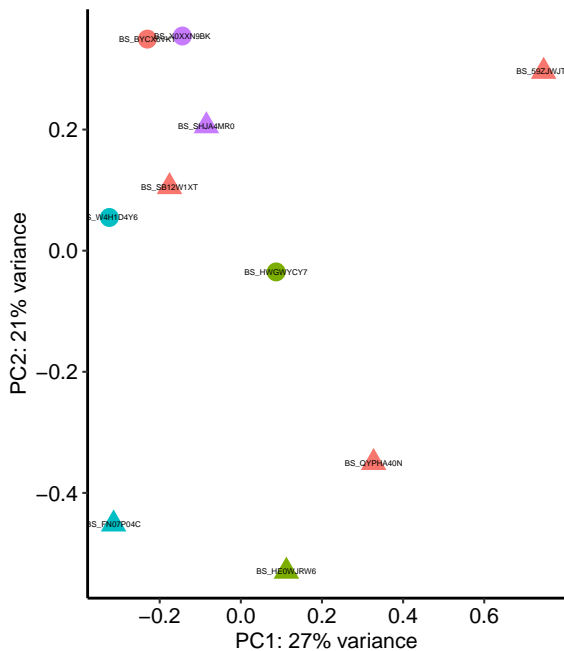
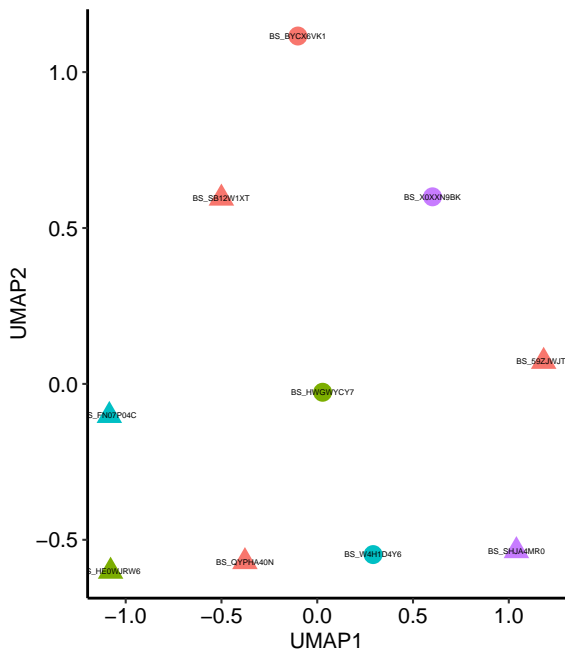


PCA: RUVg output (k = 1)

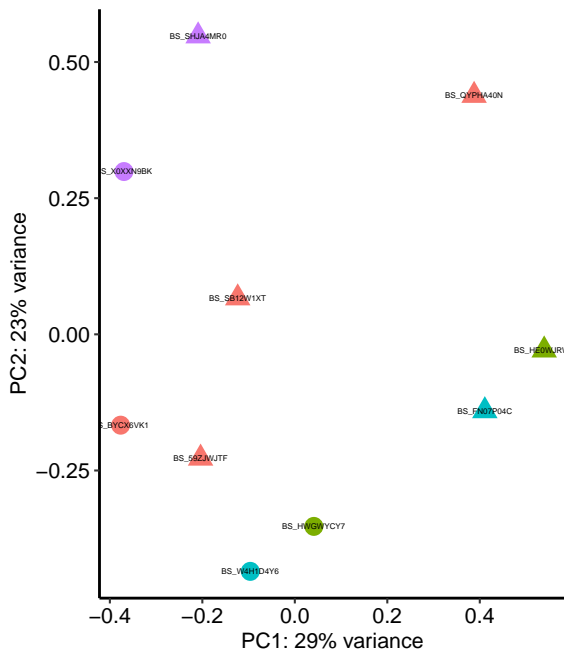


UMAP: RUVg output (k = 1)

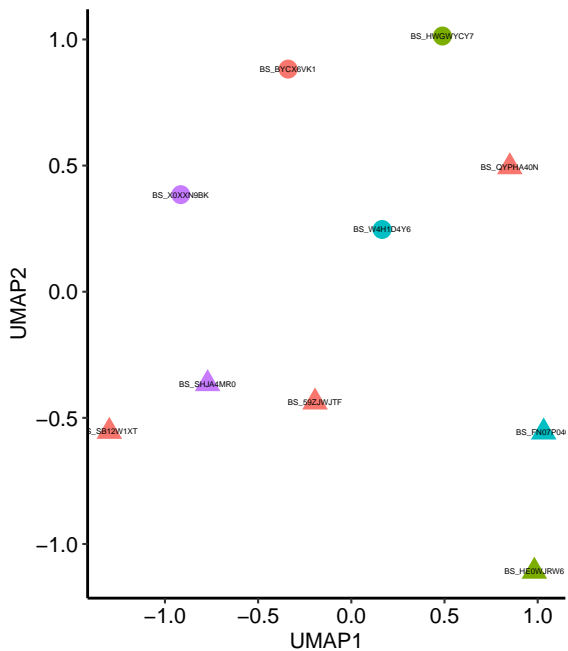


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PCA: RUVg output (k = 2)



UMAP: RUVg output (k = 2)



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PCA plot showing the first two principal components (PC1 and PC2) of the data. The x-axis represents PC1 (33% variance) and the y-axis represents PC2 (22% variance). The samples are colored by group: red (BS_54Z, BS_S612, BS_QY), green (BS_H1, BS_HE), purple (BS_XO, BS_SH), and cyan (BS_W4, BS_FN). The plot shows distinct clustering of samples within each group.

Sample	Group	PC1 (approx.)	PC2 (approx.)
BS_54Z	Red	-0.25	0.85
BS_S612	Red	0.00	-0.15
BS_QY	Red	0.45	-0.95
BS_H1	Green	-0.35	-0.75
BS_HE	Green	0.20	0.40
BS_XO	Purple	0.15	0.25
BS_SH	Purple	0.45	0.65
BS_W4	Cyan	-0.45	0.55
BS_FN	Cyan	0.10	0.95

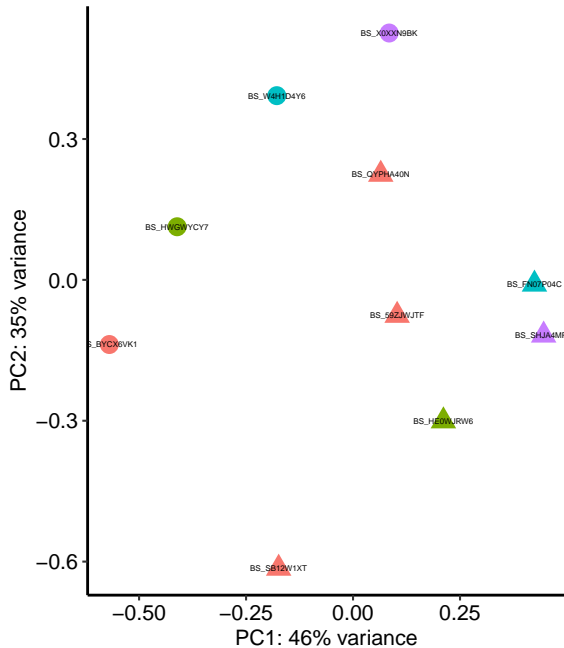
UMAP2

UMAP1

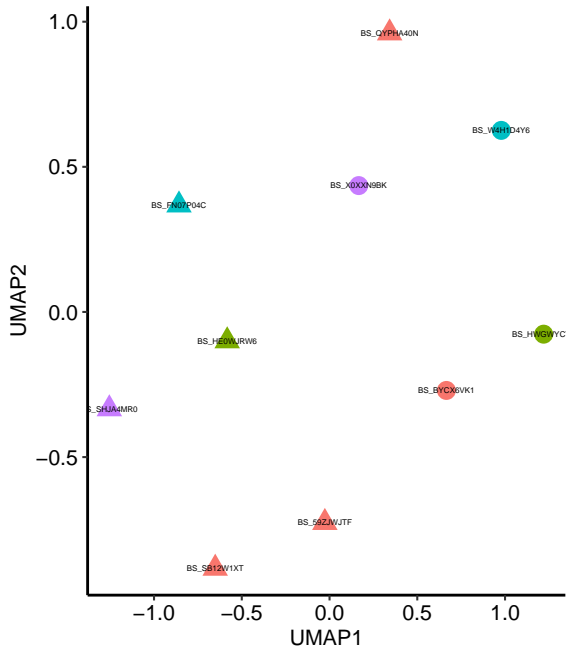
Protein Complex	UMAP1	UMAP2	Cluster
BS_BYCN6VK1	-0.6	1.1	Red Circle
BS_X0XXN9BK	0.1	1.3	Purple Circle
BS_W4H1D4Y6	-1.0	0.6	Cyan Circle
BS_HVCHWICY7	-0.4	0.4	Green Circle
BS_QYPHA40N	0.5	0.8	Red Triangle
BS_56ZMWTJF	-0.4	-0.4	Red Triangle
BS_SHUA4MR0	0.7	-0.5	Purple Triangle
BS_SB12W1XT	-0.3	-1.0	Red Triangle
BS_HE2VJRW6	0.3	-1.1	Green Triangle
BS_FN07P04	1.1	-1.0	Cyan Triangle

stranded

PCA: RUVg output (k = 4)

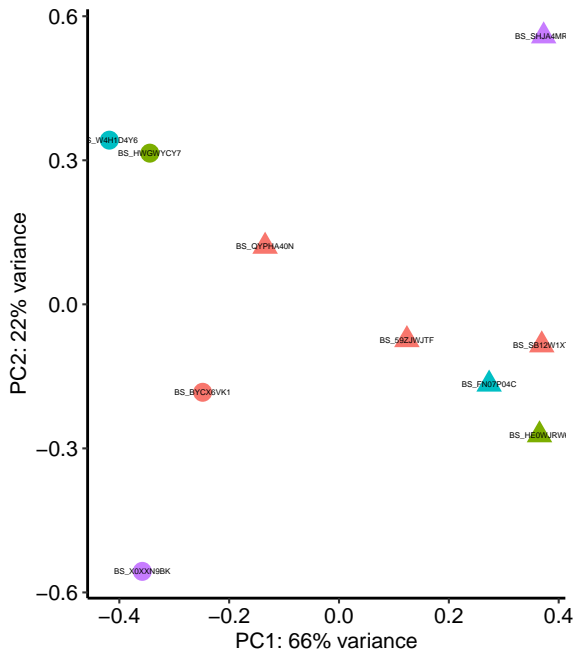


UMAP: RUVg output (k = 4)

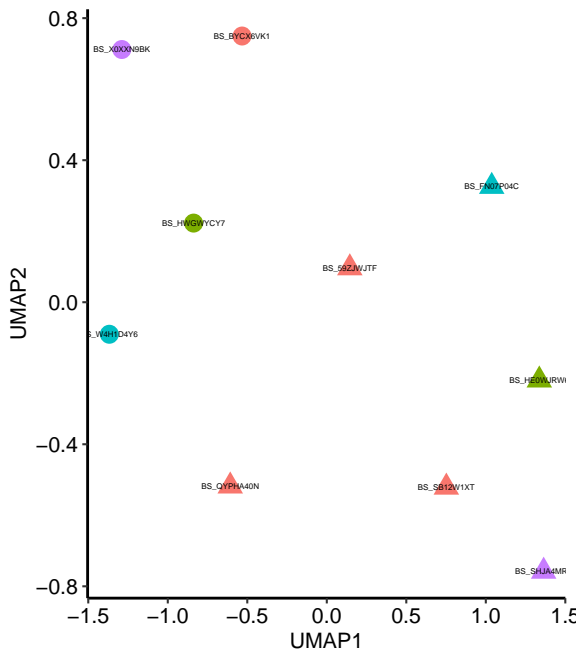


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PCA: RUVg output (k = 5)



UMAP: RUVg output (k = 5)



rna_library ● poly-A ▲ stranded