

Table 1. Table showing sequencing quality metrics for early lactation samples from Jhakrana and Jamanpari groups, including raw and clean fastQ read percentages, GC content, total sequences, and Q30 quality scores for both forward (F) and reverse (R) strands.

Group	Sample Name	Read Strand	Raw fastQ			Clean fastQ		
			% GC	M Seqs	Q30%	% GC	M Seqs	Q30%
Jhakrana Early lactation	JKE1	F	48%	58.1	87.14	46%	48	86.56
		R	49%	58.1	86.02	46%	48	91.82
	JKE2	F	52%	26	87.79	49%	20.2	86.75
		R	53%	26	81.86	49%	20.2	90.68
	JKE3	F	47%	33.8	88.21	46%	29	87.7
		R	47%	33.8	87.45	46%	29	91.68
Jamanpari Early lactation	JME1	F	48%	44.6	88.82	47%	37.8	88.63
		R	48%	44.6	88.41	47%	37.8	93.28
	JME2	F	52%	58.3	88.25	49%	43.5	87.13
		R	52%	58.3	84	49%	43.5	91.73
	JME3	F	50%	40.4	95.91	48%	2.6	87.96
		R	50%	40.4	90.87	48%	2.6	92.4

Table 2. Alignment statistics of RNA-Seq reads for early lactation samples from Jakhkana and Jamnapari goats, showing total clean reads, percentages of uniquely mapped reads, reads mapped to multiple loci, reads mapped to too many loci, and unmapped reads categorized by cause.

Group	Sample ID	Total clean	Uniquely mapped	Mapped to	Mapped to too many	Unmapped: short	too	Unmapped: other
Jhakrana Early lactation	JKE1	48000000	80.08	3.40	7.54	21.92		0.06
	JKE2	20200000	79.67	3.60	0.11	27.28		0.04
	JKE3	29000000	80.77	2.64	0.28	20.22		0.08
Jamanpari Early lactation	JME1	37800000	72.65	5.54	1.48	22.71		0.24
	JME2	43500000	69.07	7.95	1.91	29.33		0.34
	JME3	35300000	70.55	5.44	1.28	20.76		0.23

Table 3. Differentially expressed genes identified between Jakhkana Early (JKE) and Jamnapari Early (JME) lactation samples using edgeR. The table lists gene identifiers along with log2 fold change (logFC), average expression (logCPM), raw P-values, and false discovery rate (FDR). Genes shown were significantly upregulated, with FDR < 0.05.

Gene	logFC	logCPM	PValue	FDR
<i>LOC102176695</i>	3.317011	5.675365	8.79E-06	0.017659
<i>CTSW</i>	3.527569	5.467557	2.05E-05	0.020631

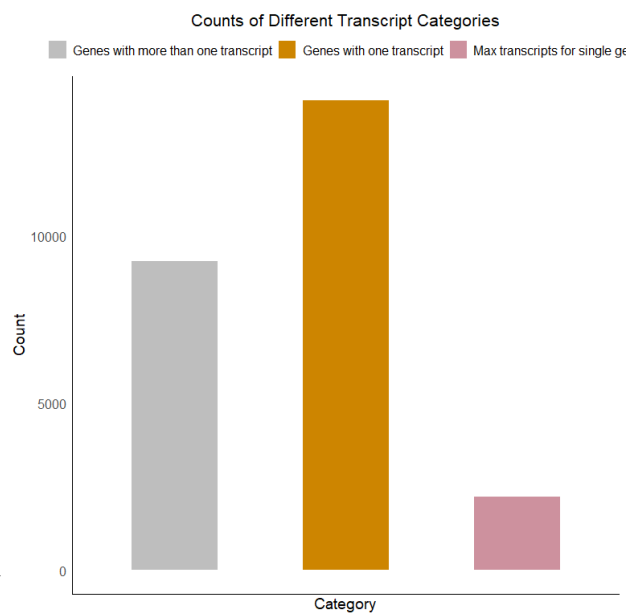
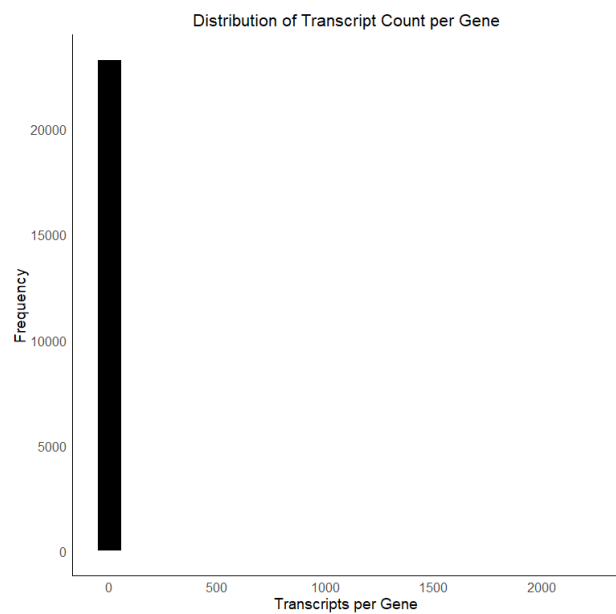


Figure 1. Histogram showing (A) the distribution of transcript counts per gene and (B) the distribution of transcript lengths in the dataset.

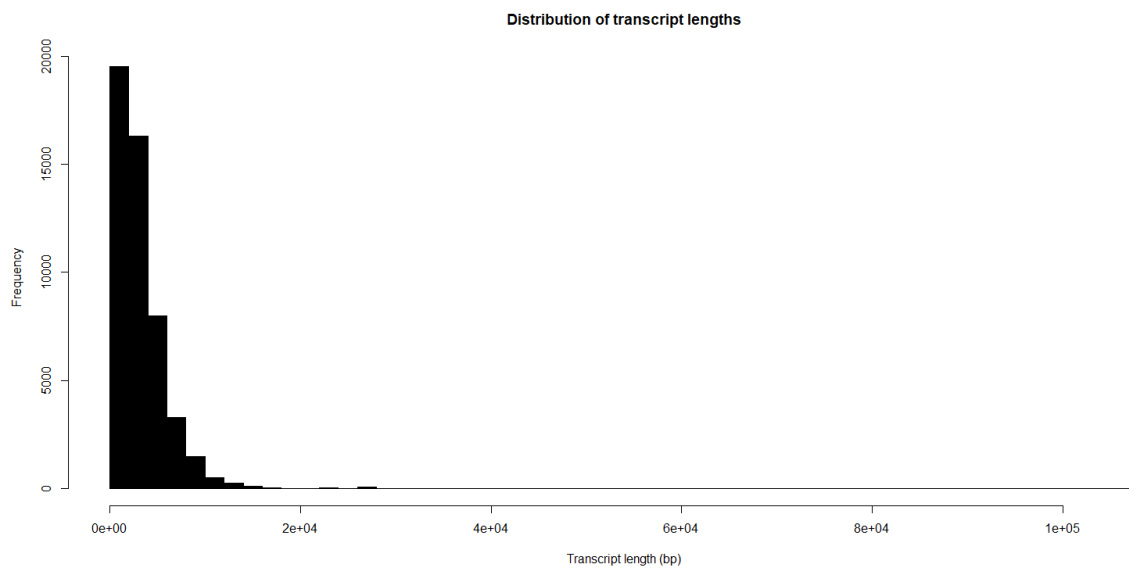


Figure 2. Distribution of transcript lengths within the dataset.

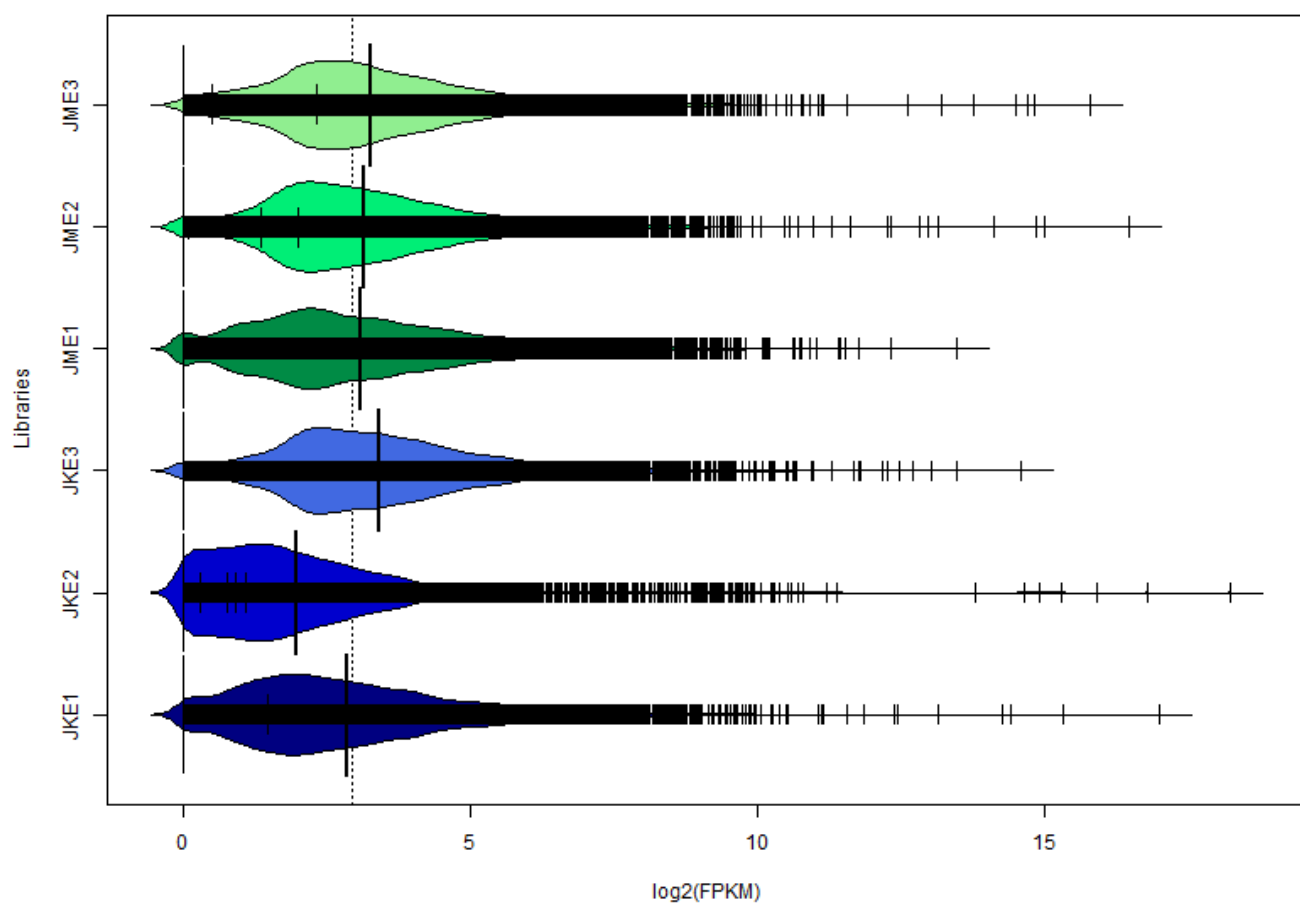


Figure 3. Violin plots (not shown) of $\log_2(\text{FPKM})$ expression values across six RNA-seq libraries (JKE1–JKE3 and JME1–JME3) illustrate right-skewed expression distributions with dominant highly expressed genes and consistent median expression levels indicative of robust normalization.

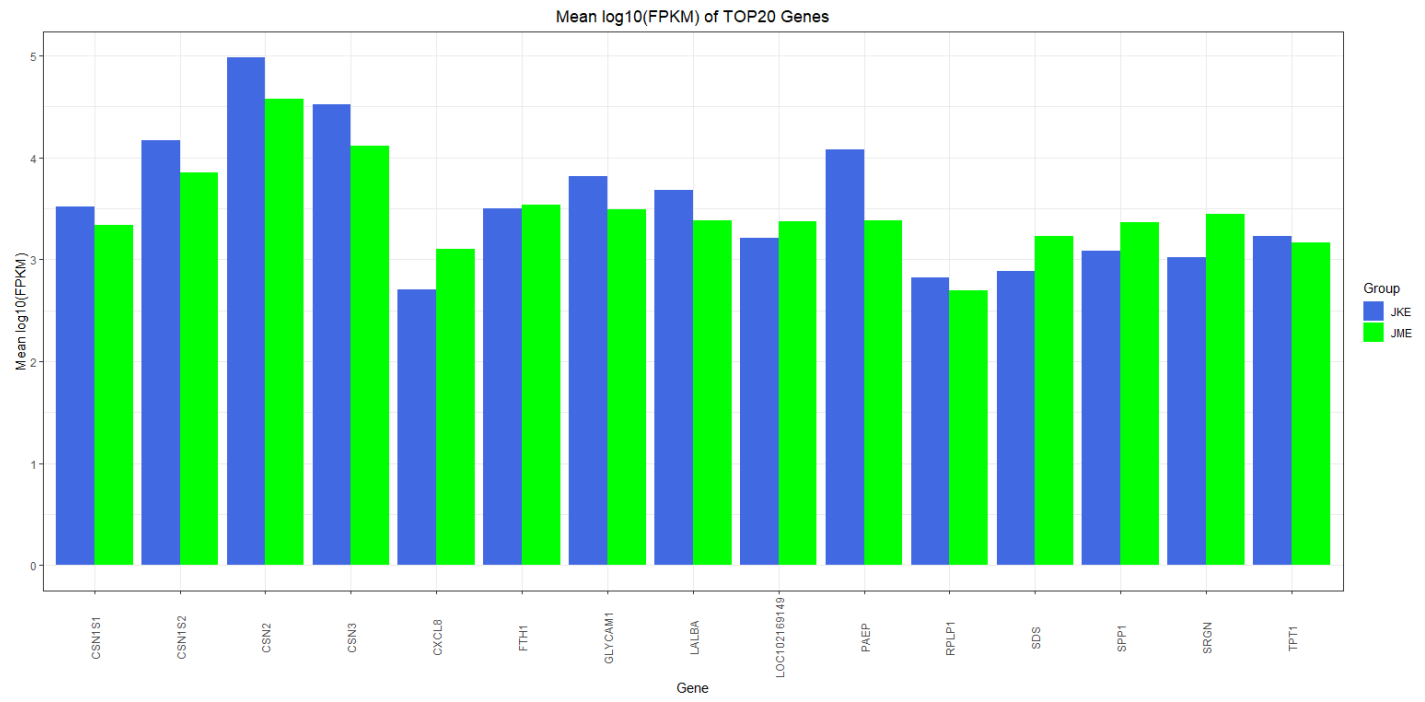


Figure 4. Contribution of the top 20 highly expressed genes to total FPKM varies across samples, highlighting milk protein and housekeeping genes as major contributors.

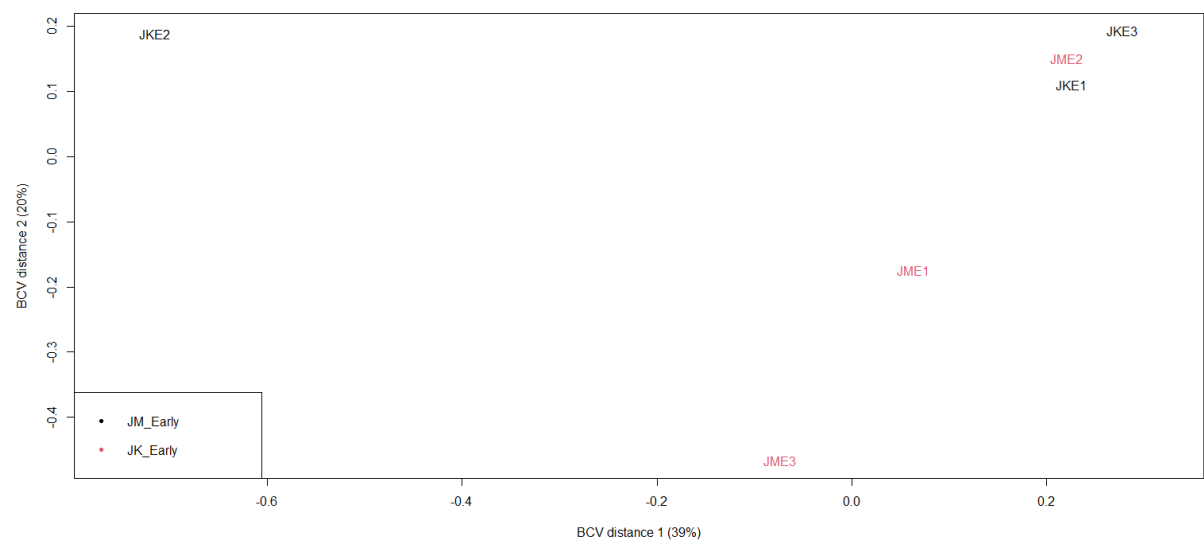


Figure 5. The multidimensional scaling plot representing the clustering of early lactation (JKE) and early lactation (JME) samples.

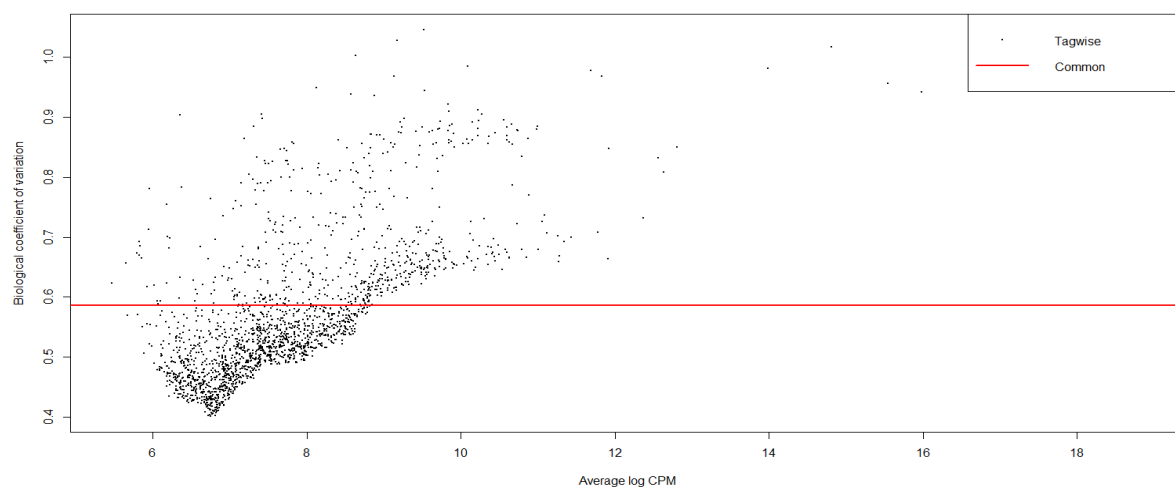


Figure 6. Biological coefficient of variation (BCV) plot showing the relationship between gene-wise biological variability and average expression levels (logCPM) across samples. Each point represents an individual gene, with tagwise BCV estimates shown as black dots and the common BCV indicated by the red horizontal line