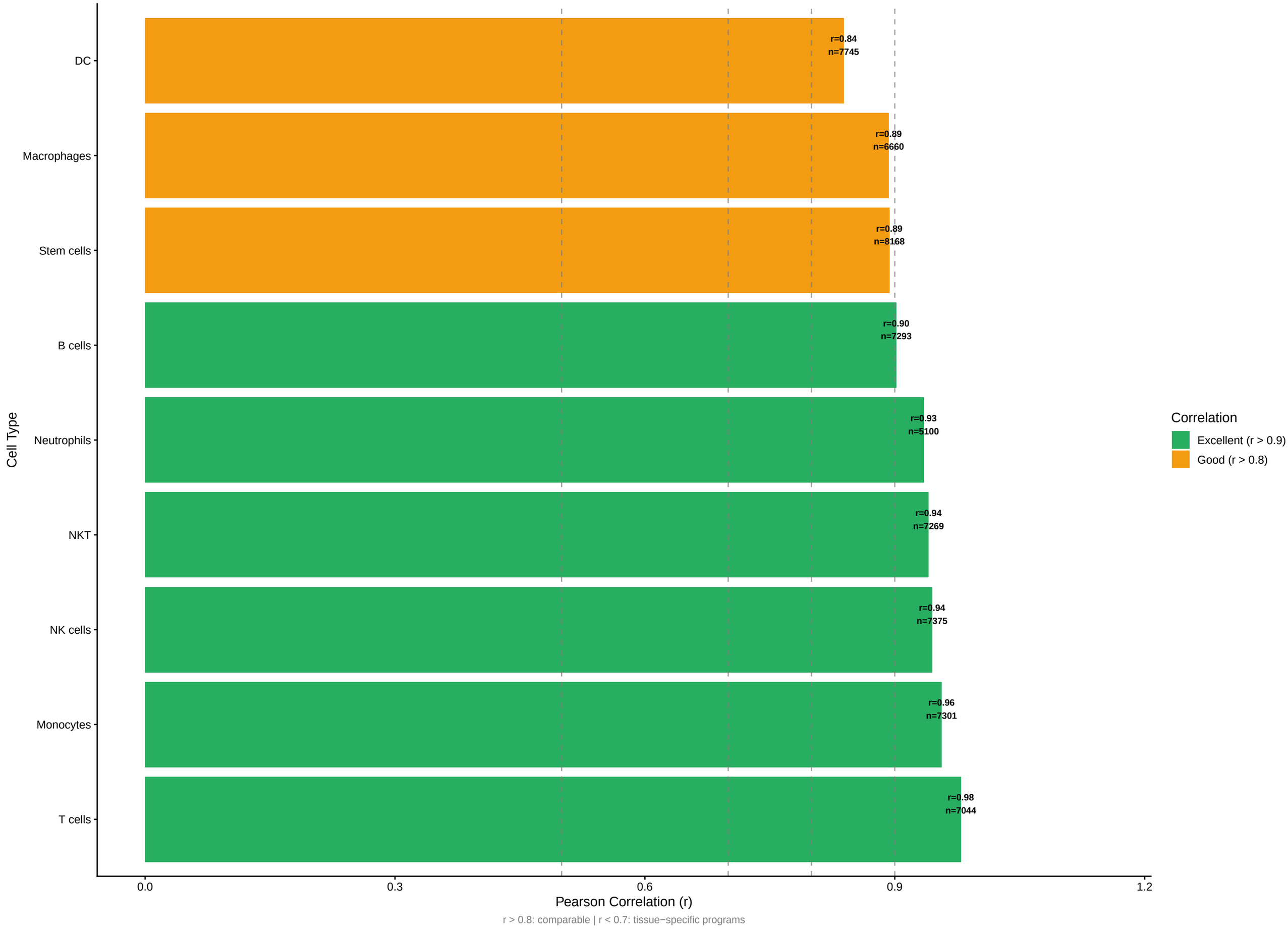
Baseline Expression Correlation Summary

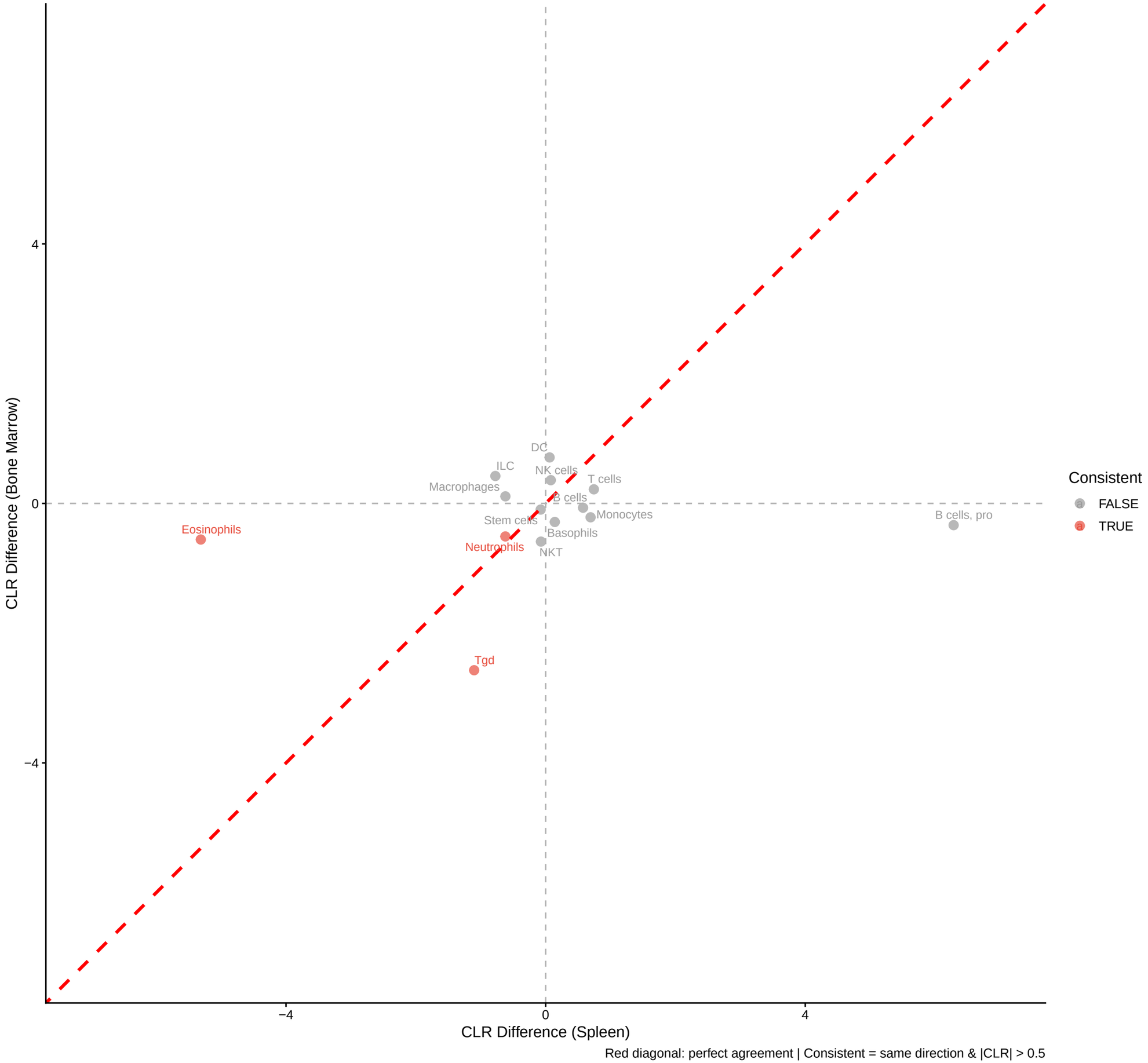
Spleen vs Bone Marrow − Are cell types comparable?



r > 0.8: comparable | r < 0.7: tissue−specific programs

Cross−Tissue CLR Comparison

r = 0.155 (p = 0.6) | 14 cell types



Red diagonal: perfect agreement | Consistent = same direction & |CLR| > 0.5

Cross−Tissue DEG Correlation Summary

Spleen vs BoneMarrow

ILC
NK cells
Basophils
NKT
Stem cells
Macrophages
DC
Neutrophils
Monocytes
B cells
T cells

0.00ns
0.00ns
0.00ns
0.00*
0.00*
0.00**
0.01***
0.03***
0.04***
0.34***
0.45***

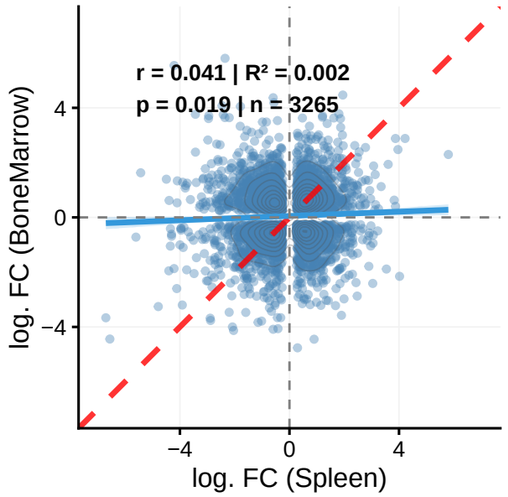
0.0
0.3
0.6
0.9
1.2
R^2

R^2
1.00
0.75
0.50
0.25
0.00

Cross−Tissue DEG Comparison: Spleen vs BoneMarrow

NKT

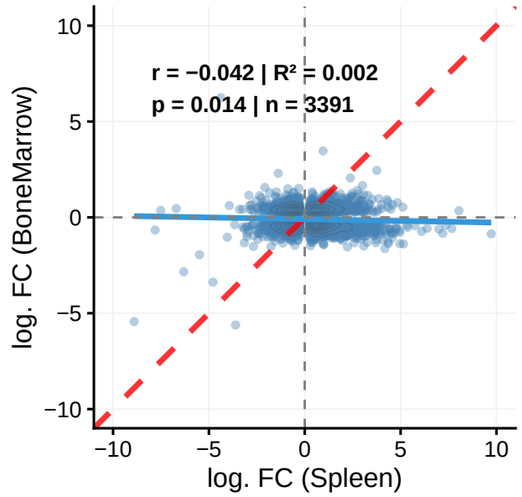
Pearson r = 0.041, R² = 0.002



Red dashed: perfect correlation (x=y) | Blue: regression

Stem cells

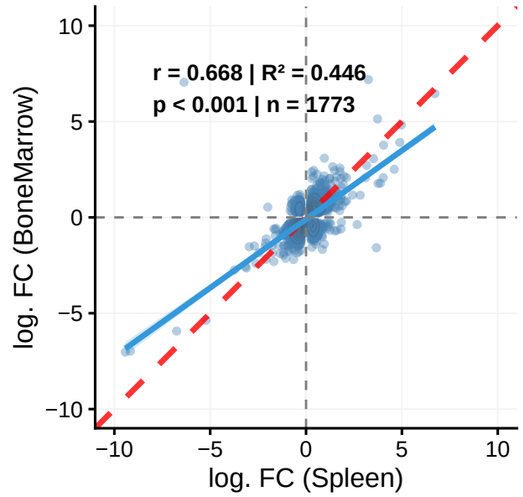
Pearson r = −0.042, R² = 0.002



Red dashed: perfect correlation (x=y) | Blue: regression

T cells

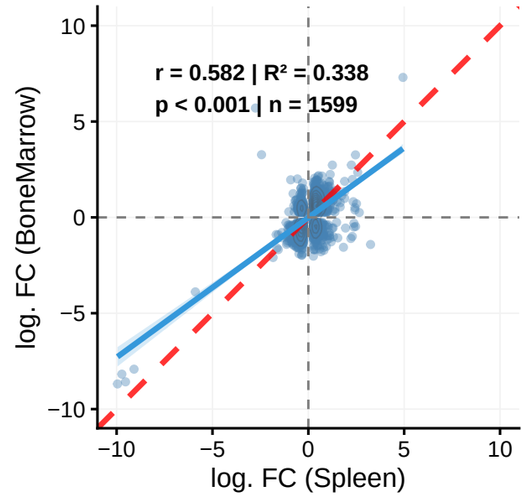
Pearson r = 0.668, R² = 0.446



Red dashed: perfect correlation (x=y) | Blue: regression

B cells

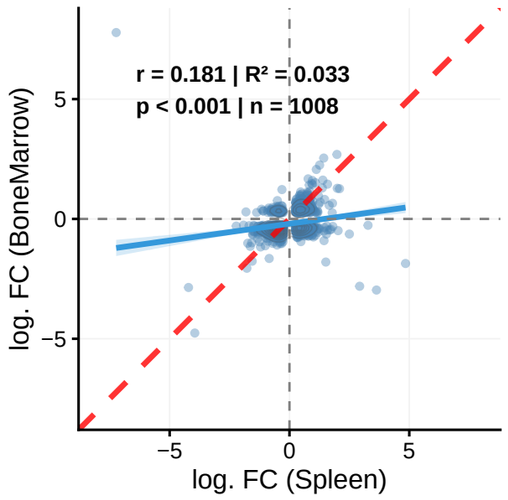
Pearson r = 0.582, R² = 0.338



Red dashed: perfect correlation (x=y) | Blue: regression

Neutrophils

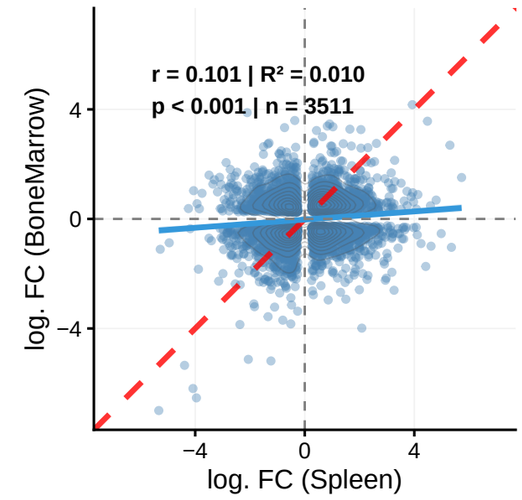
Pearson r = 0.181, R² = 0.033



Red dashed: perfect correlation (x=y) | Blue: regression

DC

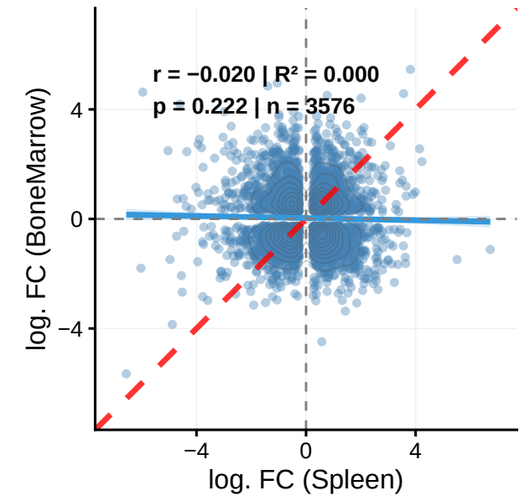
Pearson r = 0.101, R² = 0.010



Red dashed: perfect correlation (x=y) | Blue: regression

NK cells

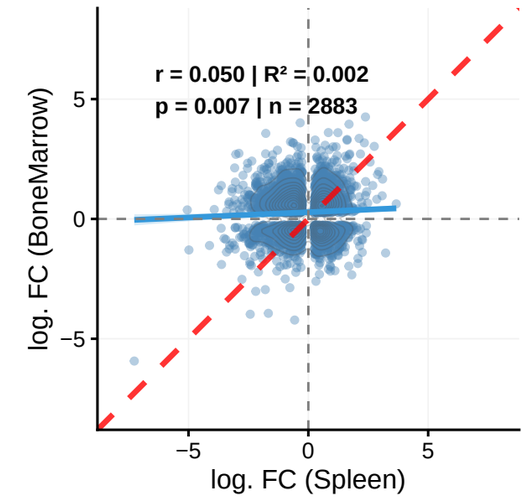
Pearson r = −0.020, R² = 0.000



Red dashed: perfect correlation (x=y) | Blue: regression

Macrophages

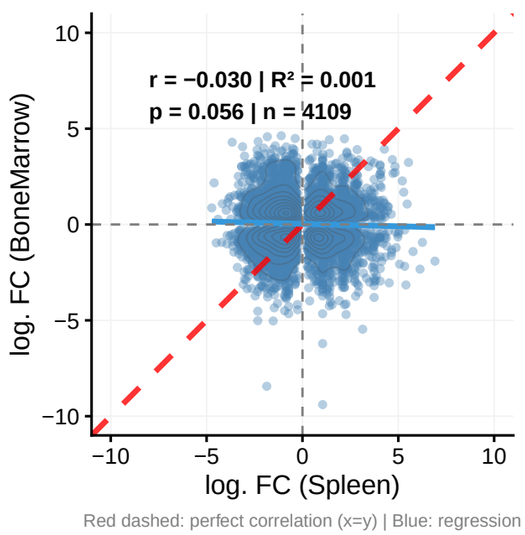
Pearson r = 0.050, R² = 0.002



Red dashed: perfect correlation (x=y) | Blue: regression

Basophils

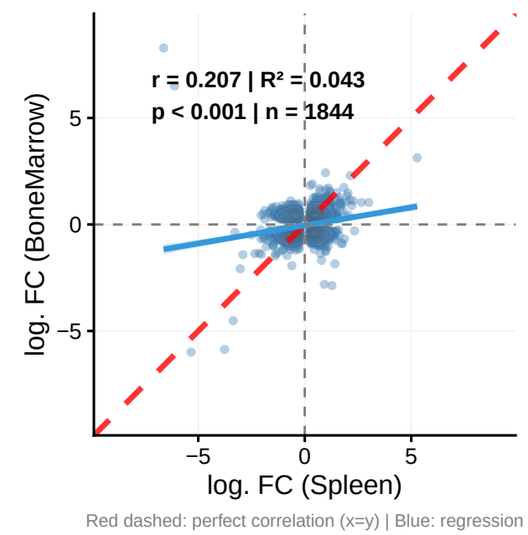
Pearson r = −0.030, R² = 0.001



Red dashed: perfect correlation (x=y) | Blue: regression

Monocytes

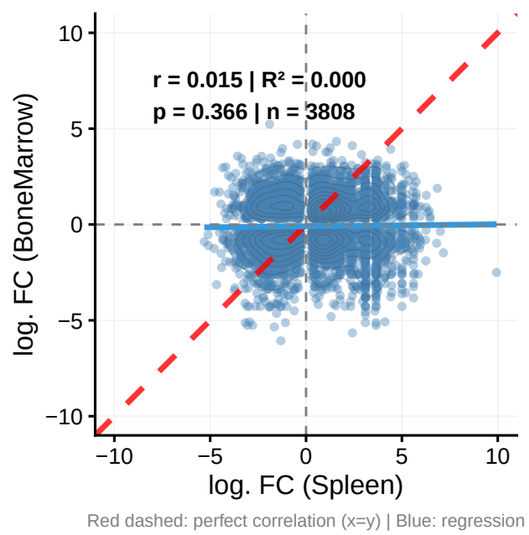
Pearson r = 0.207, R² = 0.043



Red dashed: perfect correlation (x=y) | Blue: regression

ILC

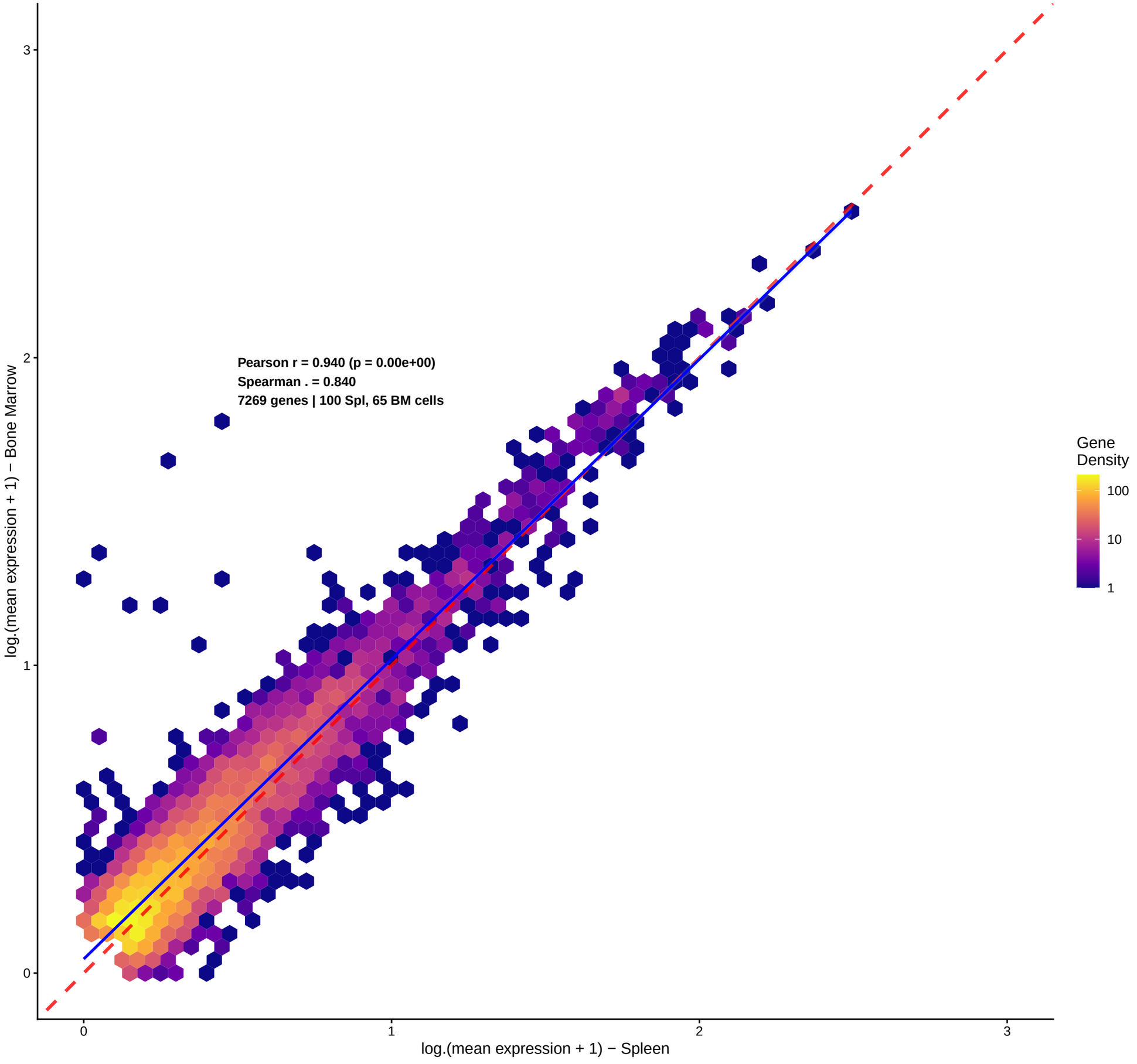
Pearson r = 0.015, R² = 0.000



Red dashed: perfect correlation (x=y) | Blue: regression

Baseline Expression − NKT

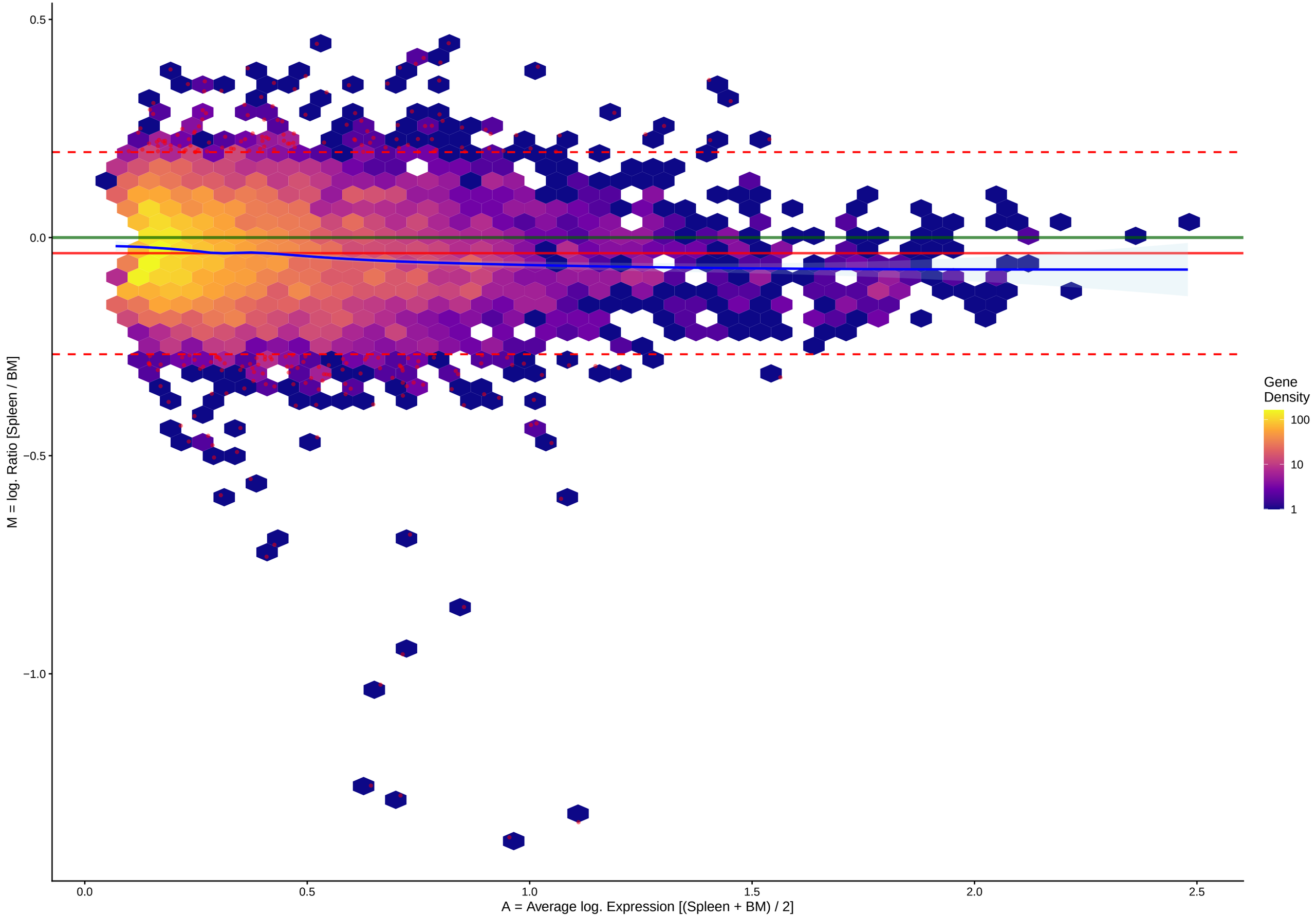
Do genes have similar expression in both tissues?



Red: perfect correlation (x=y) | Blue: regression | r > 0.8 = comparable

MA Plot − NKT

Systematic bias detection

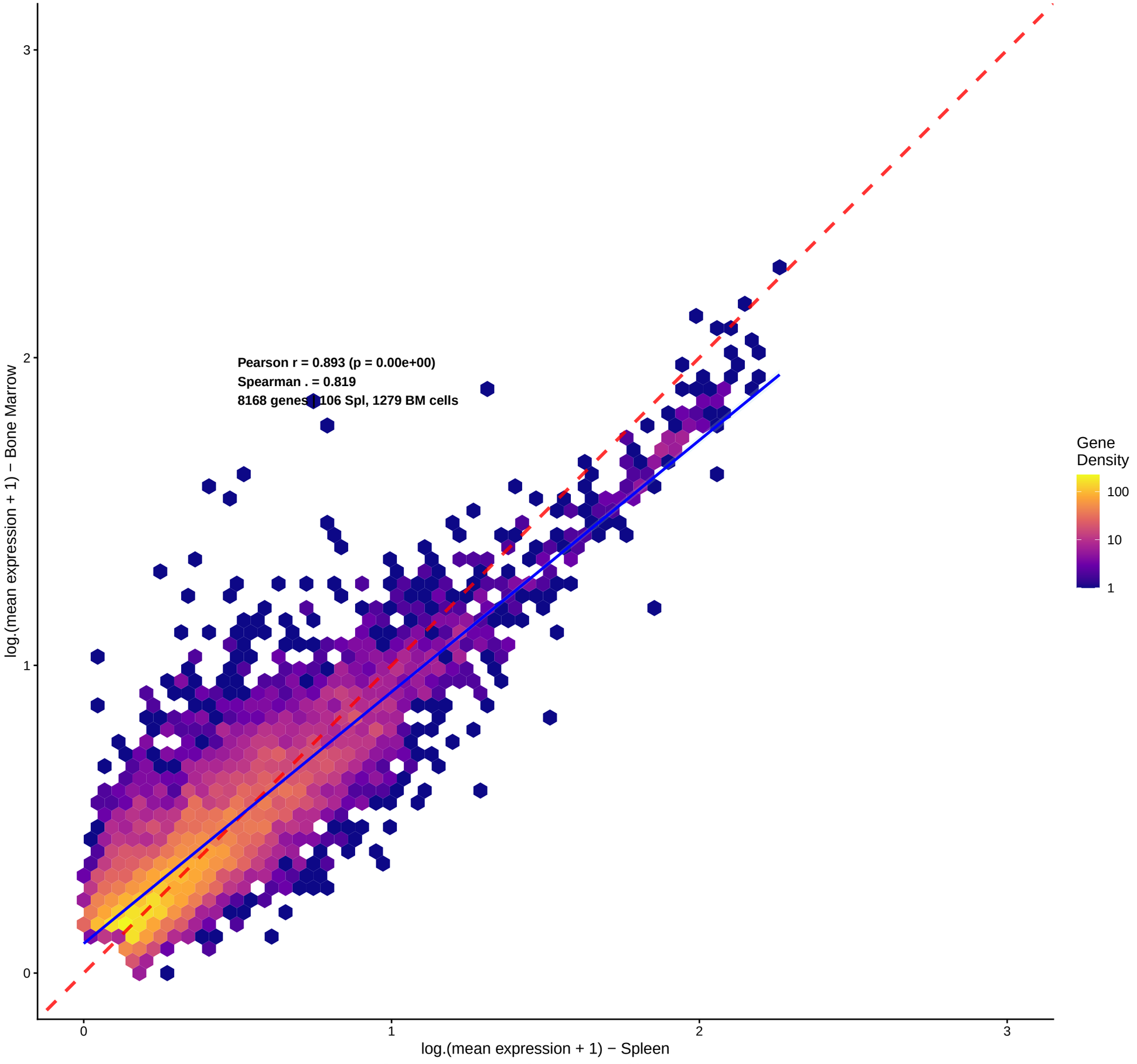


Green (M=0): no bias | Red (M=−0.04): mean bias | Dashed: ±2SD [−0.27, 0.20]

M.0 = no bias | M>0 = Spleen higher | M<0 = BM higher

Baseline Expression − Stem cells

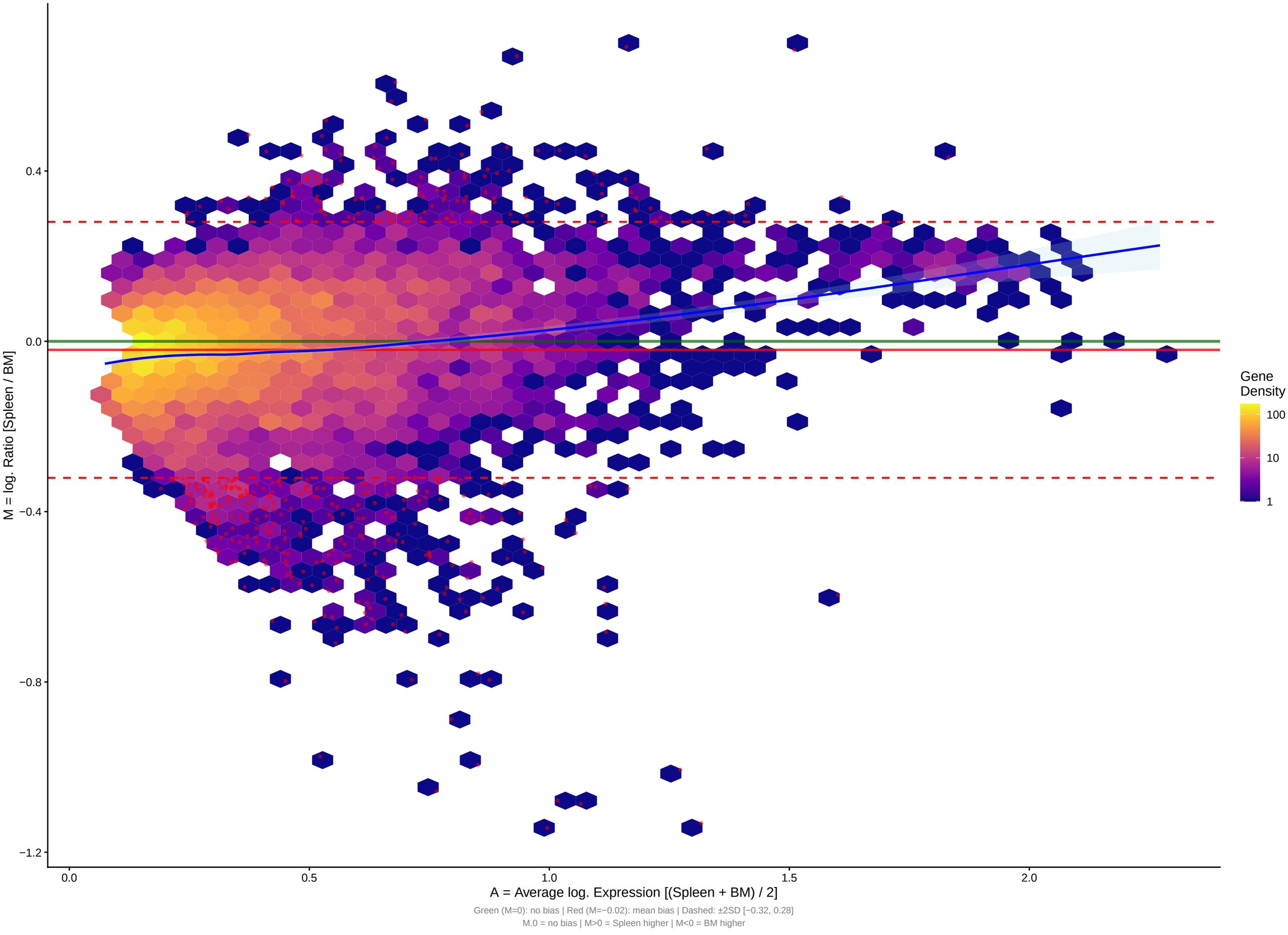
Do genes have similar expression in both tissues?



Red: perfect correlation (x=y) | Blue: regression | r > 0.8 = comparable

MA Plot − Stem cells

Systematic bias detection

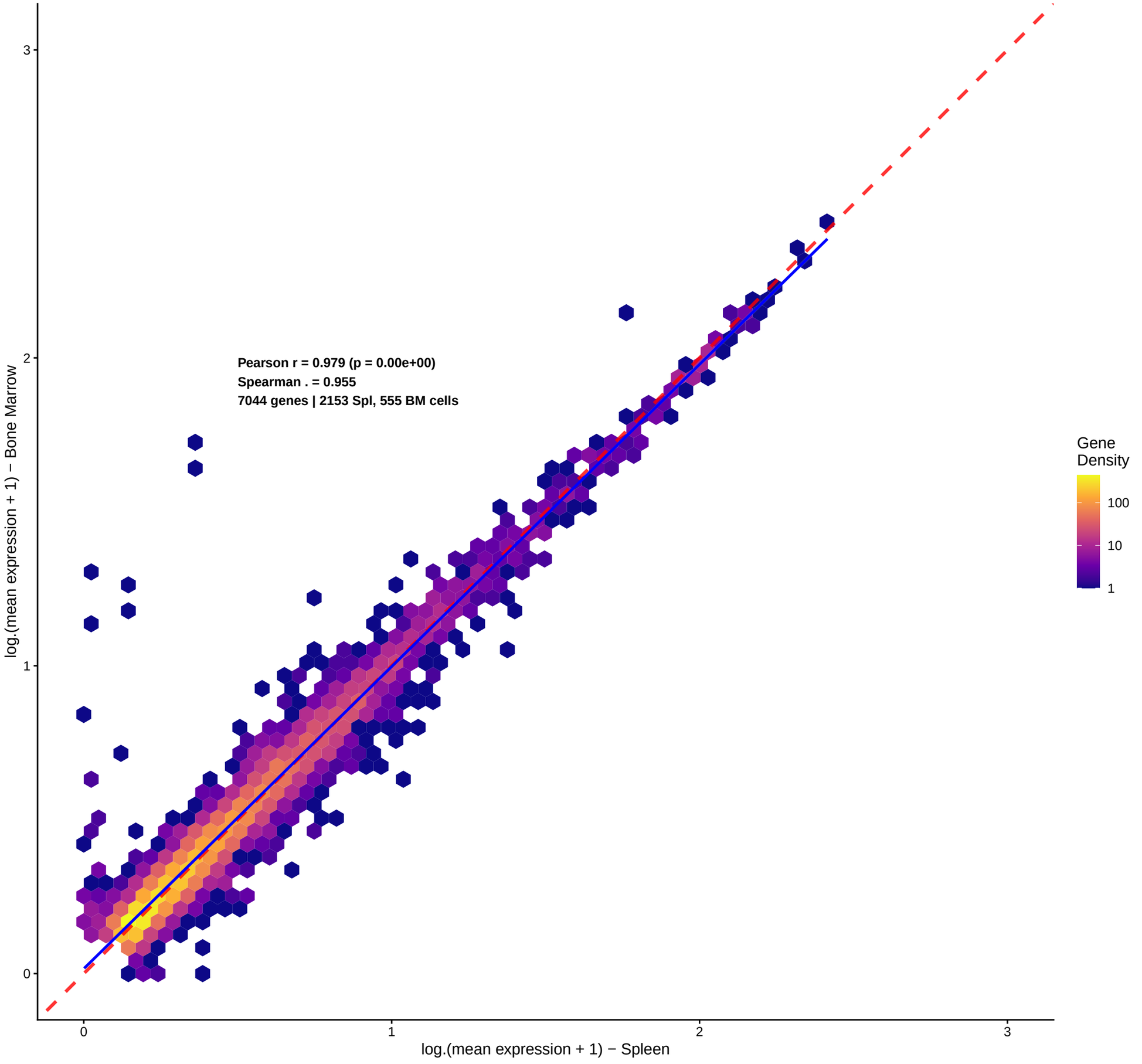


Green (M=0): no bias | Red (M=−0.02): mean bias | Dashed: ±2SD [−0.32, 0.28]

M.0 = no bias | M>0 = Spleen higher | M<0 = BM higher

Baseline Expression − T cells

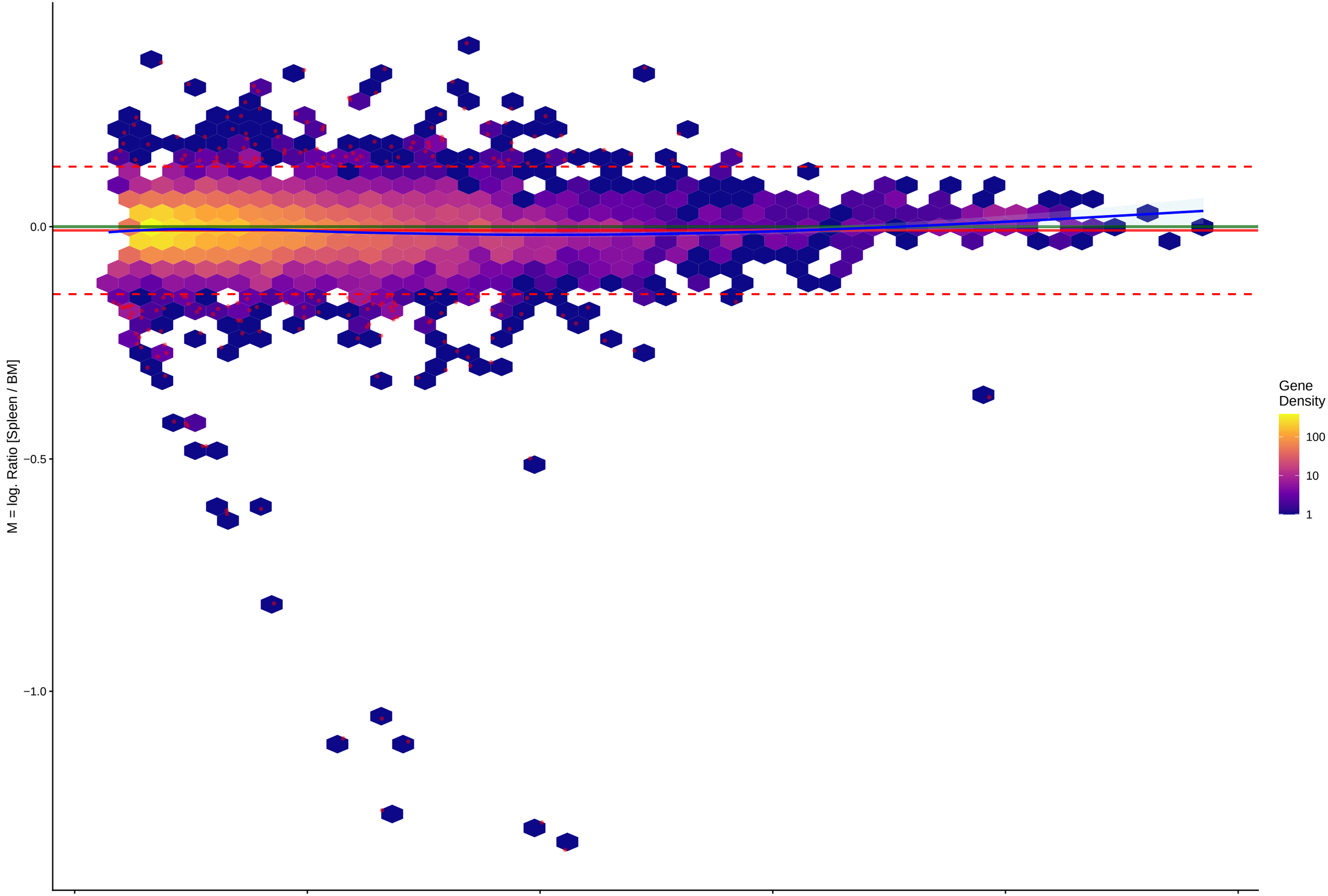
Do genes have similar expression in both tissues?



Red: perfect correlation (x=y) | Blue: regression | r > 0.8 = comparable

MA Plot − T cells

Systematic bias detection

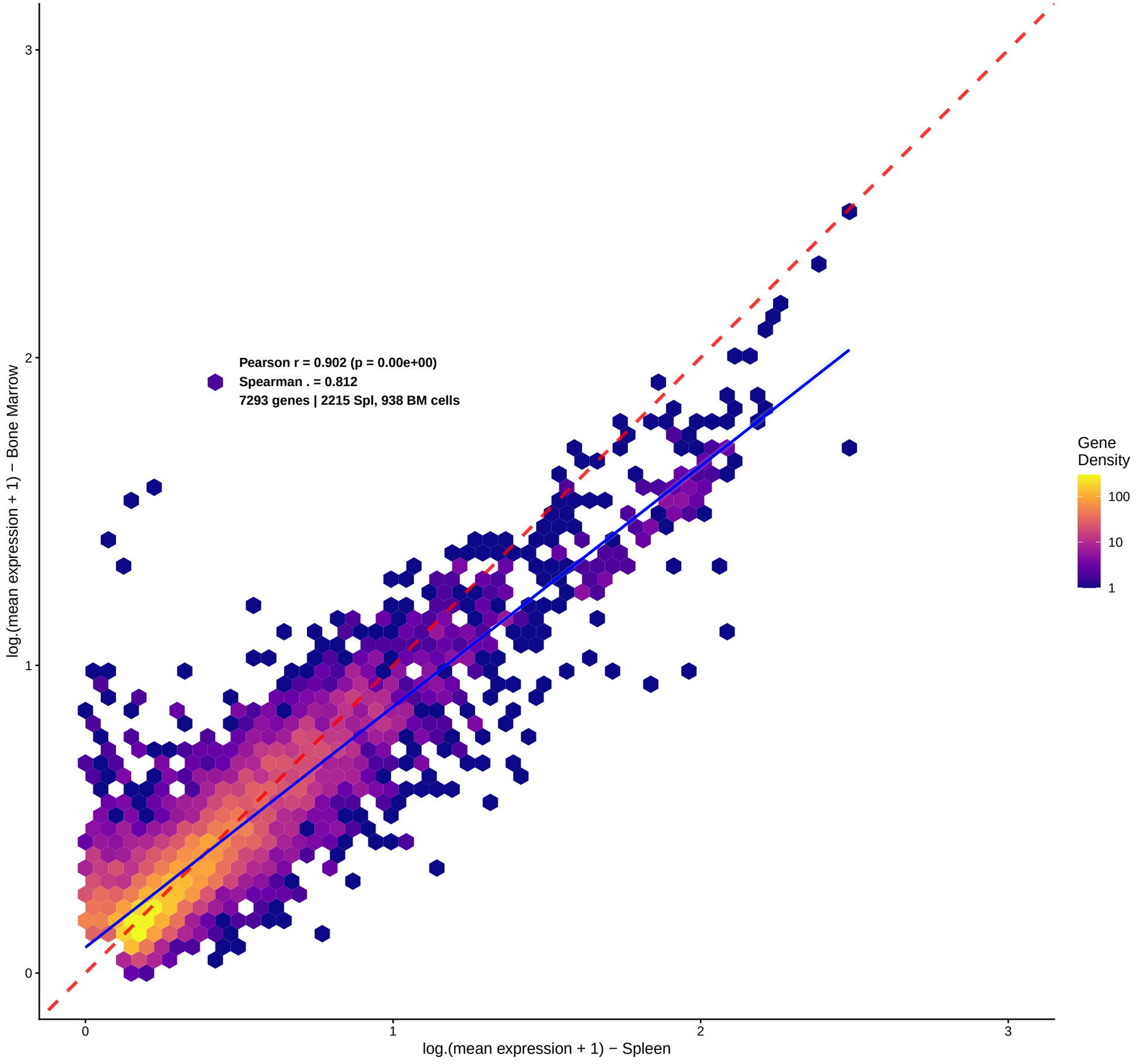


Green (M=0): no bias | Red (M=−0.01): mean bias | Dashed: ±2SD [−0.15, 0.13]

M.0 = no bias | M>0 = Spleen higher | M<0 = BM higher

Baseline Expression − B cells

Do genes have similar expression in both tissues?



Red: perfect correlation (x=y) | Blue: regression | r > 0.8 = comparable

MA Plot − B cells

Systematic bias detection

M = log. Ratio [Spleen / BM]

1.0
0.5
0.0
−0.5
−1.0
−1.5

0.0
0.5
1.0
1.5
2.0
2.5

A = Average log. Expression [(Spleen + BM) / 2]

Gene Density

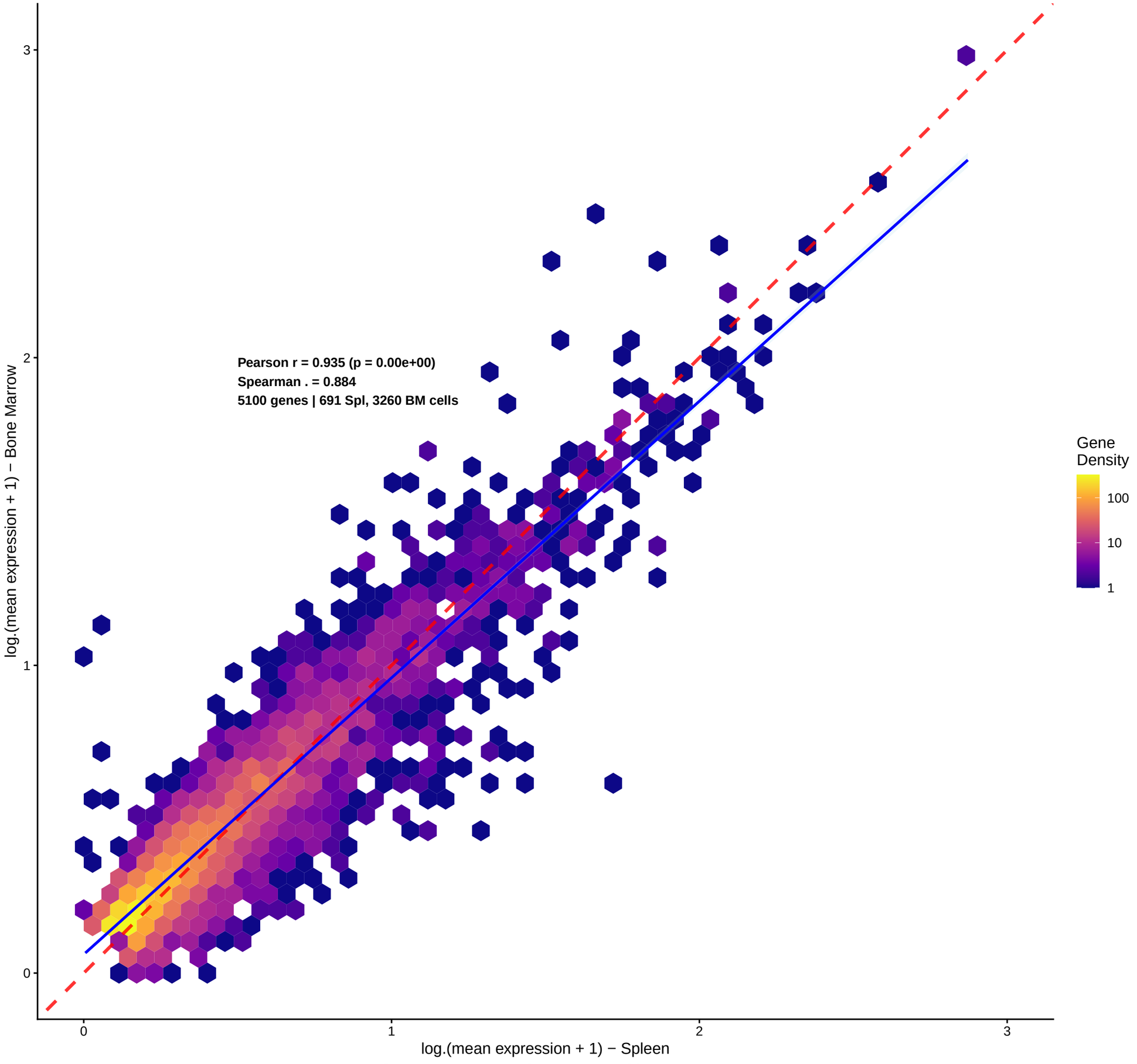
100
10
1

Green (M=0): no bias | Red (M=0.00): mean bias | Dashed: ±2SD [−0.29, 0.30]

M.0 = no bias | M>0 = Spleen higher | M<0 = BM higher

Baseline Expression − Neutrophils

Do genes have similar expression in both tissues?



Red: perfect correlation (x=y) | Blue: regression | r > 0.8 = comparable

MA Plot − Neutrophils

Systematic bias detection

M = log. Ratio [Spleen / BM]

1.0
0.5
0.0
−0.5
−1.0

0
1
2
3

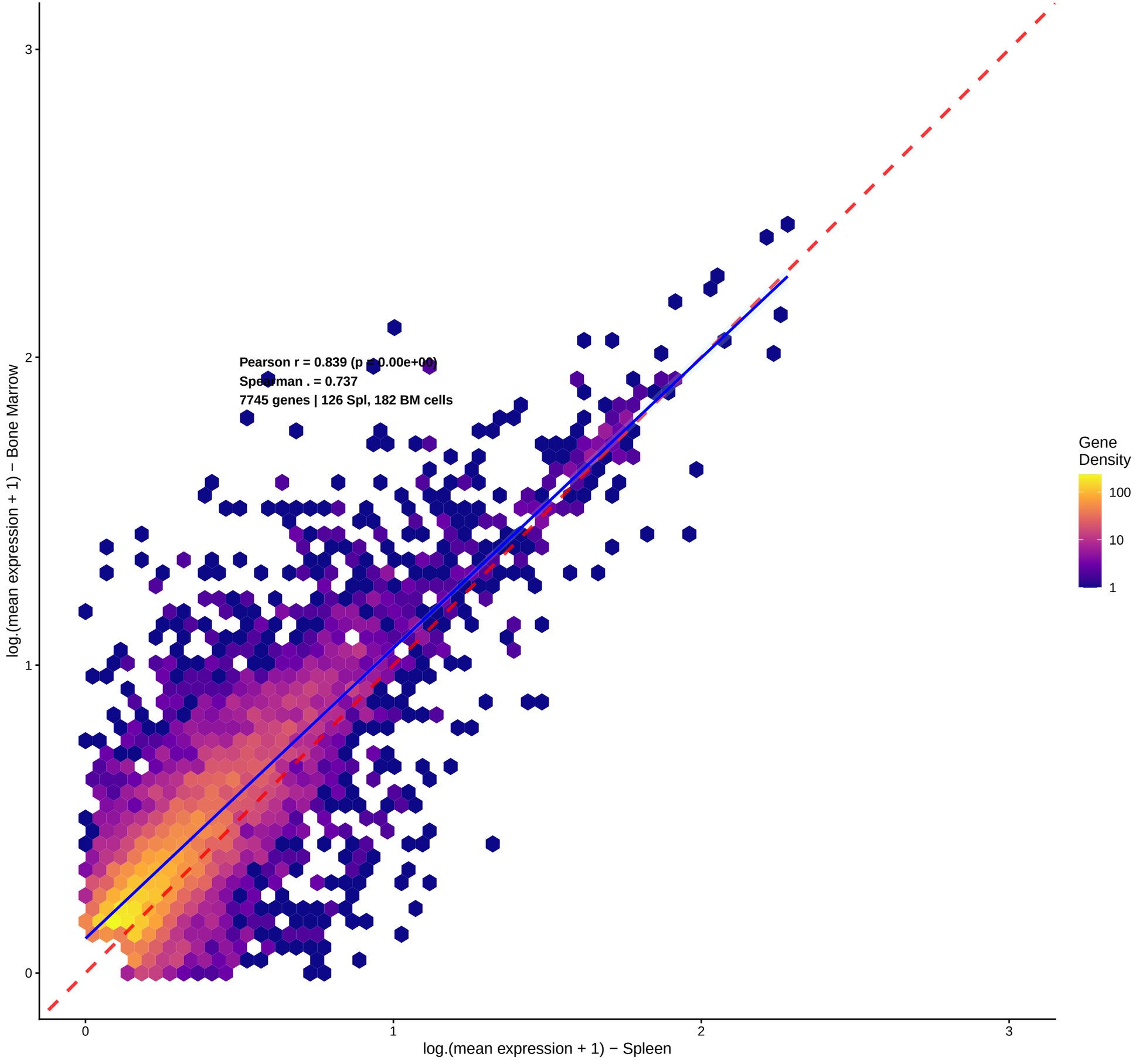
A = Average log. Expression [(Spleen + BM) / 2]

Gene Density
100
10
1

Green (M=0): no bias | Red (M=−0.02): mean bias | Dashed: ±2SD [−0.28, 0.24]
M.0 = no bias | M>0 = Spleen higher | M<0 = BM higher

Baseline Expression − DC

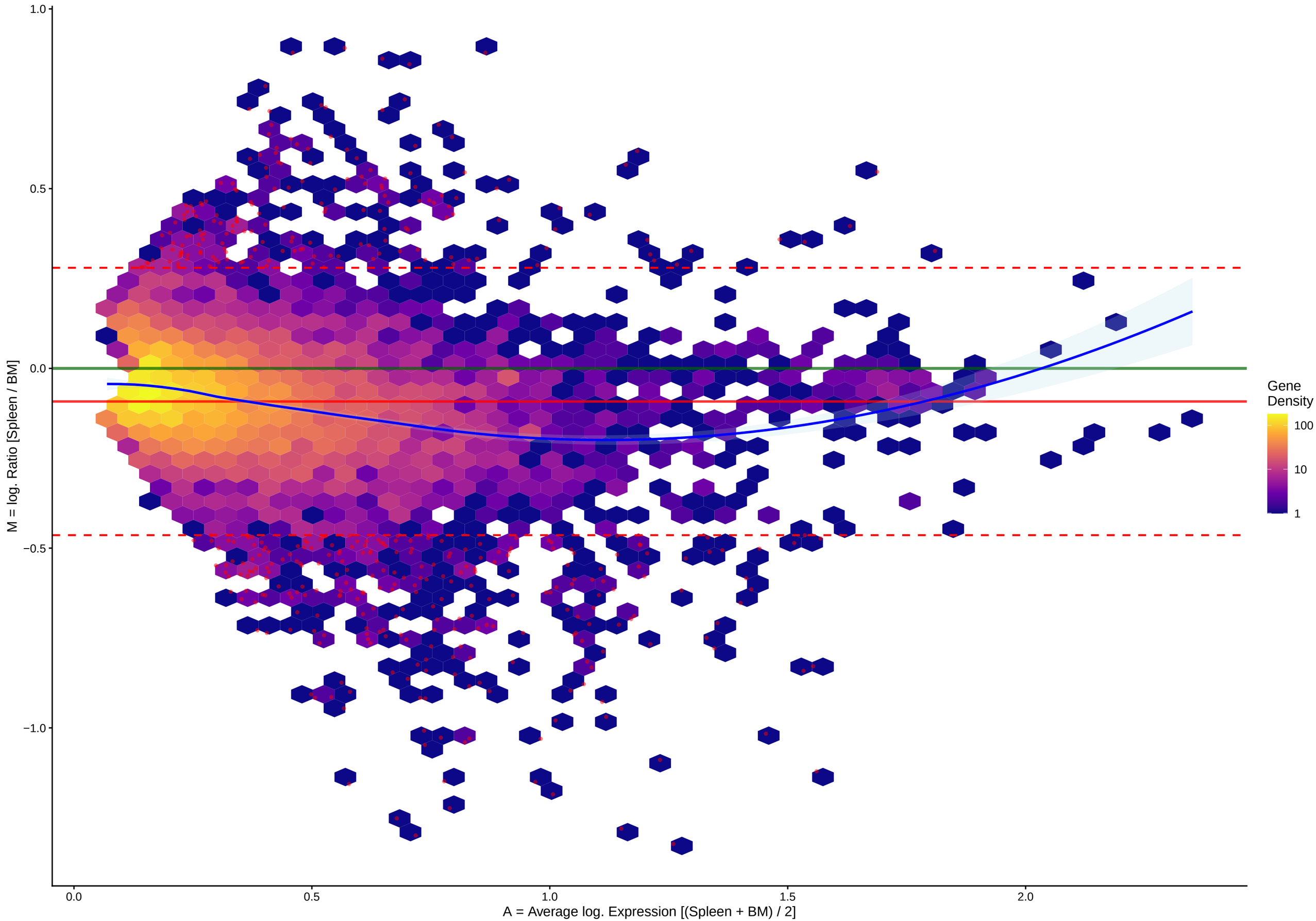
Do genes have similar expression in both tissues?



Red: perfect correlation (x=y) | Blue: regression | r > 0.8 = comparable

MA Plot – DC

Systematic bias detection

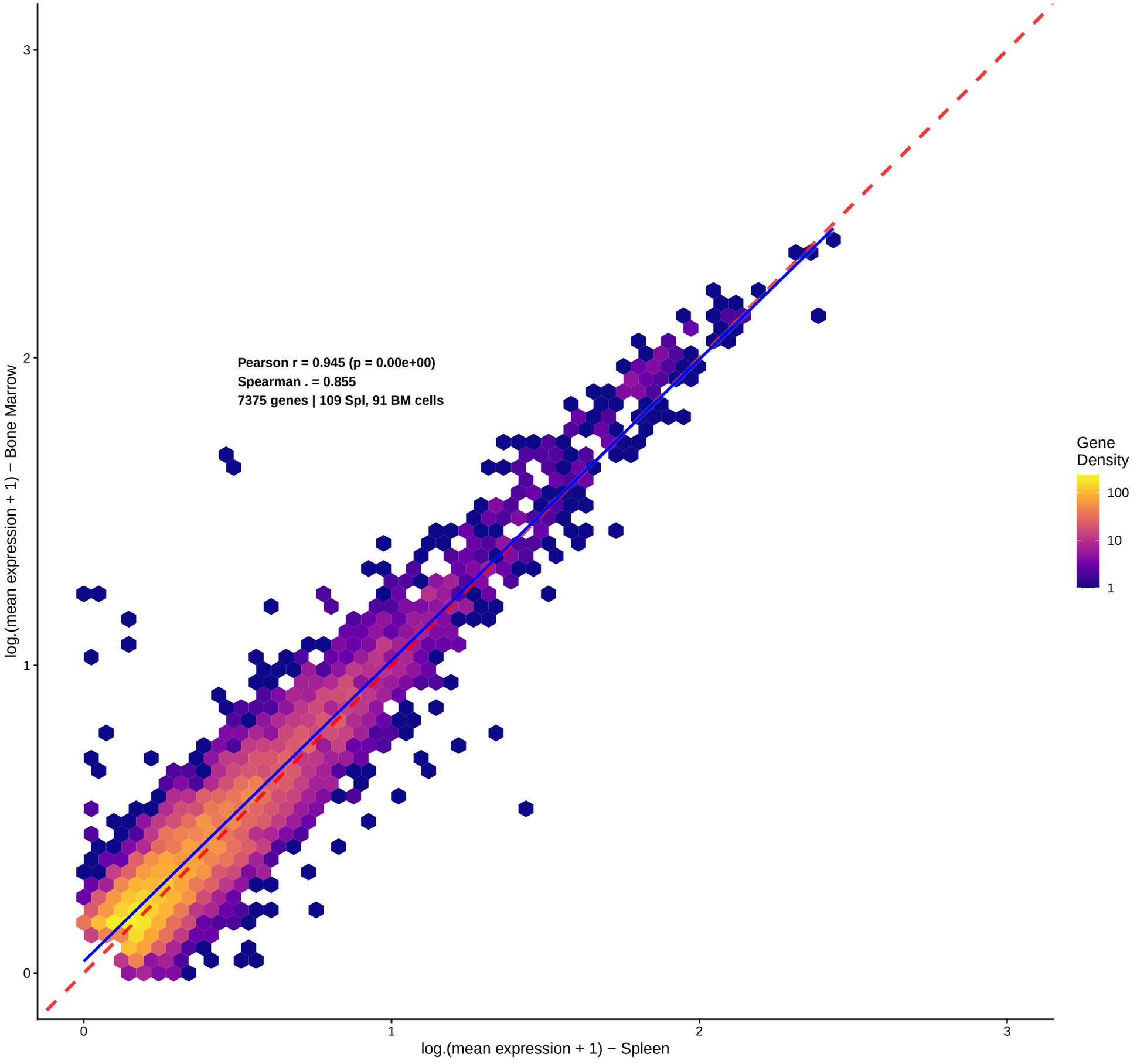


Green (M=0): no bias | Red (M=−0.09): mean bias | Dashed: ±2SD [−0.46, 0.28]

M.0 = no bias | M>0 = Spleen higher | M<0 = BM higher

Baseline Expression − NK cells

Do genes have similar expression in both tissues?



Red: perfect correlation (x=y) | Blue: regression | r > 0.8 = comparable

MA Plot − NK cells

Systematic bias detection

M = log. Ratio [Spleen / BM]

1.0
0.5
0.0
−0.5
−1.0

0.0
0.5
1.0
1.5
2.0
2.5

A = Average log. Expression [(Spleen + BM) / 2]

Gene Density

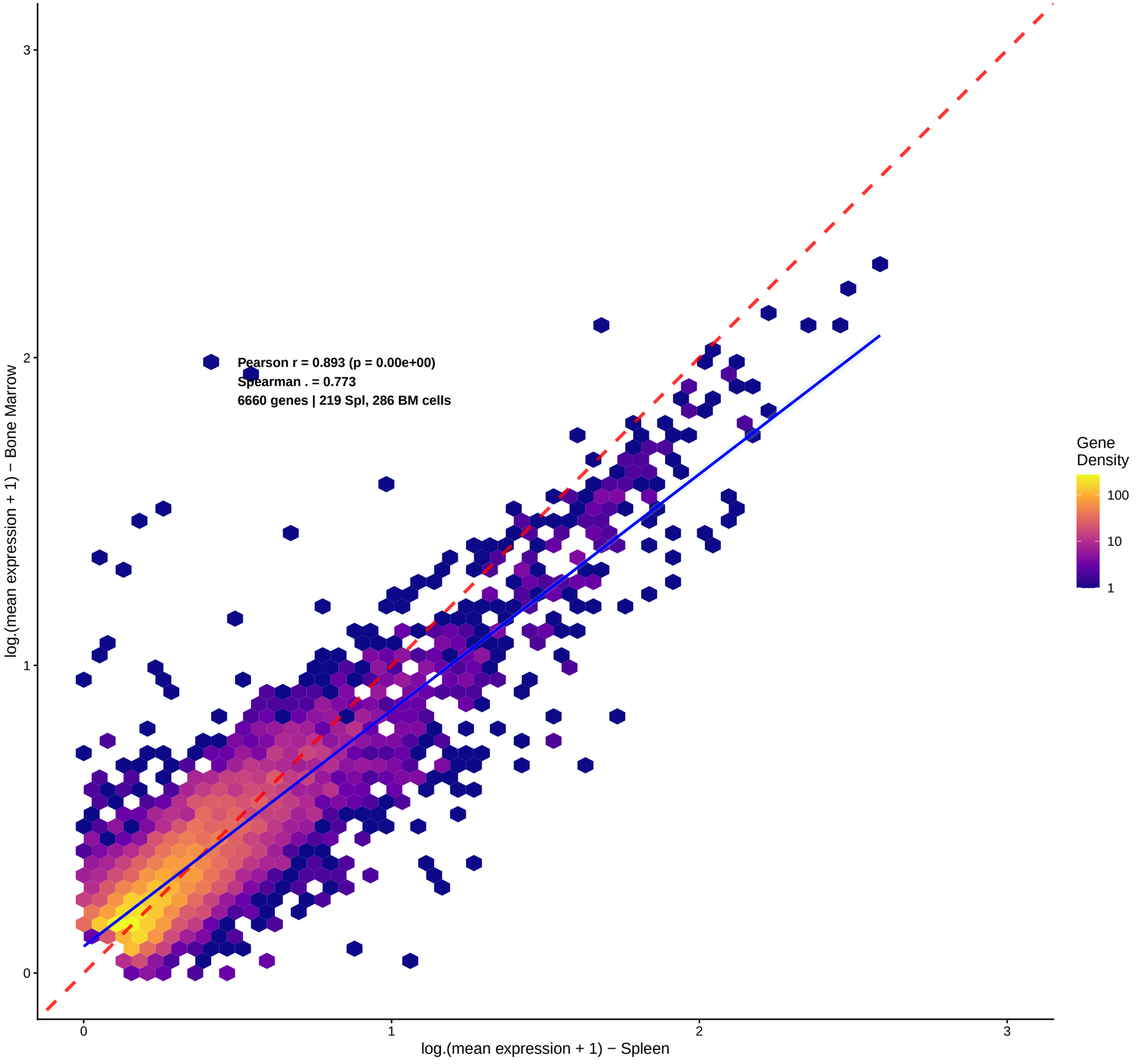
100
10
1

Green (M=0): no bias | Red (M=−0.03): mean bias | Dashed: ±2SD [−0.26, 0.20]

M.0 = no bias | M>0 = Spleen higher | M<0 = BM higher

Baseline Expression − Macrophages

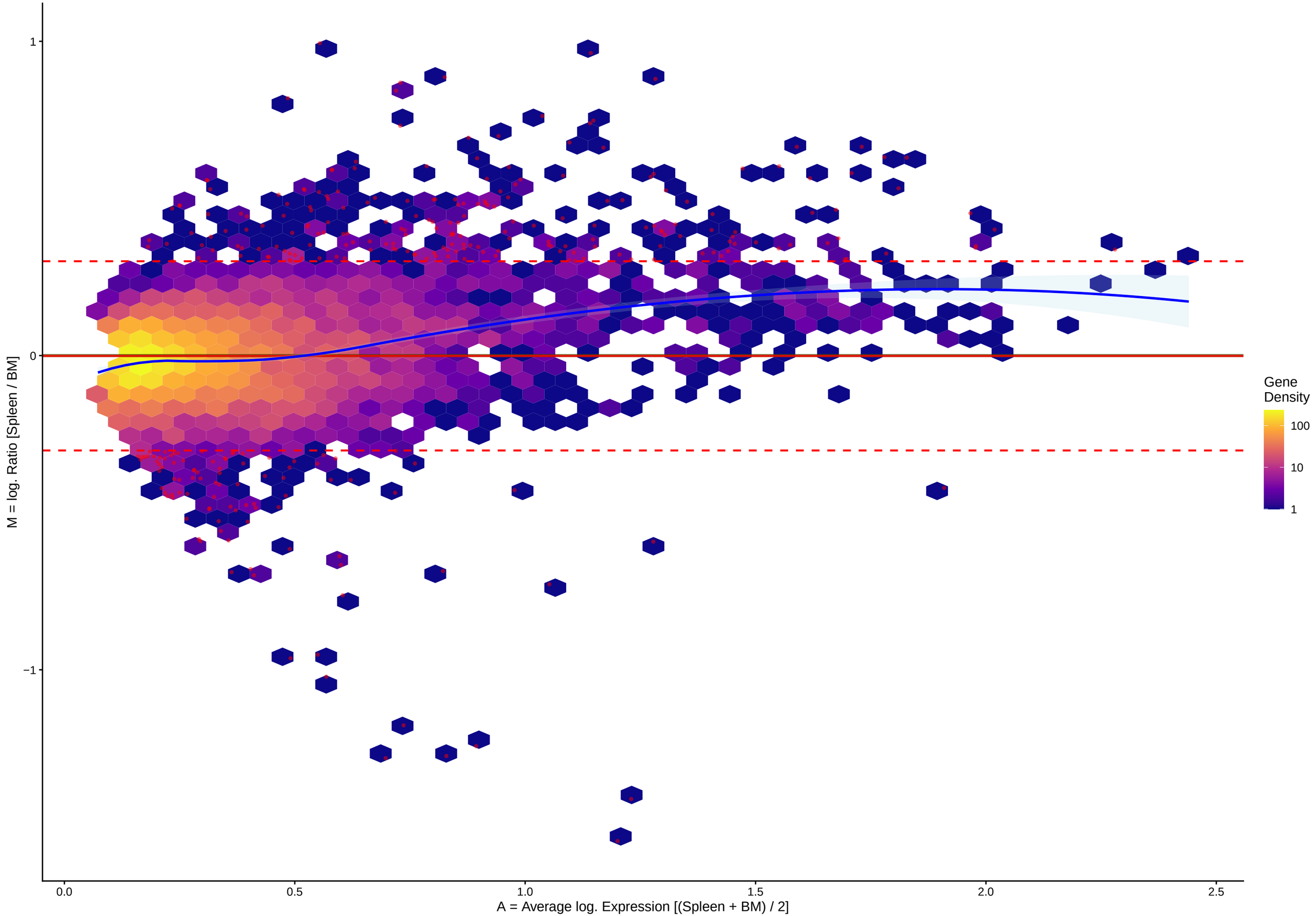
Do genes have similar expression in both tissues?



Red: perfect correlation (x=y) | Blue: regression | r > 0.8 = comparable

MA Plot − Macrophages

Systematic bias detection

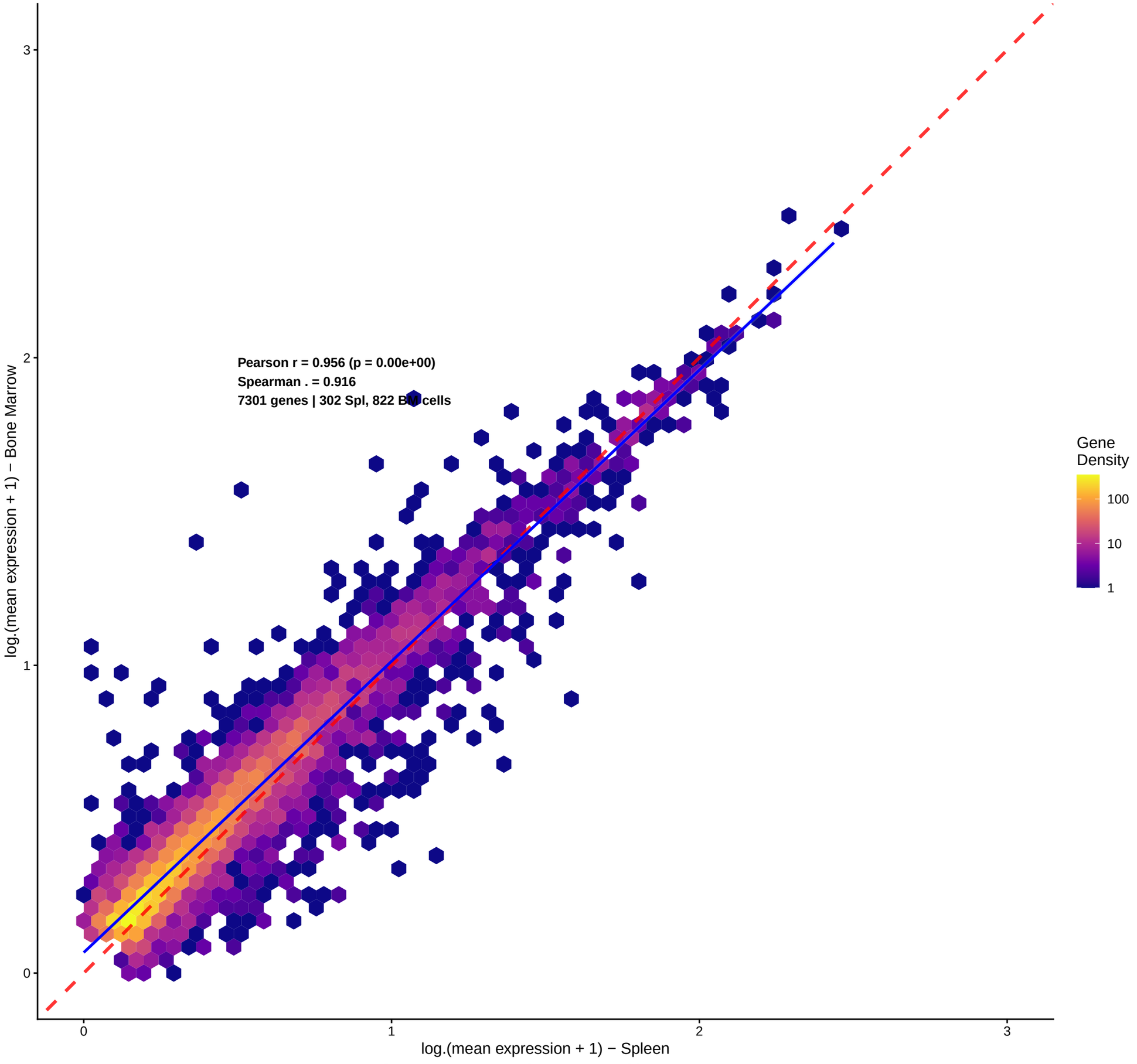


Green (M=0): no bias | Red (M=−0.00): mean bias | Dashed: ±2SD [−0.30, 0.30]

M.0 = no bias | M>0 = Spleen higher | M<0 = BM higher

Baseline Expression − Monocytes

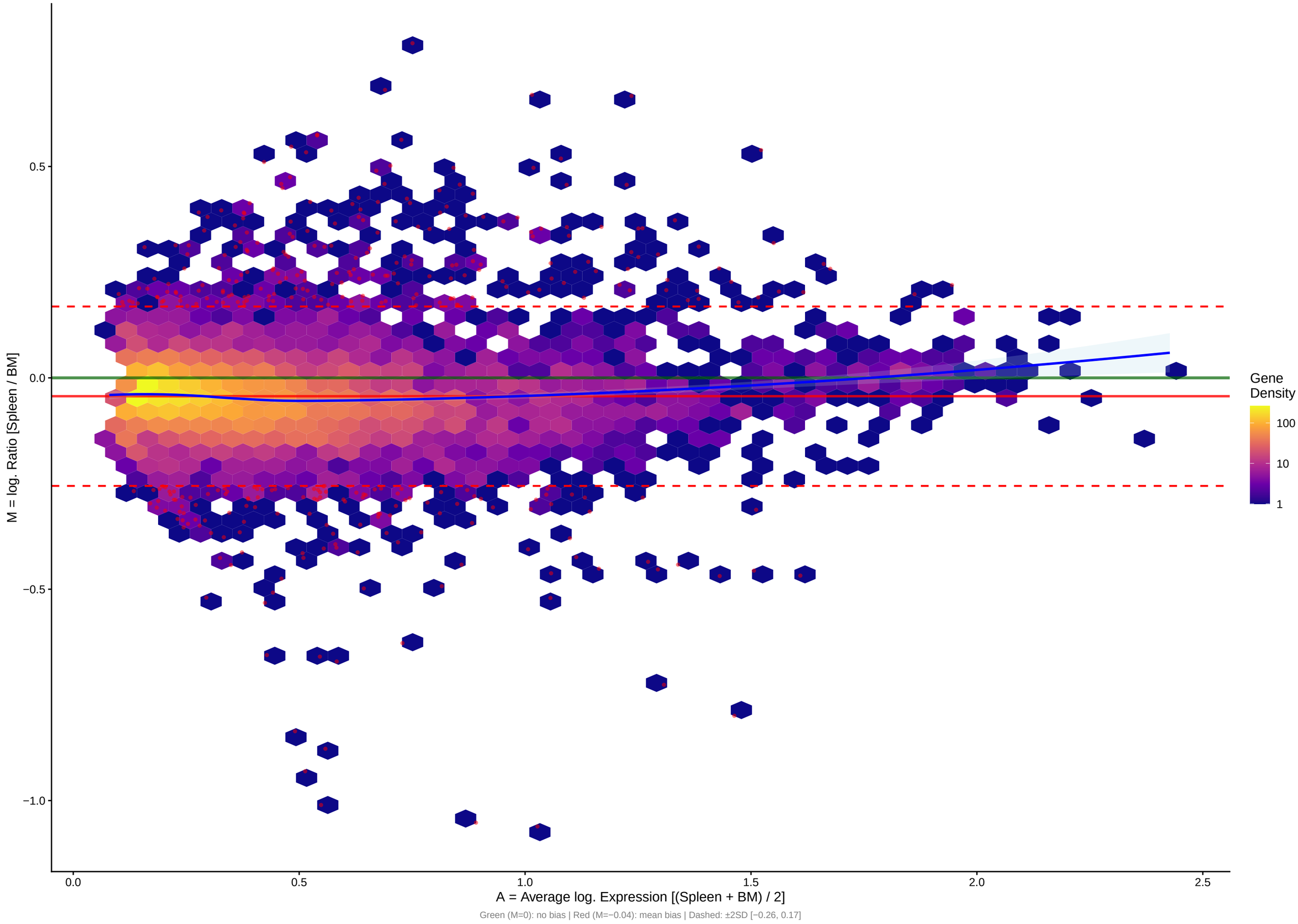
Do genes have similar expression in both tissues?



Red: perfect correlation (x=y) | Blue: regression | r > 0.8 = comparable

MA Plot − Monocytes

Systematic bias detection



Green (M=0): no bias | Red (M=−0.04): mean bias | Dashed: ±2SD [−0.26, 0.17]

M.0 = no bias | M>0 = Spleen higher | M<0 = BM higher