

SUPPLEMENTARY MATERIAL FOR INTEGRATIVE POPULATION AND FUNCTIONAL GENOMICS OF AFRICAN CATTLE

Gillian P. McHugo

Student Number: 15204236



Supplementary material for a thesis submitted to University College Dublin
in fulfilment of the requirements for the degree of Doctor of Philosophy.

UCD School of Agriculture and Food Science

Head of School: Professor Frank J. Monahan

Primary Supervisor: Professor David E. MacHugh

Secondary Supervisor: Professor Stephen V. Gordon

July, 2024

Table of contents

Table of contentsi

List of figuresii

List of tablesxi

Appendix A. Supplementary material for Chapter 2 1

Appendix B. Supplementary material for Chapter 335

Appendix C. Supplementary material for Chapter 4.....77

Bibliography..... 117

List of figures

Supplementary Figure A.1. Heatmap of mean identity-by-state values for the high-density SNP data set.	2
Supplementary Figure A.2. Tukey box plots showing the distribution of inbreeding values (F) for the high-density SNP data for each population.	3
Supplementary Figure A.3. Tukey box plots showing the distribution of inbreeding values (F) for the low-density SNP data for each population after inbreeding filters were applied.	3
Supplementary Figure A.4. A. Principal component analysis (PCA) of the selected low-density SNP data set with cattle samples coloured according to population showing the first two principal components (PC1 and PC2), and B. bar chart of the proportion of variance for the top ten PCs.	4
Supplementary Figure A.5. Hierarchical clustering of cattle samples using the high-density SNP data set.	5
Supplementary Figure A.6. Hierarchical clustering of cattle samples using the high-density SNP data set.	6
Supplementary Figure A.7. Hierarchical clustering of cattle samples using the low-density SNP data set.	7
Supplementary Figure A.8. Hierarchical clustering of cattle samples using the low-density SNP data set.	8
Supplementary Figure A.9. OptM results for the high-density SNP data set.	9
Supplementary Figure A.10. OptM results for the low-density SNP data set.	10
Supplementary Figure A.11. A. TreeMix phylogenetic tree for the high-density SNP data set with bootstrap values. B. a heatmap showing the standard error.	11
Supplementary Figure A.12. A. TreeMix phylogenetic tree for the high-density SNP data set with bootstrap values and 12 migration edges. B. a heatmap showing standard error.	11
Supplementary Figure A.13. A. TreeMix phylogenetic tree for the low-density SNP data set with bootstrap values. B. a heatmap showing the standard error.	12

Supplementary Figure A.14. A. TreeMix phylogenetic tree for the low-density SNP data set with bootstrap values and three migration edges. B. a heatmap showing standard error.	12
Supplementary Figure A.15. A. TreeMix phylogenetic tree for the high-density SNP data set with bootstrap values and 11 migration edges. B. a heatmap showing standard error.	13
Supplementary Figure A.16. Local ancestry results for chromosome 23 (BTA23) for the European hybrid group calculated using MOSAIC with the high-density SNP data set.	14
Supplementary Figure A.17. Local ancestry results for chromosome 23 (BTA23) for the African trypanotolerant hybrid group calculated using MOSAIC with the high-density SNP data set.	15
Supplementary Figure A.18. Local ancestry results for chromosome 23 (BTA23) for the African trypanosusceptible hybrid group calculated using MOSAIC with the high-density SNP data set.	16
Supplementary Figure A.19. Local ancestry results for chromosome 23 (BTA23) for the European hybrid group calculated using MOSAIC with the low-density SNP data set.	17
Supplementary Figure A.20. Local ancestry results for chromosome 23 (BTA23) for the trypanotolerant African hybrid group calculated using MOSAIC with the low-density SNP data set.	18
Supplementary Figure A.21. Local ancestry results for chromosome 23 (BTA23) for the trypanosusceptible African hybrid group calculated using MOSAIC with the low-density SNP data set.	19
Supplementary Figure A.22. Local ancestry results for chromosome 23 (BTA23) for the European hybrid group calculated using ELAI with the high-density SNP data set.	20
Supplementary Figure A.23. Local ancestry results for chromosome 23 (BTA23) for the trypanotolerant African hybrid group calculated using ELAI with the high-density SNP data set.	21
Supplementary Figure A.24. Local ancestry results for chromosome 23 (BTA23) for the trypanosusceptible African hybrid group calculated using ELAI with the high-density SNP data set.	22

Supplementary Figure A.25. Local ancestry results for chromosome 23 (BTA23) for the European hybrid group calculated using ELAI with the low-density SNP data set.	23
Supplementary Figure A.26. Local ancestry results for chromosome 23 (BTA23) for the trypanotolerant African hybrid group calculated using ELAI with the low-density SNP data set.	24
Supplementary Figure A.27. Local ancestry results for chromosome 23 (BTA23) for the trypanosusceptible African hybrid group calculated using ELAI with the low-density SNP data set.	25
Supplementary Figure A.28. Correlation plots for the European hybrid local ancestry results (high-density SNP data set).	26
Supplementary Figure A.29. Correlation plots for the trypanotolerant African hybrid local ancestry results (high-density SNP data set).	27
Supplementary Figure A.30. Correlation plots for the trypanosusceptible African hybrid local ancestry results (high-density SNP data set).	28
Supplementary Figure A.31. Correlation plots for the European hybrid local ancestry results (low-density SNP data set).	29
Supplementary Figure A.32. Correlation plots for the trypanotolerant African hybrid local ancestry results (low-density SNP data set).....	30
Supplementary Figure A.33. Correlation plots for the trypanosusceptible African hybrid local ancestry results (low-density SNP data set).....	31
Supplementary Figure A.34. g:Profiler functional enrichment of introgressed regions in European, and trypanotolerant and trypanosusceptible African hybrid populations detected with MOSAIC and low-density SNP data.	32
Supplementary Figure A.35. g:Profiler functional enrichment of introgressed regions in European, and trypanotolerant and trypanosusceptible African hybrid populations detected with ELAI and high-density SNP data.	33
Supplementary Figure A.36. g:Profiler functional enrichment of introgressed regions in European, and trypanotolerant and trypanosusceptible African hybrid populations detected with ELAI and low-density SNP data.....	34

Supplementary Figure B.1. Boxplots showing the log ₂ expression intensity of the probe sets for each sample of the A. raw and B. normalised data after quality control filtering separated into NDAM and BORA populations and coloured according to tissue.....	43
Supplementary Figure B.2. A. Principal component analysis (PCA) of the microarray data set with samples coloured according to days post infection (dpi) with the outer colour representing the tissue and shape indicating the population showing the first and third principal components (PC1 and PC3), and B. bar chart of proportion of variance of the top ten PCs.....	44
Supplementary Figure B.3. A. Principal component analysis (PCA) of the microarray data set with samples coloured according to days post infection (dpi) with the outer colour representing the tissue and shape indicating the population showing the first and fourth principal components (PC1 and PC4), and B. bar chart of proportion of variance of the top ten PCs.....	45
Supplementary Figure B.4. A. Principal component analysis (PCA) of the microarray data set with samples coloured according to tissue and shape indicating the population showing the first and fifth principal components (PC1 and PC5), and B. bar chart of proportion of variance of the top ten PCs.	46
Supplementary Figure B.5. Bar chart showing the numbers of significantly differentially expressed genes for the RESP contrasts.	47
Supplementary Figure B.6. Bar chart showing the numbers of significantly differentially expressed genes for the DIRE contrasts.	48
Supplementary Figure B.7. Bar chart showing the numbers of significantly differentially expressed genes for the NDAM contrasts.	49
Supplementary Figure B.8. Bar chart showing the numbers of significantly differentially expressed genes for the BORA contrasts.....	50
Supplementary Figure B.9. UpSet plot showing the top 20 intersections among all 64 contrasts.	51
Supplementary Figure B.10. UpSet plot showing the top 20 intersections among the RESP contrasts.	52
Supplementary Figure B.11. UpSet plot showing the top 20 intersections among the DIRE contrasts.	53

Supplementary Figure B.12. UpSet plot showing the top 20 intersections among the NDAM contrasts.	54
Supplementary Figure B.13. UpSet plot showing the top 20 intersections among the BORA contrasts.	55
Supplementary Figure B.14. Volcano plot showing the results of the RESP contrast for the peripheral blood mononuclear cell (PBMC) samples at 14 days post infection (dpi).....	56
Supplementary Figure B.15. Volcano plot showing the results of the RESP contrast for the peripheral blood mononuclear cell (PBMC) samples at 25 days post infection (dpi).....	57
Supplementary Figure B.16. Volcano plot showing the results of the RESP contrast for the liver samples at 12 days post infection (dpi).	58
Supplementary Figure B.17. Volcano plot showing the results of the RESP contrast for the liver samples at 15 days post infection (dpi).	59
Supplementary Figure B.18. Volcano plot showing the results of the RESP contrast for the liver samples at 18 days post infection (dpi).	60
Supplementary Figure B.19. Volcano plot showing the results of the RESP contrast for the liver samples at 21 days post infection (dpi).	61
Supplementary Figure B.20. Volcano plot showing the results of the RESP contrast for the liver samples at 26 days post infection (dpi).	62
Supplementary Figure B.21. Volcano plot showing the results of the RESP contrast for the liver samples at 29 days post infection (dpi).	63
Supplementary Figure B.22. Volcano plot showing the results of the RESP contrast for the liver samples at 32 days post infection (dpi).	64
Supplementary Figure B.23. Volcano plot showing the results of the RESP contrast for the liver samples at 35 days post infection (dpi).	65
Supplementary Figure B.24. Volcano plot showing the results of the RESP contrast for the lymph node samples at 21 days post infection (dpi).	66

Supplementary Figure B.25. Volcano plot showing the results of the RESP contrast for the lymph node samples at 35 days post infection (dpi).	67
Supplementary Figure B.26. Volcano plot showing the results of the RESP contrast for the spleen samples at 21 days post infection (dpi).	68
Supplementary Figure B.27. Volcano plot showing the results of the RESP contrast for the spleen samples at 35 days post infection (dpi).	69
Supplementary Figure B.28. g:Profiler functional enrichment of significantly differentially expressed genes (DEGs) in the peripheral blood mononuclear cell (PBMC) sample RESP contrasts.	70
Supplementary Figure B.29. g:Profiler functional enrichment of significantly differentially expressed genes (DEGs) in the liver sample RESP contrasts.....	71
Supplementary Figure B.30. g:Profiler functional enrichment of significantly differentially expressed genes (DEGs) in the lymph node sample RESP contrasts. Each circle represents a significantly enriched GO term with the size indicating the ratio of the intersection between the term and the DEGs.	72
Supplementary Figure B.31. g:Profiler functional enrichment of significantly differentially expressed genes (DEGs) in the spleen sample RESP contrasts.....	73
Supplementary Figure B.32. EnrichmentMap network of significantly enriched GO terms identified from g:Profiler functional enrichment of significant differentially expressed genes (DEGs) for the DIRE contrasts.....	74
Supplementary Figure B.33. EnrichmentMap network of significantly enriched GO terms identified from g:Profiler functional enrichment of significant differentially expressed genes (DEGs) for the NDAM contrasts.....	75
Supplementary Figure B.34. EnrichmentMap network of significantly enriched GO terms identified from g:Profiler functional enrichment of significant differentially expressed genes (DEGs) for the BORA contrasts.	76
Supplementary Figure C.1. Heatmap of mean identity by state values for SNP data in European, African, and Asian cattle populations.....	87

Supplementary Figure C.2. Tukey box plots showing the distribution of inbreeding values (F) for SNP data for each population of European, African, and Asian cattle.	88
Supplementary Figure C.3. A. Principal component analysis (PCA) of SNP data for cattle coloured according to population showing the first two principal components and B. bar chart of proportion of variance of the top ten principal components.	89
Supplementary Figure C.4. A. Principal component analysis (PCA) of the high-density SNP data for the cattle samples from Chapter 2 coloured according to population showing the first two principal components and B. bar chart of proportion of variance of the top ten principal components.....	90
Supplementary Figure C.5. A. Principal component analysis (PCA) of the low-density SNP data for the cattle samples from Chapter 2 coloured according to population showing the first two principal components and B. bar chart of proportion of variance of the top ten principal components.....	91
Supplementary Figure C.6. Hierarchical clustering of the SNP data for European, African, and Asian cattle populations.	92
Supplementary Figure C.7. Hierarchical clustering of the SNP data for European, African, and Asian cattle populations.	93
Supplementary Figure C.8. Hierarchical clustering of the high-density SNP data from Chapter 2 for European, African, and Asian cattle populations.	94
Supplementary Figure C.9. Hierarchical clustering of the low-density SNP data from Chapter 2 for European, African, and Asian cattle populations.	95
Supplementary Figure C.10. g:Profiler functional enrichment of introgressed regions in the African <i>B. taurus</i> cattle populations with gene expression data available according to local ancestry analysis of SNP data.....	96
Supplementary Figure C.11. g:Profiler functional enrichment of introgressed regions in the trypanotolerant African hybrid cattle populations with gene expression data available according to local ancestry analysis of SNP data.	97

Supplementary Figure C.12. g:Profiler functional enrichment of introgressed regions in the trypanosusceptible African hybrid cattle populations with gene expression data available according to local ancestry analysis of SNP data.	98
Supplementary Figure C.13. Bar chart showing the numbers of significantly differentially expressed genes for the response contrasts of the RNA-seq data.....	99
Supplementary Figure C.14. Volcano plot showing the results of the response contrast for the RNA-seq data from the LAGU population at 40 days post infection.	100
Supplementary Figure C.15. Volcano plot showing the results of the response contrast for the RNA-seq data from the BAOU population at 40 days post infection.	101
Supplementary Figure C.16. Volcano plot showing the results of the response contrast for the RNA-seq data from the NDAM population at 40 days post infection.	102
Supplementary Figure C.17. Volcano plot showing the results of the response contrast for the RNA-seq data from the BORG population at 40 days post infection.	103
Supplementary Figure C.18. Base network generated using InnateDB with the top results of a search of the GeneCards® for genes relating to the term “trypano*”.	104
Supplementary Figure C.19. Functional module identified using jActiveModules and differential expression results for the MICRO BL 34 contrast.....	105
Supplementary Figure C.20. Functional module identified using jActiveModules and differential expression results for the MICRO LI 35 contrast.....	106
Supplementary Figure C.21. Functional module identified using jActiveModules and differential expression results for the MICRO LN 35 contrast.	107
Supplementary Figure C.22. Functional module identified using jActiveModules and differential expression results for the MICRO SP 35 contrast.	108
Supplementary Figure C.23. Functional module identified using jActiveModules and differential expression results for the RNA LAGU 40 contrast.	109
Supplementary Figure C.24. Functional module identified using jActiveModules and differential expression results for the RNA BAOU 40 contrast.	110

Supplementary Figure C.25. Functional module identified using jActiveModules and differential expression results for the RNA NDAM 40 contrast.	111
Supplementary Figure C.26. Functional module identified using jActiveModules and differential expression results for the RNA BORG 40 contrast.	112
Supplementary Figure C.27. Upset plot showing the top 20 intersections between the genes in the functional modules identified using jActiveModules and differential expression results for each of the final response contrasts for the microarray and RNA-seq data.....	113
Supplementary Figure C.28. g:Profiler functional enrichment of significantly differentially expressed genes in the RNA-seq response contrasts with no background data set specified.	114
Supplementary Figure C.29. g:Profiler functional enrichment of the genes in the MICRO LI 35 functional module with no background data set specified.	115
Supplementary Figure C.30. g:Profiler functional enrichment of the genes in the base network with no background data set specified.....	116

List of tables

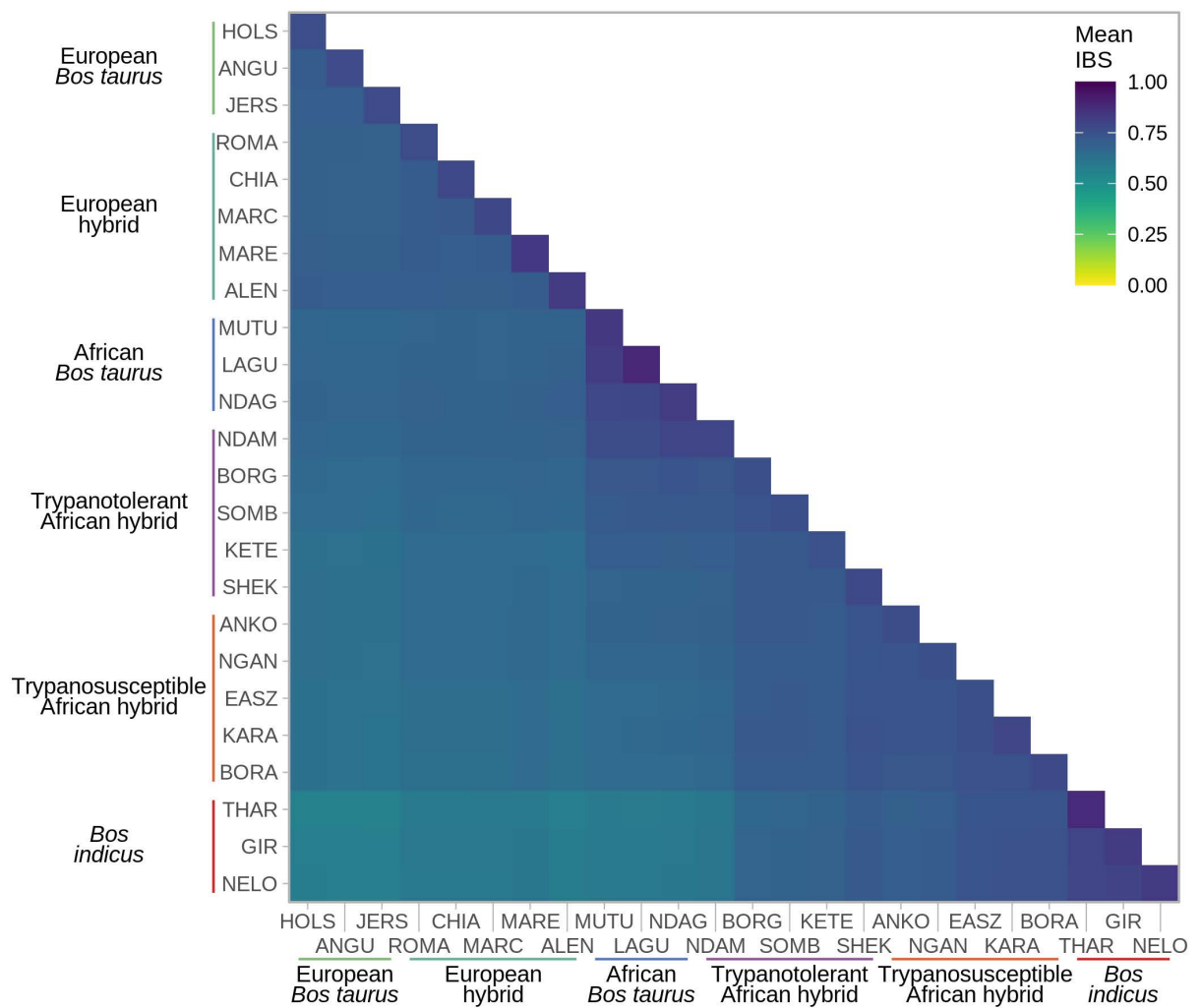
Supplementary Table A.1. Numbers of genes within 1 Mb up- and downstream of SNPs with a z -score ≥ 2.0 for weighted mean European <i>B. taurus</i> , African <i>B. taurus</i> and <i>B. indicus</i> ancestry components for the European hybrid, trypanotolerant African hybrid, and trypanosusceptible African hybrid groups across all autosomes for the MOSAIC and ELAI analyses of high- and low-density SNP data sets.	1
Supplementary Table B.1. Contrast ID, contrast type, tissue, days post infection (dpi), and formula for each of the 64 contrasts.	35
Supplementary Table B.2. Tissue, days post infection (dpi), and the top 10 most significant genes with increased and decreased expression with valid gene symbols for the direct contrasts.	37
Supplementary Table B.3. Tissue, days post infection (dpi), and the top 10 most significant genes with increased and decreased expression with valid gene symbols for the N'Dama contrasts.	39
Supplementary Table B.4. Tissue, days post infection (dpi), and the top 10 most significant genes with increased and decreased expression with valid gene symbols for the Boran contrasts.	41
Supplementary Table C.1. Numbers of SNPs with z -score ≥ 2.0 for mean European <i>B. taurus</i> , African <i>B. taurus</i> and <i>B. indicus</i> ancestry components for the six populations with gene expression data available across all autosomes.	77
Supplementary Table C.2. Numbers of genes within 1 Mb up- and downstream of SNPs with z -score ≥ 2.0 for mean European <i>B. taurus</i> , African <i>B. taurus</i> and <i>B. indicus</i> ancestry components for the six populations with gene expression data available across all autosomes.	77
Supplementary Table C.3. Population, days post infection and the significantly differentially expressed genes with increased and decreased expression with gene symbols for the response contrasts.	78
Supplementary Table C.4. Gene symbol and modules containing each of the 243 genes with valid gene symbols that were found in four or more of the eight functional modules.	79

Supplementary Table C.5. Numbers of intervals within 1 Mb up- and downstream of SNPs with z -score ≥ 2.0 for mean European *B. taurus*, African *B. taurus* and *B. indicus* ancestry components for the six populations with gene expression data available across all autosomes and groups of populations from the original local ancestry analysis. 86

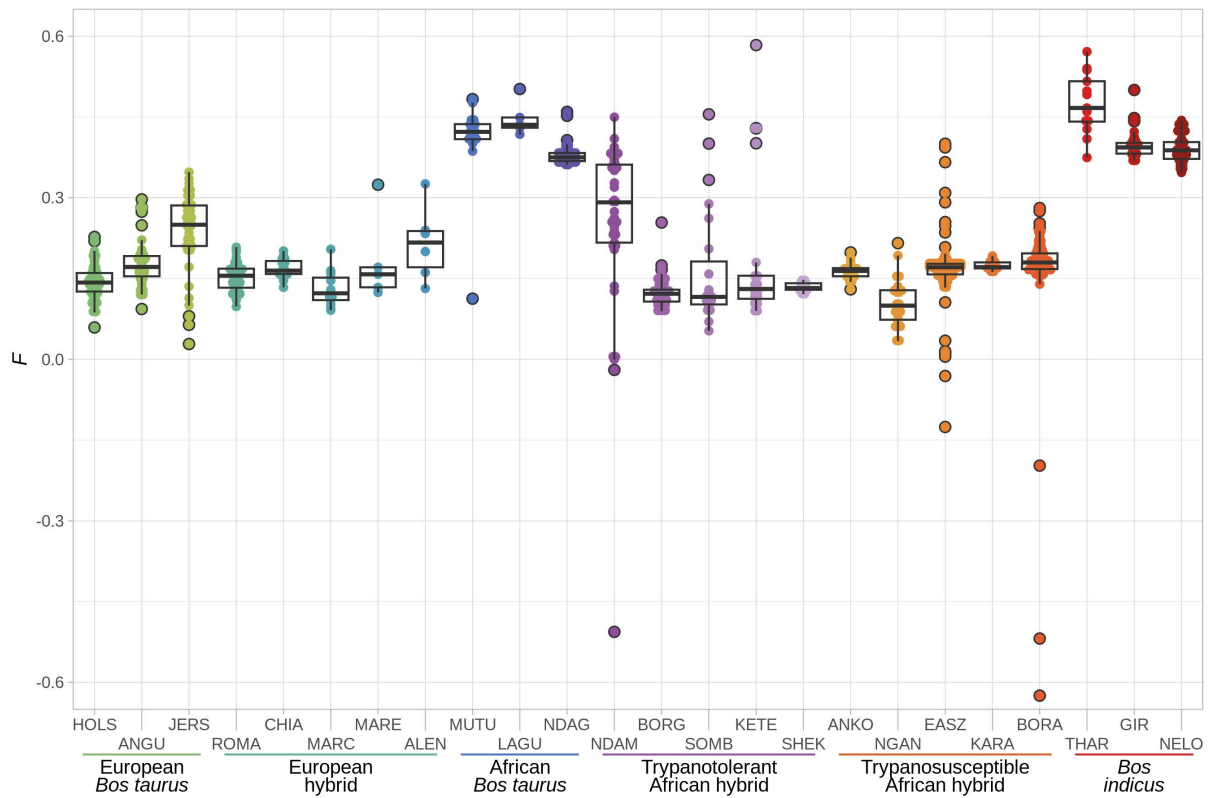
Appendix A. Supplementary material for Chapter 2

Supplementary Table A.1. Numbers of genes within 1 Mb up- and downstream of SNPs with a z-score ≥ 2.0 for weighted mean European *B. taurus*, African *B. taurus* and *B. indicus* ancestry components for the European hybrid, trypanotolerant African hybrid, and trypanosusceptible African hybrid groups across all autosomes for the MOSAIC and ELAI analyses of high- and low-density SNP data sets. The numbers in brackets indicate the percentage of the total number of SNPs in the data set.

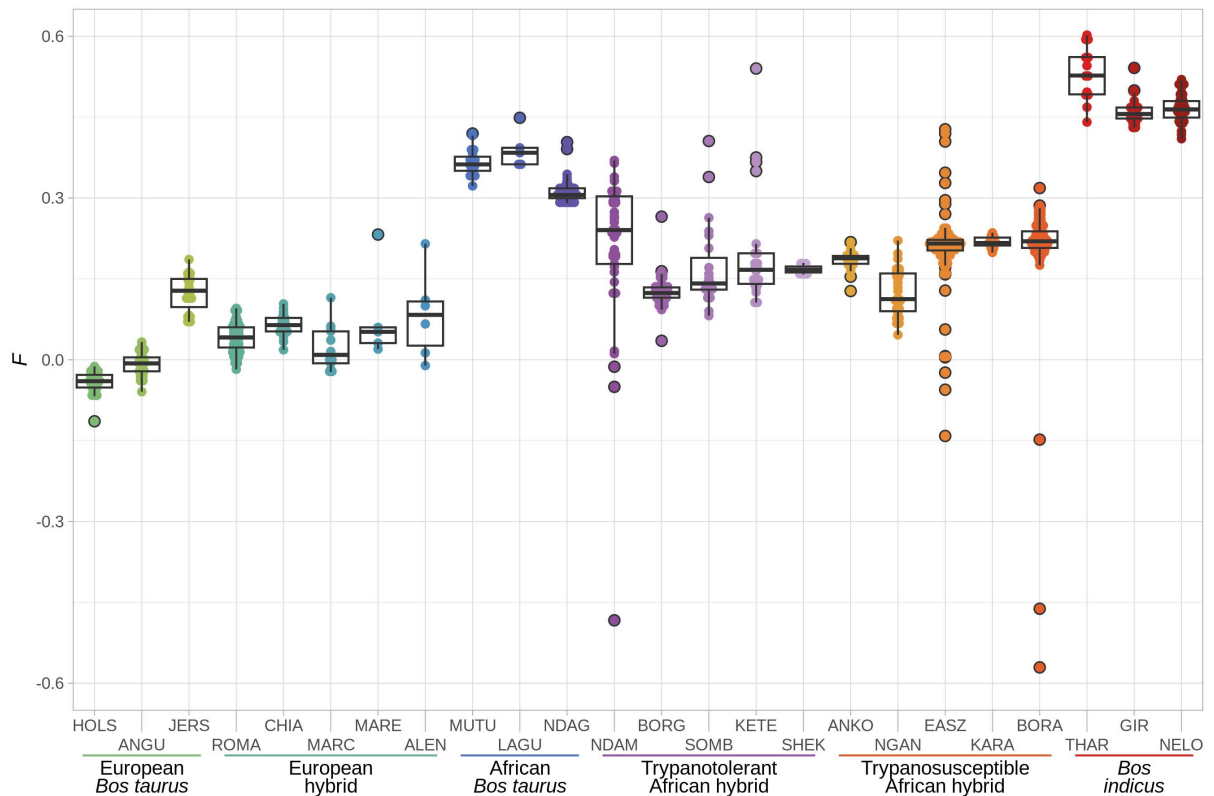
Group	Ancestry	HD MOSAIC	LD MOSAIC	HD ELAI	LD ELAI
European hybrid	European <i>B. taurus</i>	0 (0%)	0 (0%)	0 (0%)	20 (0.08%)
	African <i>B. taurus</i>	720 (2.76%)	1,980 (7.61%)	585 (2.24%)	457 (1.76%)
	<i>B. indicus</i>	1,131 (4.33%)	1,564 (6.01%)	954 (3.66%)	719 (2.76%)
Trypanotolerant African hybrid	European <i>B. taurus</i>	538 (2.06%)	689 (2.65%)	382 (1.46%)	285 (1.10%)
	African <i>B. taurus</i>	271 (1.04%)	191 (0.73%)	11 (0.04%)	192 (0.74%)
	<i>B. indicus</i>	976 (3.74%)	1,117 (4.29%)	556 (2.13%)	333 (1.28%)
Trypanosusceptible African hybrid	European <i>B. taurus</i>	540 (2.07%)	584 (2.24%)	250 (0.96%)	372 (1.43%)
	African <i>B. taurus</i>	615 (2.36%)	168 (0.65%)	268 (1.03%)	352 (1.35%)
	<i>B. indicus</i>	451 (1.73%)	686 (2.64%)	216 (0.83%)	214 (0.82%)
Total		26,101	26,017	26,101	26,017



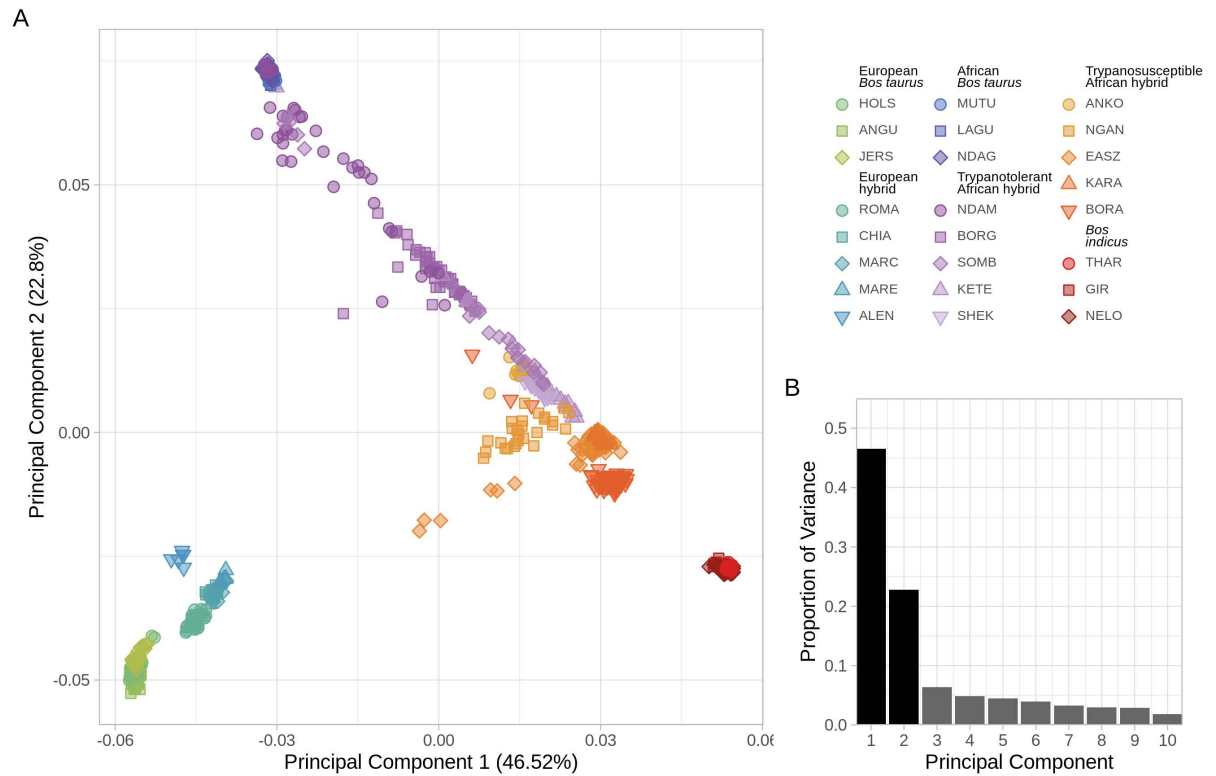
Supplementary Figure A.1. Heatmap of mean identity-by-state values for the high-density SNP data set.



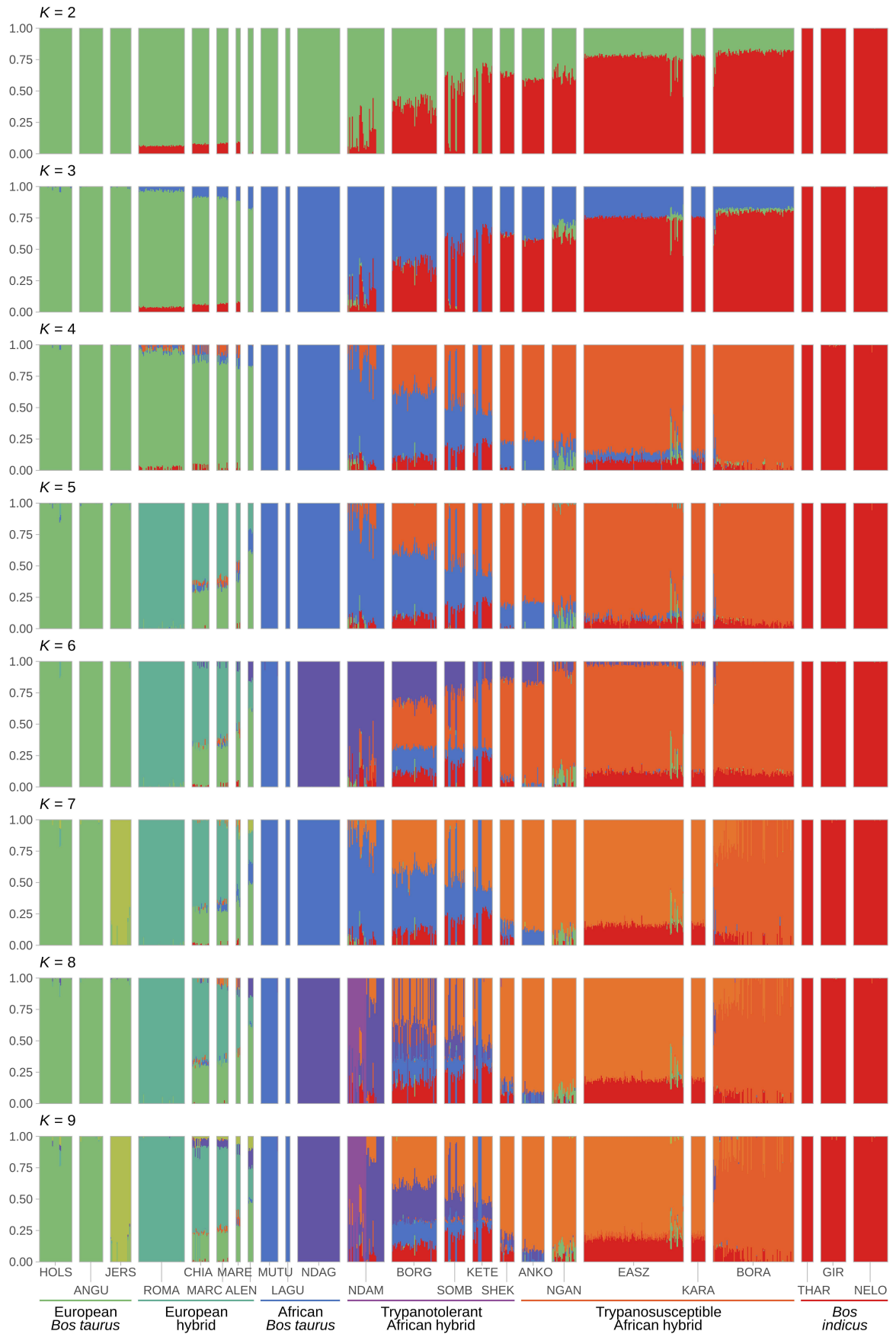
Supplementary Figure A.2. Tukey box plots showing the distribution of inbreeding values (F) for the high-density SNP data for each population. Outliers are indicated with a black outline.



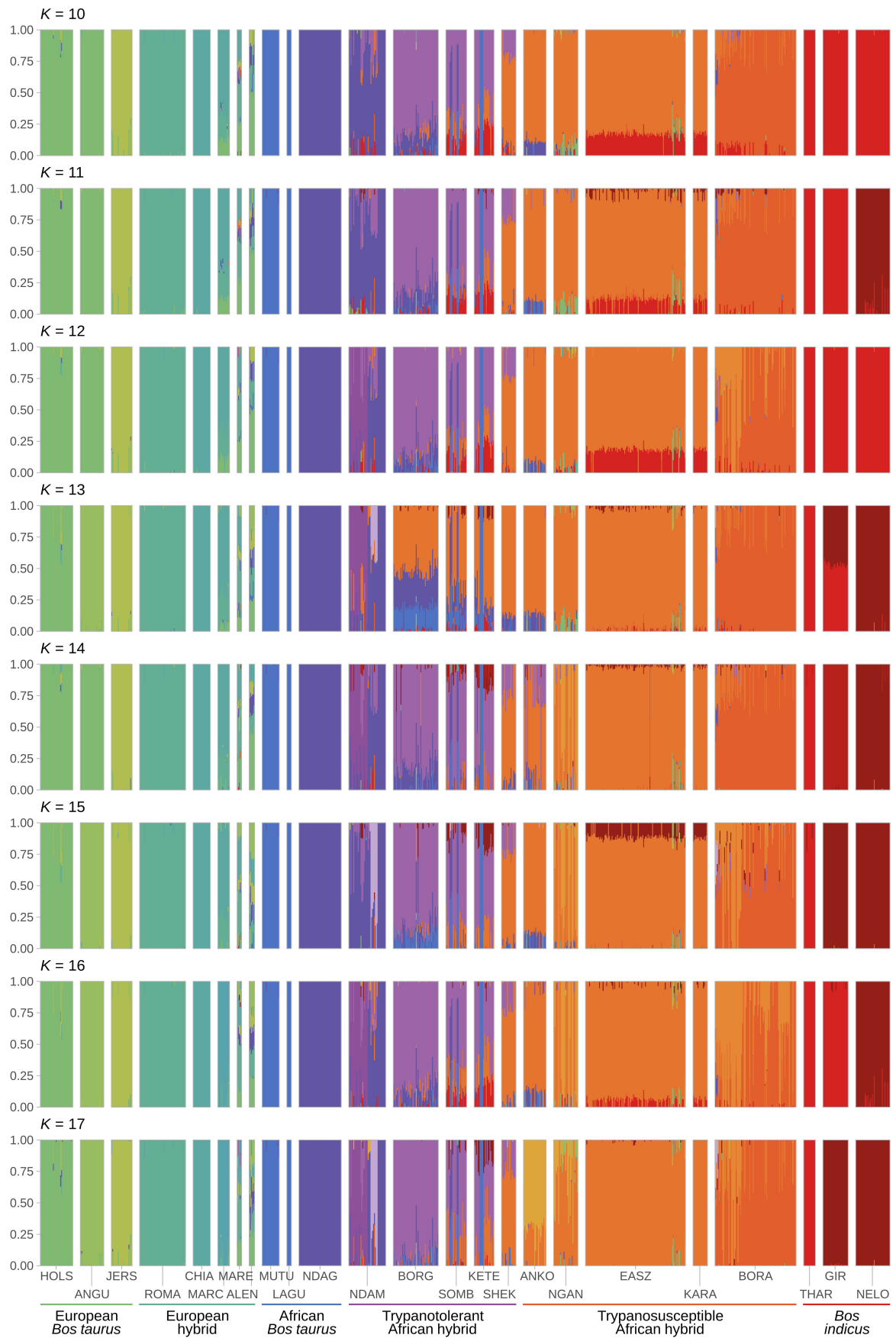
Supplementary Figure A.3. Tukey box plots showing the distribution of inbreeding values (F) for the low-density SNP data for each population after inbreeding filters were applied. Outliers are indicated with a black outline.



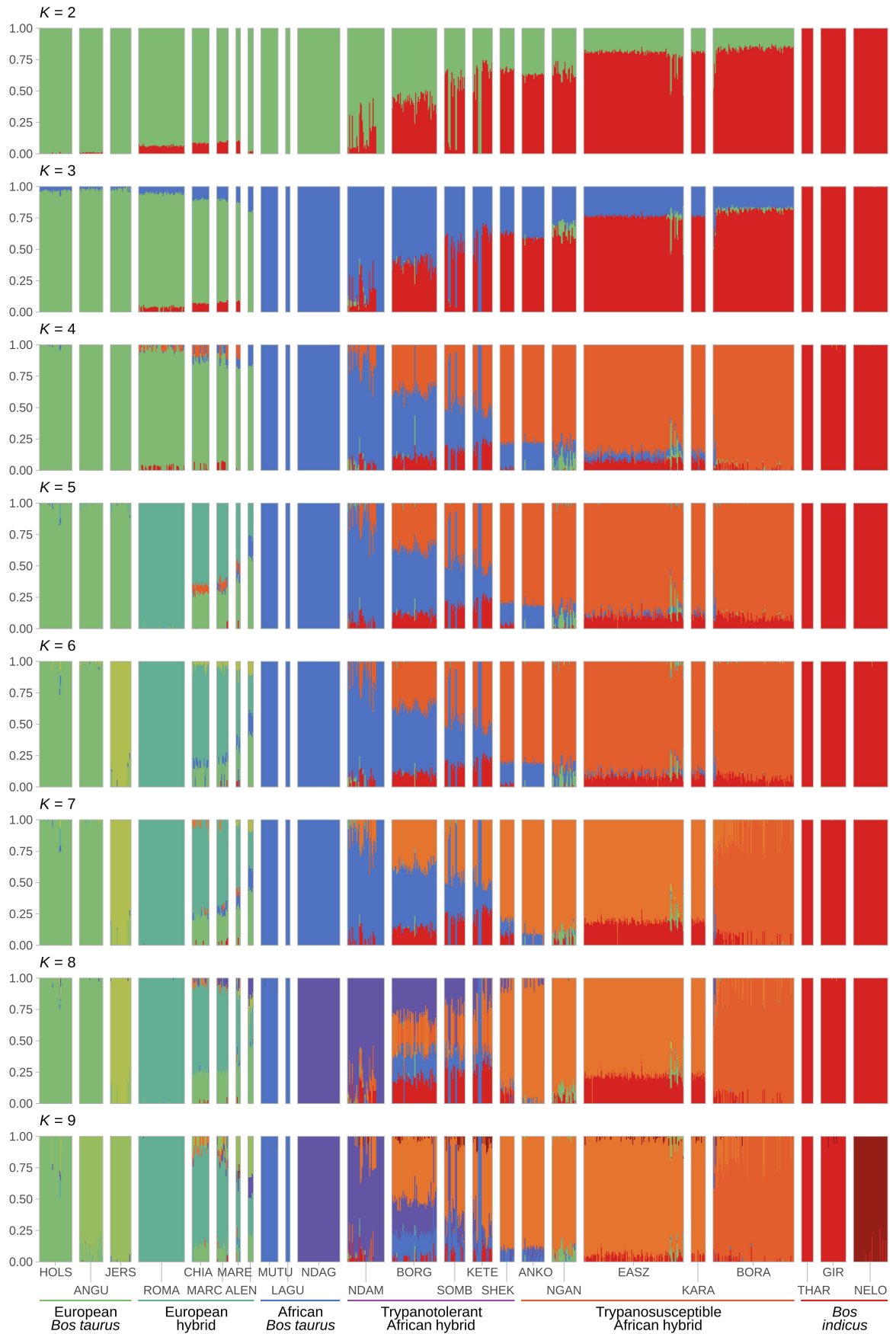
Supplementary Figure A.4. A. Principal component analysis (PCA) of the selected low-density SNP data set with cattle samples coloured according to population showing the first two principal components (PC1 and PC2), and **B.** bar chart of the proportion of variance for the top ten PCs.



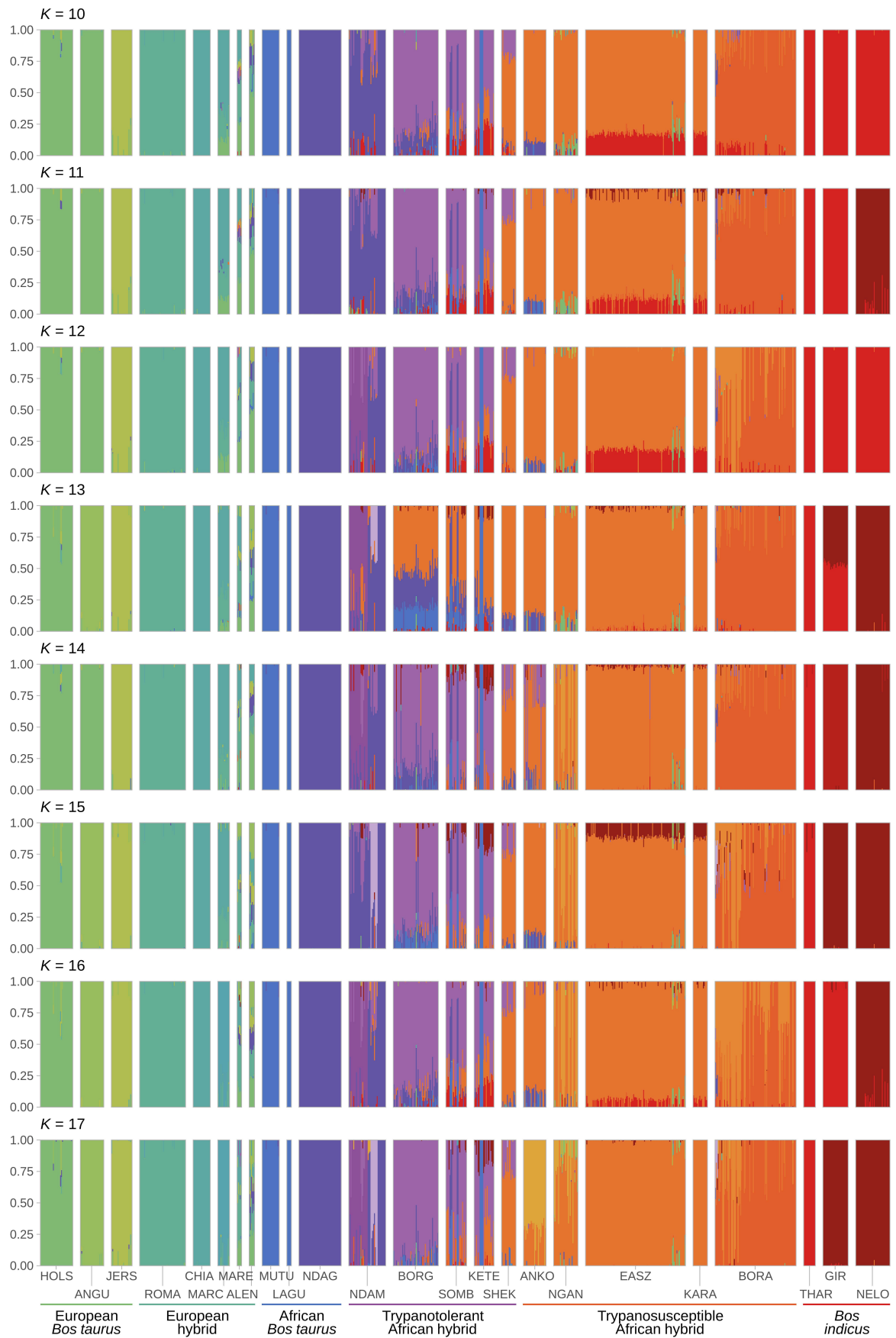
Supplementary Figure A.5. Hierarchical clustering of cattle samples using the high-density SNP data set. Results are shown for a range of assumed values for the number of ancestral populations ($K = 2-9$).



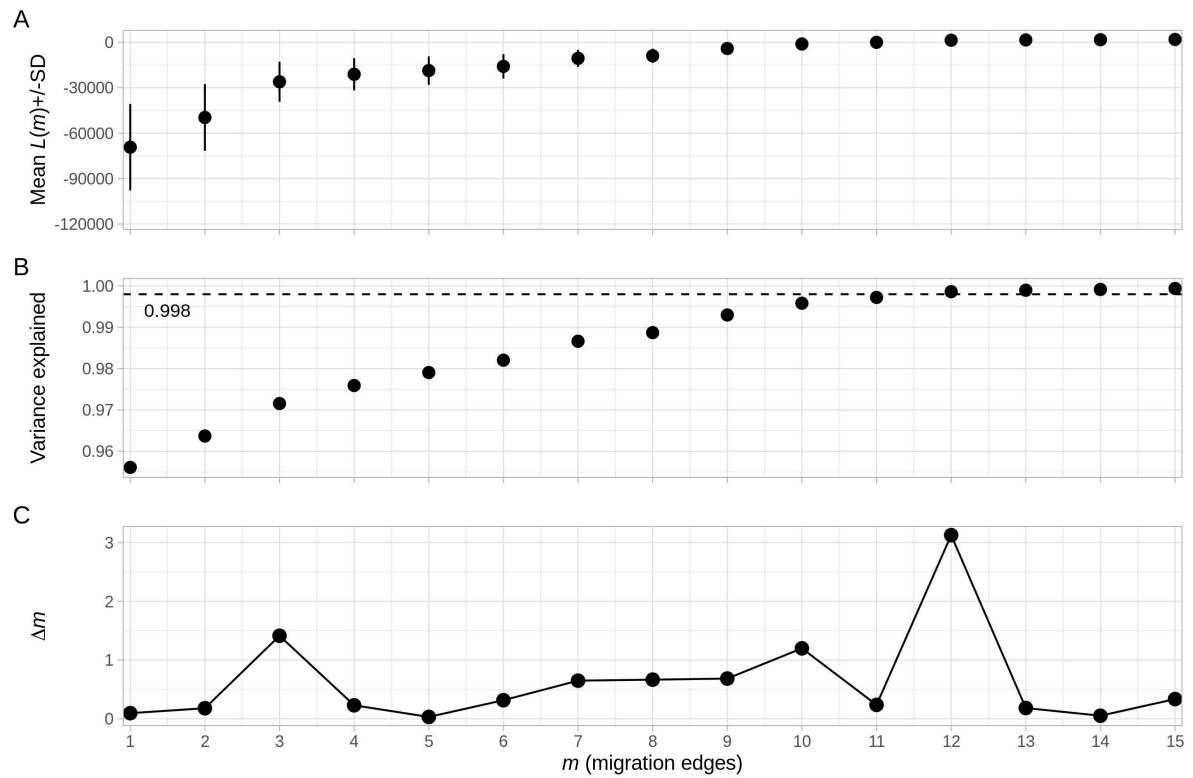
Supplementary Figure A.6. Hierarchical clustering of cattle samples using the high-density SNP data set. Results are shown for a range of assumed values for the number of ancestral populations ($K = 10\text{--}17$).



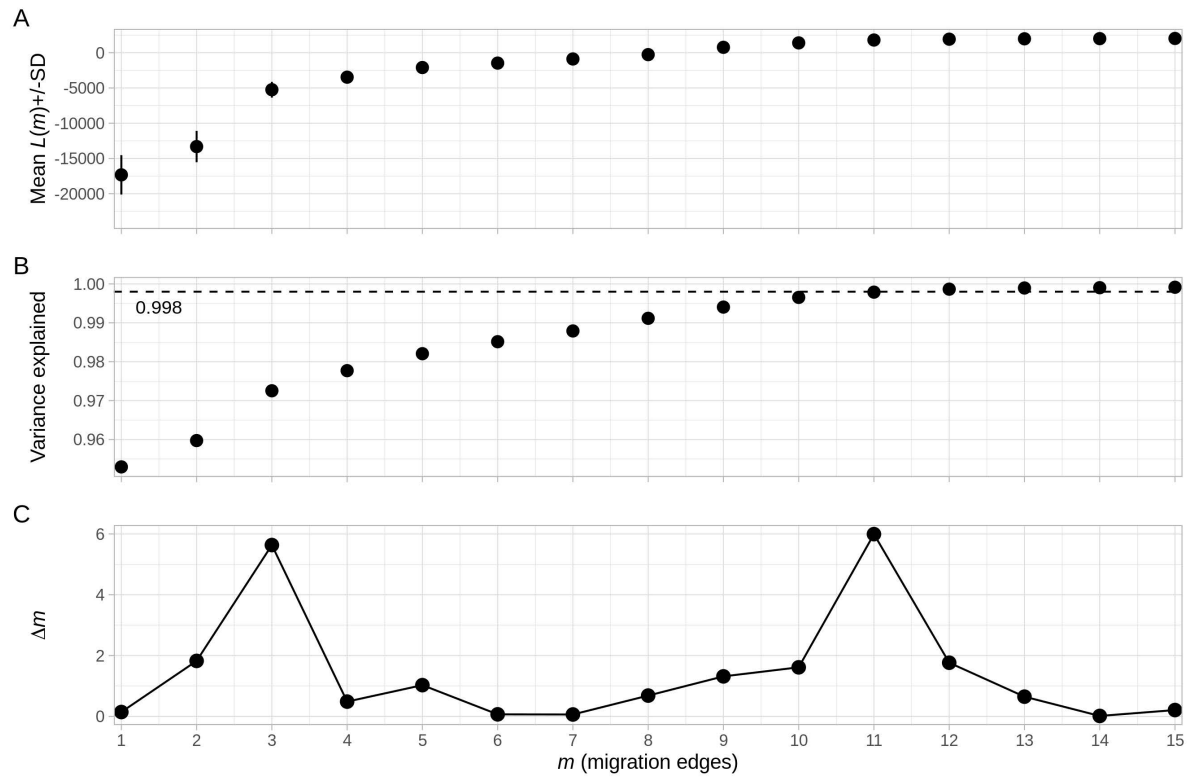
Supplementary Figure A.7. Hierarchical clustering of cattle samples using the low-density SNP data set. Results are shown for a range of assumed values for the number of ancestral populations ($K = 2-9$).



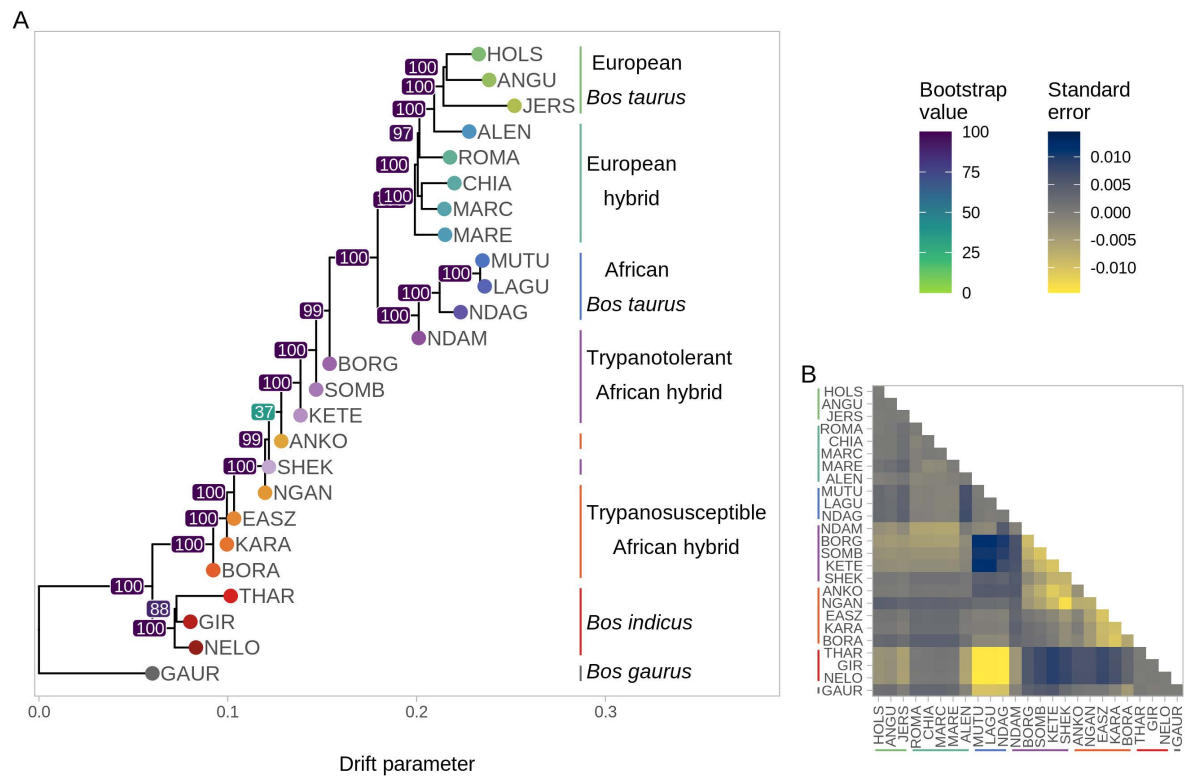
Supplementary Figure A.8. Hierarchical clustering of cattle samples using the low-density SNP data set. Results are shown for a range of assumed values for the number of ancestral populations ($K = 10$ – 17).



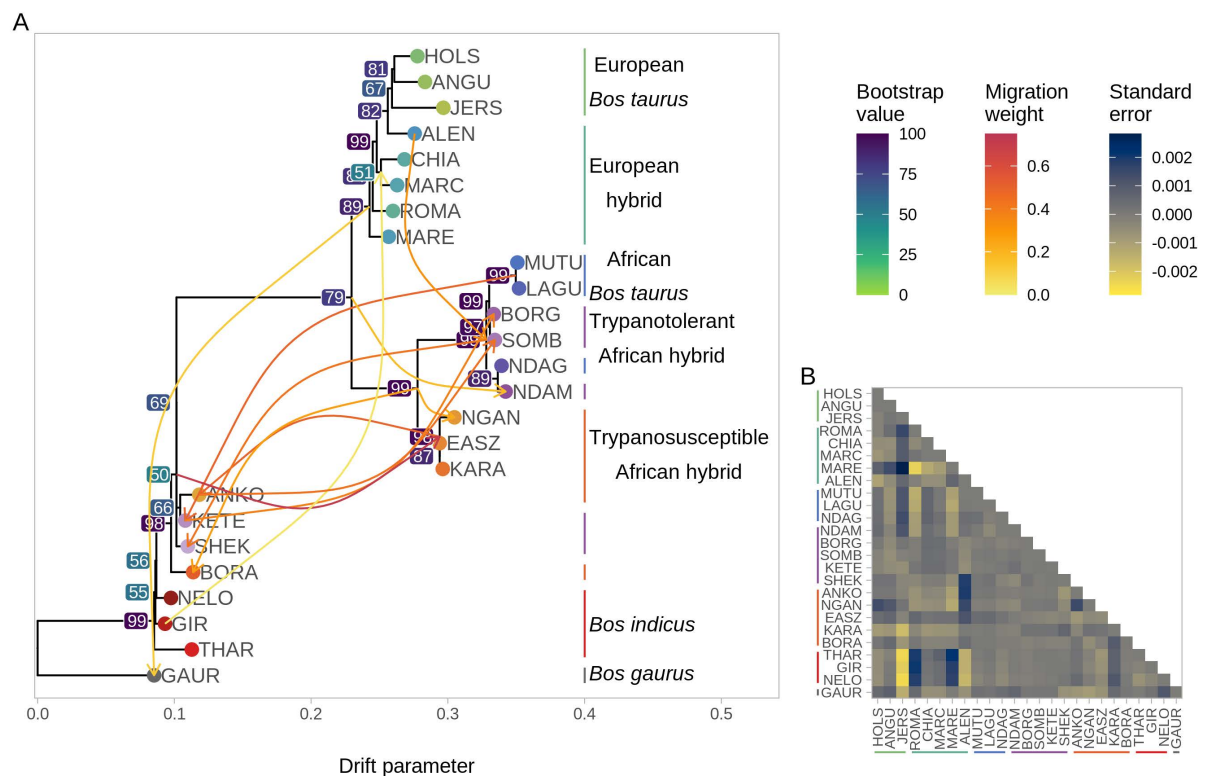
Supplementary Figure A.9. OptM results for the high-density SNP data set. **A.** the mean and standard deviation (SD) across 10 iterations for the composite likelihood ($L(m)$). **B.** the proportion of variance explained showing the 99.8% threshold (horizontal dotted line) recommended by Pickrell and Pritchard (2012). **C.** the second-order rate of change (Δm) across migration edges (m).



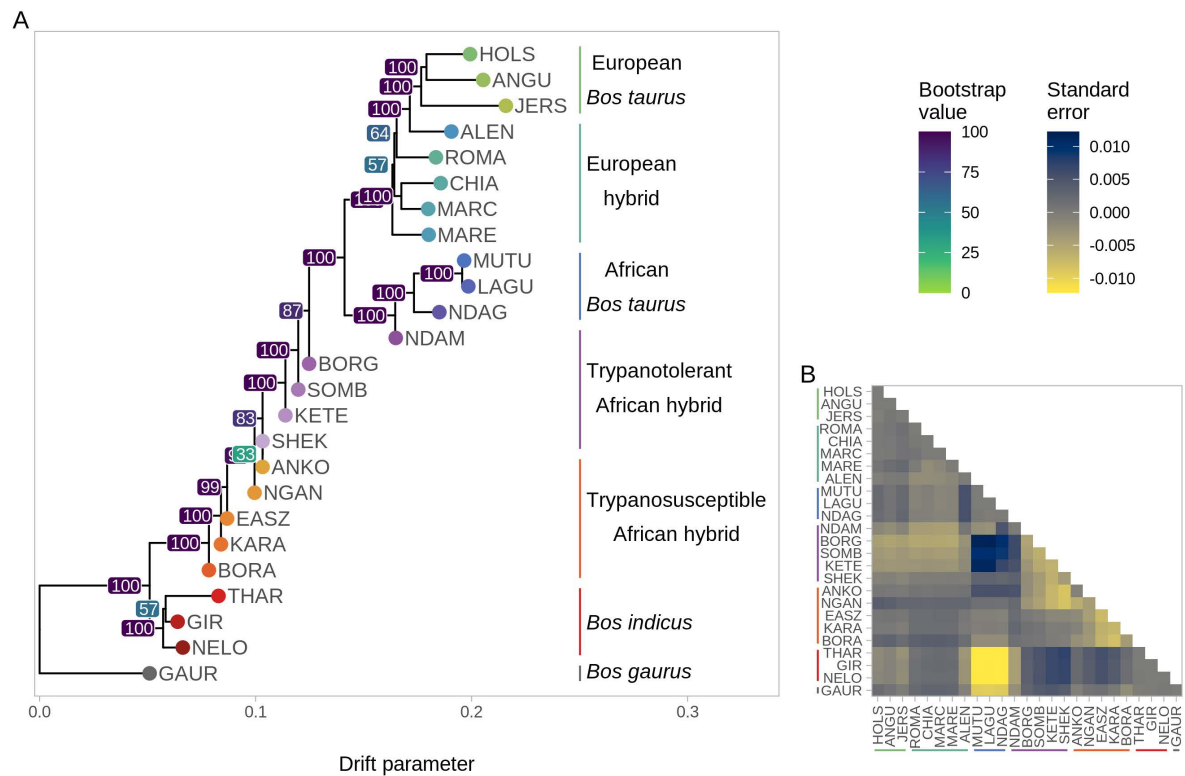
Supplementary Figure A.10. OptM results for the low-density SNP data set. **A.** the mean and standard deviation (SD) across 10 iterations for the composite likelihood ($L(m)$). **B.** the proportion of variance explained showing the 99.8% threshold (horizontal dotted line) recommended by Pickrell and Pritchard (2012). **C.** the second-order rate of change (Δm) across migration edges (m).



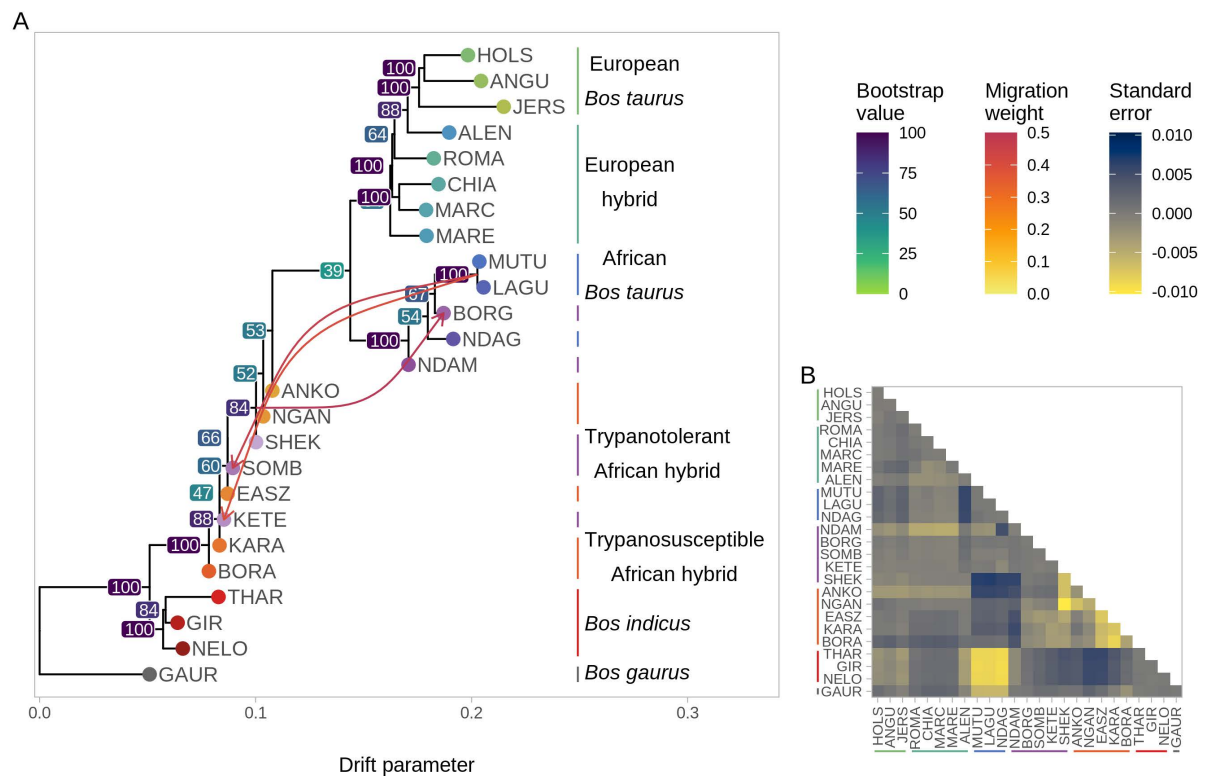
Supplementary Figure A.11. A. TreeMix phylogenetic tree for the high-density SNP data set with bootstrap values. **B.** a heatmap showing the standard error.



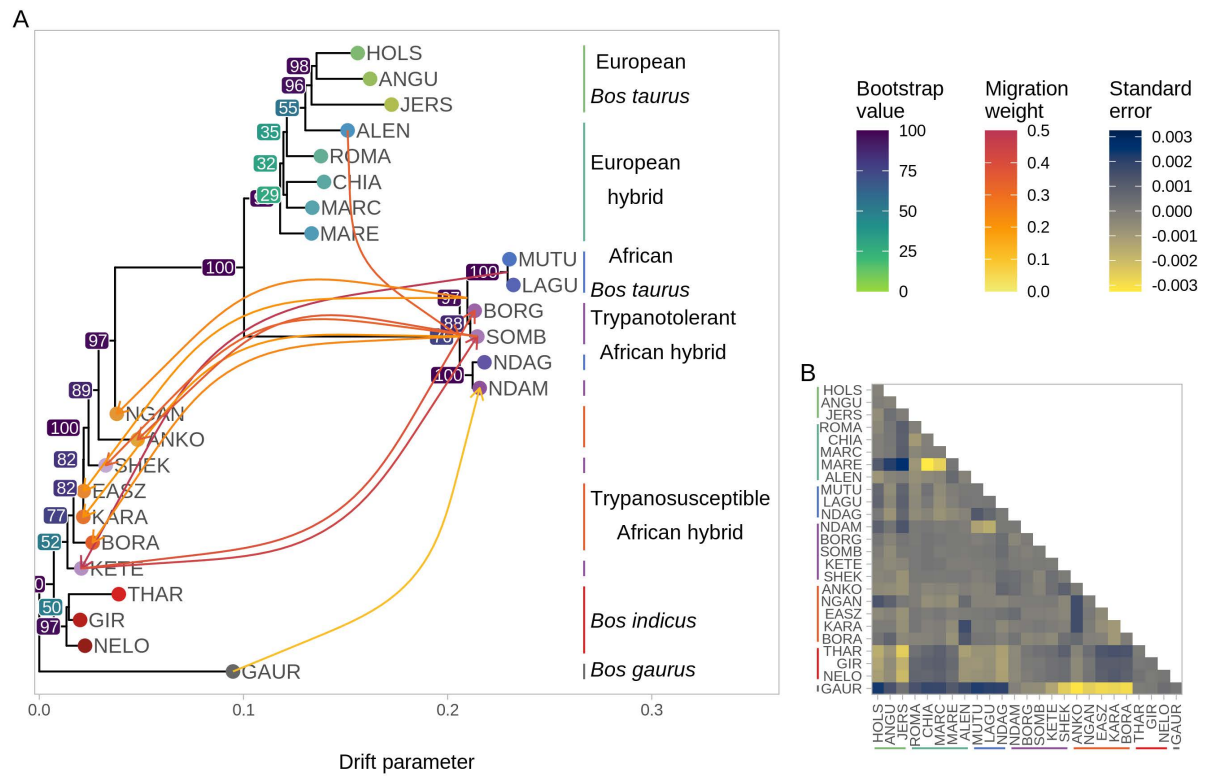
Supplementary Figure A.12. A. TreeMix phylogenetic tree for the high-density SNP data set with bootstrap values and 12 migration edges. **B.** a heatmap showing standard error.



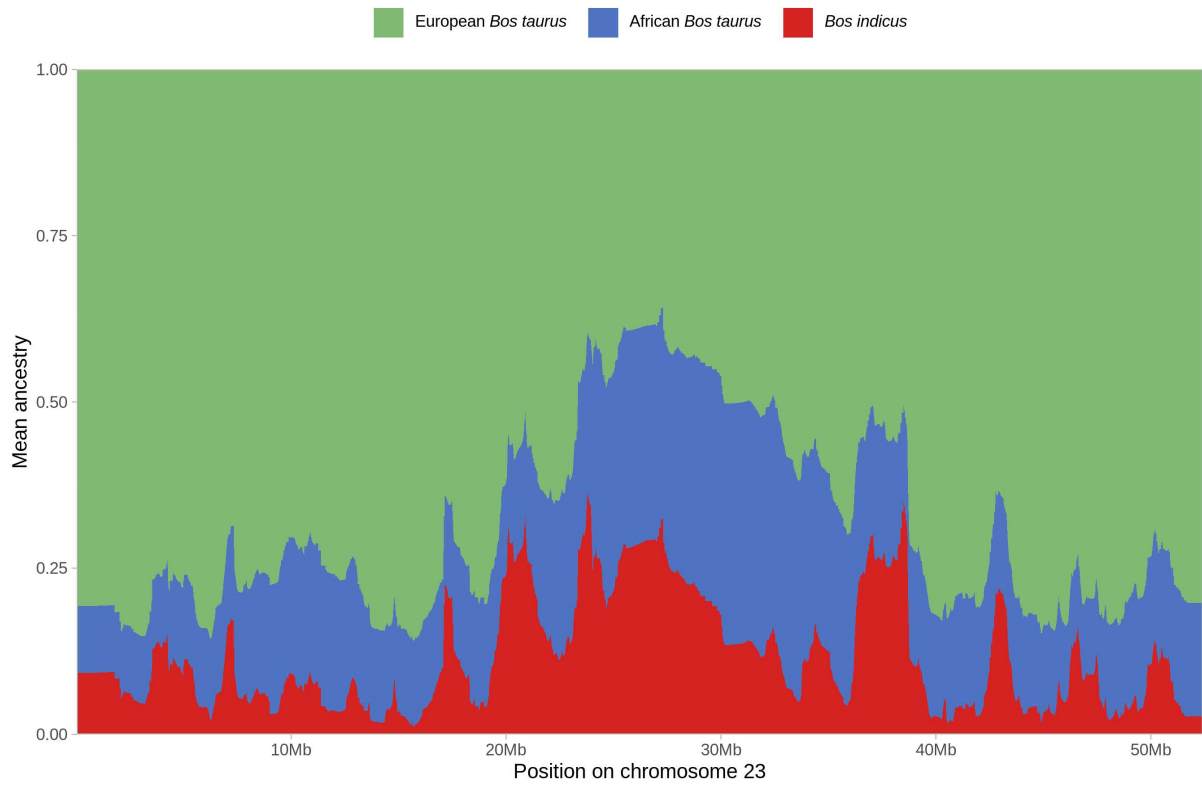
Supplementary Figure A.13. A. TreeMix phylogenetic tree for the low-density SNP data set with bootstrap values. **B.** a heatmap showing the standard error.



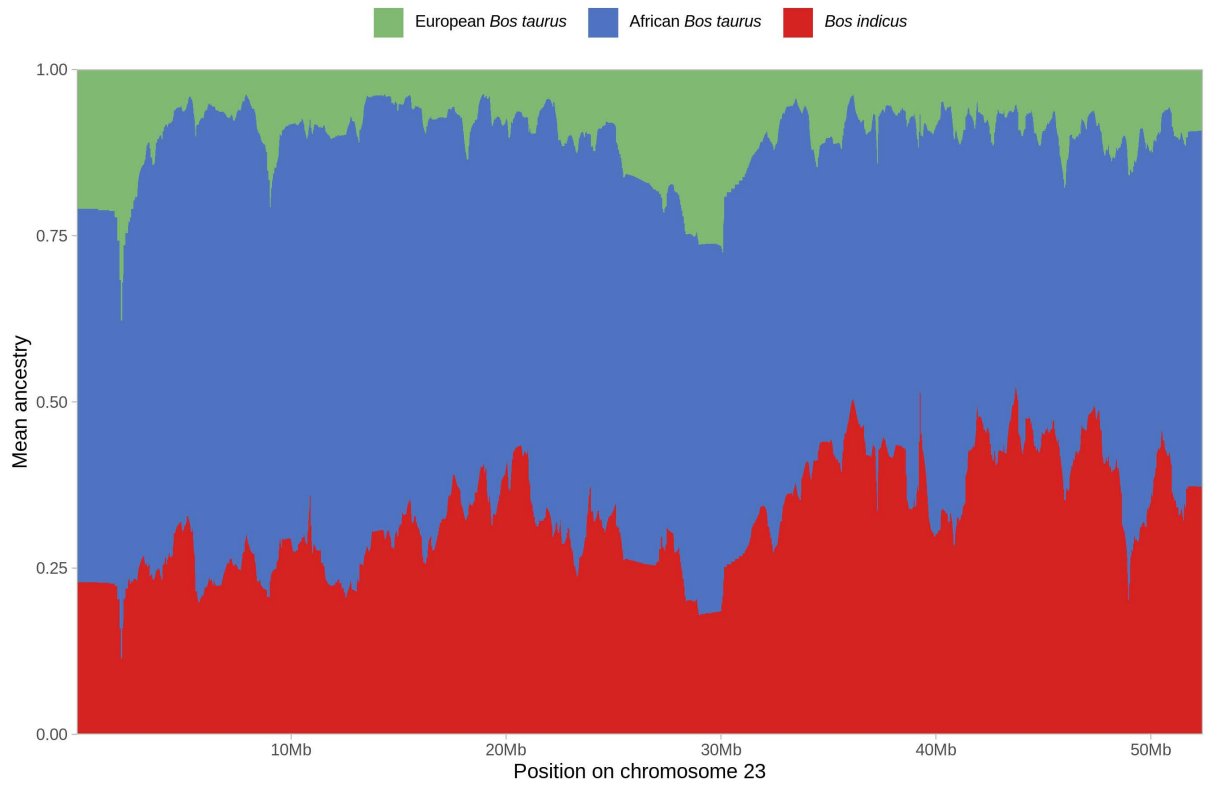
Supplementary Figure A.14. A. TreeMix phylogenetic tree for the low-density SNP data set with bootstrap values and three migration edges. **B.** a heatmap showing standard error.



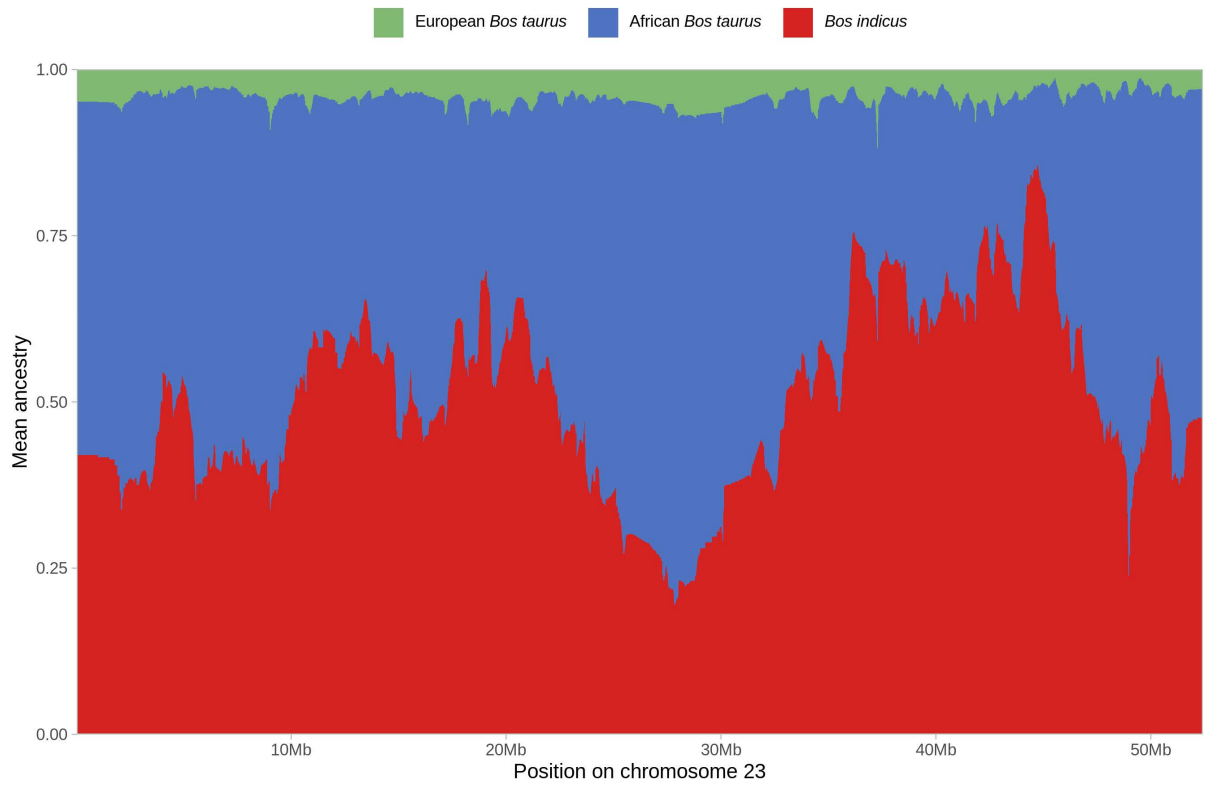
Supplementary Figure A.15. A. TreeMix phylogenetic tree for the high-density SNP data set with bootstrap values and 11 migration edges. **B.** a heatmap showing standard error.



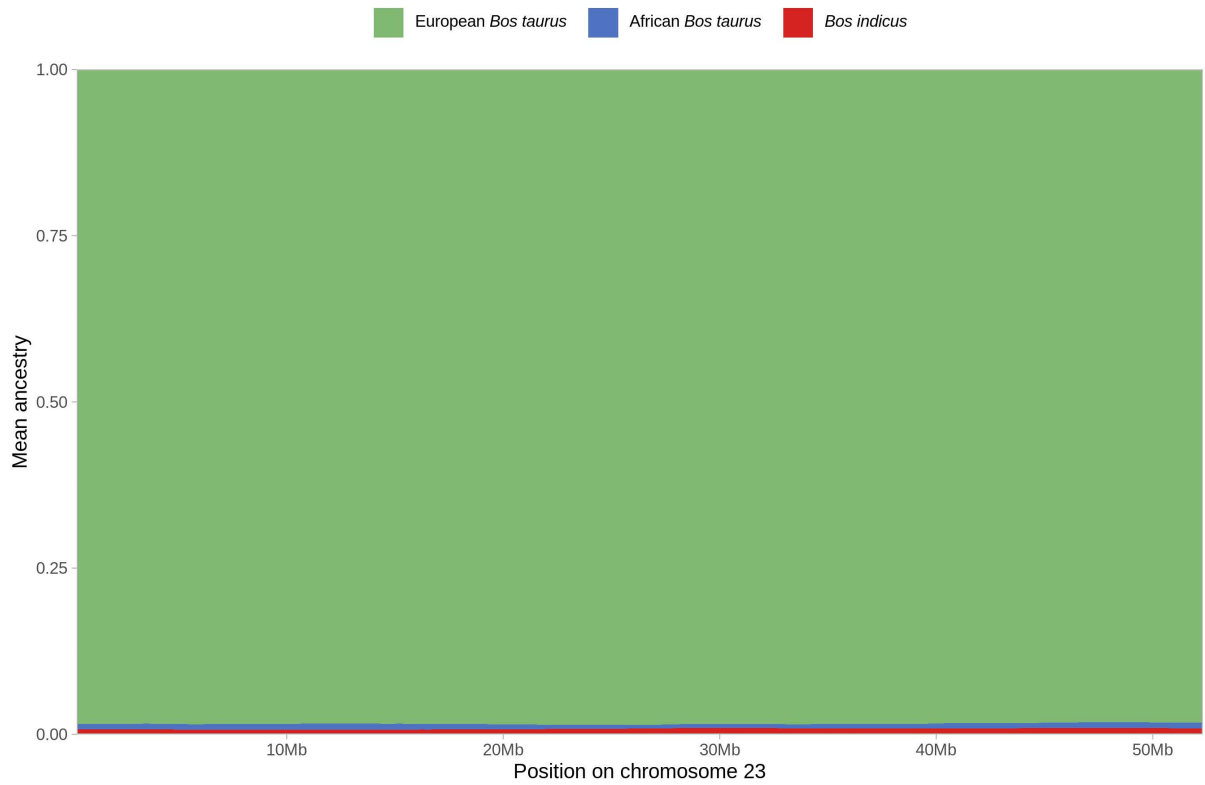
Supplementary Figure A.16. Local ancestry results for chromosome 23 (BTA23) for the European hybrid group calculated using MOSAIC with the high-density SNP data set. Each vertical line on the chromosome plot represents a SNP and is coloured according to the ancestry results.



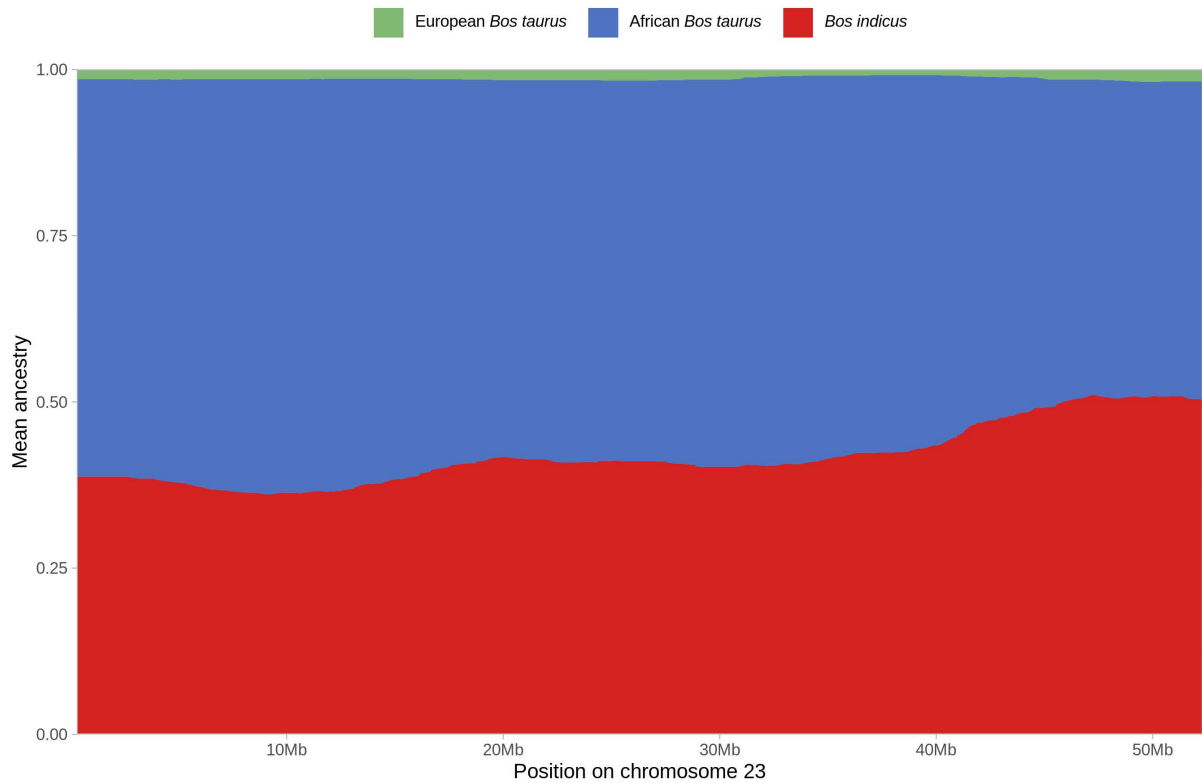
Supplementary Figure A.17. Local ancestry results for chromosome 23 (BTA23) for the African trypanotolerant hybrid group calculated using MOSAIC with the high-density SNP data set. Each vertical line on the chromosome plot represents a SNP and is coloured according to the ancestry results.



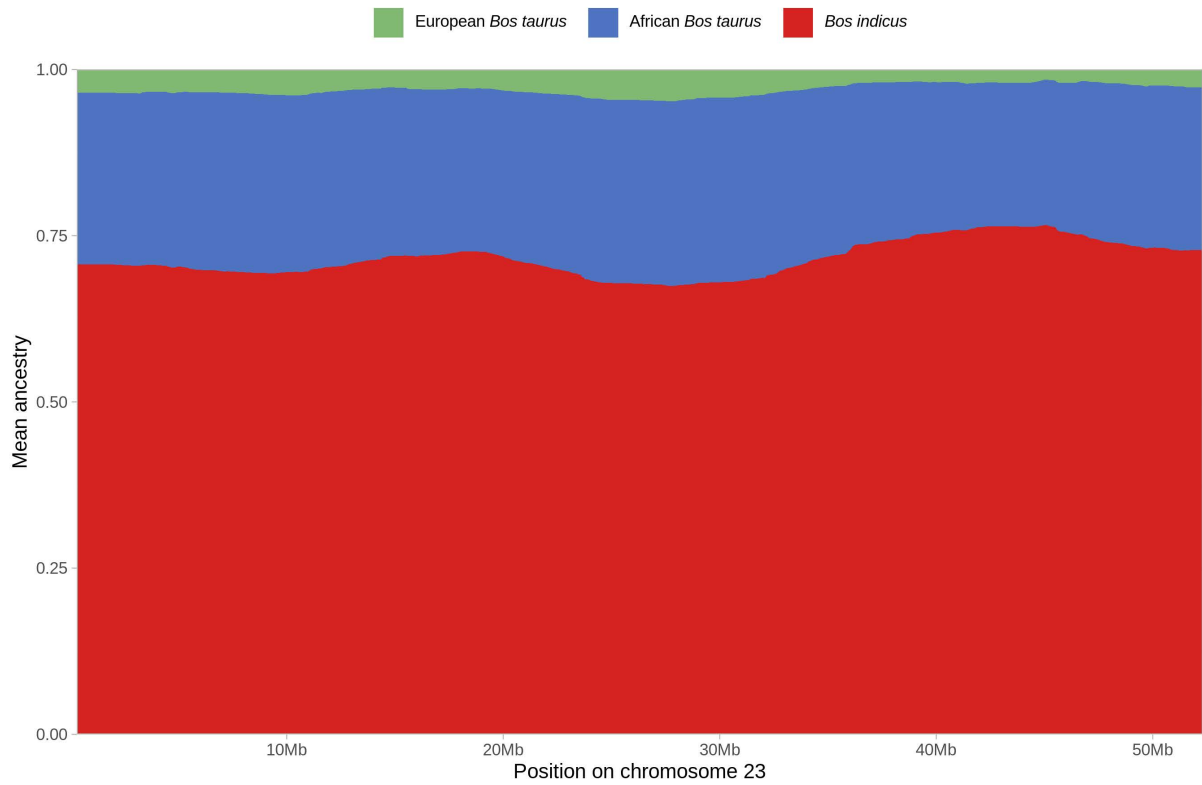
Supplementary Figure A.18. Local ancestry results for chromosome 23 (BTA23) for the African trypanosusceptible hybrid group calculated using MOSAIC with the high-density SNP data set. Each vertical line on the chromosome plot represents a SNP and is coloured according to the ancestry results.



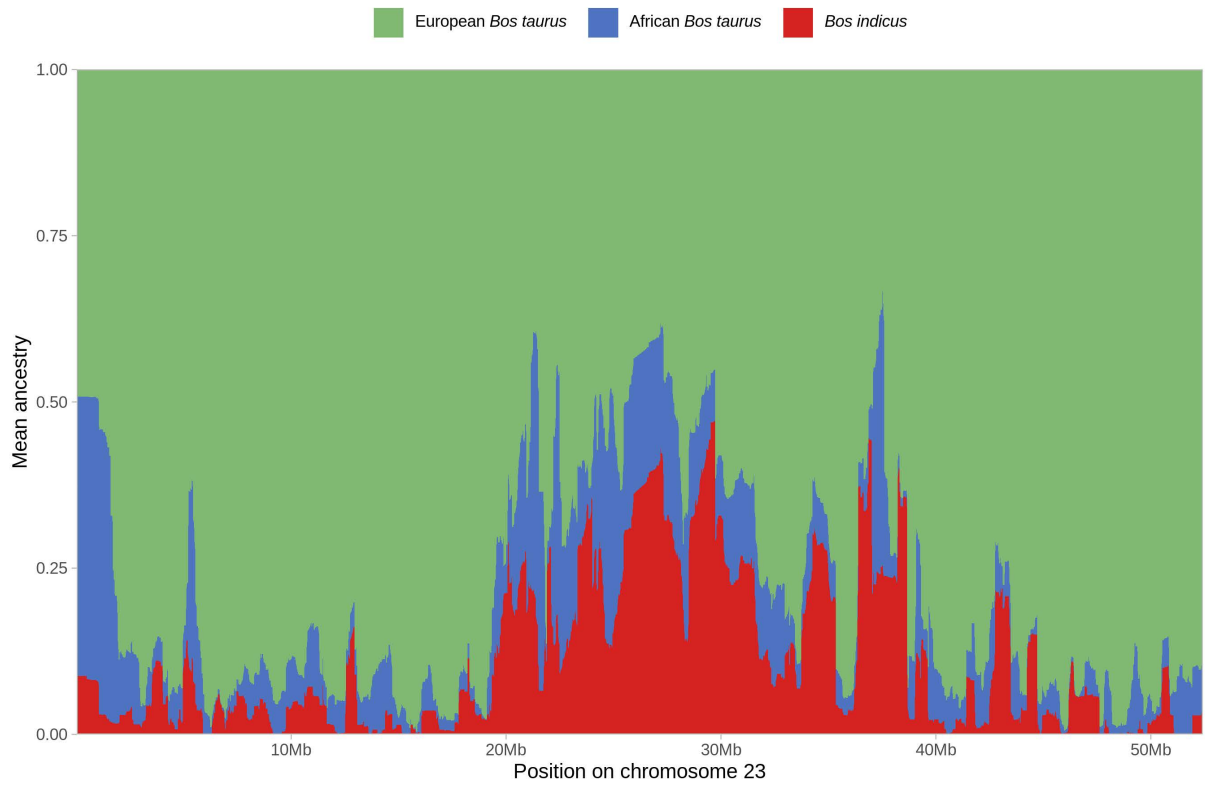
Supplementary Figure A.19. Local ancestry results for chromosome 23 (BTA23) for the European hybrid group calculated using MOSAIC with the low-density SNP data set. Each vertical line on the chromosome plot represents a SNP and is coloured according to the ancestry results.



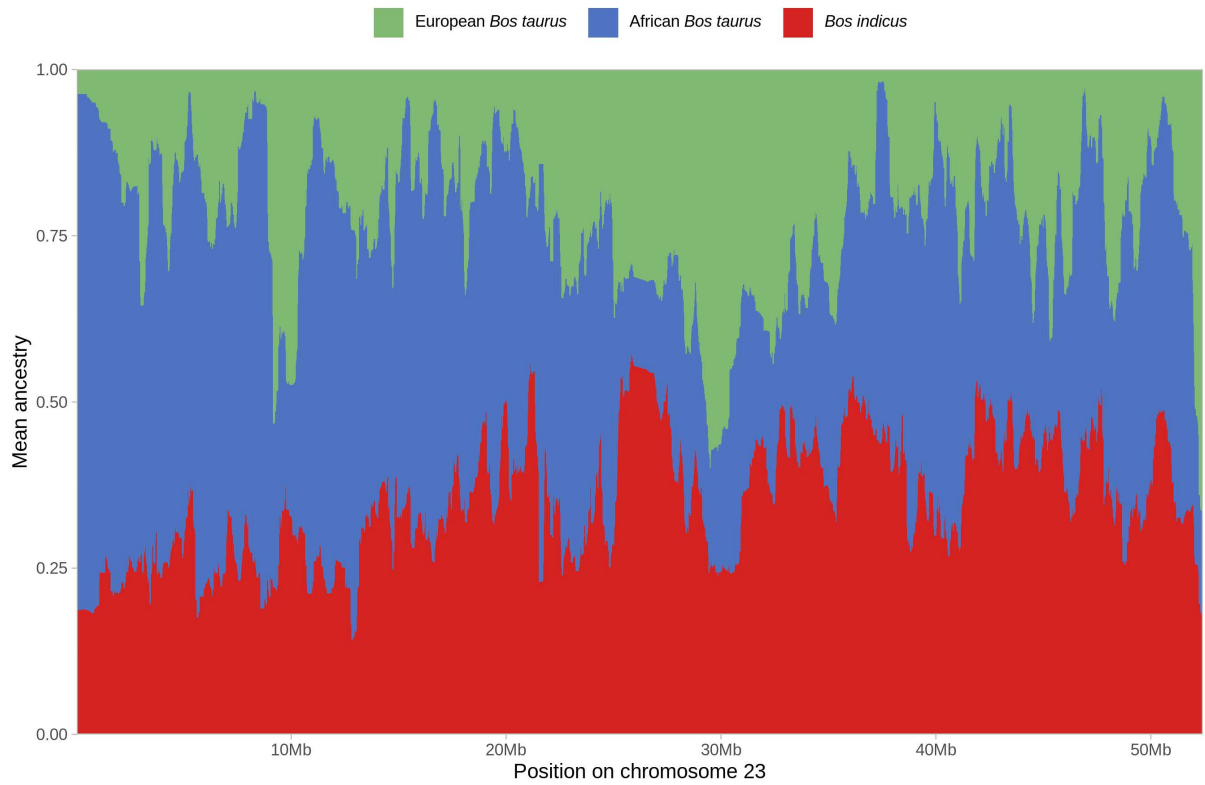
Supplementary Figure A.20. Local ancestry results for chromosome 23 (BTA23) for the trypanotolerant African hybrid group calculated using MOSAIC with the low-density SNP data set. Each vertical line on the chromosome plot represents a SNP and is coloured according to the ancestry results.



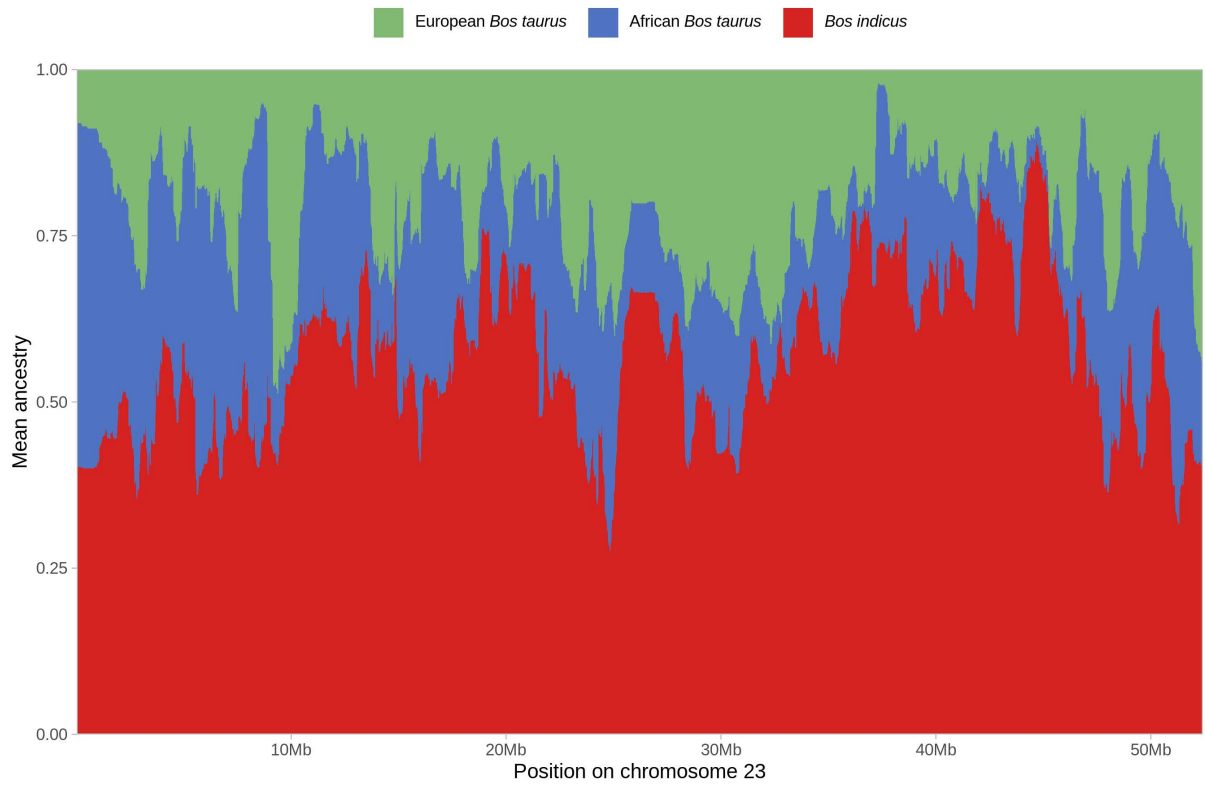
Supplementary Figure A.21. Local ancestry results for chromosome 23 (BTA23) for the trypanosusceptible African hybrid group calculated using MOSAIC with the low-density SNP data set. Each vertical line on the chromosome plot represents a SNP and is coloured according to the ancestry results.



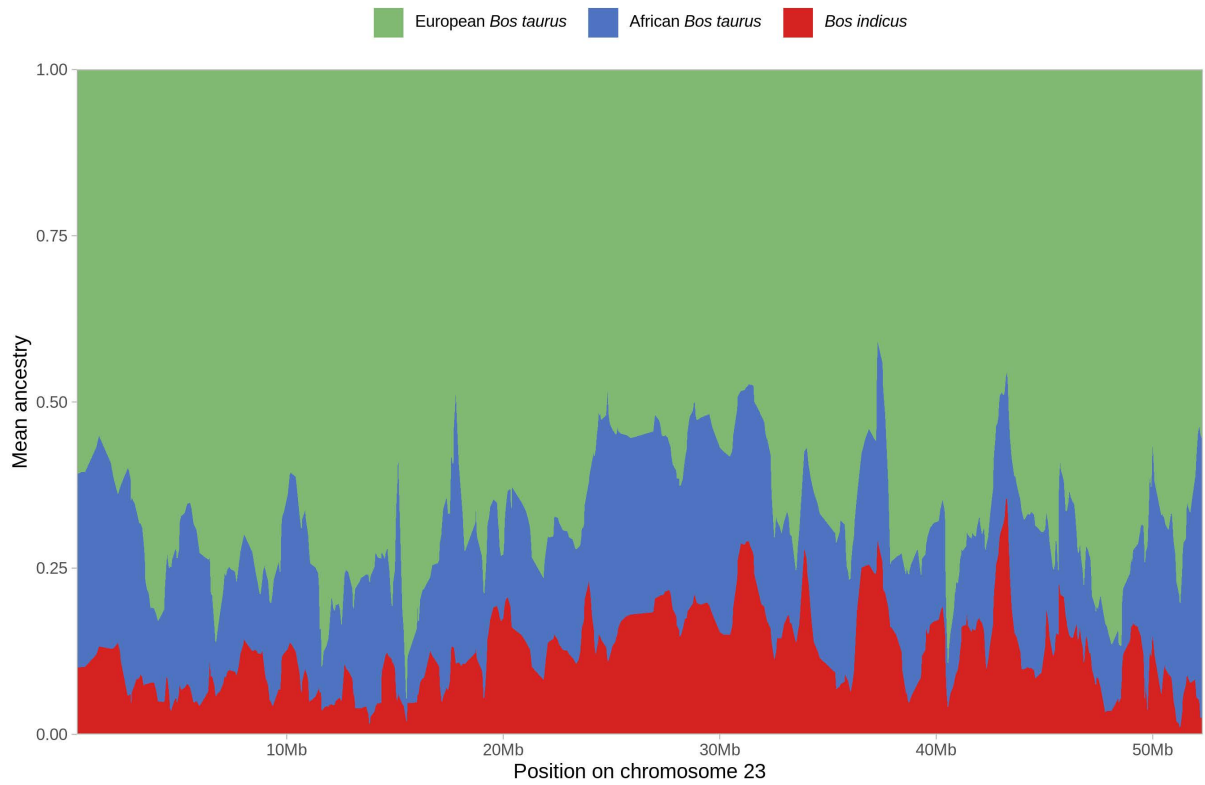
Supplementary Figure A.22. Local ancestry results for chromosome 23 (BTA23) for the European hybrid group calculated using ELAI with the high-density SNP data set. Each vertical line on the chromosome plot represents a SNP and is coloured according to the ancestry results.



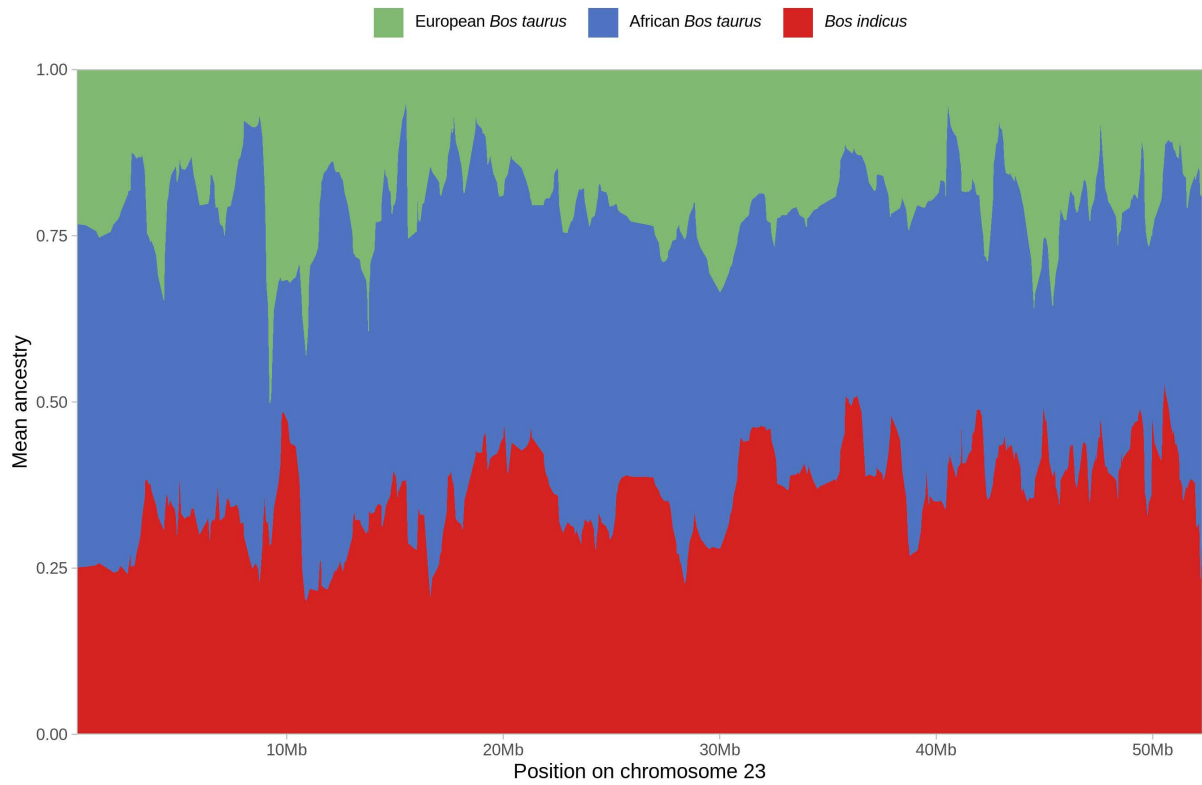
Supplementary Figure A.23. Local ancestry results for chromosome 23 (BTA23) for the trypanotolerant African hybrid group calculated using ELAI with the high-density SNP data set. Each vertical line on the chromosome plot represents a SNP and is coloured according to the ancestry results.



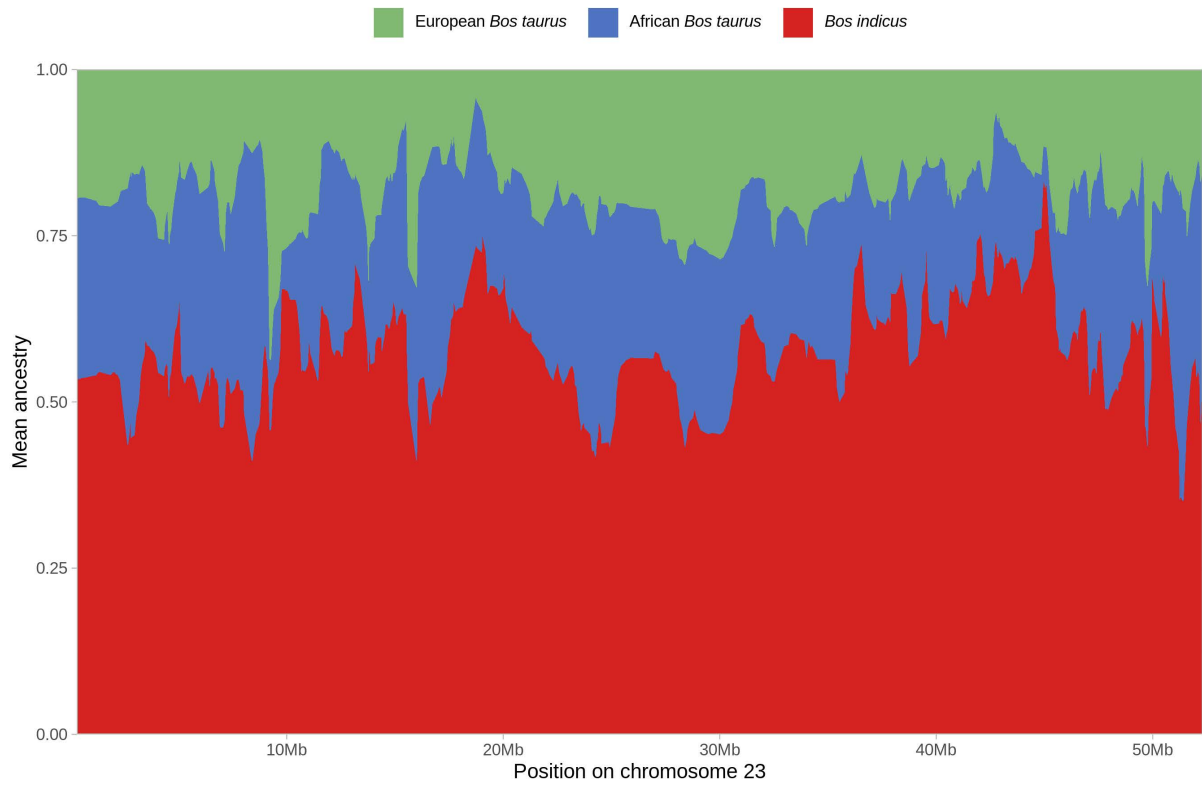
Supplementary Figure A.24. Local ancestry results for chromosome 23 (BTA23) for the trypanosusceptible African hybrid group calculated using ELAI with the high-density SNP data set. Each vertical line on the chromosome plot represents a SNP and is coloured according to the ancestry results.



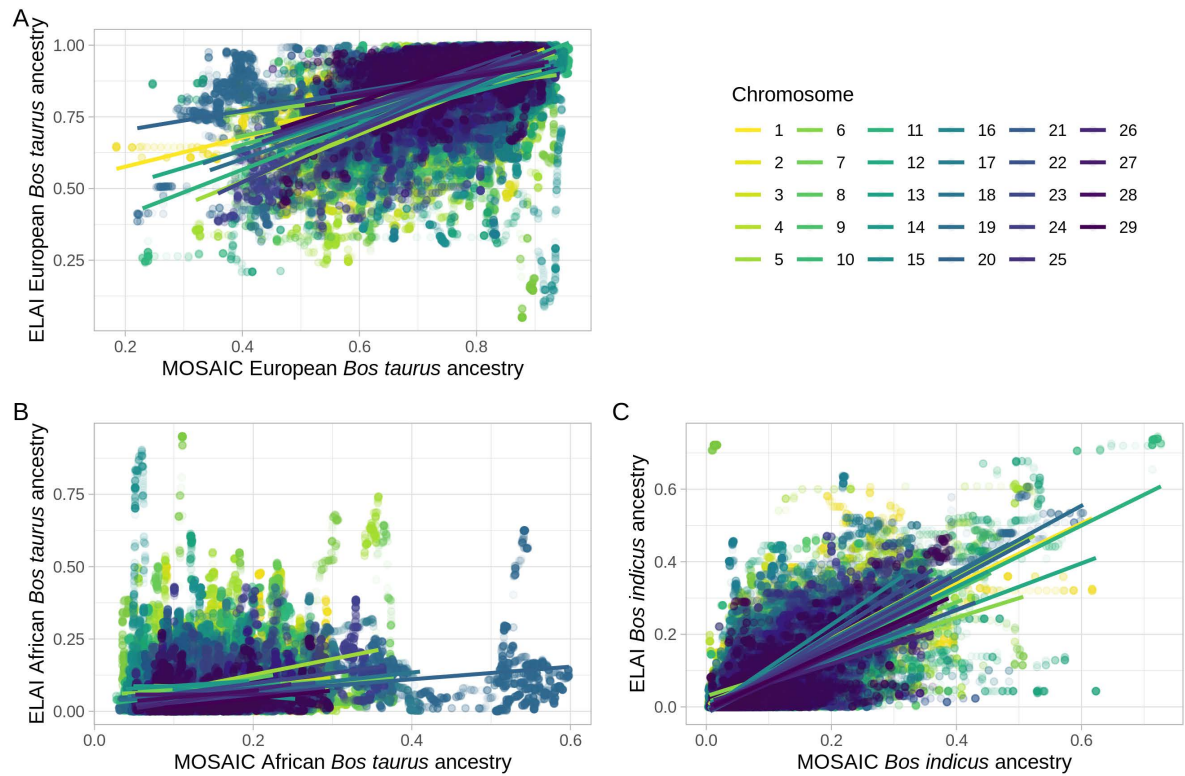
Supplementary Figure A.25. Local ancestry results for chromosome 23 (BTA23) for the European hybrid group calculated using ELAI with the low-density SNP data set. Each vertical line on the chromosome plot represents a SNP and is coloured according to the ancestry results.



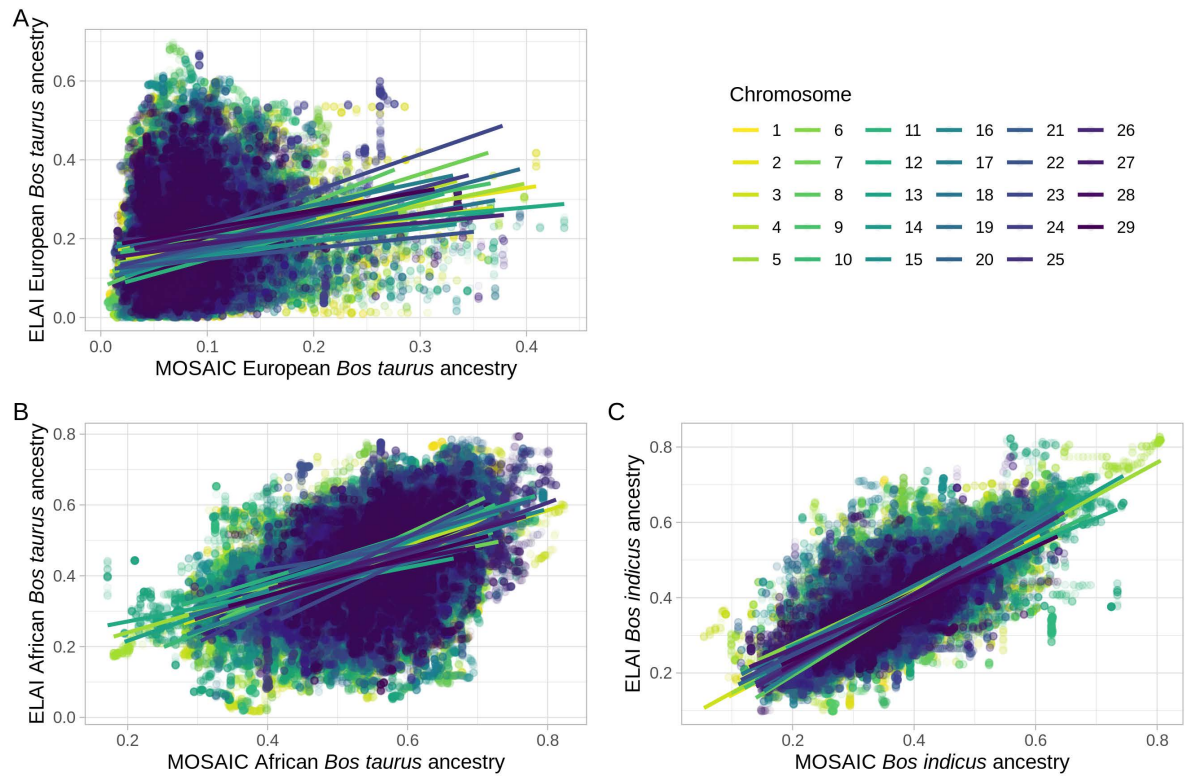
Supplementary Figure A.26. Local ancestry results for chromosome 23 (BTA23) for the trypanotolerant African hybrid group calculated using ELAI with the low-density SNP data set. Each vertical line on the chromosome plot represents a SNP and is coloured according to the ancestry results.



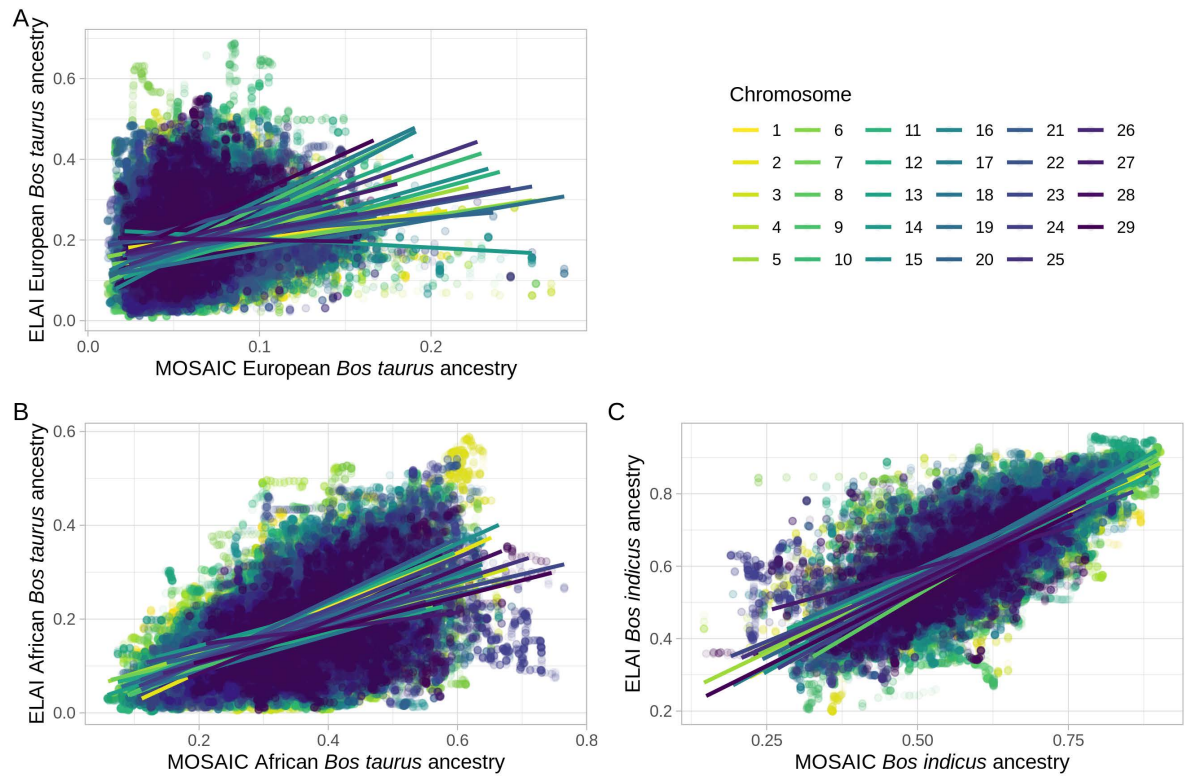
Supplementary Figure A.27. Local ancestry results for chromosome 23 (BTA23) for the trypanosusceptible African hybrid group calculated using ELAI with the low-density SNP data set. Each vertical line on the chromosome plot represents a SNP and is coloured according to the ancestry results.



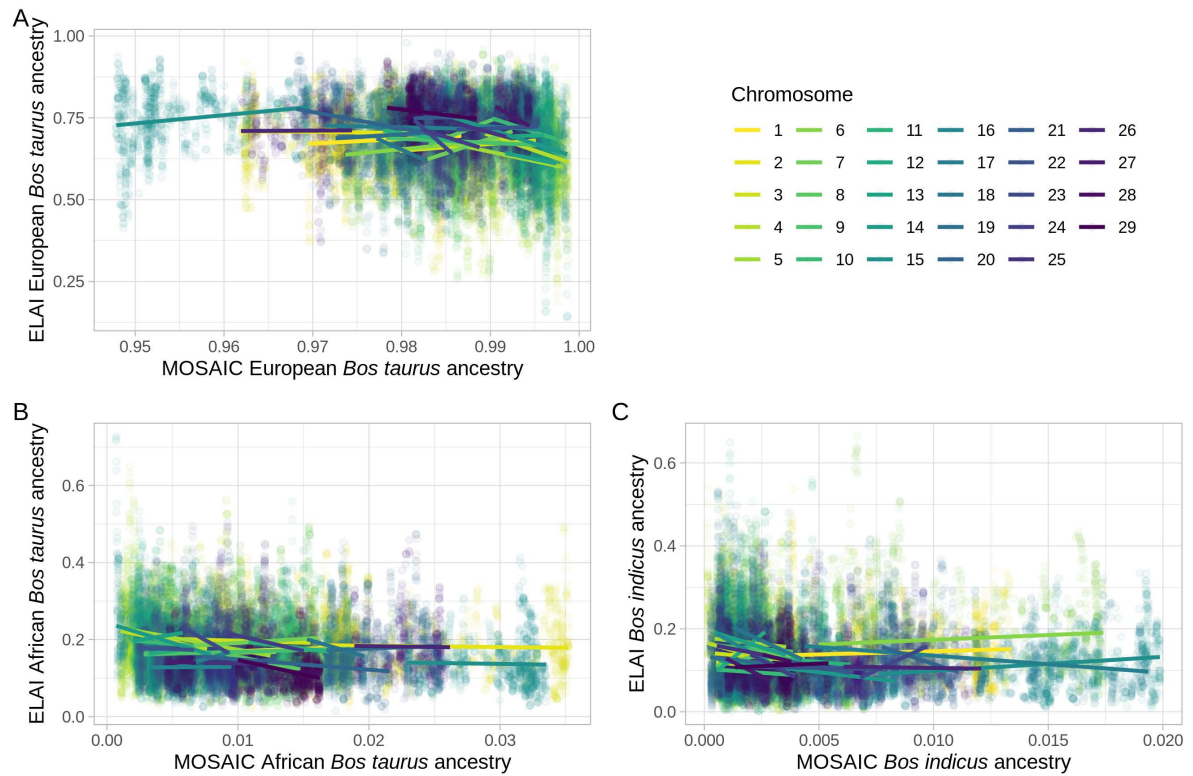
Supplementary Figure A.28. Correlation plots for the European hybrid local ancestry results (high-density SNP data set). Each dot represents a SNP coloured according to chromosome. The positions on the x- and y-axes indicate the weighted mean ancestry proportions for that SNP according to MOSAIC and ELAI, respectively. **A.** European *B. taurus*, **B.** African *B. taurus*, and **C.** *B. indicus* ancestry components. The lines represent linear models for each chromosome, coloured accordingly.



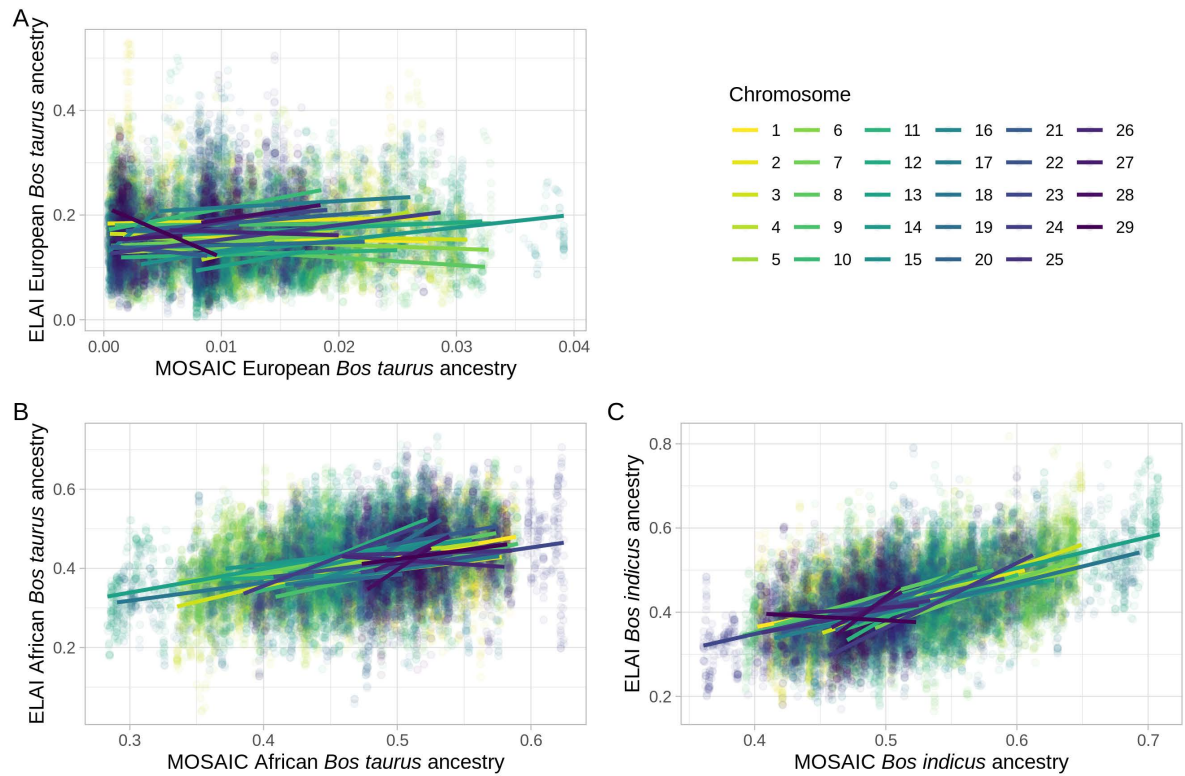
Supplementary Figure A.29. Correlation plots for the trypanotolerant African hybrid local ancestry results (high-density SNP data set). Each dot represents a SNP coloured according to chromosome. The positions on the x- and y-axes indicate the weighted mean ancestry proportions for that SNP according to MOSAIC and ELAI, respectively. **A.** European *B. taurus*, **B.** African *B. taurus*, and **C.** *B. indicus* ancestry components. The lines represent linear models for each chromosome, coloured accordingly.



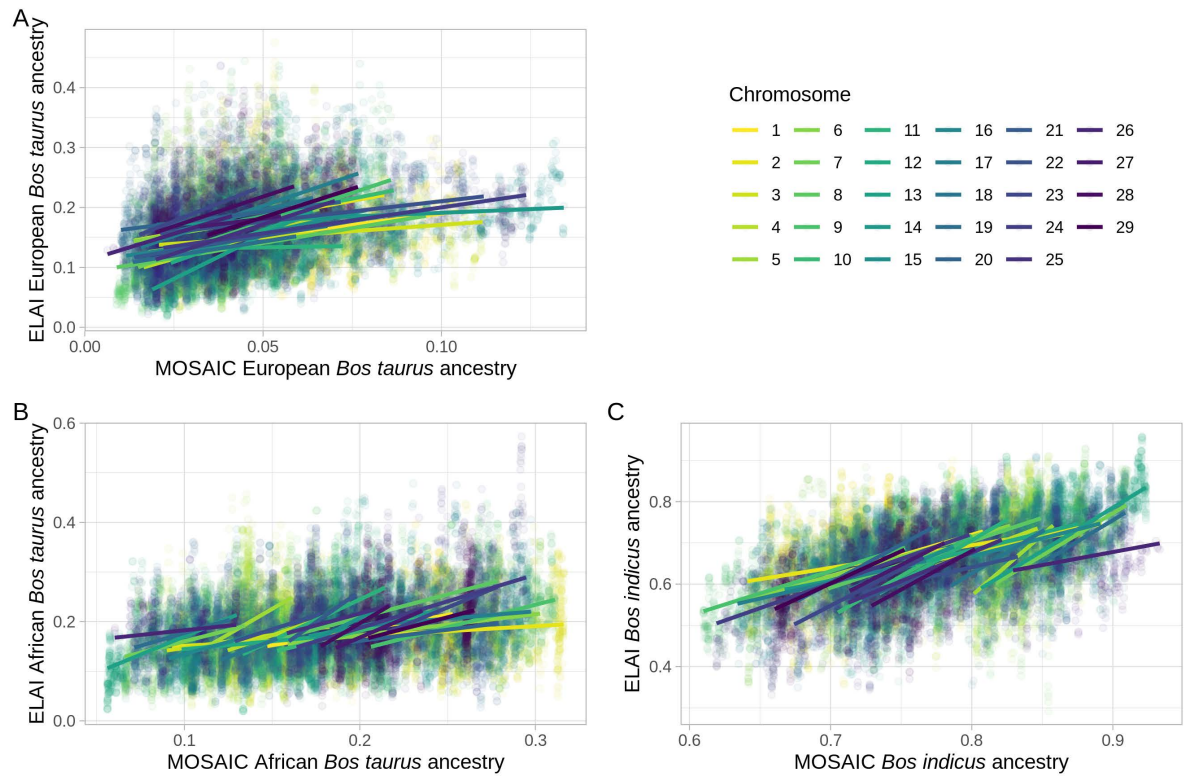
Supplementary Figure A.30. Correlation plots for the trypanosusceptible African hybrid local ancestry results (high-density SNP data set). Each dot represents a SNP coloured according to chromosome. The positions on the x- and y-axes indicate the weighted mean ancestry proportions for that SNP according to MOSAIC and ELAI, respectively. **A.** European *B. taurus*, **B.** African *B. taurus*, and **C.** *B. indicus* ancestry components. The lines represent linear models for each chromosome, coloured accordingly.



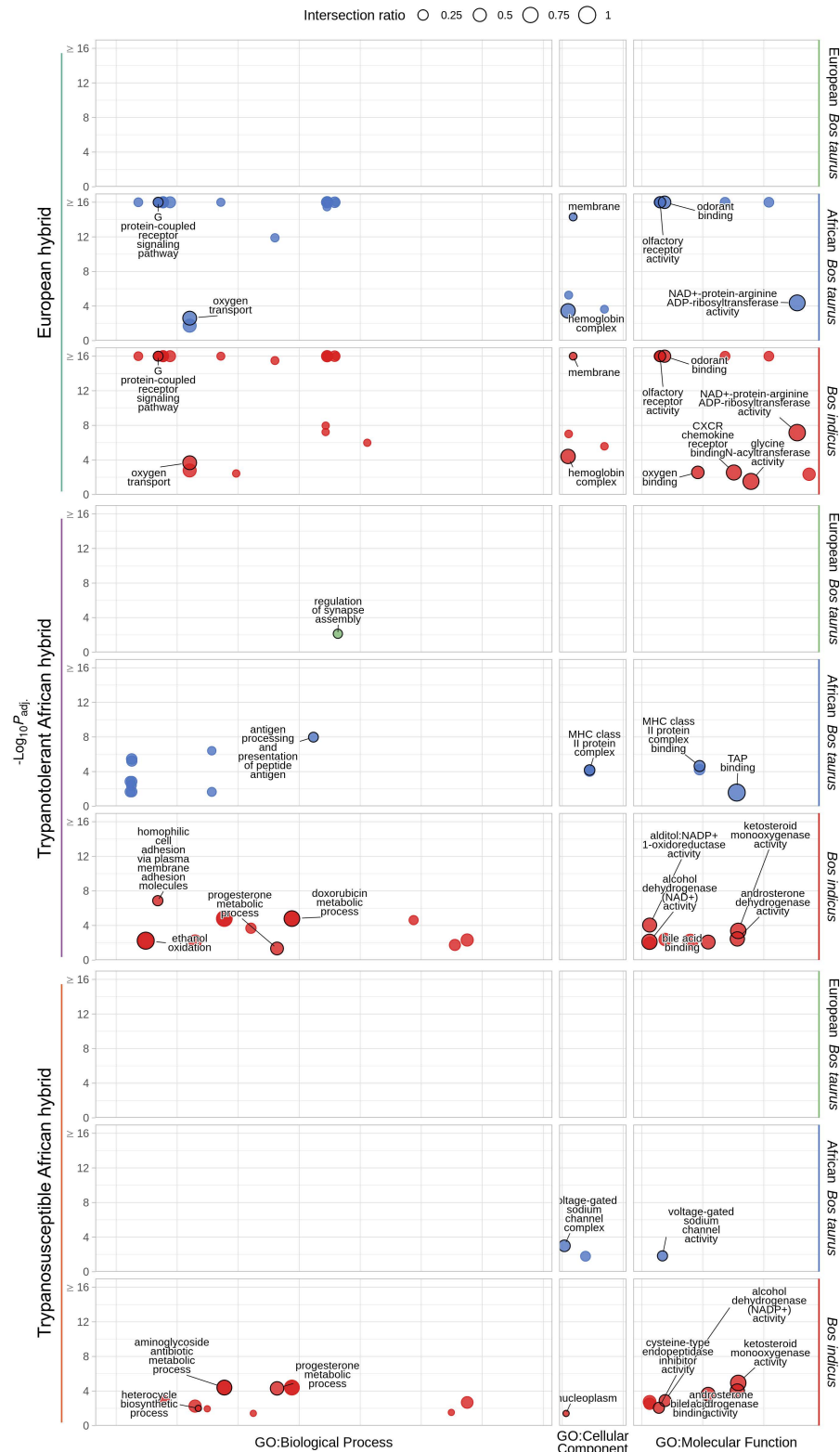
Supplementary Figure A.31. Correlation plots for the European hybrid local ancestry results (low-density SNP data set). Each dot represents a SNP coloured according to chromosome. The positions on the x- and y-axes indicate the weighted mean ancestry proportions for that SNP according to MOSAIC and ELAI, respectively. **A.** European *B. taurus*, **B.** African *B. taurus*, and **C.** *B. indicus* ancestry components. The lines represent linear models for each chromosome, coloured accordingly.



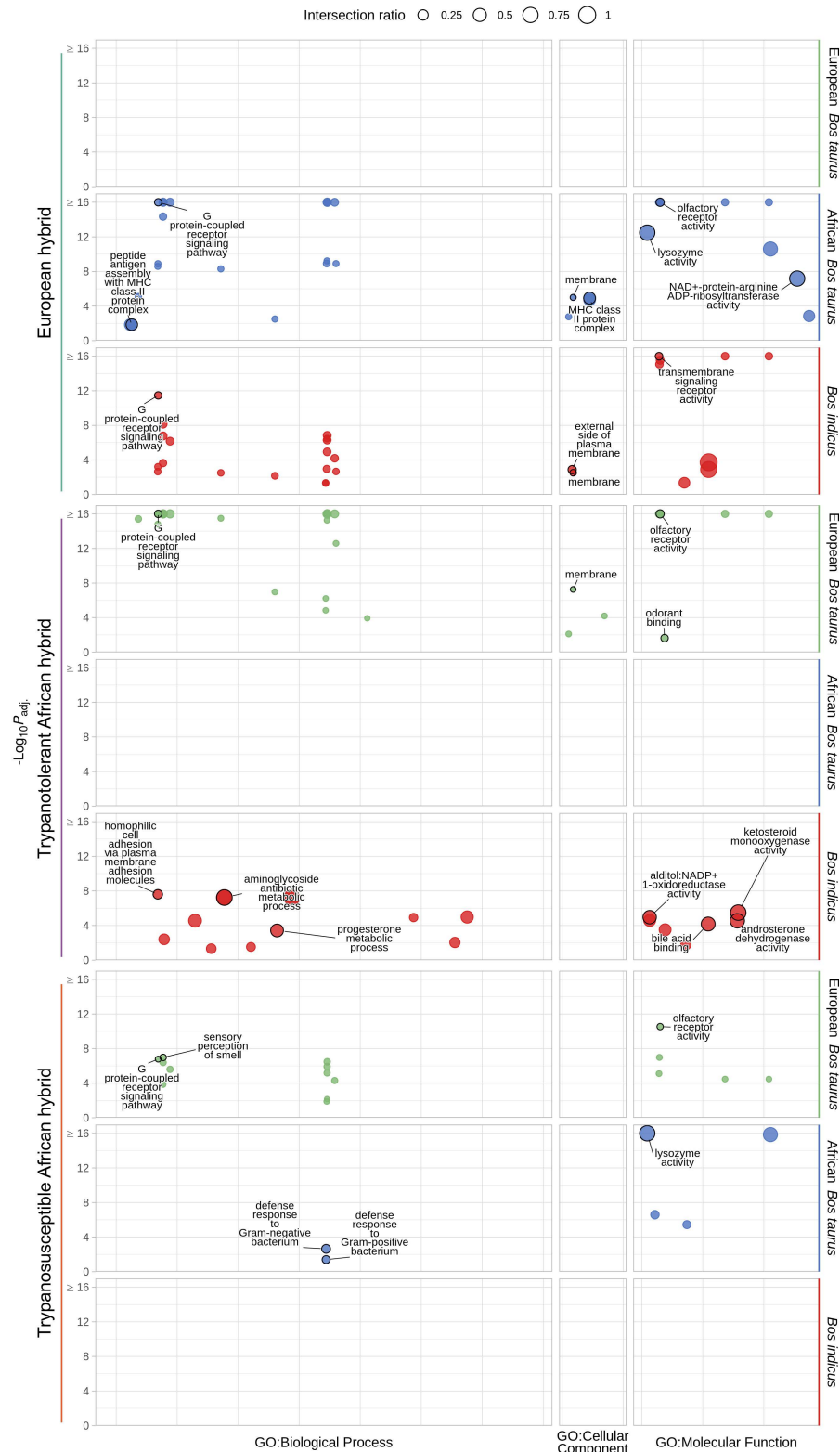
Supplementary Figure A.32. Correlation plots for the trypanotolerant African hybrid local ancestry results (low-density SNP data set). Each dot represents a SNP coloured according to chromosome. The positions on the x- and y-axes indicate the weighted mean ancestry proportions for that SNP according to MOSAIC and ELAI, respectively. **A.** European *B. taurus*, **B.** African *B. taurus*, and **C.** *B. indicus* ancestry components. The lines represent linear models for each chromosome, coloured accordingly.



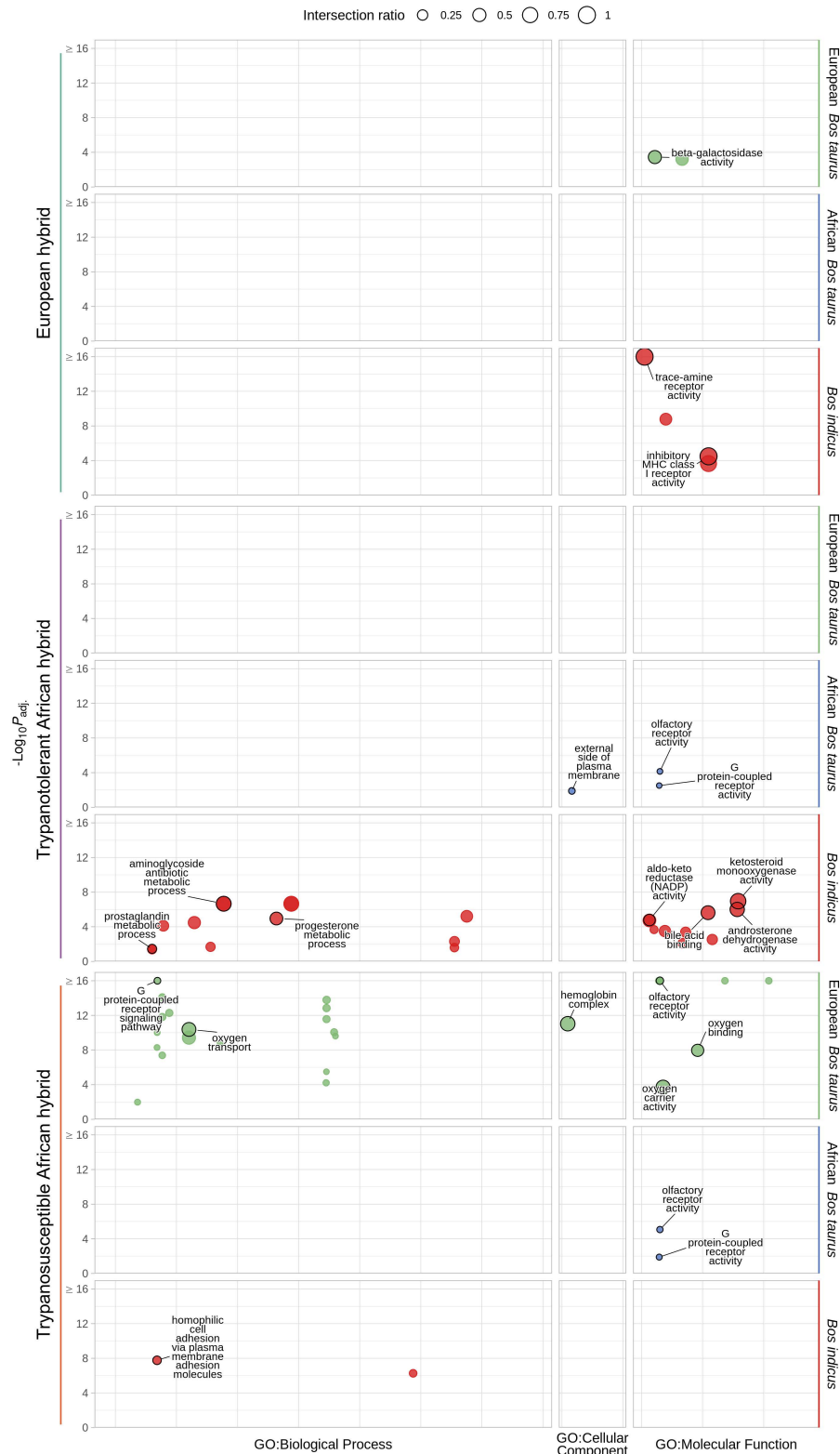
Supplementary Figure A.33. Correlation plots for the trypanosusceptible African hybrid local ancestry results (low-density SNP data set). Each dot represents a SNP coloured according to chromosome. The positions on the x- and y-axes indicate the weighted mean ancestry proportions for that SNP according to MOSAIC and ELAI, respectively. **A.** European *B. taurus*, **B.** African *B. taurus*, and **C.** *B. indicus* ancestry components. The lines represent linear models for each chromosome, coloured accordingly.



Supplementary Figure A.34. g:Profiler functional enrichment of introgressed regions in European, and trypanotolerant and trypanosusceptible African hybrid populations detected with MOSAIC and low-density SNP data. Each circle represents a significantly enriched GO term with the size indicating the ratio of the intersection between the term and the introgressed genes. The y-axis shows the $-\log_{10}P_{adj}$ value and the horizontal panels and colours indicate the ancestry component. The vertical panels indicate the source of the term, and position within each panel groups terms from the same GO subtree. The top driver GO terms (up to a maximum of 10) are indicated with a black outline and label.



Supplementary Figure A.35. g:Profiler functional enrichment of introgressed regions in European, and trypanotolerant and trypanosusceptible African hybrid populations detected with ELAI and high-density SNP data. Each circle represents a significantly enriched GO term with the size indicating the ratio of the intersection between the term and the introgressed genes. The y-axis shows the $-\log_{10}P_{adj.}$ value and the horizontal panels and colours indicate the ancestry component. The vertical panels indicate the source of the term, and position within each panel groups terms from the same GO subtree. The top driver GO terms (up to a maximum of 10) are indicated with a black outline and label.



Supplementary Figure A.36. g:Profiler functional enrichment of introgressed regions in European, and trypanotolerant and trypanosusceptible African hybrid populations detected with ELAI and low-density SNP data. Each circle represents a significantly enriched GO term with the size indicating the ratio of the intersection between the term and the introgressed genes. The y-axis shows the $-\log_{10}P_{adj}$ value and the horizontal panels and colours indicate the ancestry component. The vertical panels indicate the source of the term, and position within each panel groups terms from the same GO subtree. The top driver GO terms (up to a maximum of 10) are indicated with a black outline and label.

Appendix B. Supplementary material for Chapter 3

Supplementary Table B.1. Contrast ID, contrast type, tissue, days post infection (dpi), and formula for each of the 64 contrasts.

Contrast ID	Contrast	Tissue	dpi	Contrast formula
RESP BL 14	RESP	BL	14	(NDAM BL 14 - NDAM BL 00) - (BORA BL 14 - BORA BL 00)
RESP BL 25	RESP	BL	25	(NDAM BL 25 - NDAM BL 00) - (BORA BL 25 - BORA BL 00)
RESP BL 34	RESP	BL	34	(NDAM BL 34 - NDAM BL 00) - (BORA BL 34 - BORA BL 00)
RESP LI 12	RESP	LI	12	(NDAM LI 12 - NDAM LI 00) - (BORA LI 12 - BORA LI 00)
RESP LI 15	RESP	LI	15	(NDAM LI 15 - NDAM LI 00) - (BORA LI 15 - BORA LI 00)
RESP LI 18	RESP	LI	18	(NDAM LI 18 - NDAM LI 00) - (BORA LI 18 - BORA LI 00)
RESP LI 21	RESP	LI	21	(NDAM LI 21 - NDAM LI 00) - (BORA LI 21 - BORA LI 00)
RESP LI 26	RESP	LI	26	(NDAM LI 26 - NDAM LI 00) - (BORA LI 26 - BORA LI 00)
RESP LI 29	RESP	LI	29	(NDAM LI 29 - NDAM LI 00) - (BORA LI 29 - BORA LI 00)
RESP LI 32	RESP	LI	32	(NDAM LI 32 - NDAM LI 00) - (BORA LI 32 - BORA LI 00)
RESP LI 35	RESP	LI	35	(NDAM LI 35 - NDAM LI 00) - (BORA LI 35 - BORA LI 00)
RESP LN 21	RESP	LN	21	(NDAM LN 21 - NDAM LN 00) - (BORA LN 21 - BORA LN 00)
RESP LN 35	RESP	LN	35	(NDAM LN 35 - NDAM LN 00) - (BORA LN 35 - BORA LN 00)
RESP SP 21	RESP	SP	21	(NDAM SP 21 - NDAM SP 00) - (BORA SP 21 - BORA SP 00)
RESP SP 35	RESP	SP	35	(NDAM SP 35 - NDAM SP 00) - (BORA SP 35 - BORA SP 00)
DIRE BL 00	DIRE	BL	0	NDAM BL 00 - BORA BL 00
DIRE BL 14	DIRE	BL	14	NDAM BL 14 - BORA BL 14
DIRE BL 25	DIRE	BL	25	NDAM BL 25 - BORA BL 25
DIRE BL 34	DIRE	BL	34	NDAM BL 34 - BORA BL 34
DIRE LI 00	DIRE	LI	0	NDAM LI 00 - BORA LI 00
DIRE LI 12	DIRE	LI	12	NDAM LI 12 - BORA LI 12
DIRE LI 15	DIRE	LI	15	NDAM LI 15 - BORA LI 15
DIRE LI 18	DIRE	LI	18	NDAM LI 18 - BORA LI 18
DIRE LI 21	DIRE	LI	21	NDAM LI 21 - BORA LI 21
DIRE LI 26	DIRE	LI	26	NDAM LI 26 - BORA LI 26
DIRE LI 29	DIRE	LI	29	NDAM LI 29 - BORA LI 29
DIRE LI 32	DIRE	LI	32	NDAM LI 32 - BORA LI 32
DIRE LI 35	DIRE	LI	35	NDAM LI 35 - BORA LI 35

Supplementary Table B.1 continued.

Contrast ID	Contrast	Tissue	dpi	Contrast formula
DIRE LN 00	DIRE	LN	0	NDAM LN 00 - BORA LN 00
DIRE LN 21	DIRE	LN	21	NDAM LN 21 - BORA LN 21
DIRE LN 35	DIRE	LN	35	NDAM LN 35 - BORA LN 35
DIRE SP 21	DIRE	SP	21	NDAM SP 21 - BORA SP 21
DIRE SP 35	DIRE	SP	35	NDAM SP 35 - BORA SP 35
NDAM BL 14	NDAM	BL	14	NDAM BL 14 - NDAM BL 00
NDAM BL 25	NDAM	BL	25	NDAM BL 25 - NDAM BL 00
NDAM BL 34	NDAM	BL	34	NDAM BL 34 - NDAM BL 00
NDAM LI 12	NDAM	LI	12	NDAM LI 12 - NDAM LI 00
NDAM LI 15	NDAM	LI	15	NDAM LI 15 - NDAM LI 00
NDAM LI 18	NDAM	LI	18	NDAM LI 18 - NDAM LI 00
NDAM LI 21	NDAM	LI	21	NDAM LI 21 - NDAM LI 00
NDAM LI 26	NDAM	LI	26	NDAM LI 26 - NDAM LI 00
NDAM LI 29	NDAM	LI	29	NDAM LI 29 - NDAM LI 00
NDAM LI 32	NDAM	LI	32	NDAM LI 32 - NDAM LI 00
NDAM LI 35	NDAM	LI	35	NDAM LI 35 - NDAM LI 00
NDAM LN 21	NDAM	LN	21	NDAM LN 21 - NDAM LN 00
NDAM LN 35	NDAM	LN	35	NDAM LN 35 - NDAM LN 00
NDAM SP 21	NDAM	SP	21	NDAM SP 21 - NDAM SP 00
NDAM SP 35	NDAM	SP	35	NDAM SP 35 - NDAM SP 00
BORA BL 14	BORA	BL	14	BORA BL 14 - BORA BL 00
BORA BL 25	BORA	BL	25	BORA BL 25 - BORA BL 00
BORA BL 34	BORA	BL	34	BORA BL 34 - BORA BL 00
BORA LI 12	BORA	LI	12	BORA LI 12 - BORA LI 00
BORA LI 15	BORA	LI	15	BORA LI 15 - BORA LI 00
BORA LI 18	BORA	LI	18	BORA LI 18 - BORA LI 00
BORA LI 21	BORA	LI	21	BORA LI 21 - BORA LI 00
BORA LI 26	BORA	LI	26	BORA LI 26 - BORA LI 00
BORA LI 29	BORA	LI	29	BORA LI 29 - BORA LI 00
BORA LI 32	BORA	LI	32	BORA LI 32 - BORA LI 00
BORA LI 35	BORA	LI	35	BORA LI 35 - BORA LI 00
BORA LN 21	BORA	LN	21	BORA LN 21 - BORA LN 00
BORA LN 35	BORA	LN	35	BORA LN 35 - BORA LN 00
BORA SP 21	BORA	SP	21	BORA SP 21 - BORA SP 00
BORA SP 35	BORA	SP	35	BORA SP 35 - BORA SP 00

Supplementary Table B.2. Tissue, days post infection (dpi), and the top 10 most significant genes with increased and decreased expression with valid gene symbols for the direct contrasts.

Tissue	dpi	Genes with increased expression
BL	0	<i>TTLL1, PGA5, USP42, OLFM4, GPR132, MED27, WLS, SH3GLB2, PMF1, EIF2B2</i>
BL	14	<i>TTLL1, USP42, GPR132, UPK3B, TM9SF5, WLS, KLC1, MRPS6, TIPIN, BLK</i>
BL	25	<i>TTLL1, TM9SF5, TBXA2R, ADRA2A, RUM1, DHPS, ARL6IP4, ZNF318, KLHDC8A, APOL3</i>
BL	34	<i>TTLL1, SPDEF, KLHDC8A, TM9SF5, DHPS, KCNN4, RUM1, ARL6IP4, CDK20, FCRL3</i>
LI	0	<i>DOCK11, MAGIX, AGA, MEP1B, TMLHE, TCIRG1, SETD9, IRAK4, TRIM13, GSTM1</i>
LI	12	<i>DOCK11, AGA, MAGIX, CYP4F47, SETD9, IRAK4, IL18BP, TCIRG1, CHIA, TMEM41A</i>
LI	15	<i>MAGIX, DOCK11, ALDH7A1, AGA, TMLHE, CYP4A59, CYP4A11, INTS8, PON3, CYP4F47</i>
LI	18	<i>DOCK11, MAGIX, AGA, EPCAM, PDLIM4, ARL4D, ADTRP, TTLL1, SETD9, LTF</i>
LI	21	<i>AGA, CYP2D43, CYP2D14, COL12A1, EPPK1, DOCK11, MAGIX, TRIM13, IRAK4, ALDH7A1</i>
LI	26	<i>UGT2B10, DOCK11, TSPAN6, CCDC191, MAGIX, RTN2, SETD9, AGA, MMAA, DBI</i>
LI	29	<i>UGT2B10, DOCK11, CYP4A59, CYP4A11, AGA, DPYS, ATPAF1, QPRT, CYP4F47, MAGIX</i>
LI	32	<i>DOCK11, AGA, ADTRP, LTF, MAGIX, UGT2B10, APLNR, bta-mir-30f, GSTM1, EPCAM</i>
LI	35	<i>DOCK11, AGA, CYP2D43, CYP2D14, CYP4F47, CHIA, TSPAN6, PTPRM, RETSAT, CTDSP2</i>
LN	0	<i>CLDN11, TTLL1, BRB, CYP4B1, STAB1, PROS1, HEPH, CTSK, C1QTNF5, MT3</i>
LN	21	<i>TTLL1, SLC38A11, SUCLG1, SNORA73, EIF2B2, TXNDC11, MZB1, SLC25A26, PDIA5, ORC1</i>
LN	35	<i>TTLL1, SNORA73, LXN, MYB, DEFB4A, SLC38A11, CHD1L, TRNAU1AP, bta-mir-221, ORC1</i>
SP	0	<i>TTLL1, F2RL2, FABP3, RGS5, KIF3A, BMP2, TNFAIP6, NDN, SYT1, ITGA8</i>
SP	21	<i>TTLL1, ECRG4, TRMT10B, PTGDS, STMN2, KCNA3, CD38, CD2, CFI, MSN</i>
SP	35	<i>TTLL1, SNCA, LXN, RNASE4, MSN, ECRG4, STMN2, MAB21L1, TIPIN, TM9SF5</i>
Tissue	dpi	Genes with decreased expression
BL	0	<i>PHF12, VCAN, S100A7, PPP1R15A, CXCL5, ADAMDEC1, PLAU, CLECL1P, SAP18, CRYGS</i>
BL	14	<i>PHF12, GABARAPL2, OASL, MORN4, CRYGS, UCHL3, SEL1L3, MED16, SAP18, ERAP1</i>
BL	25	<i>VCAN, PFKFB4, PROCR, MORN4, JAM3, SELENOP, PHF12, DHRS7, SLC25A17, MTURN</i>
BL	34	<i>PROCR, MTURN, SLC25A17, MORN4, DHRS7, SMOX, TUBB1, ISCU, MFSD2B, ITGA2</i>
LI	0	<i>RFTN1, CYP4F2, TMEM45B, TPD52L1, MANEA, SPTSSB, PSMC5, PLBD1, SAP18, MED16</i>

Supplementary Table B.2 continued.

Tissue	dpi	Genes with decreased expression
LI	12	<i>SPTSSB, RFTN1, CYP4F2, MANEA, DNAJC22, TPD52L1, TMEM45B, TMLHE, BAMBI, TBC1D7</i>
LI	15	<i>SPTSSB, CYP4F2, RFTN1, PLBD1, TMEM45B, RAC1, TPD52L1, MANEA, ERAP1, GPX1</i>
LI	18	<i>CYP4F2, BAMBI, TPD52L1, RFTN1, SPTSSB, DNAJC22, PTER, MANEA, DNASE1L3, DCXR</i>
LI	21	<i>TPD52L1, PTER, KBTBD6, CYP4F2, MANEA, CRCP, RCBTB2, SLC5A6, TMLHE, JSP.1</i>
LI	26	<i>RFTN1, CYP4F2, ARSB, COX10, MANEA, ARPC1B, PAMR1, TMLHE, LCP1, NAGK</i>
LI	29	<i>JCHAIN, WWOX, PEG3, RFTN1, DNMT1, TPD52L1, PTER, ARSB, UBR7, OTULINL</i>
LI	32	<i>RFTN1, TPD52L1, CYP4F2, MANEA, PTER, SLC38A11, PIGR, JCHAIN, VPS41, HTATSF1</i>
LI	35	<i>RFTN1, TPD52L1, PARP11, TMLHE, MANEA, AVPR1A, CRCP, TBC1D7, C29H11orf86, JCHAIN</i>
LN	0	<i>SELE, CCL20, SEL1L3, EFHD1, ATP4B, SPP1, CXCL13, ALB, PLOD2, MME</i>
LN	21	<i>FOXO1, SEL1L3, COL16A1, ADAMDEC1, DDT, MOSMO, ATP4B, SELE, EFHD1, LTBP2</i>
LN	35	<i>LTBP2, DNER, IGFBP3, FOXO1, EFEMP1, RARRES2, DNASE1L3, DEFB10, VPS41, TBC1D7</i>
SP	0	<i>CFH, CYP4B1, EFHD1, LTBP2, EXOC7, FAM83D, MCPH1, TM4SF18, DDT, HCLS1</i>
SP	21	<i>CFH, FOXO1, DDT, SCG2, THBS1, BCAT2, PTER, RARRES2, MORN4, C6</i>
SP	35	<i>NELL2, CFH, RARRES2, SCG2, GPD2, PLA2, SAP18, JSP.1, CD14, FOXO1</i>

Supplementary Table B.3. Tissue, days post infection (dpi), and the top 10 most significant genes with increased and decreased expression with valid gene symbols for the N'Dama contrasts.

Tissue	dpi	Genes with increased expression
BL	14	<i>SRSF11, HNRNPH1, UPK3B, CEP95, LAP3, NUPR1, PRPF40A, CCAR1, SNORD24, ABCC10</i>
BL	25	<i>NEB, ADORA2B, CMTM3, CPLANE1, CERS4, UPK3B, RHBDF2, ADRA2A, SRSF11, KCNN4</i>
BL	34	<i>NEB, CERS4, ADRA2A, UPK3B, FCRL3, KCNN4, WDR73, CMTM3, RHBDF2, LCAT</i>
LI	12	<i>CXCL11, UBD, TMSB10, WARS1, TAP1, PSMB9, BCL2A1, IRF1, BIRC3, PSMB10</i>
LI	15	<i>TMSB10, ADA, CYRIB, CD48, HCK, SPI1, PTPRC, JCHAIN, SLA, TMSB4X</i>
LI	18	<i>TMSB10, CYRIB, PTPRC, SPI1, CD48, TMSB4X, ADA, HCK, ARHGDIB, CD53</i>
LI	21	<i>TMSB10, CYRIB, PTPRC, TMSB4X, ARHGDIB, SPI1, CD48, CD53, RAC2, ADA</i>
LI	26	<i>TMSB10, TMSB4X, CYRIB, PTPRC, SPI1, CD53, CD48, CCDC191, CD55, SLA</i>
LI	29	<i>TMSB10, TMSB4X, PTPRC, CYRIB, SPI1, CD53, CD55, CD48, TMSB4, HTRA4</i>
LI	32	<i>TMSB10, TMSB4X, CYRIB, PTPRC, CD53, SPI1, CD55, CD48, RAP1B, TMSB4</i>
LI	35	<i>TMSB10, TMSB4X, PTPRC, CYRIB, CD53, SPI1, ARHGDIB, SLA, CD48, RAP1B</i>
LN	21	<i>ORC1, MZB1, CDC6, SKA3, UBE2S, SPAG5, SLC25A5, SPDL1, NDUFA4, CDC20</i>
LN	35	<i>SPAG5, ORC1, MKI67, TOP2A, TPX2, BUB1, AURKB, CDC6, CENPT, ASPM</i>
SP	21	<i>IRF4, CDC6, SPAG5, KIF2C, ESPL1, MKI67, CENPT, H2AC18, H2AC19, KRTCAP2</i>
SP	35	<i>MKI67, ORC1, AURKB, SPAG5, IRF4, ESPL1, BUB1, CDC6, ASPM, UBE2C</i>
Tissue	dpi	Genes with decreased expression
BL	14	<i>VAT1L, OLFM4, JAML, PGA5, PMF1, GZMB, ALOX15, FCER1A, PTGDR2, RAVR1, ICAM3</i>
BL	25	<i>JAML, CSF3R, OLFM4, RAVR1, ICAM3, VAT1L, PIP5K1B, GZMB, NFAM1, PTGDR2</i>
BL	34	<i>JAML, PIP5K1B, VAT1L, RAVR1, ICAM3, OLFM4, GZMB, PTGDR2, CSF3R, FCER1A</i>
LI	12	<i>MAPK6, SLC25A15, NUDT12, EEF1A1, CRYZ, GLCE, EPB41L5, PHKB, MYO1B, GNA14</i>
LI	15	<i>SIGLEC1, IGFBP6, GSTA2, CDK3, TEN1, ACSM5, GALT, MAPK6, SLC51B, JOSD2</i>
LI	18	<i>SIGLEC1, GCAT, AS3MT, PPOX, SLC51B, PMVK, IGFBP6, EPB41L5, NTN5, RORC</i>
LI	21	<i>RORC, GCAT, FAM83H, SIGLEC1, C15H11orf52, DVL1, CARD19, PTPRF, MOSPD1, NAA30</i>
LI	26	<i>SIGLEC1, GCAT, FOXA2, GUCD1, HPN, HOMER2, PTPRF, HSD17B14, THOP1, GPLD1</i>
LI	29	<i>SIGLEC1, GCAT, IYD, SHPK, NMRAL1, GRHPR, PPP2R2B, KHK, ACY1, FARP1</i>

Supplementary Table B.3 continued.

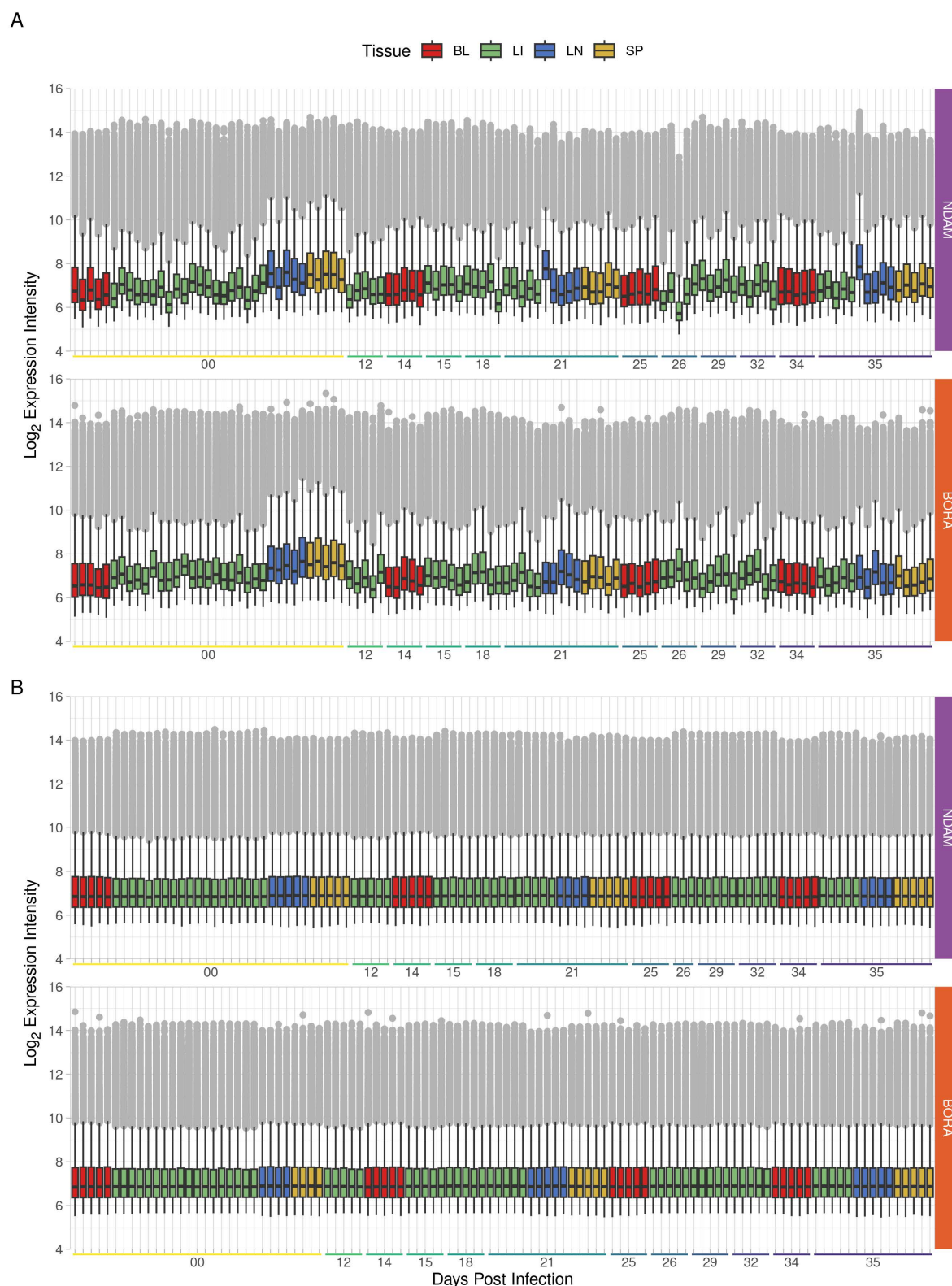
Tissue	dpi	Genes with decreased expression
LI	32	<i>GCAT, SIGLEC1, ACY1, FOXA2, MGC152281, PDK2, FAAH, GRHPR, GUCD1, SLC27A4</i>
LI	35	<i>SIGLEC1, NIT1, AS3MT, EPB41L5, GCAT, PDZK1, PLPP6, GSR, GRHPR, C15H11orf52</i>
LN	21	<i>CLDN11, ELOVL7, SNTB2, SMCHD1, BRB, SMAD5, CFLAR, NR2F1, ADGRF5, HEPH</i>
LN	35	<i>CLDN11, BRB, ELOVL7, SMYD2, HEPH, NR2F1, TJP1, SCARA5, MEIS2, ADGRF5</i>
SP	21	<i>SYT1, GDPD2, NTRK2, NTN4, IGFBP6, DNASE1L3, NDN, FGF2, PENK, F2RL2</i>
SP	35	<i>SYT1, GDPD2, IGFBP6, NTRK2, NTN4, NDN, FBLN5, PGM5, PENK, PYGM</i>

Supplementary Table B.4. Tissue, days post infection (dpi), and the top 10 most significant genes with increased and decreased expression with valid gene symbols for the Boran contrasts.

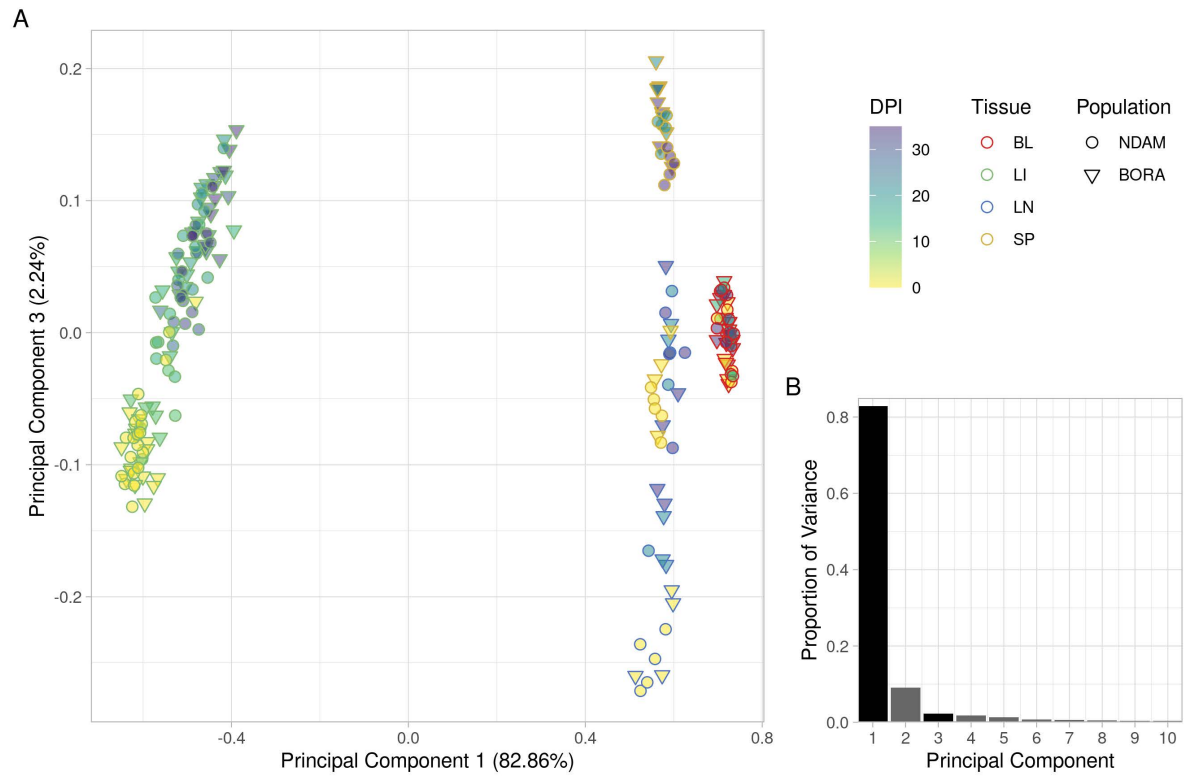
Tissue	dpi	Genes with increased expression
BL	14	<i>GZMB, LAP3, SLAMF8, IRF1, FCRL3, NUB1, NLRC5, OASL, WARS1, GBP5</i>
BL	25	<i>CPLANE1, CSTB, NEB, ADORA2B, CMTM3, SRSF11, PIK3C2B, SEC11A, INPP5B, UPK3B</i>
BL	34	<i>NEB, ADORA2B, CPLANE1, CMTM3, INPP5B, SLC25A12, CERS4, PIK3C2B, ADRA2A, PYGO1</i>
LI	12	<i>TAP1, UBD, IRF1, PSMB9, TMSB10, CXCL11, B2M, PSMB10, CXCL10, NLRC5</i>
LI	15	<i>TMSB10, CYRIB, ADA, CD48, SPI1, HCK, PTPRC, ARHGDIB, GNG2, CORO1A</i>
LI	18	<i>TMSB10, CYRIB, SPI1, PTPRC, CD48, ADA, ARHGDIB, HCK, PLTP, CD53</i>
LI	21	<i>TMSB10, CYRIB, CD53, SPI1, PTPRC, TMSB4X, ARHGDIB, ADA, CD48, ACTR3</i>
LI	26	<i>TMSB10, CYRIB, PTPRC, SPI1, CD53, TMSB4X, PLTP, CDH5, HCK, ARHGDIB</i>
LI	29	<i>CYRIB, TMSB10, SPI1, PTPRC, CD53, PLTP, TMSB4X, RAP1B, ARHGDIB, DOCK2</i>
LI	32	<i>TMSB10, CYRIB, PTPRC, SPI1, CD53, TMSB4X, PLTP, CD55, HCK, RAP1B</i>
LI	35	<i>TMSB10, CYRIB, CD53, PTPRC, SPI1, TMSB4X, PLTP, RAP1B, CD48, VAV1</i>
LN	21	<i>MEA1, ATP5ME, MRPL52, POLR2L, RNASEH2C, SLC25A5, MZB1, COX6B1, TXNDC5, FAM32A</i>
LN	35	<i>MEA1, NDUFA4, COX6B1, KIFC1, SPAG5, ATP5ME, AQP3, MKI67, TXNDC5, TOP2A</i>
SP	21	<i>CDC6, IRF4, KRTCAP2, RNASEH2C, CSTB, MYDGF, BUB1, TUBG1, CENPT, ESPL1</i>
SP	35	<i>CSTB, LAP, IRF4, CD14, CTLA4, CDC6, MYDGF, TUBG1, ACSL5, NOLC1</i>
Tissue	dpi	Genes with decreased expression
BL	14	<i>PIP5K1B, ADAMDEC1, IFT27, CA5B, S100A7, FCER1A, RGCC, JAML, FOSB, NR4A2</i>
BL	25	<i>JAML, PIP5K1B, CXCR1, CXCR2, IFT27, GZMB, ALOX15, CSF3R, VAT1L, PTGDR2</i>
BL	34	<i>JAML, IFT27, PIP5K1B, CA5B, S100A7, PARP8, CSF3R, CXCL8, NFAM1, PTGDR2</i>
LI	12	<i>RPS2, SNORA64, CA5A, TRIM6, PAF1, FGA, HSD17B14, 7SK, SLC7A9, HEXIM2</i>
LI	15	<i>COLEC11, TCEA3, EPB41L5, SIGLEC1, IMMP2L, PYURF, AS3MT, AUH, APOM, AGMAT</i>
LI	18	<i>SIGLEC1, PTPRF, PMVK, TEAD2, APLNR, TCEA3, DHRS11, EPB41L5, ANKS4B, CBS</i>
LI	21	<i>PHACTR4, APLNR, TCEA3, RORC, GCGR, GCAT, SIGLEC1, FAM149A, ST7L, CRYBG2</i>
LI	26	<i>PMVK, SIGLEC1, GCAT, CBS, HSD17B14, PTPRF, ACY1, HAGH, CIDEA, PAFAH2</i>
LI	29	<i>GCAT, GRHPR, FAAH, EPB41L5, DPYS, PMVK, CBS, NIPSNAP1, TCEA3, ACY1</i>

Supplementary Table B.4 continued.

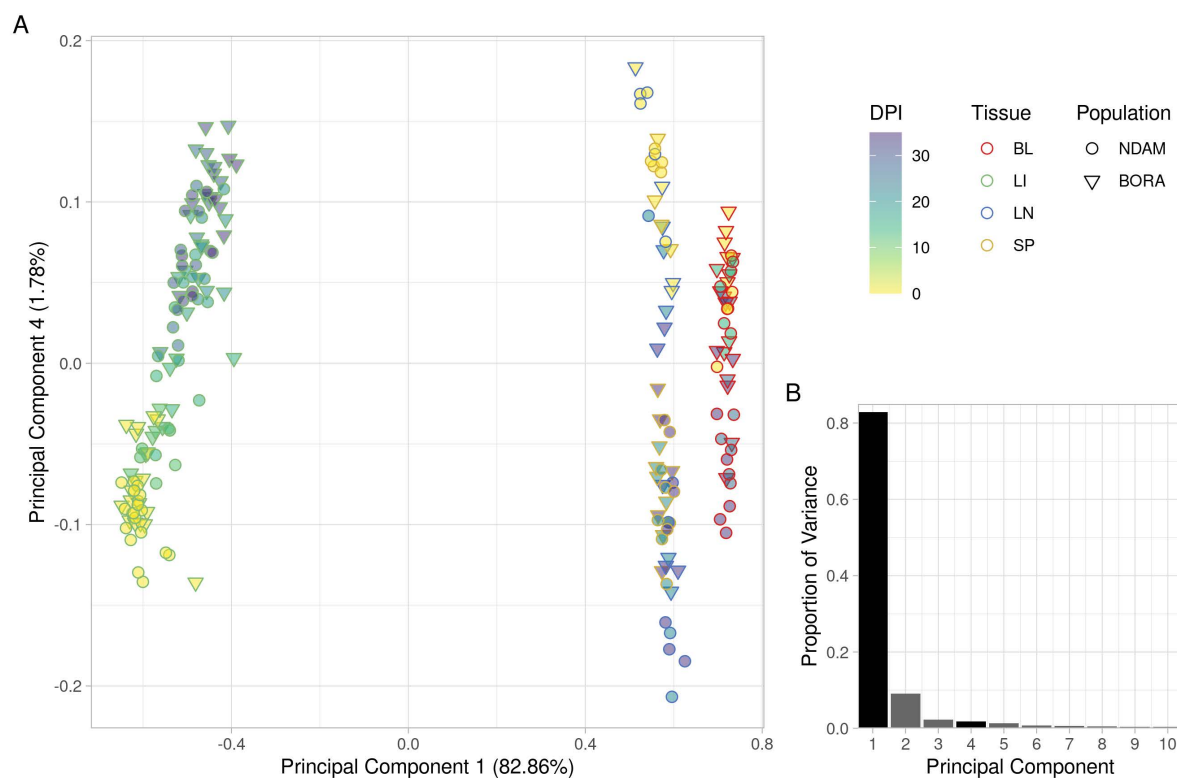
Tissue	dpi	Genes with decreased expression
LI	32	<i>GCAT, PMVK, CES1, SIGLEC1, KCTD21, ACY1, FAAH, EBP, FOXA2, MMAB</i>
LI	35	<i>GCAT, GCGR, EBP, PMVK, ACY1, GRHPR, PTPRF, FAH, NTN5, HPN</i>
LN	21	<i>MSANTD2, MFSD4A, SMCHD1, NPNT, SHISA3, ZNF318, MDFIC, BPTF, KMT2C, TSC1</i>
LN	35	<i>MSANTD2, LUM, CLDN11, SMCHD1, MFSD4A, KMT2C, MINDY2, COL6A3, NR2F1, AGO3</i>
SP	21	<i>SYT1, NTN4, DNASE1L3, GDPD2, IGFBP6, NTRK2, PGM5, NXPH1, FBLN5, GPR34</i>
SP	35	<i>NTRK2, IGFBP6, GDPD2, SYT1, NTN4, FBLN5, PGM5, PYGM, DNASE1L3, TPM2</i>



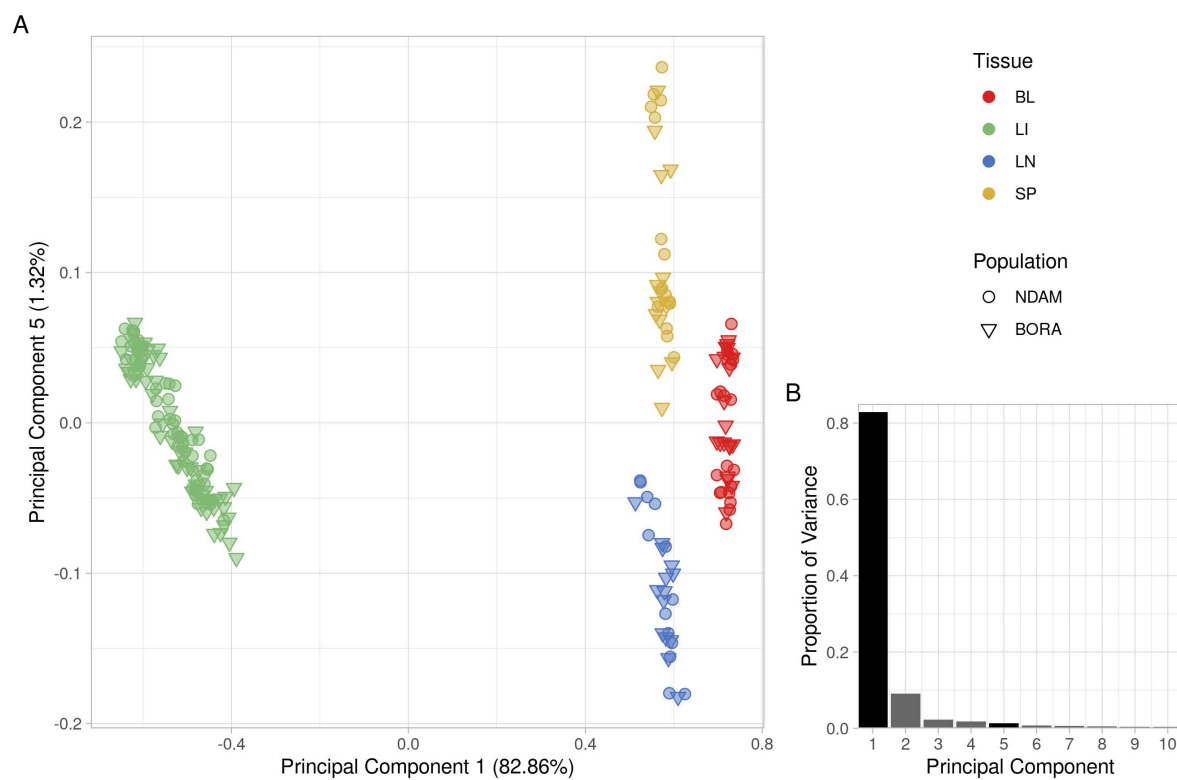
Supplementary Figure B.1. Boxplots showing the log₂ expression intensity of the probe sets for each sample of the **A.** raw and **B.** normalised data after quality control filtering separated into NDAM and BORA populations and coloured according to tissue. The position along the horizontal axis indicates the days post infection. Outlier probe sets are shown as grey dots.



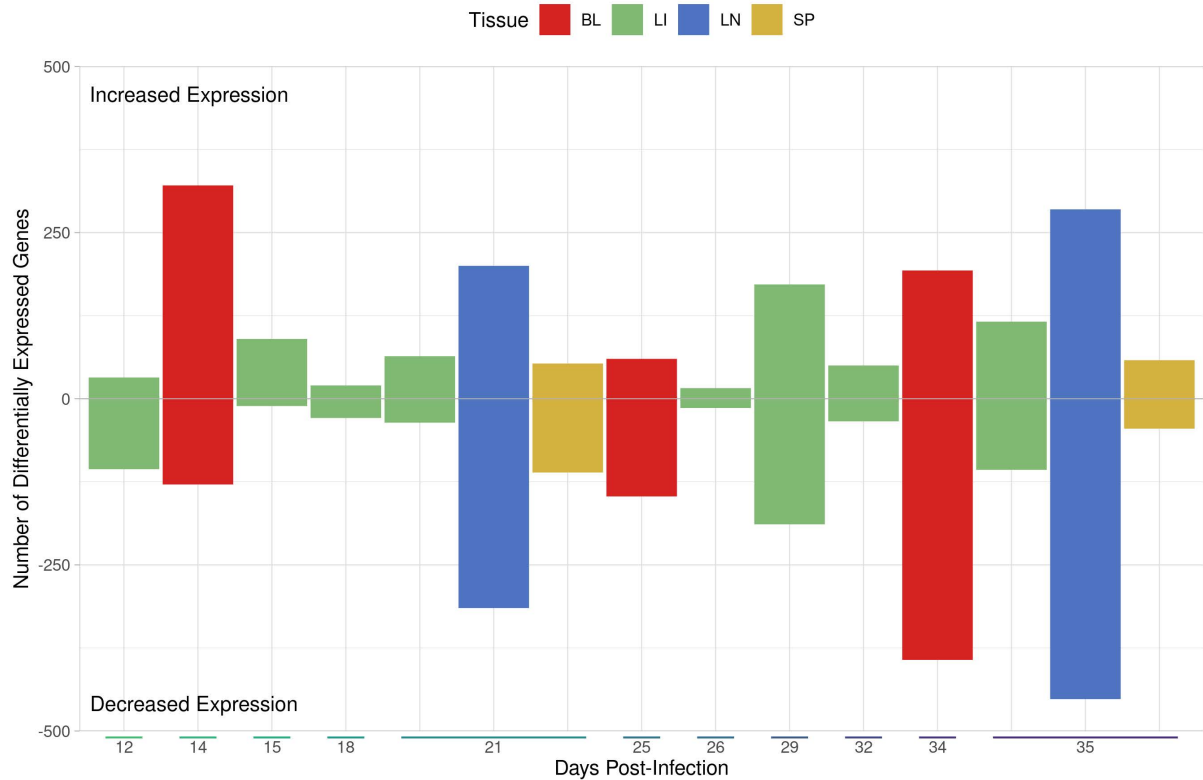
Supplementary Figure B.2. A. Principal component analysis (PCA) of the microarray data set with samples coloured according to days post infection (dpi) with the outer colour representing the tissue and shape indicating the population showing the first and third principal components (PC1 and PC3), and **B.** bar chart of proportion of variance of the top ten PCs.



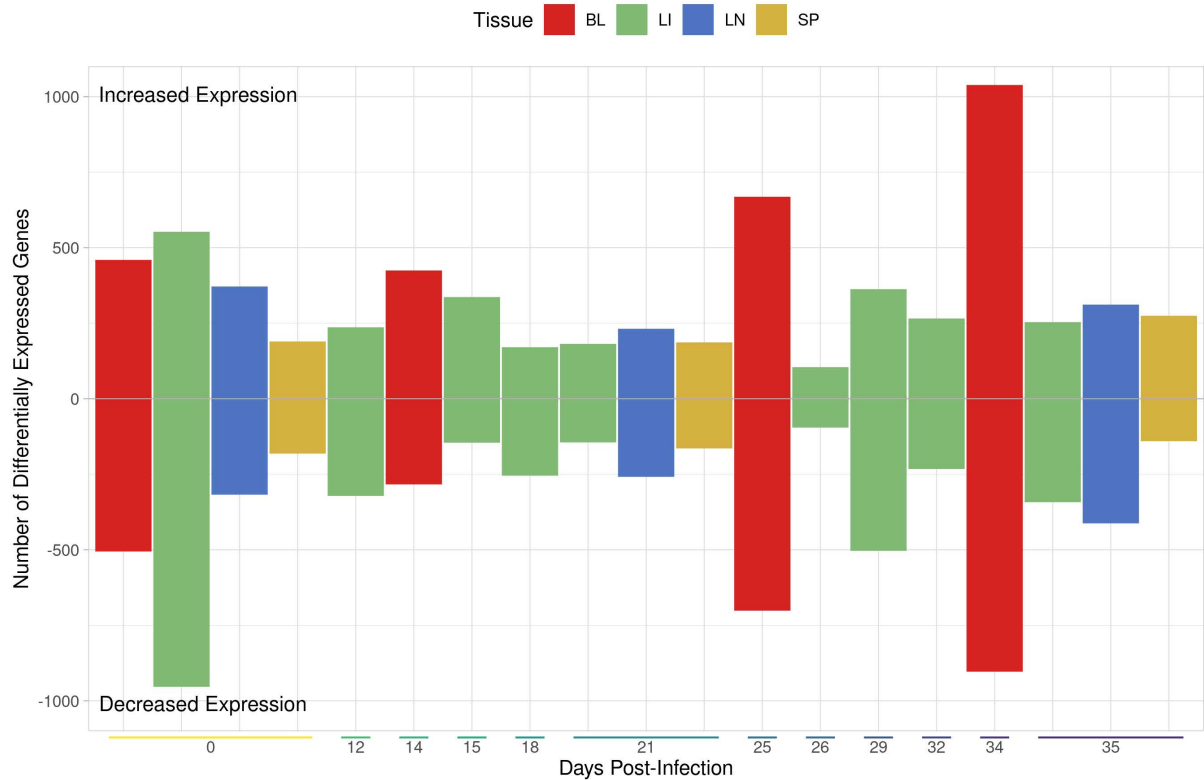
Supplementary Figure B.3. A. Principal component analysis (PCA) of the microarray data set with samples coloured according to days post infection (dpi) with the outer colour representing the tissue and shape indicating the population showing the first and fourth principal components (PC1 and PC4), and **B.** bar chart of proportion of variance of the top ten PCs.



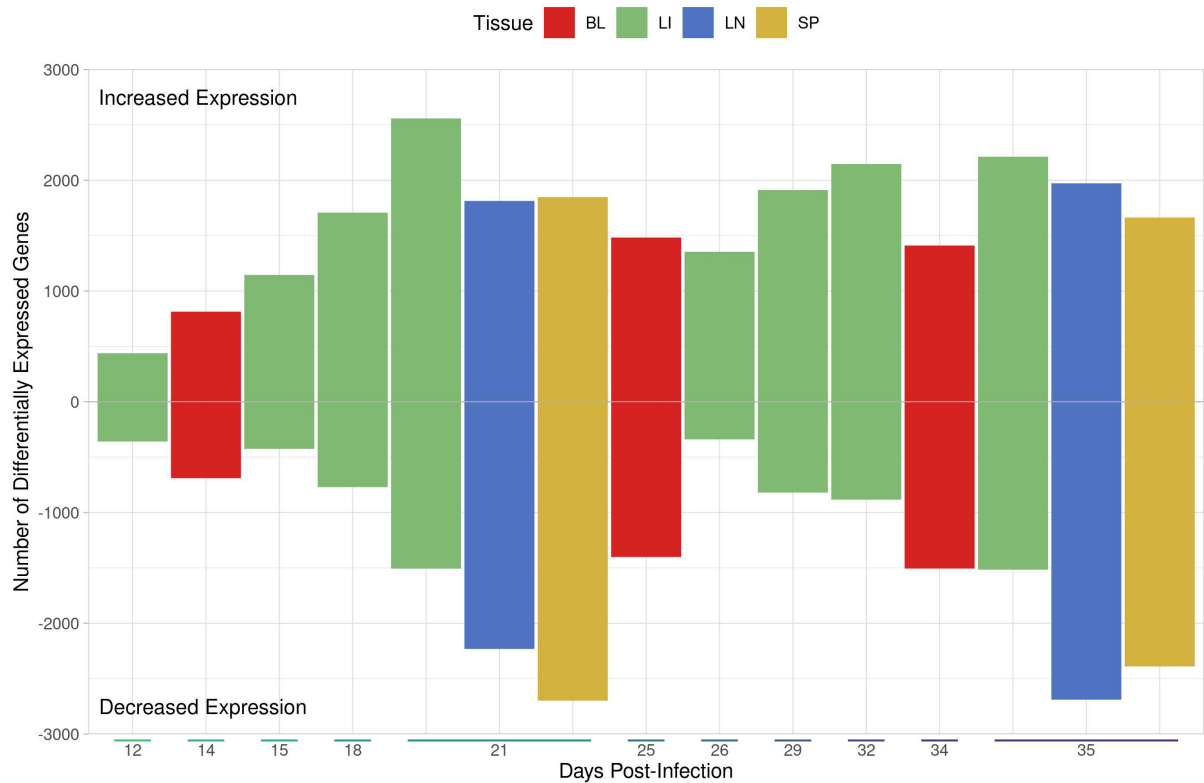
Supplementary Figure B.4. A. Principal component analysis (PCA) of the microarray data set with samples coloured according to tissue and shape indicating the population showing the first and fifth principal components (PC1 and PC5), and **B.** bar chart of proportion of variance of the top ten PCs.



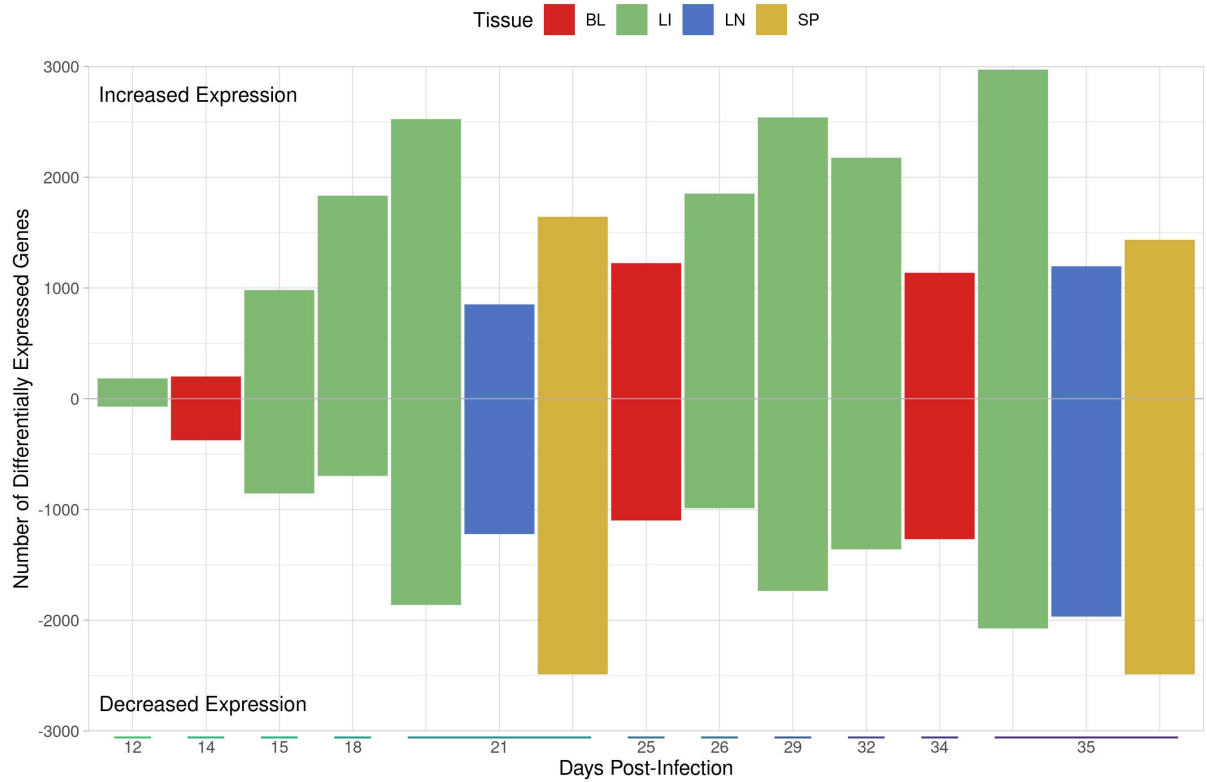
Supplementary Figure B.5. Bar chart showing the numbers of significantly differentially expressed genes for the RESP contrasts. The extent of the bar above and below 0 on the vertical axis indicates the numbers of significantly differentially expressed genes (DEGs) with increased and decreased expression, respectively. The position on the horizontal indicates the number of days post infection (dpi) and the colour of the bars represents the tissue.



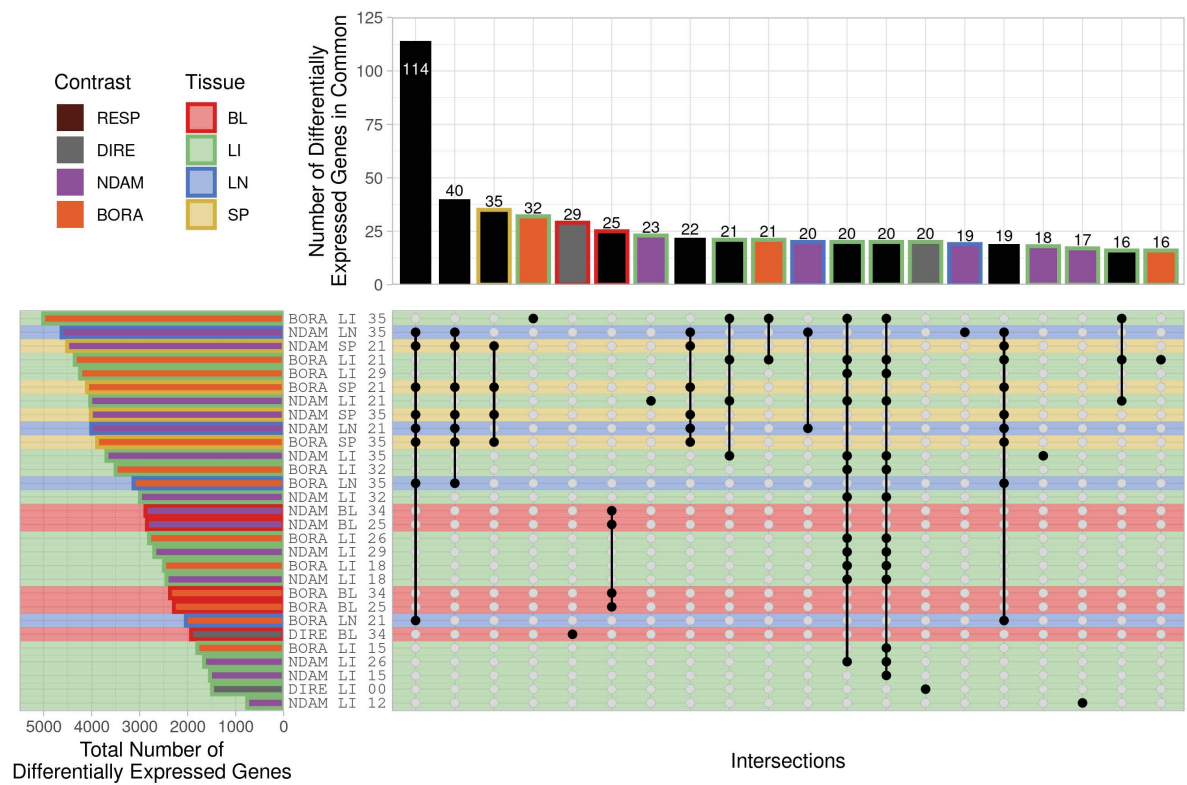
Supplementary Figure B.6. Bar chart showing the numbers of significantly differentially expressed genes for the DIRE contrasts. The extent of the bar above and below 0 on the vertical axis indicates the numbers of significantly differentially expressed genes (DEGs) with increased and decreased expression, respectively. The position on the horizontal indicates the number of days post infection (dpi) and the colour of the bars represents the tissue.



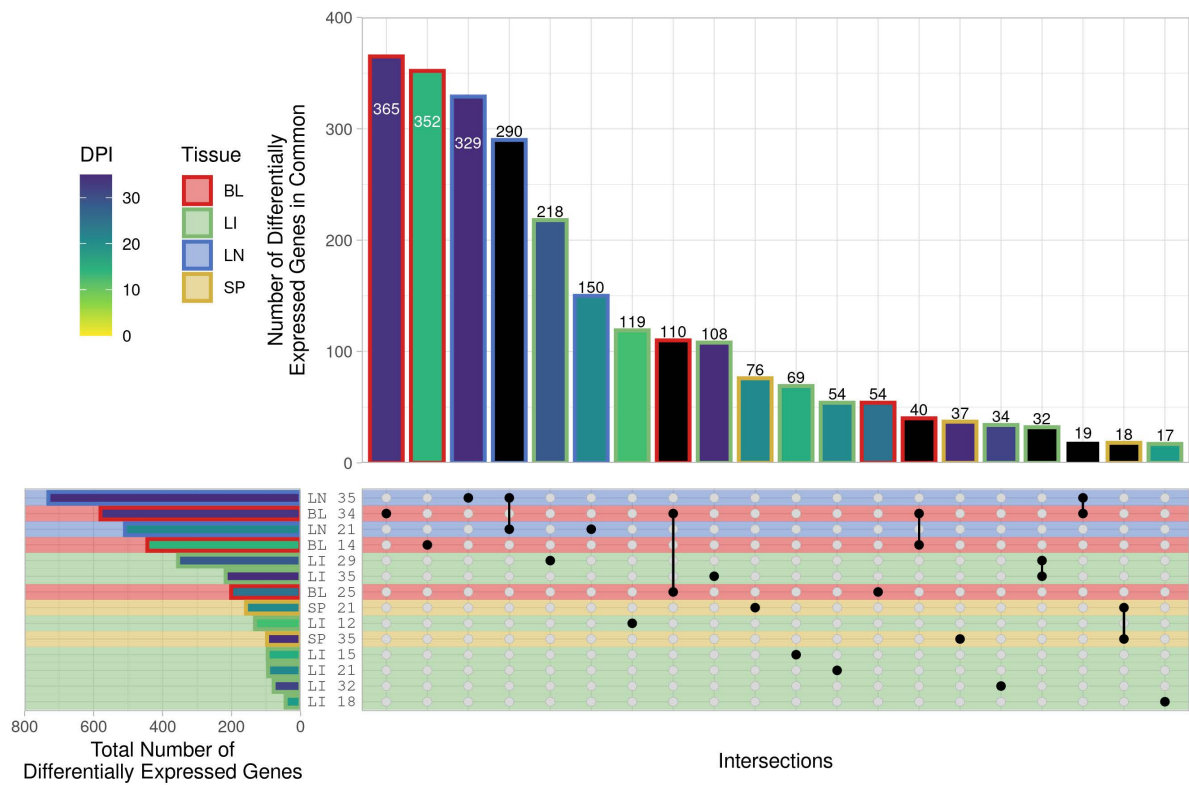
Supplementary Figure B.7. Bar chart showing the numbers of significantly differentially expressed genes for the NDAM contrasts. The extent of the bar above and below 0 on the vertical axis indicates the numbers of significantly differentially expressed genes (DEGs) with increased and decreased expression, respectively. The position on the horizontal indicates the number of days post infection (dpi) and the colour of the bars represents the tissue.



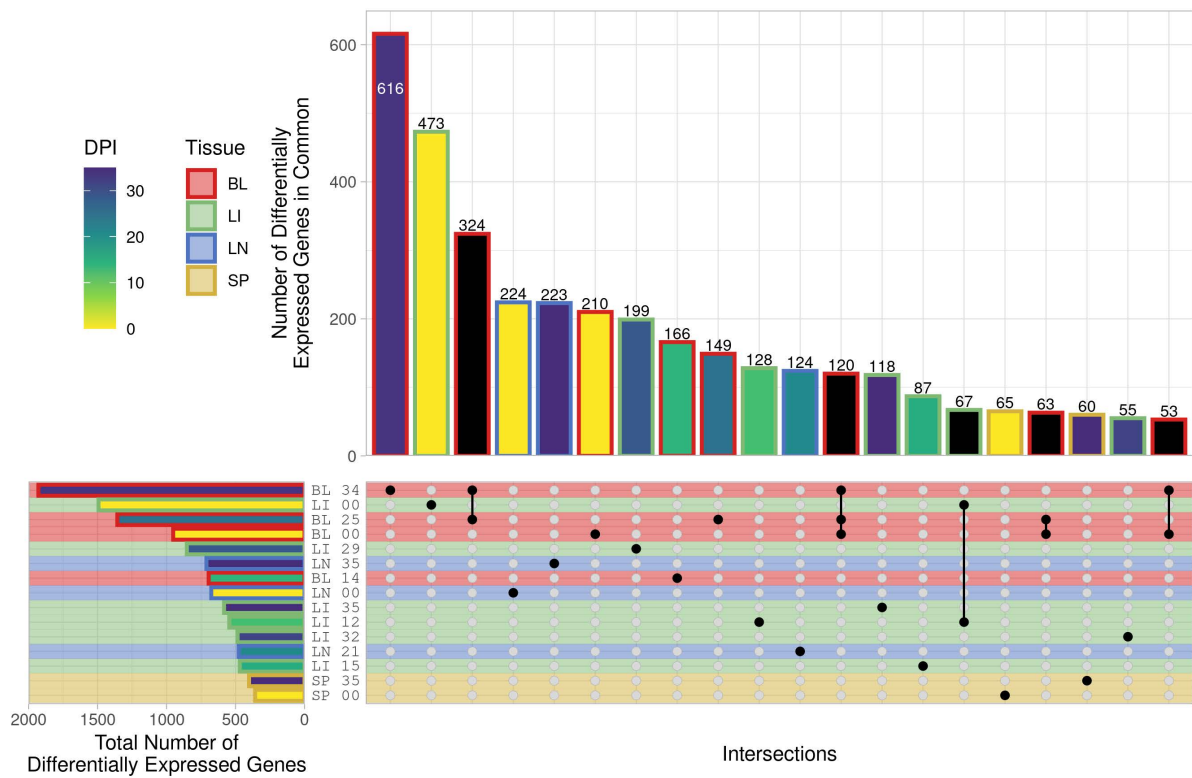
Supplementary Figure B.8. Bar chart showing the numbers of significantly differentially expressed genes for the BORA contrasts. The extent of the bar above and below 0 on the vertical axis indicates the numbers of significantly differentially expressed genes (DEGs) with increased and decreased expression, respectively. The position on the horizontal indicates the number of days post infection (dpi) and the colour of the bars represents the tissue.



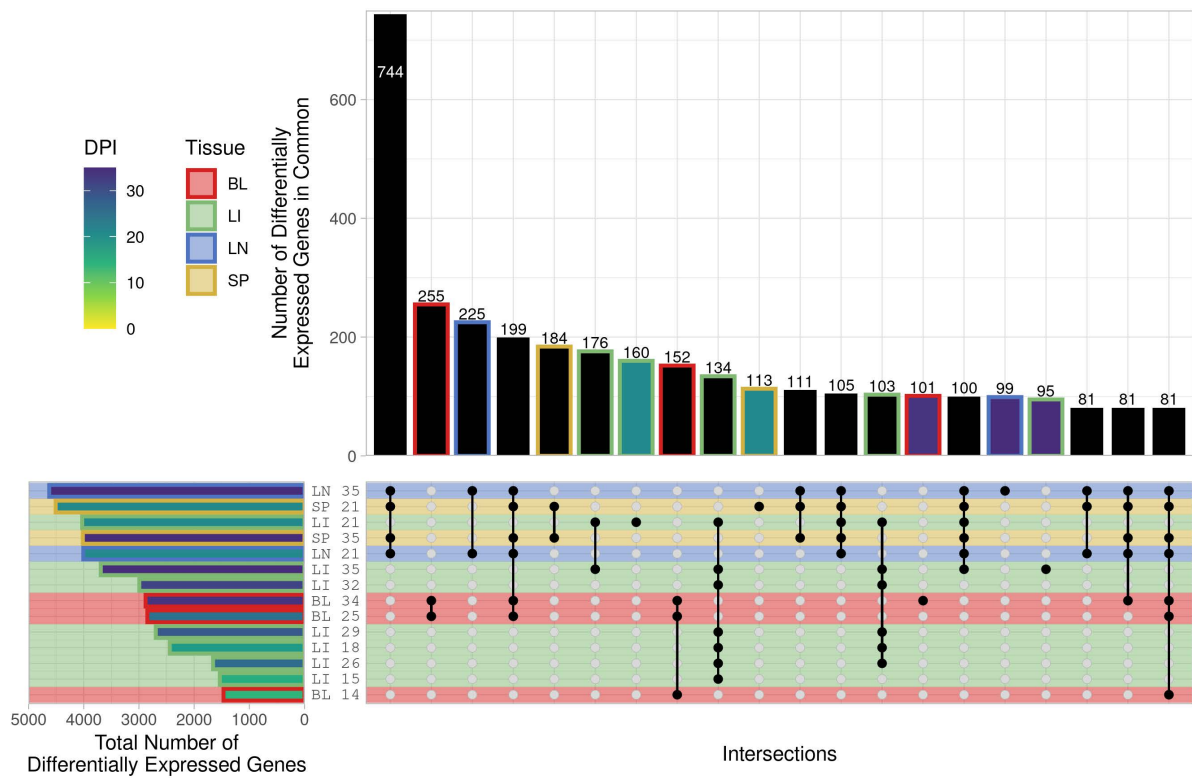
Supplementary Figure B.9. UpSet plot showing the top 20 intersections among all 64 contrasts. The horizontal bars indicate the total number of significant differentially expressed genes (DEGs) for each contrast while the vertical bars indicate the number of significant DEGs in common between the contrasts annotated with black dots connected by lines in the intersection matrix. The background colour of the stripes in the intersection matrix and horizontal bars represents the tissue. The colour of the bars represents the contrast type with black bars indicating an overlap between different contrast types. The outline colour of the bars also represents the tissue with no outline representing an overlap between different tissues.



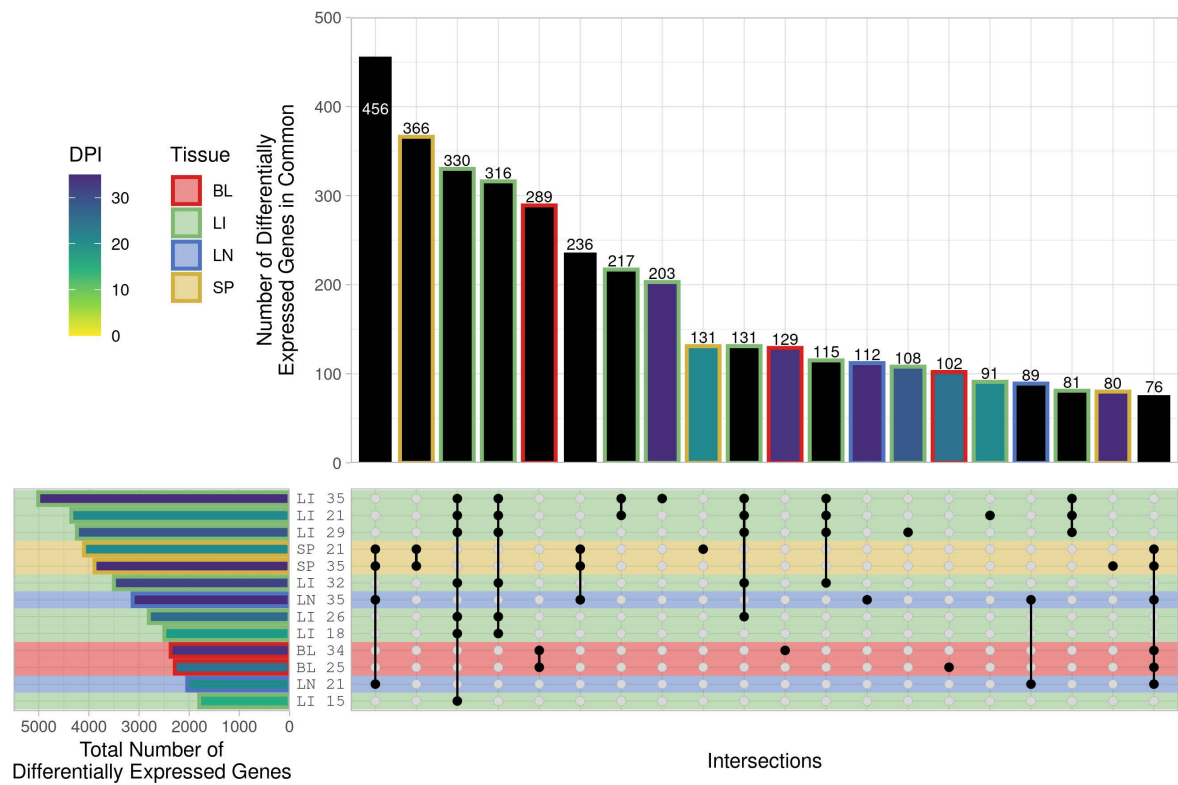
Supplementary Figure B.10. UpSet plot showing the top 20 intersections among the RESP contrasts. The horizontal bars indicate the total number of significant differentially expressed genes (DEGs) for each contrast while the vertical bars indicate the number of significant DEGs in common between the contrasts annotated with black dots connected by lines in the intersection matrix. The background colour of the stripes in the intersection matrix and horizontal bars represents the tissue. The colour of the bars represents the days post infection (dpi) with black bars indicating an overlap between different timepoints. The outline colour of the bars also represents the tissue with no outline representing an overlap between different tissues.



Supplementary Figure B.11. UpSet plot showing the top 20 intersections among the DIRE contrasts. The horizontal bars indicate the total number of significant differentially expressed genes (DEGs) for each contrast while the vertical bars indicate the number of significant DEGs in common between the contrasts annotated with black dots connected by lines in the intersection matrix. The background colour of the stripes in the intersection matrix and horizontal bars represents the tissue. The colour of the bars represents the days post infection (dpi) with black bars indicating an overlap between different timepoints. The outline colour of the bars also represents the tissue with no outline representing an overlap between different tissues.



Supplementary Figure B.12. UpSet plot showing the top 20 intersections among the NDAM contrasts. The horizontal bars indicate the total number of significant differentially expressed genes (DEGs) for each contrast while the vertical bars indicate the number of significant DEGs in common between the contrasts annotated with black dots connected by lines in the intersection matrix. The background colour of the stripes in the intersection matrix and horizontal bars represents the tissue. The colour of the bars represents the days post infection (dpi) with black bars indicating an overlap between different timepoints. The outline colour of the bars also represents the tissue with no outline representing an overlap between different tissues.



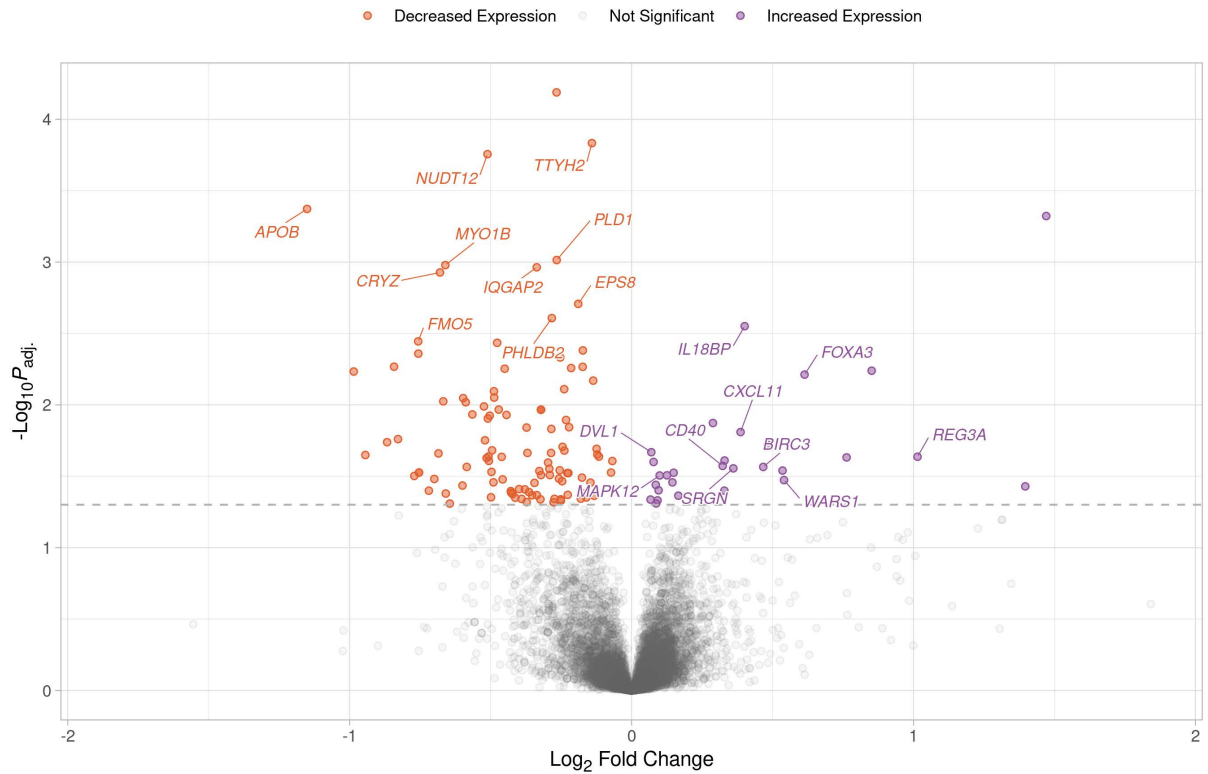
Supplementary Figure B.13. UpSet plot showing the top 20 intersections among the BORA contrasts. The horizontal bars indicate the total number of significant differentially expressed genes (DEGs) for each contrast while the vertical bars indicate the number of significant DEGs in common between the contrasts annotated with black dots connected by lines in the intersection matrix. The background colour of the stripes in the intersection matrix and horizontal bars represents the tissue. The colour of the bars represents the days post infection (dpi) with black bars indicating an overlap between different timepoints. The outline colour of the bars also represents the tissue with no outline representing an overlap between different tissues.



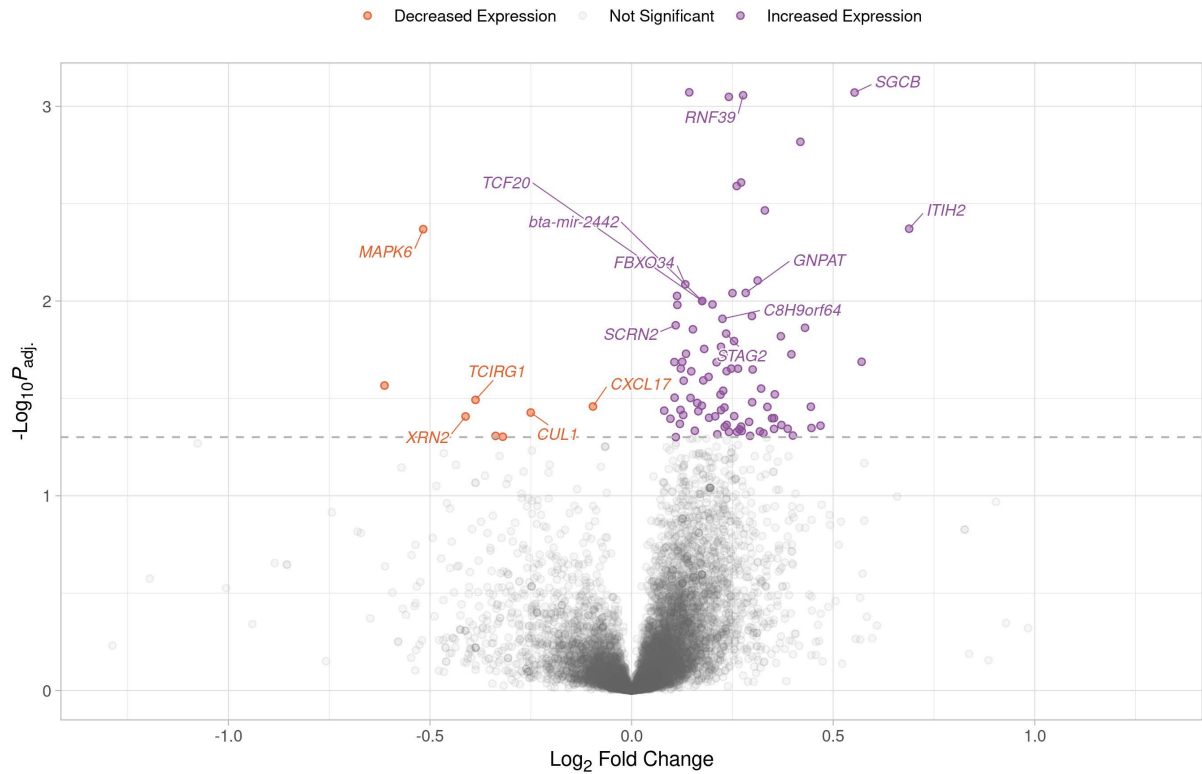
Supplementary Figure B.14. Volcano plot showing the results of the RESP contrast for the peripheral blood mononuclear cell (PBMC) samples at 14 days post infection (dpi). Each data point represents a gene with the position on the x- and y-axes indicating the \log_2 fold change and $-\log_{10}P_{adj.}$, respectively. Genes above the horizontal dashed line are significantly differentially expressed with the colours representing the change in expression. The top 10 most significant genes for increased and decreased expression with gene symbols are labelled.



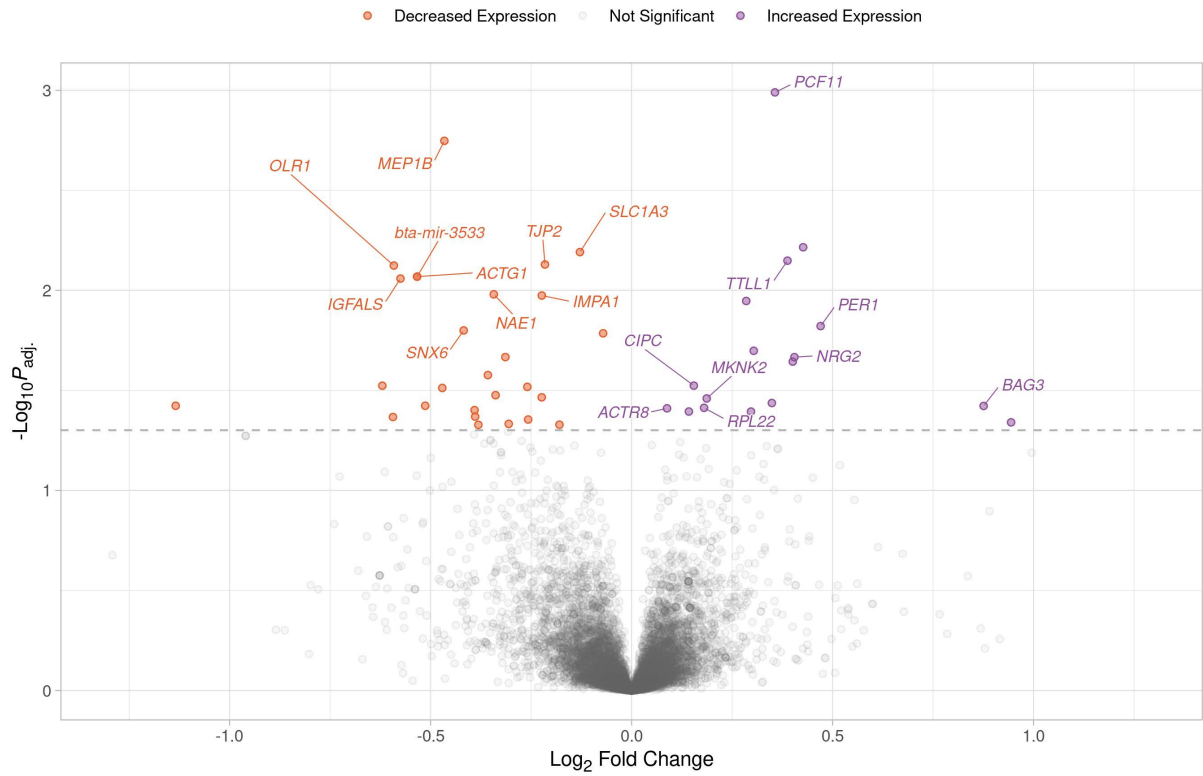
Supplementary Figure B.15. Volcano plot showing the results of the RESP contrast for the peripheral blood mononuclear cell (PBMC) samples at 25 days post infection (dpi). Each data point represents a gene with the position on the x- and y-axes indicating the \log_2 fold change and $-\log_{10}P_{adj.}$, respectively. Genes above the horizontal dashed line are significantly differentially expressed with the colours representing the change in expression. The top 10 most significant genes for increased and decreased expression with gene symbols are labelled.



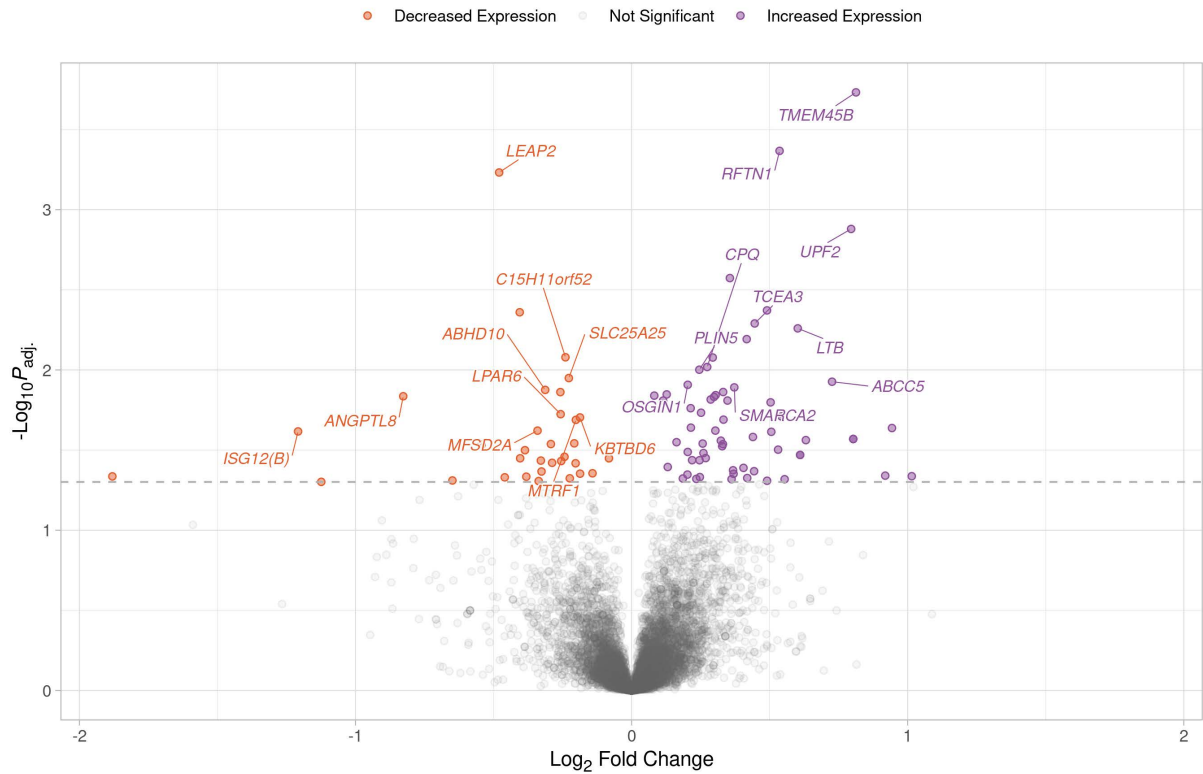
Supplementary Figure B.16. Volcano plot showing the results of the RESP contrast for the liver samples at 12 days post infection (dpi). Each data point represents a gene with the position on the x- and y-axes indicating the \log_2 fold change and $-\log_{10}P_{adj.}$, respectively. Genes above the horizontal dashed line are significantly differentially expressed with the colours representing the change in expression. The top 10 most significant genes for increased and decreased expression with gene symbols are labelled.



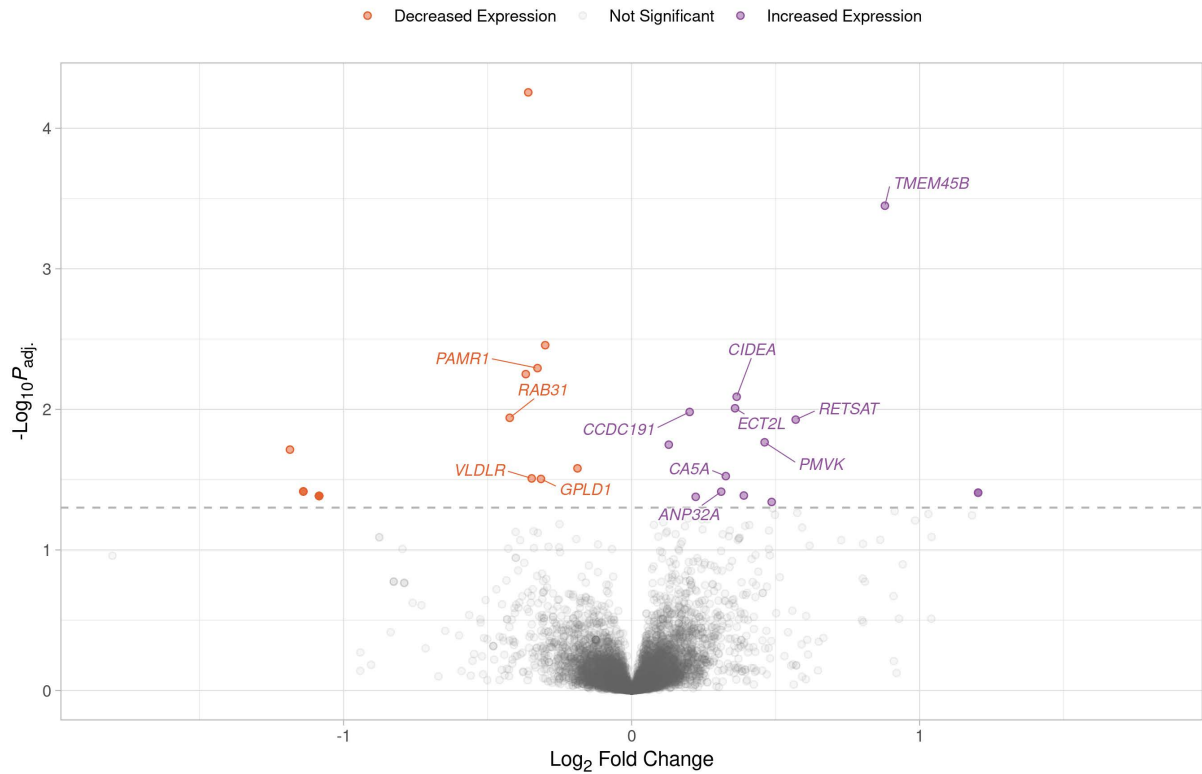
Supplementary Figure B.17. Volcano plot showing the results of the RESP contrast for the liver samples at 15 days post infection (dpi). Each data point represents a gene with the position on the x- and y-axes indicating the \log_2 fold change and $-\log_{10}P_{adj.}$, respectively. Genes above the horizontal dashed line are significantly differentially expressed with the colours representing the change in expression. The top 10 most significant genes for increased and decreased expression with gene symbols are labelled.



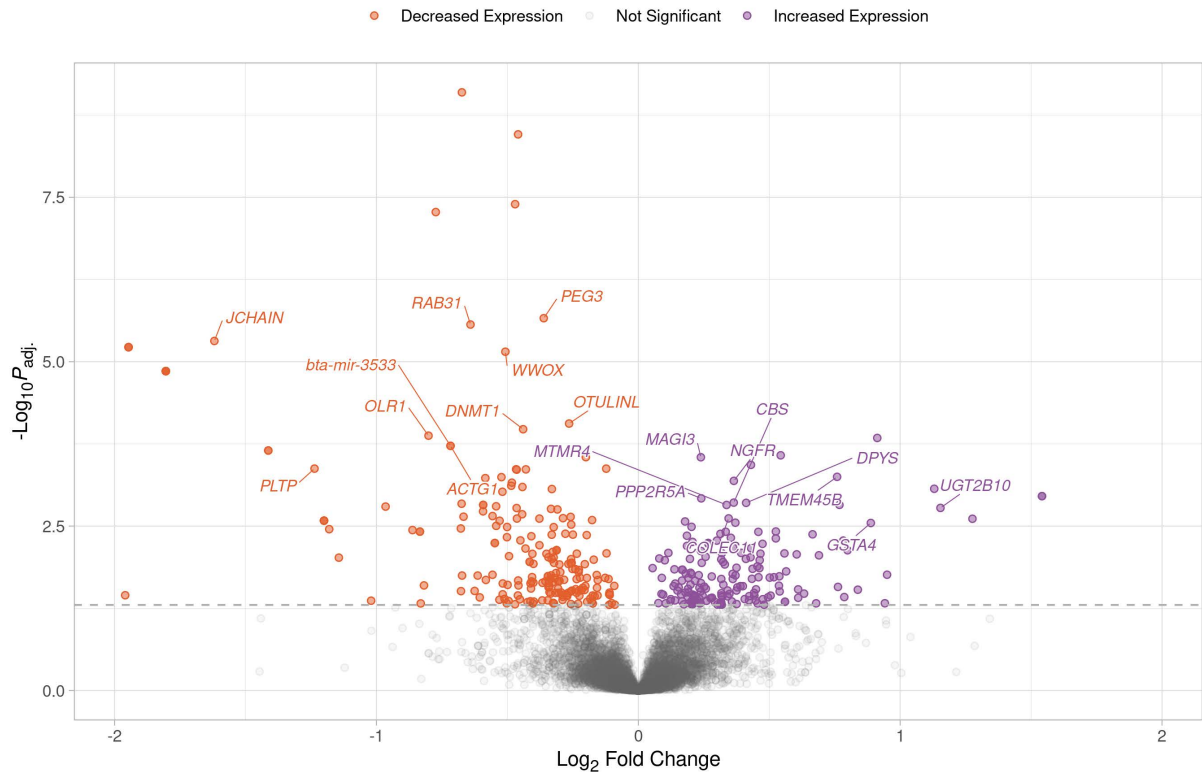
Supplementary Figure B.18. Volcano plot showing the results of the RESP contrast for the liver samples at 18 days post infection (dpi). Each data point represents a gene with the position on the x- and y-axes indicating the \log_2 fold change and $-\log_{10} P_{adj.}$, respectively. Genes above the horizontal dashed line are significantly differentially expressed with the colours representing the change in expression. The top 10 most significant genes for increased and decreased expression with gene symbols are labelled.



Supplementary Figure B.19. Volcano plot showing the results of the RESP contrast for the liver samples at 21 days post infection (dpi). Each data point represents a gene with the position on the x- and y-axes indicating the \log_2 fold change and $-\log_{10}P_{adj.}$, respectively. Genes above the horizontal dashed line are significantly differentially expressed with the colours representing the change in expression. The top 10 most significant genes for increased and decreased expression with gene symbols are labelled.



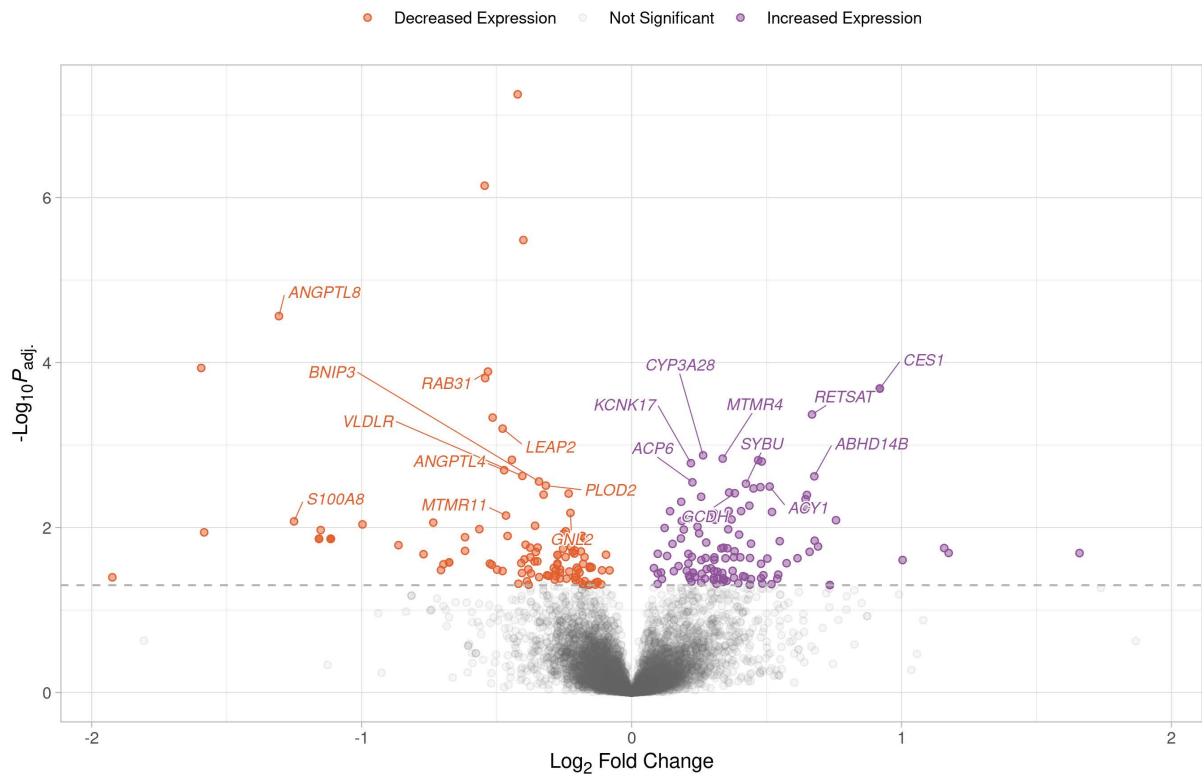
Supplementary Figure B.20. Volcano plot showing the results of the RESP contrast for the liver samples at 26 days post infection (dpi). Each data point represents a gene with the position on the x- and y-axes indicating the \log_2 fold change and $-\log_{10} P_{adj.}$, respectively. Genes above the horizontal dashed line are significantly differentially expressed with the colours representing the change in expression. The top 10 most significant genes for increased and decreased expression with gene symbols are labelled.



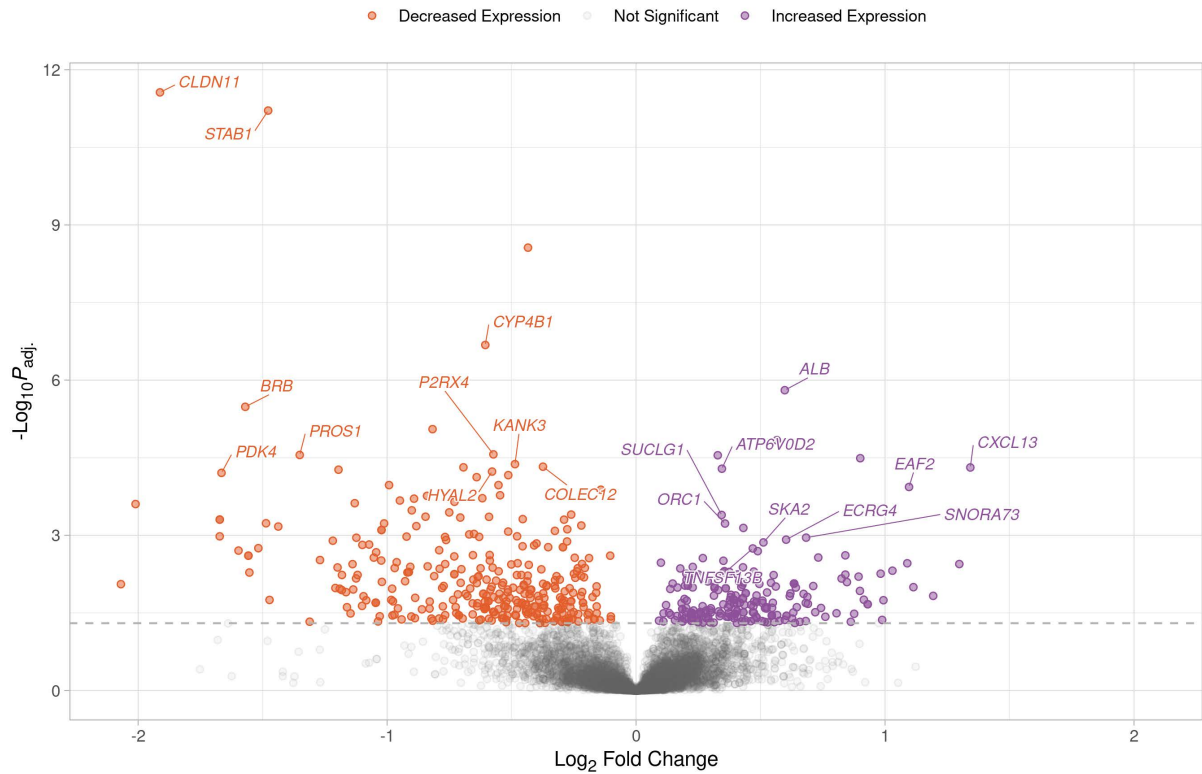
Supplementary Figure B.21. Volcano plot showing the results of the RESP contrast for the liver samples at 29 days post infection (dpi). Each data point represents a gene with the position on the x- and y-axes indicating the \log_2 fold change and $-\log_{10} P_{adj.}$, respectively. Genes above the horizontal dashed line are significantly differentially expressed with the colours representing the change in expression. The top 10 most significant genes for increased and decreased expression with gene symbols are labelled.



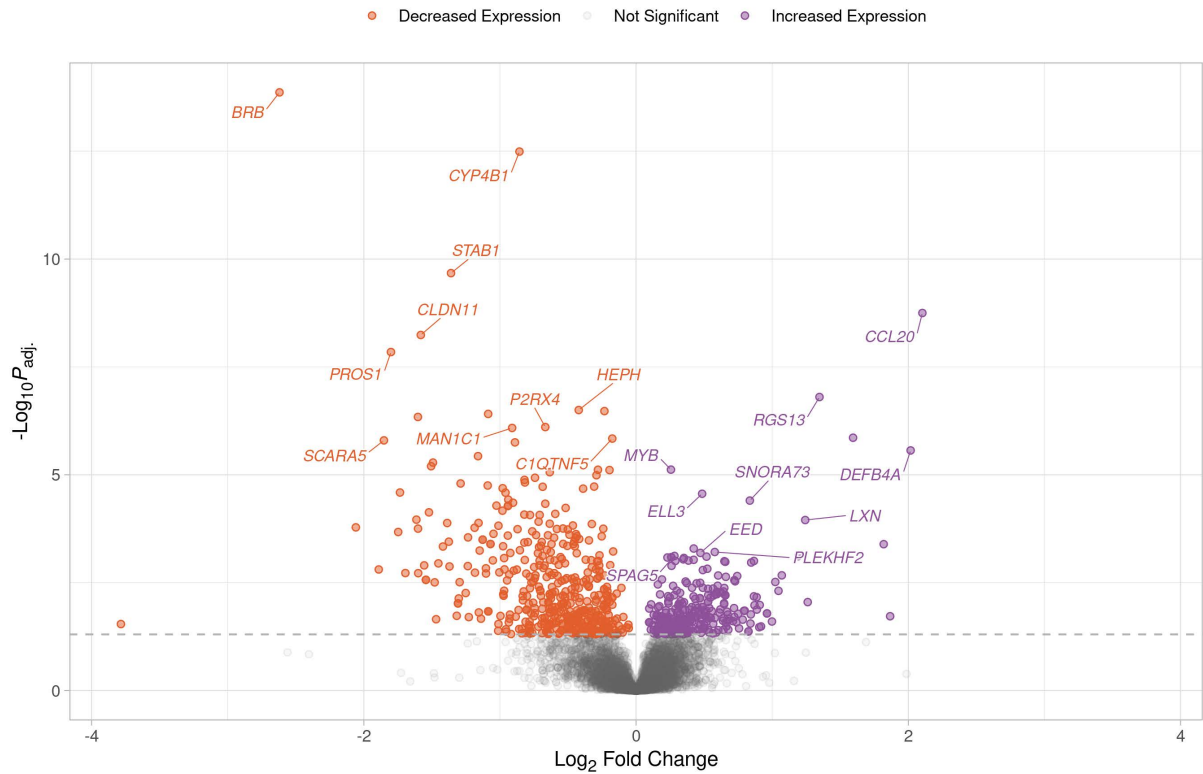
Supplementary Figure B.22. Volcano plot showing the results of the RESP contrast for the liver samples at 32 days post infection (dpi). Each data point represents a gene with the position on the x- and y-axes indicating the \log_2 fold change and $-\log_{10} P_{adj.}$, respectively. Genes above the horizontal dashed line are significantly differentially expressed with the colours representing the change in expression. The top 10 most significant genes for increased and decreased expression with gene symbols are labelled.



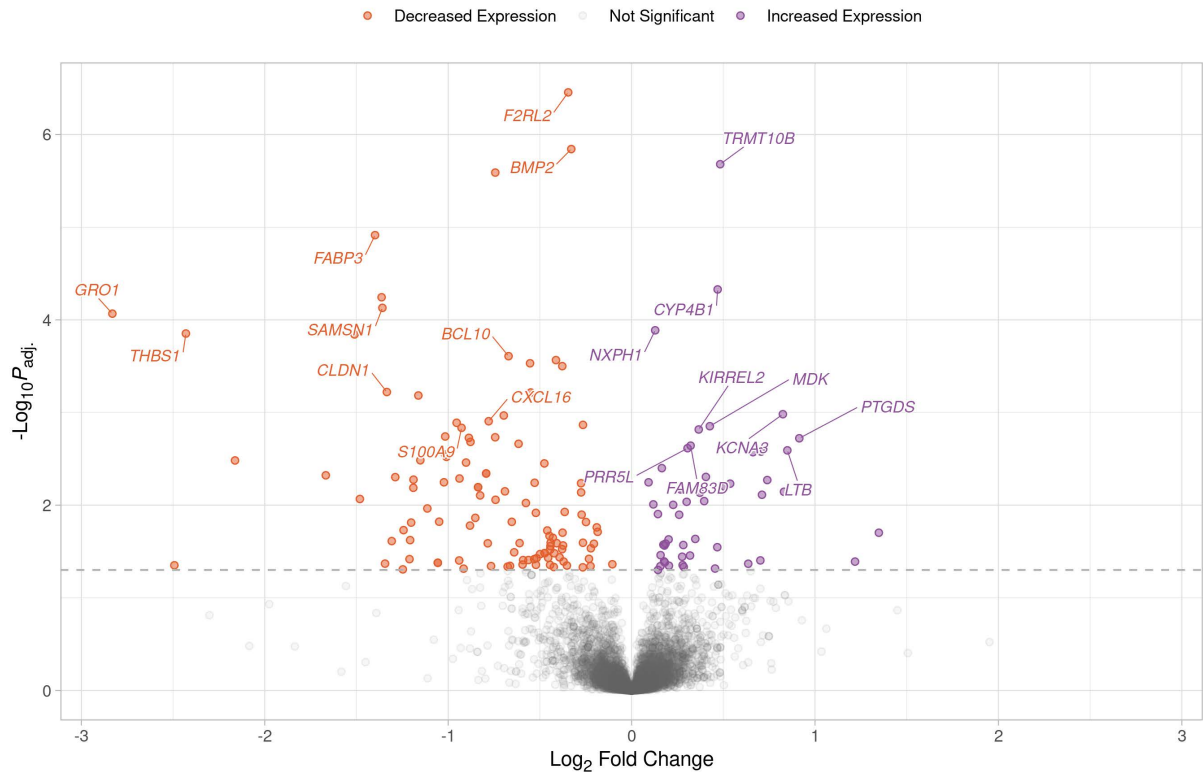
Supplementary Figure B.23. Volcano plot showing the results of the RESP contrast for the liver samples at 35 days post infection (dpi). Each data point represents a gene with the position on the x- and y-axes indicating the \log_2 fold change and $-\log_{10} P_{adj.}$, respectively. Genes above the horizontal dashed line are significantly differentially expressed with the colours representing the change in expression. The top 10 most significant genes for increased and decreased expression with gene symbols are labelled.



Supplementary Figure B.24. Volcano plot showing the results of the RESP contrast for the lymph node samples at 21 days post infection (dpi). Each data point represents a gene with the position on the x- and y-axes indicating the \log_2 fold change and $-\log_{10} P_{adj.}$, respectively. Genes above the horizontal dashed line are significantly differentially expressed with the colours representing the change in expression. The top 10 most significant genes for increased and decreased expression with gene symbols are labelled.



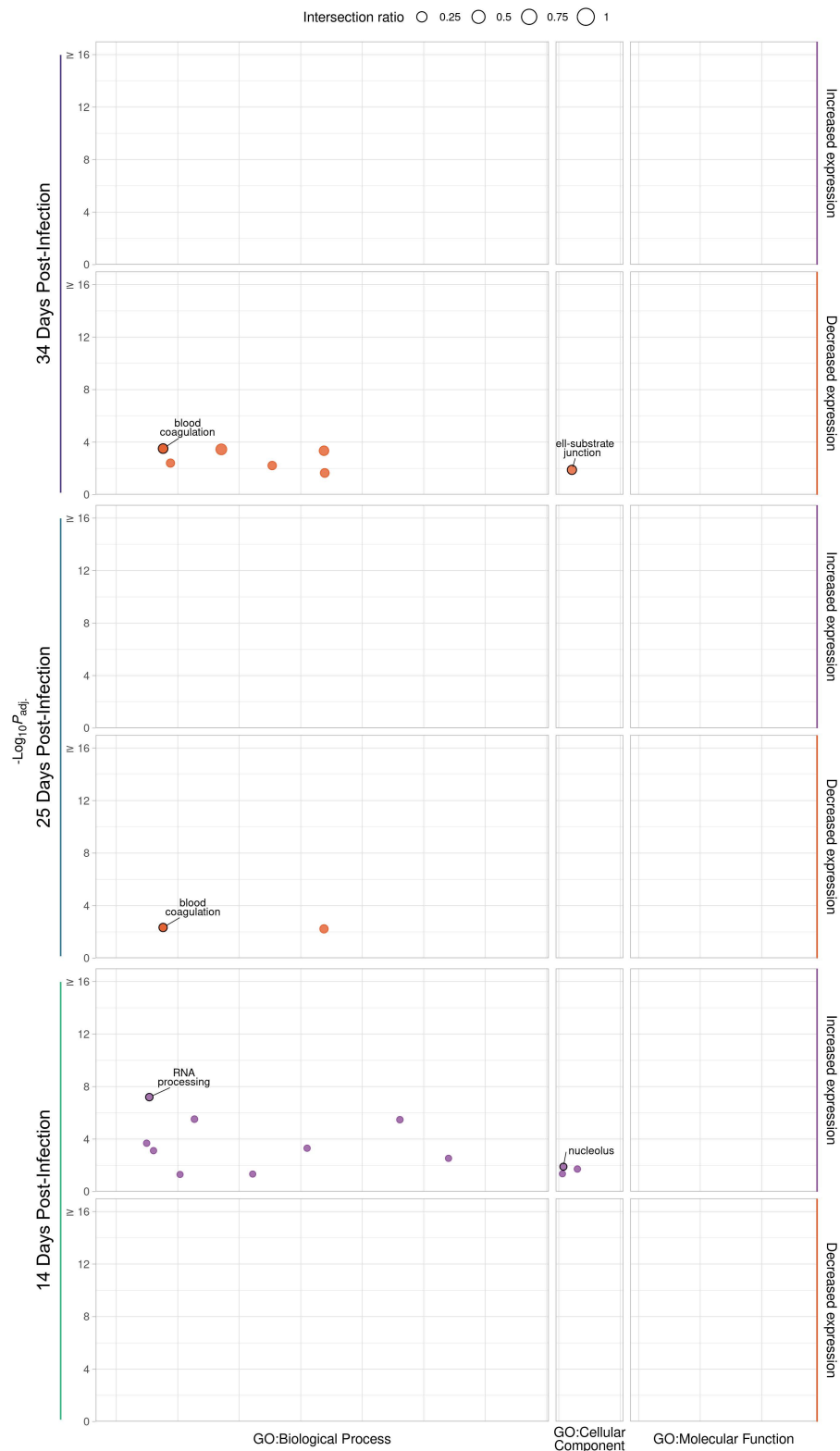
Supplementary Figure B.25. Volcano plot showing the results of the RESP contrast for the lymph node samples at 35 days post infection (dpi). Each data point represents a gene with the position on the x- and y-axes indicating the \log_2 fold change and $-\log_{10} P_{adj.}$, respectively. Genes above the horizontal dashed line are significantly differentially expressed with the colours representing the change in expression. The top 10 most significant genes for increased and decreased expression with gene symbols are labelled.



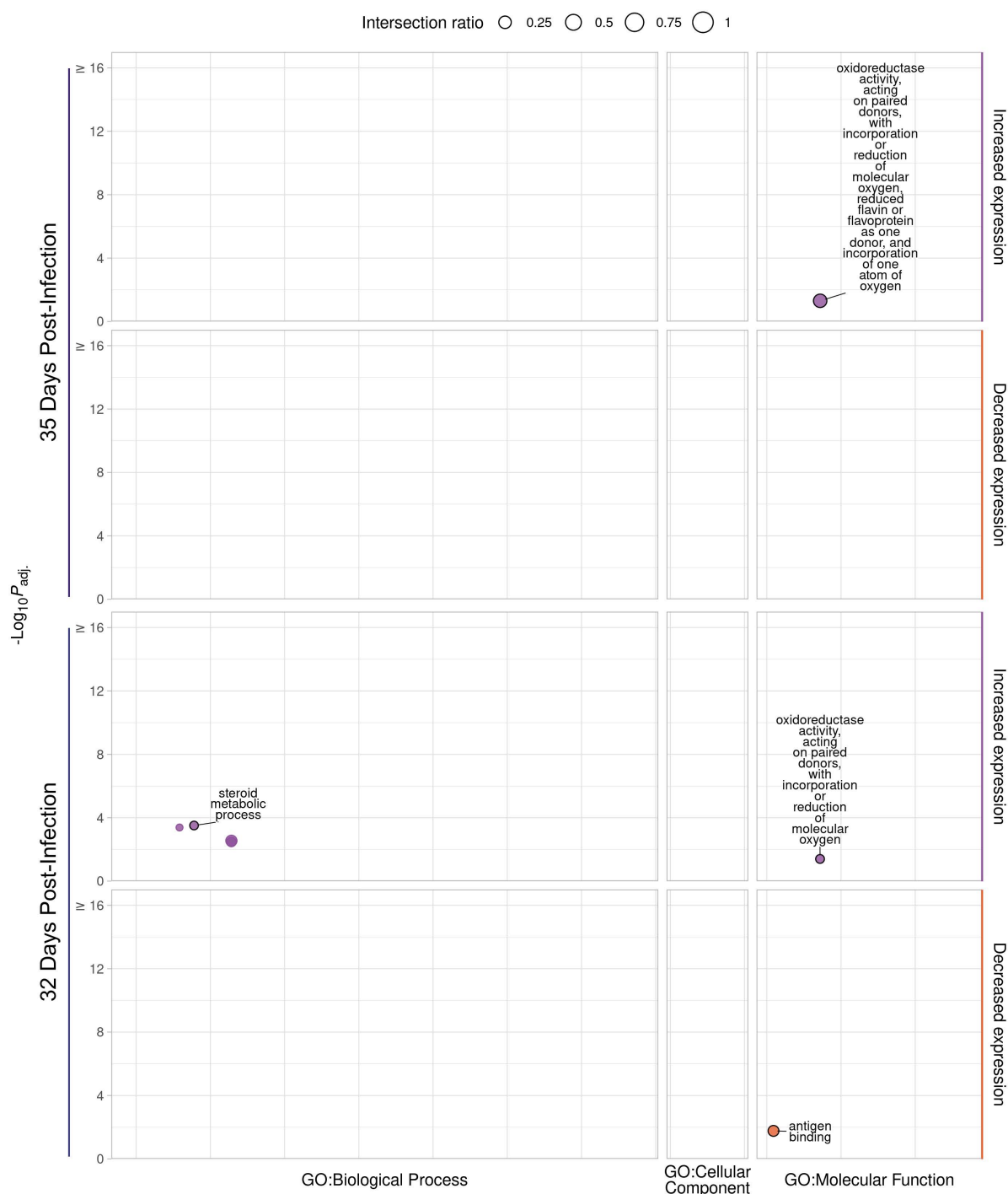
Supplementary Figure B.26. Volcano plot showing the results of the RESP contrast for the spleen samples at 21 days post infection (dpi). Each data point represents a gene with the position on the x- and y-axes indicating the \log_2 fold change and $-\log_{10}P_{adj.}$, respectively. Genes above the horizontal dashed line are significantly differentially expressed with the colours representing the change in expression. The top 10 most significant genes for increased and decreased expression with gene symbols are labelled.



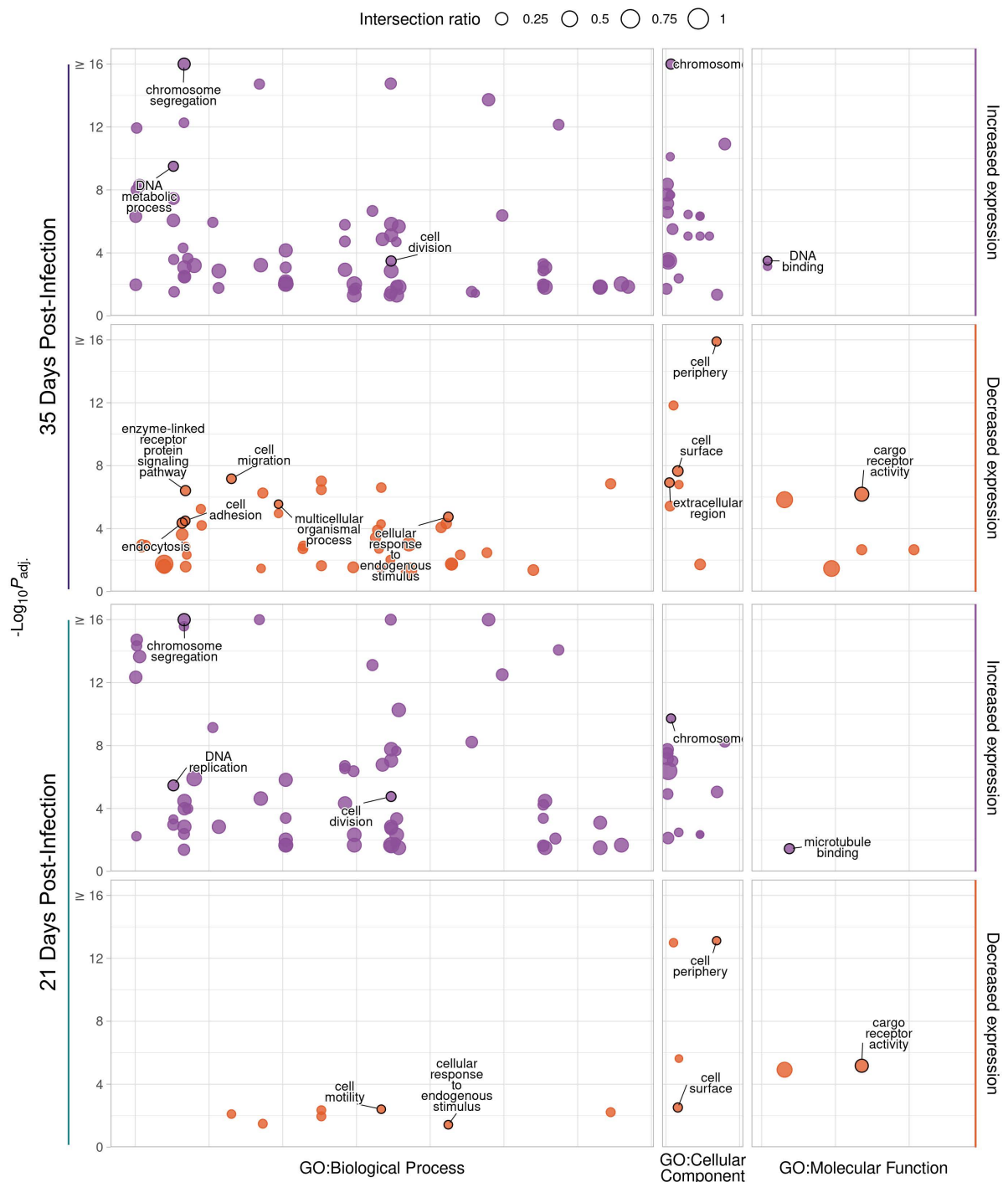
Supplementary Figure B.27. Volcano plot showing the results of the RESP contrast for the spleen samples at 35 days post infection (dpi). Each data point represents a gene with the position on the x- and y-axes indicating the \log_2 fold change and $-\log_{10} P_{adj.}$, respectively. Genes above the horizontal dashed line are significantly differentially expressed with the colours representing the change in expression. The top 10 most significant genes for increased and decreased expression with gene symbols are labelled.



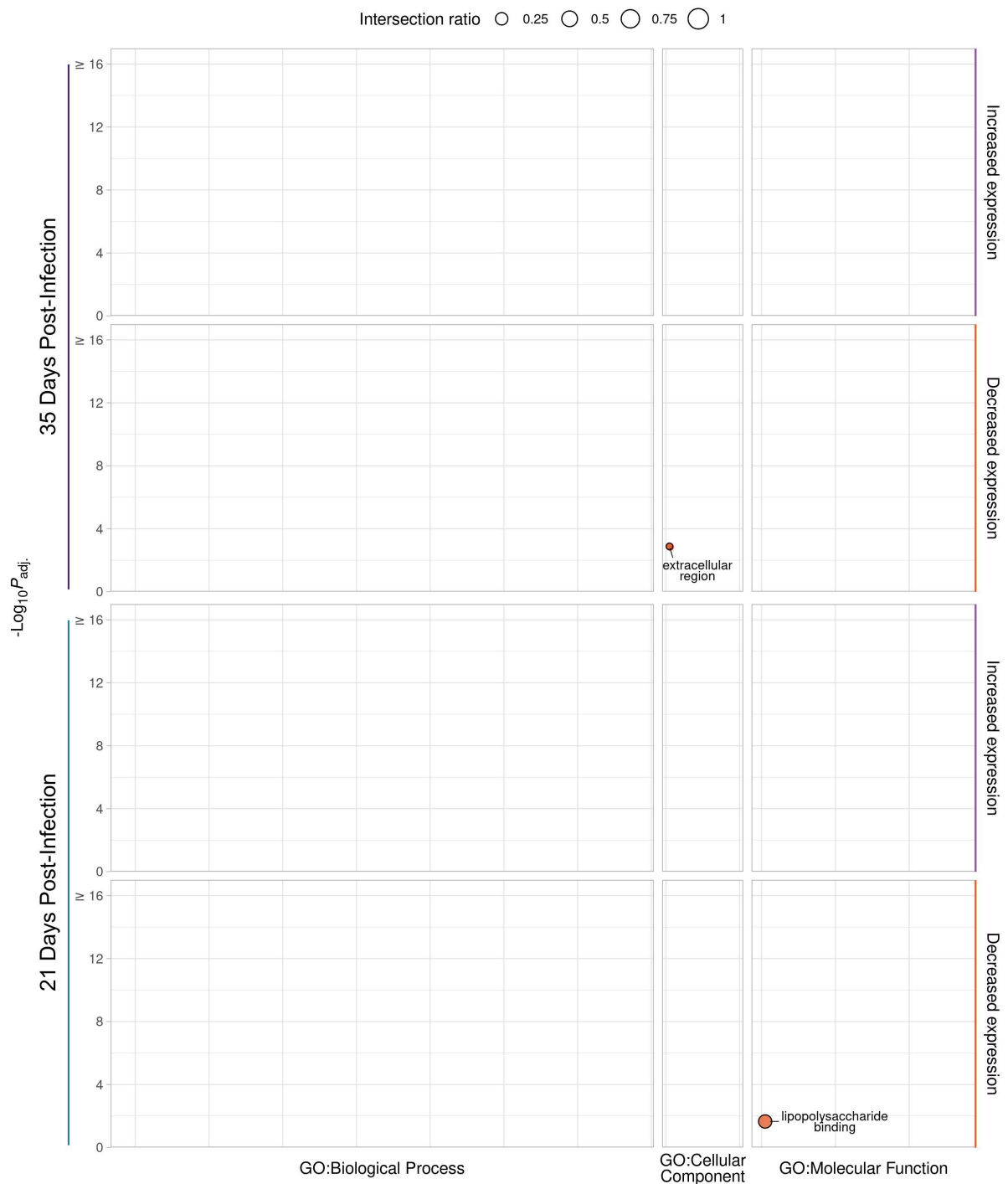
Supplementary Figure B.28. g:Profiler functional enrichment of significantly differentially expressed genes (DEGs) in the peripheral blood mononuclear cell (PBMC) sample RESP contrasts. Each circle represents a significantly enriched GO term with the size indicating the ratio of the intersection between the term and the DEGs. The vertical axis shows the $-\log_{10}P_{adj.}$ value and the vertical panels and colours indicate the direction of change in expression. The horizontal panels indicate the source of the term and the position within the panels groups terms from the same GO subtree. The top driver GO terms (up to a maximum of 10) are indicated with a black outline and label.



Supplementary Figure B.29. g:Profiler functional enrichment of significantly differentially expressed genes (DEGs) in the liver sample RESP contrasts. Each circle represents a significantly enriched GO term with the size indicating the ratio of the intersection between the term and the DEGs. The vertical axis shows the $-\log_{10}P_{\text{adj.}}$ value and the vertical panels and colours indicate the direction of change in expression. The horizontal panels indicate the source of the term and the position within the panels groups terms from the same GO subtree. The top driver GO terms (up to a maximum of 10) are indicated with a black outline and label.



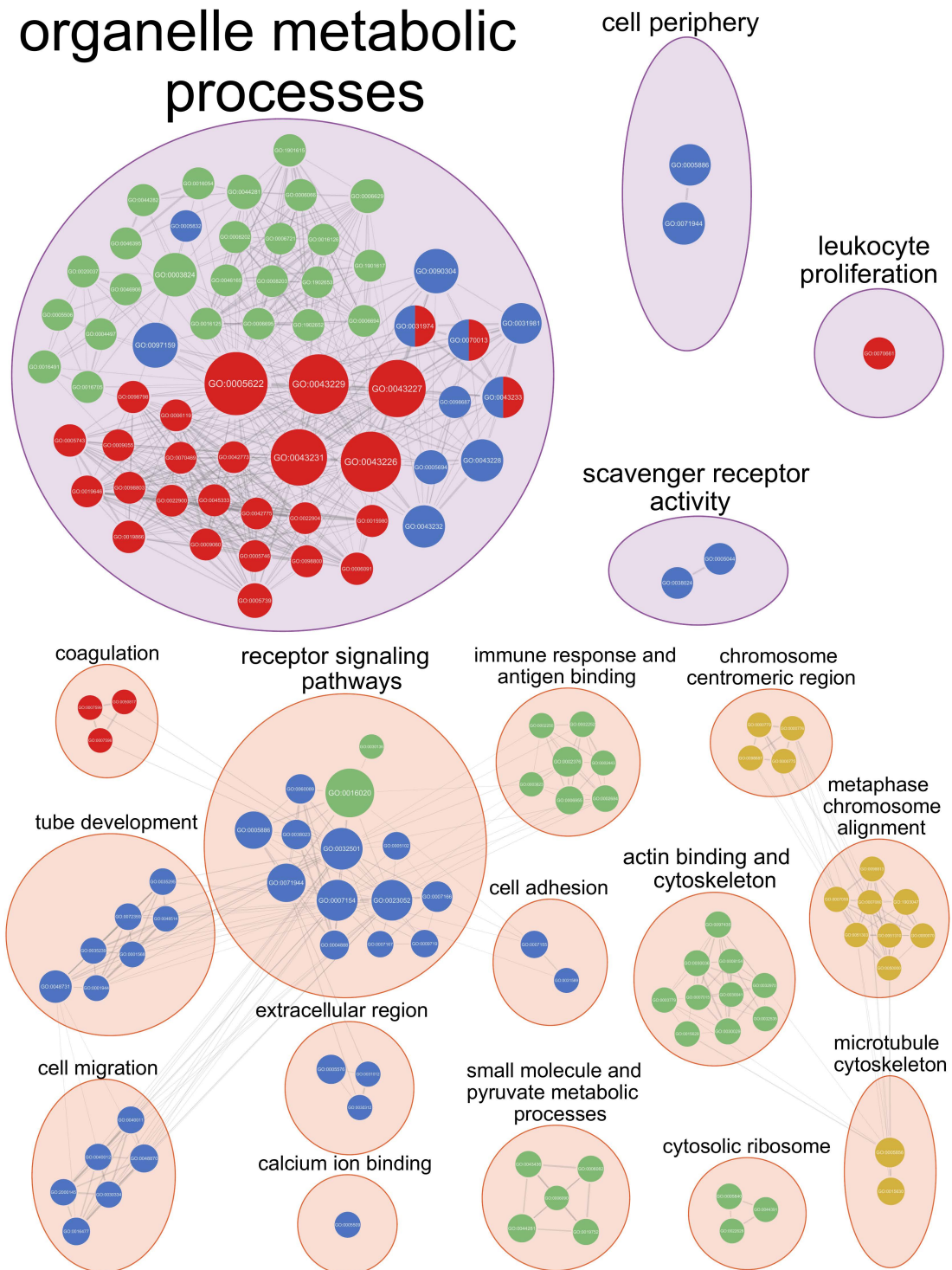
Supplementary Figure B.30. g:Profiler functional enrichment of significantly differentially expressed genes (DEGs) in the lymph node sample RESP contrasts. Each circle represents a significantly enriched GO term with the size indicating the ratio of the intersection between the term and the DEGs. The vertical axis shows the $-\log_{10} P_{adj.}$ value and the vertical panels and colours indicate the direction of change in expression. The horizontal panels indicate the source of the term and the position within the panels groups terms from the same GO subtree. The top driver GO terms (up to a maximum of 10) are indicated with a black outline and label.



Supplementary Figure B.31. g:Profiler functional enrichment of significantly differentially expressed genes (DEGs) in the spleen sample RESP contrasts. Each circle represents a significantly enriched GO term with the size indicating the ratio of the intersection between the term and the DEGs. The vertical axis shows the $-\log_{10}P_{\text{adj.}}$ value and the vertical panels and colours indicate the direction of change in expression. The horizontal panels indicate the source of the term and the position within the panels groups terms from the same GO subtree. The top driver GO terms (up to a maximum of 10) are indicated with a black outline and label.

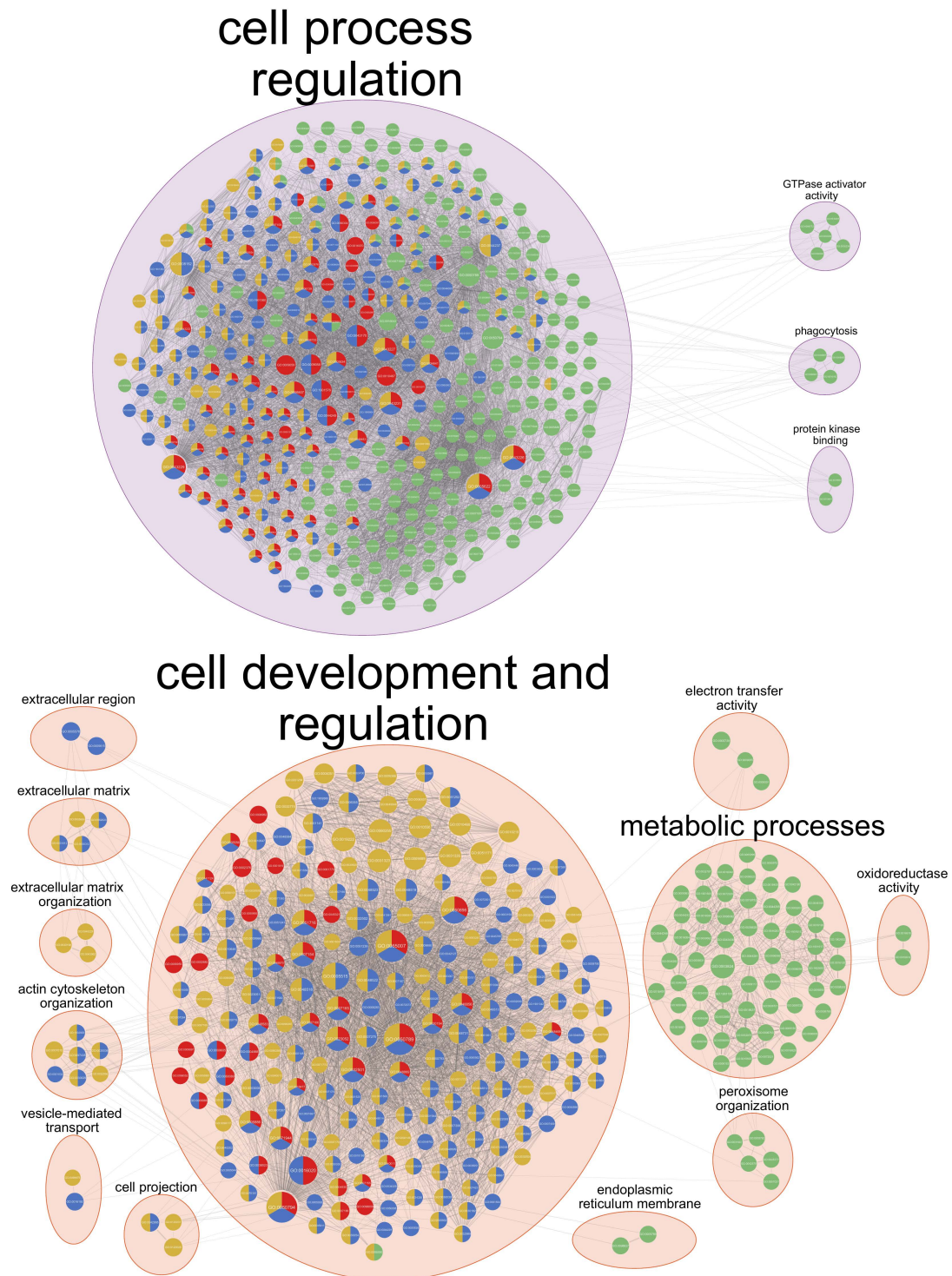
Expression ● Increased ● Decreased Tissue ● BL ● LI ● LN ● SP

organelle metabolic processes



Supplementary Figure B.32. EnrichmentMap network of significantly enriched GO terms identified from g:Profiler functional enrichment of significant differentially expressed genes (DEGs) for the DIRE contrasts. Each node represents a GO term with the colour of the node representing the tissue and the size representing the number of genes in the GO term. The edges indicate overlap between the GO terms with the width of the edges representing the similarity coefficient for the connected GO terms. The GO terms are clustered by AutoAnotate with the background colour of the clusters representing the direction of expression. The clusters are labelled with the size of the label scaling with the number of GO terms in the cluster.

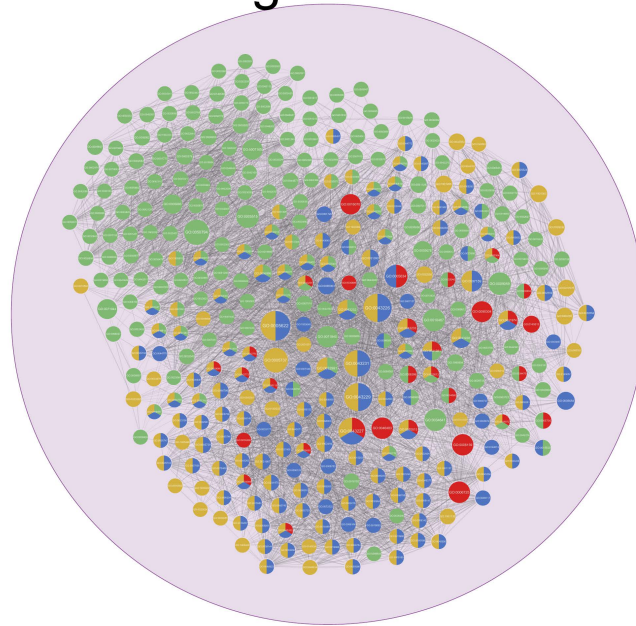
Expression ● Increased ● Decreased Tissue ● BL ● LI ● LN ● SP



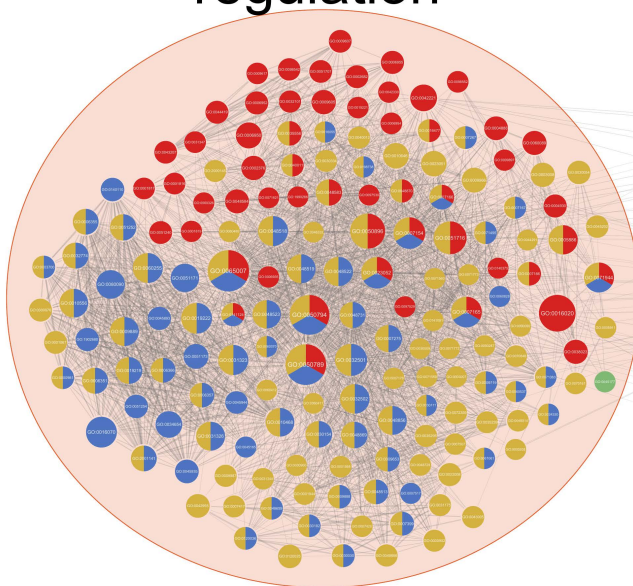
Supplementary Figure B.33. EnrichmentMap network of significantly enriched GO terms identified from g:Profiler functional enrichment of significant differentially expressed genes (DEGs) for the NDAM contrasts. Each node represents a GO term with the colour of the node representing the tissue and the size representing the number of genes in the GO term. The edges indicate overlap between the GO terms with the width of the edges representing the similarity coefficient for the connected GO terms. The GO terms are clustered by AutoAnotate with the background colour of the clusters representing the direction of expression. The clusters are labelled with the size of the label scaling with the number of GO terms in the cluster.

Expression ● Increased ● Decreased Tissue ● BL ● LI ● LN ● SP

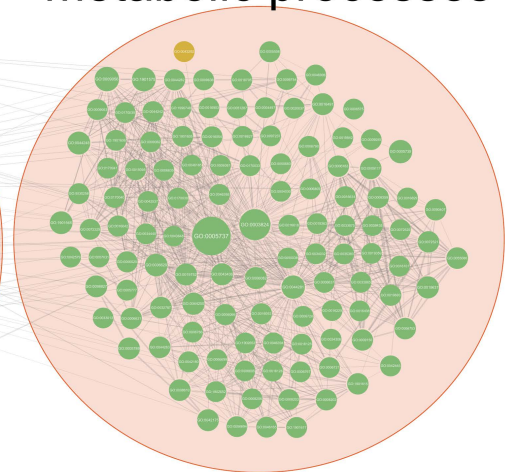
cell process
regulation



cell response
regulation



metabolic processes



Supplementary Figure B.34. EnrichmentMap network of significantly enriched GO terms identified from g:Profiler functional enrichment of significant differentially expressed genes (DEGs) for the BORA contrasts. Each node represents a GO term with the colour of the node representing the tissue and the size representing the number of genes in the GO term. The edges indicate overlap between the GO terms with the width of the edges representing the similarity coefficient for the connected GO terms. The GO terms are clustered by AutoAnotate with the background colour of the clusters representing the direction of expression. The clusters are labelled with the size of the label scaling with the number of GO terms in the cluster.

Appendix C. Supplementary material for Chapter 4

Supplementary Table C.1. Numbers of SNPs with z-score ≥ 2.0 for mean European *B. taurus*, African *B. taurus* and *B. indicus* ancestry components for the six populations with gene expression data available across all autosomes. The numbers in brackets indicate the percentage of the total 29,869 SNPs in the data set.

Group	Population	European <i>Bos taurus</i> ancestry	African <i>Bos taurus</i> ancestry	<i>Bos indicus</i> ancestry
African <i>Bos taurus</i>	LAGU	1,348 (4.51%)	0 (0%)	1,257 (4.21%)
African <i>Bos taurus</i>	BAOU	1,359 (4.55%)	0 (0%)	1,190 (3.98%)
Trypanotolerant African hybrid	NDAM	1,407 (4.71%)	112 (0.37%)	1,148 (3.84%)
Trypanotolerant African hybrid	BORG	1,193 (3.99%)	455 (1.52%)	958 (3.21%)
Trypanosusceptible African hybrid	FULA	1,251 (4.19%)	754 (2.52%)	654 (2.19%)
Trypanosusceptible African hybrid	BORA	1,282 (4.29%)	1,125 (3.77%)	300(1.00%)

Supplementary Table C.2. Numbers of genes within 1 Mb up- and downstream of SNPs with z-score ≥ 2.0 for mean European *B. taurus*, African *B. taurus* and *B. indicus* ancestry components for the six populations with gene expression data available across all autosomes. The numbers in brackets indicate the percentage of the total 34,080 genes in the data set.

Group	Population	European <i>Bos taurus</i> ancestry	African <i>Bos taurus</i> ancestry	<i>Bos indicus</i> ancestry
African <i>Bos taurus</i>	LAGU	845 (2.48%)	0 (0%)	1,076 (3.16%)
African <i>Bos taurus</i>	BAOU	947 (2.78%)	0 (0%)	1,060 (3.11%)
Trypanotolerant African hybrid	NDAM	1,006 (2.95%)	45 (0.13%)	842 (2.47%)
Trypanotolerant African hybrid	BORG	561 (1.65%)	82 (0.24%)	1,232 (3.62%)
Trypanosusceptible African hybrid	FULA	943 (2.77%)	171 (0.50%)	516 (1.51%)
Trypanosusceptible African hybrid	BORA	796 (2.34%)	569 (1.67%)	129 (0.38%)

Supplementary Table C.3. Population, days post infection and the significantly differentially expressed genes with increased and decreased expression with gene symbols for the response contrasts.

Population	Days post infection	Significantly differentially expressed genes with increased expression
NDAM	20	<i>PDK4, SLC11A1, CPT1A, DCTN5</i>
BAOU	30	<i>SRXN1, GNG11</i>
NDAM	30	<i>SLC11A1</i>
LAGU	40	<i>IL12RB2, SLC25A36, NFAT5, E2F3, PHF20L1, PTPN4, ZC3HAV1, PIGR, PICALM, TTBK2, RAB11FIP2, MYSM1, PDPR, LOC100366216, SLC38A4, ZBTB37, CD55, GPATCH2L, NT5C2, TET2</i>
NDAM	40	<i>FKBP5</i>
Population	Days post infection	Significantly differentially expressed genes with decreased expression
NDAM	30	<i>SNX9, LZTS3</i>
LAGU	40	<i>OXER1, NEIL2, FADS1, NAB2, ANXA6</i>
BAOU	40	<i>SPARC</i>
NDAM	40	<i>GATA1, IGF2, STK36, PRKCG, NEIL2, SYNGR3, PDLIM1, LZTS3</i>
BORG	40	<i>NEIL2</i>

Supplementary Table C.4. Gene symbol and modules containing each of the 243 genes with valid gene symbols that were found in four or more of the eight functional modules.

Symbol	Modules
<i>CBL</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>CNOT1</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>EDN1</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>EIF2C2</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>IL1B</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>RIPK1</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>TRAF2</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>BIKBA</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>CAV3</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>CCND1</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>CFTR</i>	MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>CTNNB1</i>	MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>HPRT1</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>IKBKB</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>IL2RB</i>	MICRO BL 34, MICRO LI 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>IQCB1</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40, RNA BORG 40
<i>JUN</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA BORG 40
<i>LAMP2</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40
<i>LBR</i>	MICRO BL 34, MICRO LI 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>MAPK10</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>MYD88</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA BORG 40
<i>PARP1</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40, RNA BORG 40
<i>PIK3R1</i>	MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>PKD1</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40
<i>REL</i>	MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40

Supplementary Table C.4 continued.

Symbol	Modules
<i>SELE</i>	MICRO BL 34, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>SKP1</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA BORG 40
<i>TLR2</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40
<i>TP53</i>	MICRO BL 34, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>ALB</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>APOE</i>	MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>CCND2</i>	MICRO BL 34, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40, RNA BORG 40
<i>CDC37</i>	MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>CDKN1A</i>	MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>COPS6</i>	MICRO BL 34, MICRO LI 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40
<i>CTR9</i>	MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40
<i>ERBB3</i>	MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>GRIN1</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA NDAM 40, RNA BORG 40
<i>HRMT1L2</i>	MICRO LI 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>IL1R2</i>	MICRO LI 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>IL2RA</i>	MICRO BL 34, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>IRAK1</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40
<i>KRT18</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>MT-CO2</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA NDAM 40, RNA BORG 40
<i>NEK2</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40
<i>NTRK2</i>	MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>PLCG1</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BORG 40
<i>RFC1</i>	MICRO BL 34, MICRO LN 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>SF3B14</i>	MICRO BL 34, MICRO LN 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>SIRT1</i>	MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>SLC11A1</i>	MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40, RNA BORG 40

Supplementary Table C.4 continued.

Symbol	Modules
<i>TBK1</i>	MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40
<i>TRADD</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40
<i>ACTC1</i>	MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>ACTN1</i>	MICRO BL 34, MICRO LN 35, RNA LAGU 40, RNA NDAM 40, RNA BORG 40
<i>AR</i>	MICRO LN 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>ARF1</i>	MICRO LI 35, MICRO LN 35, RNA LAGU 40, RNA NDAM 40, RNA BORG 40
<i>ARRB1</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40
<i>ATF2</i>	MICRO LN 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>CD14</i>	MICRO BL 34, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40
<i>CDK4</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA NDAM 40
<i>CDK9</i>	MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40, RNA BORG 40
<i>CHUK</i>	MICRO LN 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>CREBBP</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40
<i>CSF3</i>	MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>CTTN</i>	MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40
<i>CUL2</i>	MICRO LI 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA BORG 40
<i>CXCL10</i>	MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40
<i>DDX58</i>	MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>DLG4</i>	MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40
<i>DST</i>	MICRO LI 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>EEF1B</i>	MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>EIF2C1</i>	MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>EIF2S1</i>	MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40
<i>FBXW11</i>	MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40
<i>FLIP</i>	MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>GRK5</i>	MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40, RNA BORG 40
<i>HNRNPD</i>	MICRO BL 34, MICRO LI 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>HSP90AA1</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40
<i>HSPA9</i>	MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40, RNA BORG 40
<i>IL12RB2</i>	MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>IL17A</i>	MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>IRF1</i>	MICRO BL 34, MICRO LI 35, MICRO SP 35, RNA BAOU 40, RNA BORG 40
<i>IRF3</i>	MICRO BL 34, MICRO SP 35, RNA LAGU 40, RNA NDAM 40, RNA BORG 40
<i>IRF4</i>	MICRO LI 35, MICRO LN 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>LRRK2</i>	MICRO LI 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40

Supplementary Table C.4 continued.

Symbol	Modules
<i>LYN</i>	MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40
<i>MAP3K7</i>	MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40
<i>MCL1</i>	MICRO BL 34, MICRO LI 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>MDM2</i>	MICRO BL 34, MICRO SP 35, RNA LAGU 40, RNA NDAM 40, RNA BORG 40
<i>METTL21B</i>	MICRO LI 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>MT-ND4</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40
<i>NCOA6</i>	MICRO BL 34, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40
<i>NGF</i>	MICRO LN 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>NPHP1</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA BAOU 40
<i>NPHP4</i>	MICRO BL 34, MICRO LN 35, MICRO SP 35, RNA BAOU 40, RNA BORG 40
<i>PLAA</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA NDAM 40
<i>PML</i>	MICRO BL 34, MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>PPP2R1A</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40
<i>PPP2R4</i>	MICRO LI 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>PSMD10</i>	MICRO LI 35, MICRO LN 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>PTK2</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, RNA LAGU 40, RNA BORG 40
<i>PTPN11</i>	MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40
<i>RAB11A</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA NDAM 40
<i>RELB</i>	MICRO BL 34, MICRO LI 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40
<i>RRM2</i>	MICRO BL 34, MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40
<i>SF1</i>	MICRO BL 34, MICRO LN 35, RNA LAGU 40, RNA NDAM 40, RNA BORG 40
<i>SF3A2</i>	MICRO BL 34, MICRO LI 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>SHC1</i>	MICRO BL 34, MICRO LN 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>SMARCA4</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, RNA LAGU 40, RNA BORG 40
<i>SP1</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA BAOU 40
<i>STAT3</i>	MICRO BL 34, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40
<i>SYNCRIP</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, RNA BAOU 40, RNA NDAM 40
<i>TCN2</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40
<i>TCP1</i>	MICRO BL 34, MICRO LI 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40
<i>TRAF6</i>	MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA NDAM 40, RNA BORG 40
<i>TRIM21</i>	MICRO BL 34, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40
<i>TUBB5</i>	MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>TXNRD1</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA NDAM 40
<i>XIAP</i>	MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40
<i>YWHAE</i>	MICRO BL 34, MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>A2M</i>	MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40
<i>AHCY</i>	MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40
<i>AKAP8</i>	MICRO BL 34, MICRO LI 35, MICRO SP 35, RNA NDAM 40
<i>APAF1</i>	MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40
<i>APLP2</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35
<i>APOA2</i>	MICRO LI 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>APP</i>	MICRO BL 34, MICRO LN 35, RNA LAGU 40, RNA NDAM 40
<i>ASPM</i>	MICRO BL 34, MICRO LN 35, MICRO SP 35, RNA NDAM 40

Supplementary Table C.4 continued.

Symbol	Modules
<i>ATF3</i>	MICRO BL 34, MICRO LI 35, MICRO SP 35, RNA NDAM 40
<i>ATP5J</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>ATR</i>	MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40
<i>BCAR3</i>	MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40
<i>BCR</i>	MICRO BL 34, MICRO LN 35, MICRO SP 35, RNA LAGU 40
<i>BDNF</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>BECN1</i>	MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA LAGU 40
<i>BIRC3</i>	MICRO LN 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40
<i>C20ORF18</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>C2ORF29</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>C3H1orf52</i>	MICRO BL 34, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>CCR5</i>	MICRO BL 34, MICRO LN 35, MICRO SP 35, RNA LAGU 40
<i>CCRL1</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>CD28</i>	MICRO BL 34, MICRO LN 35, MICRO SP 35, RNA LAGU 40
<i>CDC25C</i>	MICRO BL 34, MICRO SP 35, RNA LAGU 40, RNA NDAM 40
<i>CDC73</i>	MICRO BL 34, MICRO LI 35, RNA LAGU 40, RNA BAOU 40
<i>CDK1</i>	MICRO LN 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>CLU</i>	MICRO BL 34, MICRO SP 35, RNA LAGU 40, RNA NDAM 40
<i>CMYA5</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>CNOT6</i>	MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40
<i>CNOT7</i>	MICRO BL 34, MICRO LI 35, MICRO SP 35, RNA BORG 40
<i>CNTF</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>CRYAB</i>	MICRO LI 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>CSF2</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>CSNK1G1</i>	MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40
<i>CSNK2A2</i>	MICRO BL 34, MICRO SP 35, RNA LAGU 40, RNA NDAM 40
<i>CTPS</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>CXCR7</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>DDIT4</i>	MICRO LI 35, RNA LAGU 40, RNA NDAM 40, RNA BORG 40
<i>DHFR</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35
<i>DPF1</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>DVL2</i>	MICRO BL 34, MICRO LI 35, MICRO SP 35, RNA NDAM 40
<i>EIF2AK2</i>	MICRO LI 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40
<i>ELA2</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>EP300</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>FBXO32</i>	MICRO LN 35, RNA LAGU 40, RNA BAOU 40, RNA BORG 40
<i>FBXO5</i>	MICRO LN 35, MICRO SP 35, RNA BAOU 40, RNA BORG 40
<i>FKBP5</i>	MICRO SP 35, RNA LAGU 40, RNA NDAM 40, RNA BORG 40
<i>FLJ20565</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>FN1</i>	MICRO LN 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>GEMIN2</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35
<i>GNB2L1</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>GR-A</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>GRB2</i>	MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40
<i>HGS</i>	MICRO LI 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40

Supplementary Table C.4 continued.

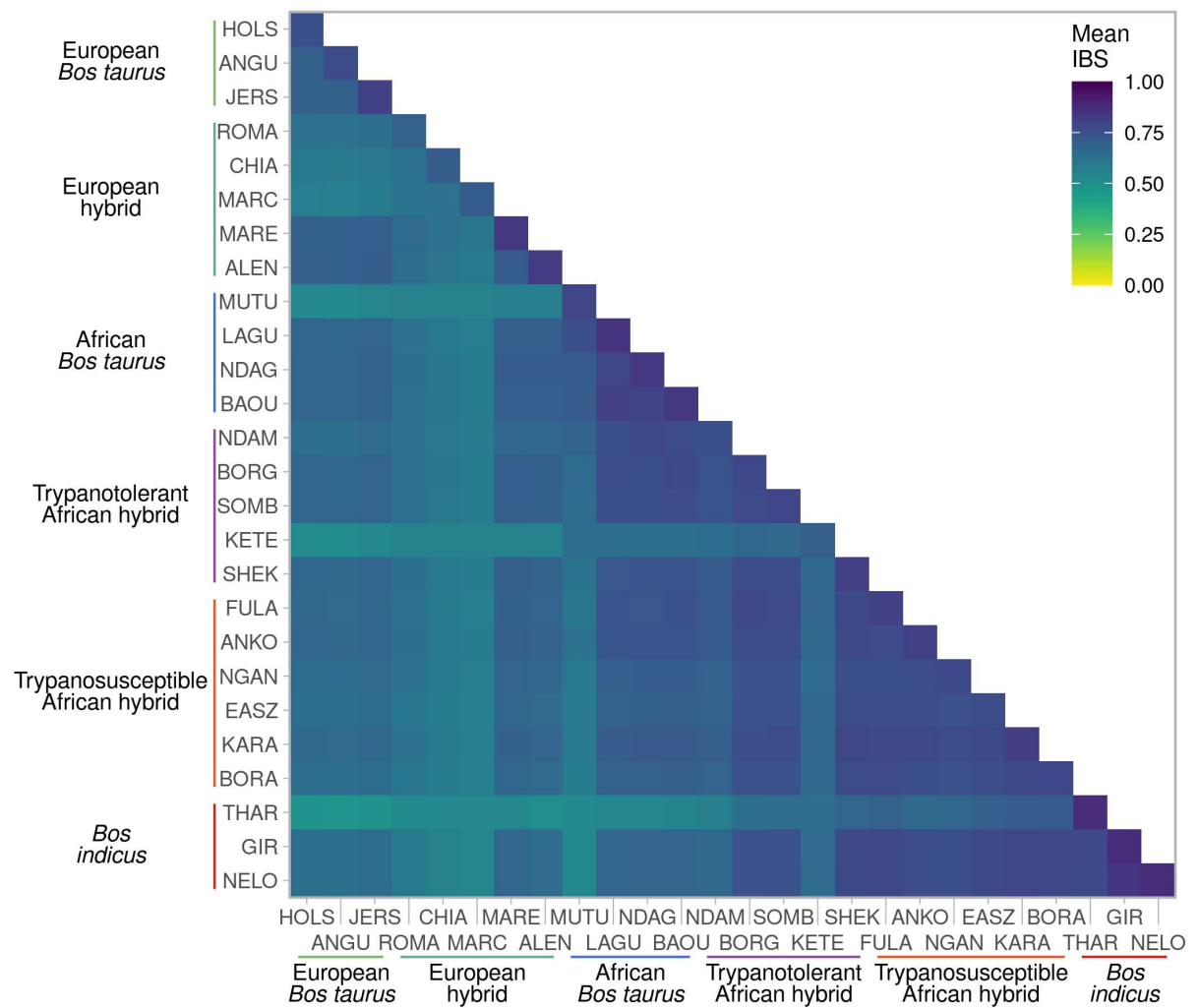
Symbol	Modules
<i>HMGA2</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>HMGB1</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35
<i>HTT</i>	MICRO BL 34, MICRO LN 35, MICRO SP 35, RNA BORG 40
<i>ICT1</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>IL10</i>	MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40
<i>IL11</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>IL12A</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>ILF3</i>	MICRO BL 34, MICRO LN 35, MICRO SP 35, RNA NDAM 40
<i>IRF2</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35
<i>ISG15</i>	MICRO BL 34, MICRO LN 35, MICRO SP 35, RNA LAGU 40
<i>ITGB2</i>	MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40
<i>JAKMIP1</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>KAT5</i>	MICRO BL 34, MICRO LN 35, RNA LAGU 40, RNA BORG 40
<i>KSR1</i>	MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40
<i>LARS</i>	MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA NDAM 40
<i>LCK</i>	MICRO LN 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40
<i>LEO1</i>	MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40
<i>LIFR</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>MAFG</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35
<i>MAP3K7IP1</i>	MICRO BL 34, MICRO SP 35, RNA BAOU 40, RNA NDAM 40
<i>MAPK6</i>	MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40
<i>MDH2</i>	MICRO LI 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>MIB1</i>	MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40
<i>NANOG</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>NANOS2</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>NFAT5</i>	MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA BORG 40
<i>NFATC2</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35
<i>NFKBIE</i>	MICRO BL 34, MICRO SP 35, RNA LAGU 40, RNA BAOU 40
<i>NFKBIL1</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35
<i>NPM1</i>	MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA BAOU 40
<i>NR4A1</i>	MICRO BL 34, MICRO LI 35, MICRO SP 35, RNA NDAM 40
<i>PCAF</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>PGD</i>	MICRO BL 34, MICRO LI 35, RNA LAGU 40, RNA NDAM 40
<i>PGHS-2</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>PGR</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>PIK3R2</i>	MICRO BL 34, MICRO SP 35, RNA LAGU 40, RNA NDAM 40
<i>POU2F1</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, RNA LAGU 40
<i>PPP2R1B</i>	MICRO LI 35, MICRO LN 35, RNA LAGU 40, RNA NDAM 40
<i>PRDX5</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, RNA LAGU 40
<i>PRKCI</i>	MICRO BL 34, MICRO LN 35, MICRO SP 35, RNA LAGU 40
<i>PROS1</i>	MICRO LN 35, MICRO SP 35, RNA BAOU 40, RNA NDAM 40
<i>PTPN1</i>	MICRO LN 35, MICRO SP 35, RNA LAGU 40, RNA NDAM 40
<i>PTPN6</i>	MICRO BL 34, MICRO SP 35, RNA BAOU 40, RNA BORG 40
<i>RAG1</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>RAG2</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40

Supplementary Table C.4 continued.

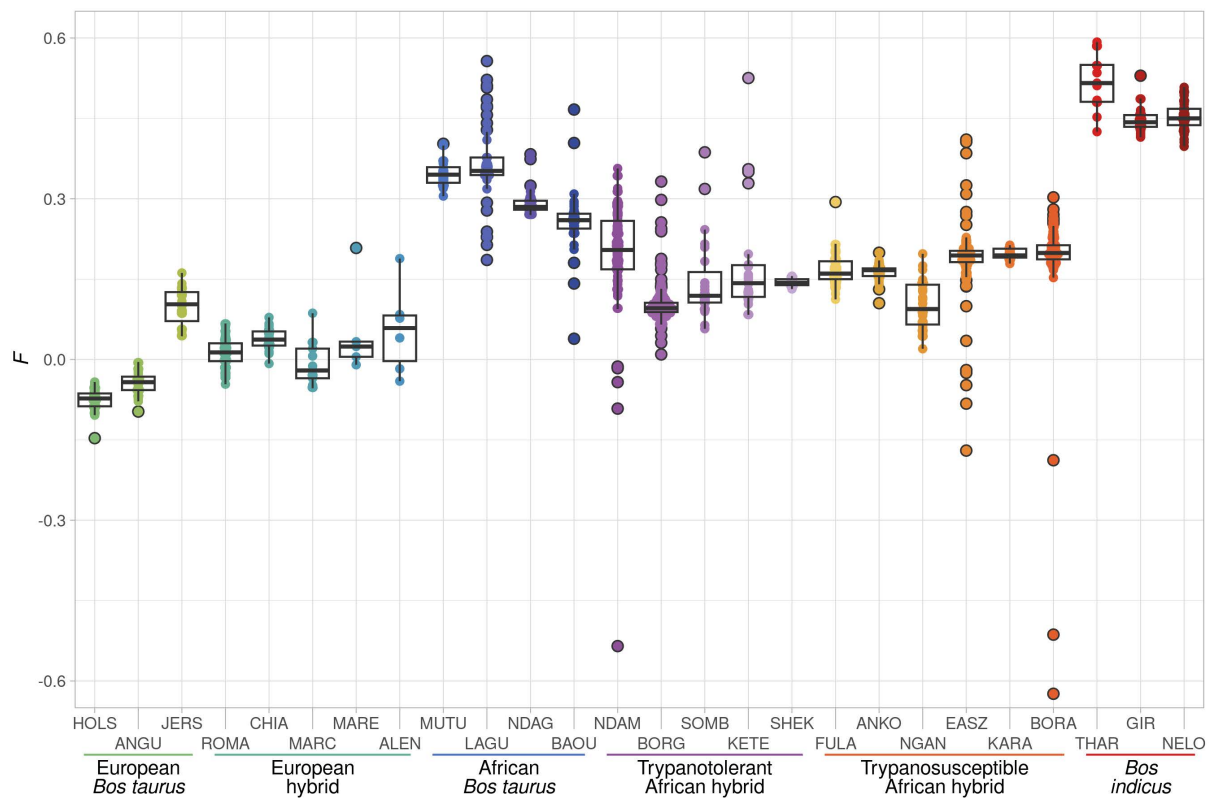
Symbol	Modules
<i>RGS7</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>RQCD1</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>RRM2B</i>	MICRO BL 34, MICRO LN 35, MICRO SP 35, RNA LAGU 40
<i>SELL</i>	MICRO BL 34, MICRO LI 35, MICRO SP 35, RNA LAGU 40
<i>SNCA</i>	MICRO BL 34, MICRO SP 35, RNA NDAM 40, RNA BORG 40
<i>SRRM2</i>	MICRO BL 34, MICRO LI 35, RNA BAOU 40, RNA BORG 40
<i>STAT5B</i>	MICRO BL 34, MICRO LI 35, RNA BAOU 40, RNA BORG 40
<i>TBPL1</i>	MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA NDAM 40
<i>TGFB1</i>	MICRO BL 34, MICRO SP 35, RNA LAGU 40, RNA NDAM 40
<i>TLR4</i>	MICRO BL 34, MICRO LI 35, MICRO SP 35, RNA LAGU 40
<i>TMEM66</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>TNF</i>	MICRO LI 35, MICRO SP 35, RNA LAGU 40, RNA BAOU 40
<i>TNIP3</i>	MICRO SP 35, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40
<i>TOMM70A</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>TRAIP</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>UBA1</i>	MICRO BL 34, MICRO LI 35, MICRO LN 35, MICRO SP 35
<i>UBE2D1</i>	MICRO BL 34, MICRO LI 35, MICRO SP 35, RNA LAGU 40
<i>UBE2N</i>	MICRO LI 35, MICRO LN 35, MICRO SP 35, RNA BORG 40
<i>UNC5CL</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>VDR</i>	MICRO BL 34, MICRO LN 35, MICRO SP 35, RNA LAGU 40
<i>VIM</i>	MICRO BL 34, RNA LAGU 40, RNA BAOU 40, RNA NDAM 40
<i>VPS4A</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>WDR96</i>	MICRO SP 35, RNA BAOU 40, RNA NDAM 40, RNA BORG 40
<i>YY1</i>	MICRO BL 34, MICRO LI 35, MICRO SP 35, RNA BAOU 40

Supplementary Table C.5. Numbers of intervals within 1 Mb up- and downstream of SNPs with z-score ≥ 2.0 for mean European *B. taurus*, African *B. taurus* and *B. indicus* ancestry components for the six populations with gene expression data available across all autosomes and groups of populations from the original local ancestry analysis.

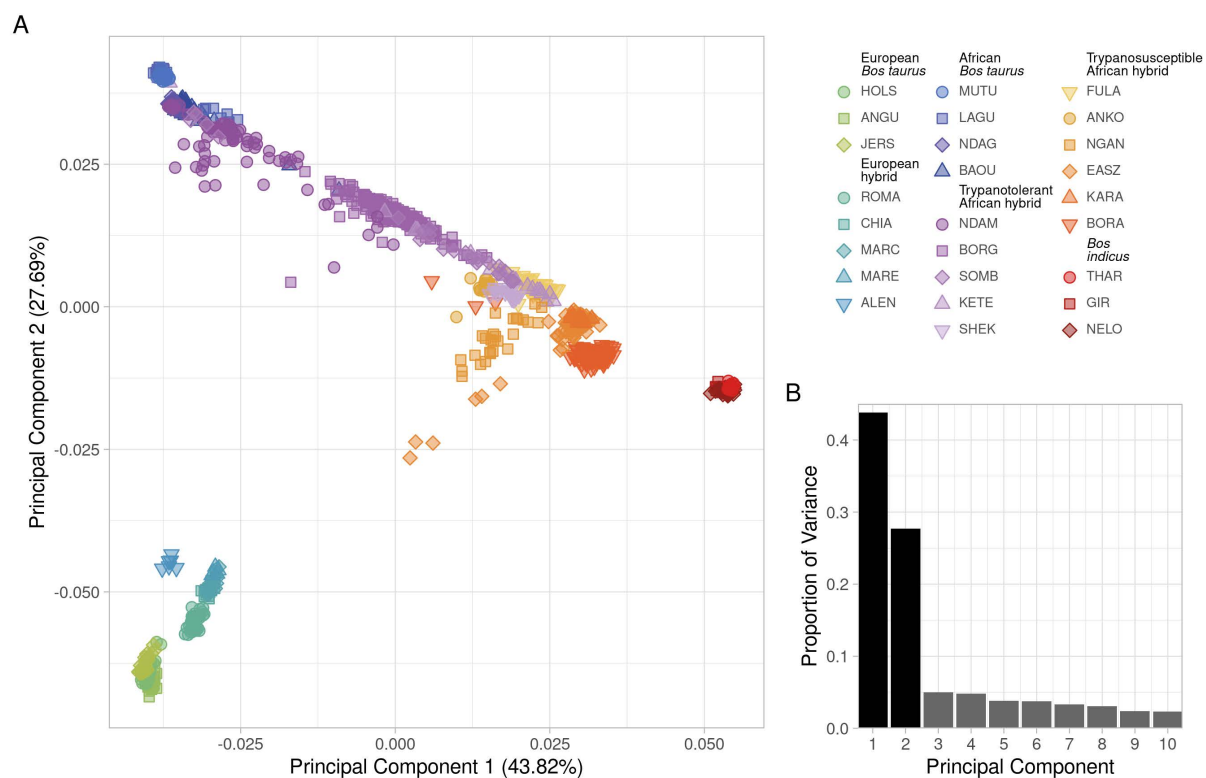
Analysis	Software	Data	Group/Population	European <i>Bos taurus</i> intervals	African <i>Bos taurus</i> intervals	<i>Bos indicus</i> intervals
Updated	ELAI	LD	LAGU	1,237	0	1,169
Updated	ELAI	LD	BAOU	1,262	0	1,111
Updated	ELAI	LD	NDAM	1,302	102	1,049
Updated	ELAI	LD	BORG	1,084	426	864
Updated	ELAI	LD	FULA	1,150	711	580
Updated	ELAI	LD	BORA	1,203	1,053	260
Original	ELAI	HD	Selected European hybrids	0	9,296	12,898
Original	ELAI	HD	Selected trypanotolerant African hybrids	10,748	3,408	6,966
Original	ELAI	HD	Trypanosusceptible African hybrids	10,273	8,930	2,871
Original	ELAI	LD	Selected European hybrids	132	1,220	1,306
Original	ELAI	LD	Selected trypanotolerant African hybrids	1,153	582	738
Original	ELAI	LD	Trypanosusceptible African hybrids	1,091	1,013	398
Original	MOSAIC	HD	Selected European hybrids	0	6,737	12,802
Original	MOSAIC	HD	Selected trypanotolerant African hybrids	9,924	3,457	6,774
Original	MOSAIC	HD	Trypanosusceptible African hybrids	10,634	7,352	3,415



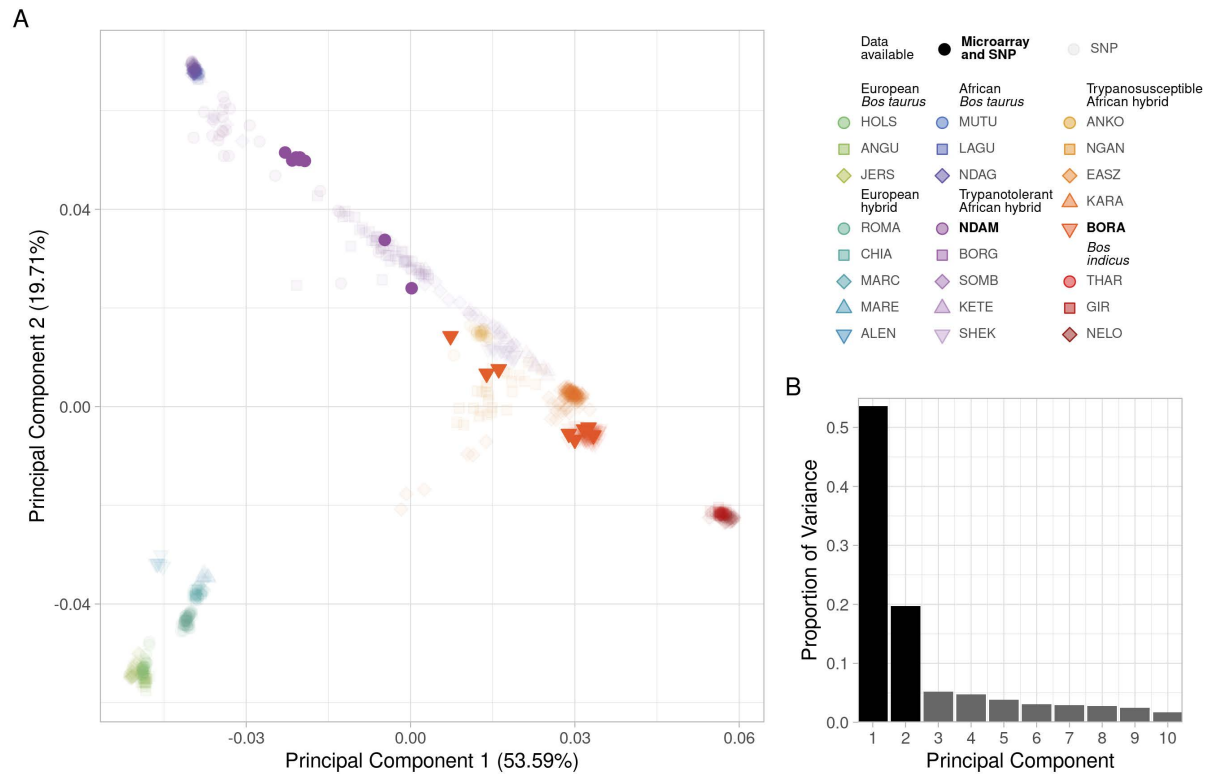
Supplementary Figure C.1. Heatmap of mean identity by state values for SNP data in European, African, and Asian cattle populations.



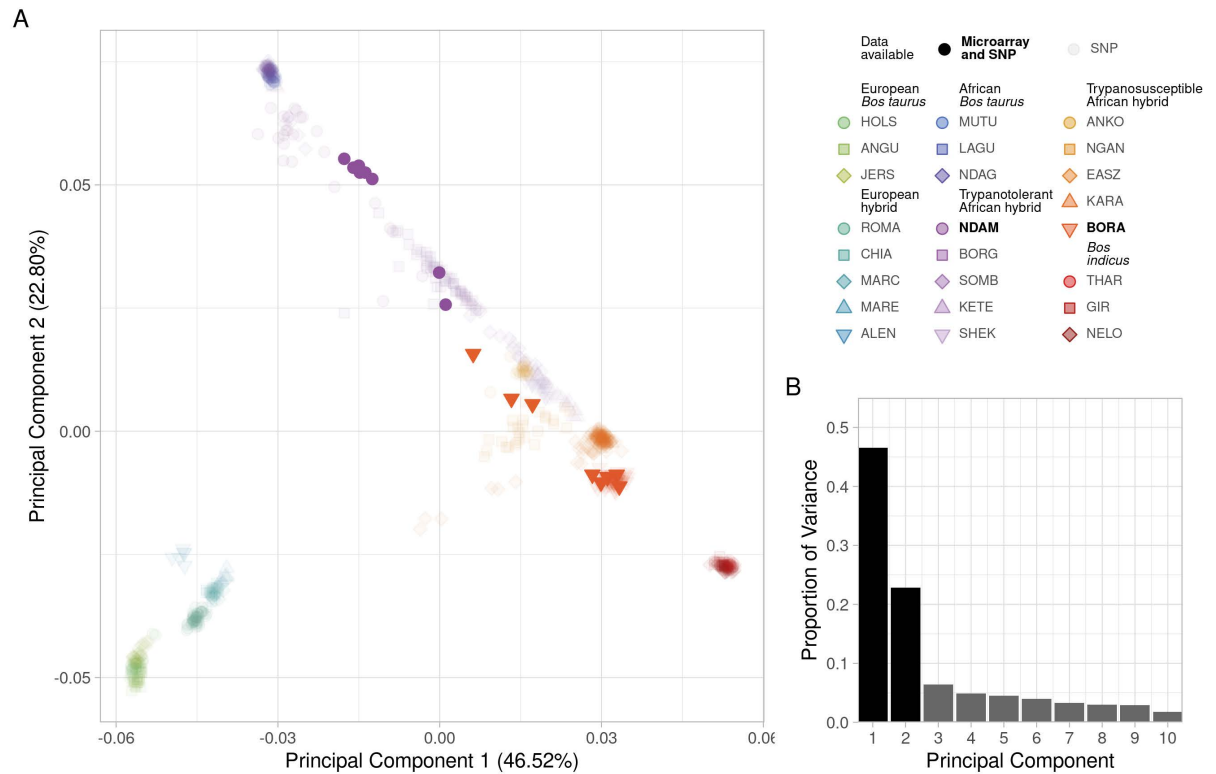
Supplementary Figure C.2. Tukey box plots showing the distribution of inbreeding values (F) for SNP data for each population of European, African, and Asian cattle. Outliers are indicated with a black outline.



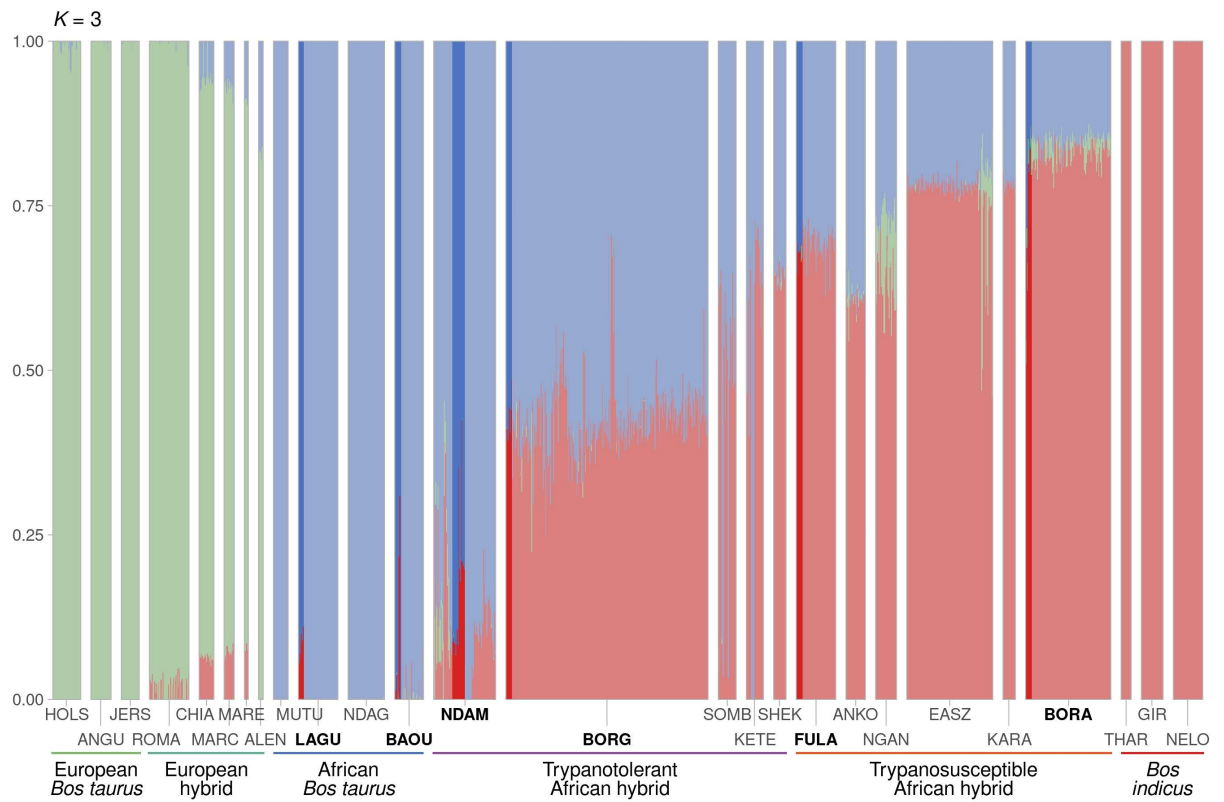
Supplementary Figure C.3. A. Principal component analysis (PCA) of SNP data for cattle coloured according to population showing the first two principal components and **B.** bar chart of proportion of variance of the top ten principal components.



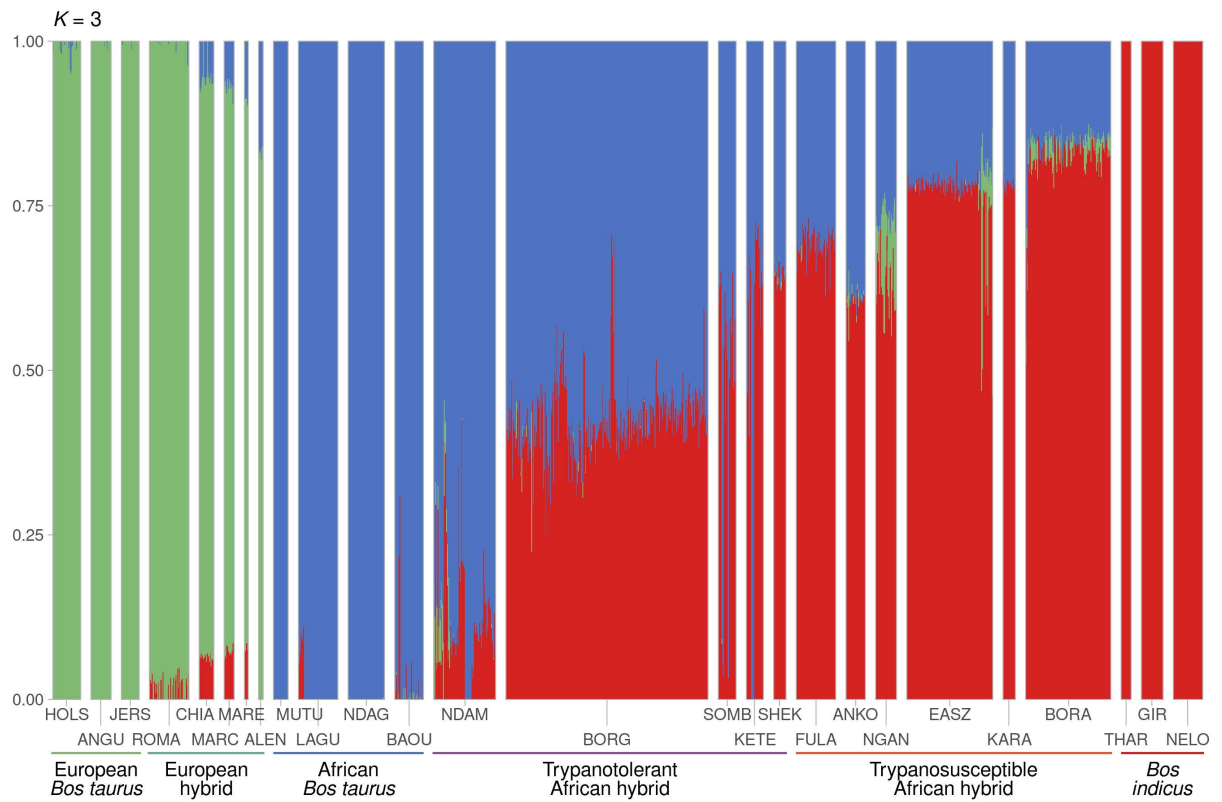
Supplementary Figure C.4. A. Principal component analysis (PCA) of the high-density SNP data for the cattle samples from **Chapter 2** coloured according to population showing the first two principal components and **B.** bar chart of proportion of variance of the top ten principal components. The transparency indicates the availability of microarray gene expression data for the sample.



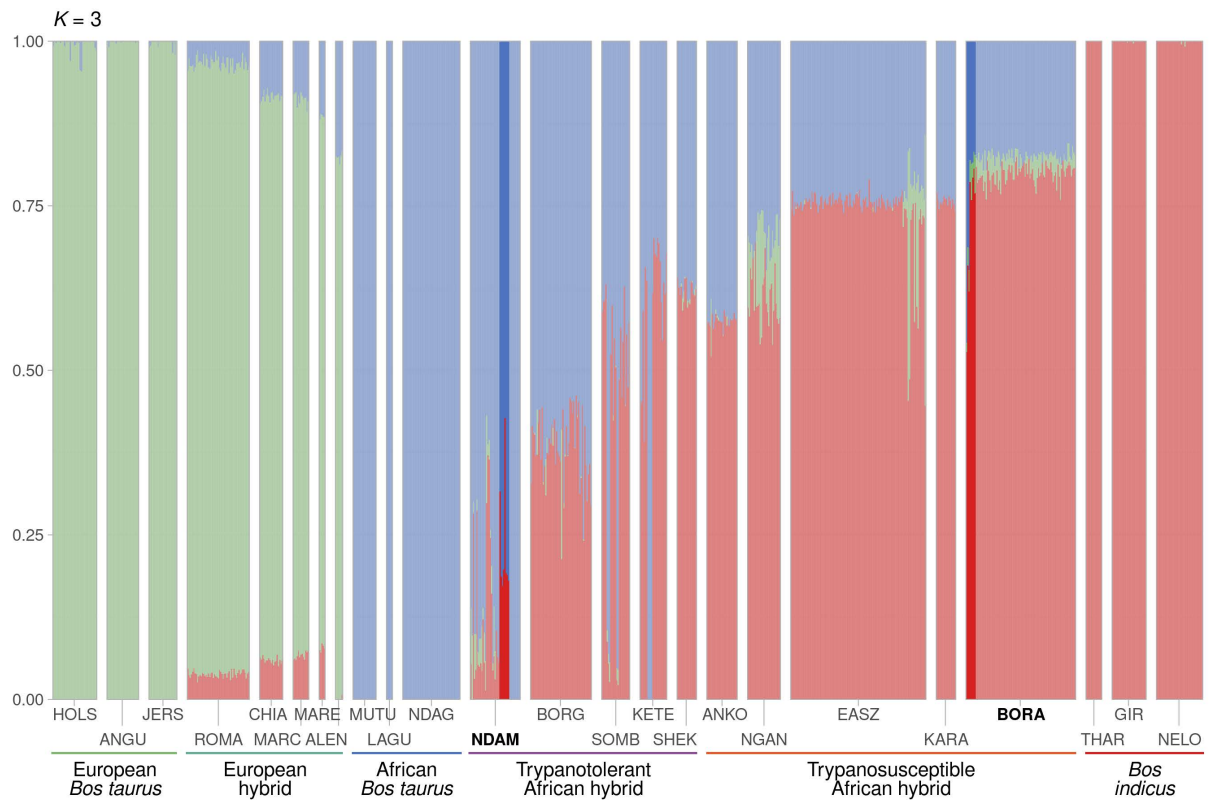
Supplementary Figure C.5. A. Principal component analysis (PCA) of the low-density SNP data for the cattle samples from **Chapter 2** coloured according to population showing the first two principal components and **B.** bar chart of proportion of variance of the top ten principal components. The transparency indicates the availability of microarray gene expression data for the sample.



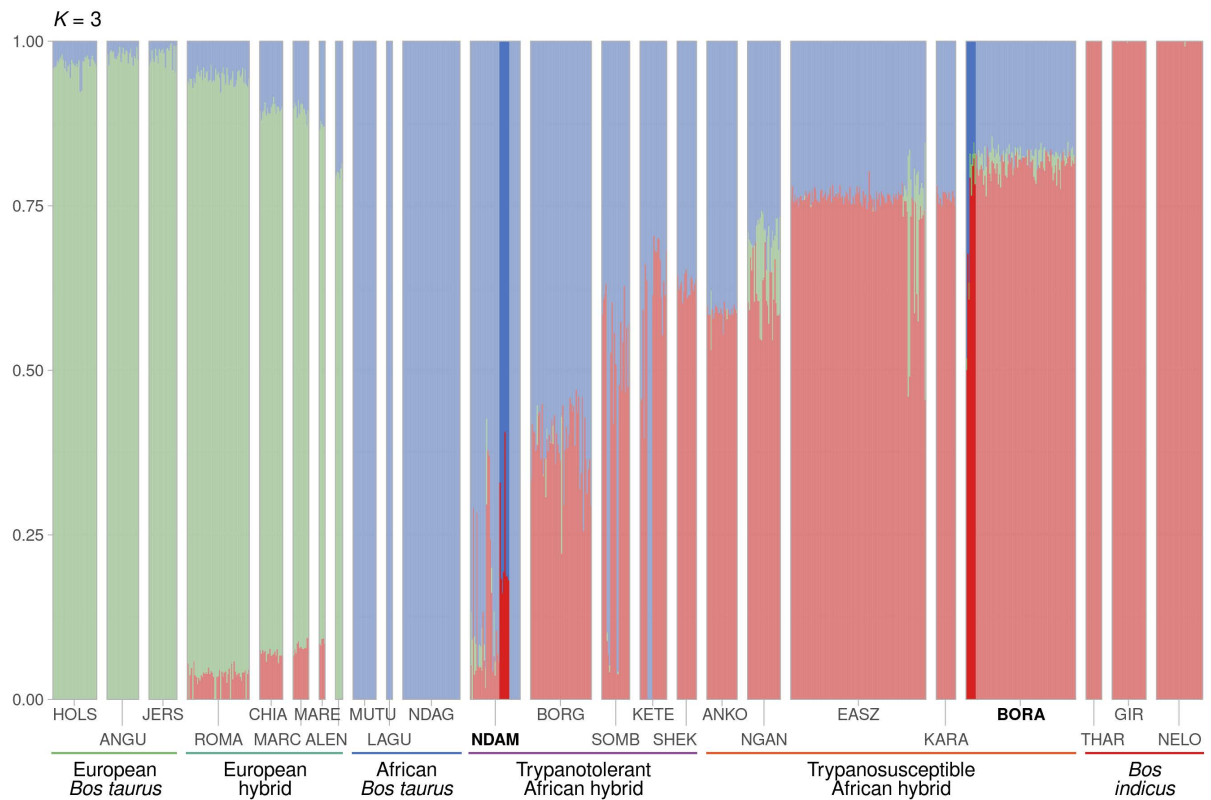
Supplementary Figure C.6. Hierarchical clustering of the SNP data for European, African, and Asian cattle populations. Results are shown for an assumed value of the number of ancestral populations $K = 3$. The transparency indicates the availability of gene expression data for the sample.



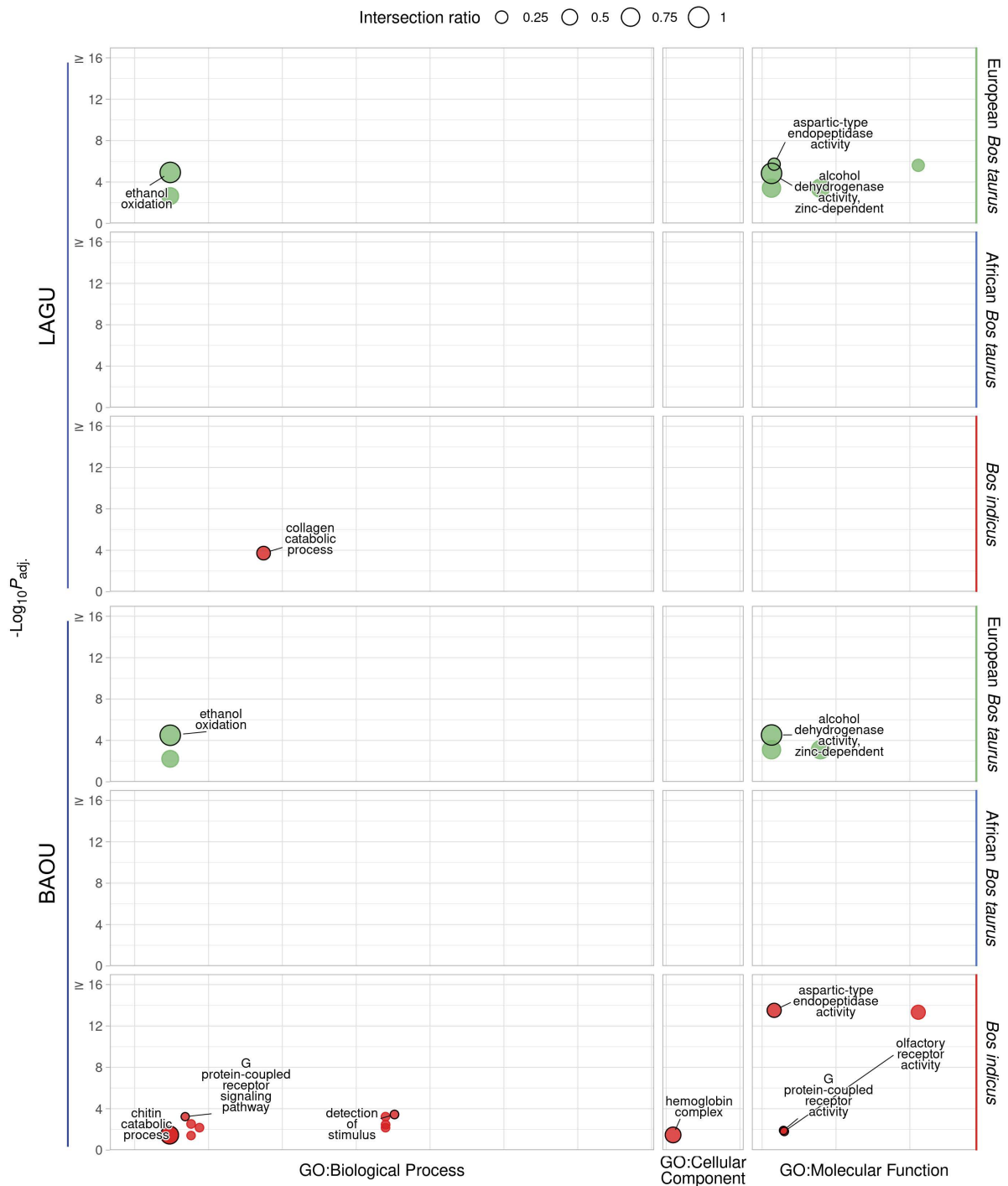
Supplementary Figure C.7. Hierarchical clustering of the SNP data for European, African, and Asian cattle populations. Results are shown for an assumed value of the number of ancestral populations $K = 3$.



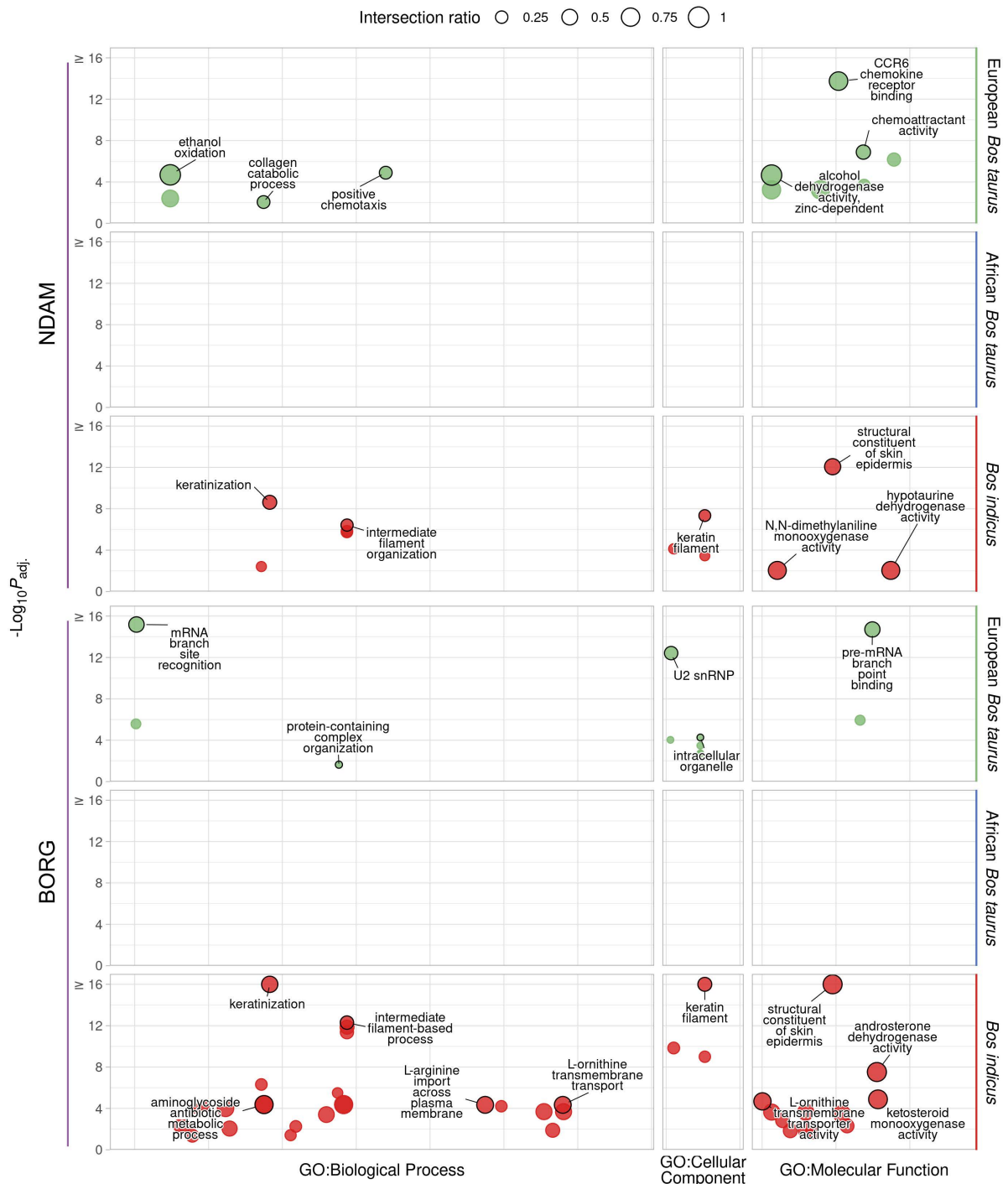
Supplementary Figure C.8. Hierarchical clustering of the high-density SNP data from **Chapter 2** for European, African, and Asian cattle populations. Results are shown for an assumed value of the number of ancestral populations $K = 3$. The transparency indicates the availability of microarray gene expression data for the sample.



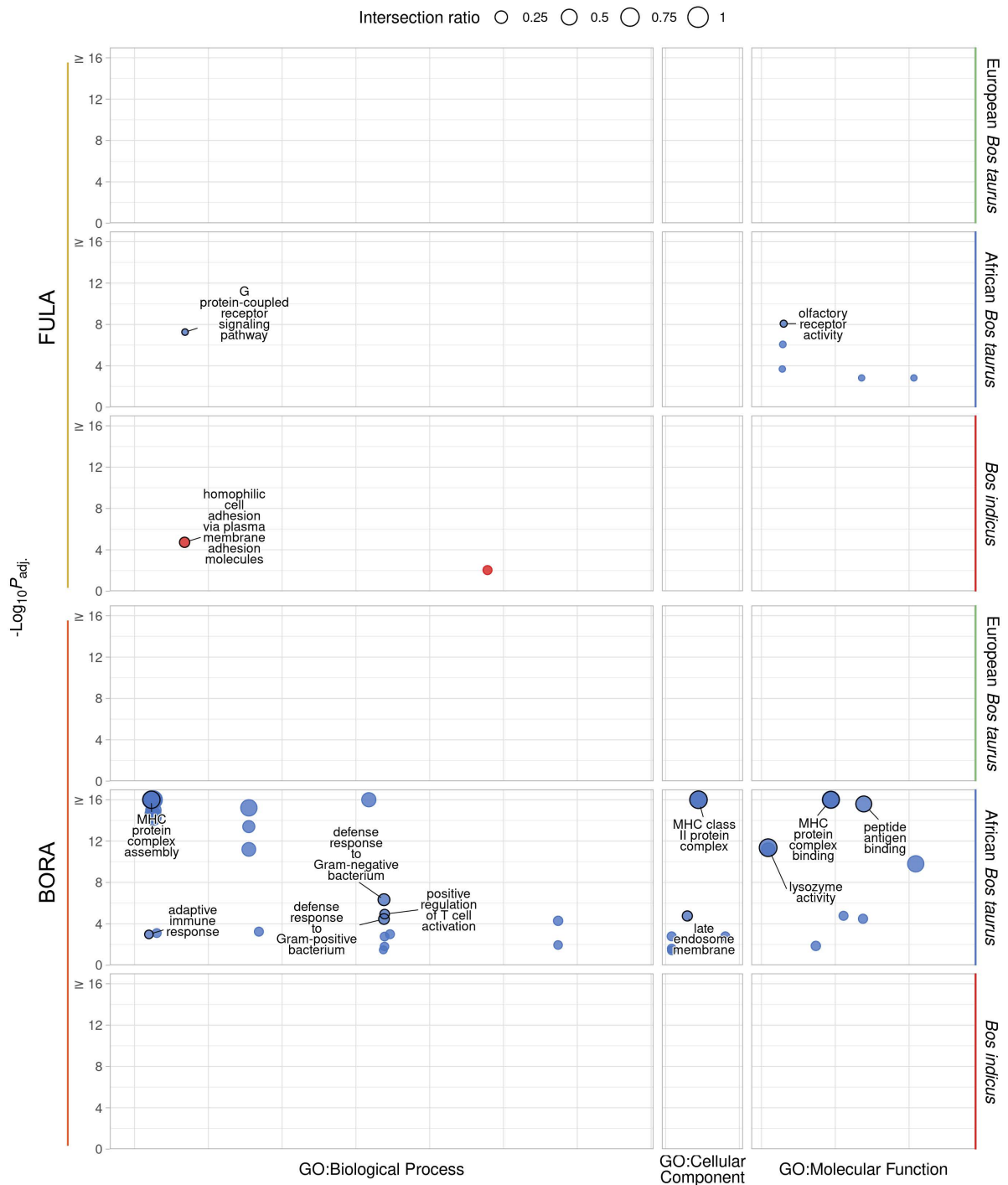
Supplementary Figure C.9. Hierarchical clustering of the low-density SNP data from **Chapter 2** for European, African, and Asian cattle populations. Results are shown for an assumed value of the number of ancestral populations $K = 3$. The transparency indicates the availability of microarray gene expression data for the sample.



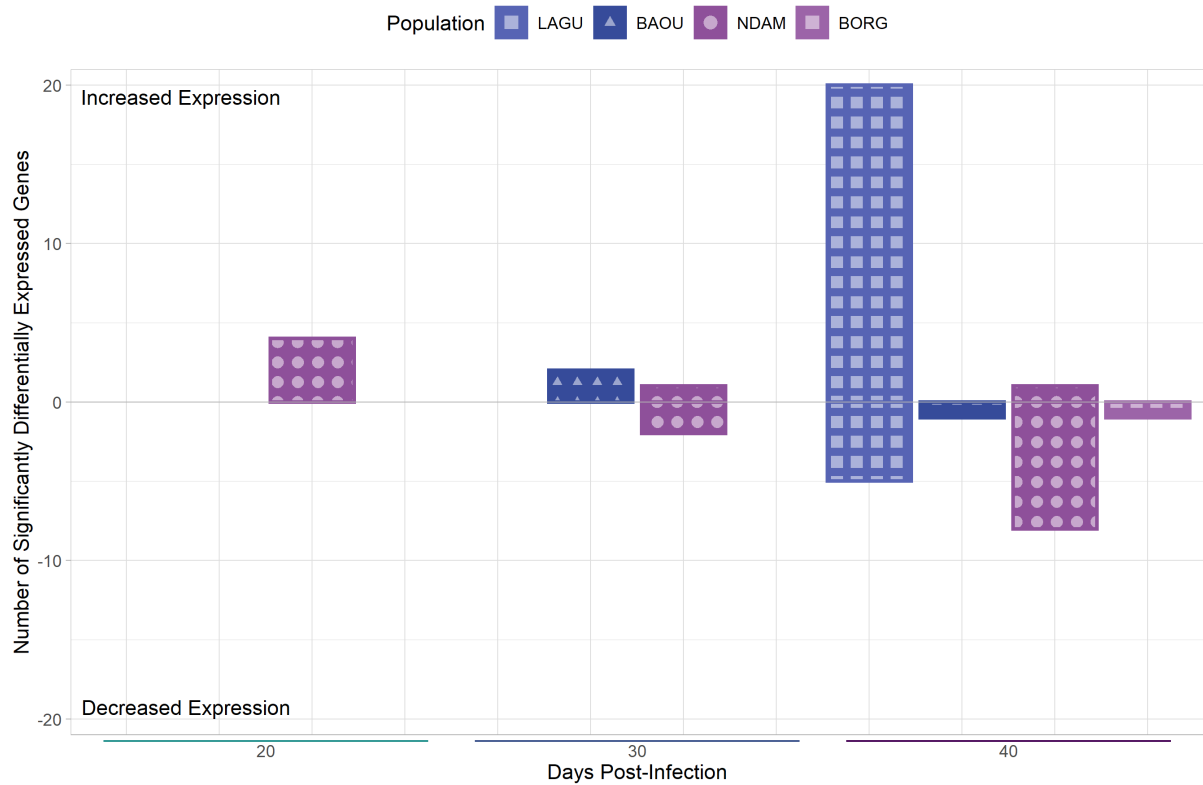
Supplementary Figure C.10. g:Profiler functional enrichment of introgressed regions in the African *B. taurus* cattle populations with gene expression data available according to local ancestry analysis of SNP data. Each dot represents a significantly enriched GO term with the size indicating the ratio of the intersection between the term and the introgressed genes. The y-axis shows the $-\log_{10}P_{adj.}$ value up to a maximum of 16 and the panels along the y-axis and colours indicate the ancestry component. The panels along the x-axis indicate the source of the term and the position within the panels groups terms from the same GO subtree. The top driver GO terms up to a maximum of ten are indicated with a black outline and label.



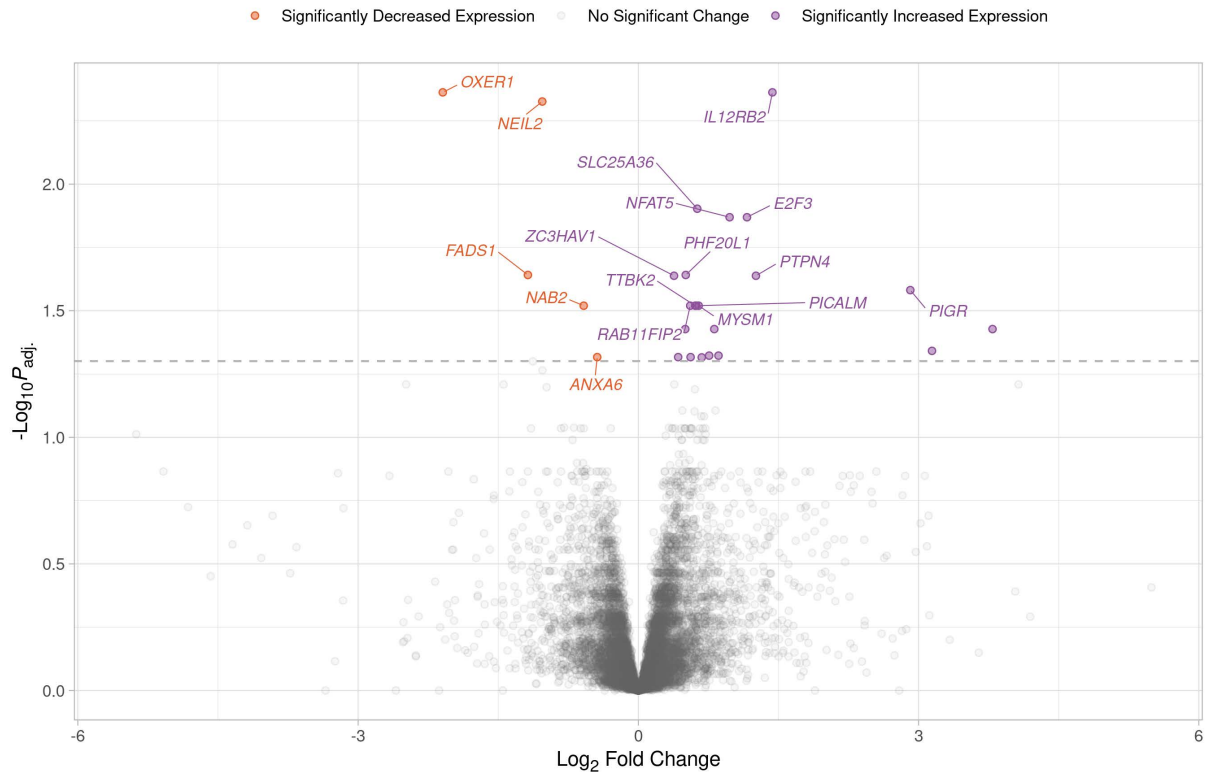
Supplementary Figure C.11. g:Profiler functional enrichment of introgressed regions in the trypanotolerant African hybrid cattle populations with gene expression data available according to local ancestry analysis of SNP data. Each dot represents a significantly enriched GO term with the size indicating the ratio of the intersection between the term and the introgressed genes. The y-axis shows the $-\log_{10} P_{adj}$ value up to a maximum of 16 and the panels along the y-axis and colours indicate the ancestry component. The panels along the x-axis indicate the source of the term and the position within the panels groups terms from the same GO subtree. The top driver GO terms up to a maximum of ten are indicated with a black outline and label.



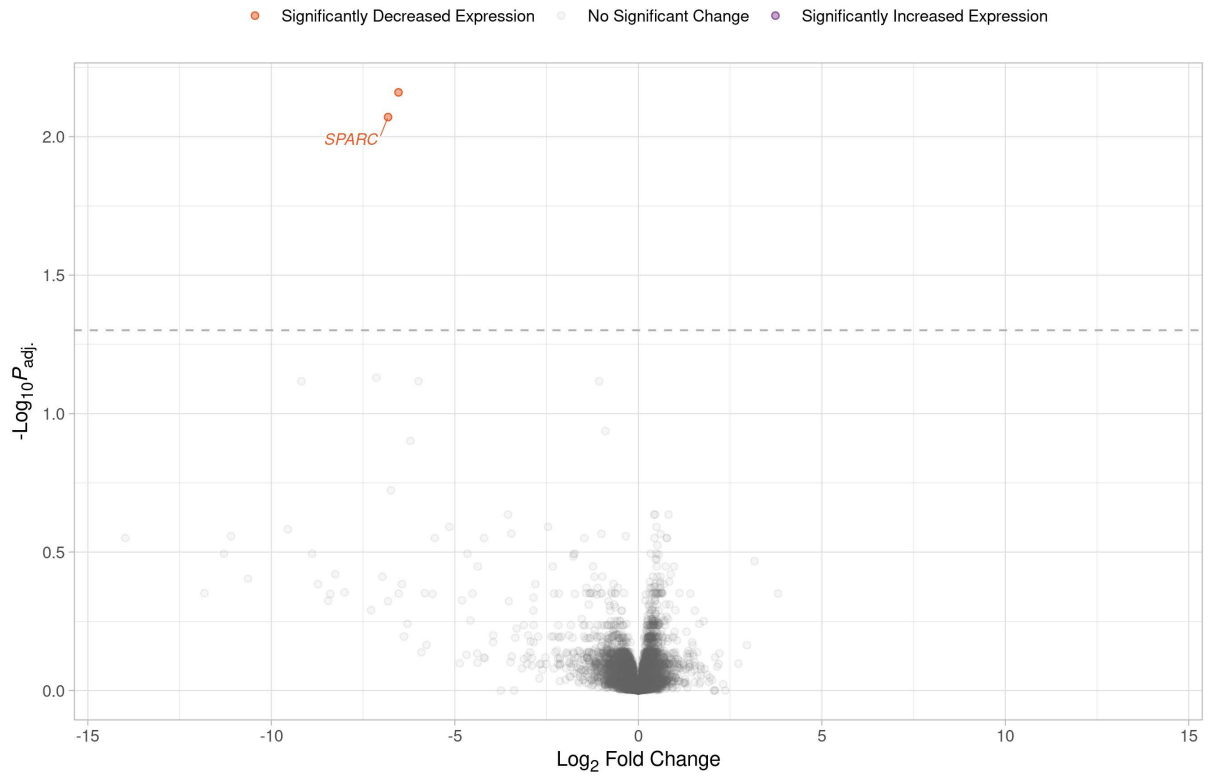
Supplementary Figure C.12. g:Profiler functional enrichment of introgressed regions in the trypanosusceptible African hybrid cattle populations with gene expression data available according to local ancestry analysis of SNP data. Each dot represents a significantly enriched GO term with the size indicating the ratio of the intersection between the term and the introgressed genes. The y-axis shows the $-\log_{10}P_{\text{adj.}}$ value up to a maximum of 16 and the panels along the y-axis and colours indicate the ancestry component. The panels along the x-axis indicate the source of the term and the position within the panels groups terms from the same GO subtree. The top driver GO terms up to a maximum of ten are indicated with a black outline and label.



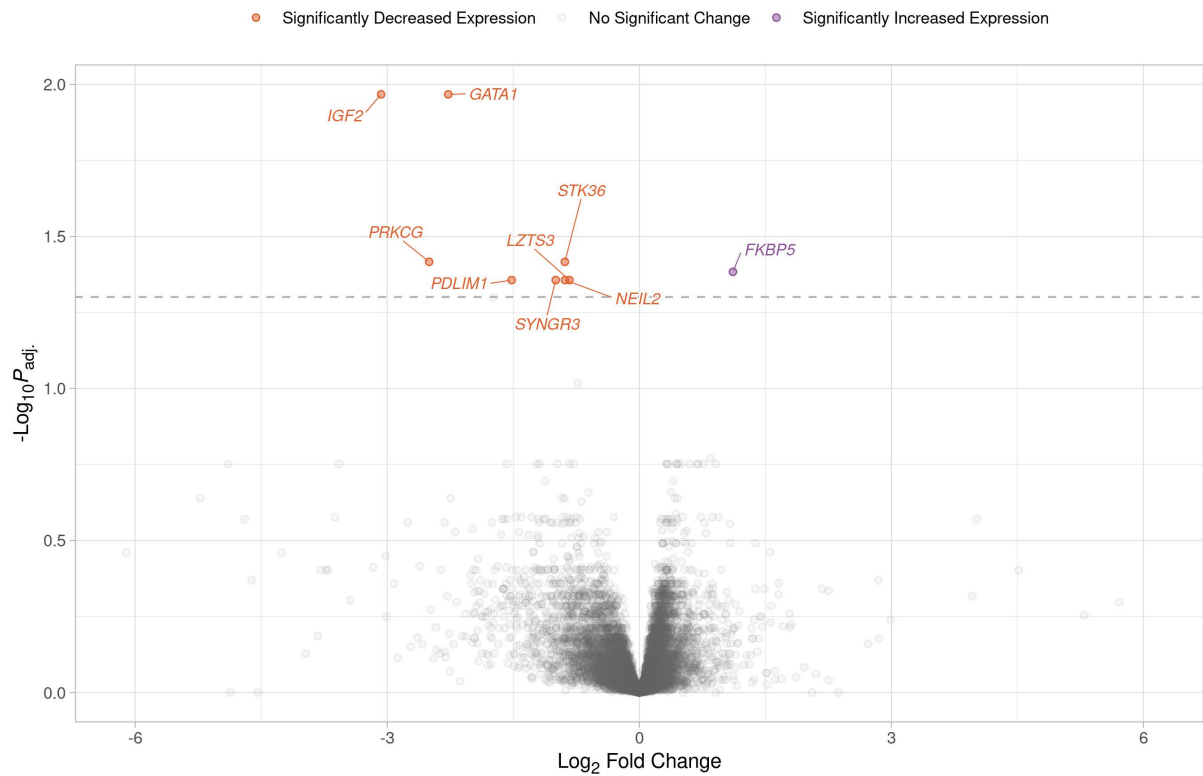
Supplementary Figure C.13. Bar chart showing the numbers of significantly differentially expressed genes for the response contrasts of the RNA-seq data. The extent of the bar above and below 0 on the y-axis indicates the numbers of significantly differentially expressed genes with increased and decreased expression respectively. The position on the x-axis indicates the number of days post infection and the colour and shapes within the bars represent the population.



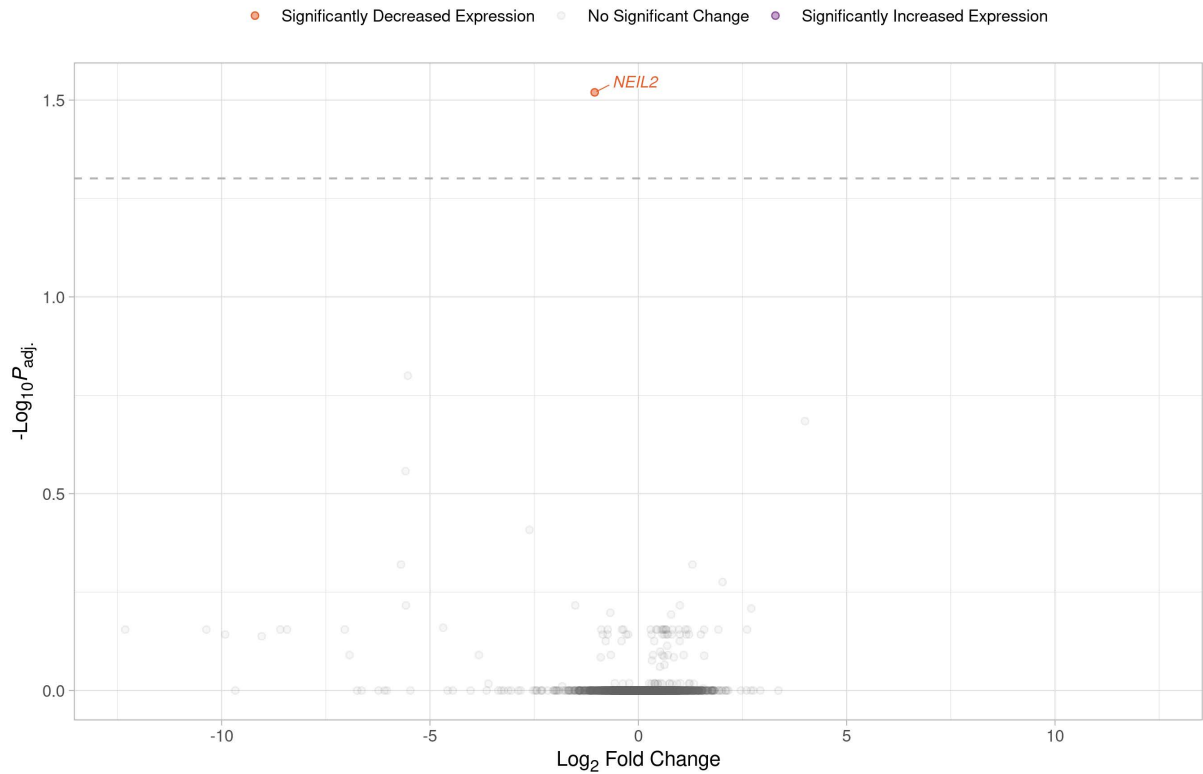
Supplementary Figure C.14. Volcano plot showing the results of the response contrast for the RNA-seq data from the LAGU population at 40 days post infection. Each dot represents a gene with the position on the x- and y-axes indicating the \log_2 fold change and $-\log_{10}P_{adj.}$, respectively. Genes above the horizontal dashed line are significantly differentially expressed with the colours representing the change in expression. The top 10 most significant genes for increased and decreased expression with gene symbols are labelled.



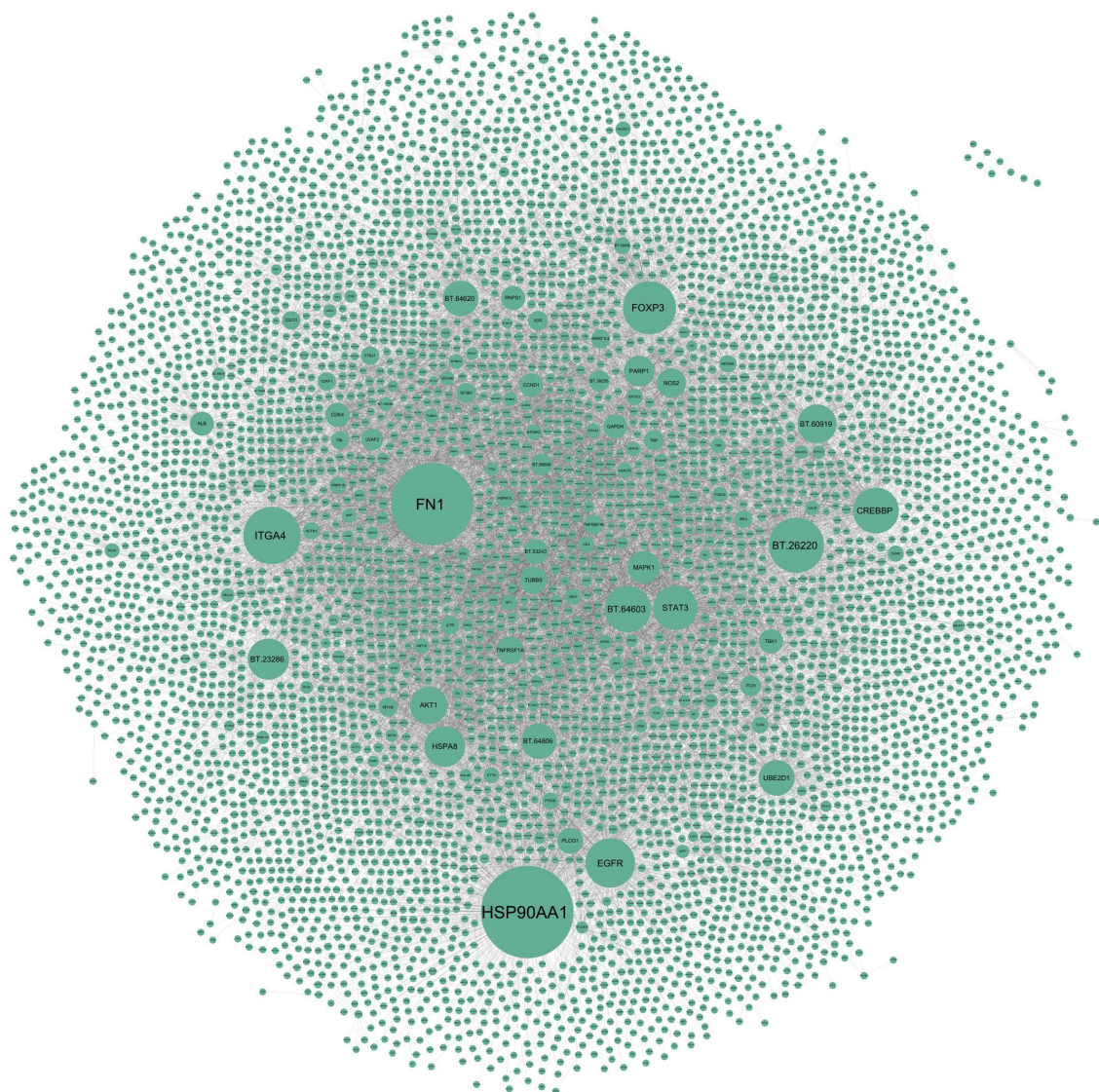
Supplementary Figure C.15. Volcano plot showing the results of the response contrast for the RNA-seq data from the BAOU population at 40 days post infection. Each dot represents a gene with the position on the x- and y-axes indicating the \log_2 fold change and $-\log_{10} P_{adj.}$, respectively. Genes above the horizontal dashed line are significantly differentially expressed with the colours representing the change in expression. The top 10 most significant genes for increased and decreased expression with gene symbols are labelled.



Supplementary Figure C.16. Volcano plot showing the results of the response contrast for the RNA-seq data from the NDAM population at 40 days post infection. Each dot represents a gene with the position on the x- and y-axes indicating the \log_2 fold change and $-\log_{10} P_{adj.}$, respectively. Genes above the horizontal dashed line are significantly differentially expressed with the colours representing the change in expression. The top 10 most significant genes for increased and decreased expression with gene symbols are labelled.

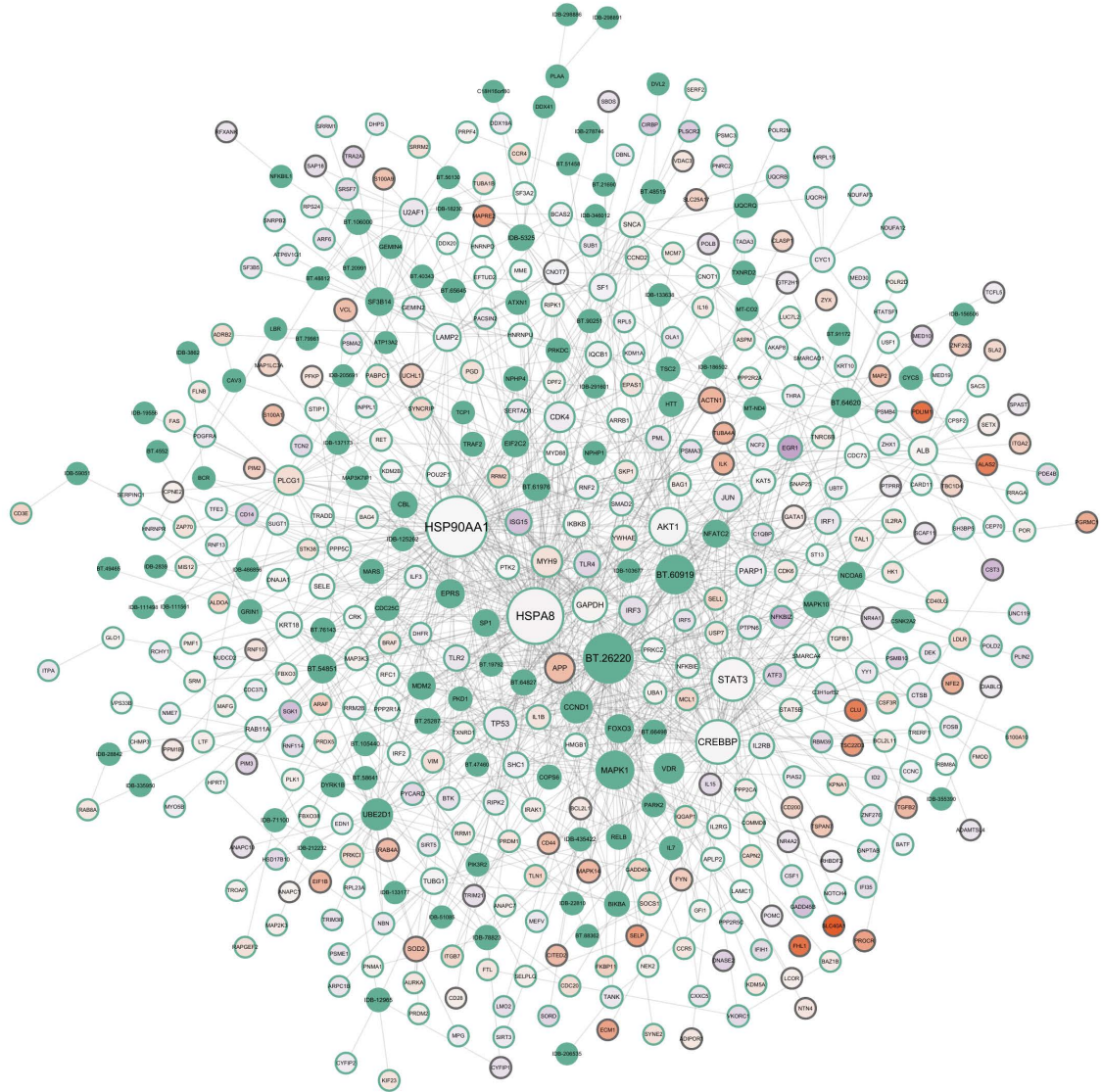


Supplementary Figure C.17. Volcano plot showing the results of the response contrast for the RNA-seq data from the BORG population at 40 days post infection. Each dot represents a gene with the position on the x- and y-axes indicating the \log_2 fold change and $-\log_{10} P_{adj.}$, respectively. Genes above the horizontal dashed line are significantly differentially expressed with the colours representing the change in expression. The top 10 most significant genes for increased and decreased expression with gene symbols are labelled.



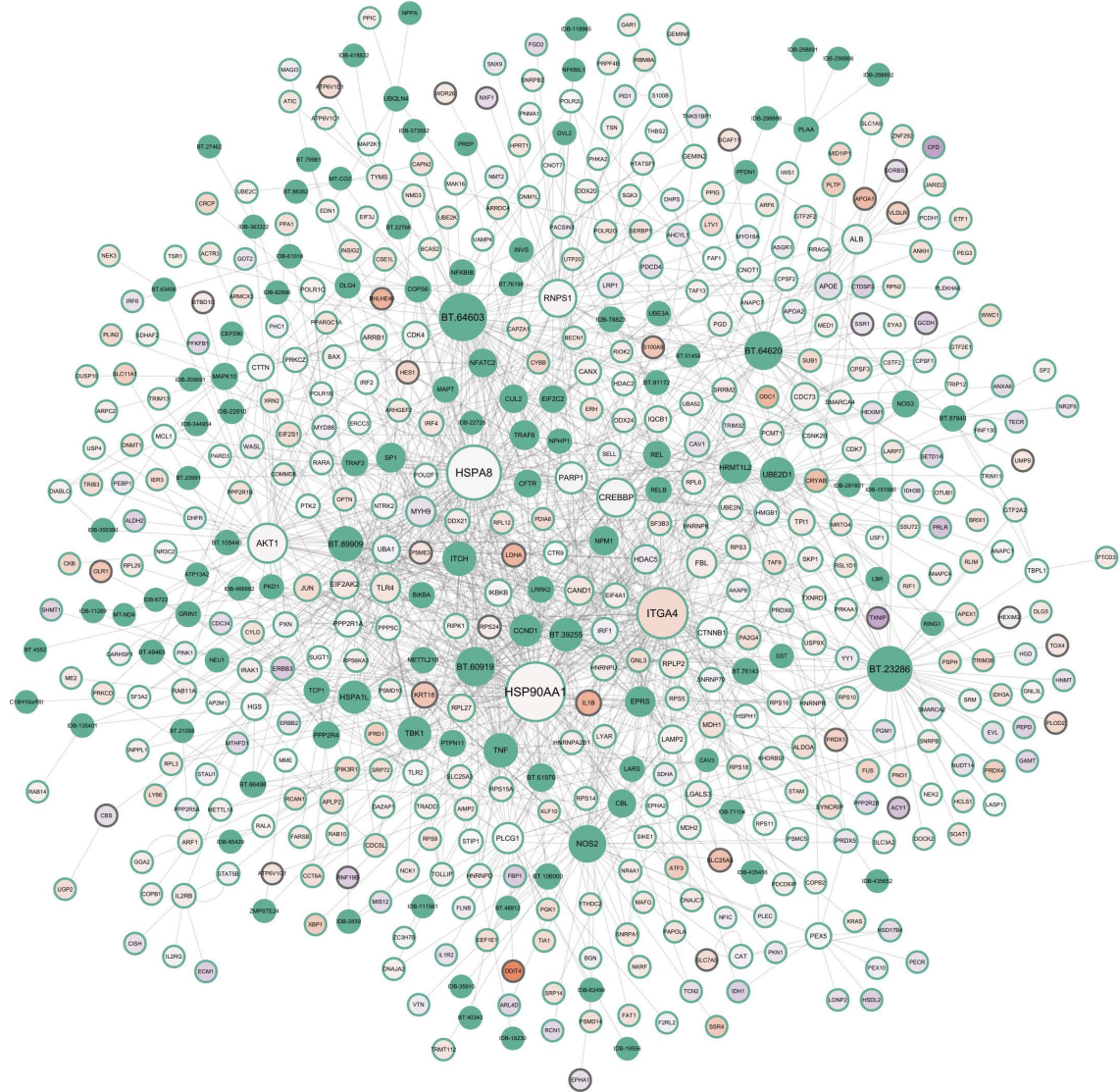
Supplementary Figure C.18. Base network generated using InnateDB with the top results of a search of the GeneCards® for genes relating to the term “trypano*”. Each node in the network represents a gene while the edges connecting the nodes represent gene interactions. The nodes are sized according to their degree or number of interactions.

● Base Network
 ● Increased Expression
 ● Decreased Expression
 ○ Significantly Differentially Expressed
 ○ No Significant Change



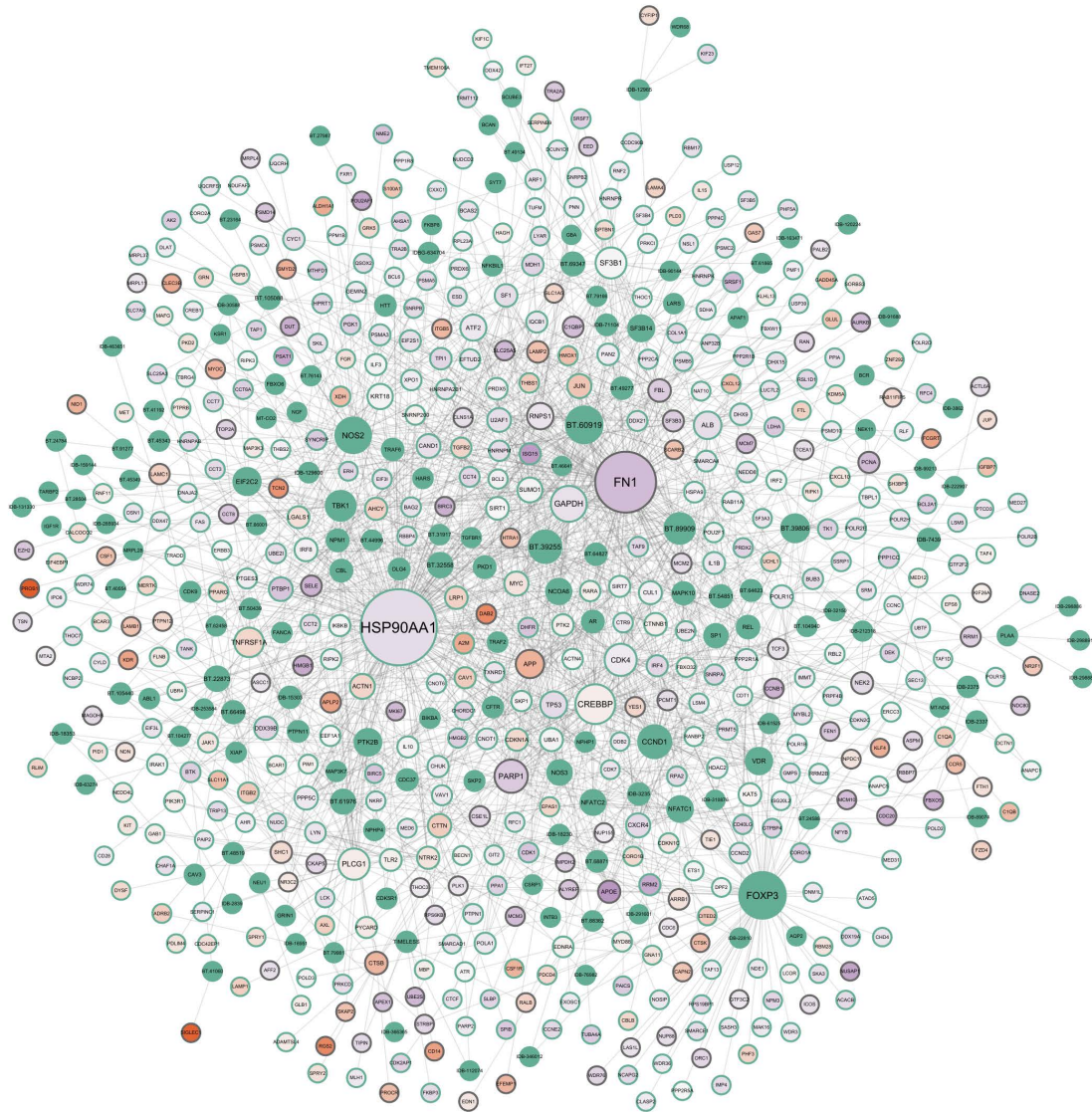
Supplementary Figure C.19. Functional module identified using jActiveModules and differential expression results for the MICRO BL 34 contrast. Each node in the network represents a gene coloured according to expression with significant differential expression indicated by the outline. The edges connecting the nodes represent gene interactions and the nodes are sized according to their number of interactions or degree.

● Base Network
 ● Increased Expression
 ● Decreased Expression
 ○ Significantly Differentially Expressed
 ○ No Significant Change



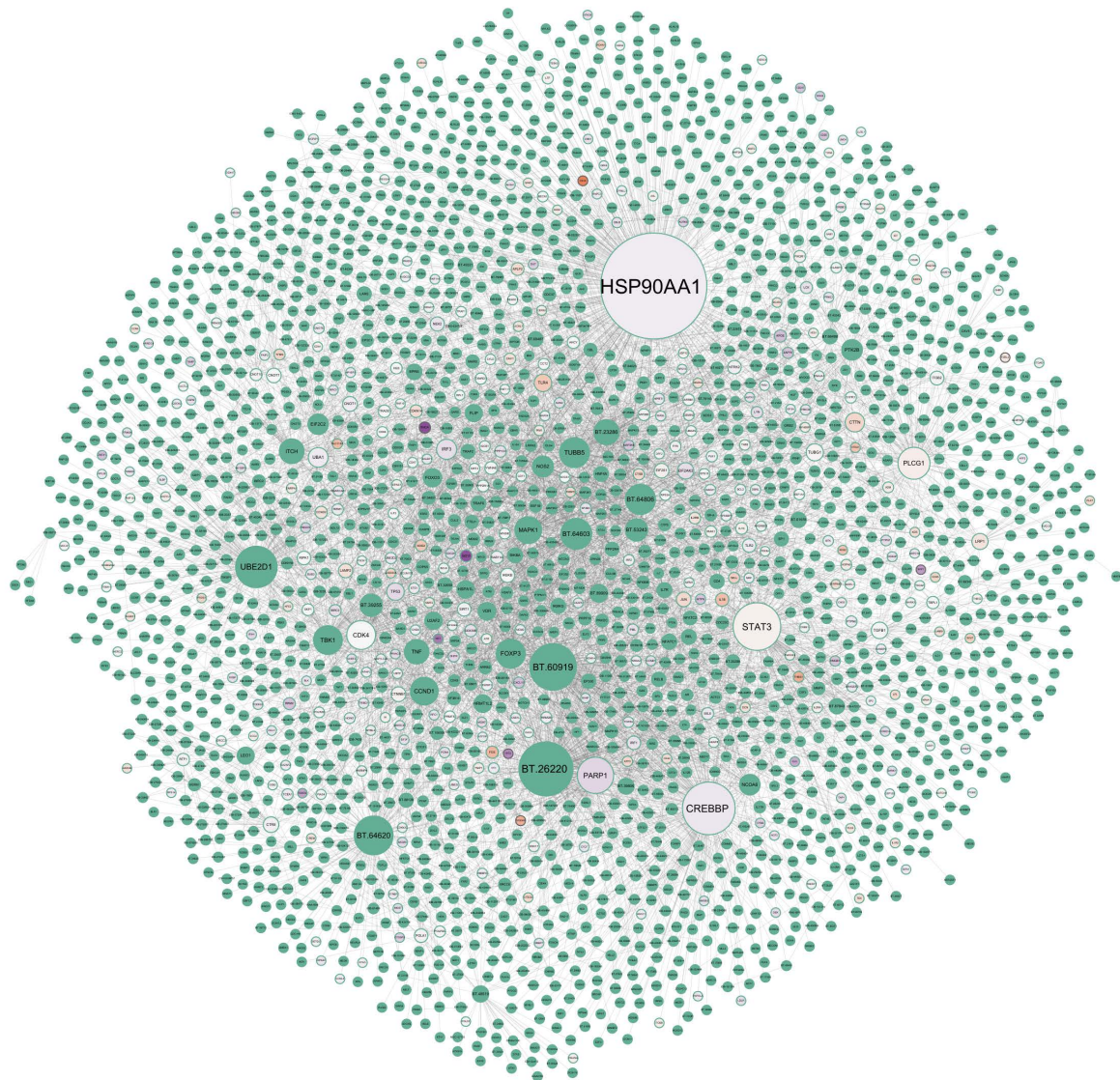
Supplementary Figure C.20. Functional module identified using jActiveModules and differential expression results for the MICRO LI 35 contrast. Each node in the network represents a gene coloured according to expression with significant differential expression indicated by the outline. The edges connecting the nodes represent gene interactions and the nodes are sized according to their number of interactions or degree.

● Base Network
 ● Increased Expression
 ● Decreased Expression
 ○ Significantly Differentially Expressed
 ○ No Significant Change



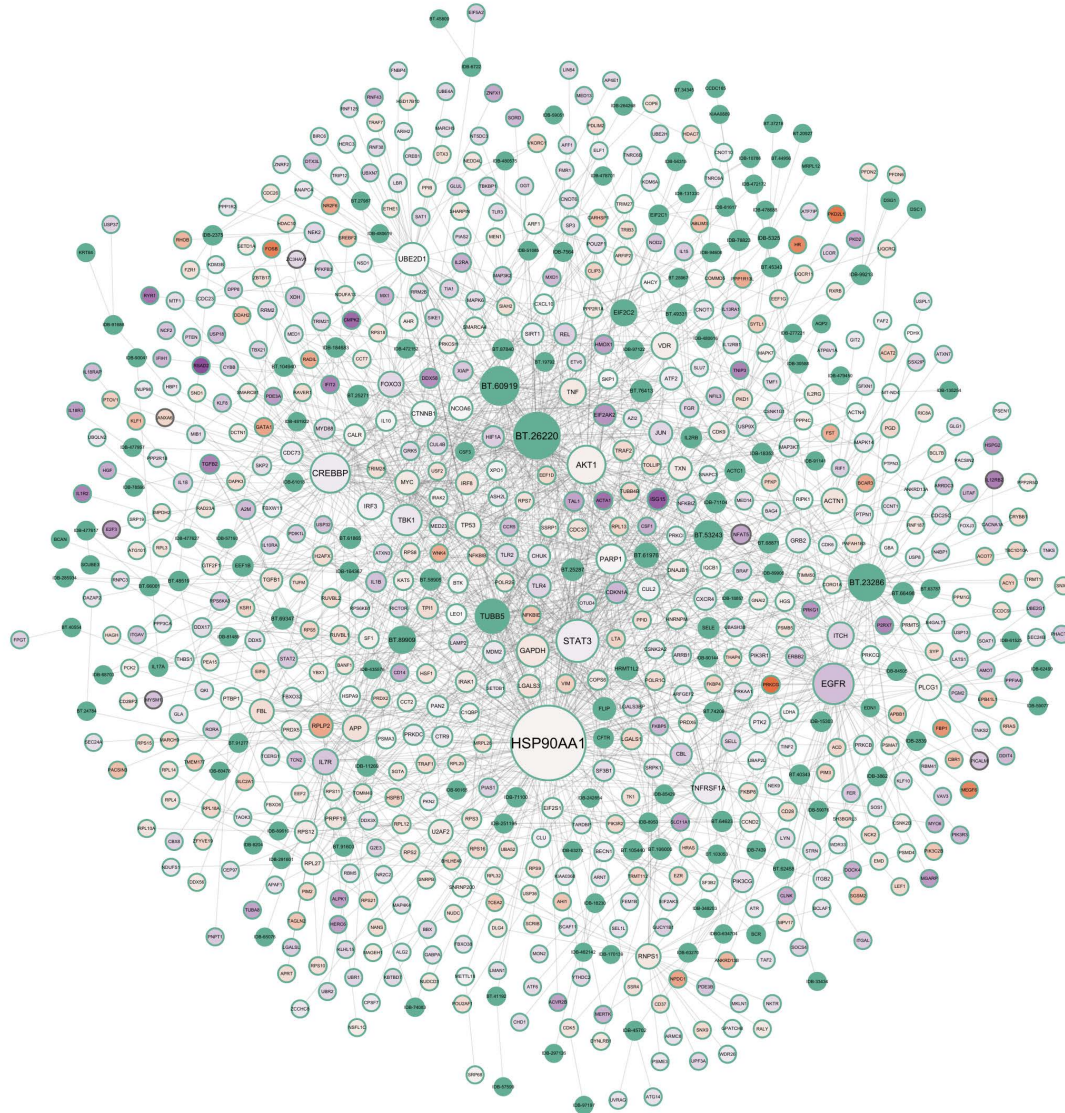
Supplementary Figure C.21. Functional module identified using jActiveModules and differential expression results for the MICRO LN 35 contrast. Each node in the network represents a gene coloured according to expression with significant differential expression indicated by the outline. The edges connecting the nodes represent gene interactions and the nodes are sized according to their number of interactions or degree.

● Base Network
 ● Increased Expression
 ● Decreased Expression
 Significantly Differentially Expressed
 No Significant Change

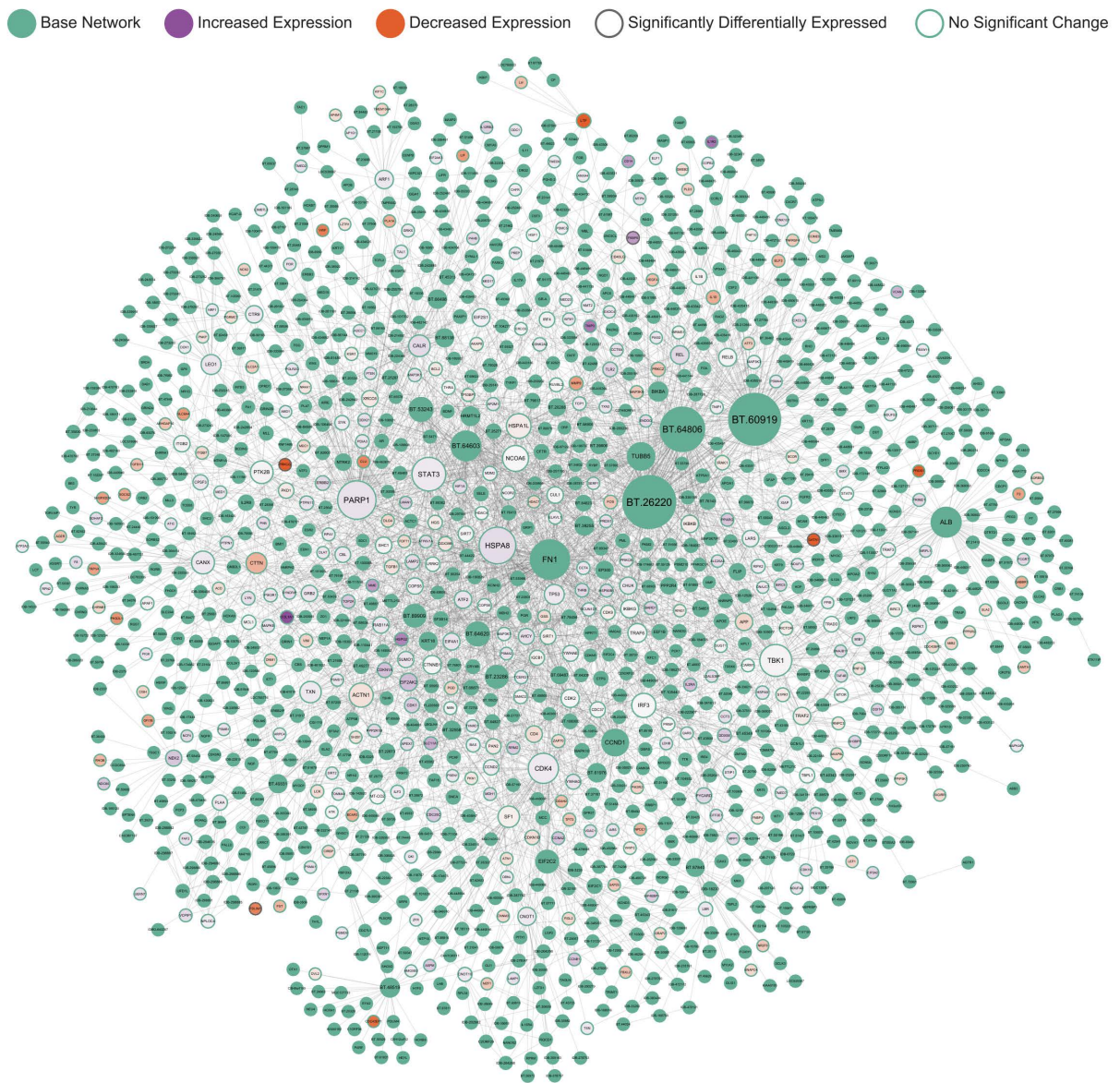


Supplementary Figure C.22. Functional module identified using jActiveModules and differential expression results for the MICRO SP 35 contrast. Each node in the network represents a gene coloured according to expression with significant differential expression indicated by the outline. The edges connecting the nodes represent gene interactions and the nodes are sized according to their number of interactions or degree.

● Base Network
 ● Increased Expression
 ● Decreased Expression
 ○ Significantly Differentially Expressed
 ○ No Significant Change

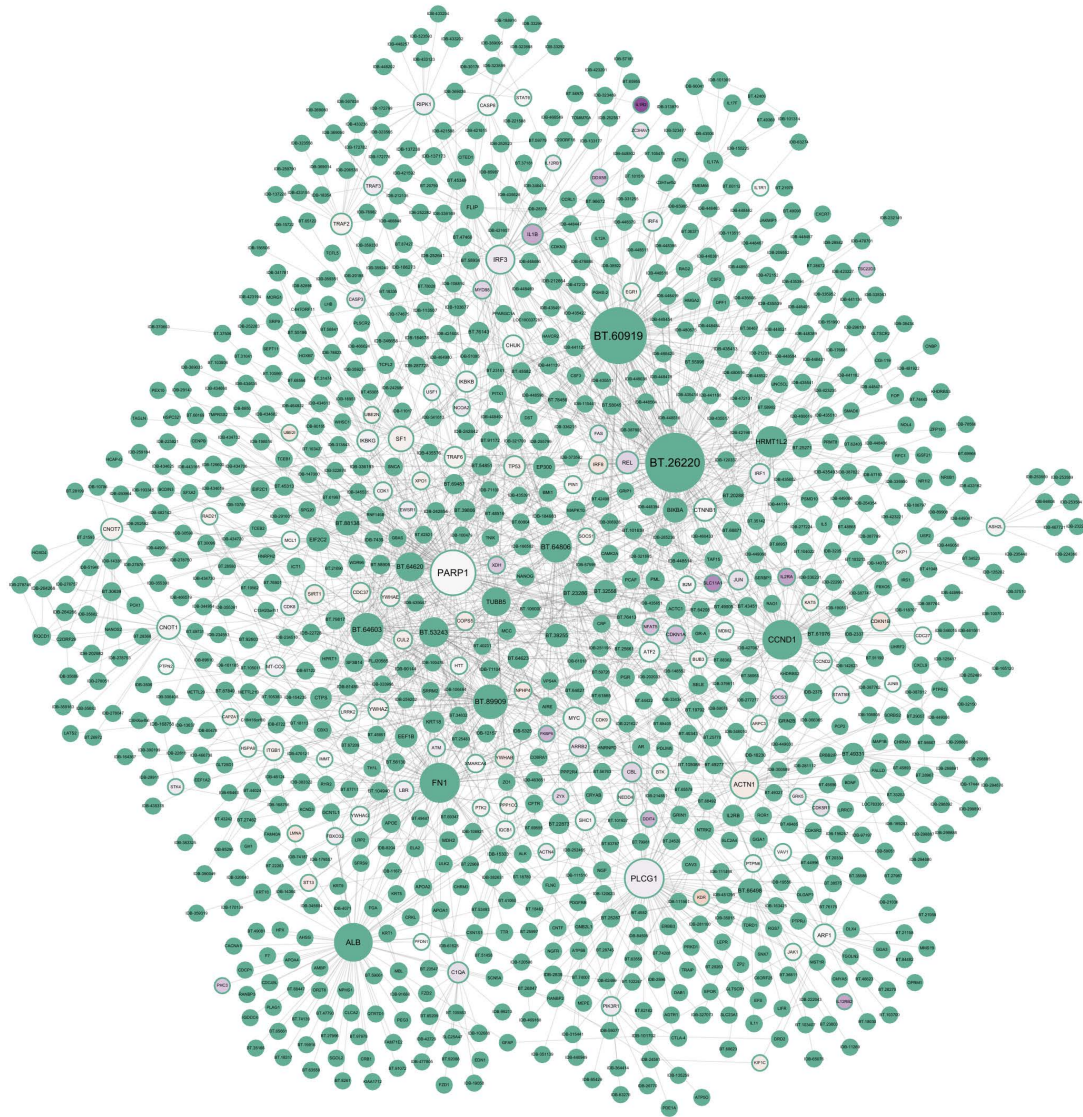


Supplementary Figure C.23. Functional module identified using jActiveModules and differential expression results for the RNA LAGU 40 contrast. Each node in the network represents a gene coloured according to expression with significant differential expression indicated by the outline. The edges connecting the nodes represent gene interactions and the nodes are sized according to their number of interactions or degree.

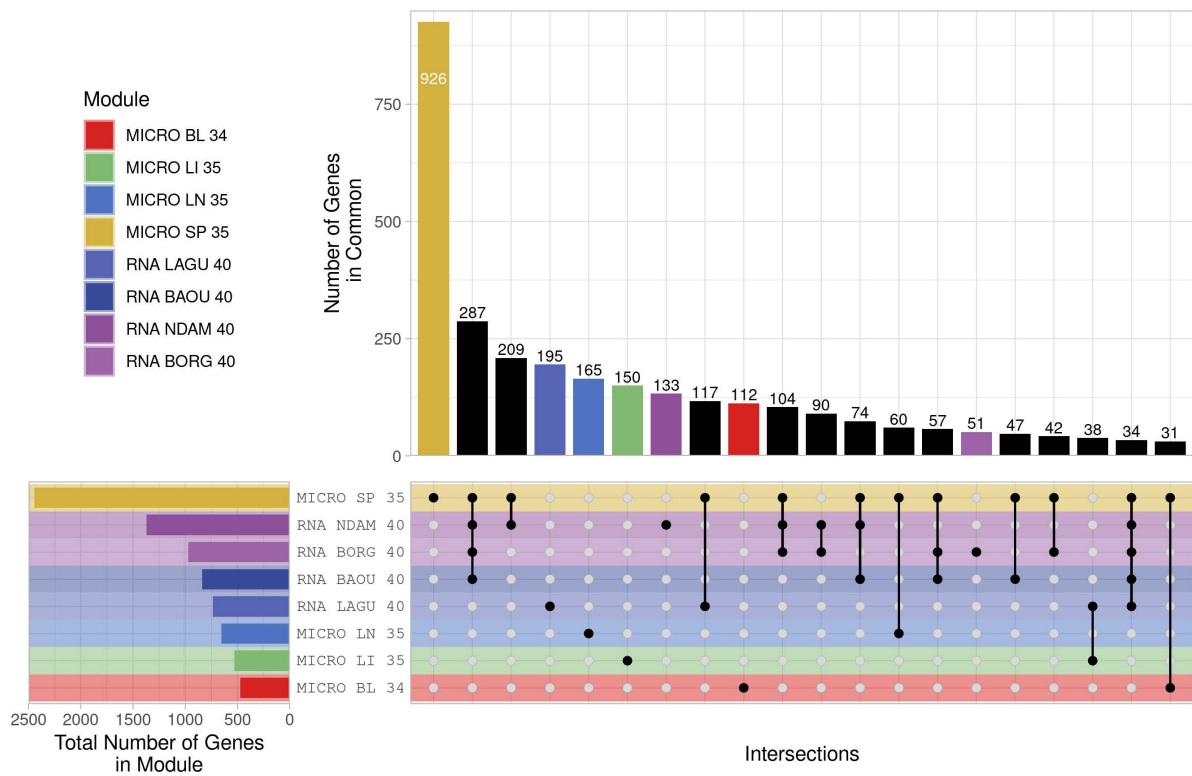


Supplementary Figure C.25. Functional module identified using jActiveModules and differential expression results for the RNA NDAM 40 contrast. Each node in the network represents a gene coloured according to expression with significant differential expression indicated by the outline. The edges connecting the nodes represent gene interactions and the nodes are sized according to their number of interactions or degree.

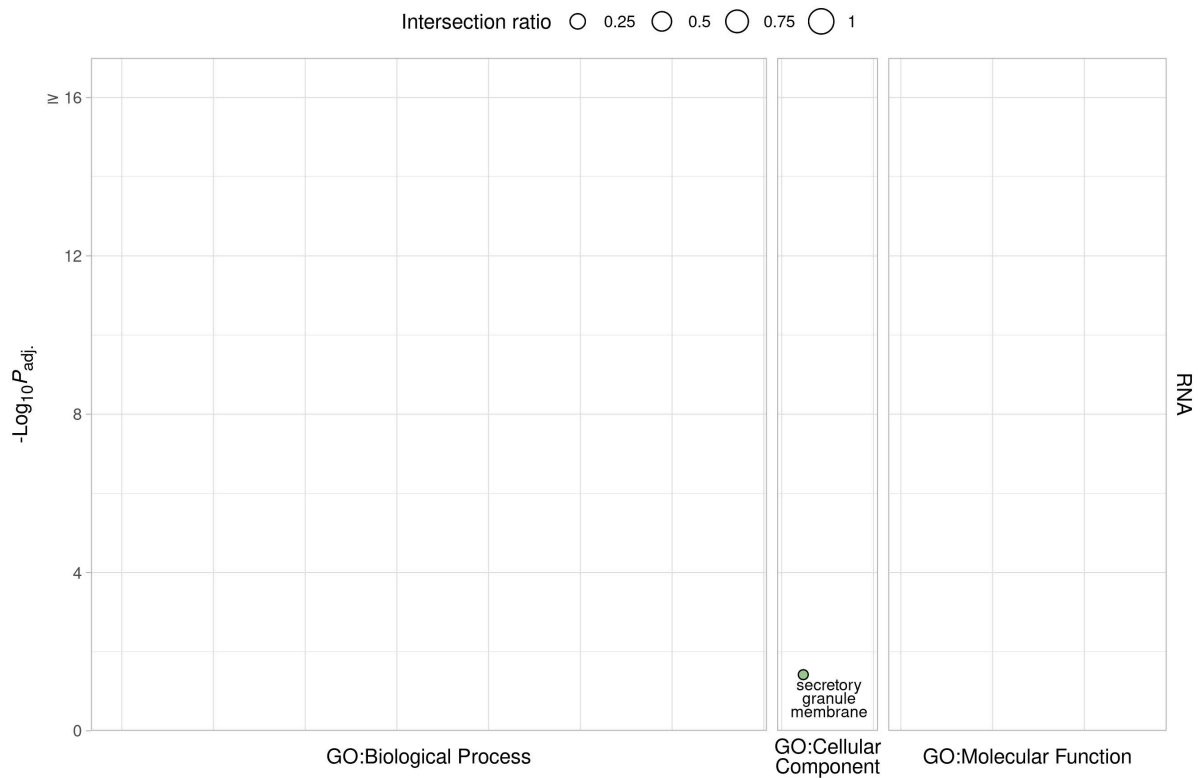
● Base Network
 ● Increased Expression
 ● Decreased Expression
 Significantly Differentially Expressed
 No Significant Change



Supplementary Figure C.26. Functional module identified using jActiveModules and differential expression results for the RNA BORG 40 contrast. Each node in the network represents a gene coloured according to expression with significant differential expression indicated by the outline. The edges connecting the nodes represent gene interactions and the nodes are sized according to their number of interactions or degree.



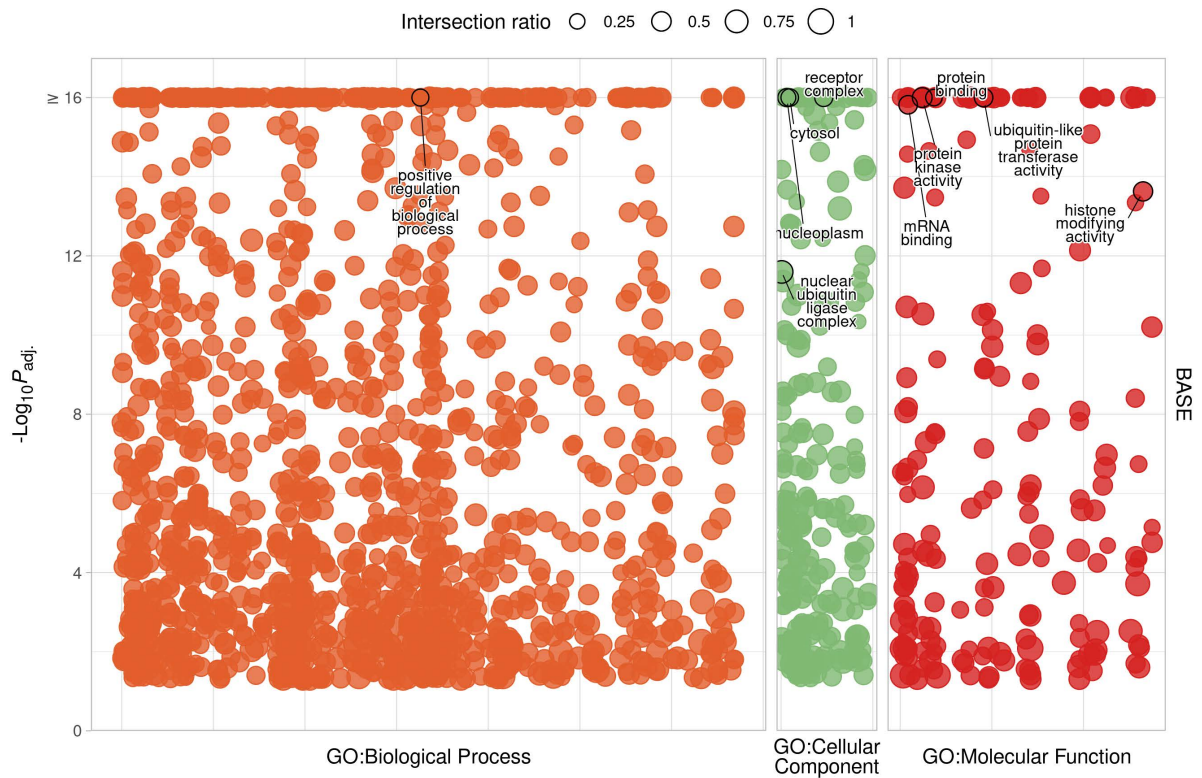
Supplementary Figure C.27. Upset plot showing the top 20 intersections between the genes in the functional modules identified using jActiveModules and differential expression results for each of the final response contrasts for the microarray and RNA-seq data. The horizontal bars indicate the total number of genes in each module while the vertical bars indicate the number of genes in common between the modules annotated with black dots connected by lines in the intersection matrix. The background colour of the stripes in the intersection matrix and colour of the horizontal and vertical bars represent the module. Black bars indicate an overlap between different modules.



Supplementary Figure C.28. g:Profiler functional enrichment of significantly differentially expressed genes in the RNA-seq response contrasts with no background data set specified. Each dot represents a significantly enriched GO term with the size indicating the ratio of the intersection between the term and the introgressed genes. The y-axis shows the $-\log_{10}P_{adj.}$ value up to a maximum of 16 and the panels along the y-axis and colours indicate the module. The panels along the x-axis indicate the source of the term and the position within the panels groups terms from the same GO subtree. The top driver GO terms up to a maximum of ten are indicated with a black outline and label.



Supplementary Figure C.29. g:Profiler functional enrichment of the genes in the MICRO LI 35 functional module with no background data set specified. Each dot represents a significantly enriched GO term with the size indicating the ratio of the intersection between the term and the introgressed genes. The y-axis shows the $-\log_{10}P_{adj.}$ value up to a maximum of 16 and the panels along the y-axis and colours indicate the module. The panels along the x-axis indicate the source of the term and the position within the panels groups terms from the same GO subtree. The top driver GO terms up to a maximum of ten are indicated with a black outline and label.



Supplementary Figure C.30. g:Profiler functional enrichment of the genes in the base network with no background data set specified. Each dot represents a significantly enriched GO term with the size indicating the ratio of the intersection between the term and the introgressed genes. The y-axis shows the $-\log_{10}P_{adj.}$ value up to a maximum of 16 and the panels along the y-axis and colours indicate the module. The panels along the x-axis indicate the source of the term and the position within the panels groups terms from the same GO subtree. The top driver GO terms up to a maximum of ten are indicated with a black outline and label.

Bibliography

Pickrell J.K. & Pritchard J.K. (2012) Inference of population splits and mixtures from genome-wide allele frequency data. *PLoS Genet* 8, e1002967.