Visualization methods for RNA-sequencing data analysis



Presenter: Lindsay Rutter

Advisor: Dr. Dianne Cook

Graduate and Professional Student Research Conference






GENE 1	96	75	32	56	12	6
GENE 2	40	33	37	70	60	20
GENE 3	100	57	40	72	43	79
GENE 4	150	146	152	8	4	12
GENE 5	37	6	37	35	37	28
GENE 6	99	48	63	14	81	79
GENE 7	10	88	42	63	7	2
GENE 8	6	9	52	39	39	37
GENE 9	75	52	58	64	99	81
GENE 10	36	75	57	14	94	92
GENE 11	13	78	30	50	19	49
GENE 12	27	39	89	44	43	42
GENE 13	34	68	22	95	26	53
GENE 14	0	1	2	50	46	51
GENE 15	16	43	11	82	3	95
...	...	...	...	...	...	...

Healthy

H.1 H.2 H.3






GENE 1	96	75	32	56	12	6
GENE 2	40	33	37	70	60	20
GENE 3	100	57	40	72	43	79
GENE 4	150	146	152	8	4	12
GENE 5	37	6	37	35	37	28
GENE 6	99	48	63	14	81	79
GENE 7	10	88	42	63	7	2
GENE 8	6	9	52	39	39	37
GENE 9	75	52	58	64	99	81
GENE 10	36	75	57	14	94	92
GENE 11	13	78	30	50	19	49
GENE 12	27	39	89	44	43	42
GENE 13	34	68	22	95	26	53
GENE 14	0	1	2	50	46	51
GENE 15	16	43	11	82	3	95
...	...	...	...	...	...	...

	Healthy			Unhealthy		
	H.1	H.2	H.3	U.1	U.2	U.3
						
GENE 1	96	75	32	56	12	6
GENE 2	40	33	37	70	60	20
GENE 3	100	57	40	72	43	79
GENE 4	150	146	152	8	4	12
GENE 5	37	6	37	35	37	28
GENE 6	99	48	63	14	81	79
GENE 7	10	88	42	63	7	2
GENE 8	6	9	52	39	39	37
GENE 9	75	52	58	64	99	81
GENE 10	36	75	57	14	94	92
GENE 11	13	78	30	50	19	49
GENE 12	27	39	89	44	43	42
GENE 13	34	68	22	95	26	53
GENE 14	0	1	2	50	46	51
GENE 15	16	43	11	82	3	95
...	...	...	...	...	...	...

	Healthy			Unhealthy		
	H.1	H.2	H.3	U.1	U.2	U.3
						
GENE 1	96	75	32	56	12	6
GENE 2	40	33	37	70	60	20
GENE 3	100	57	40	72	43	79
GENE 4	150	146	152	8	4	12
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GENE 6	99	48	63	14	81	79
GENE 7	10	88	42	63	7	2
GENE 8	6	9	52	39	39	37
GENE 9	75	52	58	64	99	81
GENE 10	36	75	57	14	94	92
GENE 11	13	78	30	50	19	49
GENE 12	27	39	89	44	43	42
GENE 13	34	68	22	95	26	53
GENE 14	0	1	2	50	46	51
GENE 15	16	43	11	82	3	95
...	...	...	...	...	...	...

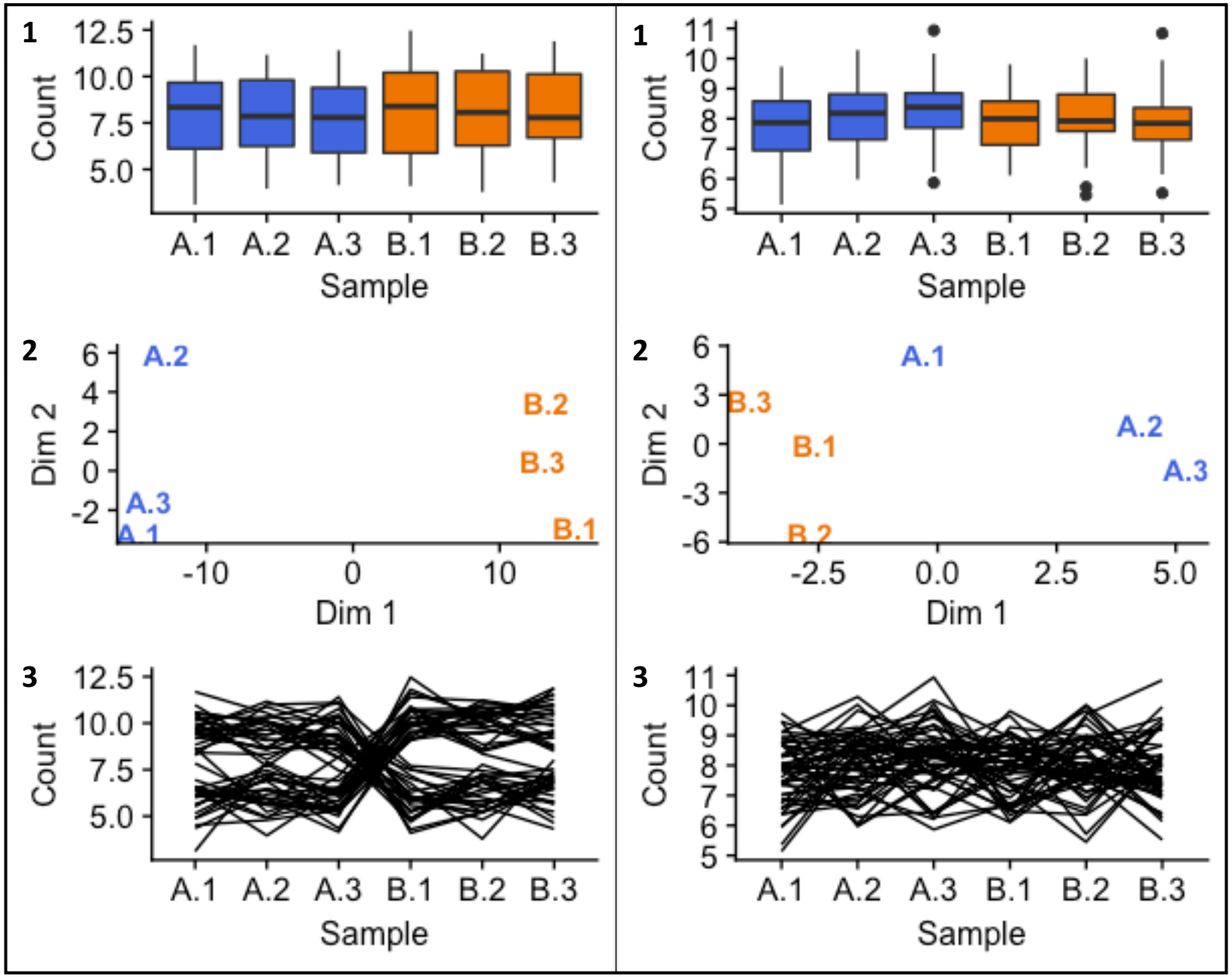
DEGs

(Differentially Expressed Genes)

Healthy

Unhealthy

GENE 1	96	75	32	56	12	6
GENE 2	40	33	37	70	60	20
GENE 3	100	57	40	72	43	79
GENE 4	150	146	152	8	4	12
GENE 5	37	6	37	35	37	28
GENE 6	99	48	63	14	81	79
GENE 7	10	88	42	63	7	2
GENE 8	6	9	52	39	39	37
GENE 9	75	52	58	64	99	81
GENE 10	36	75	57	14	94	92
GENE 11	13	78	30	50	19	49
GENE 12	27	39	89	44	43	42
GENE 13	34	68	22	95	26	53
GENE 14	0	1	2	50	46	51
GENE 15	16	43	11	82	3	95
...	...	...	...	...	...	...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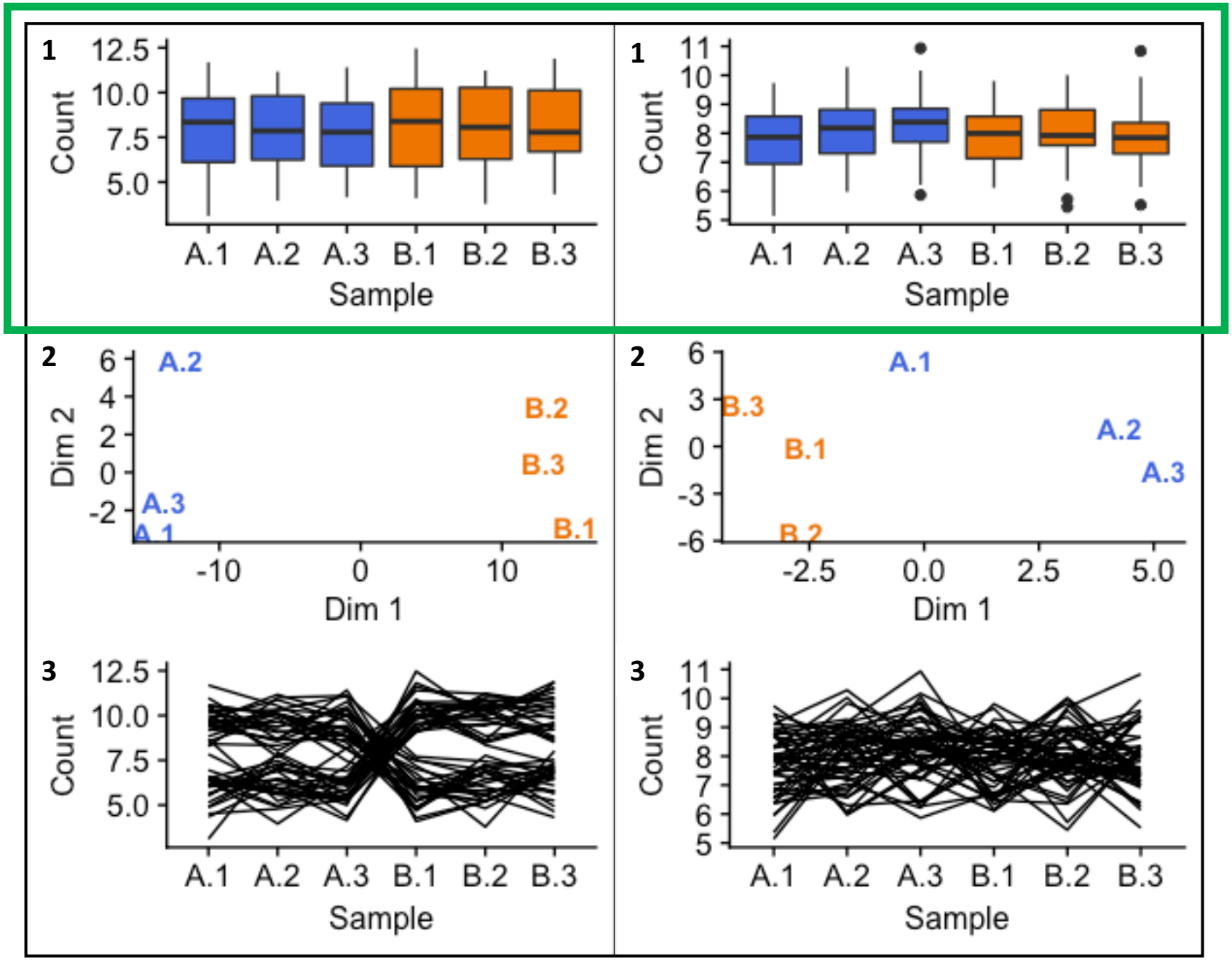
Count
12.5
10.0
7.5
5.0
A.1 A.2 A.3 B.1 B.2 B.3
Sample
1
Count
11
10
9
8
7
6
5
A.1 A.2 A.3 B.1 B.2 B.3
Sample
2
Dim 2
6
4
2
0
-2
A.2
B.2
B.3
A.3
A.1
B.1
-10 0 10
Dim 1
2
Dim 2
6
3
0
-3
-6
A.1
B.3
B.1
A.2
A.3
B.2
-2.5 0.0 2.5 5.0
Dim 1
3
Count
12.5
10.0
7.5
5.0
A.1 A.2 A.3 B.1 B.2 B.3
Sample
3
Count
11
10
9
8
7
6
5
A.1 A.2 A.3 B.1 B.2 B.3
Sample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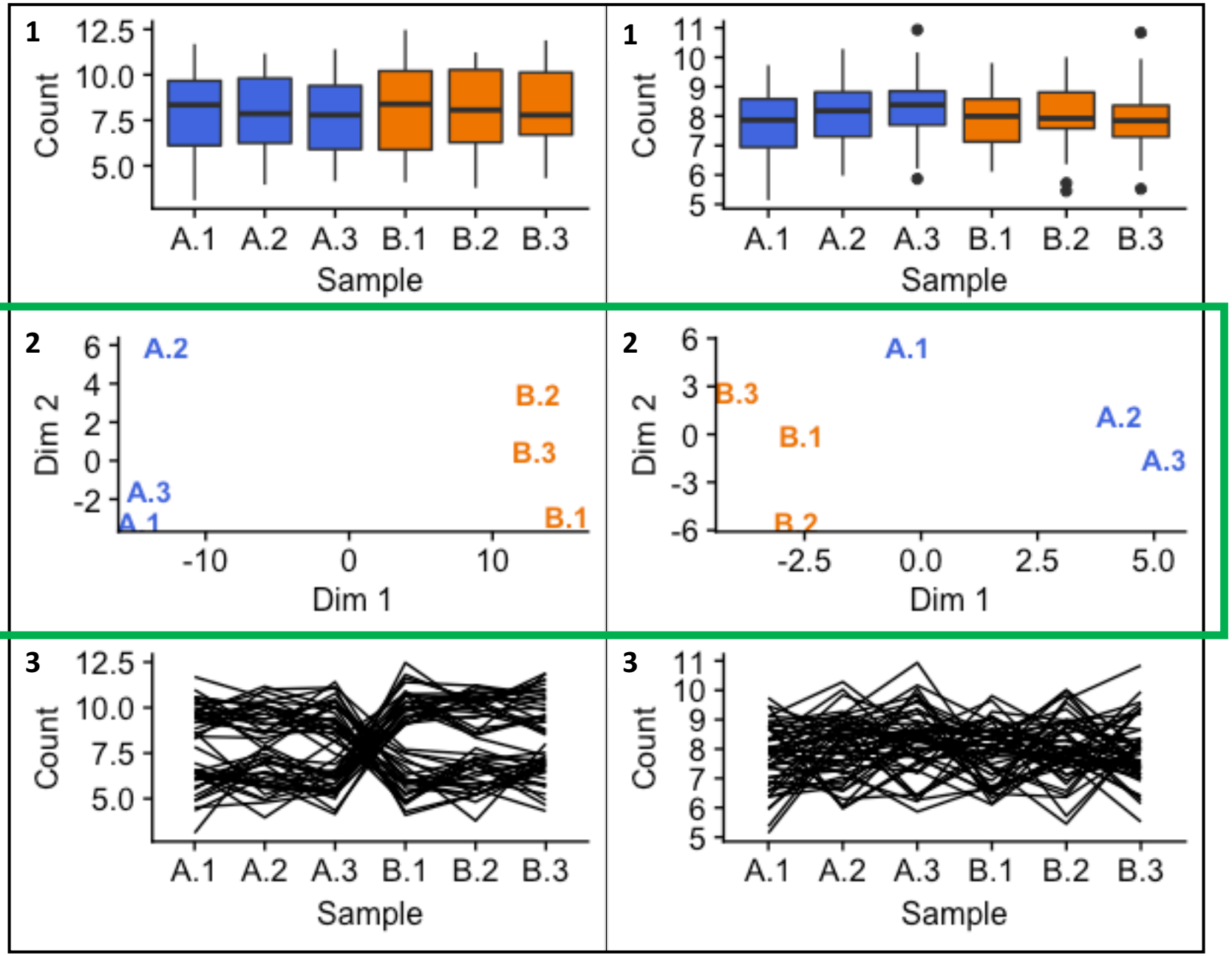
Count
12.5
10.0
7.5
5.0
A.1 A.2 A.3 B.1 B.2 B.3
Sample
1
Count
11
10
9
8
7
6
5
A.1 A.2 A.3 B.1 B.2 B.3
Sample
2
Dim 2
6
4
2
0
-2
A.2
B.2
B.3
A.3
A.1
B.1
-10 0 10
Dim 1
2
Dim 2
6
3
0
-3
-6
A.1
B.3
B.1
A.2
A.3
B.2
-2.5 0.0 2.5 5.0
Dim 1
3
Count
12.5
10.0
7.5
5.0
A.1 A.2 A.3 B.1 B.2 B.3
Sample
3
Count
11
10
9
8
7
6
5
A.1 A.2 A.3 B.1 B.2 B.3
Sample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Count
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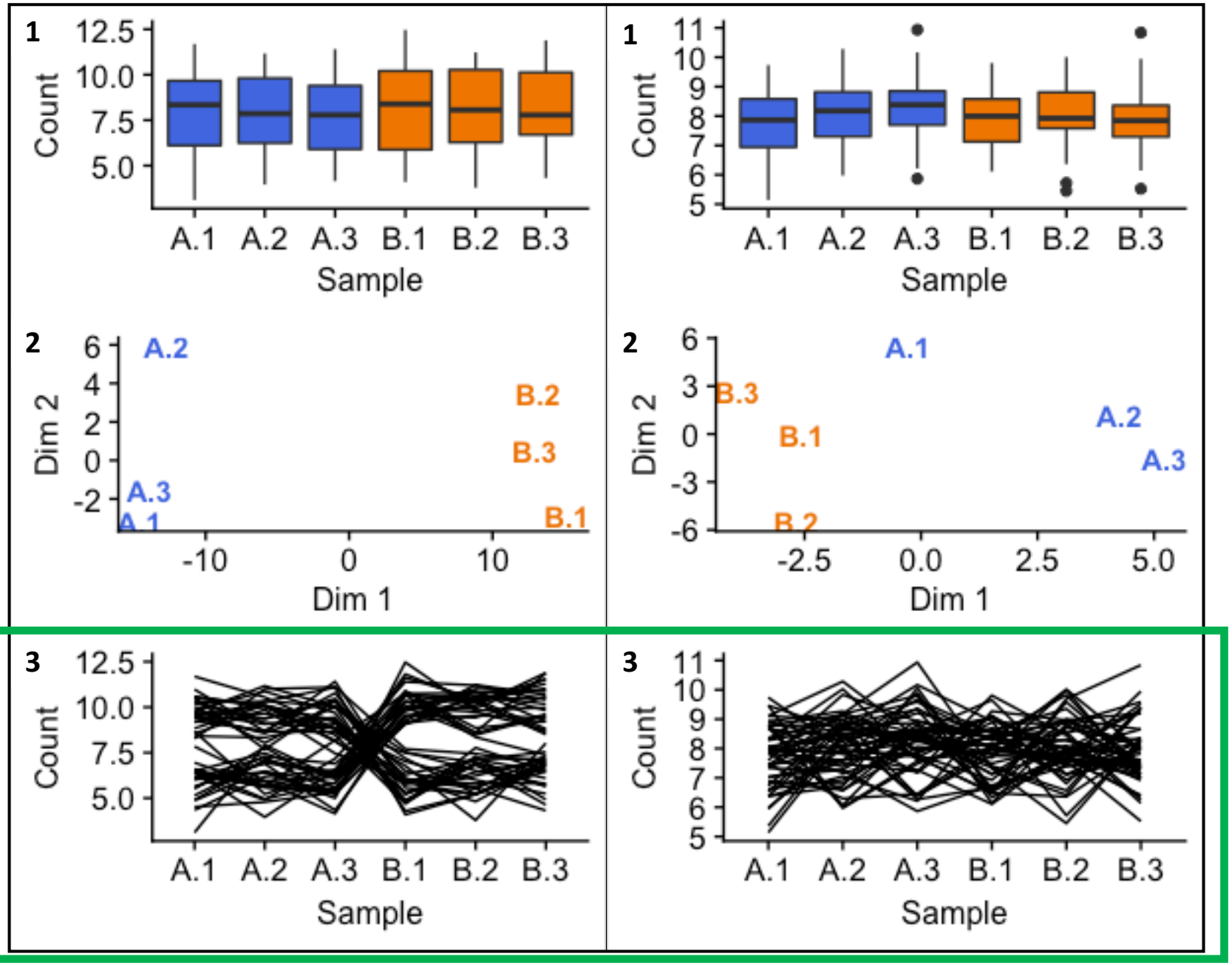
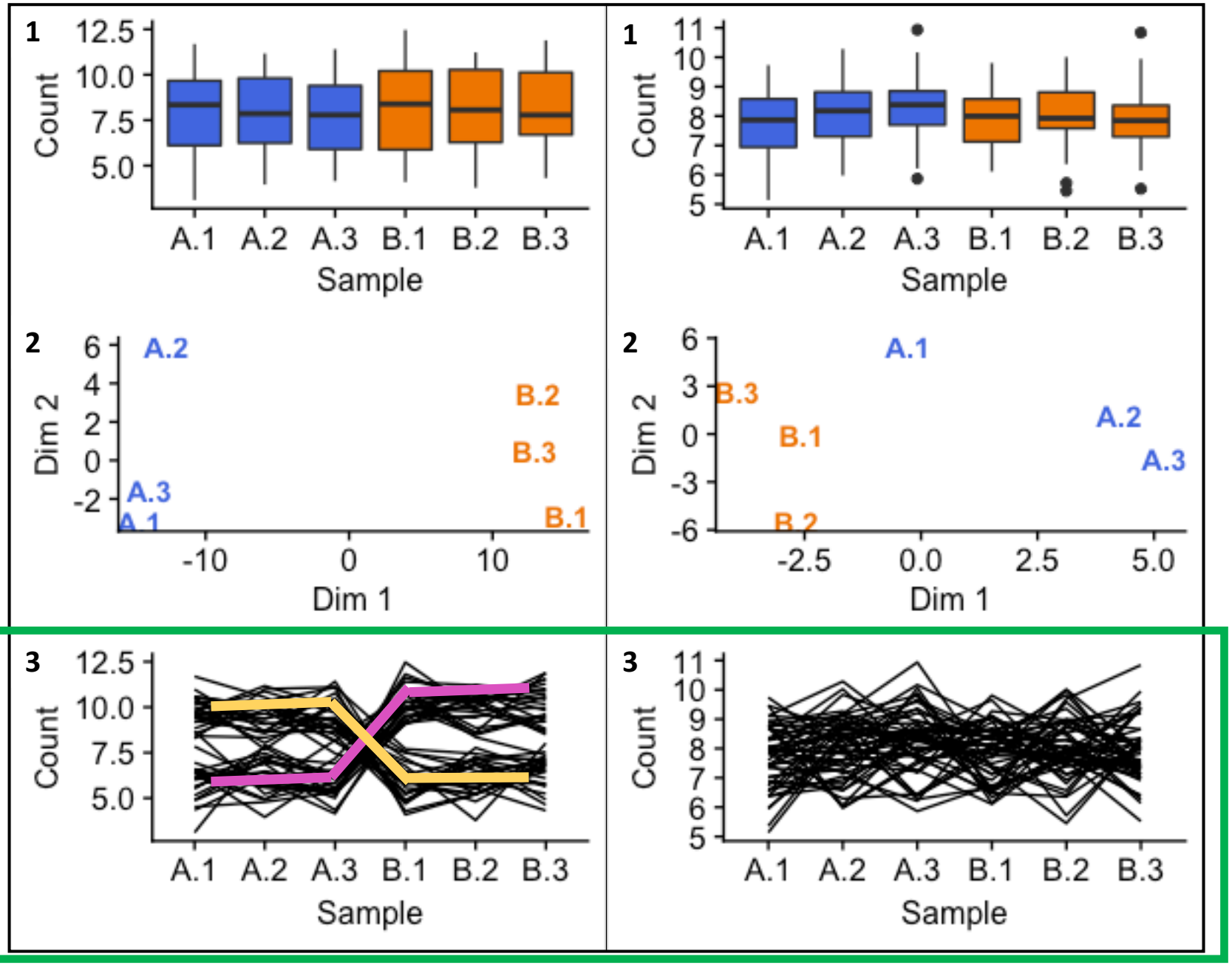
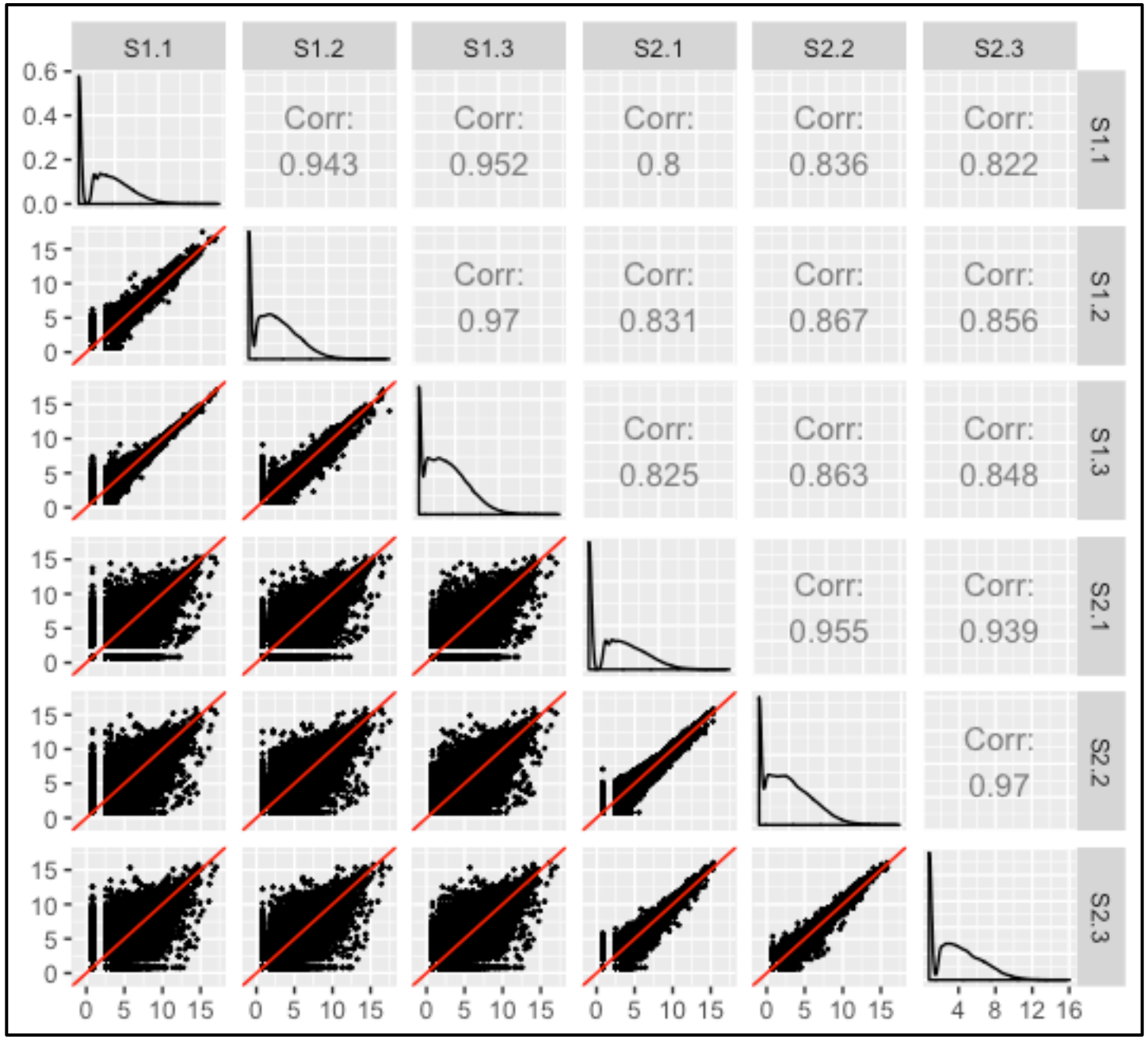
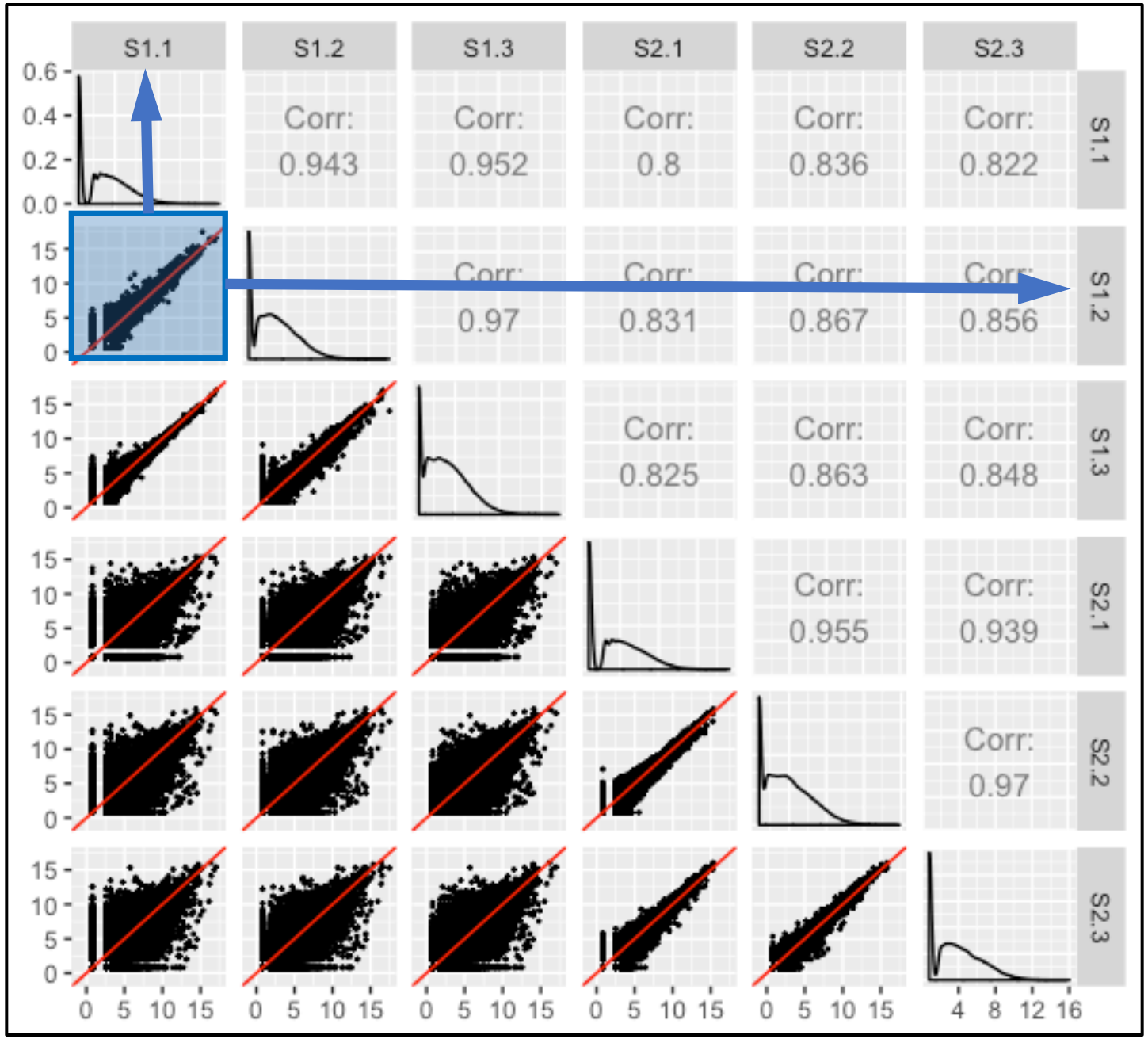
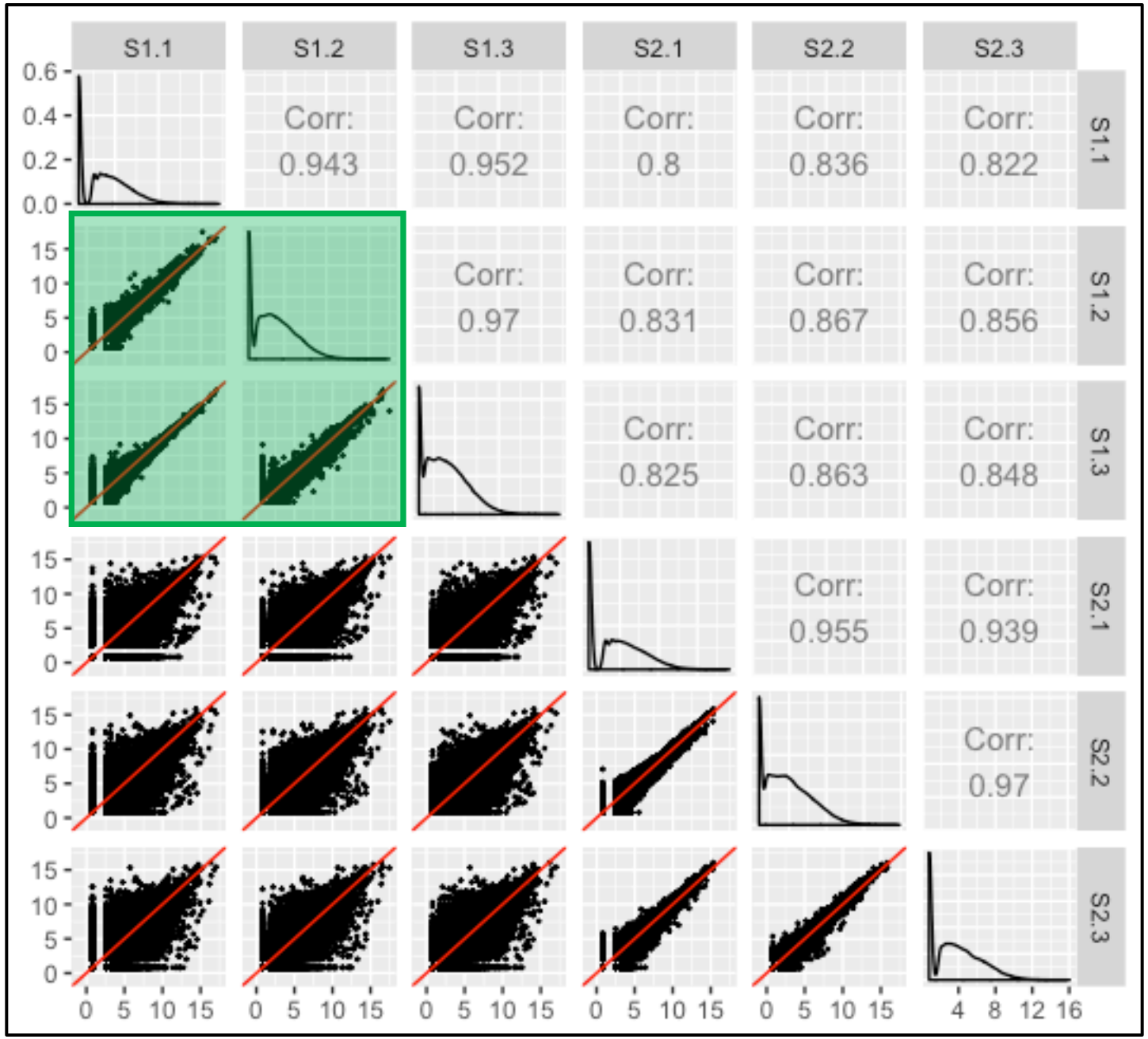
10.0
7.5
5.0
A.1 A.2 A.3 B.1 B.2 B.3
Sample
1
Count
11
10
9
8
7
6
5
A.1 A.2 A.3 B.1 B.2 B.3
Sample
2
Dim 2
6
4
2
0
-2
A.2
B.2
B.3
A.3
A.1
B.1
-10 0 10
Dim 1
2
Dim 2
6
3
0
-3
-6
A.1
B.3
B.1
A.2
A.3
B.2
-2.5 0.0 2.5 5.0
Dim 1
3
Count
12.5
10.0
7.5
5.0
A.1 A.2 A.3 B.1 B.2 B.3
Sample
3
Count
11
10
9
8
7
6
5
A.1 A.2 A.3 B.1 B.2 B.3
Sample

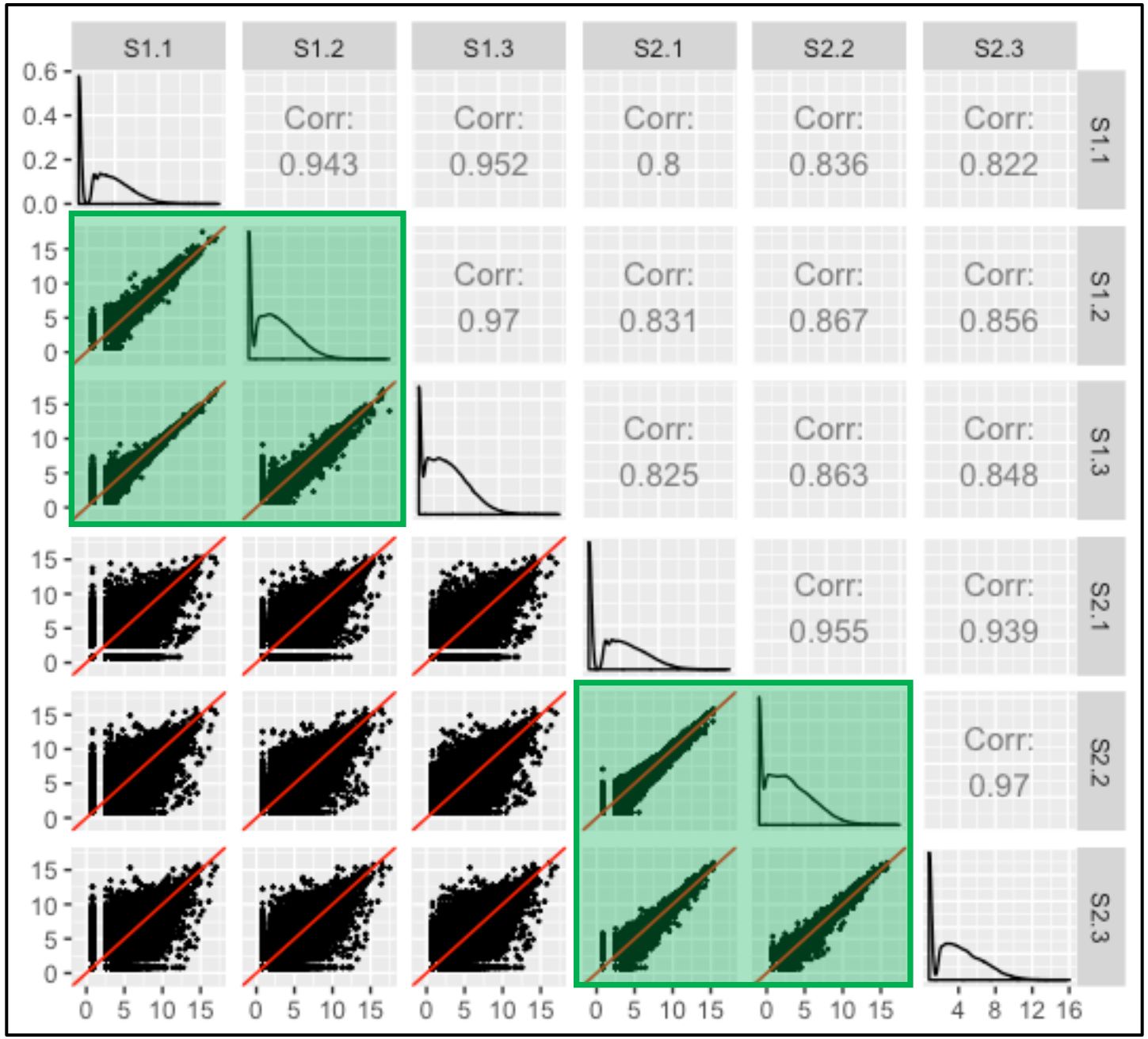

1
Count
12.5
10.0
7.5
5.0
A.1 A.2 A.3 B.1 B.2 B.3
Sample
1
Count
11
10
9
8
7
6
5
A.1 A.2 A.3 B.1 B.2 B.3
Sample
2
Dim 2
6
4
2
0
-2
A.2
B.2
B.3
A.3
A.1
B.1
-10 0 10
Dim 1
2
Dim 2
6
3
0
-3
-6
A.1
B.3
B.1
A.2
A.3
B.2
-2.5 0.0 2.5 5.0
Dim 1
3
Count
12.5
10.0
7.5
5.0
A.1 A.2 A.3 B.1 B.2 B.3
Sample
3
Count
11
10
9
8
7
6
5
A.1 A.2 A.3 B.1 B.2 B.3
Sample

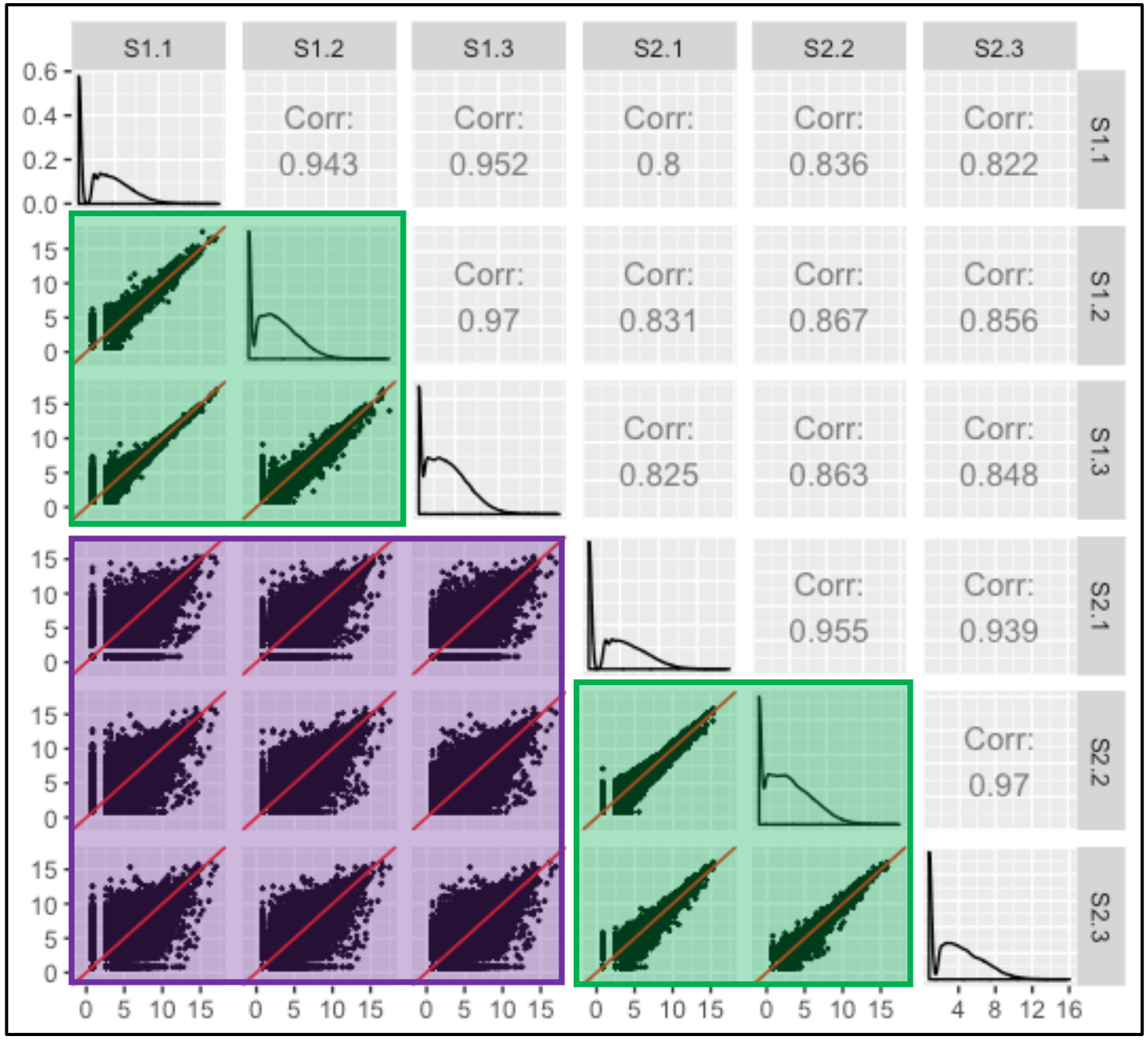

1
Count
12.5
10.0
7.5
5.0
A.1 A.2 A.3 B.1 B.2 B.3
Sample
1
Count
11
10
9
8
7
6
5
A.1 A.2 A.3 B.1 B.2 B.3
Sample
2
Dim 2
6
4
2
0
-2
A.2
B.2
B.3
A.3
A.1
B.1
-10
0
10
Dim 1
2
Dim 2
6
3
0
-3
-6
A.1
B.3
B.1
A.2
A.3
B.2
-2.5
0.0
2.5
5.0
Dim 1
3
Count
12.5
10.0
7.5
5.0
A.1 A.2 A.3 B.1 B.2 B.3
Sample
3
Count
11
10
9
8
7
6
5
A.1 A.2 A.3 B.1 B.2 B.3
Sample

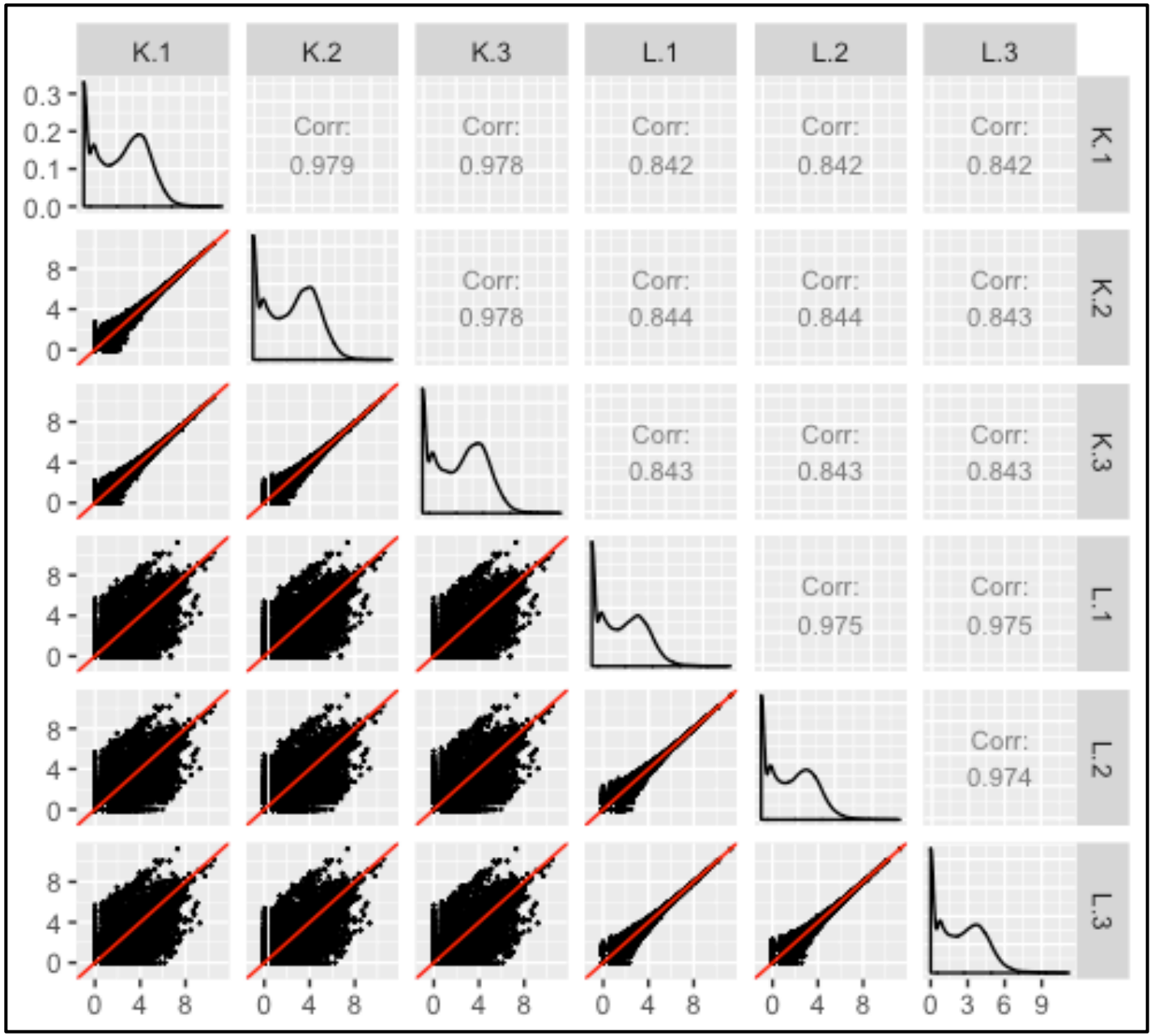

S1.1
S1.2
S1.3
S2.1
S2.2
S2.3
Corr: 0.943
Corr: 0.952
Corr: 0.8
Corr: 0.836
Corr: 0.822
Corr: 0.97
Corr: 0.831
Corr: 0.867
Corr: 0.856
Corr: 0.825
Corr: 0.863
Corr: 0.848
Corr: 0.955
Corr: 0.939
Corr: 0.97
0.6
0.4
0.2
0.0
15
10
5
0
0 5 10 15
4 8 12 16


S1.1
S1.2
S1.3
S2.1
S2.2
S2.3
Corr: 0.943
Corr: 0.952
Corr: 0.8
Corr: 0.836
Corr: 0.822
Corr: 0.97
Corr: 0.831
Corr: 0.867
Corr: 0.856
Corr: 0.825
Corr: 0.863
Corr: 0.848
Corr: 0.955
Corr: 0.939
Corr: 0.97
0.6
0.4
0.2
0.0
15
10
5
0
0 5 10 15
4 8 12 16

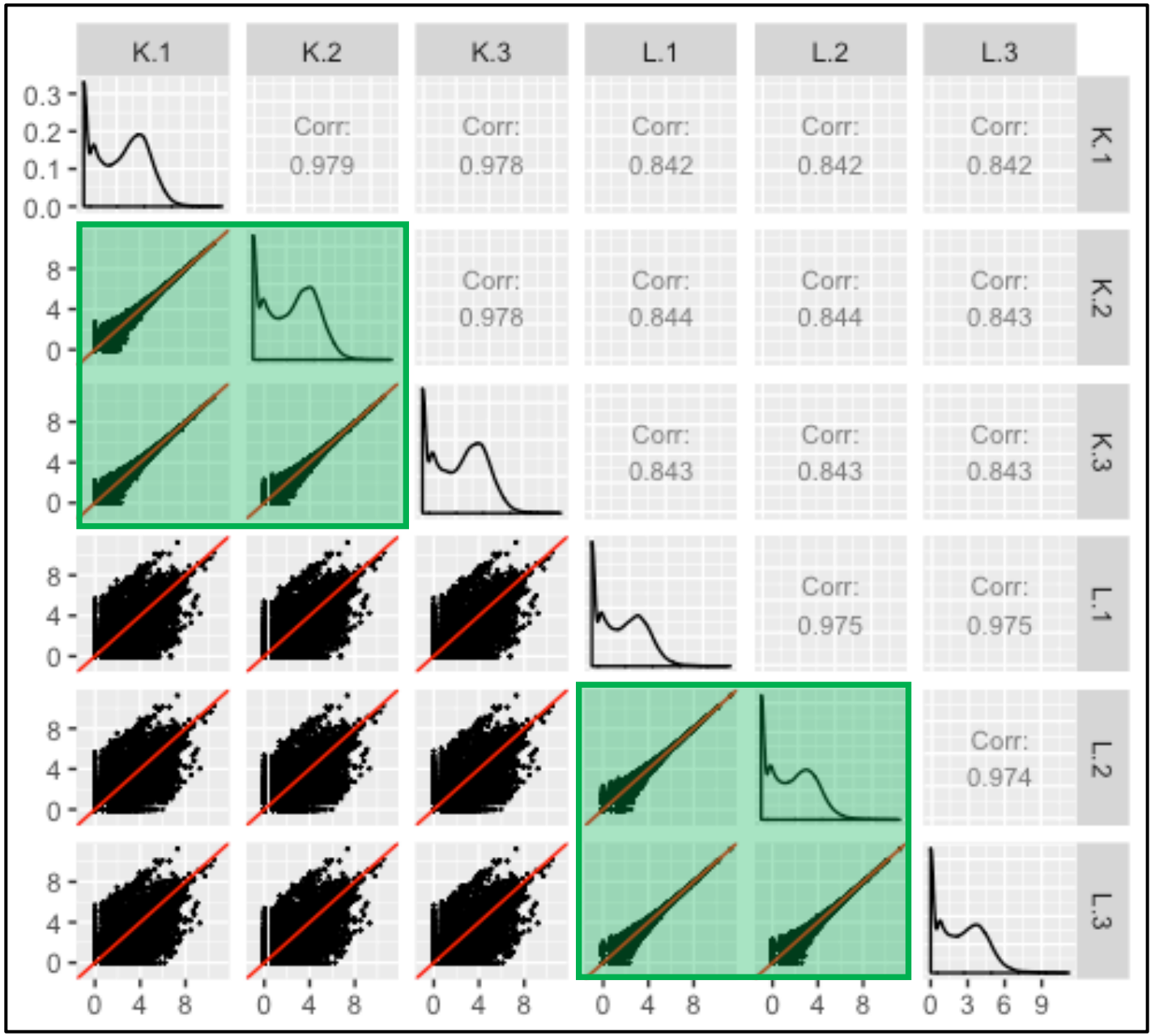

S1.1
S1.2
S1.3
S2.1
S2.2
S2.3
Corr: 0.943
Corr: 0.952
Corr: 0.8
Corr: 0.836
Corr: 0.822
Corr: 0.97
Corr: 0.831
Corr: 0.867
Corr: 0.856
Corr: 0.825
Corr: 0.863
Corr: 0.848
Corr: 0.955
Corr: 0.939
Corr: 0.97
0.6
0.4
0.2
0.0
15
10
5
0
0 5 10 15
4 8 12 16


S1.1
S1.2
S1.3
S2.1
S2.2
S2.3
Corr: 0.943
Corr: 0.952
Corr: 0.8
Corr: 0.836
Corr: 0.822
Corr: 0.97
Corr: 0.831
Corr: 0.867
Corr: 0.856
Corr: 0.825
Corr: 0.863
Corr: 0.848
Corr: 0.955
Corr: 0.939
Corr: 0.97
0.6
0.4
0.2
0.0
15
10
5
0
0 5 10 15
4 8 12 16


S1.1
S1.2
S1.3
S2.1
S2.2
S2.3
Corr: 0.943
Corr: 0.952
Corr: 0.8
Corr: 0.836
Corr: 0.822
Corr: 0.97
Corr: 0.831
Corr: 0.867
Corr: 0.856
Corr: 0.825
Corr: 0.863
Corr: 0.848
Corr: 0.955
Corr: 0.939
Corr: 0.97
0.0
0.2
0.4
0.6
0
5
10
15
4
8
12
16



Marioni, J.C., Mason, C.E., Mane, S.M., Stephens, M., and Gilad, Y. (2008) RNA-seq: An assessment of technical reproducibility and comparison with gene expression arrays. *Genome Research*, **18**, 1509–1517.



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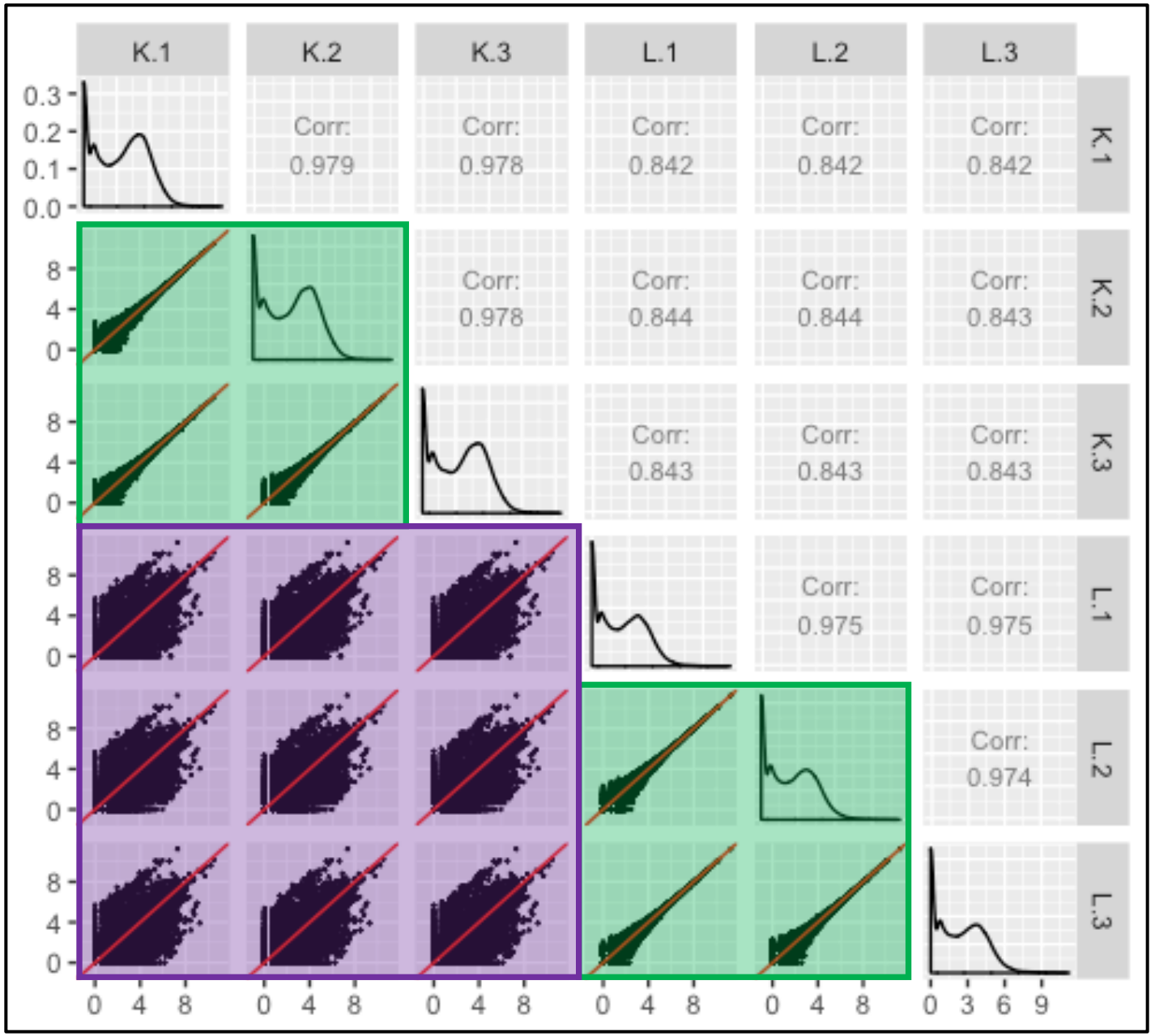
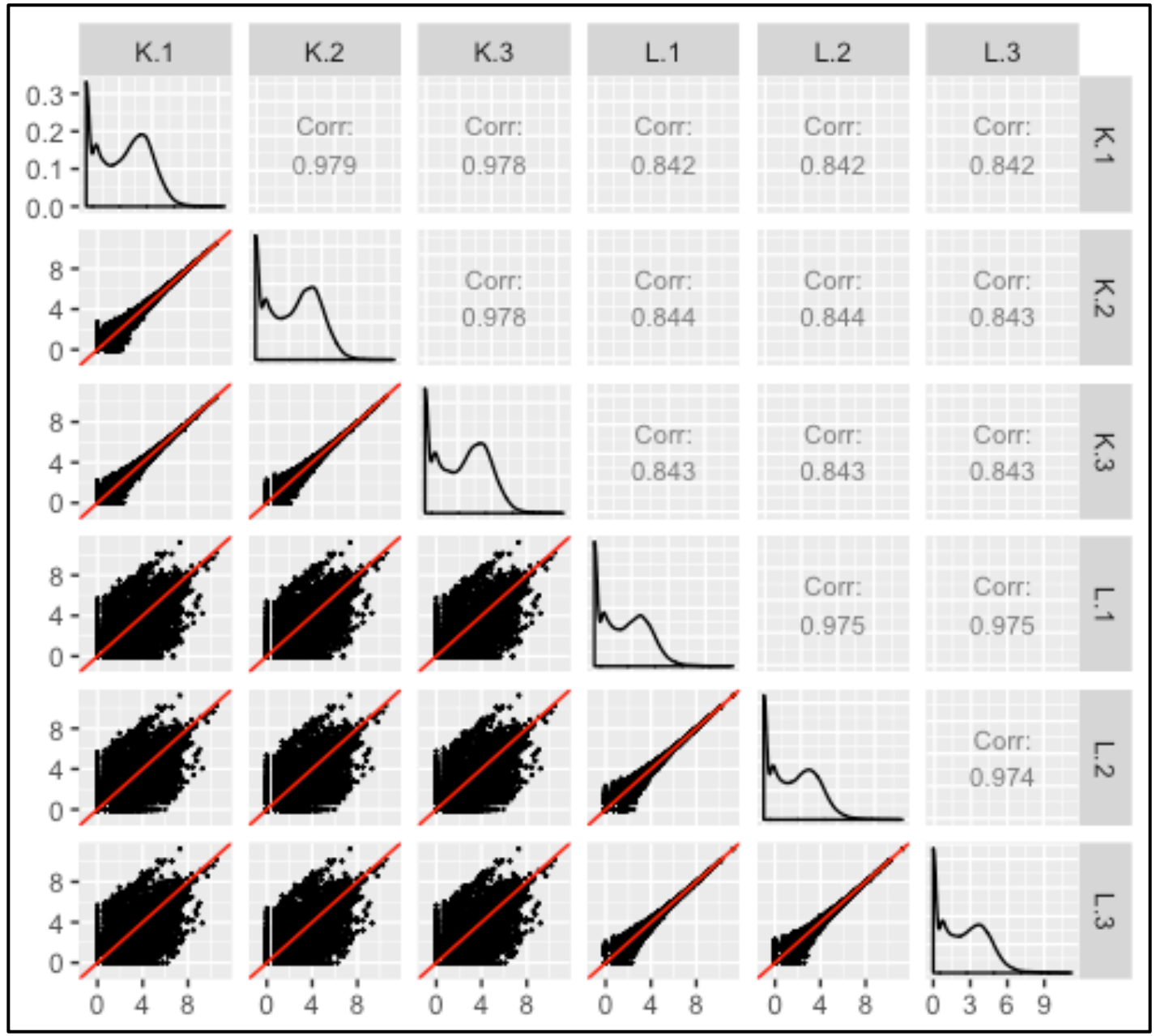
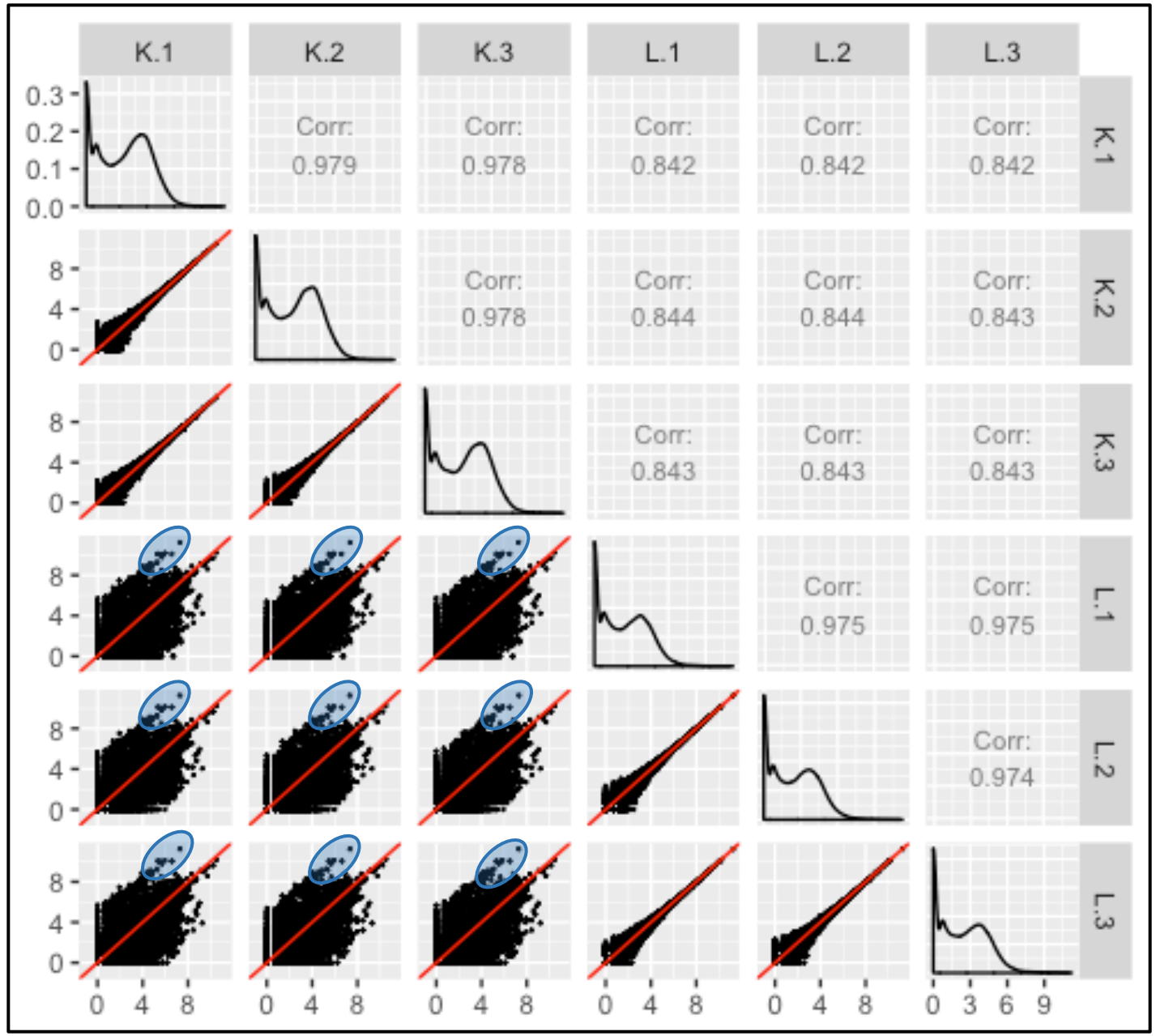
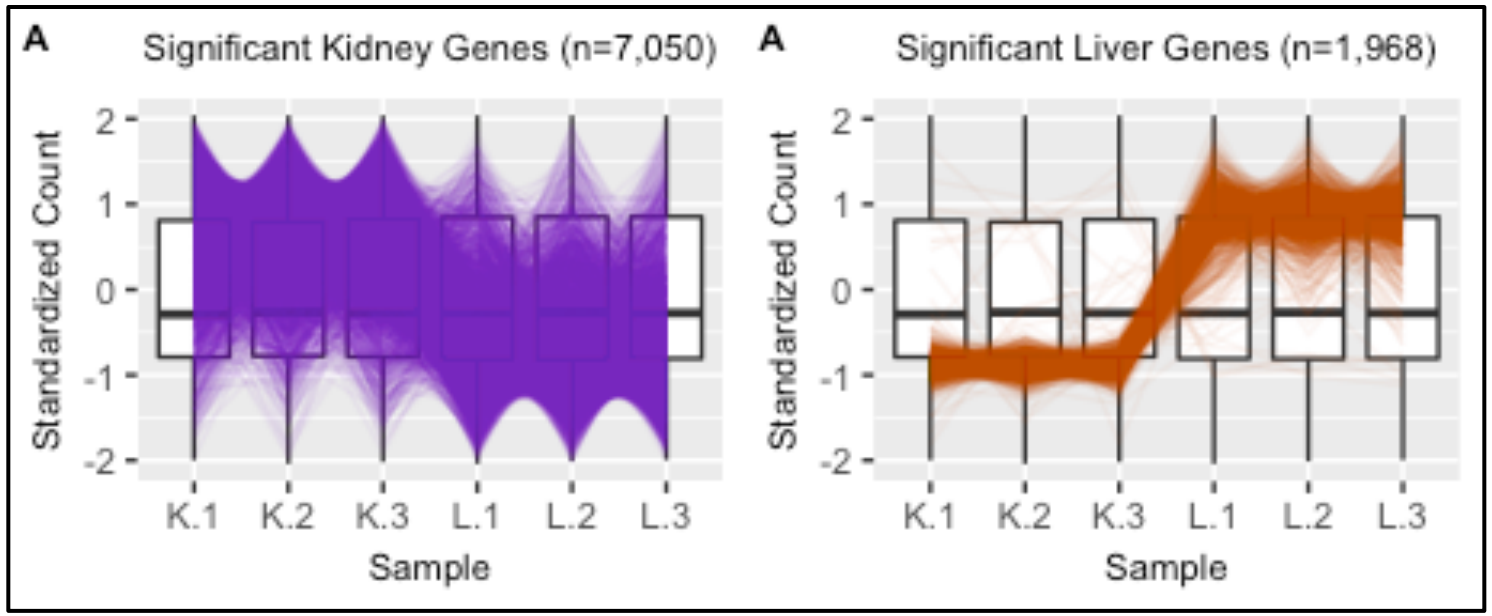


Marioni, J.C., Mason, C.E., Mane, S.M., Stephens, M., and Gilad, Y. (2008) RNA-seq: An assessment of technical reproducibility and comparison with gene expression arrays. *Genome Research*, **18**, 1509–1517.


K.1
K.2
K.3
L.1
L.2
L.3
Corr: 0.979
Corr: 0.978
Corr: 0.842
Corr: 0.842
Corr: 0.842
Corr: 0.978
Corr: 0.844
Corr: 0.844
Corr: 0.843
Corr: 0.843
Corr: 0.843
Corr: 0.843
Corr: 0.975
Corr: 0.975
Corr: 0.974
0.3
0.2
0.1
0.0
8
4
0
0 4 8
0 3 6 9

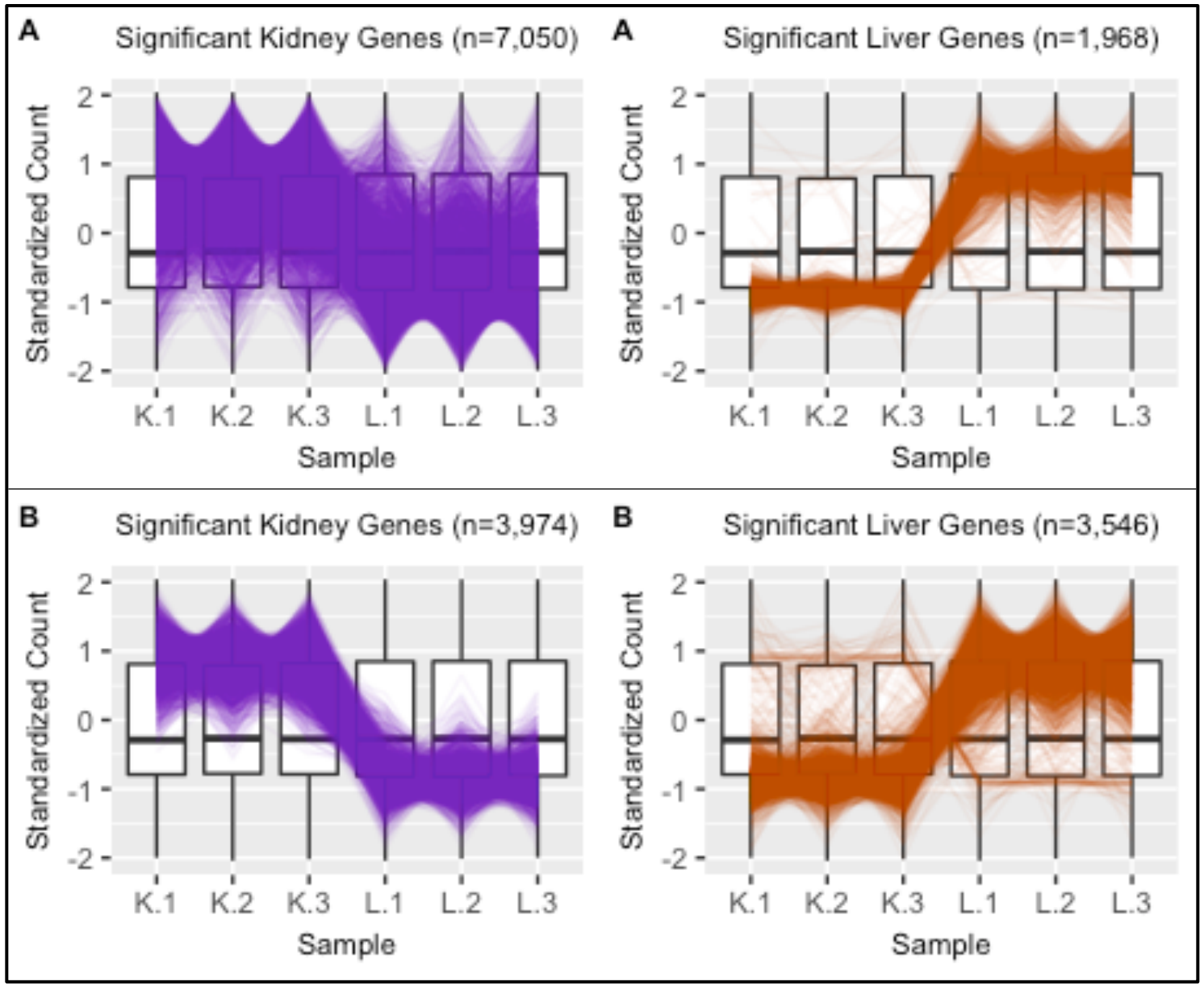

K.1
K.2
K.3
L.1
L.2
L.3
Corr: 0.979
Corr: 0.978
Corr: 0.842
Corr: 0.842
Corr: 0.842
Corr: 0.978
Corr: 0.844
Corr: 0.844
Corr: 0.843
Corr: 0.843
Corr: 0.843
Corr: 0.843
Corr: 0.975
Corr: 0.975
Corr: 0.974
0.3
0.2
0.1
0.0
8
4
0
0 4 8
0 3 6 9

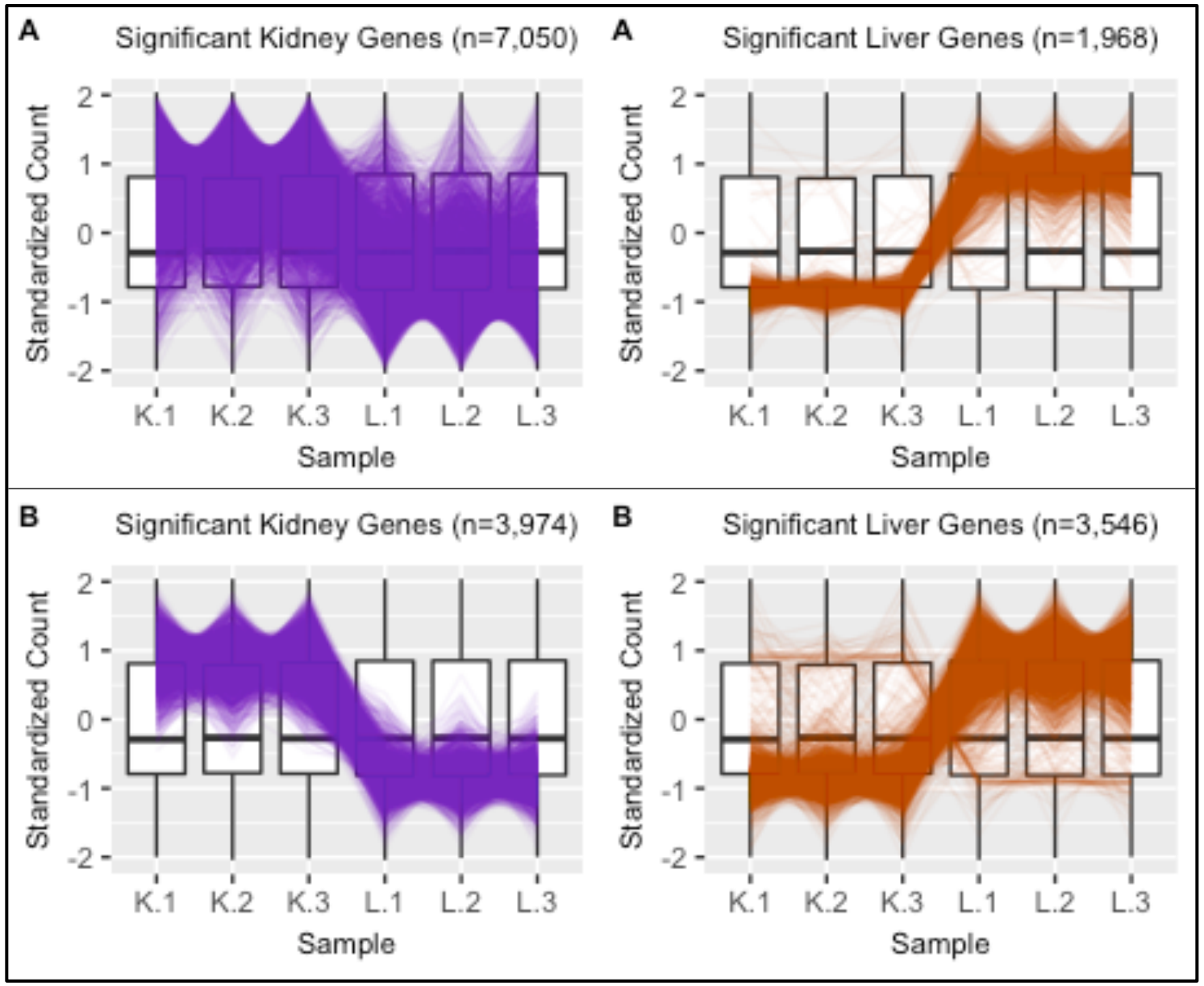
Library Lane Normalization



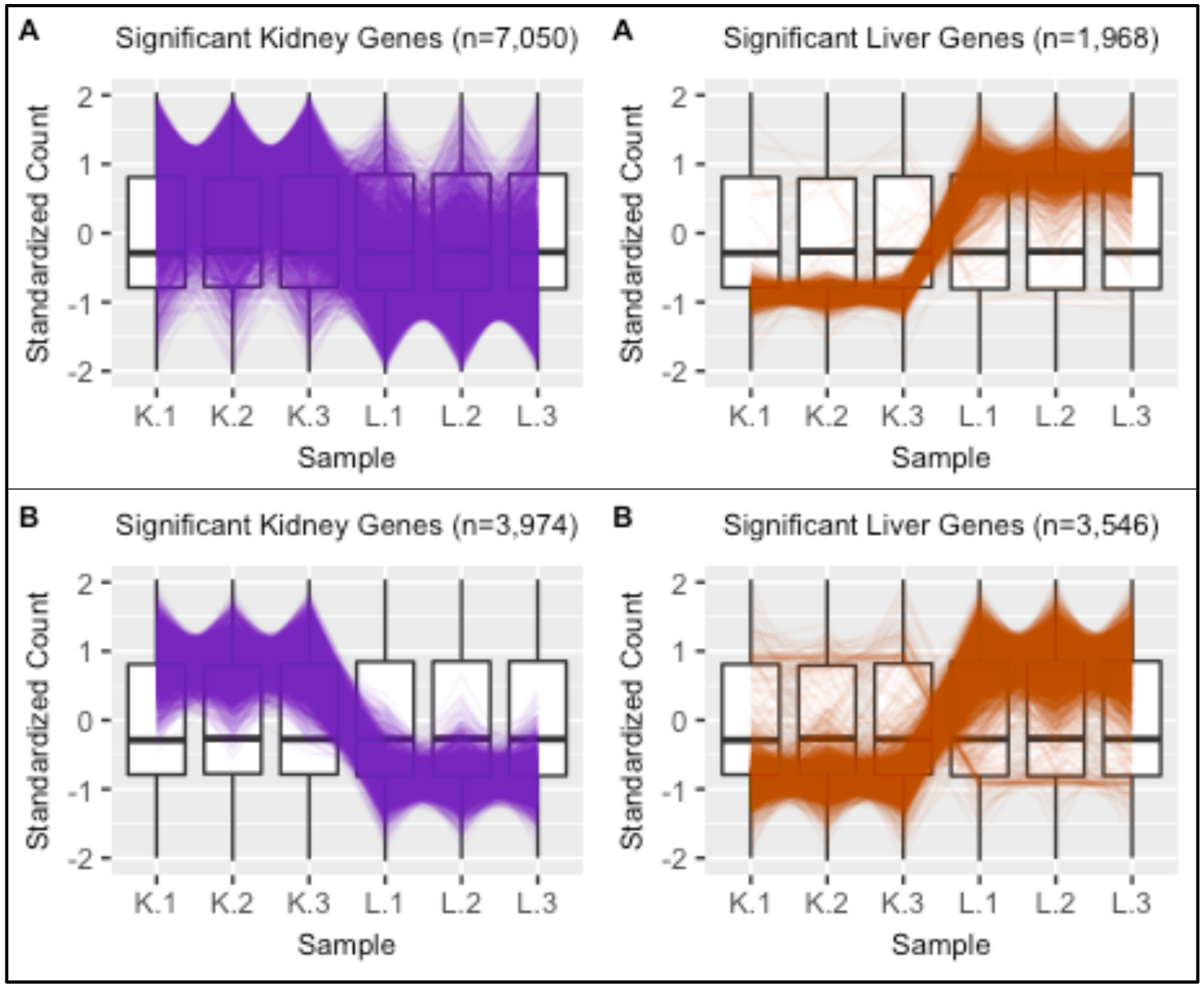
Library Lane Normalization

Trimmed Mean Normalization





Kept Kidney DEGs
(n = 3,974)

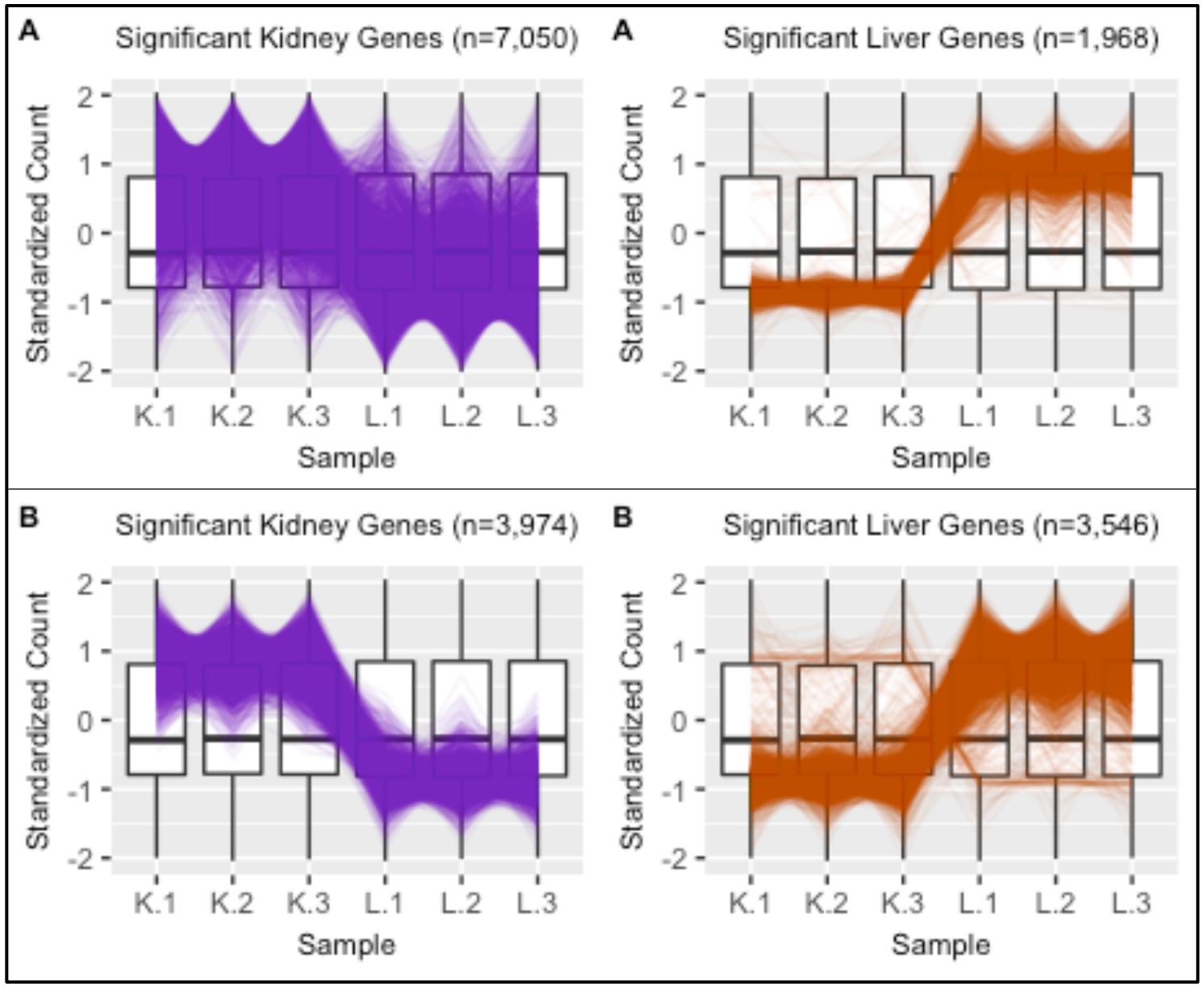


Kept Kidney DEGs
(n = 3,974)

Original Liver DEGs
(n = 1,968)

Removed Kidney DEGs
(n = 3,076)

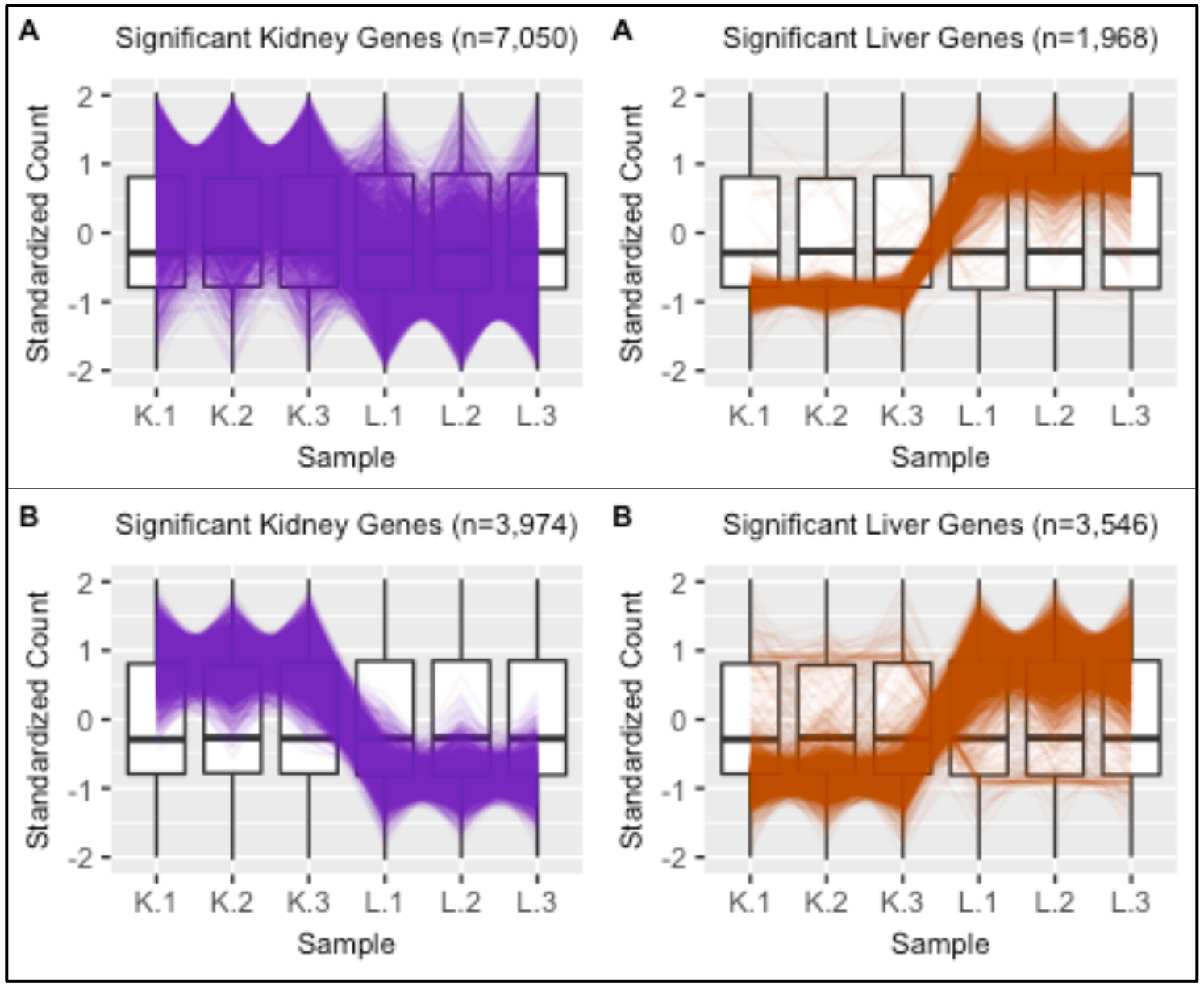
Kept Kidney DEGs
(n = 3,974)



Original Liver DEGs
(n = 1,968)

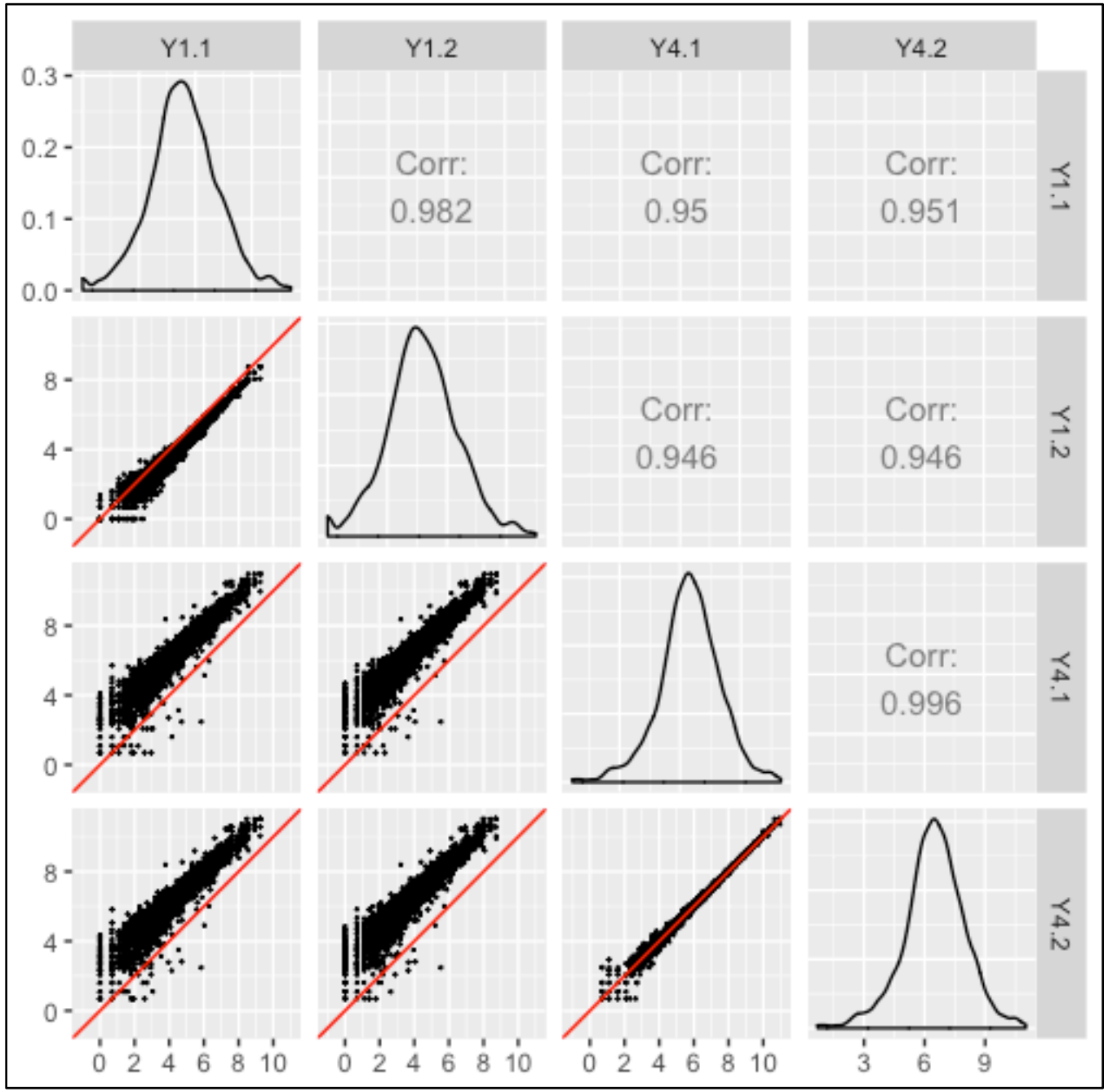
Removed Kidney DEGs
(n = 3,076)

Kept Kidney DEGs
(n = 3,974)

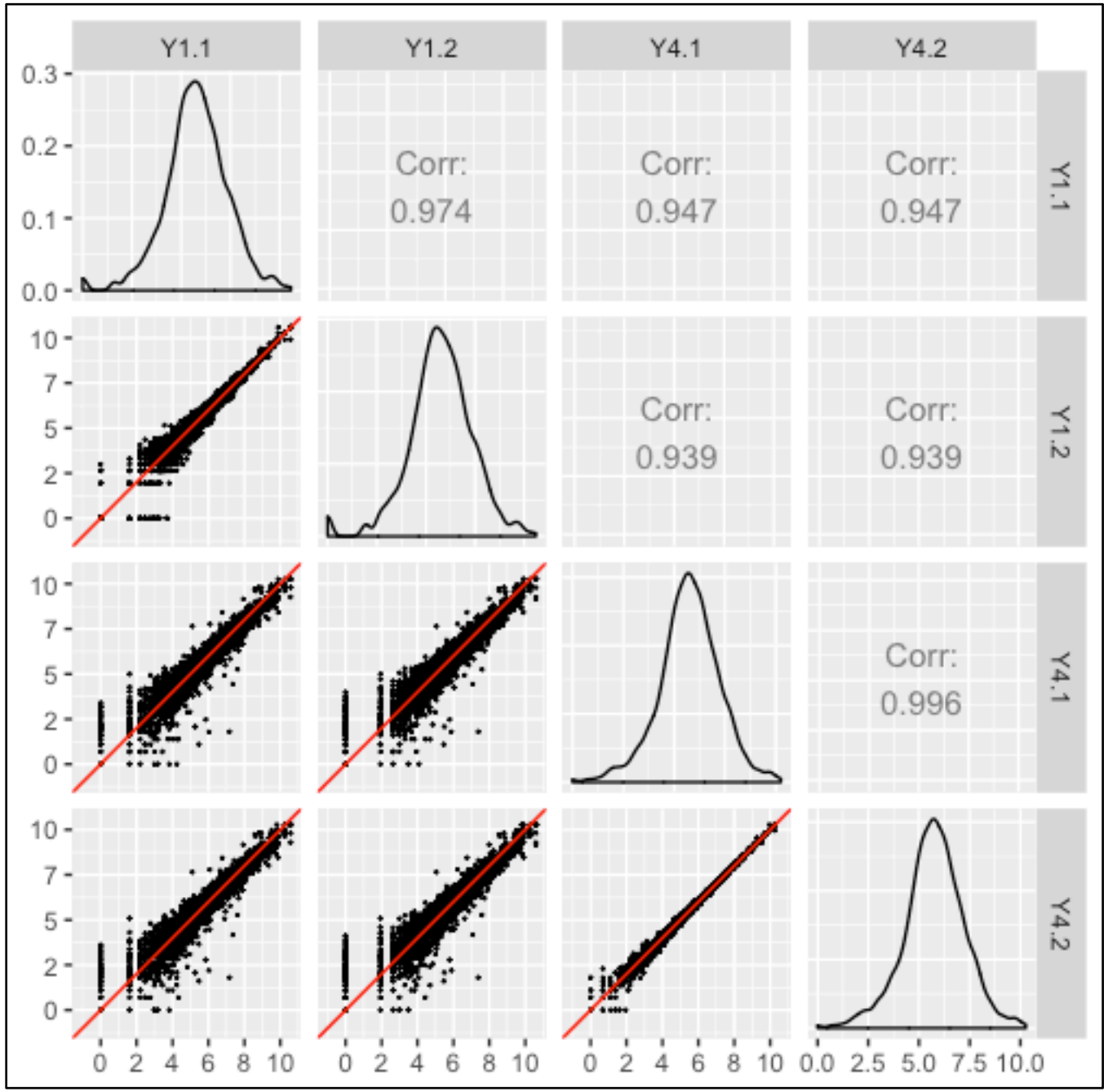


Original Liver DEGs
(n = 1,968)

Added Liver DEGs
(n = 1,578)



Within Lane Normalization



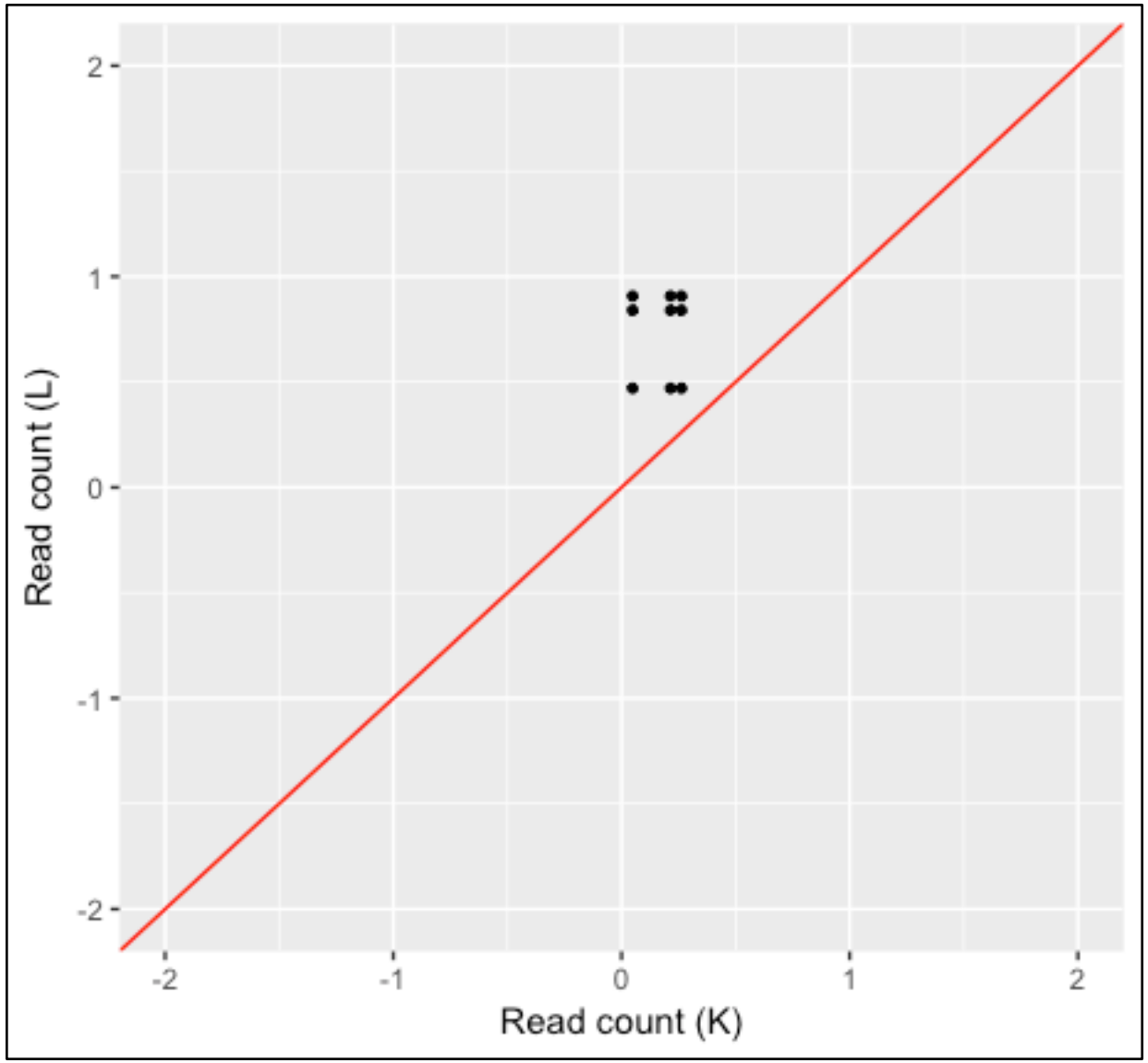
Within and Between Lane Normalization

repLIcate TREatment ("litre") plot

	L1	L2	L3
K1	K1, L1	K1, L2	K1, L3
K2	K2, L1	K2, L2	K2, L3
K3	K3, L1	K3, L2	K3, L3

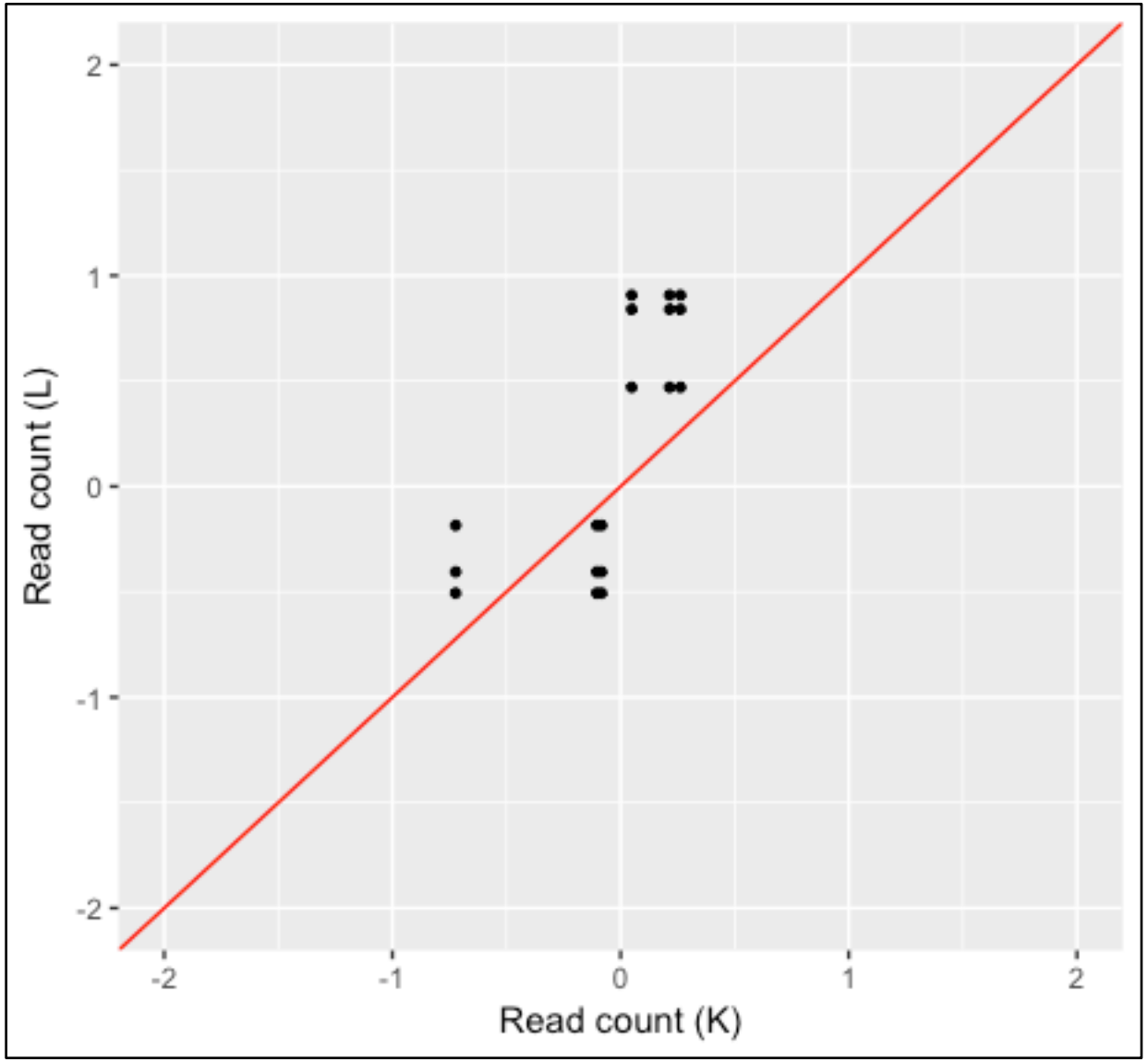
repLIcate TREatment ("litre") plot

	L1	L2	L3
K1	K1, L1	K1, L2	K1, L3
K2	K2, L1	K2, L2	K2, L3
K3	K3, L1	K3, L2	K3, L3



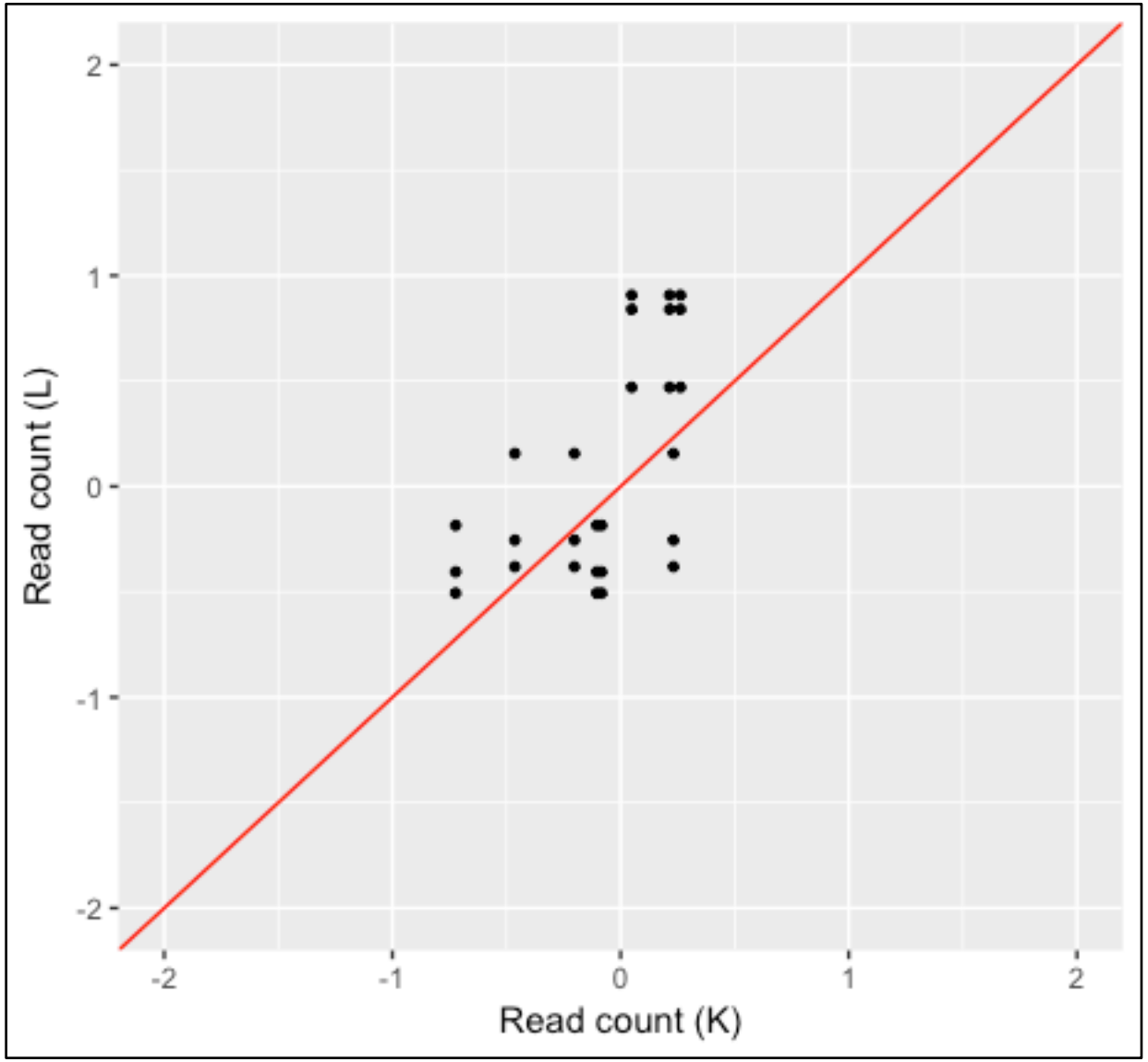
repLIcate TREatment ("litre") plot

	L1	L2	L3
K1	K1, L1	K1, L2	K1, L3
K2	K2, L1	K2, L2	K2, L3
K3	K3, L1	K3, L2	K3, L3



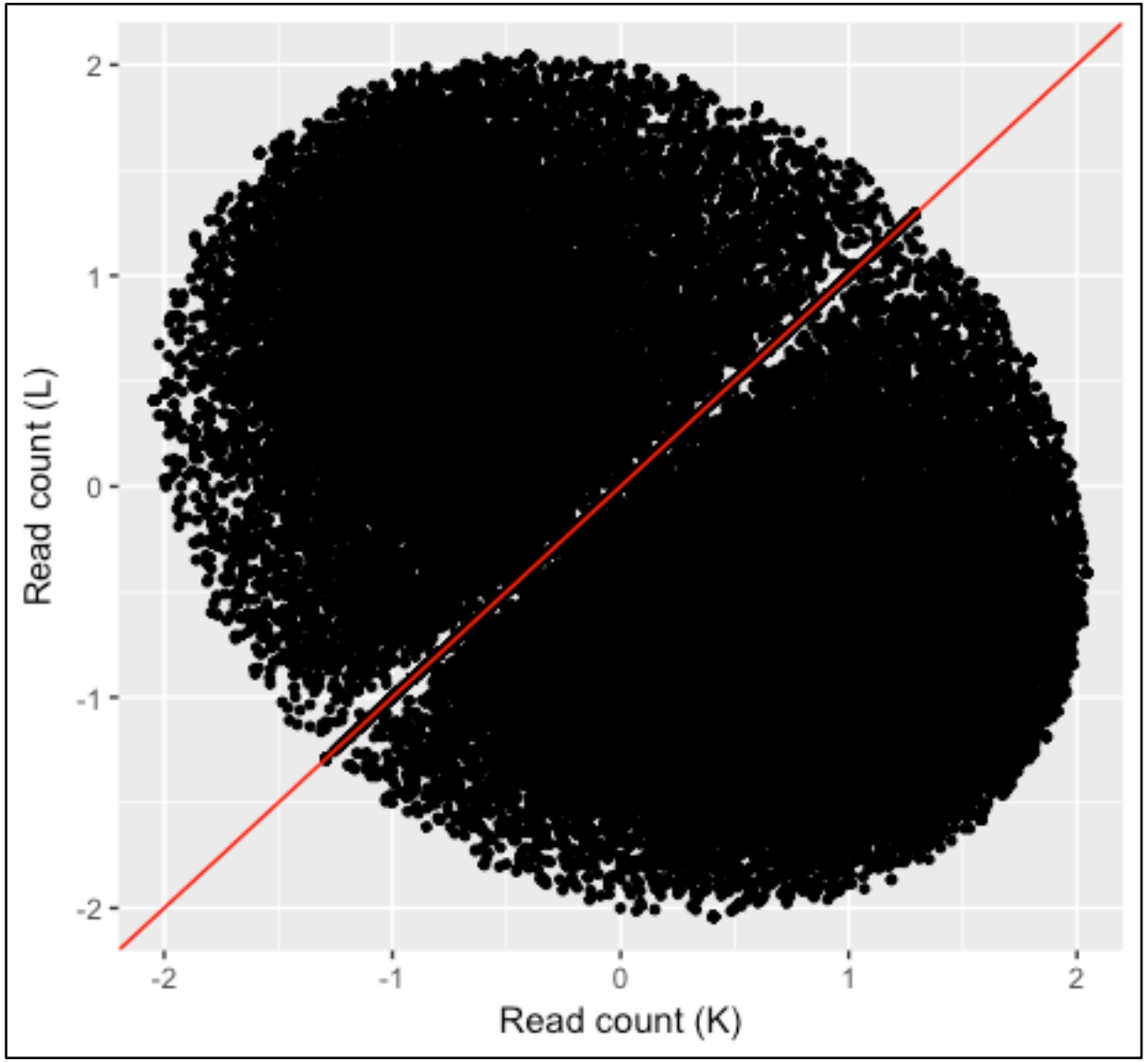
repLIcate TREatment ("litre") plot

	L1	L2	L3
K1	K1, L1	K1, L2	K1, L3
K2	K2, L1	K2, L2	K2, L3
K3	K3, L1	K3, L2	K3, L3



repLIcate TREatment ("litre") plot

	L1	L2	L3
K1	K1, L1	K1, L2	K1, L3
K2	K2, L1	K2, L2	K2, L3
K3	K3, L1	K3, L2	K3, L3



Future Directions

- Convince scientists iteration between models and visuals is crucial
- Provide easy-to-use tools to do so