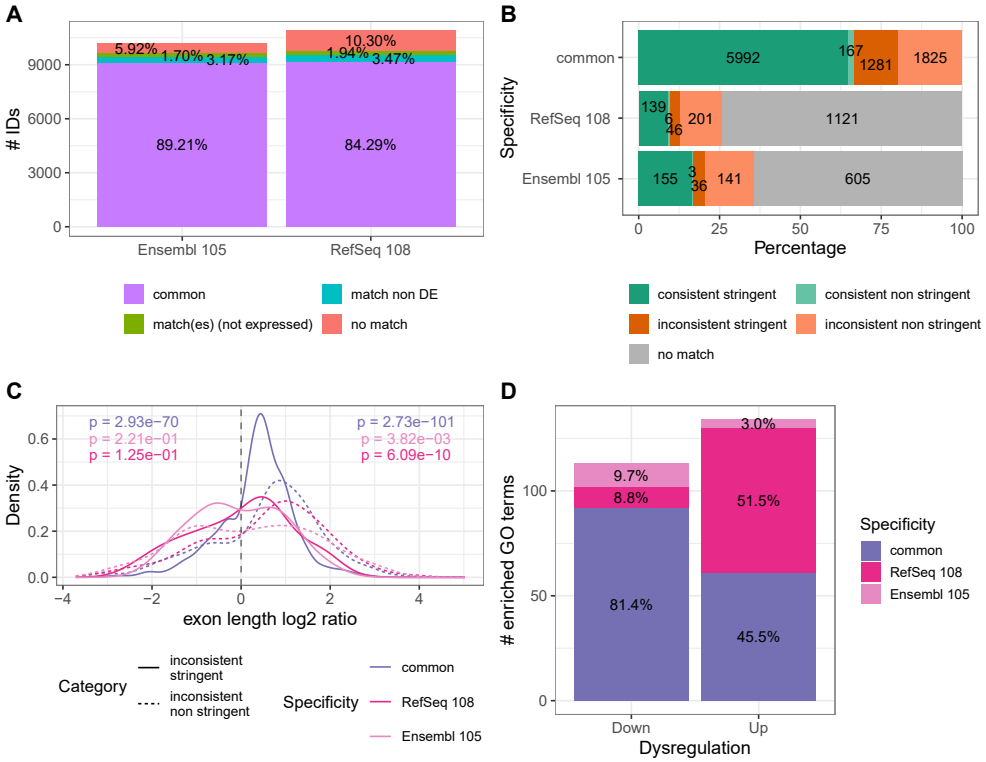
Supplementary fig. 8 Impact of *Rattus norvegicus* reference genomes on the comparison of CA3 subregion to other subregions. Samples of the CA1, CA2, CA3 and DG subregions from the GSE179101 dataset were used for the differenrial expression anlalysis. A: gene identifier matching, genes with multiple matches and genes whose match is not expressed were gathered in the same category, B: differentially expressed (DE) gene counts per category defined by consistency and stringency, C: distribution of cumulative exon length ratio in the annotations of the two reference genomes for inconsistent DE genes, p-values of one-sided Wilcoxon signed-rank tests for paired difference in exon length where the alternative is a greater exon length in RefSeq 108 annotations are displayed per specificity and for inconsistent stringent genes (left) and inconsistent non stringent genes (right). D: enriched Gene Ontology term counts among down-regulated and upregulated genes.



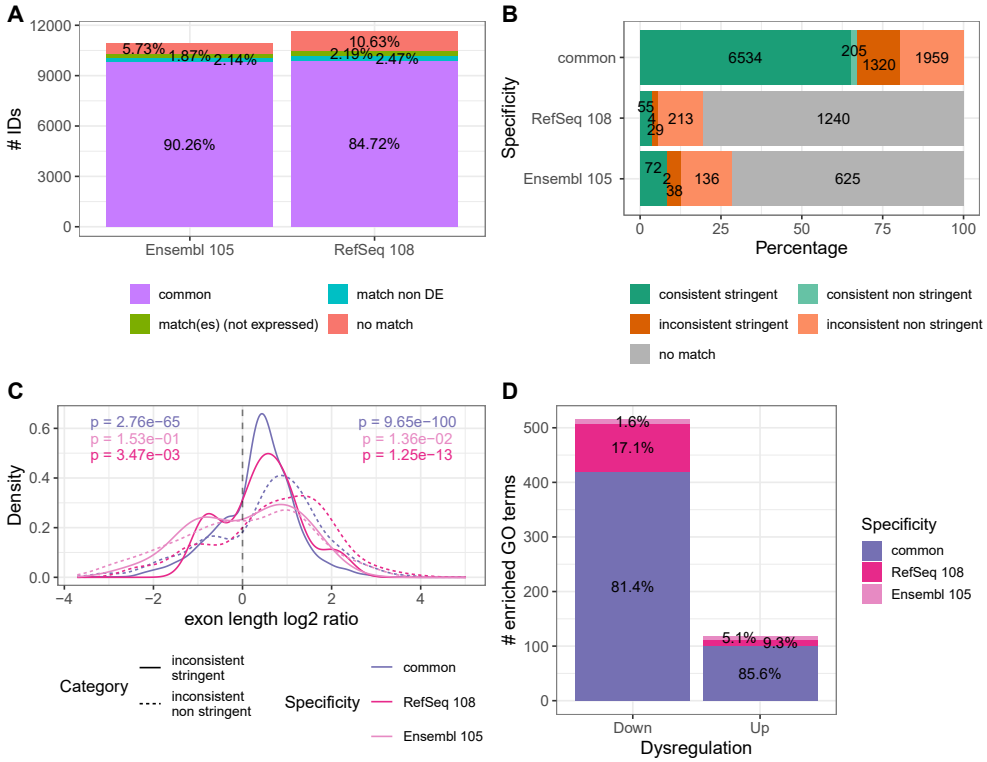
Supplementary fig. 9 Impact of *Rattus norvegicus* reference genomes on the comparison of DG subregion to other subregions. Samples of the CA1, CA2, CA3 and DG subregions from the GSE179101 dataset were used for the differenrial expression anlalysis. A: gene identifier matching, genes with multiple matches and genes whose match is not expressed were gathered in the same category, B: differentially expressed (DE) gene counts per category defined by consistency and stringency, C: distribution of cumulative exon length ratio in the annotations of the two reference genomes for inconsistent DE genes, p-values of one-sided Wilcoxon signed-rank tests for paired difference in exon length where the alternative is a greater exon length in RefSeq 108 annotations are displayed per specificity and for inconsistent stringent genes (left) and inconsistent non stringent genes (right). D: enriched Gene Ontology term counts among down-regulated and upregulated genes.



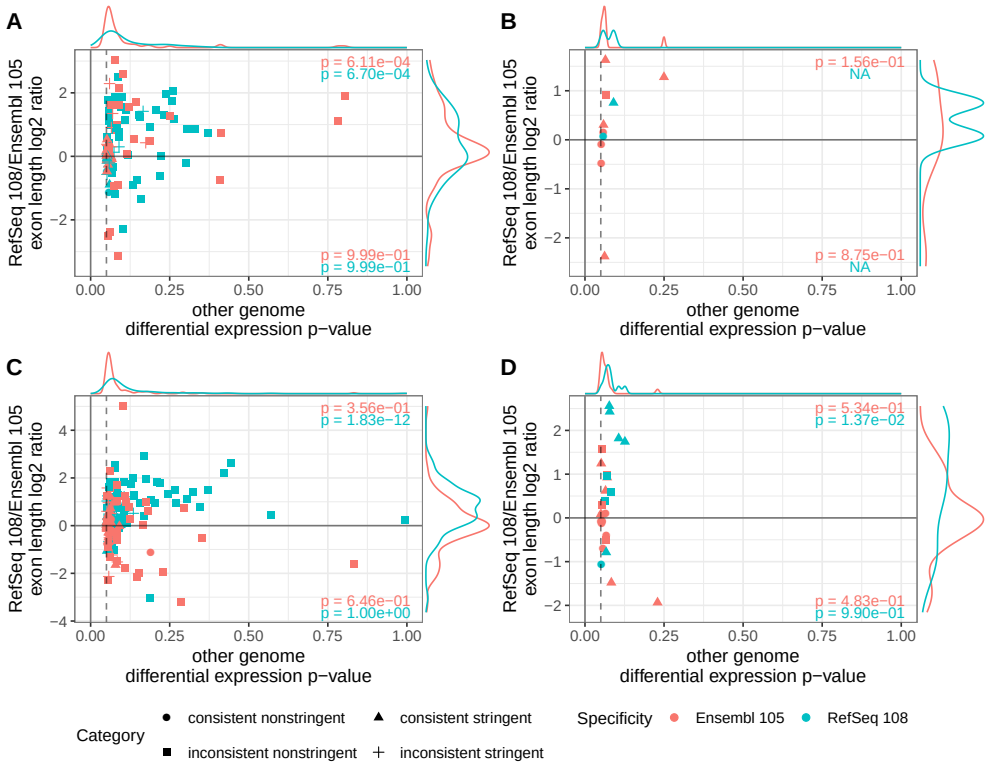
Supplementary fig. 10 Impact of *Rattus norvegicus* reference genomes on the comparison of CA1 subregion to other subregions. Samples of the CA1, CA3 and DG subregions from the GSE140420 dataset were used for the differenrial expression anlalysis. A: gene identifier matching, genes with multiple matches and genes whose match is not expressed were gathered in the same category, B: differentially expressed (DE) gene counts per category defined by consistency and stringency, C: distribution of cumulative exon length ratio in the annotations of the two reference genomes for inconsistent DE genes, p-values of one-sided Wilcoxon signed-rank tests for paired difference in exon length where the alternative is a greater exon length in RefSeq 108 annotations are displayed per specificity and for inconsistent stringent genes (left) and inconsistent non stringent genes (right). D: enriched Gene Ontology term counts among down-regulated and upregulated genes.



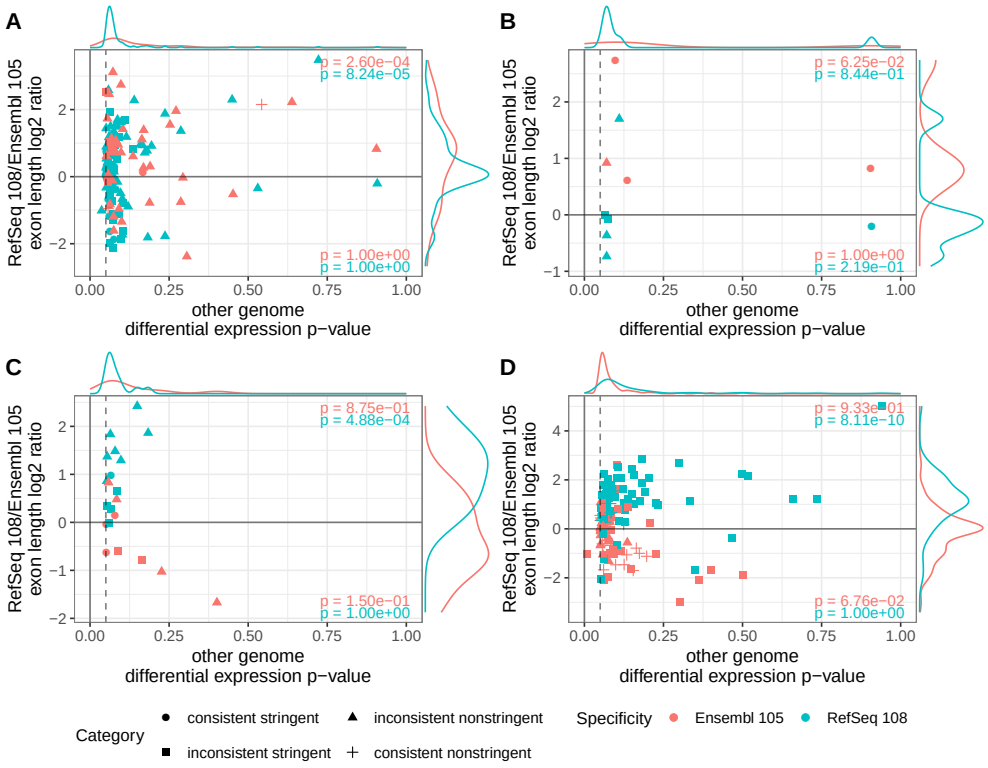
Supplementary fig. 11 Impact of *Rattus norvegicus* reference genomes on the comparison of CA3 subregion to other subregions. Samples of the CA1, CA3 and DG subregions from the GSE140420 dataset were used for the differenrial expression anlalysis. A: gene identifier matching, genes with multiple matches and genes whose match is not expressed were gathered in the same category, B: differentially expressed (DE) gene counts per category defined by consistency and stringency, C: distribution of cumulative exon length ratio in the annotations of the two reference genomes for inconsistent DE genes, p-values of one-sided Wilcoxon signed-rank tests for paired difference in exon length where the alternative is a greater exon length in RefSeq 108 annotations are displayed per specificity and for inconsistent stringent genes (left) and inconsistent non stringent genes (right). D: enriched Gene Ontology term counts among down-regulated and upregulated genes.



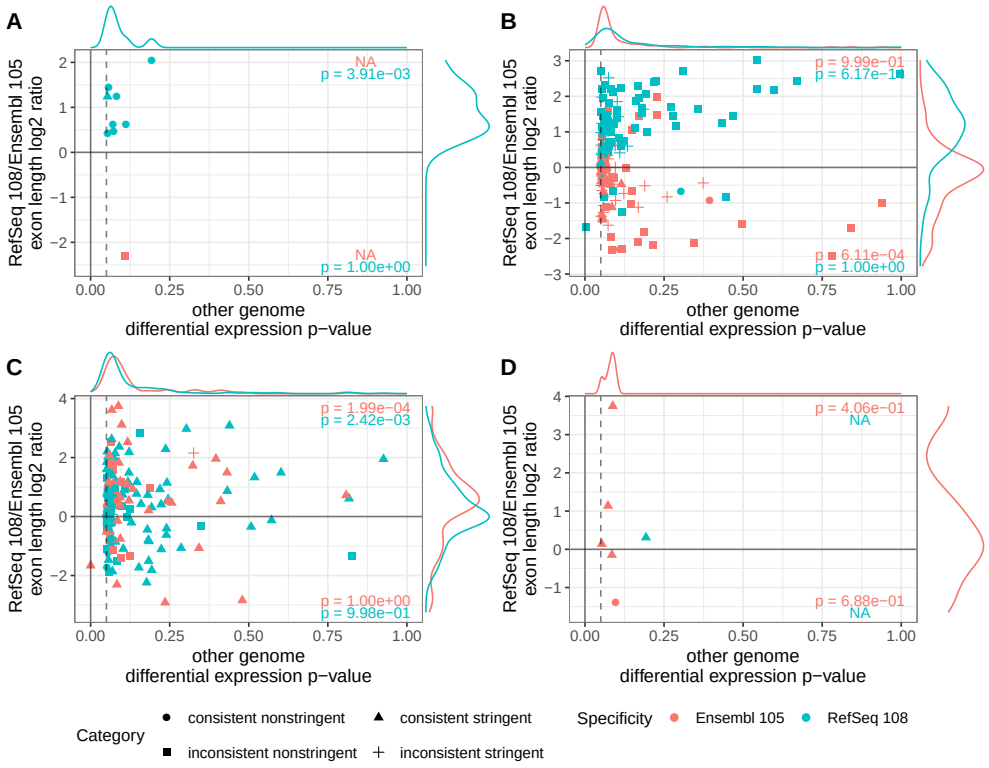
Supplementary fig. 12 Impact of *Rattus norvegicus* reference genomes on the comparison of DG subregion to other subregions. Samples of the CA1, CA3 and DG subregions from the GSE140420 dataset were used for the differenrial expression anlalysis. A: gene identifier matching, genes with multiple matches and genes whose match is not expressed were gathered in the same category, B: differentially expressed (DE) gene counts per category defined by consistency and stringency, C: distribution of cumulative exon length ratio in the annotations of the two reference genomes for inconsistent DE genes, p-values of one-sided Wilcoxon signed-rank tests for paired difference in exon length where the alternative is a greater exon length in RefSeq 108 annotations are displayed per specificity and for inconsistent stringent genes (left) and inconsistent non stringent genes (right). D: enriched Gene Ontology term counts among down-regulated and upregulated genes.



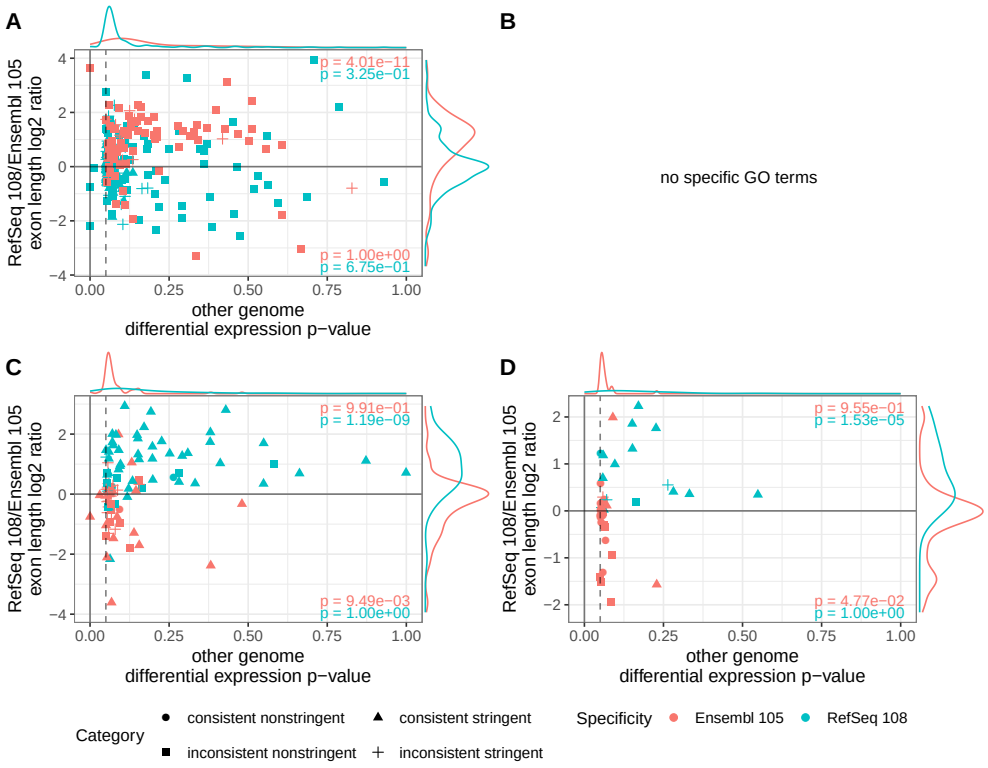
Supplementary fig. 13 Genome-specific differentially expressed genes related to specifically enriched Gene Ontology terms. Exon length log ratio and p-value obtained with the other reference genome for the comparison of CA2 subregion to all other subregions using samples from the GSE179101 dataset. Results are stratified by dysregulation and by genome specificity: specifically enriched GO terms identified among upregulated genes with RefSeq 108 genome (A), upregulated genes with Ensembl 105 genome (B), downregulated genes with RefSeq 108 genome (C), downregulated genes with Ensembl 105 genome (D). P-values of one-sided Wilcoxon signed-rank tests for paired difference in exon length where the alternative is a greater exon length or a lower exon length in RefSeq 108 annotations are displayed on top or bottom of the panels respectively for differentially expressed genes specifically identified with the two different genomes.



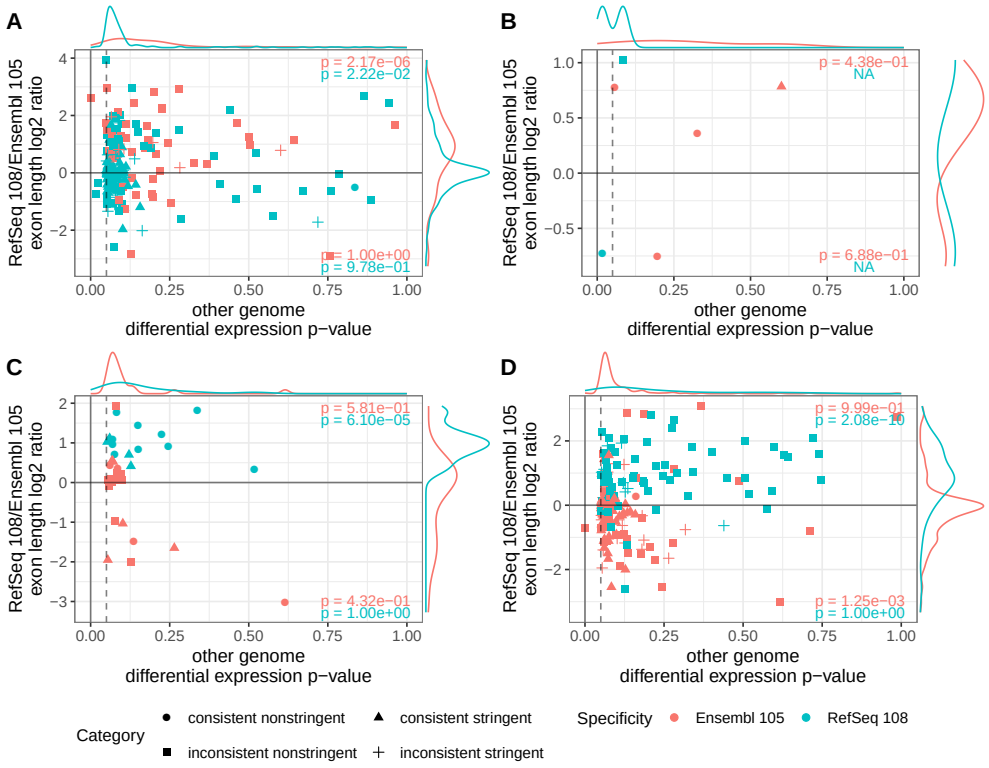
Supplementary fig. 14 Genome-specific differentially expressed genes related to specifically enriched Gene Ontology terms. Exon length log ratio and p-value obtained with the other reference genome for the comparison of CA3 subregion to all other subregions using samples from the GSE179101 dataset. Results are stratified by dysregulation and by genome specificity: specifically enriched GO terms identified among upregulated genes with RefSeq 108 genome (A), upregulated genes with Ensembl 105 genome (B), downregulated genes with RefSeq 108 genome (C), downregulated genes with Ensembl 105 genome (D). P-values of one-sided Wilcoxon signed-rank tests for paired difference in exon length where the alternative is a greater exon length or a lower exon length in RefSeq 108 annotations are displayed on top or bottom of the panels respectively for differentially expressed genes specifically identified with the two different genomes.



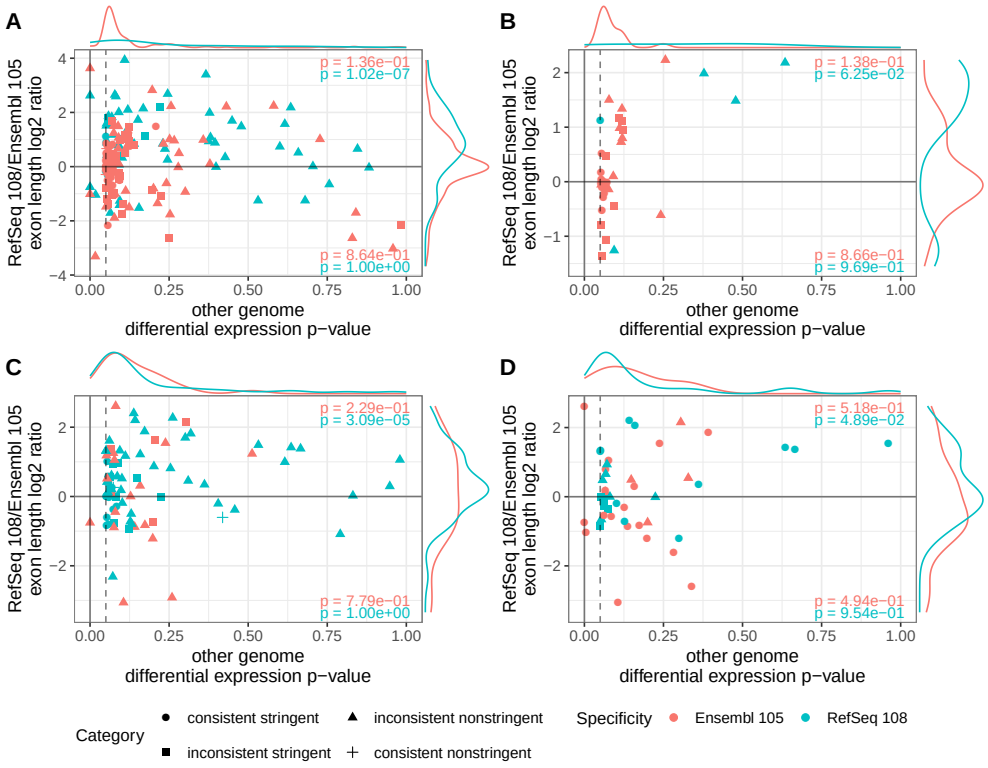
Supplementary fig. 15 Genome-specific differentially expressed genes related to specifically enriched Gene Ontology terms. Exon length log ratio and p-value obtained with the other reference genome for the comparison of DG subregion to all other subregions using samples from the GSE179101 dataset. Results are stratified by dysregulation and by genome specificity: specifically enriched GO terms identified among upregulated genes with RefSeq 108 genome (A), upregulated genes with Ensembl 105 genome (B), downregulated genes with RefSeq 108 genome (C), downregulated genes with Ensembl 105 genome (D). P-values of one-sided Wilcoxon signed-rank tests for paired difference in exon length where the alternative is a greater exon length or a lower exon length in RefSeq 108 annotations are displayed on top or bottom of the panels respectively for differentially expressed genes specifically identified with the two different genomes.



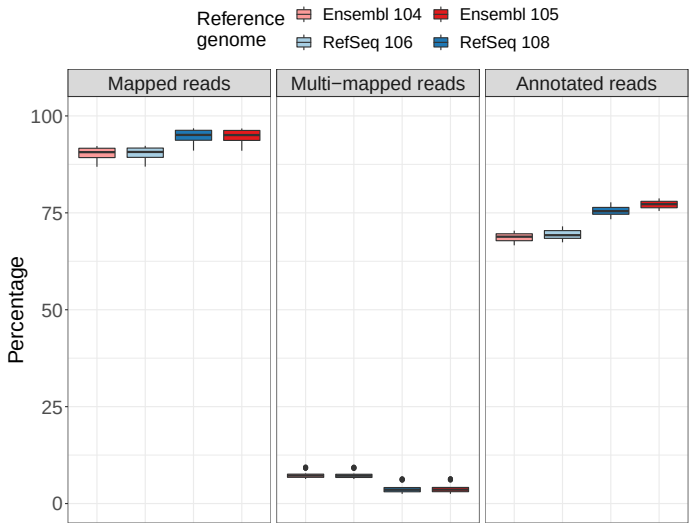
Supplementary fig. 16 Genome-specific differentially expressed genes related to specifically enriched Gene Ontology terms. Exon length log ratio and p-value obtained with the other reference genome for the comparison of CA1 subregion to all other subregions using samples from the GSE140420 dataset. Results are stratified by dysregulation and by genome specificity: specifically enriched GO terms identified among upregulated genes with RefSeq 108 genome (A), upregulated genes with Ensembl 105 genome (B), downregulated genes with RefSeq 108 genome (C), downregulated genes with Ensembl 105 genome (D). P-values of one-sided Wilcoxon signed-rank tests for paired difference in exon length where the alternative is a greater exon length or a lower exon length in RefSeq 108 annotations are displayed on top or bottom of the panels respectively for differentially expressed genes specifically identified with the two different genomes.



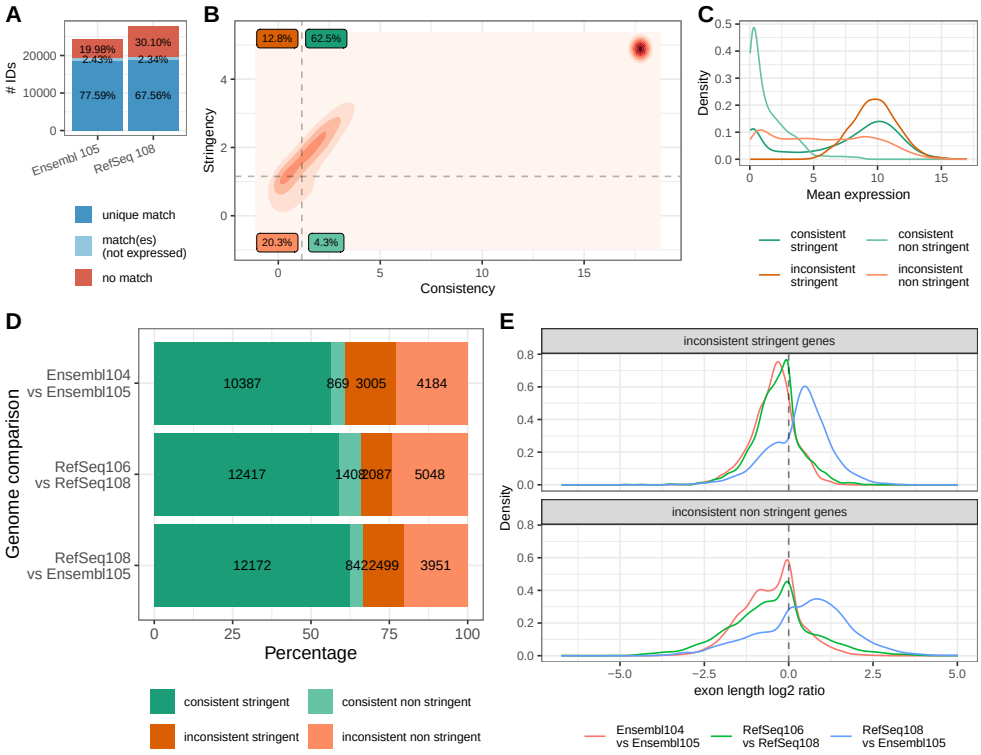
Supplementary fig. 17 Genome-specific differentially expressed genes related to specifically enriched Gene Ontology terms. Exon length log ratio and p-value obtained with the other reference genome for the comparison of CA3 subregion to all other subregions using samples from the GSE140420 dataset. Results are stratified by dysregulation and by genome specificity: specifically enriched GO terms identified among upregulated genes with RefSeq 108 genome (A), upregulated genes with Ensembl 105 genome (B), downregulated genes with RefSeq 108 genome (C), downregulated genes with Ensembl 105 genome (D). P-values of one-sided Wilcoxon signed-rank tests for paired difference in exon length where the alternative is a greater exon length or a lower exon length in RefSeq 108 annotations are displayed on top or bottom of the panels respectively for differentially expressed genes specifically identified with the two different genomes.



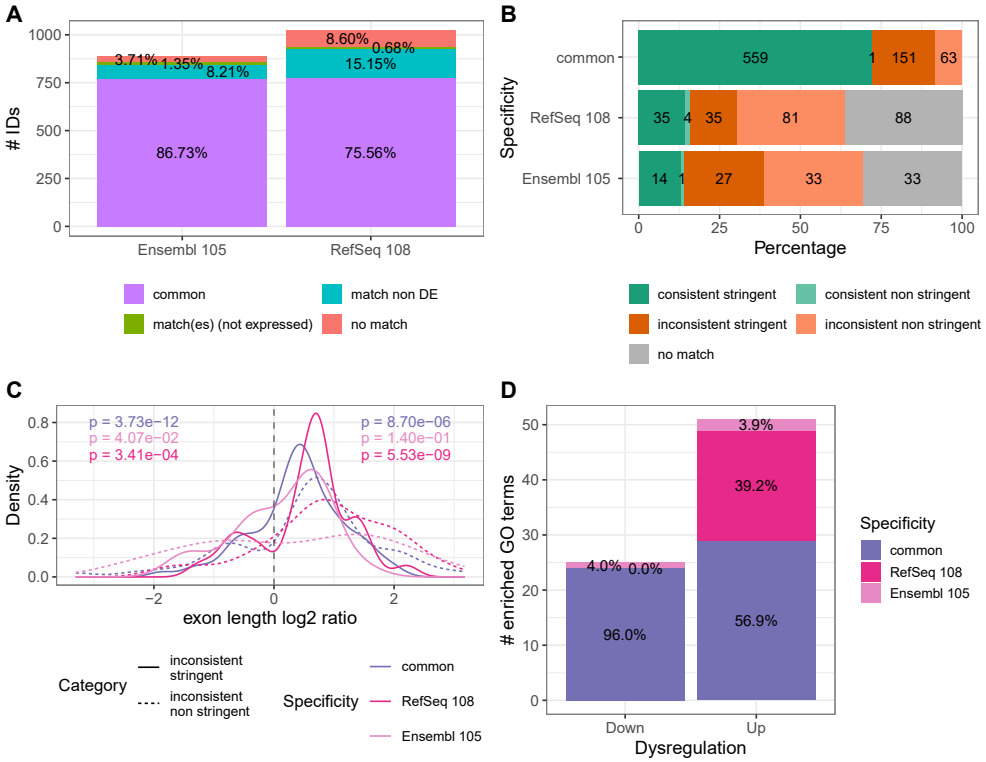
Supplementary fig. 18 Genome-specific differentially expressed genes related to specifically enriched Gene Ontology terms. Exon length log ratio and p-value obtained with the other reference genome for the comparison of DG subregion to all other subregions using samples from the GSE140420 dataset. Results are stratified by dysregulation and by genome specificity: specifically enriched GO terms identified among upregulated genes with RefSeq 108 genome (A), upregulated genes with Ensembl 105 genome (B), downregulated genes with RefSeq 108 genome (C), downregulated genes with Ensembl 105 genome (D). P-values of one-sided Wilcoxon signed-rank tests for paired difference in exon length where the alternative is a greater exon length or a lower exon length in RefSeq 108 annotations are displayed on top or bottom of the panels respectively for differentially expressed genes specifically identified with the two different genomes.



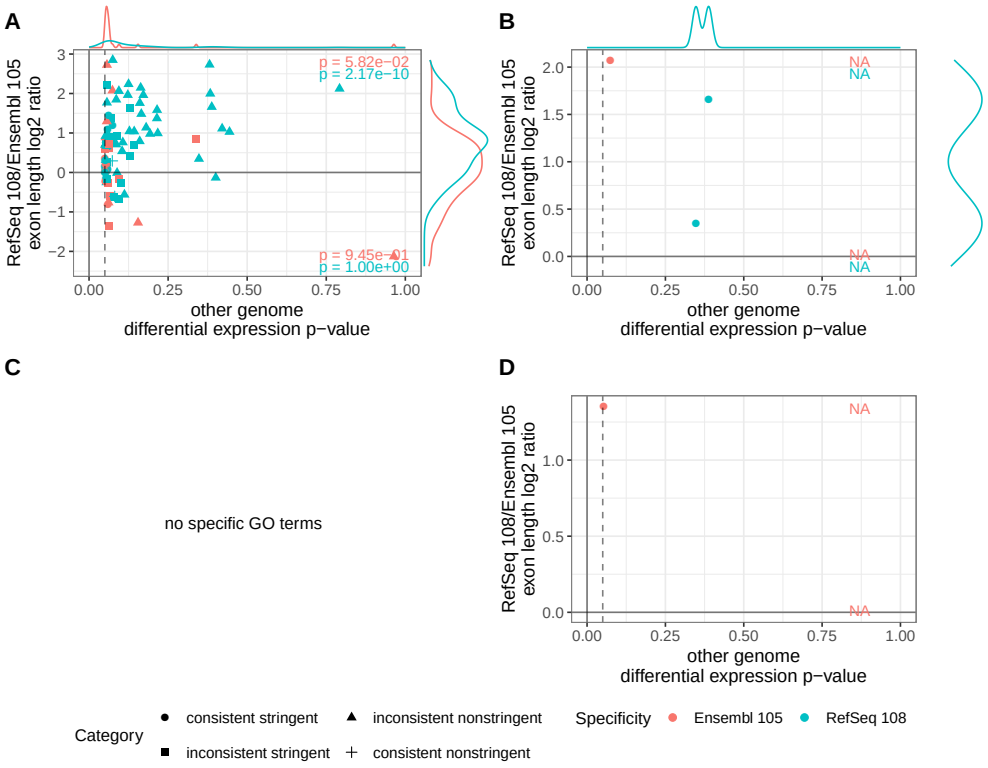
Supplementary fig. 19 Read mapping statistics with respect to *Rattus norvegicus* reference genomes for the GSE136913 dataset. The raw sequencing reads of all the samples of GSE136913 dataset were trimmed for adpaters and quality before being aligned against *Rattus norvegicus* reference genomes and assigned to annotations.



Supplementary fig. 20 Consistency and stringency of *Rattus norvegicus* reference genomes for the analysis of GSE136913 dataset. A: gene identifier matching, genes with multiple matches and genes whose match is not expressed were gathered in the same category, B: consistency and stringency for all expressed genes in both matrices, C: distribution of mean expression of all the genes expressed in the matrix generated with Ensembl 105 genome, D: gene counts per category defined by consistency and stringency for pairwise genome comparison, E: distribution of cumulative exon length ratio in the annotations of two reference genomes for inconsistent genes.



Supplementary fig. 21 Impact of *Rattus norvegicus* reference genomes on differential expression anlalysis results of GSE136913 dataset. A: gene identifier matching, genes with multiple matches and genes whose match is not expressed were gathered in the same category, B: differentially expressed (DE) gene counts per category defined by consistency and stringency, C: distribution of cumulative exon length ratio in the annotations of the two reference genomes for inconsistent DE genes, p-values of one-sided Wilcoxon signed-rank tests for paired difference in exon length where the alternative is a greater exon length in RefSeq 108 annotations are displayed per specificity and for inconsistent stringent genes (left) and inconsistent non stringent genes (right). D: enriched Gene Ontology term counts among down-regulated and upregulated genes.



Supplementary fig. 22 Genome-specific differentially expressed genes related to specifically enriched Gene Ontology terms. Exon length log ratio and p-value obtained with the other reference genome for the comparison of treated samples to control samples from the GSE136913 dataset. Results are stratified by dysregulation and by genome specificity: specifically enriched GO terms identified among upregulated genes with RefSeq 108 genome (A), upregulated genes with Ensembl 105 genome (B), downregulated genes with RefSeq 108 genome (C), downregulated genes with Ensembl 105 genome (D). P-values of one-sided Wilcoxon signed-rank tests for paired difference in exon length where the alternative is a greater exon length or a lower exon length in RefSeq 108 annotations are displayed on top or bottom of the panels respectively for differentially expressed genes specifically identified with the two different genomes.