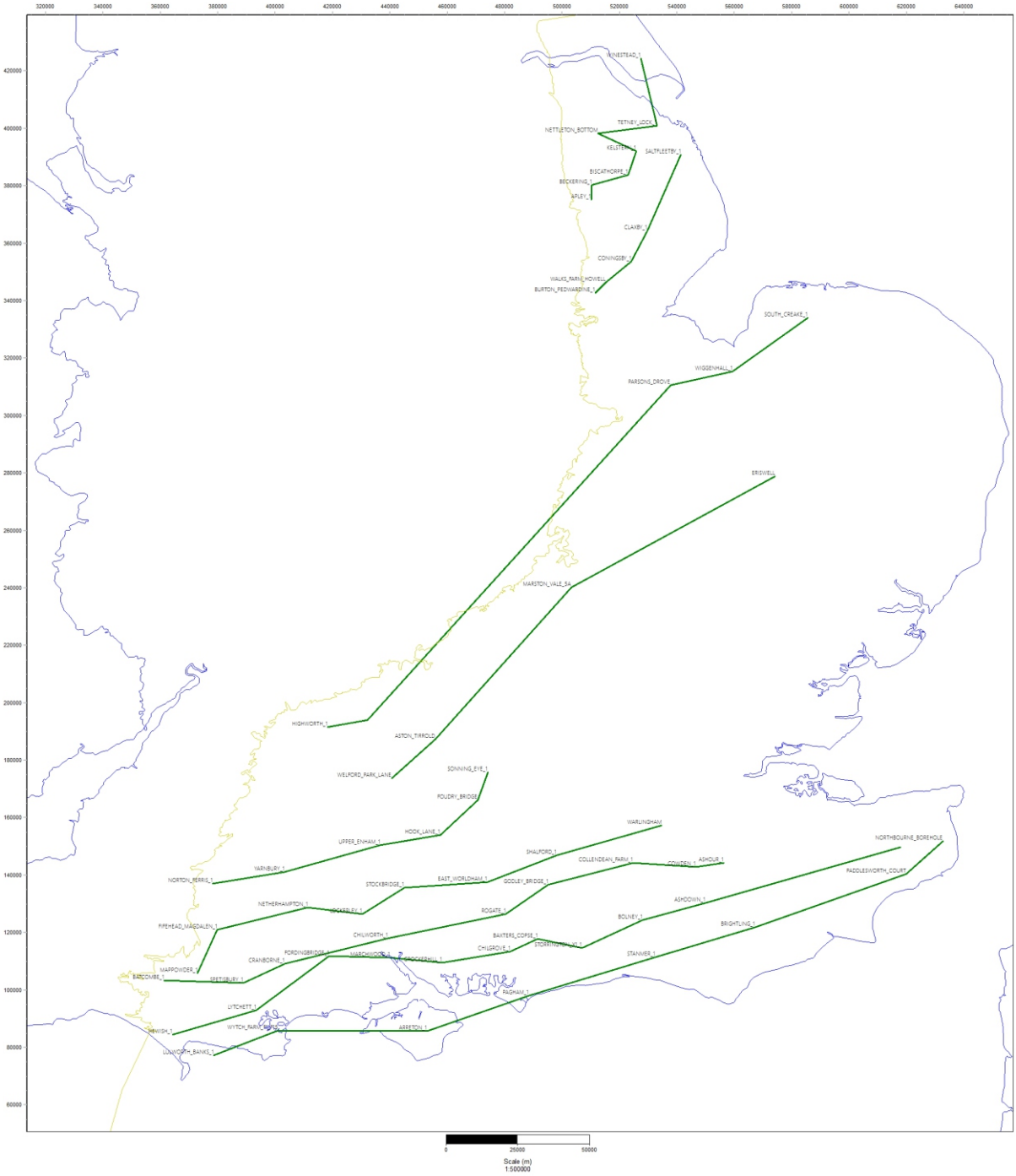
GEOPHYSICAL LOG DATA

Well Section Map



Key to abbreviations on well section lines:

Top_CB=Top of Cornbrash Formation

Top_KLB=Top of Kellaways Formation

Top_Pet=Top of Peterborough Member

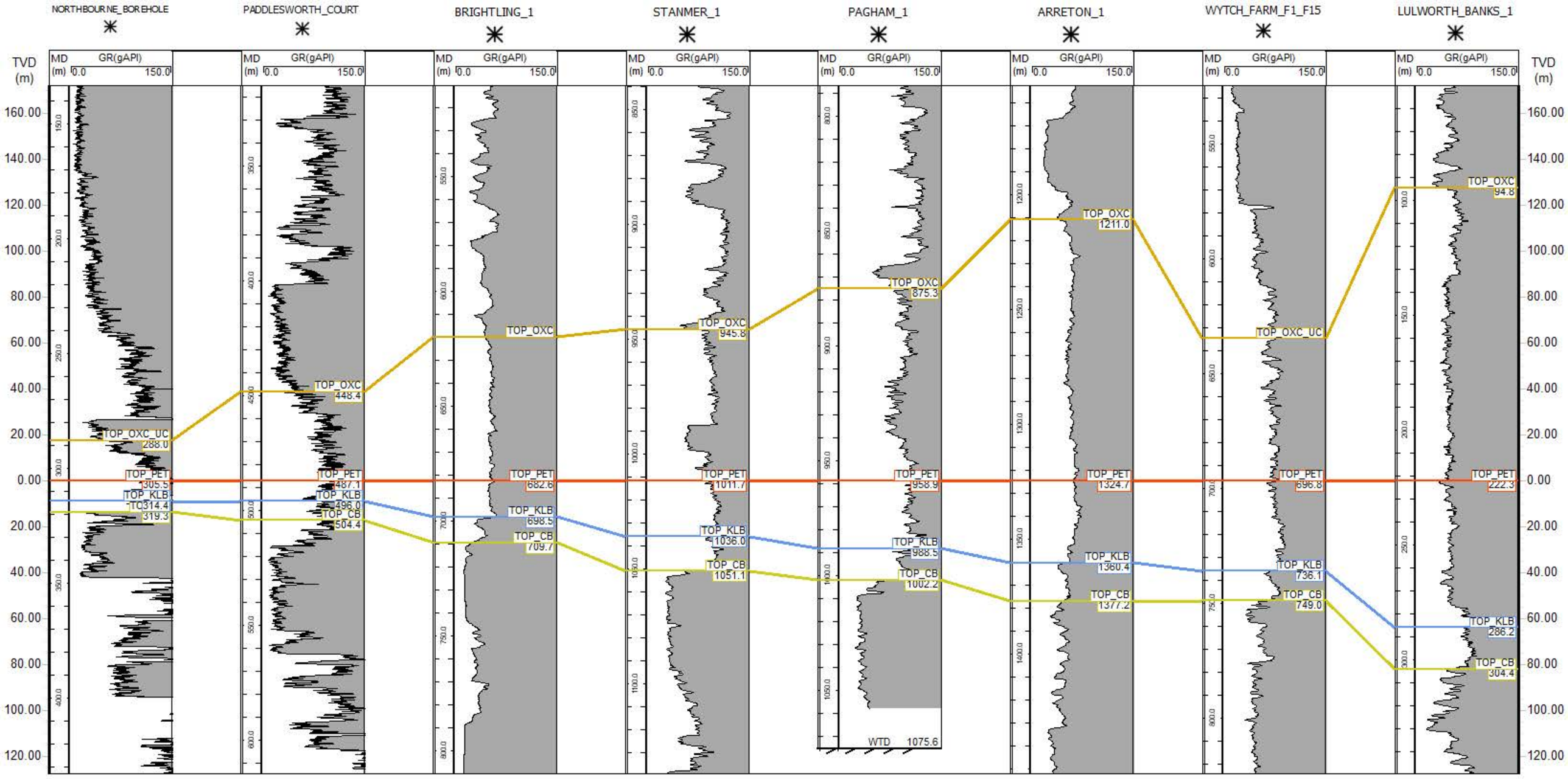
Top_OXC=Top of Oxford Clay Formation

Top_OXC_UC=Top of Oxford Clay Formation where eroded unconformity

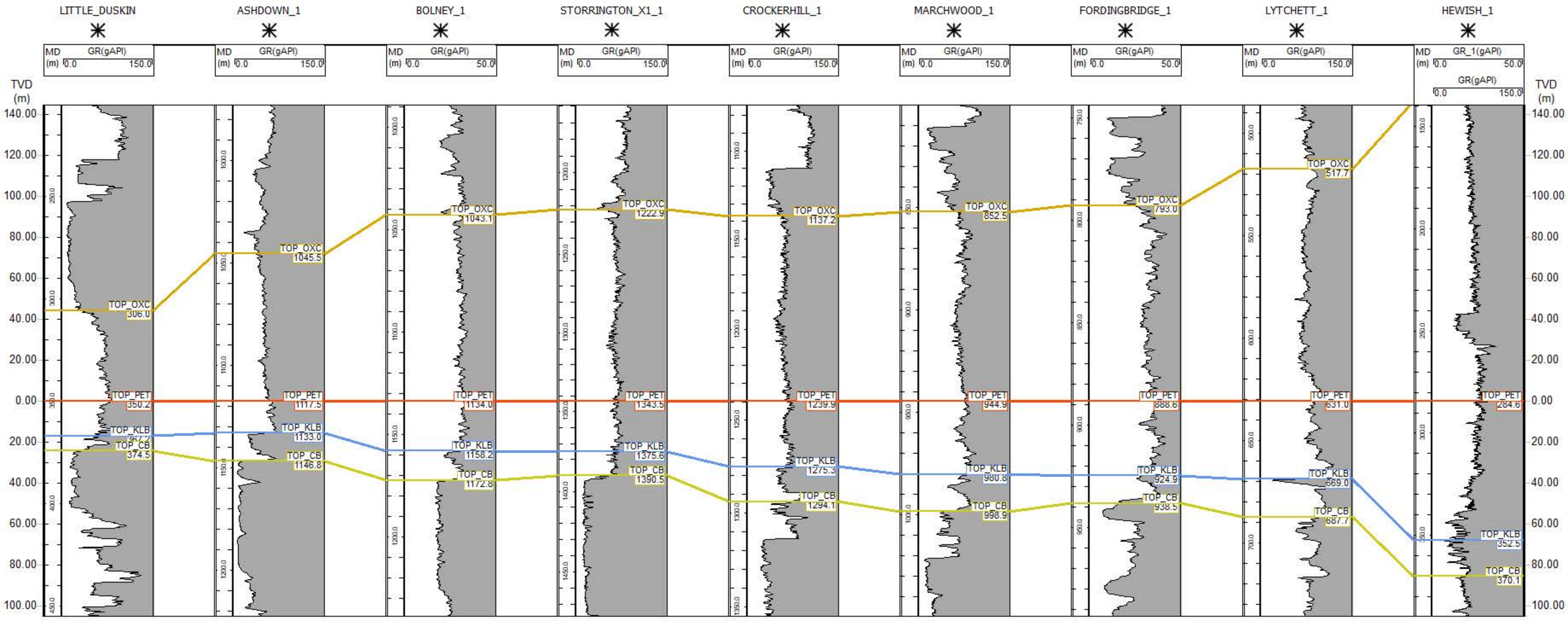
Depths on well markers indicate measured depths below well datum

All sections are flattened on Top of the Peterborough Member

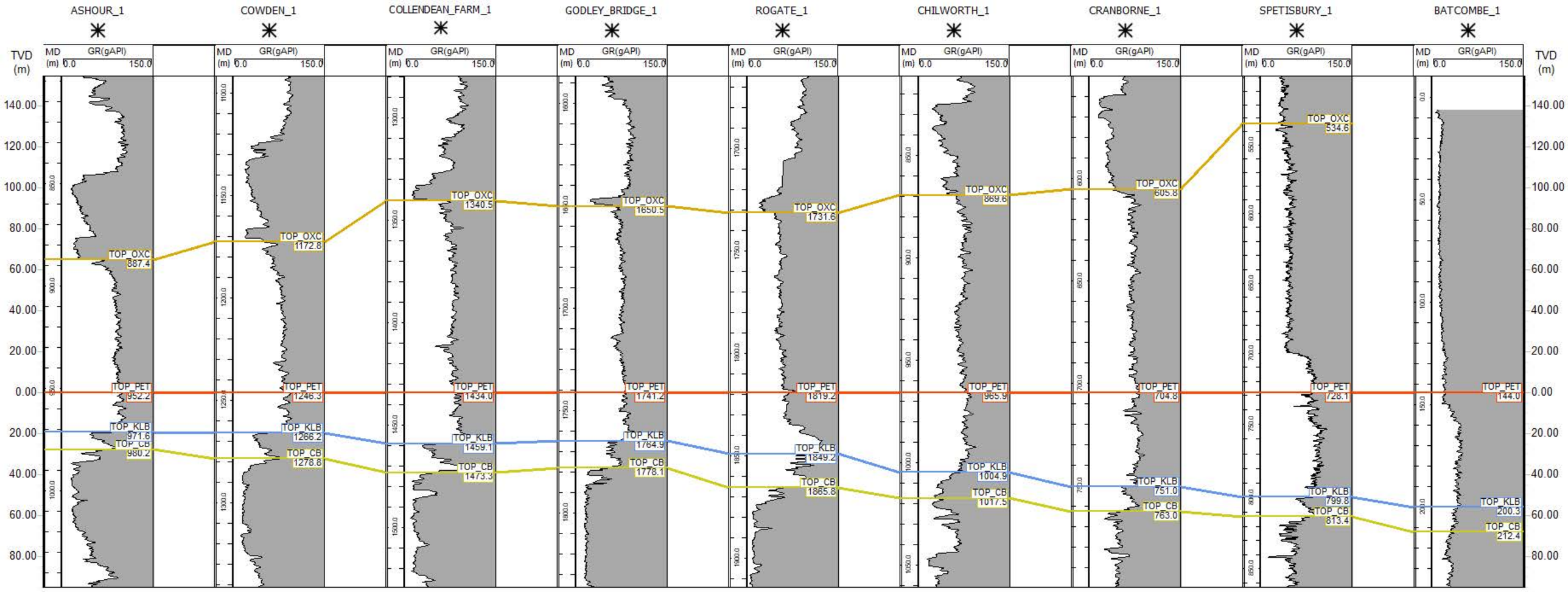
Well Section 1


NORTHBOURNE_BOREHOLE
PADDLESWORTH_COURT
BRIGHTLING_1
STANMER_1
PAGHAM_1
ARRETON_1
WYTCH_FARM_F1_F15
LULWORTH_BANKS_1
TVD (m)
MD (m)
GR(gAPI)
0.0
150.0
TOP_OXC_UC
288.0
TOP_PET
305.5
TOP_KLB
314.4
TOP_CB
319.3
TOP_OXC
448.4
TOP_PET
487.1
TOP_KLB
496.0
TOP_CB
504.4
TOP_OXC
682.6
TOP_KLB
698.5
TOP_CB
709.7
TOP_OXC
945.8
TOP_PET
1011.7
TOP_KLB
1036.0
TOP_CB
1051.1
TOP_OXC
875.3
TOP_PET
958.9
TOP_KLB
988.5
TOP_CB
1002.2
WTD 1075.6
TOP_OXC
1211.0
TOP_PET
1324.7
TOP_KLB
1360.4
TOP_CB
1377.2
TOP_OXC_UC
TOP_PET
696.8
TOP_KLB
736.1
TOP_CB
749.0
TOP_OXC
94.8
TOP_PET
222.3
TOP_KLB
286.2
TOP_CB
304.4

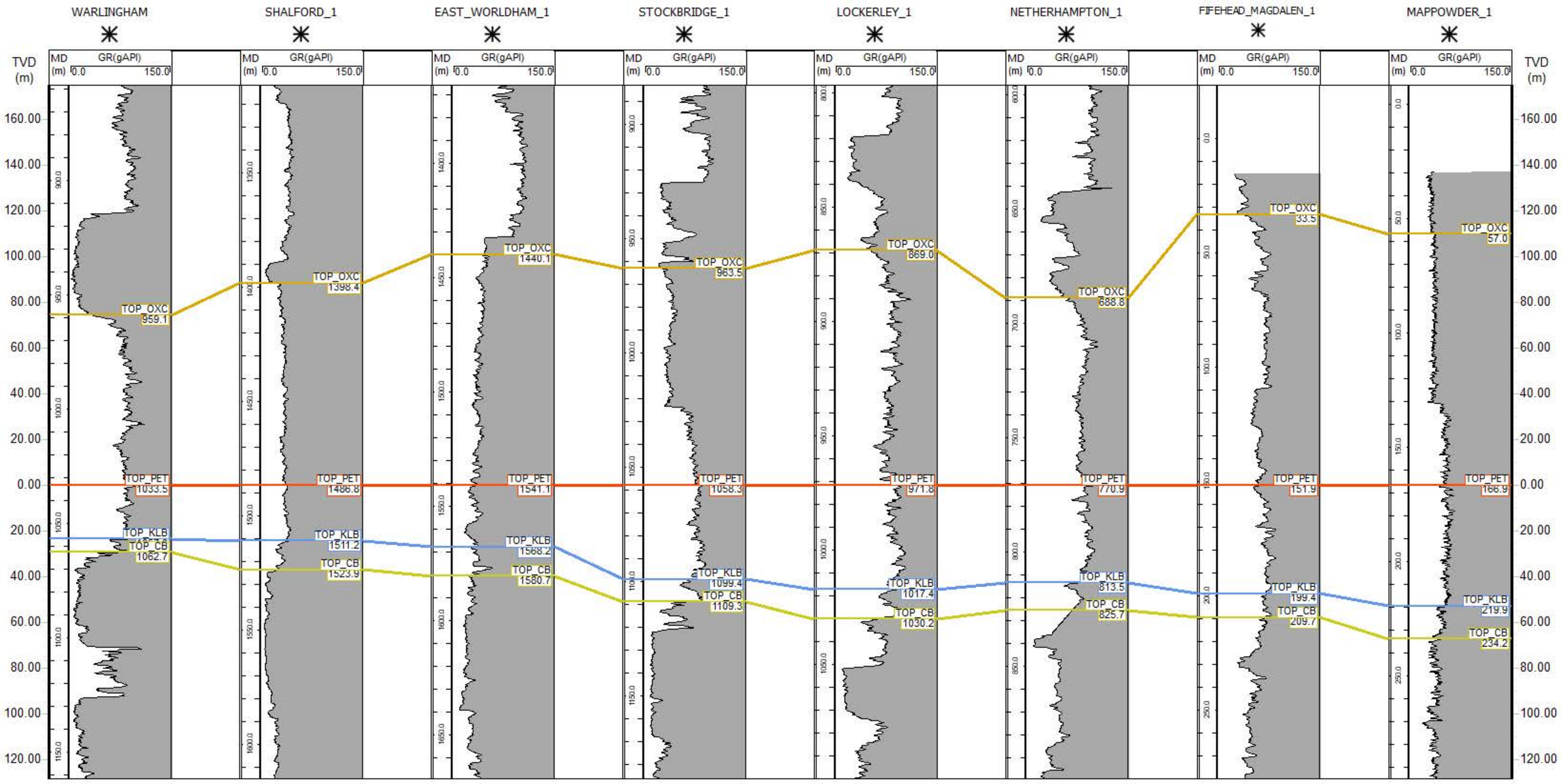
Well Section 2


LITTLE_DUSKIN
ASHDOWN_1
BOLNEY_1
STORRINGTON_X1_1
CROCKERHILL_1
MARCHWOOD_1
FORDINGBRIDGE_1
LYTCHETT_1
HEWISH_1
MD (m)
GR(gAPI)
GR_1(gAPI)
TVD (m)
TOP_OXC
TOP_PET
TOP_KLB
TOP_CB
306.0
350.2
374.5
1045.5
1117.5
1133.0
1146.8
1043.1
1134.0
1158.2
1172.8
1222.9
1343.5
1375.6
1390.5
1137.2
1239.9
1275.3
1294.1
852.5
944.9
980.8
998.9
793.0
888.6
924.9
938.5
517.7
631.0
669.0
687.7
284.6
352.5
370.1

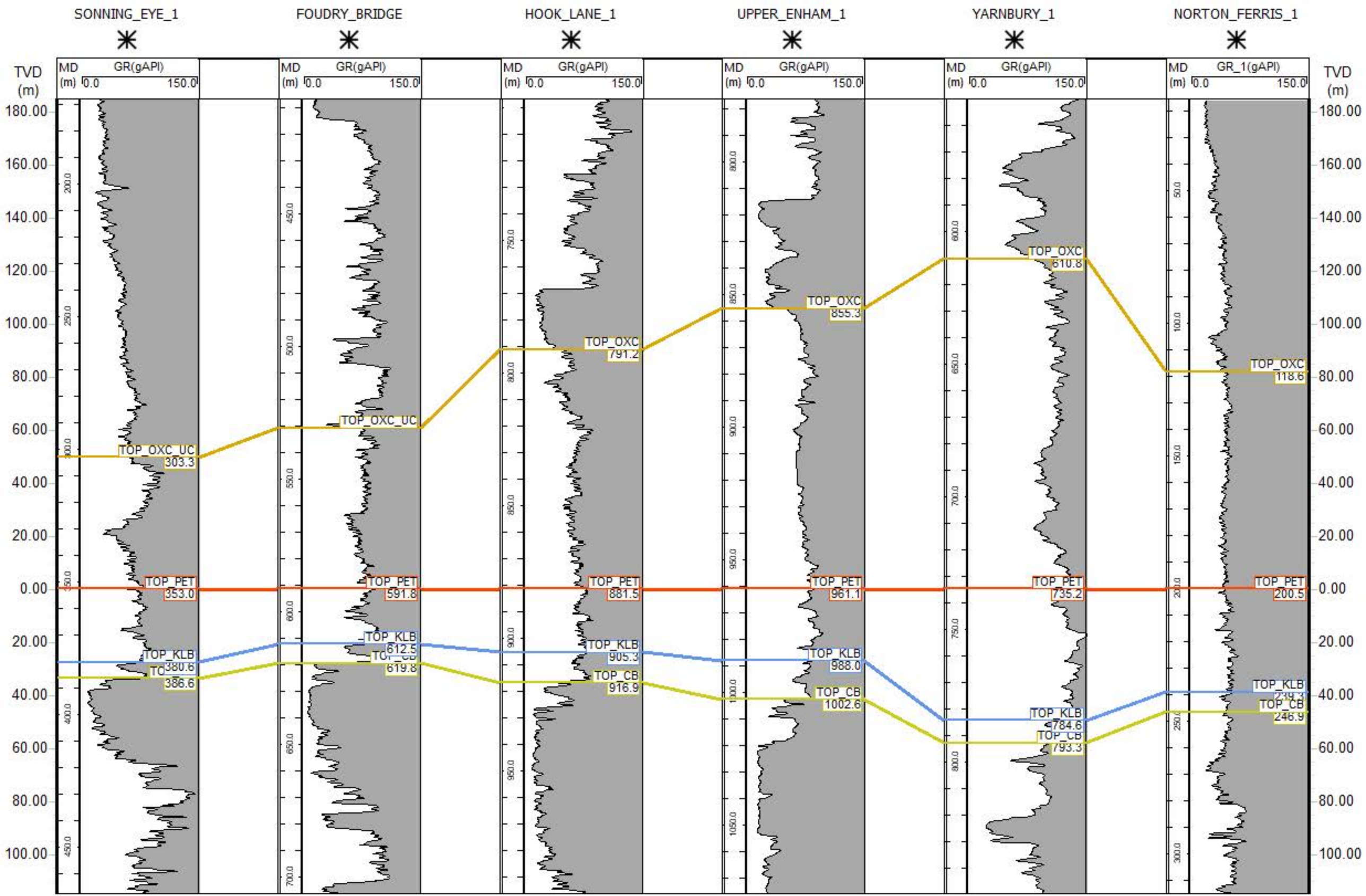
Well Section 3


ASHOUR_1
COWDEN_1
COLLENDEAN_FARM_1
GODLEY_BRIDGE_1
ROGATE_1
CHILWORTH_1
CRANBORNE_1
SPETISBURY_1
BATCOMBE_1
TVD (m)
MD (m)
GR(gAPI)
0.0
150.0
TOP_OXC
887.4
1172.8
1340.5
1650.5
1731.6
869.6
605.8
534.6
TOP_PET
952.2
1246.3
1434.0
1741.2
1819.2
965.9
704.8
728.1
144.0
TOP_KLB
971.6
1266.2
1459.1
1764.9
1849.2
1004.9
751.0
799.8
200.3
TOP_CB
980.2
1278.8
1473.3
1778.1
1865.8
1017.5
763.0
813.4
212.4

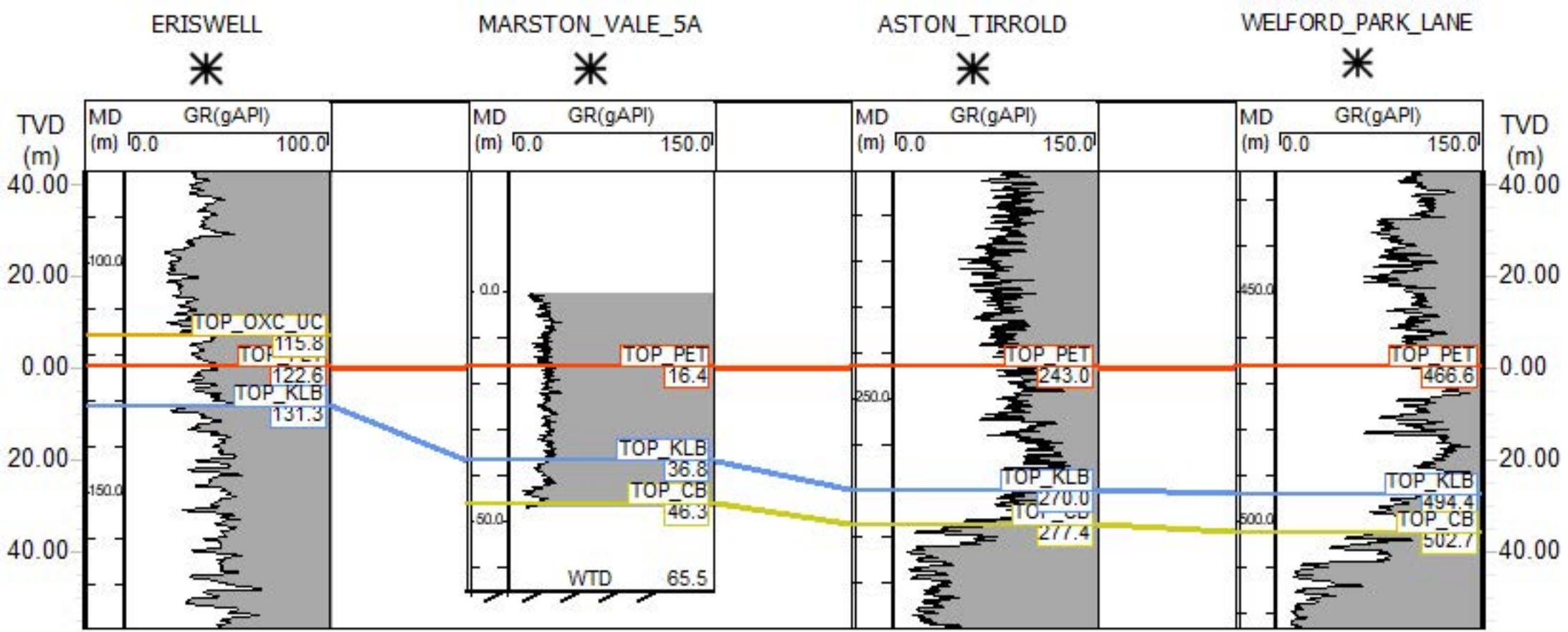
Well Section 4


WARLINGHAM
SHALFORD_1
EAST_WORLDHAM_1
STOCKBRIDGE_1
LOCKERLEY_1
NETHERHAMPTON_1
FIFEHEAD_MAGDALEN_1
MAPPOWDER_1
TVD (m)
MD (m)
GR(gAPI)
0.0
150.0
TOP_OXC
959.1
1398.4
1440.1
963.5
869.0
688.8
33.5
57.0
TOP_PET
1033.5
1486.8
1541.1
1058.3
971.8
770.9
151.9
166.9
TOP_KLB
1062.7
1511.2
1568.2
1099.4
1017.4
813.5
199.4
219.9
TOP_CB
1523.9
1580.7
1109.3
1030.2
825.7
209.7
234.2

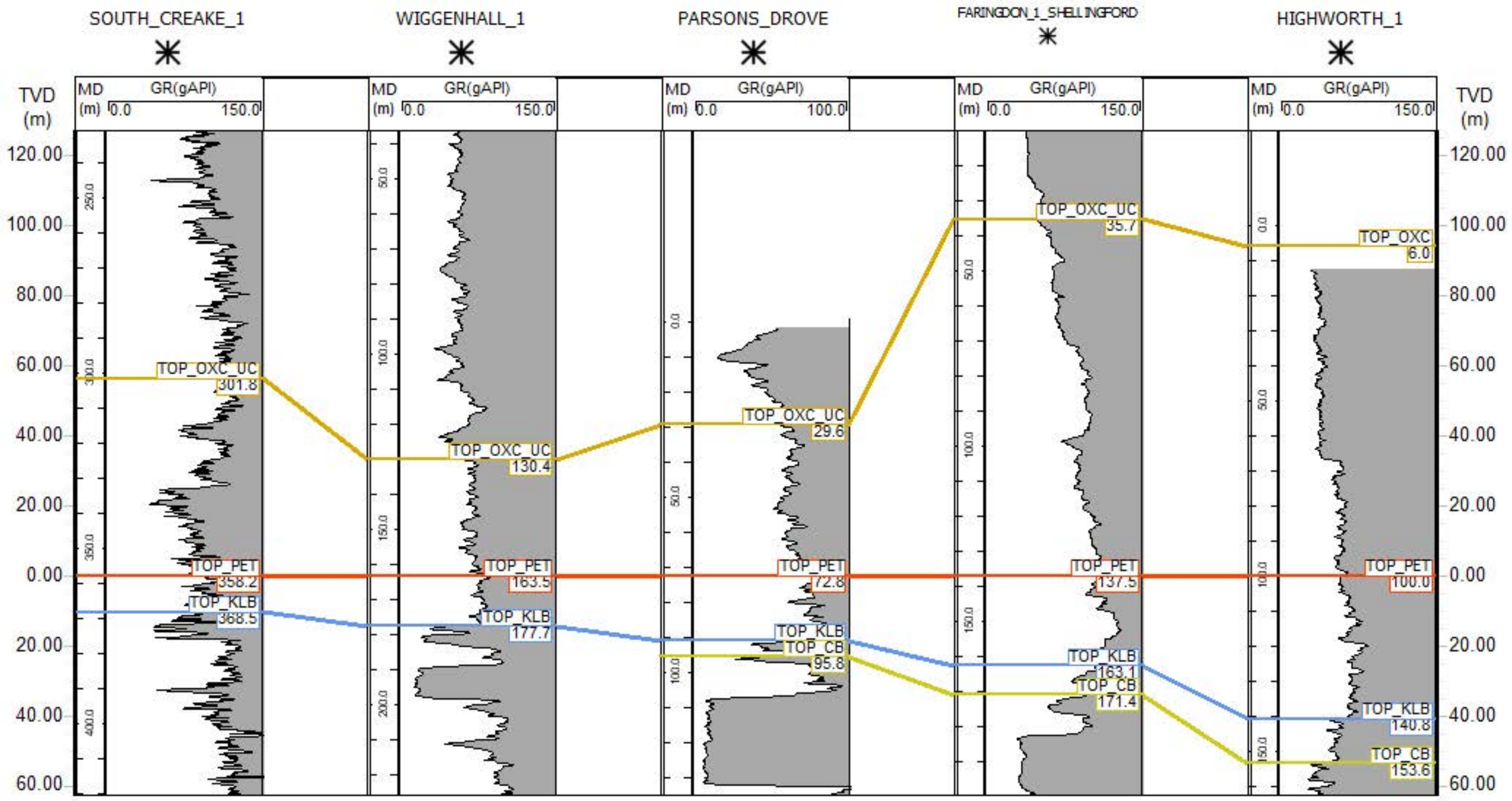
Well Section 5


SONNING_EYE_1
FOUDRY_BRIDGE
HOOK_LANE_1
UPPER_ENHAM_1
YARNBURY_1
NORTON_FERRIS_1
TVD (m)
MD (m)
GR(gAPI)
GR_1(gAPI)
0.0
150.0
TOP_OXC_UC 303.3
TOP_PET 353.0
TOP_KLB 380.6
386.6
TOP_OXC_UC
TOP_PET 591.8
TOP_KLB 612.5
619.8
TOP_OXC 791.2
TOP_PET 881.5
TOP_KLB 905.3
TOP_CB 916.9
TOP_OXC 855.3
TOP_PET 961.1
TOP_KLB 988.0
TOP_CB 1002.6
TOP_OXC 610.8
TOP_PET 735.2
TOP_KLB 784.6
TOP_CB 793.3
TOP_OXC 118.6
TOP_PET 200.5
TOP_KLB
TOP_CB 246.9

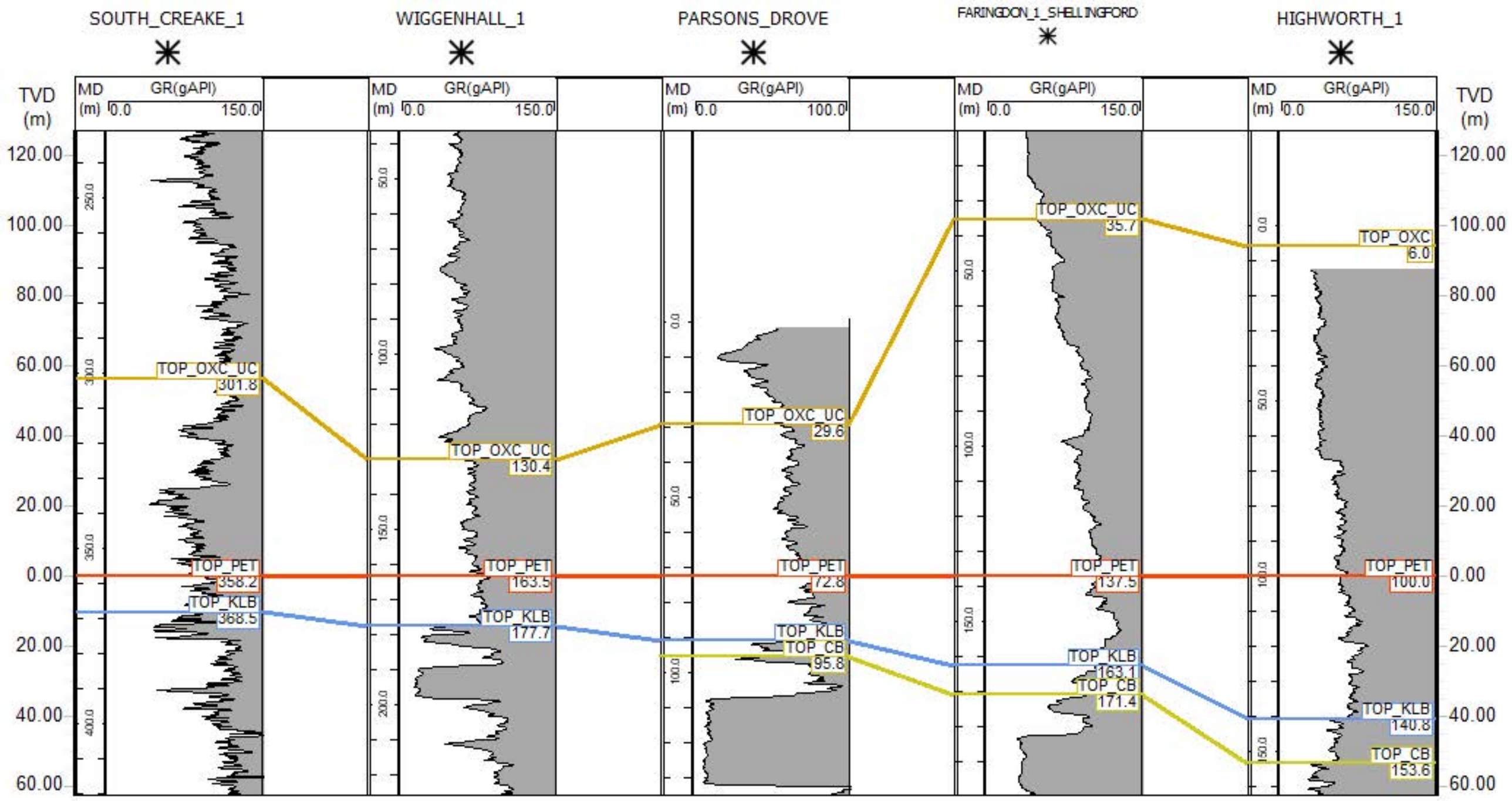
Well Section 6


ERISWELL
MARSTON_VALE_5A
ASTON_TIRROLD
WELFORD_PARK_LANE
TVD (m)
MD (m)
GR(gAPI)
0.0
100.0
150.0
40.00
20.00
0.00
TOP_OXC_UC
115.8
122.6
TOP_KLB
131.3
TOP_PET
16.4
36.8
TOP_CB
46.3
WTD
65.5
243.0
270.0
277.4
466.6
494.4
502.7

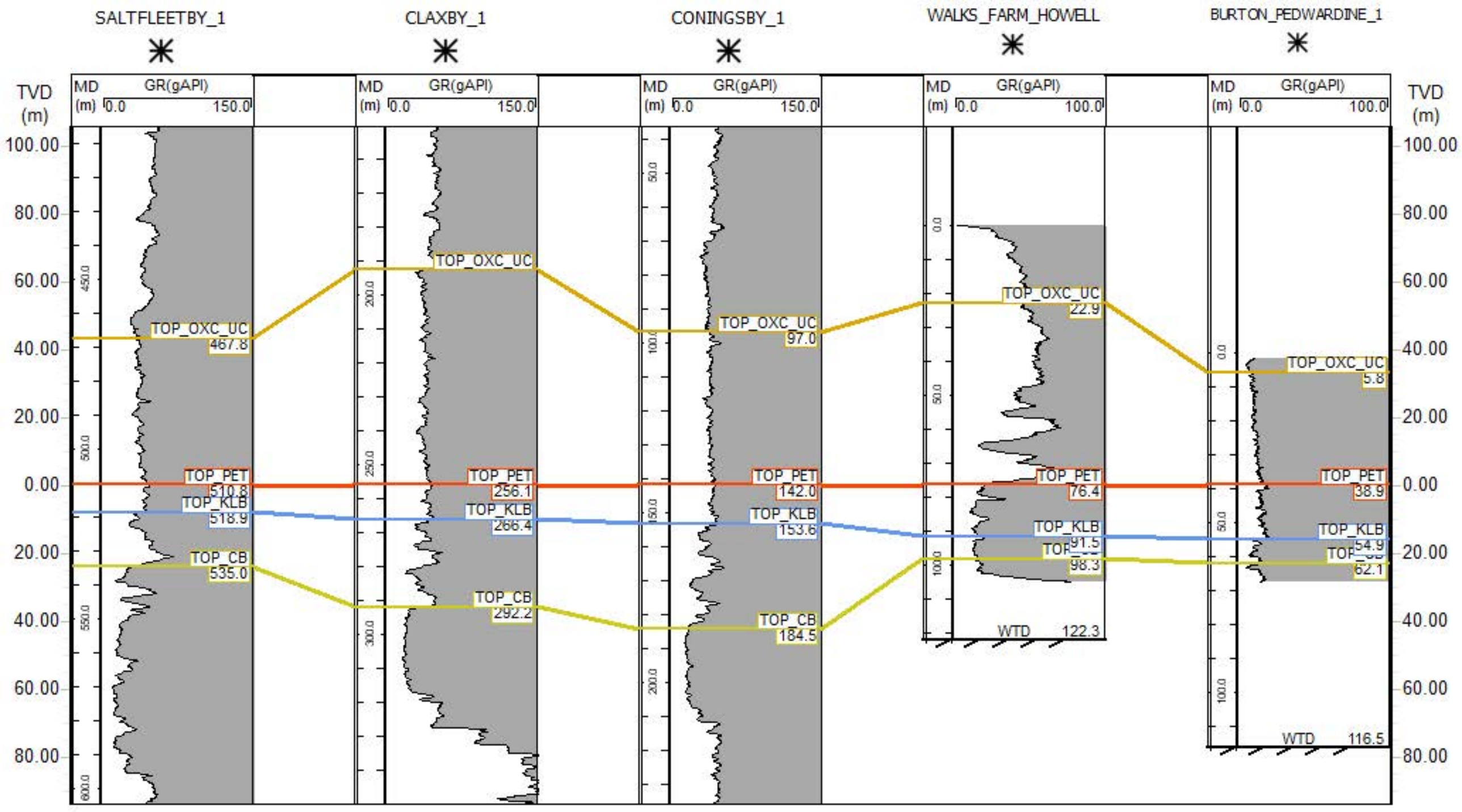
Well Section 7


SOUTH_CREAKE_1
WIGGENHALL_1
PARSONS_DROVE
FARINGDON_1_SHELLINGFORD
HIGHWORTH_1
TVD (m)
MD (m)
GR(gAPI)
0.0
150.0
100.0
TOP_OXC_UC
301.8
TOP_PET
358.2
TOP_KLB
368.5
TOP_OXC_UC
130.4
TOP_PET
163.5
TOP_KLB
177.7
TOP_OXC_UC
29.6
TOP_PET
72.8
TOP_KLB
TOP_CB
95.8
TOP_OXC_UC
35.7
TOP_PET
137.5
TOP_KLB
163.1
TOP_CB
171.4
TOP_OXC
6.0
TOP_PET
100.0
TOP_KLB
140.8
TOP_CB
153.6

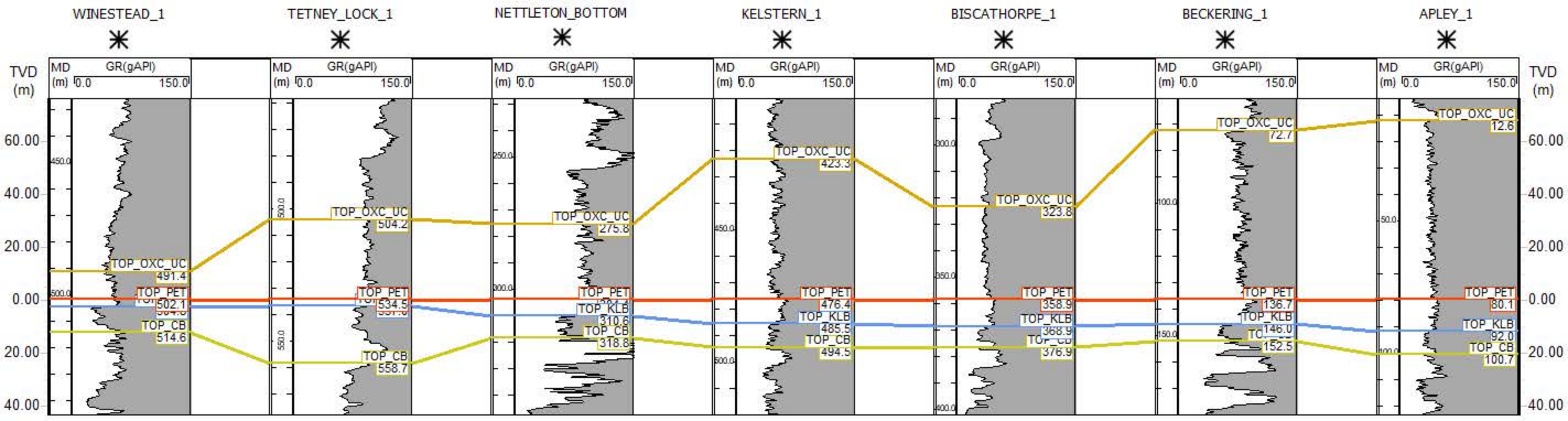
Well Section 8


SOUTH_CREAKE_1
WIGGENHALL_1
PARSONS_DROVE
FARINGDON_1_SHELLINGFORD
HIGHWORTH_1
TVD (m)
MD (m)
GR(gAPI)
0.0
150.0
100.0
TOP_OXC_UC
301.8
TOP_PET
358.2
TOP_KLB
368.5
TOP_OXC_UC
130.4
TOP_PET
163.5
TOP_KLB
177.7
TOP_OXC_UC
29.6
TOP_PET
72.8
TOP_KLB
TOP_CB
95.8
TOP_OXC_UC
35.7
TOP_PET
137.5
TOP_KLB
163.1
TOP_CB
171.4
TOP_OXC
6.0
TOP_PET
100.0
TOP_KLB
140.8
TOP_CB
153.6

Well Section 9


SALTFLEETBY_1
CLAXBY_1
CONINGSBY_1
WALKS_FARM_HOWELL
BURTON_PEDWARDINE_1
TVD (m)
MD (m)
GR(gAPI)
0.0
150.0
100.0
TOP_OXC_UC
467.8
TOP_PET
510.8
TOP_KLB
518.9
TOP_CB
535.0
256.1
266.4
292.2
97.0
142.0
153.6
184.5
22.9
76.4
91.5
98.3
WTD 122.3
5.8
38.9
54.9
62.1
WTD 116.5
100.00
80.00
60.00
40.00
20.00
0.00

Well Section 10


WINESTEAD_1
TETNEY_LOCK_1
NETTLETON_BOTTOM
KELSTERN_1
BISCATHORPE_1
BECKERING_1
APLEY_1
TVD (m)
MD (m)
GR(gAPI)
0.0
150.0
60.00
40.00
20.00
0.00
20.00
40.00
TOP_OXC_UC
TOP_PET
TOP_KLB
TOP_CB
491.4
502.1
514.6
504.2
534.5
558.7
275.8
310.6
318.8
423.3
476.4
485.5
494.5
323.8
358.9
368.9
376.9
72.7
136.7
146.0
152.5
12.6
80.1
92.0
100.7

Borehole Sample Data

Relative abundance of biofacies components in borehole core

For Christian Malford Borehole 11 the following relative abundance scale of biofacies components was applied for observations made of single bedding surfaces in half core (diameter 50 mm):

1: Present

2: Common (2 – 4 specimens)

3: Abundant (5 or more specimens)

4: Plaster

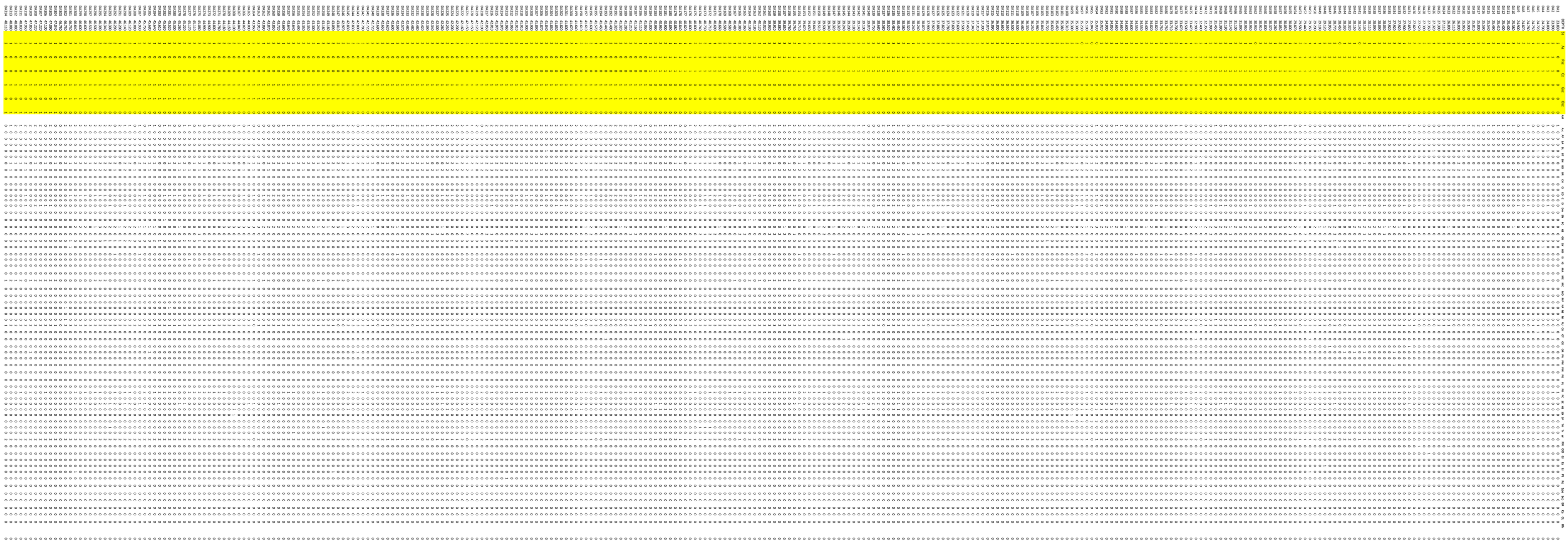
For all other boreholes, for which observations are combined from all visible surfaces of individual core samples, the following relative abundance scale for biofacies components was applied:

1: Present

2: Few

3: Abundant

See Supplementary Data (BIOFACIES/STATISTICS) for details of how these scales are applied in the accompanying data tabulation and statistical analysis.



Eriswell Borehole

	DEPTH	Sz	Az	Psz	Cz	AM	Aic	AP	BA	BL	BT	BN	BO	BR	BU	CH	CI	CO	C	DI	Dm	EN	FO	GE	GR	GY	HO	IS	IG	MA	ME	MC	MO	MP	NA	NE	NI	NU	OS	OT	OX	OR	PA	PM	PIN	PG	PL	PR	PC	SC	HS	SO	SP	TH	Tr	W	PN	OO	Cr	Es	Li	Pt	Ro	Spo	Sco	BR	Ca	CL	Rh
E1	122.660	3	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E2	122.670	3	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E3	122.680	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E4	122.690	3	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E5	122.700	3	1	1	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E6	122.720	3	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E7	122.750	3	1	1	0	0	0	0	0	0	0	2	1	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E8	122.760	3	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E9	122.770	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E10	122.770	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E11	122.780	2	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E12	122.790	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E13	122.790	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E14	122.800	3	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	3	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E15	122.810	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E16	123.020	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E17	123.040	2	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E18	123.08	3	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E19	123.1	3	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E20	123.12	3	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	1	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E21	123.14	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E22	123.24	3	1	1	0	0	0	0	0	0	0	2	1	0	1	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E23	123.26	3	1	1	0	0	0	0	0	0	0	2	1	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E24	123.32	3	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E25	123.34	1	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	2	0	0	0	1	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E26	123.36	3	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E27	123.4	3	1	1	0	1	0	0	0	0	0	2	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E28	123.4	3	1	1	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	2	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E29	123.41	3	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E30	123.43	3	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	2	0	1	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E31	123.5	3	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	1	0	0	0	0	1	1	0	0	0	0	0	0	3	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E32	123.51	3	1	1	0	1	0	0	0	0	0	2	1	0	0	0	0	2	0	1	1	0	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E33	123.51	3	1	1	0	1	0	0	0	0	0	1	1	0	0	0	0	1	0	1	1	0	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E34	123.52	1	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	2	0	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E35	123.62	3	1	1	0	0	0	0	0	0	0	2	2	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E36	123.63	1	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E37	123.63	3	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0
E38	123.7	3	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E39	123.74	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	2	0	1	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E40	123.74	3	1	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E41	123.75	3	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	2	0	1	0	0	2	0	0	0	1	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E42	123.8	3	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	2	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E43	123.89	3	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
E44	123.89	3	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
E45	123.9	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E46	124	3	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
E47	124.1	3	1	1	0	0	0	0	0	0	0	2	1	0	1	0	0	1	0	1	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
E48	124.19	3	1	1	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
E49	124.19	3	1	1	0	0	0	0	0	0	0	1	1	0	1	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E50	124.35	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
E51	124.4	2	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E52	124.45	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E53	124.45	1	1	1	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	1	0	0	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
E54	124.46	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E55	124.55	1	1	1	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0

Parson Drove Borehole

	DEPTH	Sz	Az	Psz	Cz	AM	Aic	AP	BA	BL	BT	BN	BO	BR	CH	Cl	CO	C	DI	Dm	EN	FO	GE	GR	GY	HO	IS	IG	MA	ME	MC	MO	MP	NA	NE	NI	NU	OS	OT	OX	OR	PA	PM	PIN	PG	PL	PR	PC	SC	HS	SO	SP	TH	Tr	W	PN	OO	Cr	Es	Li	Pt	Ro	Spo	Sco	BR	Ca	CL	Rh
P1	69.020	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P2	69.230	3	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P3	69.350	2	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P4	69.530	3	1	1	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P5	69.550	2	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P6	69.600	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P7	69.780	3	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P8	69.970	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P9	70.000	3	1	1	0	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P10	70.200	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P11	70.380	3	1	1	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P12	70.400	1	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P13	70.810	3	1	1	0	1	0	0	0	1	1	0	0	0	0	0	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P14	70.810	3	1	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P15	71.000	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P16	71.100	2	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P17	71.210	3	1	1	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P18	71.410	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P19	71.620	3	1	1	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P20	72.610	1	1	1	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P21	72.700	3	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P22	73.000	2	1	1	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P23	73.050	3	1	1	0	0	0	0	0	0	0	2	2	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P24	73.560	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P25	73.820	3	1	1	0	2	0	0	0	0	0	1	2	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P26	?75	2	1	1	0	1	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P27	75.000	3	1	1	0	0	0	0	0	0	0	2	2	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P28	75.490	1	1	1	0	1	0	0	0	0	0	0	2	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P29	75.500	3	1	1	0	1	0	0	0	0	0	1	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P30	77.000	2	1	1	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P31	77.600	3	1	1	0	2	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P32	77.650	3	1	1	0	1	0	0	0	0	0	2	2	0	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P33	77.700	2	1	1	0	2	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P34	77.800	1	1	1	0	1	0	0	0	0	0	0	3	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P35	78.150	1	1	1	0	2	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P36	78.300	2	1	1	0	1	0	0	0	0	0	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P37	78.410	3	1	1	0	1	0	0	0	0	0	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P38	78.400	3	1	1	0	1	0	0	0	0	0	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P39	78.510	3	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P40	78.590	2	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P41	78.670	3	1	1	0	2	0	0	0	0	0	2	2	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P42	78.700	3	1	1	0	0	0	0	0	0	0	1	3	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P43	79.000	3	1	1	0	1	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P44	79.020	1	1	1	0	1	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P45	79.200	1	1	1	0	1	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P46	79.330	3	1	1	0	2	0	0	0	0	0	1	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P47	79.460	3	1	1	0	1	0	0	0	0	0	1	2	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P48	79.470	2	1	1	0	1	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P49	79.470	1	1	1	0	1	0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P50	79.470	1	1	1	0	1	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P51	79.480	3	1	1	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P52	79.670	3	1	1	0	2	0	0	0	0	0	2	2	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P53	79.790	3	1	1	0	1	0	0	0	0	0	2	3	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P54	79.870	3	1	1	0	2	0	0	0	0	0	2	3	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P55	79.900	3	1	1	0	2	0	0	0	0	0	2	3	0	0

Ashdown 2 Borehole

	DEPTH	Sz	Cz	AM	Aic	AP	BA	BL	BT	BN	BO	BR	CH	CI	CO	C	DI	Dm	EN	FO	GE	GR	GY	HO	IS	IG	MA	ME	MC	MO	MP	NA	NE	NI	NU	OS	OT	OX	OR	PA	PM	PIN	PG	PL	PR	PC	SC	HS	SO	SP	TH	Tr	W	PN	OO	Cr	Es	Li	Pt	Ro	Spo	Sco	BR	Ca	CL	Rh
A1	1103.376	3	1	0	0	0	0	0	0	2	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A2	1103.681	3	1	2	0	0	0	0	0	2	2	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A3	1103.986	2	1	2	0	0	0	0	0	2	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A4	1104.4428	3	1	1	0	0	0	0	0	2	2	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A5	1104.595	2	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A6	1104.748	3	1	0	0	0	0	0	0	2	2	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A7	1104.900	2	1	0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A8	1105.205	2	1	0	0	0	0	0	0	2	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A9	1105.5096	2	1	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A10	1105.662	3	1	0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A11	1105.814	2	1	0	0	0	0	0	0	2	2	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A12	1105.967	3	1	1	0	0	0	0	0	2	2	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A13	1106.119	2	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A14	1106.424	2	1	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A15	1106.729	2	1	0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A16	1107.034	2	1	0	0	0	0	0	0	2	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A17	1107.338	2	1	0	0	0	0	0	0	2	2	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A18	1107.643	3	1	0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A19	1107.796	3	1	1	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A20	1107.872	3	1	2	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A21	1108.253	2	1	1	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A22	1108.558	2	1	1	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A23	1108.862	3	1	2	0	0	0	0	0	2	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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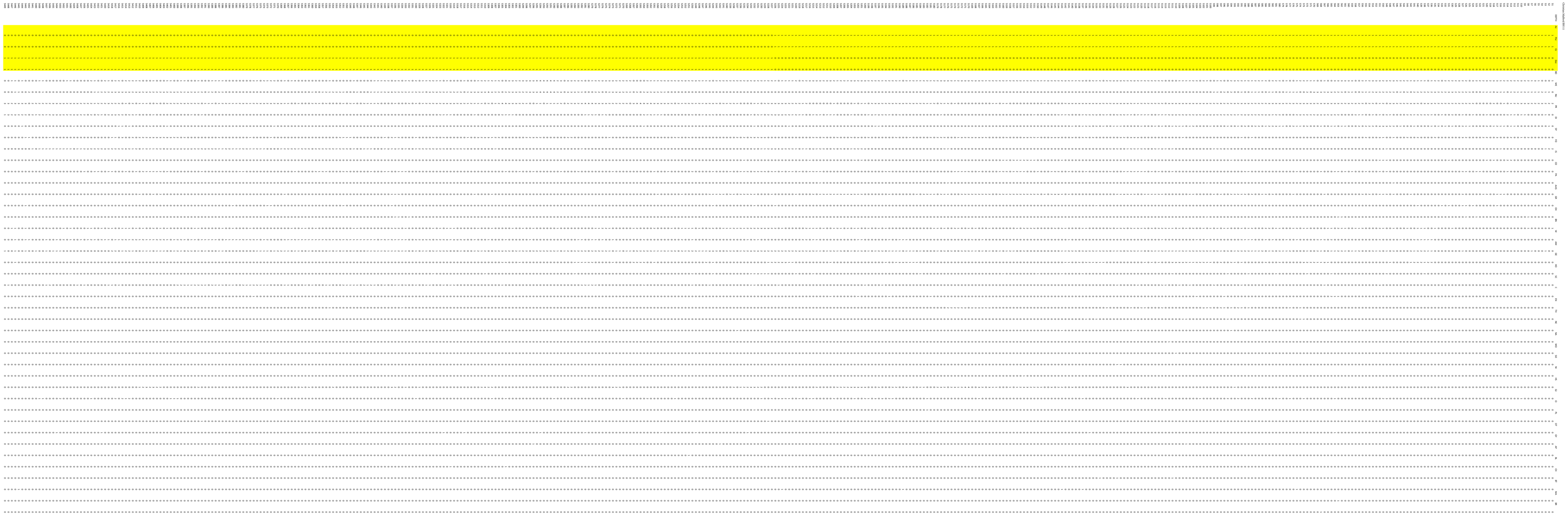
Kimmeridge 2 Borehole

	DEPTH	Sz	CJC	AM	Aic	AP	BA	BL	BT	BN	BO	BR	CH	Cl	C	DI	Dm	EN	FO	GE	GR	GY	HO	IS	IG	MA	ME	MC	MO	MP	NA	NE	NI	NU	OS	OT	OX	OR	PA	PM	PIN	PG	PL	PR	PC	SC	HS	SO	SP	TH	Tr	W	PN	OO	Cr	Es	Li	Pt	Ro	Spo	Sco	BR	Ca	CL	Rh
K1	573.024	3	1	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K2	573.1002	3	1	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K3	573.1256	3	1	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K4	573.1764	3	1	2	0	0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K5	573.2526	3	1	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K6	573.278	3	1	2	0	0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K7	573.3034	3	1	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K8	573.3796	3	1	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K9	573.405	3	1	2	0	0	0	0	0	1	2	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K10	573.5574	3	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K11	573.634	3	1	2	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K12	573.8876	3	1	1	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K13	573.938	3	1	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K14	574.04	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K15	574.243	3	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K16	574.3956	3	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K17	574.4972	3	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K18	574.548	3	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K19	574.6242	3	1	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K20	574.853	3	1	2	0	0	0	0	0	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K21	575.158	3	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K22	575.2338	3	1	1	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K23	575.3608	3	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K24	575.4116	1	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K25	575.462	3	1	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K26	575.5386	3	1	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K27	575.6402	1	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K28	575.7164	3	1	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K29	575.767	3	1	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K30	575.8434	3	1	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K31	575.9196	3	1	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K32	576.0466	3	1	2	0	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K33	576.072	3	1	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K34	576.0974	3	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K35	576.4276	3	1	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K36	576.6816	3	1	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K37	576.707	3	1	0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K38	576.834	3	1	0	0	0	0	0	0	1	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K39	576.9102	3	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K40	576.986	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K41	577.1134	3	1	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K42	577.1642	3	1	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K43	577.291	3	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K44	577.342	3	1	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K45	577.469	3	1	2	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K46	577.5452	3	1	2	0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K47	577.596	3	1	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K48	577.7484	3	1	0	0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K49	577.901	3	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K50	578.0278	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K51	578.206	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K52	578.510	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K53	578.739	3	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K54	578.815	3	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K55	578.9676	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K56	579.120	3	1	1	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
K57	579.374	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0



Christian Malford BH9

	DEPTH	Az	Psz	BO	ME	NU	PR	DI	SP	FO	IS	CO	PA	AmS	GR	OX	BN	W	AM	GE	HO	SC	C	EN	TH	NE	NA	MO	SO	NI	HS	GJ	CI	PL	OT	GY	AP	BL	CH	BT	MA	BR
B9_1		1	1	0	2	2	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B9_2		1	1	1	2	2	2	1	0	0	0	0	0	0	0	0	1	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B9_3		1	1	0	1	2	1	1	2	0	0	1	0	1	0	0	0	2	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
B9_4		1	1	1	0	3	0	1	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B9_5		1	1	1	0	2	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B9_6		1	1	0	1	2	1	1	0	0	0	1	0	1	0	0	1	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
B9_7		1	1	1	0	3	1	1	0	0	0	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0
B9_8		1	1	3	1	2	2	2	0	0	0	1	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
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B9_10		1	1	0	1	1	0	0	0	0	0	1	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
B9_11		1	1	0	0	2	1	0	0	0	0	0	0	1	1	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0
B9_12		1	1	0	1	2	3	1	0	0	0	1	0	1	0	0	1	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B9_13		1	1	0	0	4	2	1	0	1	0	1	0	0	0	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0
B9_14		1	1	2	0	1	1	1	1	1	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0
B9_15		1	1	0	1	0	2	1	0	1	0	0	0	0	0	0	0	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B9_16		1	1	0	0	2	1	1	0	1	0	0	0	0	0	0	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B9_17		1	1	2	1	3	1	1	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B9_18		1	1	3	1	0	1	2	2	0	0	1	0	1	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
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B9_32		1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B9_33		1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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B9_36		1	1	0	3	2	1	2	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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B9_38		1	1	1	2	1	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
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B9_74		1	1	0	2	2	1	0	0	2	0	0	0	0	0	0	0	2	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
B9_75		1	1	0	2	2	1	1	0	2	0	0	0	0	0	0	0	2	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B9_76		1	1	0	2	1	0	0	0	3	0	0	0	1	0	0	1	3	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B9_77		1	1	1	2	1	0	1	0	3	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B9_78		1	1	1	1	1	0	1	0	1	0	0	0	0	0	0	1	0	0	1	0	3	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
B9_79		1	1	0	1	1	1	0	0	2	0	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B9_80		1	1	0	1	1	1	1	2	3	0	0	0	1	0	0	0	3	0	0	1	1	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0
B9_81		1	1	1	2	2	1	1	0	1	0	0	0	1	0	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B9_82		1	1	1	2	2	1	0	0	0	0	0	0	1	0	0	1	1	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B9_83		1	1	3	3	0	1	2	3	1	0	0	0	0	0	0	0	2	1	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B9_84		1	1	0	4	0	0	1	2	0	0	0	0	1	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
B9_85		1	1	3	3	1	0	2	2	2	0	0	0	0	0	0	1	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B9_86		1	1	1	3	0	0	3	4	3	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B9_87		1	1	0	2	0	0	1	0	2	2	0	0	0	0	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0
B9_88		1	1	0	2	0	1	2	4	3	2	1	0	1	0	0	2	2	1	0	1	1	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0
B9_89		1	1	1	2	0	0	2	3	3	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
B9_90		1	1	1	2	0	0	1	2	2	1	0	0	2	0	0	1	2	1	0	0	1	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0
B9_91		1	1	1	2	0	1	0	0	2	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
B9_92		1	1	3	2	0

Combe Throop Borehole

	DEPTH	Sz	Az	Psz	Cz	Jz	Jsz	Msz	Caz	Esz	Csz	AM	Alc	AP	BA	BL	BT	BN	BO	BR	CH	Cl	CO	C	Di	Dm	EN	FO	GE	GR	GY	HO	IS	IG	MA	ME	MC	MO	MP	NA	NE	NI	NU	OS	OT	OX	OR	Orb	PA	PM	PN	PG	PL	PR	PC	SC	HS	SO	SP	TH	Tri	W	PN	OO	Cr	Es	Li	Pt	Ro	Spo	Sco	Ga	CL	Rh
CT1	8.3	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CT2	11.5	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
CT3	11.66	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0	0	0	1	0	0	0	0	2	0	0	0	0	1	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
CT4	11.7	2	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2	0	0	0	1	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
CT5	11.9	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
CT6	11.95	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	2	0	0	2	0	2	0	0	0	0	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
CT7	11.96	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
CT8	11.97	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	2	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
CT9	12.04	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	2
CT10	12.15	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	2	0	0	0	0	2	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	2	0	0	0	0	0	0
CT11	12.17	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	2	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
CT12	12.2	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	2	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
CT13	12.35	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
CT14	12.4	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
CT15	12.72	3	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
CT16	13.25	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
CT17	13.27	2	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
CT18	13.2	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
CT19	13.24	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
CT20	13.32	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
CT21	13.34	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	2	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
CT22	13.38	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	2	0	0	0	0	3	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
CT23	13.6	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
CT24	13.8	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
CT25	14.1	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
CT26	14.12	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
CT27	14.5	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0	2	0	2	0	0	0	0	0	0	0	0	0	0	0
CT28	14.51	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	1	0	0	2	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
CT29	14.62	3	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	2	0	2	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
CT30	14.63	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0	0	0	2	0	2	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	3	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
CT31	14.64	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	2	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0
CT32	14.85	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0	0	0	0	0	3	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CT33	14.86	3	1	1	0	0	0	0	0	0	0	0	2	0	0	0	0	2	2	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0	2	0	2	0	2	0	0	0	0	0	0	0	0	0	0	0
CT34	15	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	1	0	0	2	0	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0
CT35	15.08	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	2	0	0	0	0	0	1	0	0	0	1	0	0	1	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	2	0	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0
CT36	15.1	3	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	2	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
CT37	15.52	3	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	2	2	0	0	0	2	0	2	0	0	3	0	0	0	0	2	0	0	2	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0	1	0	0	3	0	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0
CT38	15.44	3	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	2	2	0	0	0	2	0	2	0	0	2	0	0	0	0	1	0	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	3	0	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0
CT39	15.48	2	1	1	0	0	0	0	0	0	0	2	1	0	0	0	0	2	1	0	0	0	3	0	1	0	0	3	0	0	0	0	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0	3	0	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0
CT40	15.6	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	3	2	0	0	1	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
CT41	15.63	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
CT42	15.65	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
CT43	16.02	3	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	3	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
CT44	16.03	2	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0
CT45	16.1	2	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	2	0	0	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
CT46	16.12	3	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	2	0	0	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
CT47	16.35	2	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
CT48	16.43	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	1	0	2	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CT49	16.62	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
CT50	16.64	3	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CT51	16.36	2	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0

Geochemistry: Christian Malford Borehole 11

Reading No	depth (m)	Sr	Rb	Fe	Ti	Ca	K	Ca/K	Ti/K
775	3.02	104.85	83.32	17153.61	2603.38	18306.47	11356.63	1.611963	0.229239
776	3.03	102.02	91.77	16804.29	3019.45	20947.46	12356.19	1.695301	0.244367
777	3.04	81.74	71.29	15509.85	2354.32	13560.9	8937.94	1.517229	0.263407
778	3.05	82.77	69.3	15426.81	3113.36	14688.54	12550	1.170402	0.248076
779	3.06	87.44	80.94	16277.63	3081.25	15385.51	13019.85	1.181696	0.236658
780	3.07	101.6	75.1	16670.96	3058.04	15352.43	13947.65	1.100718	0.219251
781	3.08	92.13	70.29	17235.05	2975.11	14630.41	12798.48	1.143137	0.232458
782	3.09	91.31	88.1	17343.37	3250.76	13774.42	12386.13	1.112084	0.262452
783	3.1	90.21	83.49	16328.36	2825.98	13996.03	11035.63	1.268258	0.256078
784	3.11	100.63	87.02	17702.85	3134.21	13219.64	13018.25	1.01547	0.240755
785	3.12	83.87	80.45	17510.97	3013.02	14718.47	11438.43	1.286756	0.263412
786	3.13	95.4	74.98	17605.45	3018.67	16925.74	12006.85	1.409674	0.251412
787	3.14	105.97	81.95	16813.27	3043.82	14525.6	11865.89	1.224148	0.256518
788	3.15	97.34	80.92	17125.34	3034.02	15874.94	11973.46	1.325844	0.253395
789	3.16	118.68	78.19	17572.52	3189.15	20503.85	11907.3	1.721956	0.267831
790	3.17	124.97	87.57	17761.34	3117.15	17593.43	12873.97	1.366589	0.242128
791	3.18	115.19	78.72	17643.74	3199.27	18516.41	12317.37	1.503276	0.259736
792	3.19	164.52	76.96	18117.57	2908.42	24586.65	11478.25	2.142021	0.253385
793	3.2	113.53	77.27	17600.1	3075.05	17824.3	11509.32	1.548684	0.267179
794	3.21	126.52	68.84	19313.35	3152.68	21456.45	12530.86	1.712289	0.251593
795	3.22	140.63	67.96	17105.16	2328.96	34070.17	8795.17	3.873736	0.2648
796	3.23	121.55	84.13	16804.08	3050.22	19464.5	11372.31	1.71157	0.268215
797	3.24	113.6	87.3	16672.99	2829.64	18103.38	12045.53	1.502913	0.234912
798	3.25	110.68	69.74	17723.49	2991.21	16939.63	11323.21	1.49601	0.264166
799	3.26	125.95	96.8	18968.47	3136.81	19819.83	12349.98	1.604847	0.253993
800	3.27	120.97	72.24	18233.67	2988.95	20540.02	11082.88	1.853311	0.269691
801	3.28	105.03	79.62	17772.19	2730	17852.84	10639.35	1.678001	0.256595
802	3.29	117.67	87.46	17115.47	2745.27	16092.12	10653.14	1.510552	0.257696
803	3.3	134.55	83.68	18151.66	2515.53	18085.02	10253.09	1.76386	0.245344
804	3.31	133.86	82.37	18878.16	2856.94	22095.46	12983.42	1.701821	0.220045
805	3.32	161.25	78.66	16485.28	3042.23	26390.22	12710.32	2.076283	0.239351
806	3.33	154.79	76.91	17896.8	3135.14	28908.11	12760.72	2.265398	0.245687
807	3.34	146.64	83.66	19402.54	2868.9	23937.24	12618.22	1.897038	0.227362
808	3.35	123.31	84.05	17734.44	3008.78	24212.74	13814.24	1.752738	0.217803
809	3.36	167.81	102.06	20070.08	3000.31	25155.03	13474.07	1.866921	0.222673
810	3.37	140.41	83.95	18545.95	3118.42	23660.37	13401.82	1.765459	0.232686
811	3.38	169.09	86.01	16772.23	3048.45	34224.09	13321.38	2.56911	0.228839
812	3.39	155.25	91.57	15950.37	2825.44	23651.63	12744.89	1.855774	0.221692
813	3.4	131.54	82.41	17152.47	3300.89	26113.04	14246.1	1.832996	0.231705
814	3.41	160.52	96.56	17270.17	2867.6	33126.33	14634.61	2.263561	0.195946
815	3.42	144.1	84.56	16872.27	3088.34	27324.95	15144.36	1.804299	0.203927
816	3.43	135	98.36	18183.9	3000.2	28368.3	15164.22	1.870739	0.197847
817	3.44	146.42	92.02	17827.93	2359.44	25492.57	10768.37	2.367356	0.219108
818	3.45	126.27	92.04	16864.58	2647.91	23487.15	12553.48	1.870967	0.21093
819	3.46	198.65	96.21	17667.56	2699.11	35800.03	14621.05	2.448527	0.184604
820	3.47	162.16	94.4	16590.15	2604.53	39325.13	14531.24	2.706247	0.179237
821	3.48	180.5	90.94	18207.78	2857.57	36667.83	14148.67	2.59161	0.201967
823	3.49	151.4	80.47	17061.71	2389.87	27779.98	11756.76	2.362894	0.203276
824	3.5	133.76	70.29	17301	2585.38	27492.23	13586.27	2.02353	0.190294
825	3.51	142.93	91.5	17638.24	2669.57	29011.17	14799.53	1.960276	0.180382
826	3.52	150.59	84.04	18413.21	2665.76	29093.59	15642.86	1.859864	0.170414
827	3.53	178.38	92.58	18314.22	2620.75	35874.37	14561.63	2.463623	0.179976
828	3.54	152.68	76.82	17688.79	2594.74	35968.73	12989.7	2.769019	0.199754
831	3.55	152.69	80.55	18807.17	2320.37	38997.93	13320.66	2.927627	0.174193
832	3.56	163.43	63.8	17572.96	2261.25	48351.22	13554.91	3.567063	0.166821
833	3.57	185.35	68.91	17420.09	2014.3	57131.47	13084.75	4.366264	0.153943
834	3.58	193.75	79.85	18567.79	1695.66	46249.82	11071.8	4.177263	0.153151
835	3.59	160.03	62.87	17956.54	2051.57	52596.19	13198.38	3.985049	0.155441
836	3.6	182.9	75.56	17999.85	1965.58	52600.12	13020	4.039948	0.150966
838	3.61	158.85	80.04	18002.53	2200.63	47271.14	14583.67	3.241375	0.150897
840	3.62	174.55	94.6	18901.82	1914.65	33905.63	11819.77	2.868552	0.161987
841	3.63	153.16	74.26	18244.2	2619.1	37622.17	13578.65	2.770686	0.192884
842	3.64	160.94	93.17	18552.7	2431.21	35401.04	14266.51	2.481409	0.170414
843	3.65	134.87	85.78	19982.83	2615.65	32690.8	15413.2	2.120961	0.169702
844	3.66	150.71	70.56	17876.06	2190.22	29983.19	11796.24	2.541758	0.185671
845	3.67	165.2	91.44	19072.86	2665.96	39835.43	13535.64	2.943003	0.196959
849	3.68	145.33	98.53	19299.1	2389.79	36945.08	14878.65	2.483094	0.160619
851	3.69	162.2	87.13	19404.82	2439.29	34823.25	15127.86	2.301928	0.161245
852	3.7	129.75	88.37	20723.48	2508.29	35236.9	14564.11	2.419434	0.172224
853	3.71	158.92	99.76	18599.35	2562.38	41189.19	14505.82	2.839494	0.176645
854	3.72	148.13	83.63	19486.36	2439.59	34443.21	13115.7	2.626105	0.186005
855	3.73	148.97	77.73	20997.08	2628.02	28824.77	14269.08	2.020086	0.184176
857	3.74	119.69	91.58	21205.4	2763.34	26898.96	14505.93	1.854342	0.190497
858	3.75	137.83	88.21	20070.19	2574.31	26068.62	12885.33	2.023124	0.199786
859	3.76	124.21	99.16	20338.61	2473.15	20876.62	13445.95	1.552633	0.183933
860	3.77	132.9	83.06	18913.84	2582.57	18236.42	12292.99	1.483481	0.210085
861	3.78	122.15	95.24	19310.61	2833	19364.69	13744.94	1.40886	0.206112
862	3.79	101.72	99.44	18827.16	2663.07	14152.69	11566.58	1.223585	0.230238
863	3.8	108.92	99.09	20990.91	3015.74	19254.03	14120.18	1.363582	0.213577
864	3.81	114.2	102.8	21979.55	2934.04	14483.15	13765.44	1.052139	0.213145
865	3.82	119.78	90.39	21897.27	2946.27	19029.08	12719.13	1.496099	0.231641
866	3.83	104	88	20939.56	3334.38	18172.68	15022.58	1.209691	0.221958
867	3.84	97.04	91.25	21484.6	3331.77	10349.62	13790.39	0.750495	0.241601
868	3.86	112.3	82.65	19226.86	3046.31	23725.62	11992.48	1.978375	0.254018
891	3.87	137.39	84.57	20325.61	3042.72	32393.92	12524.46	2.586452	0.242942
890	3.88	125.8	96.12	20603.16	3188.38	24562.26	13152.98	1.867429	0.242407
882	3.89	127.34	85.09	19913.28	3337.72	26445.19	13574.63	1.948133	0.245879
883	3.9	113.99	104.42	20822.12	3422.93	26656.96	12712	2.096992	0.269268
884	3.91	156.96	86.89	26715.8	3446.95	24224.3	14257.77	1.699024	0.241759
885	3.92	197.18	65.56	28970.86	3200.3	31615.84	12822.82	2.465592	0.249578
886	3.93	163.83	77.66	27374.39	3247.19	23035.33	13493.68	1.70712	0.240645
887	3.94	136.73	86.67	22088.83	3238.4	23634.72	13655.25	1.730816	0.237154
888	3.95	139.57	100.05	22728.06	3091.39	28614.34	12490.49	2.29089	0.247499
889	3.96	138.78	84.58	21571.16	3043.24	26057.87	13402.16	1.944304	0.227071
669	4.02	121.72	82.4	19496.97	2865.38	14098.12	12889.67	1.093753	0.2223
670	4.03	108.98	89.43	21363.65	2850.81	15127.05	12232.59	1.236619	0.23305
671	4.04	142.05	94.57	22747.25	2309.99	13942.97	10320.94	1.35094	0.223816
672	4.05	148.31	101.44	20799.22	2891.1	17860.8	12624.16	1.414811	0.229013
673	4.06	131.72	89.16	19333.67	2561.67	15941.43	10932.66	1.458147	0.234314
674	4.07	139.6	83.04	21600.08	2588.71	16850.38	11624.71	1.449531	0.22269
675	4.08	155.86	96.23	21672.48	2560.07	19201.05	11684.82	1.643247	0.219094
676	4.09	142.5	93.2	19261.77	2444.92	23378.46	11565.98	2.021313	0.211389
677	4.1	168.24	93.66	19008.02	2570.58	26886.52	12161.59	2.210773	0.211369
678	4.11	145.04	98.31	21033.29	2196.14	21861.62	10902.19	2.00525	0.20144
679	4.12	244.65	81.34	16809.78	1651.92	43912.67	9656.03	4.547694	0.171077
681	4.13	229.64	66.88	20268.54	1863.88	43772.09	9709.18	4.50832	0.191971
682	4.14	187.85	85.59	19974.12	2468.73	31729.05	12223.17	2.595812	0.201971
683	4.15	195.55	83.26	19257.59	2486.63	33871.05	13047.11	2.596058	0.190589
684	4.16	172.63	65.39	19159.74	2417.98	39415.43	13564.07	2.90587	0.178264
685	4.17	206.84	72.07	18167.04	2273.56	40787.16	13095.09	3.114691	0.173619
686	4.18	150.38	71.69	17526.37	2143.03	30712.76	11925.14	2.575463	0.179707
687	4.19	119.57	102.17	18370.36	2665.7	19037.9	12849.58	1.481597	0.207454
688	4.2	195.79	95.87	18094.97	2240.46	48102.68	12966.18	3.709857	0.172793
689	4.21	165.96	99.76	17966.55	2323.37	25633.58	13443.33	1.906788	0.172827
690	4.22	172.44	94.17	19080.85	2446.07	31950.24	13306.89	2.40103	0.18382
691	4.23	149.38	103.51	20444.98	2533.88	33197.63	13048.7	2.544133	0.194186
692	4.24	139.78	104.04	19536.79	2739.94	22180.21	15067.79	1.472028	0.181841
693	4.25	176.26	90.91	18583.12	2824.46	26489.06	14247.48	1.85921	0.198243
694	4.26	170.33	88.31	17789.75	2661.14	25645	13259.75	1.934049	0.200693
695	4.27	145.64	96.98	17498.44	2895.21	23768.58	14050.1	1.691702	0.206063
696	4.28	148.62	95.75	19565.54	2971.36	26409.23	14675.54	1.799541	0.20247
697	4.29	149.64	97.95	20398.17	2857.91	23723.11	14723.7	1.611219	0.194103
698	4.3	125.47	97.76	18478.41	2843.05	30112.73	14537.3	2.071411	0.195569
699	4.31	145.66	82.66	18776.78	2666.39	29222.11	14434.24	2.024499	0.184727
700	4.32	194.37	101.06	19311.34	2488.63	42466.41	13491.44	3.147656	0.18446
701	4.33	152.09	86.27	18775.58	2418.73	45396.43	13995	3.243761	0.172828
703	4.34	161.21	85.61	19171.12	2583.33	34183.64	13321.34	2.566081	0.193924
705	4.35	168.23	91.23	20116.79	2555.02	33373.45	14403.71	2.317004	0.177386
706	4.36	152.46	83.73	20018.91	2850.11	29562.62	13277.75	2.226478	0.214653
707	4.37	154.47	93.27	20205.31	2878.37	26065.47	15055.38	1.731306	0.191185
708	4.38	140.16	81.67	20002.76	2747.59	27224.49	15624.84	1.742385	0.175848
709	4.39	165.75	101.53	20075.13	2728.11	27516.67	14912.31	1.845232	0.182943
710	4.4	161.1	99.24	21152.49	2613.48	29927.53	13613.54	2.198365	0.191977
711	4.41	161.11	95.01	19205.35	2533.58	42953.39	13492.72	3.183449	0.187774
712	4.42	169.46	105.02	20034.53	2622.24	37240.85	15316.96	2.431347	0.171198
713	4.43	150.56	90.17	20393.24	2607.53	34271.76	13735.94	2.495043	0.189833
714	4.44	186.98	83.33	17217.01	2701.76	46849.46	14019.33	3.341776	0.192717
715	4.45	155.26	91.76	19038.17	2716.83	39791.51	13613.8	2.92288	0.199564
716	4.46	116.34	91.18	21914.2	2944.68	25908.26	14400.01	1.799183	0.204492
717	4.47	225.41	81.91	27603.41	2294.51	51102.62	12794.79	3.994018	0.179332
718	4.48	165.51	84.04	19782.7	2945.81	34536.52	13861.99	2.491455	0.21251
719	4.49	128.49	83.45	21866.96	2627.32	25470.2	11675.06	2.181591	0.225037
720	4.5	164.2	88.67	20877.14	2630.69	28342.64	13506.28	2.098479	0.194775
721	4.51	179.17	84.82	18804.29	2941.96	35736.09	12276.24	2.910996	0.239647
722	4.52	160.78	89.24	18284.41	2823.78	33296.56	12393.3	2.686658	0.227847
723	4.53	166.4	79.31	17425.82	2750.41	41573.68	13728.7	3.028231	0.20034
724	4.54	271.91	82.89	20499.73	1951.89	70847.13	11028.33	6.424103	0.176989
725	4.55	181.78	77.12	22473.93	2757.87	35591.42	13636.49	2.610013	0.202242
726	4.56	135.22	91.13	16987.97	2962.76	27405.2	13165.54	2.081586	0.225039
727	4.57	191.19	79.21	18285.11	2736.12	30376.52	12176.26	2.494733	0.224709
728	4.58	152.3	100.91	17906.5	2771.85	24867.27	12567.94	1.978627	0.220549
729	4.59	146.54	73.42	18965.91	2926.31	26014.37	12101.55	2.149673	0.241813
730	4.6	171.01	89	19958.16	2944.36	32674.68	12300.56	2.656357	0.239368
731	4.61	181.34	76.53	19820.56	2924.59	38385.91	11634.88	3.29921	0.251364
732	4.62	174.7	82.34	18979.55	2963.36	32822.05	13345.93	2.45933	0.222042
733	4.63	150.95	79.37	19258.63	3076.22	29610.17	13387.79	2.211729	0.229778
734	4.64	156.99	83.01	18045.75	2735.8	26902.44	11734.21	2.29265	0.233147
735	4.65	147.1	76.68	20568.19	3064.68	26168.88	12451.58	2.101651	0.246128
736	4.66	164.39	76.65	17786.65	3003.26	34808.28	13002.8	2.676983	0.23097
737	4.67	155.87	81.87	17908.33	2837.42	33031.04	11814.5	2.795805	0.240164
739	4.68	207.53	99.7	19268.95	2897.93	37094.39	13170.39	2.816499	0.220034
740	4.69	167.17	85.8	17741.18	2609.87	40937.6	12400.04	3.301409	0.210473
741	4.7	137.06	79.37	17843.9	2825	27844.78	12609.18	2.208294	0.224043
742	4.71	178.08	91.98	16853.51	2766.92	38479.08	13142.72	2.927787	0.210529
743	4.72	159.61	91.05	18915.29	3102.8	29623.26	14399.08	2.057302	0.215486
744	4.73	168.18	105.71	19353.37	2368.63	39061.67	11500.25	3.396593	0.205963
747	4.74	199.62	84.53	17107.53	2701.05	34253.88	13131.89	2.60845	0.205686
748	4.75	176.54	88.69	17794.35	2852.35	25825.52	15305.34	1.687354	0.186363
749	4.76	149.36	83	20625.79	3192.93	21520.37	15029.35	1.43189	0.212446
750	4.77	139.42	81.11	17218.25	2845.72	26121.03	14849.83	1.759012	0.191633
751	4.78	159.3	108.37	18703.38	3039.46	29649.81	13244.45	2.238659	0.229489
752	4.79	145.67	105.82	18326.14	3125.81	23921.97	13860.81	1.725871	0.225514
753	4.8	130.82	103.56	17743.3	3243.94	17689.6	15844.91	1.116422	0.204731
755	4.81	145.74	102.57	18521.44	3100.09	20614.23	14660.83	1.406075	0.211454
756	4.82	152.49	100.47	21143.28	3028.23	23410.46	14407.23	1.624911	0.210188
757	4.83	159.47	90.25	19930.45	3358.97	20754.55	14783.42	1.403907	0.227212
758	4.84	148.31	105.8	18296.2	3374.4	18170.87	14613.45	1.243435	0.230911
759	4.85	133.67	112.85	20077.9	3200.99	18236.93	14993.68	1.216308	0.213489
760	4.86	130.99	78.86	19054.6	3270.92	18593.52	14590.98	1.274316	0.224174
761	4.87	164.21	87.32	20349.88	3268.37	21240.08	15105.19	1.406145	0.216374
762	4.88	153.89	90.31	21927.75	3156.84	24049.08	14342.91	1.676723	0.220098
763	4.89	163.71	92.18	18375	3202.93	21696.62	15816.08	1.371808	0.202511
764	4.9	160.25	93.1	21312.41	3151.86	22872.51	14464.77	1.581256	0.217899
765	4.91	162.45	98.51	20865.13	3134.6	21612.08	15854.13	1.363183	0.197715
767	4.92	151.74	94.25	17613.89	3322.58	26746.65	15716.36	1.701835	0.211409
768	4.93	134.56	95.68	18957.31	3269.29	20352.66	14961.71	1.360316	0.21851
769	4.94	193.08	88.38	22138.77	3101.89	32279.21	14794.06	2.181903	0.209671
770	4.95	182.22	85.55	18604.15	3024.85	30406.37	14698.05	2.068735	0.205799
771	4.96	170.3	88.62	18426.96	2998.01	26375.17	14488.37	1.820437	0.206925
772	4.97	161.27	85.12	18038.13	3045.95	25440.22	16172.09	1.573094	0.188346
881	4.99	148.07	95.02	19239.8	3381.47	18484.15	13498.87	1.369311	0.2505
556	5.02	149.78	89.58	17531.95	3474.63	18043.24	14943.93	1.207396	0.232511
557	5.03	153.98	93.12	18878.74	3253.86	23712.24	14651.05	1.618467	0.222091
558	5.04	163.08	93.54	18807.36	3214.76	25902.72	13848.14	1.870484	0.232144
559	5.05	153.82	95.27	21593.56	3285.72	20800.53	13486.13	1.542365	0.243637
560	5.06	162.3	90.5	19508.95	3304.52	21384.06	13843.54	1.544696	0.238705
561	5.07	163.31	93.29	19669.65	3263.28	22703.1	14713.46	1.543016	0.221789
562	5.08	160.3	101.51	21439.56	3282.09	19776	13376.93	1.478366	0.245355
563	5.09	177.82	102.45	20421.73	3012.56	25580.98	13083.33	1.955235	0.230259
564	5.1	161.09	83.01	20714.97	3081.72	19993.52	13166.53	1.518511	0.234057
565	5.11	196.92	104.24	19353.96	3152.59	28453.91	14037.51	2.026991	0.224583
566	5.12	172.54	102.84	20416.93	3179.1	34156.98	13325.4	2.563299	0.238574
567	5.13	152.76	97.67	19880.35	2877.07	32071.39	12998.02	2.467406	0.221347
568	5.14	180.68	84.64	18915.8	2852.62	37367.28	13122.88	2.847491	0.217378
569	5.15	154.04	91.91	19156.82	3321.66	24892.16	14015.94	1.775989	0.236992
574	5.16	145.59	106.43	19892.59	3185.4	20998.17	13955.86	1.504613	0.228248
575	5.17	153.87	83.23	20014.35	3028.27	22057.79	13876.55	1.589573	0.218229
576	5.18	195.35	95.27	20173.59	3163.51	33651.13	13649.36	2.4654	0.23177
577	5.19	178.1	97.55	19973.32	3241.83	25335.14	13313.28	1.902998	0.243503
578	5.2	165.14	101.2	19920.37	3151.88	28248.95	13828.18	2.042854	0.227932
579	5.21	177.64	77.46	19014.41	3171.98	30736.37	13471.15	2.281644	0.235465
580	5.22	162.4	95.72	18796.3	2769.09	31713.12	12760.87	2.485185	0.216999
581	5.23	135.14	86.47	19874.49	3010.35	16634.99	14476.26	1.149122	0.207951
582	5.24	176.57	100.27	19790.03	2765.46	23756.51	12325.68	1.9274	0.224366
583	5.25	171.58	92.31	21959.29	2854.5	34933.55	12279.37	2.844898	0.232463
584	5.26	182.3	78.02	19173.99	2671.83	37560.78	12316.52	3.049626	0.216931
585	5.27	170.49	87.34	18923.77	2907.7	27844.42	12262.53	2.270691	0.237121
587	5.28	151.88	99.33	19878.81	2958.44	26388.07	12978.64	2.033192	0.227947
588	5.29	148.36	100.51	20947.86	3008.39	25202.38	13207.24	1.908225	0.227783
589	5.3	197.91	82.96	19895.23	2727.41	39251.29	13177.07	2.978757	0.206982
590	5.31	171.95	87.93	20356.48	2847.44	30577.07	12984.25	2.354935	0.2193
591	5.32	179.88	81.73	21853.4	2657.79	41984.12	11274.36	3.723858	0.235738
592	5.33	252.59	71.98	24286.42	2220.6	57094.13	9442.33	6.046615	0.235175
593	5.34	201.81	86.78	25718.81	2237.6	54135.51	10292.93	5.259485	0.217392
594	5.35	226.41	73.82	25111.04	1994.83	53696.61	11489.05	4.673721	0.173629
595	5.36	293.22	75.19	28473.57	1944.83	68205.23	10246.28	6.656585	0.189808
596	5.37	199.46	88.92	21576.97	2023.35	54971.32	10037.43	5.476633	0.20158
597	5.38	279.95	76.22	31361.43	1787.58	69266.17	9439.34	7.338031	0.189376
598	5.39	318.16	49.13	28420.61	1620.33	89025.86	9070.18	9.815225	0.178644
600	5.4	234.7	80.45	23936.17	1912.51	57109.5	10741.04	5.316943	0.178056
601	5.41	214.94	88.75	20896.65	2529.32	55421.8	13391.97	4.138435	0.188868
602	5.42	194.73	96.94	20164.62	2381.71	37910.74	13755.62	2.756018	0.173145
603	5.43	186.85	85.72	19214.57	2176.52	40424.25	12807.61	3.156268	0.16994
604	5.44	164.77	92.57	19125.97	2384	34262.5	13652.73	2.509571	0.174617
605	5.45	193.35	83.98	18732.46	2464.05	38036.11	13732.85	2.769717	0.179427
606	5.46	207.72	73.33	18563.76	2130.98	32767.36	13411.37	2.443252	0.158894
607	5.47	197.27	95.53	17287.96	2588.57	38811.67	13847.65	2.802762	0.186932
608	5.48	181.01	80.86	17915.85	2017.55	35286.89	12206.03	2.890939	0.165291
609	5.49	172.82	87.83	16976.05	2078.18	37509.86	12308.89	3.04738	0.168836
610	5.5	205.35	91.25	17536.53	2195.23	52217.03	13814.84	3.779778	0.158904
611	5.51	199.79	91.76	20474.08	2626.09	37233.66	14396.12	2.586368	0.182417
612	5.52	174.78	98.13	18626.72	2479.09	39

Geochemistry: Christian Malford Borehole 9

sample (SSK)	depth (m)	Sr	Rb	Fe	Ti	Ca	K	Ca/K	Ti/K
57590	0.01	138.65	106.78	24680.64	4576.18	29015.82	25048.4	1.15839	0.182694
57589	0.0275	162.68	104.27	25471.79	4154.12	33719.27	24867.68	1.355948	0.167049
57588	0.045	167.23	104.27	24382.48	3927.84	42799.99	24085.36	1.777013	0.16308
57587	0.0625	164.57	110.06	26218.18	4400.67	36534.8	24697.46	1.479294	0.178183
57586	0.08	194.73	107.54	27385.91	4372.43	39404.05	25308.92	1.556923	0.172762
57585	0.09	181.14	104.25	31476.5	4411.86	36489.24	25155.06	1.450573	0.175387
57584	0.1	203.93	104.15	29364.8	4449.92	39306.11	24154.66	1.627268	0.184226
57583	0.11	227.43	110.76	30365.38	4183.99	45686.33	24829.17	1.840026	0.168511
57582	0.12	202.16	111.57	32870.89	4246.8	42836.47	25330.13	1.691127	0.167658
57581	0.13	174.22	99.76	29075.95	4581.27	33545.49	26092.6	1.285632	0.175577
57580	0.14	194.41	118.19	25570.69	4528.36	36026.8	26146.25	1.377895	0.173193
57579	0.1575	233.19	100.16	26129.19	4089.36	50860.57	24213.81	2.100478	0.168885
57578	0.17	173.18	100.89	24694.92	4195.79	39419.89	25534.07	1.543815	0.164321
57577	0.215	210.25	105.45	25271.47	3918.33	52666.17	25704.7	2.048893	0.152436
57576	0.26	189.11	113.42	25580.54	4064.88	47086.14	25823.34	1.823395	0.157411
57575	0.27	185.18	103.27	24778.05	3994.28	49425.32	26014.13	1.899941	0.153543
57574	0.28	180.99	111.52	26399.18	3816.87	52623.25	24835.12	2.118905	0.153688
57573	0.29	186.63	110.89	25319.98	3724.14	55750.42	25763.79	2.163906	0.144549
57572	0.3	171.24	96.41	26817.43	3551.83	54493.34	24736.68	2.202937	0.143586
57571	0.31	161.26	102.36	26371.17	3883.12	44331.87	24424.19	1.81508	0.158987
57570	0.32	153.51	115.95	27117.25	4884.17	28890.21	25923.88	1.114425	0.188404
57569	0.33	138.71	104.16	26450.04	5170.59	26306.21	26404.32	0.996284	0.195824
57568	0.34	155.21	111.33	27140.55	5305.2	26353.97	25903.47	1.017391	0.204807
57567	0.35	171.51	114.37	28852.28	4904.88	30148.36	25577.96	1.178685	0.191762
57566	0.375	197.65	101.24	28469.72	4680.05	34050.8	24915.44	1.366655	0.187837
57565	0.4	129.17	110.34	27019.11	5033.71	20225.04	24155.79	0.837275	0.208385
57564	0.425	185.94	121.29	27170.87	4951.05	32256.81	24436.43	1.32003	0.202609
57563	0.45	189.97	110.18	27660.29	4653.29	35987.17	23644.23	1.522028	0.196804
57562	0.475	209.17	103.17	27732.7	4629.19	42209.04	23756.58	1.77673	0.194859
57561	0.485	177.41	104.18	27874.32	4850.22	30661.95	24429.78	1.255105	0.198537
57560	0.495	178.99	95.98	26074.07	4642.93	32433.68	24482.8	1.324754	0.18964
57559	0.53	196.64	99.19	27424.47	4501.61	41863.65	24119.57	1.735671	0.186637
57558	0.57	153.12	100.6	25761.79	4451.49	36205.81	24094.65	1.502649	0.18475
57557	0.61	202.2	92.54	26400.41	4075.26	47546.52	23382.15	2.033454	0.174289
57556	0.69	171.35	87.12	23160.39	4112.37	44784.25	23418.46	1.912348	0.175604
57555	0.71	182.75	92.87	22126.86	3820.83	55443.69	22667.44	2.445962	0.16856
57554	0.84	199.25	109.01	25577.32	4529.93	36019.77	24139.94	1.492123	0.187653
57553	0.86	145.75	98.92	21712.22	4070.26	50005.14	21410.96	2.335493	0.190102
57552	0.9	158.89	83.99	22331.41	4019.4	49818.51	22852.3	2.180022	0.175886
57551	0.94	143.84	83.59	21610.59	3845.95	54629.5	21983.23	2.485053	0.174949
57550	0.98	162.81	90.05	22082.46	3793.89	57150.71	22406.46	2.550635	0.169321
57549	1	153.31	82.03	22077.44	3728.52	59658.38	21320.97	2.798108	0.174876
57548	1.02	172.18	87.53	24595.06	4105.97	44904.43	25161.23	1.784668	0.163186
57547	1.04	161.54	96.04	25391.37	4275.14	37919.86	26328.19	1.440276	0.162379
57546	1.08	179.48	96.17	30642.06	5026.25	40851.08	26259.14	1.55569	0.19141
57545	1.1	216.99	106.9	23975.08	3925.32	47012.3	25929.75	1.813064	0.151383
57544	1.12	193.22	91.12	23620.8	3638.82	53541.13	25050.51	2.137327	0.145259
57543	1.14	204.47	95.11	25355.14	3507.7	57016.91	25349.88	2.249198	0.138371
57593	1.18	184.14	89.78	27033.8	3584.41	55350.77	24170.18	2.290044	0.148299
57542	1.22	208.03	93	26149.19	3369.94	62158.09	24447.7	2.542492	0.137843
57541	1.26	259.75	80.62	29636.57	3031.26	84055.21	23462.57	3.582524	0.129196
57540	1.3	208.89	91.96	27428.39	2933.34	74301.99	23933.29	3.104546	0.122563
57539	1.34	135.32	108.47	25229.53	4728.29	21970.94	25501.13	0.861567	0.185415
57538	1.365	131.63	109.49	25939.69	4781.88	22581.82	25097.5	0.899764	0.190532
57537	1.4	164.35	120.59	26271.64	4967.68	26732.38	25361.37	1.054059	0.195876
57536	1.4133	130.77	116.71	24644.01	5090.91	19085.24	26056.91	0.732444	0.195377
57535	1.4266	162.26	104.69	25475.68	4899.34	29199.19	25496.57	1.14522	0.192157
57534	1.4366	159.09	108.05	26699.21	4912.67	28487.83	25100.87	1.134934	0.195717
57533	1.4466	171.36	119.7	26343.31	4848.84	29845.82	24937.91	1.196805	0.194437
57532	1.4566	163.76	114.18	24893.12	4761.68	31699.82	25176.56	1.259101	0.189131
57531	1.47	176.63	116.34	26180.29	4740.64	34654.72	24246.78	1.42925	0.195516
57530	1.4833	167.16	96.84	24987.56	4687.12	34136.74	24269.4	1.406575	0.193129
57529	1.4966	166.74	118.13	26458.79	4827.77	31682.49	25214.7	1.256509	0.191466
57528	1.51	172.26	112.54	27522.56	4676.32	32749.71	25701.78	1.27422	0.181945
57527	1.52	181.43	114	26746.34	4725.89	35409.65	26095.28	1.356937	0.181101
57526	1.53	167.5	126.81	28085.01	4713.7	31508.3	25709.66	1.225543	0.183344
57525	1.54	185.2	122.49	26593.43	4675.91	34394.25	26833.4	1.28177	0.174257
57524	1.55	191.3	117.44	26288.98	4663.2	31354.71	26504.16	1.183011	0.175942
57523	1.56	179.71	112.65	24234.89	4557.87	37926.78	27043.62	1.40243	0.168538
57522	1.62	186.89	124.18	25560.47	4497.28	38069.59	27898.12	1.364593	0.161204
57521	1.64	210.1	83.12	25155.19	3249.38	72410.3	24707.88	2.930656	0.131512
57520	1.66	235.26	82.58	24861.05	2727.23	94441.18	24079.5	3.922057	0.113259
57518	1.7	242.45	89.58	23884.76	2816.61	96597.69	24124.48	4.004136	0.116753
57517	1.73	225.51	108.98	28132.96	3030.36	77009.96	24689.47	3.119142	0.122739
57516	1.76	202.73	111.57	26130.41	3758.97	57495.95	26355.18	2.181581	0.142627
57515	1.81	200.75	106.11	27872	3746.52	54974.21	26681.05	2.060422	0.140419
57514	1.91	221.78	120.79	28267.21	3756.66	54991.94	27601.99	1.992318	0.136101
57513	1.95	186.5	109.99	26992.97	3926.83	43801.33	26970.86	1.624024	0.145595
57512	1.98	193.91	116.02	27473.85	4347.74	36745.18	27424.86	1.339849	0.158533
57511	2.01	190.54	109.75	26872.55	4579.13	30765.98	26696.39	1.15244	0.171526
57510	2.04	147.98	111.22	28405.23	5057.02	21180.14	25474.36	0.83143	0.198514
57509	2.08	173.04	113.85	29013.02	4950.66	23999.31	24912.08	0.96336	0.198725
57508	2.11	167.24	113.15	28698.39	4857.52	25254.76	24957.39	1.011915	0.194633
57507	2.14	204.53	112.1	33623.34	4704.02	31047.5	24513.95	1.266524	0.191892
57506	2.17	192.95	120.22	30432.34	4741.51	28193.22	25236.85	1.117145	0.18788
57505	2.2	189.43	118.11	29807.21	4817.48	27634.28	26195.27	1.054934	0.183906
57504	2.21	175.15	125.07	28479.37	5000.43	25268.19	26807.71	0.942572	0.18653
57503	2.22	172.34	132.01	27197.56	4882.4	24373.05	26863.81	0.907282	0.181746
57502	2.23	191.56	133.87	27587.18	4704.97	30150.97	27598.55	1.092484	0.170479
57601	2.24	240.73	122.83	26904.36	3841.21	58819.38	26212.91	2.243909	0.146539
57501	2.25	203.8	116.29	28145.02	4565.79	34762.61	26716.6	1.301161	0.170897
57604	2.26	183.16	113.72	25108.49	3887.72	45743.38	26962.68	1.696544	0.144189
57594	2.27	279.79	92.55	30159.82	2961.28	82496.2	23767	3.47104	0.124596
57500	2.28	233.51	107.83	27252.51	3938.55	53519.18	26537.23	2.016758	0.148416
57499	2.308	212.04	118.49	26198.26	4616.75	37381.56	27492.93	1.359679	0.167925
57498	2.336	193.37	125.1	26386.09	4572.66	34707.85	27232.12	1.274519	0.167914
57592	2.364	211.06	121.44	26241.35	4117.98	45567.23	27517.75	1.655921	0.149648
57497	2.392	257.35	99.81	26368.96	3705.68	62438.08	26580.06	2.349057	0.139416
57595	2.42	242.14	118.46	27577.67	4037.18	54954.81	28146.01	1.95249	0.143437
57496	2.448	186.78	125.23	26557.52	4244.07	38552.52	28658.24	1.345251	0.148092
48496	2.476	221.2	134.47	25771.05	4288.64	38764.27	28922.12	1.340298	0.148282
48495	2.504	200.52	115.43	25539.43	4167.55	45556.09	28473.13	1.599968	0.146368
48494	2.532	235.15	132.23	28631.84	4140.49	42136.22	27710.42	1.520591	0.14942
48493	2.56	239.84	122.66	25767.02	4104.33	50939.23	27386.15	1.860036	0.149869
48492	2.58	235.31	108.2	27599.97	4150.34	44214.07	27435.2	1.611582	0.151278
48491	2.6	205.44	109.21	26147.56	4449.61	38383.56	26719.83	1.43652	0.166528

Appendix 2 for ‘Rolling back the ‘mudstone blanket’: complex geometric and facies responses to basin architecture in the epicontinental Oxford Clay Formation (Jurassic, UK)’

The statistical analysis of the fossil content of the Oxford Clay Formation in nine UK boreholes.

Contents

Boreholes 3

Palaeontological Data 3

Statistical analysis: procedure 3

Data Acquisition and Exploratory Data Analysis 4
- Script 1: EDA_Removing rares 4
- Script 2: Number of clusters 4

Data manipulation 5
- Script 3: Non-Euclidian relational clustering 5
- Script 4: DCA analysis using the upper quartile taxa 6
- Script 5: Hierarchical clustering 6

Results 6

References 7

Ashdown 2 (AD) 8
Christian Malford 11 (CM11) 24
Christian Malford 9 (CM9) 40
Combe Throop (CT) 51
Down Ampney (DA) 67
Eriswell (EW) 83
Kimmeridge 2 (KR) 101
Parson Drove (PD) 117
Warlingham (WH) 134

Boreholes

The nine boreholes are listed in Table A.1 alongside their code used throughout this document. Their approximate stratigraphic coverage is shown in Figure 2 of the paper.

Table A.1: Borehole codes

Borehole	Code
Ashdown 2	AD
Christian Malford 9	CM9
Christian Malford 11	CM11
Coombethroop	CT
Down Ampney	DA
Eriswell	EW
Kimmeridge 2	KR
Parson Drove	PD
Warlingham	WH

Palaeontological Data

Palaeontological data was captured using a scale from 0 to 3, except for borehole CM11 where a scale of 0 to 4 was employed. For the purpose of the subsequent statistical analysis and to improve comparison between the boreholes, all results were brought back to the same scale. Table A.2 shows that scale point 1 in 8 boreholes was taken as '1 or a few' which corresponds to scale points 1 (present (1)) and 2 (common (2–4) in CM11. Therefore, scale points 1 and 2 in CM11 were merged to scale point 1 and scale points 3 (abundant) and 4 (plaster) were converted to 2 and 3 respectively. In total 79 taxa were recognized in the Oxford Clay material of the nine boreholes. In the statistical analyses, the faunal codes of Appendix 1 were employed.

Table A.2: scoring of the palaeontological content of the Oxford Clay material

Scale	Abundance	CM11	Abundance	Converted
0	absent	0	0	0
1	1 or a few	1	present (1)	1
2	many	2	common (2-4)	1
3	plaster	3	abundant	2
		4	plaster	3

Statistical analysis: procedure

All the statistical analyses were performed in the open source environment R (R Development Core Team, 2020). Six scripts were written to perform the necessary transformations to produce the figures following this introduction. These six scripts use functions from the following R packages: *Hmisc* (v4.4-1; Harrell, 2020), *vegan* (v2.5-6; Oksanen et al., 2020), *rioja* (v0.9-21; Juggins, 2017), *tidyverse* (Wickham et al., 2019), *fossil* (v0.4.0; Vavrek, 2011), *ecodist* (v2.0.7; Goslee and Urban, 2007), *cluster* (v2.1.0; Maechler et al., 2019), *NbClust* (v3.0; Charrad et al., 2014), *dendextend* (v1.14.0; Galili, 2015), and *factoextra* (v1.0.7; Kassambra and Mundt, 2020).

The six scripts perform specific tasks in the statistical workflow. The ultimate aim of the statistical analysis in the current study is twofold:

1. Understand the pattern of biofacies for each borehole (and the extent to which biofacies successions for individual boreholes can be merged into a unified set of biofacies for all the boreholes).
2. Understand how zones / subzones vary or are similar between borehole locations – this is reflected in the biofacies patterns for those zones / ubzones.

The workflow is divided into three stages: data acquisition, data manipulation and interpretation. Appendix 1 focuses on the first two stages for the nine UK boreholes where extra data was acquired which lay the foundation for the interpretation discussed in the main text. We are focusing on each borehole separately to fulfil goal 1: visualizing and interpreting the changes in biofacies in each borehole to understand the palaeo-ecological changes.

Data Acquisition and Exploratory Data Analysis

The palaeontological analysis was performed by PW and MAW on cored materials proving the Peterborough Member of the Oxford Clay Formation. Horizons parallel to sub-parallel to the prevailing bedding orientation were scanned using zoom stereomicroscopes. Palaeontological data was captured on a 0 to 3 scale except for CM11 where a 0 to scale was employed (see Table A.2), a semi-quantitative method.

Script 1: EDA_Removing rares

This script performs the pre-processing analysis of the data (EDA = exploratory data analysis) and can be summarized as follows:

Remove Sz, Az, PsZ, Cz, Gsz, OsZ, CJC, Jz, Jsz, MsZ, Esz, Csz and AmS. These variables describe stratigraphic position and sample size and have to be removed. AmS is a bin term combining taxa of very different origin, the ecology of which cannot be resolved by the statistical analyses.

The faunal code for Nanogyra was changed from NA to NG. This is because NA clashes with the R language which assumes NA signifies missing data (NA = Not Available).

The following taxa were merged: NU + MC; MP + TR; AP + AM.

A preliminary detrended correspondence analysis (DCA) was run on the resulting raw dataset. This gives an idea of the number of clusters required to effectively see the changes in biofacies. It also generates a list of species statistical weights, which can be used to select the upper quartile species for the ordination analysis.

A second DCA was run only on the taxa with an upper quartile statistical weight.

Script 2: Number of clusters

To determine the number of clusters to be utilised in each borehole, we use the *NbClust* (v3.0; Charrad et al., 2014) package. It draws on >20 methods to perform cluster analysis. The function NbClust performs tests all methods and reaches a conclusion informing the most suggested number of clusters. As an input, this function requires a minimum and maximum number of clusters to consider. We use the 'Elbow' plot in combination with the initial DCA plot to provide that information. The two other methods we relied on for the current analysis are the gap statistic (function clusGap) and the silhouette plot (function fviz_nbclust). Based on these four lines of evidence, we choose an appropriate number of clusters for each borehole.

Data manipulation

We employ two multivariate methods to evaluate the recovered fauna in the nine UK boreholes:

Clustering which assumes discontinuities to exist in the dataset which form the basis to recognise discrete groups. This technique is desirable in heterogeneous datasets. The outcome of cluster analysis is a two-dimensional dendrogram. No relationships between the clusters and underlying environmental gradients can be discerned directly, although the clusters may be interpreted as representing communities, biofacies, or faunal provinces.

Ecological **ordination**: the ordering or arrangement of samples and/or variables (taxa) in an ecological space in relation to environmental gradients. Ordination extracts major directions of variation from the original data by rearranging the data points in a multidimensional space so that they are concentrated on the first few, preferably two, principal axes. No assumption of a grouping structure is made, instead, ordinations assume continuity in the data. The outcome is a two-dimensional scatter plot in which the samples and/or variables are located relative to on another according to their variations on these axes. Natural groupings of samples and/or variables are revealed in this way.

We employed three multivariate techniques: two clustering techniques: (Non-Euclidian Relational Clustering (NERC) and hierarchical clustering) and one ordination technique (detrended correspondence analysis (DCA)). NERC is considered to be the most reliable clustering method for palaeontology and palaeobiology datasets because it scores better on incomplete datasets (Vavrek, 2016). However, in the current study we exclusively use borehole data which introduces an inescapable relationship between the samples: a stratigraphical ordering, which assuming the absence of faulting or folding, means an ordering by age. This is typically more easily visualized by dendrograms and therefore we have utilised a combination of both clustering techniques: a dendrogram coloured using the NERC clustering. To better understand the clustering results, we use the same NERC colours for the DCA plots to allow downhole interpretations of palaeoecological changes.

A further ordination technique, Non-Metric Multidimensional Scaling (NMDS) (using metaMDS in *vegan*) was attempted as it is a good indicator to assess cluster distinctiveness and is also commonly used on palaeontological data (e.g. Danise et al., 2013). However, it was specifically designed for quantitative data (Kruskal, 1964) and we found it performed suboptimally for our purposes where only semi-quantitative data were available.

Script 3: Non-Euclidian relational clustering

Most functions for multivariate analysis require an ecological distance matrix as input, constructed by applying a formula to the raw counts or the semiquantitative scores. We used the Sørenson dissimilarity index (or Dice or coincidence index, Dice, 1945). It is one of the most commonly used indices and is regarded as one of the most effective presence/absence dissimilarity measures (Southwood & Henderson, 2000; Magurran, 2004) and is the recommended input for NERC (Vavrek, 2011).

We follow the recommendations of Legendre and Legendre (2012): when dealing with species abundances that are not raw abundances and without associated probability levels, the Sørenson index is one of the recommended dependence measures. In general, it is not recommended to discard semi-quantitative data when available, but we are dealing with three different ways of capturing data: two semi-quantitative scales in the 9 boreholes and full quantitative counts collected by another study (Appendix 3). Therefore, we choose to use a dependence measure that can be applied equally on all datasets of the current study.

In R, this conversion is performed by the ecol.dist function of the ecodist package. The resulting distance matrix was then used for the rclust function of the fossil package, with the specified number of clusters to be recognized (see above) to perform the NERC analysis.

Script 4: DCA analysis using the upper quartile taxa

Script 1 results in an initial DCA plot based on the full, raw dataset for each borehole. However, in many cases interpretations will be made almost impossible because the presence of rare taxa forces the isolation of a few samples, while the majority of samples is packed in one tight cluster. A common technique to avoid skewing the DCA plots, is to consider only the taxa with an upper quartile statistical weight. Using script 1, we subset the original dataset to isolate the upper quartile taxa and ran a DCA analysis using the decorana function of the vegan package. We then coloured the datapoints using the NERC clusters. For each borehole, a figure with only the samples and a figure with samples and taxa is provided.

Script 5: Hierarchical clustering

To perform hierarchical clustering, we utilised the chclust function of the rioja package. This is the only function that allows hierarchical clustering whilst maintaining sample ordering. It also allows the samples to be spaced using depths. Two dendrograms per borehole are provided: a first one where the samples are in order, not spaced using the depths, and coloured using the NERC clustering with a NERC colour bar. A second vertical dendrogram where sample distances are scaled using depths, but labels are not coloured instead, a basic line diagram indicating the NERC colours is added.

Results

On the pages following the references, the results of the statistical analysis of all the boreholes are shown. The figures provided are:

1. DCA of samples and all taxa
2. DCA of samples and only upper quartile (UQ) taxa
3. Elbow plot to determine optimal amount of clusters
4. Gap statistic plot to help determine the optimal amount of clusters
5. A silhouette plot to help determine the optimal amount of clusters
6. A DCA plot of NERC coloured samples and (UQ) taxa
7. A DCA plot of NERC coloured samples
8. Dendrogram (hierarchical clustering) with NERC colour bar
9. Dendrogram (hierarchical clustering); samples spaced using depths; NERC colour bar

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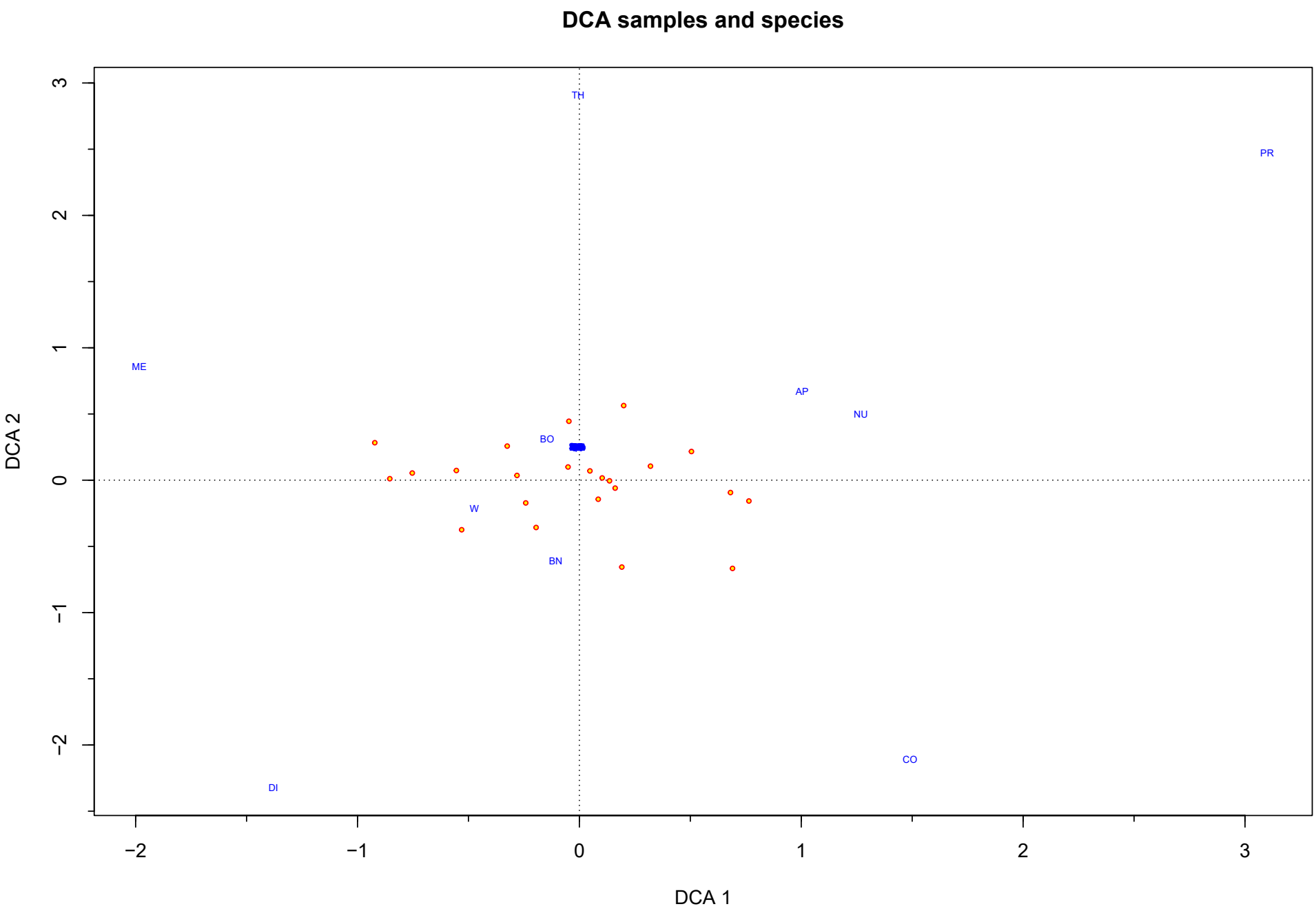
Ashdown 2 (AD)


DCA samples and species
TH
PR
ME
AP
NU
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DCA 1
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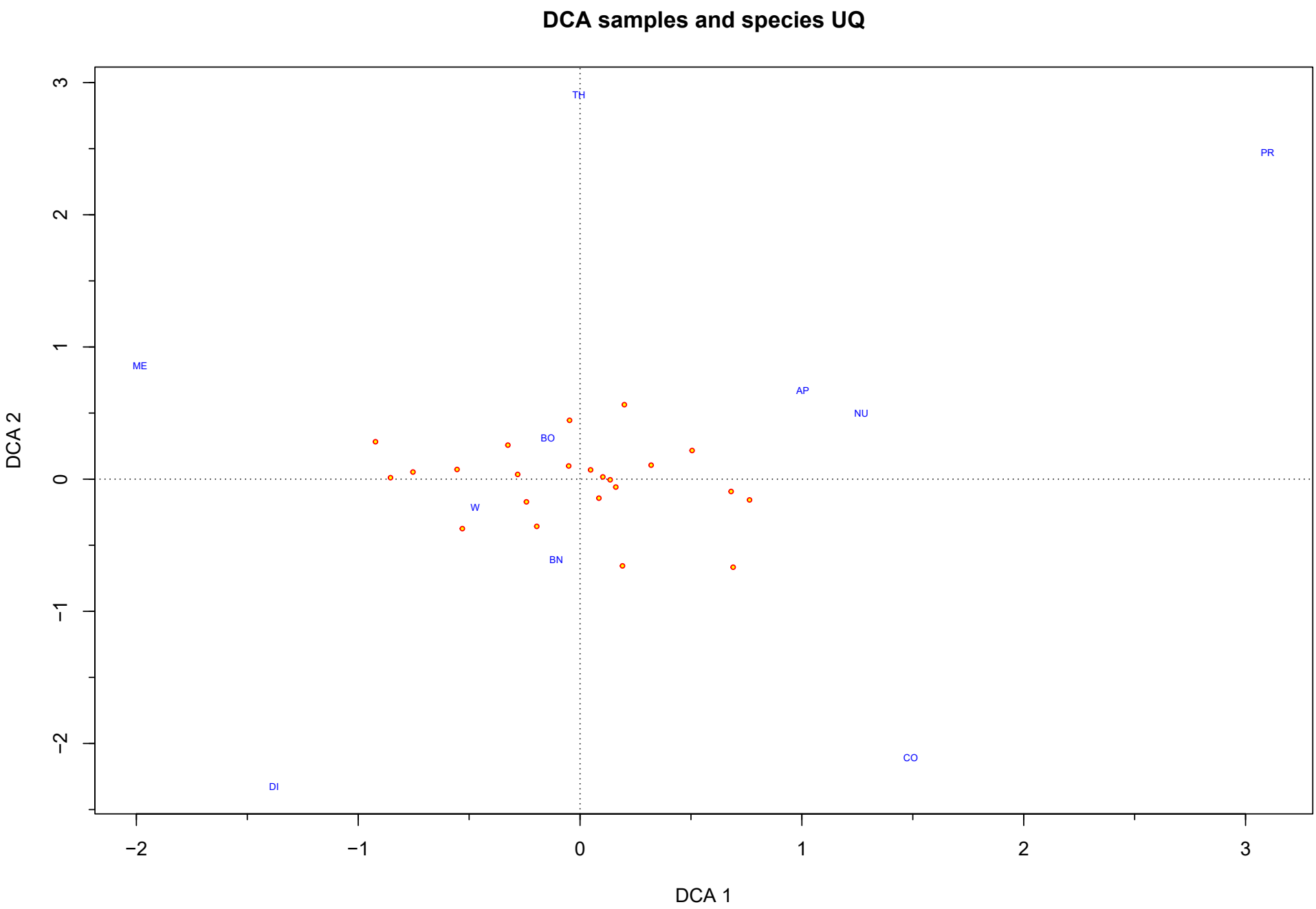
DCA samples and species UQ
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PR
ME
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NU
BO
W
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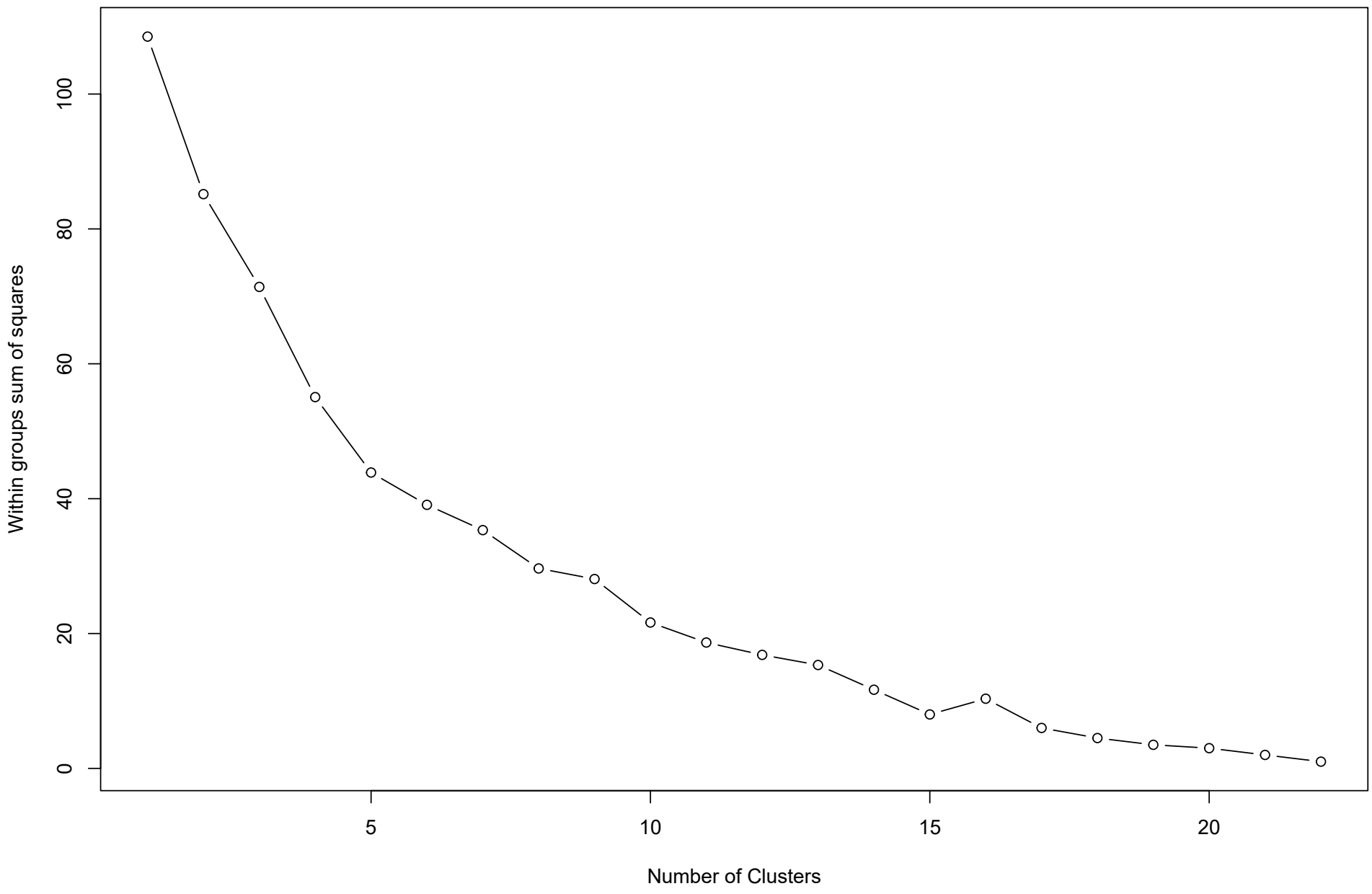
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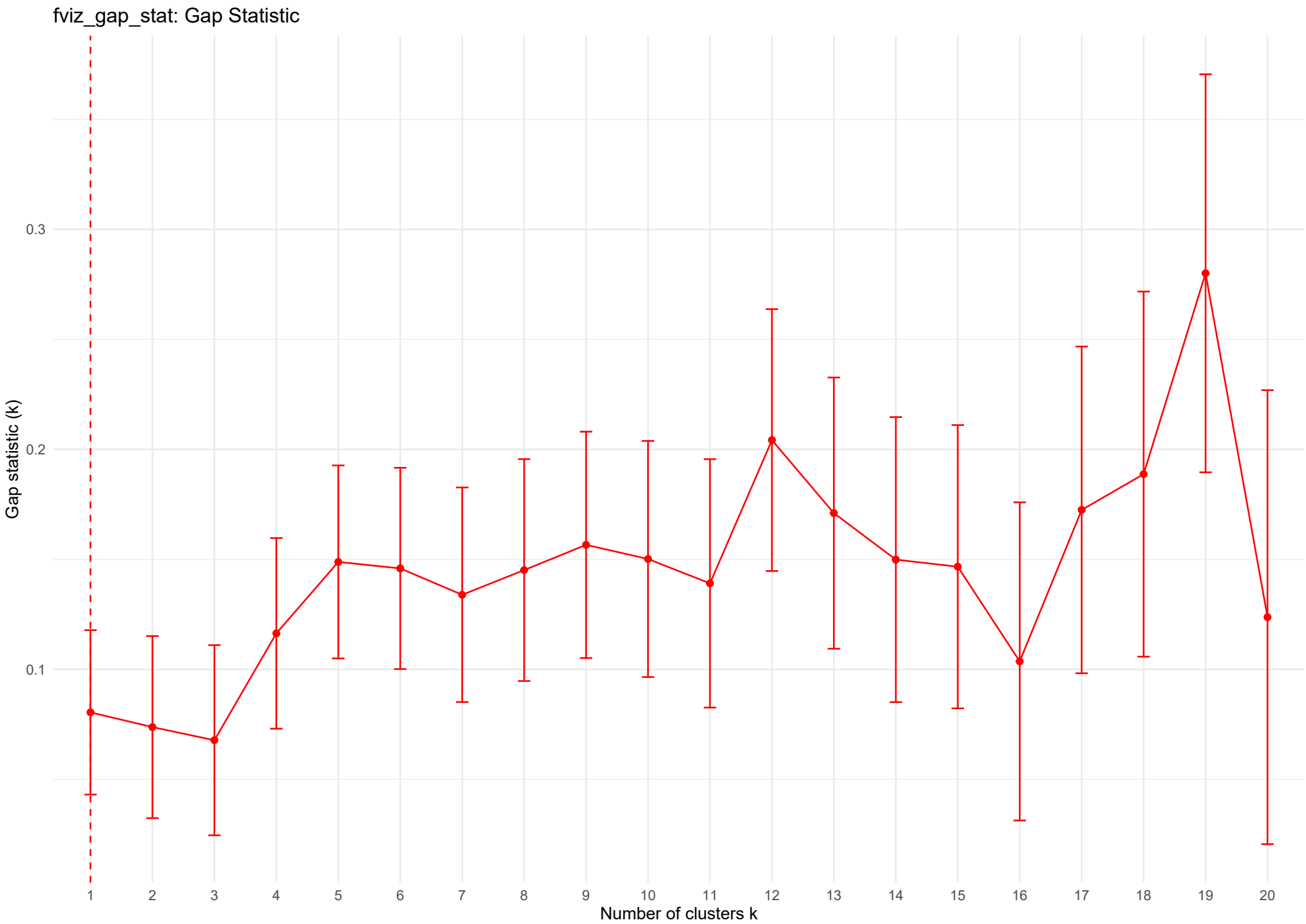
40
60
80
100
5
10
15
20
Number of Clusters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Gap statistic (k)
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0.2
0.1
1
2
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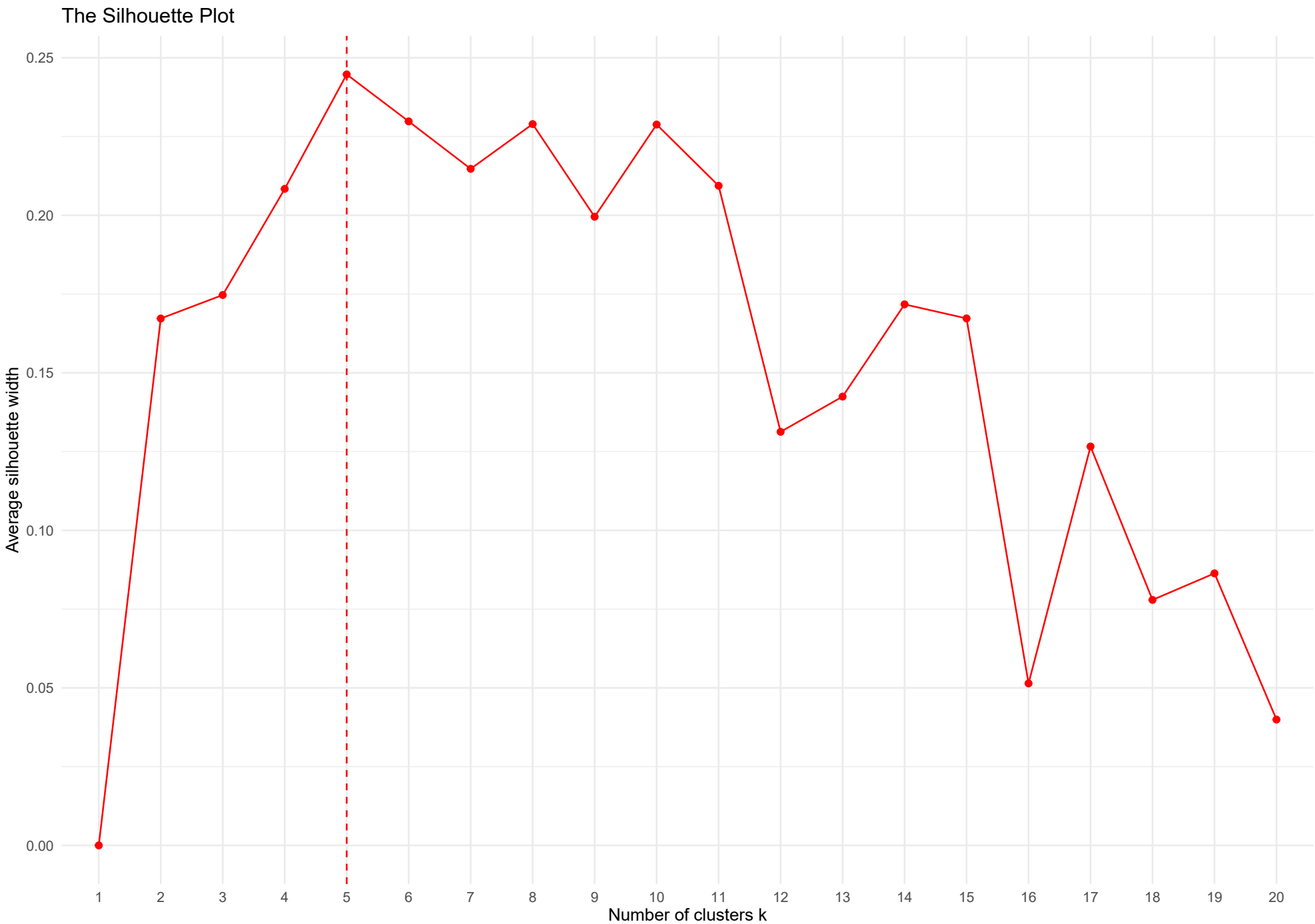
7
8
9
10
11
12
13
14
15
16
17
18
19
20
Number of clusters k


The Silhouette Plot
Average silhouette width
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0.20
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0.10
0.05
0.00
1
2
3
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12
13
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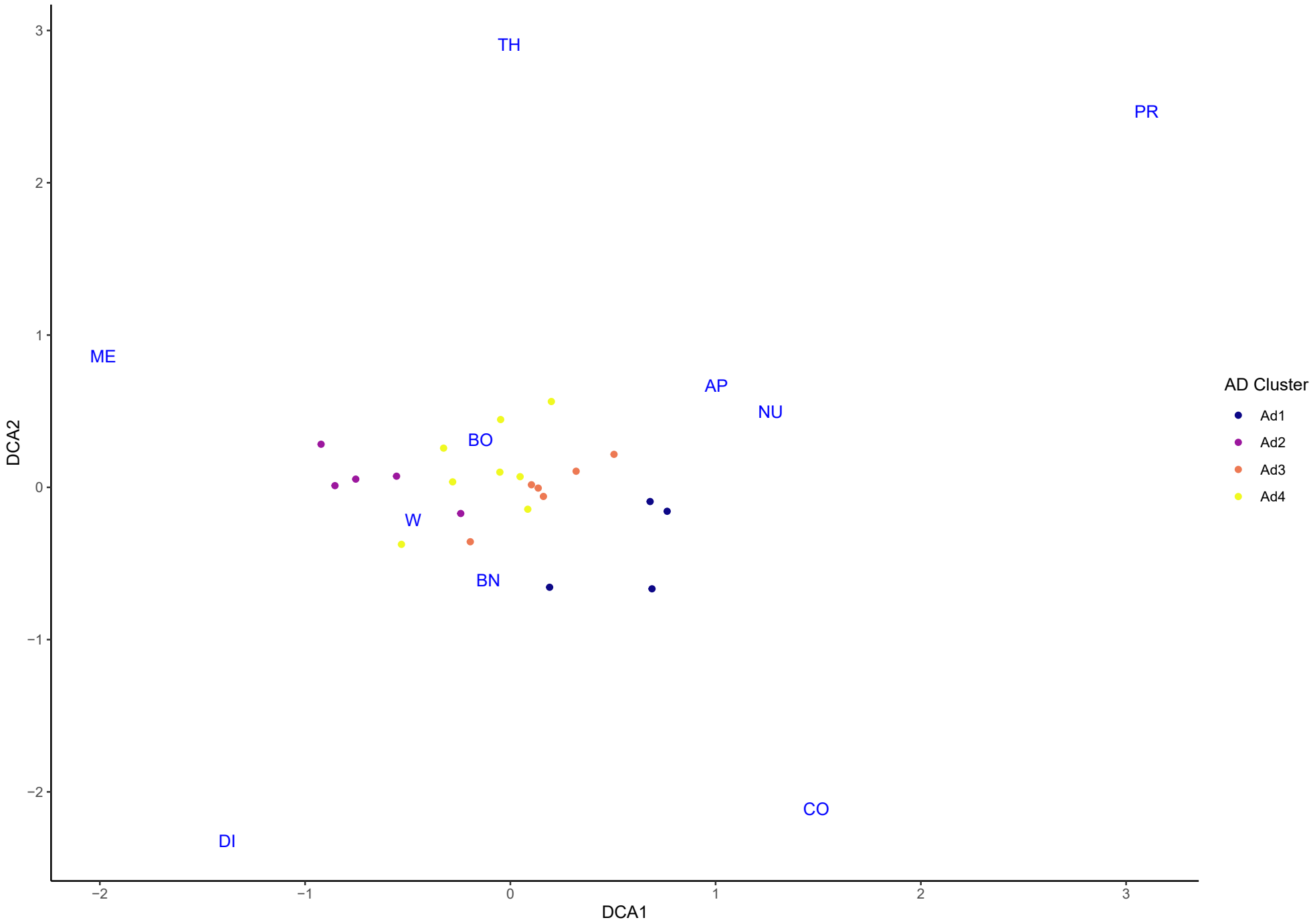
15
16
17
18
19
20
Number of clusters k


TH
PR
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BO
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DCA2
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−1
0
1
2
3
AD Cluster
Ad1
Ad2
Ad3
Ad4

AD_18
AD_3
AD_10
AD_5
AD_20
AD_19
AD_2
AD_9
AD_23
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AD_1
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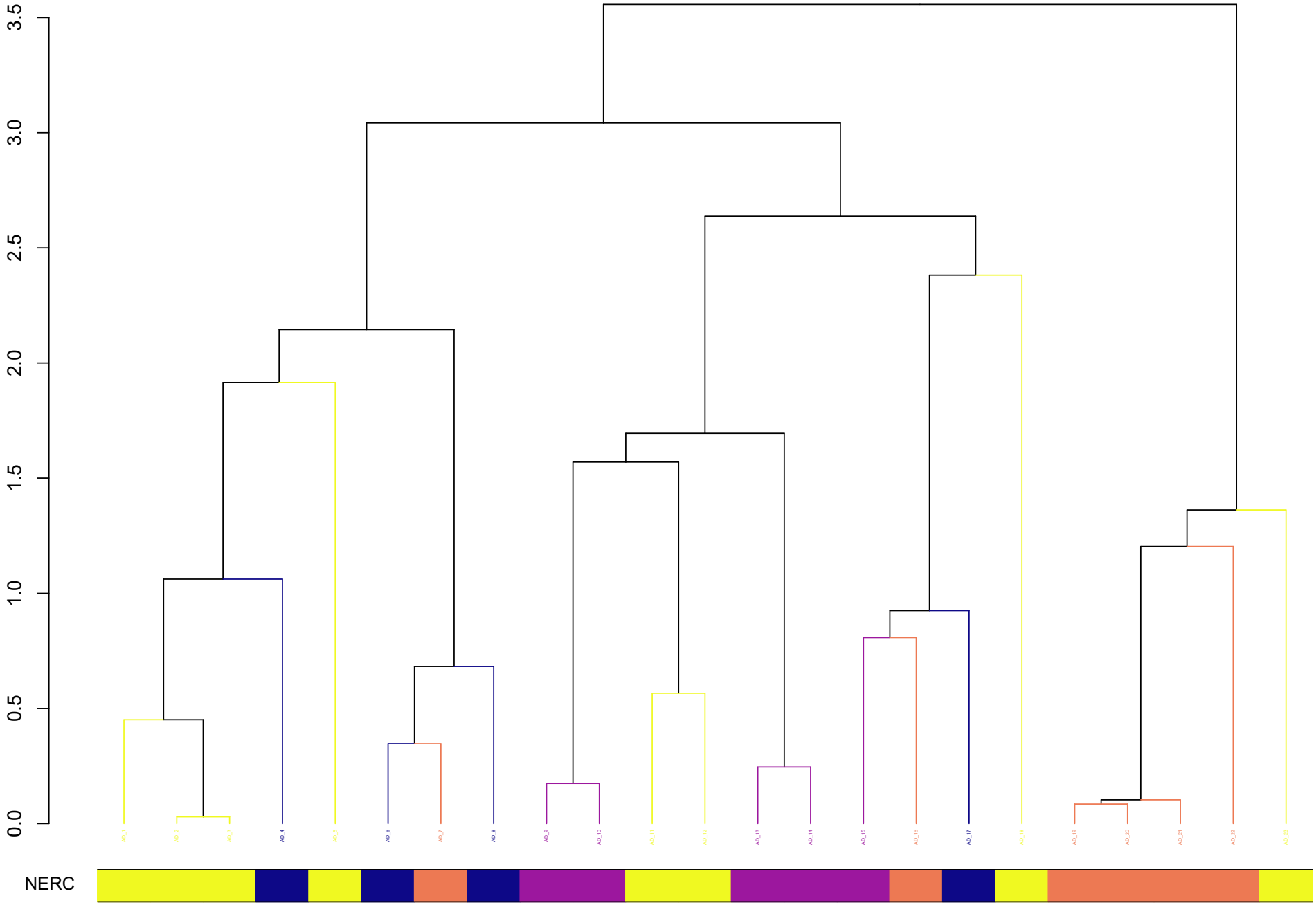
AD Cluster
Ad1
Ad2
Ad3
Ad4

Ashdown 2 (AD)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AD_2
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AD_6
AD_7
AD_8
AD_9
AD_10
AD_11
AD_12
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AD_19
AD_20
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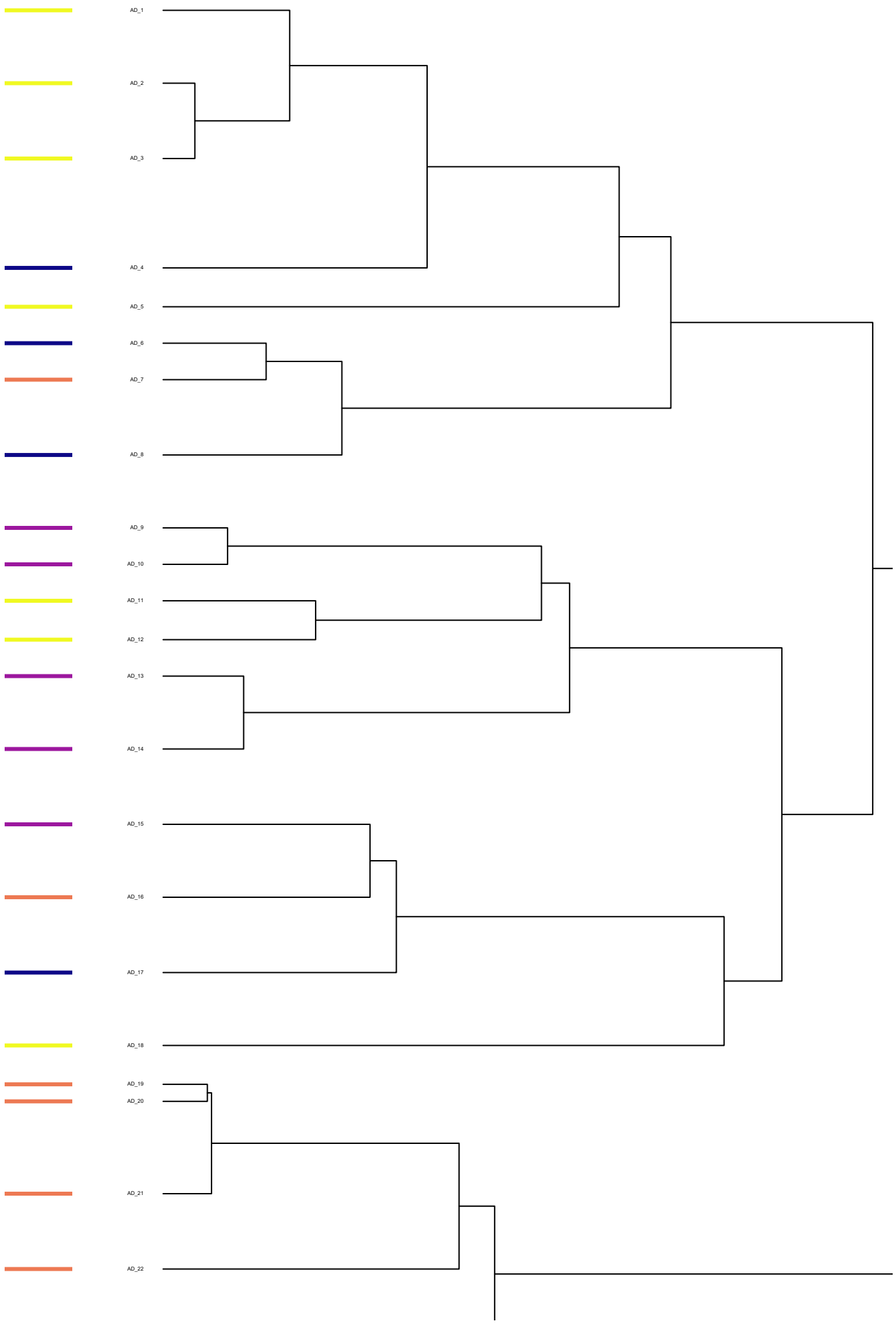
AD_22
AD_23
NERC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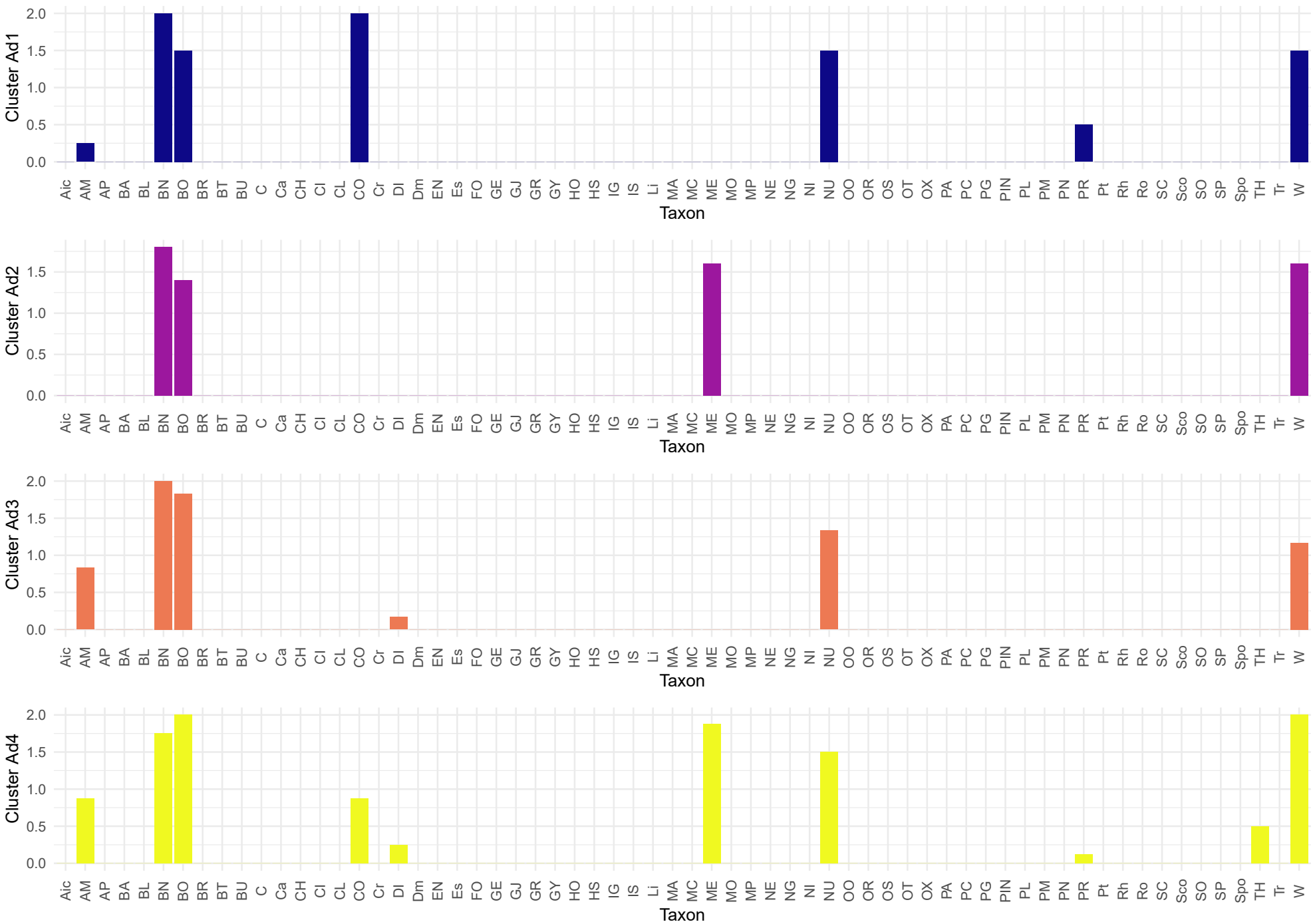
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Cluster Ad2
Cluster Ad3
Cluster Ad4
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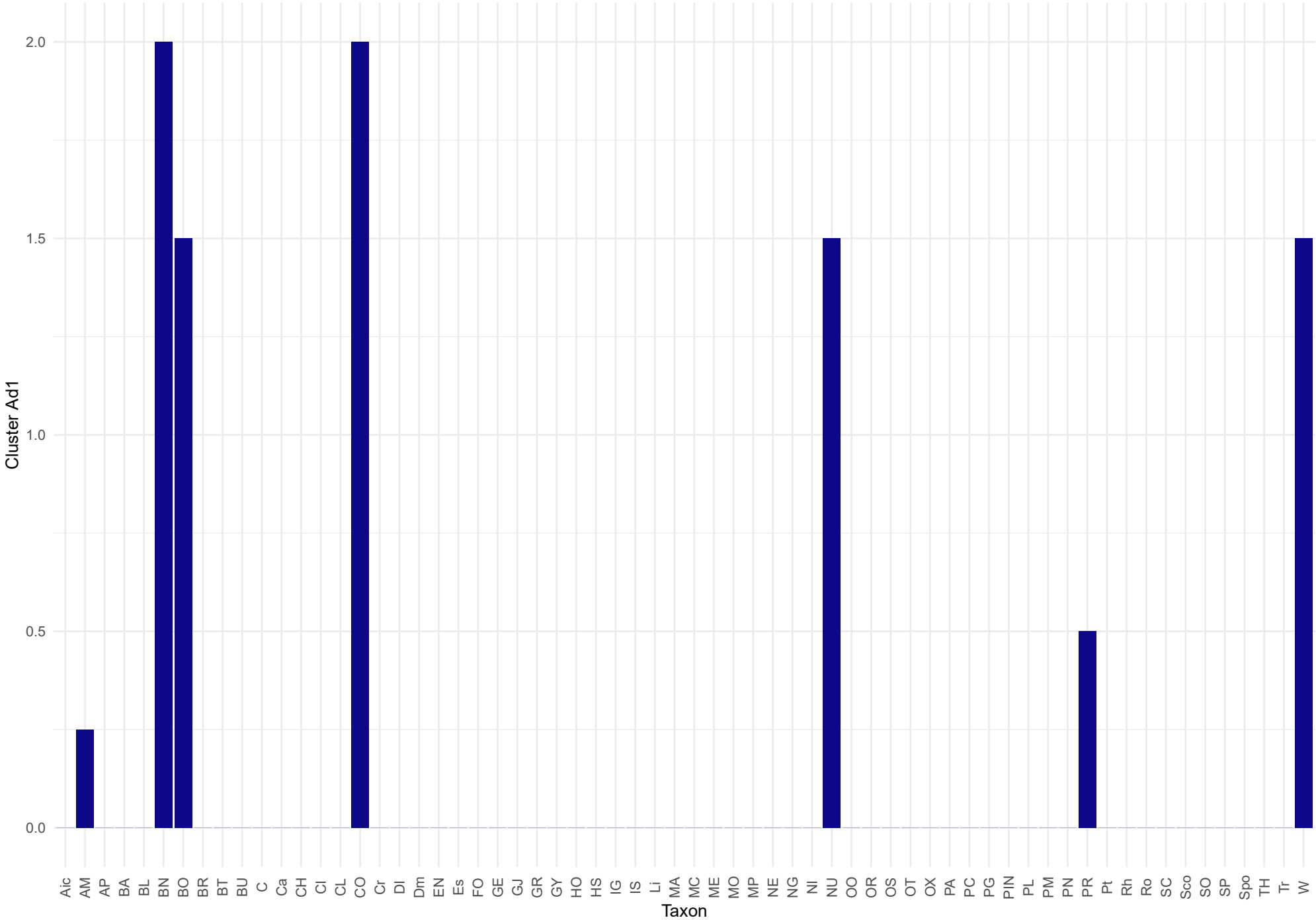
Taxon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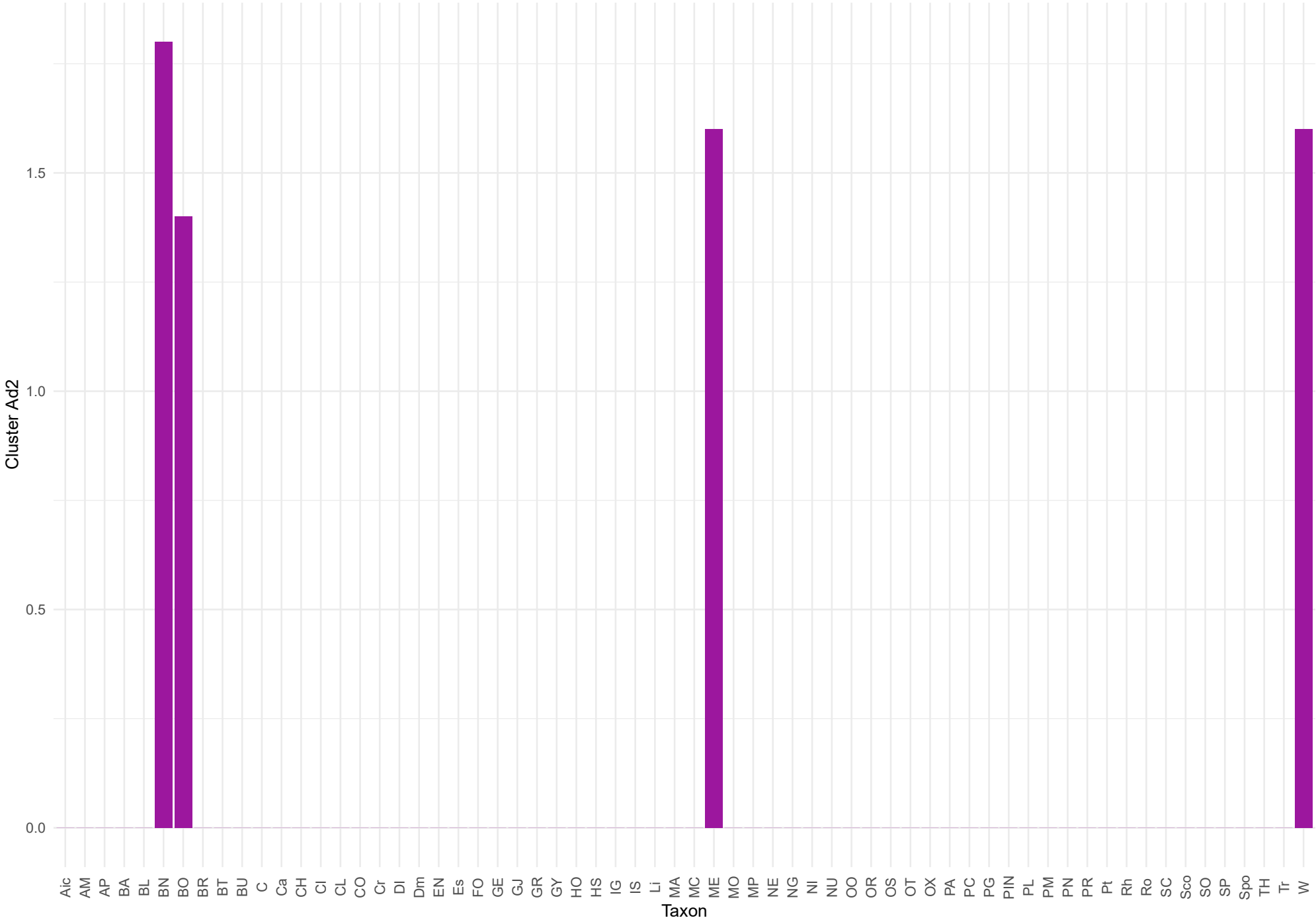
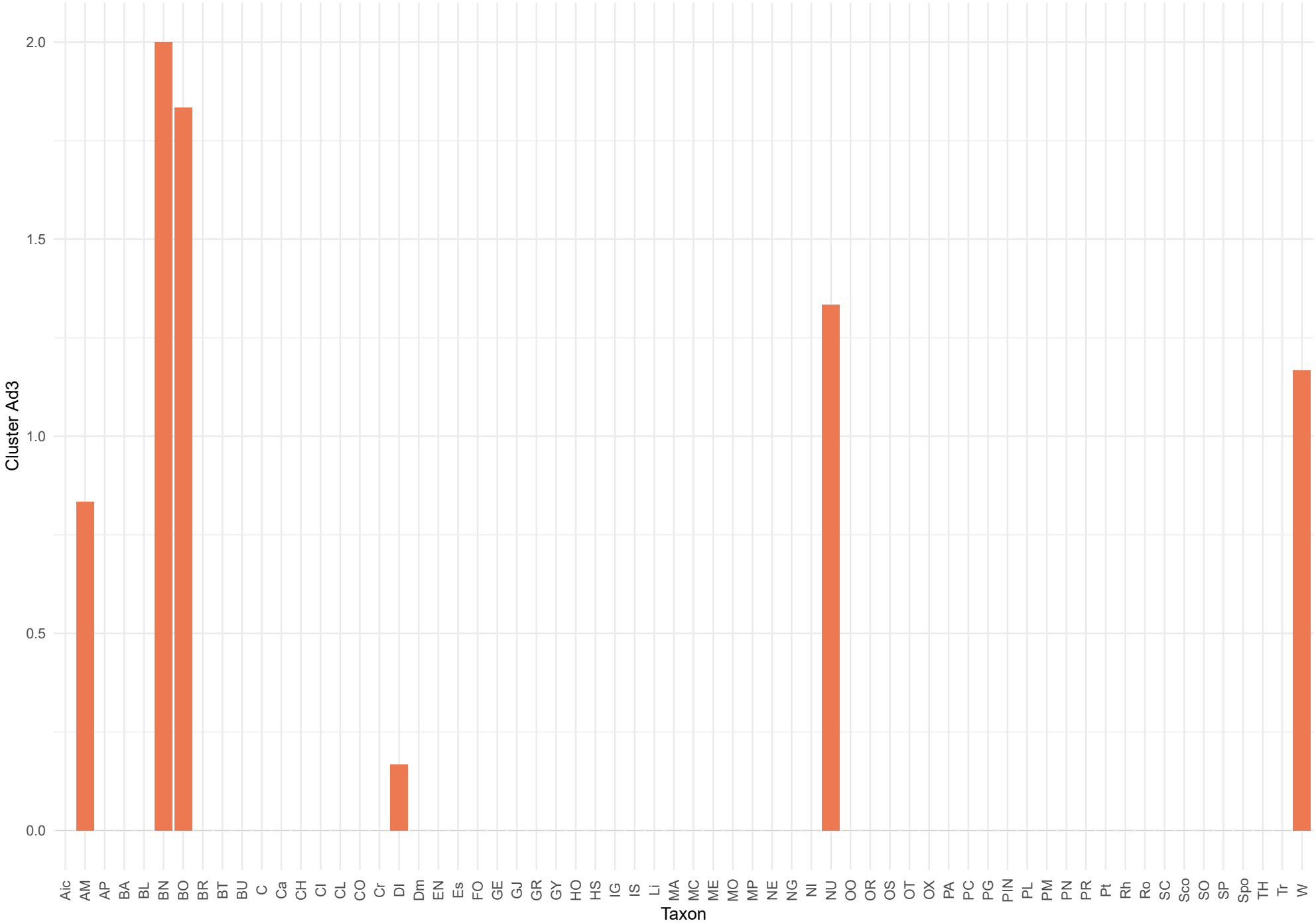
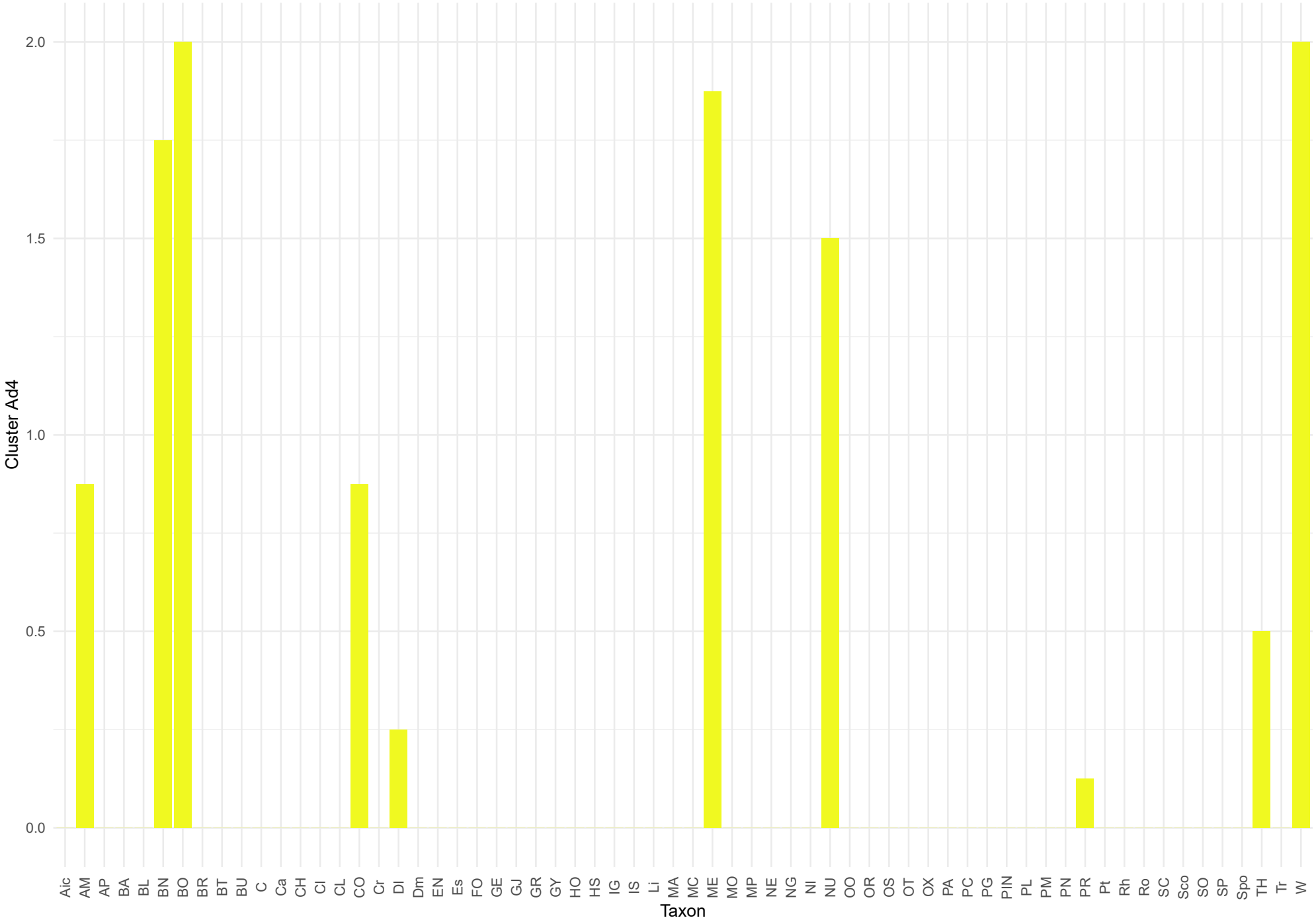
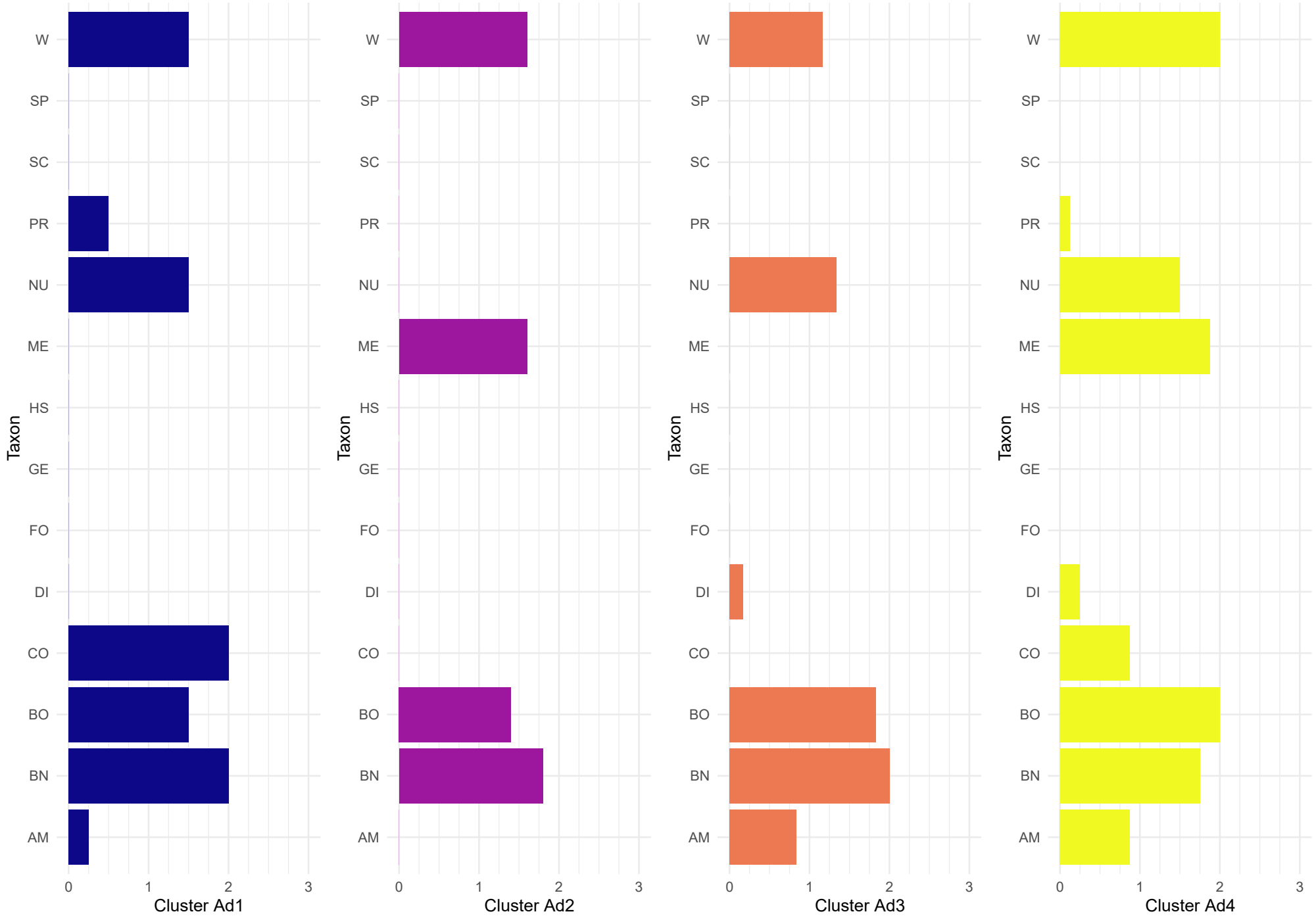
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon


Cluster Ad2
0.0
0.5
1.0
1.5
Aic AM AP BA BL BN BO BR BT BU C Ca CH Cl CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon

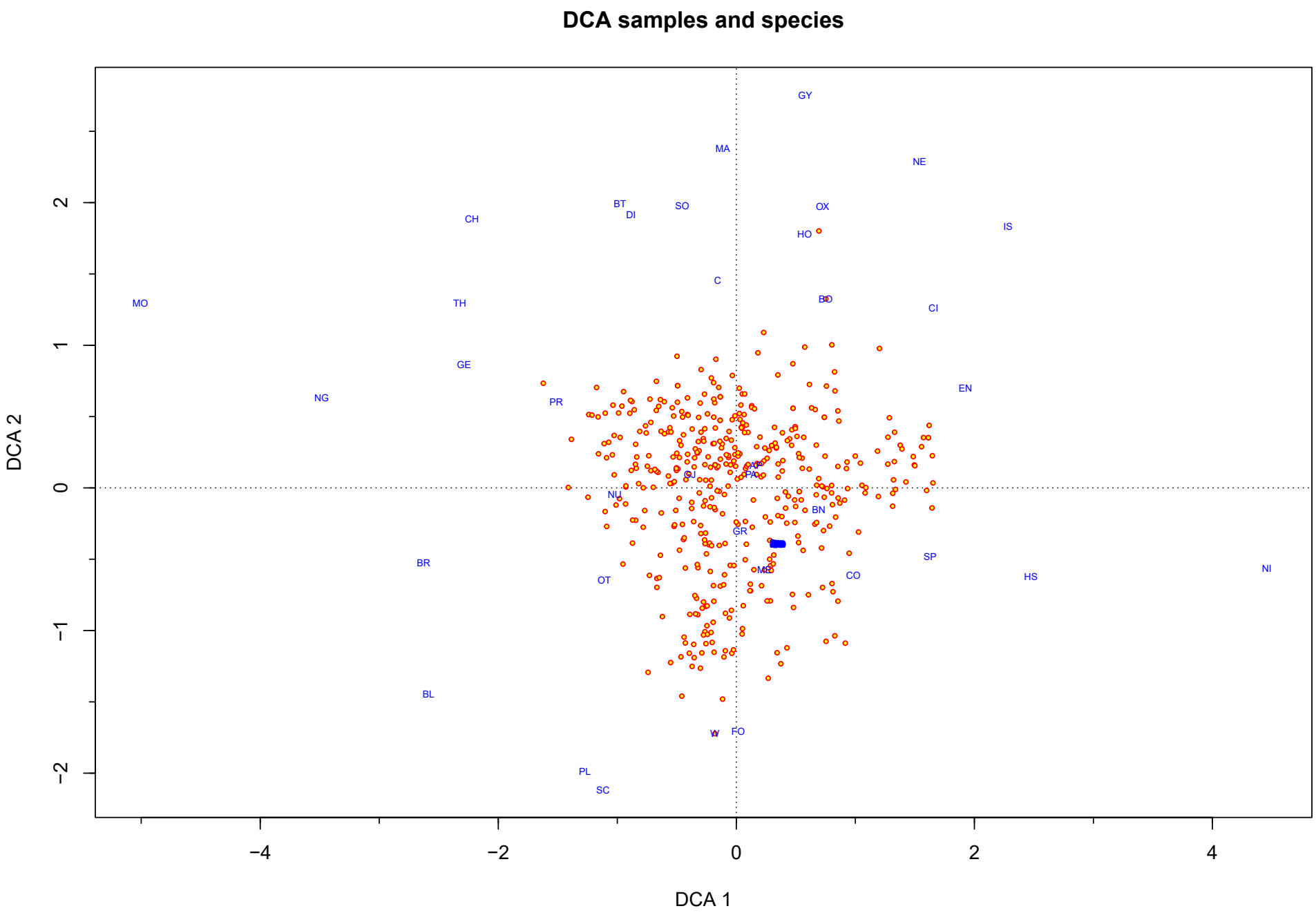
Ashdown 2 (AD)


Cluster Ad3
2.0
1.5
1.0
0.5
0.0
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon

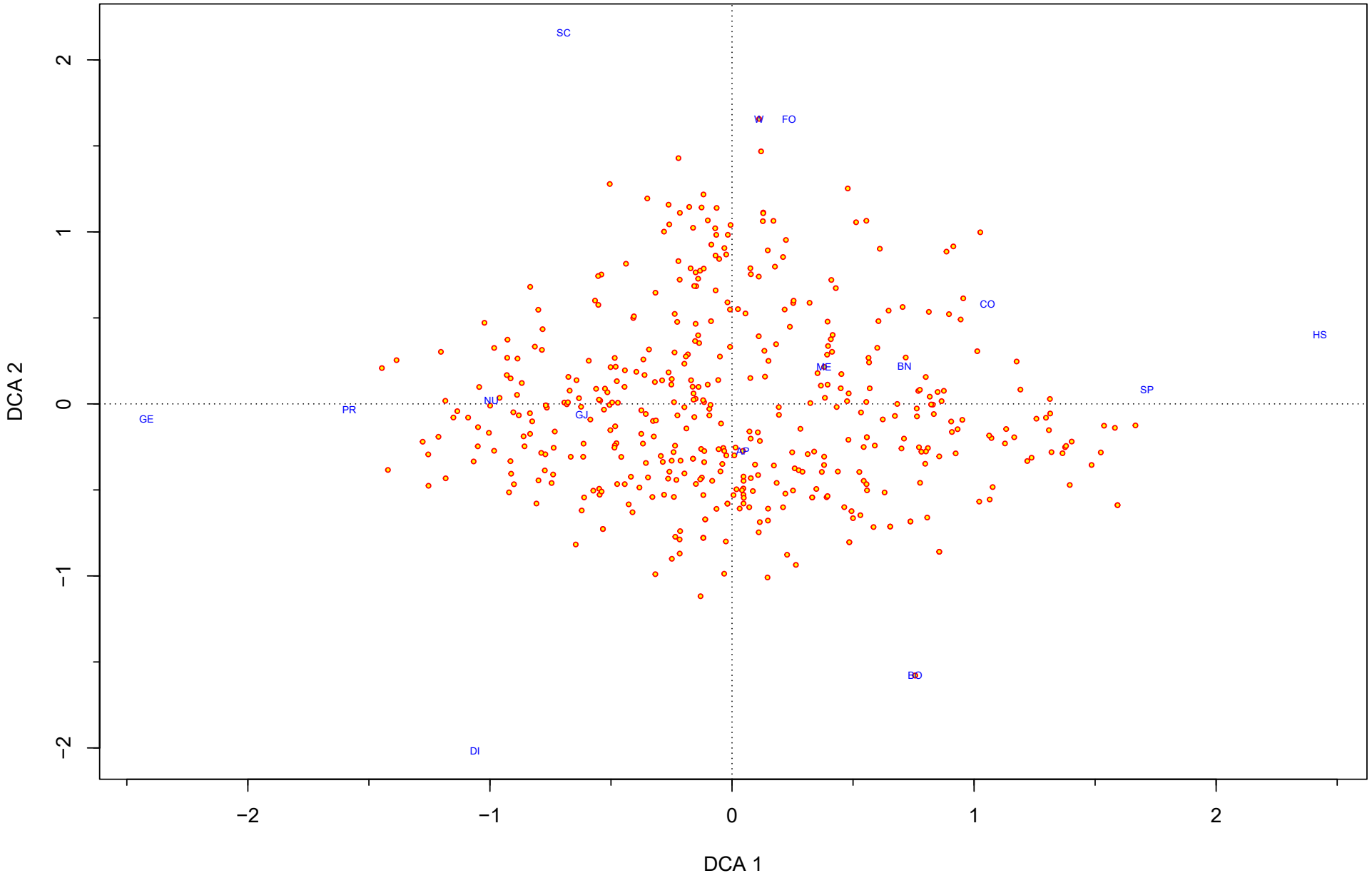

Cluster Ad4
2.0
1.5
1.0
0.5
0.0
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon

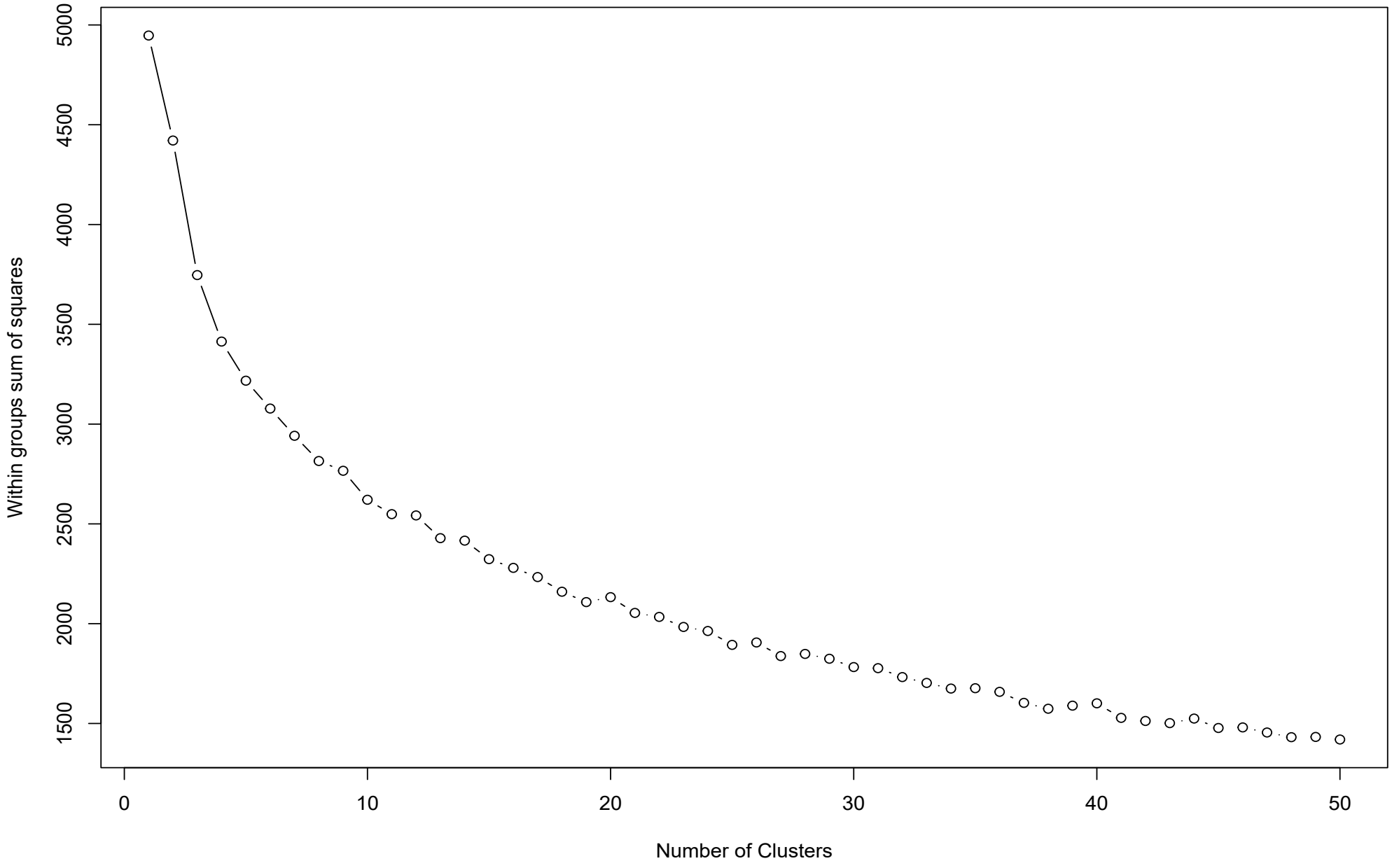

Taxon
W
SP
SC
PR
NU
ME
HS
GE
FO
DI
CO
BO
BN
AM
0
1
2
3
Cluster Ad1
Cluster Ad2
Cluster Ad3
Cluster Ad4

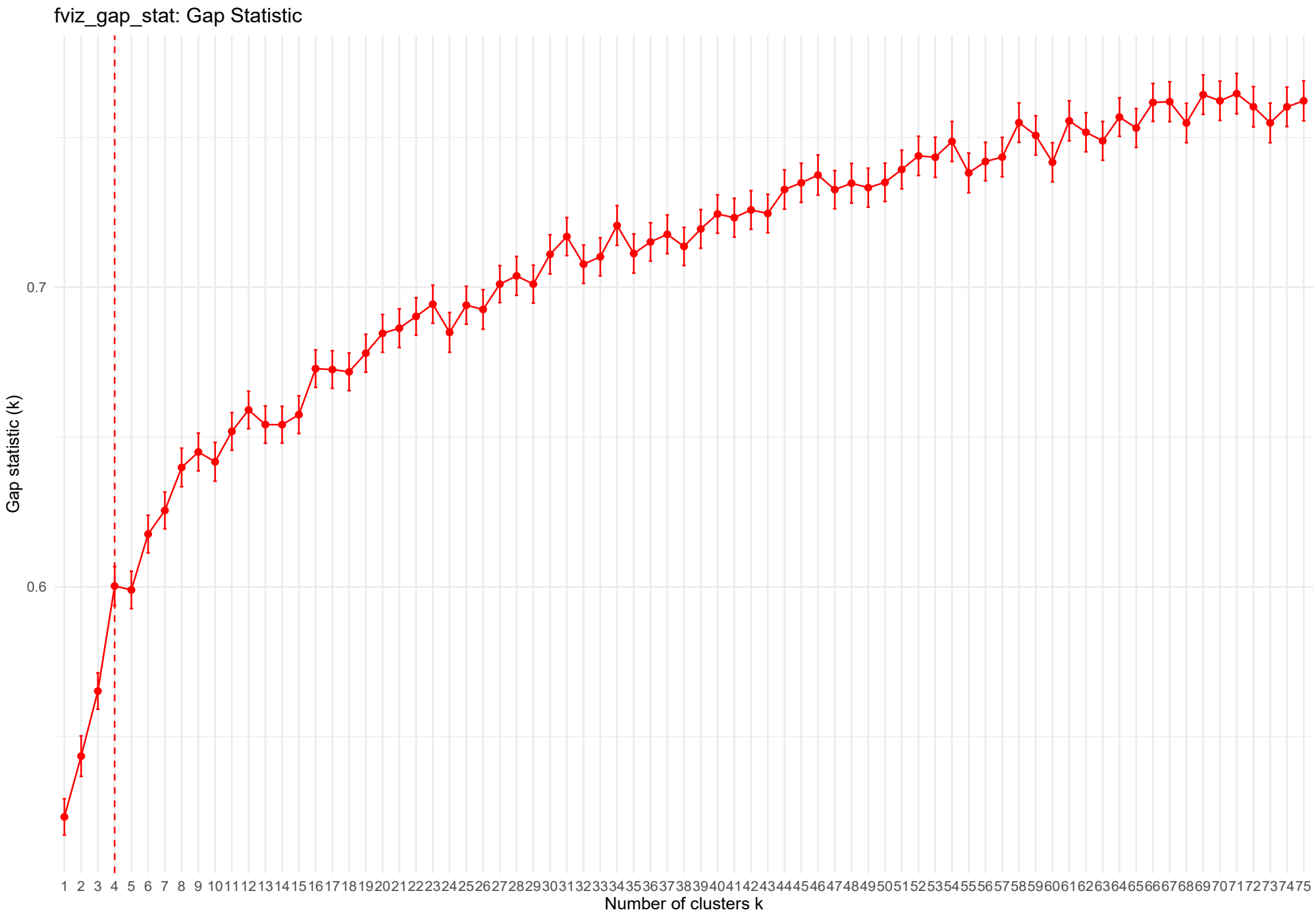
Christian Malford 11 (CM11)

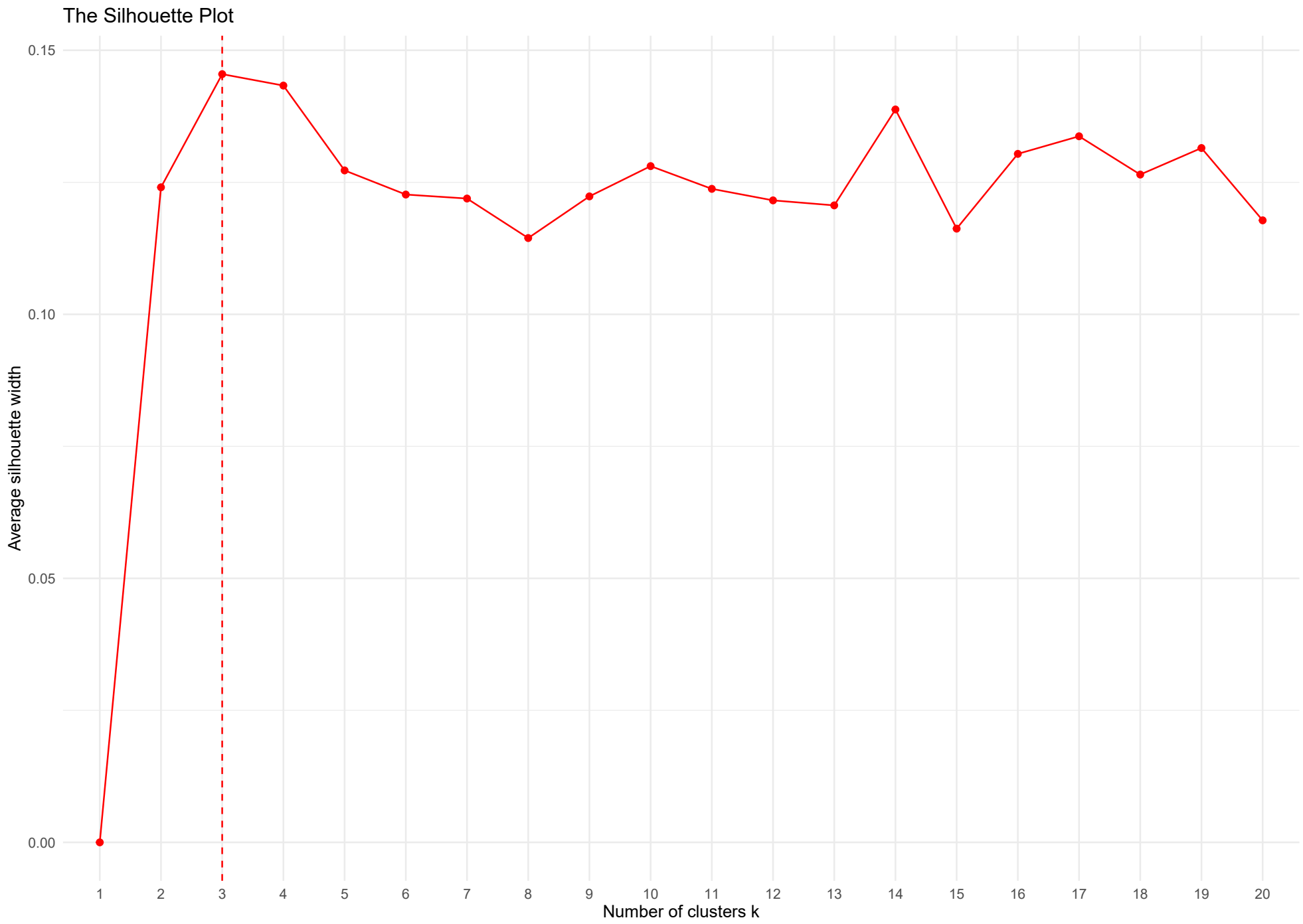

DCA samples and species
GY
MA
NE
BT
DI
SO
OX
CH
IS
HO
C
MO
TH
BO
CI
GE
EN
NG
PR
CJ
PA
NU
BN
GR
SP
BR
OT
CO
HS
NI
BL
FO
PL
SC
DCA 2
DCA 1
−4
−2
0
2
4
−2
−1
0
1
2

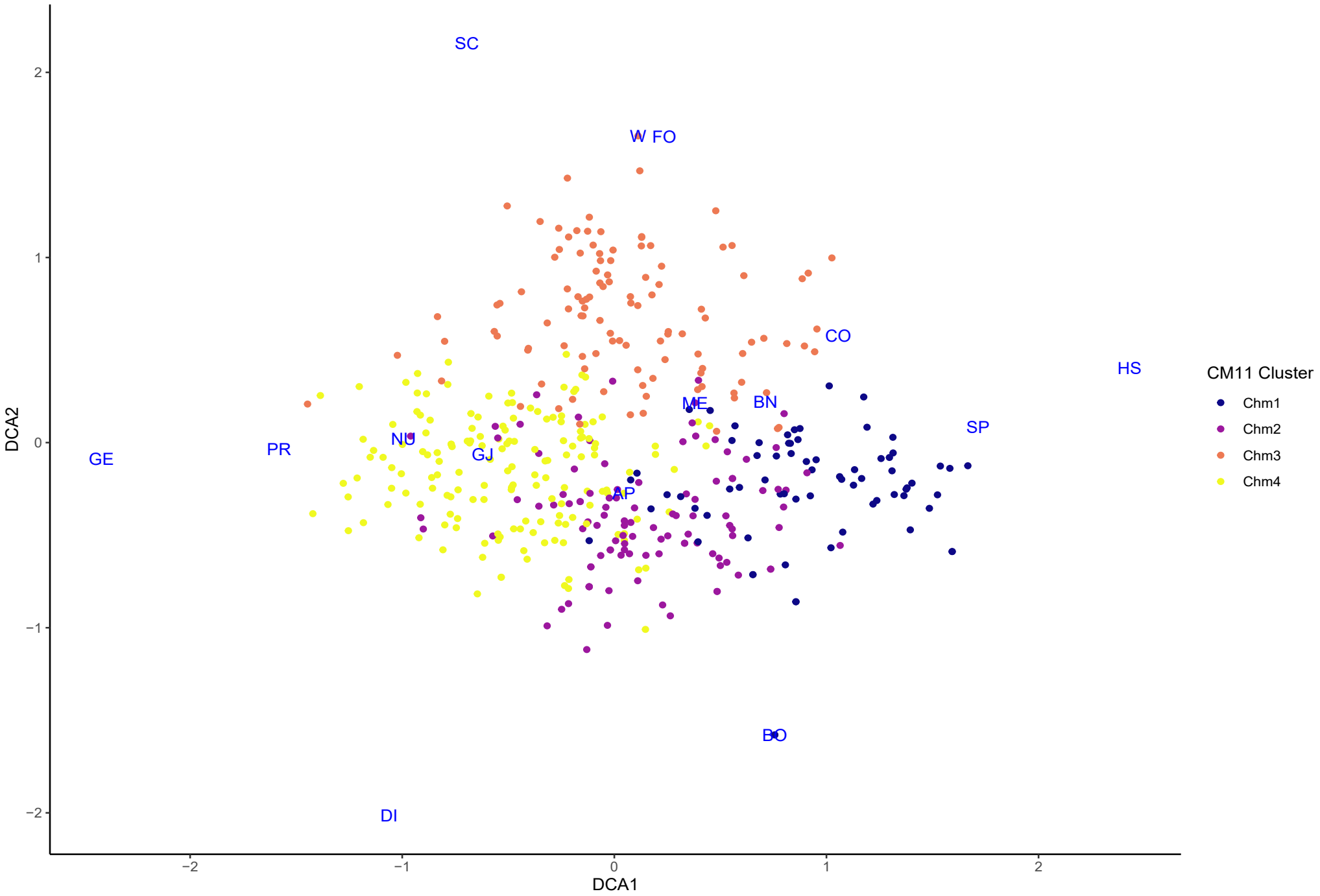
DCA samples and species UQ

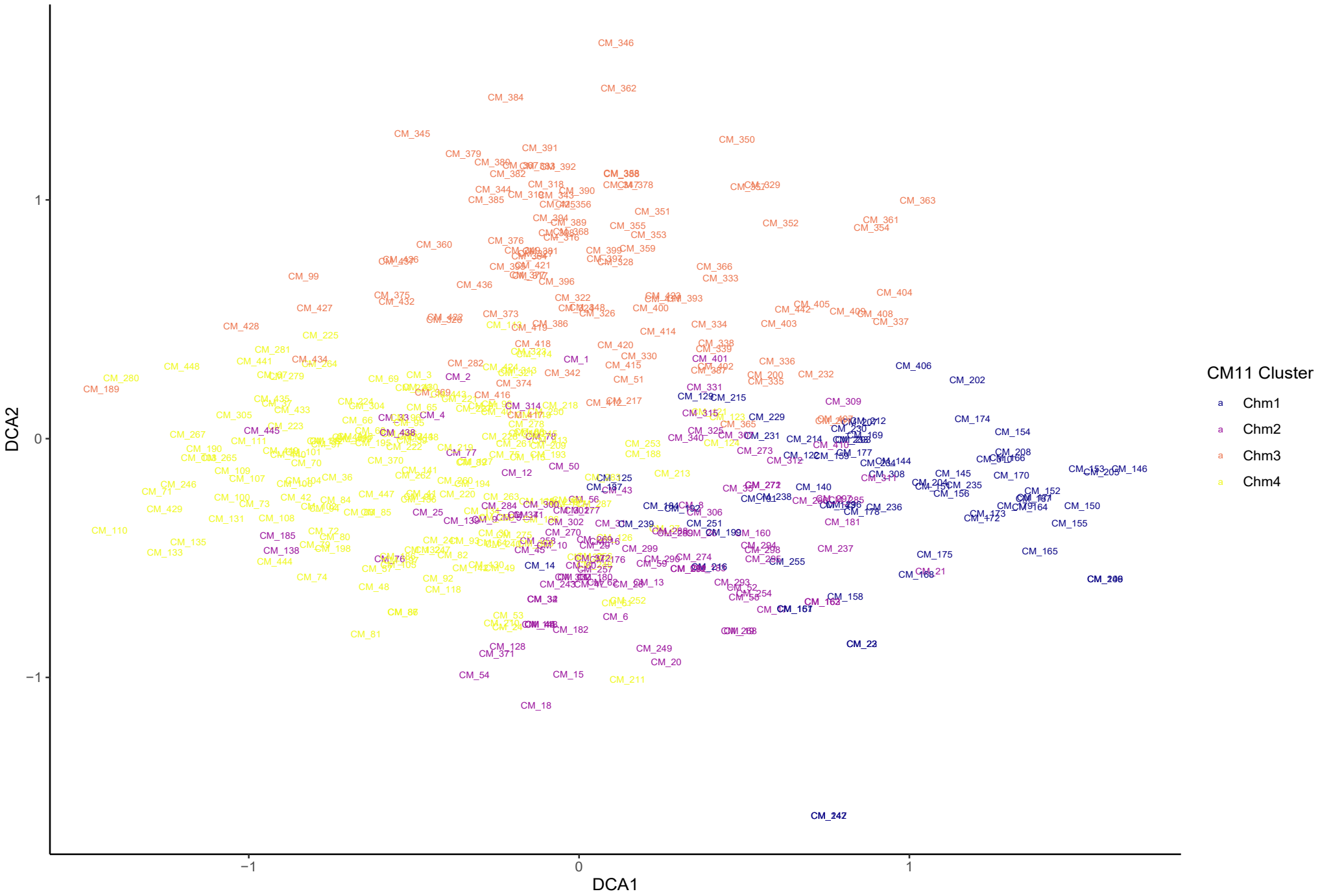


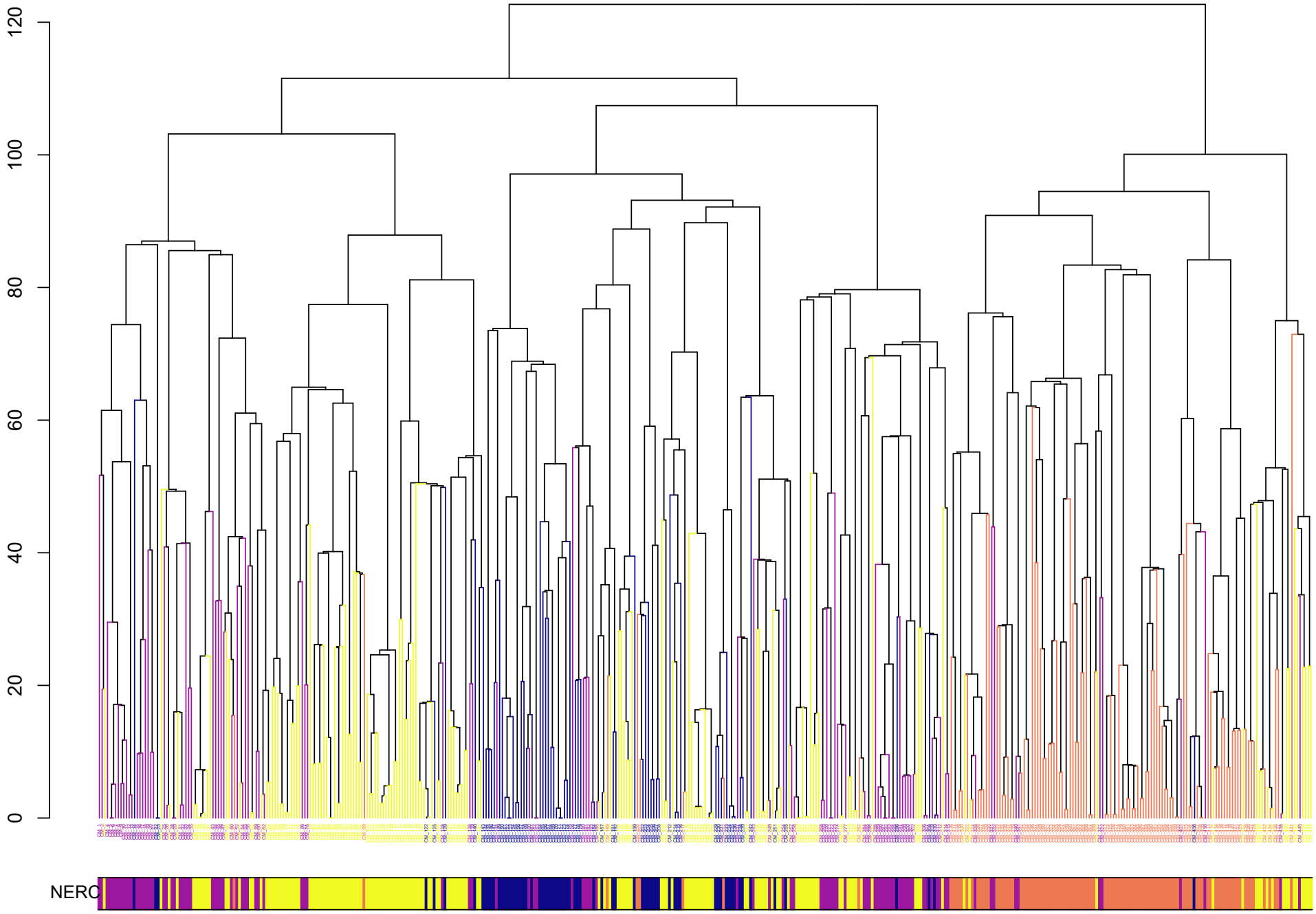

Within groups sum of squares
5000
4500
4000
3500
3000
2500
2000
1500
0
10
20
30
40
50
Number of Clusters

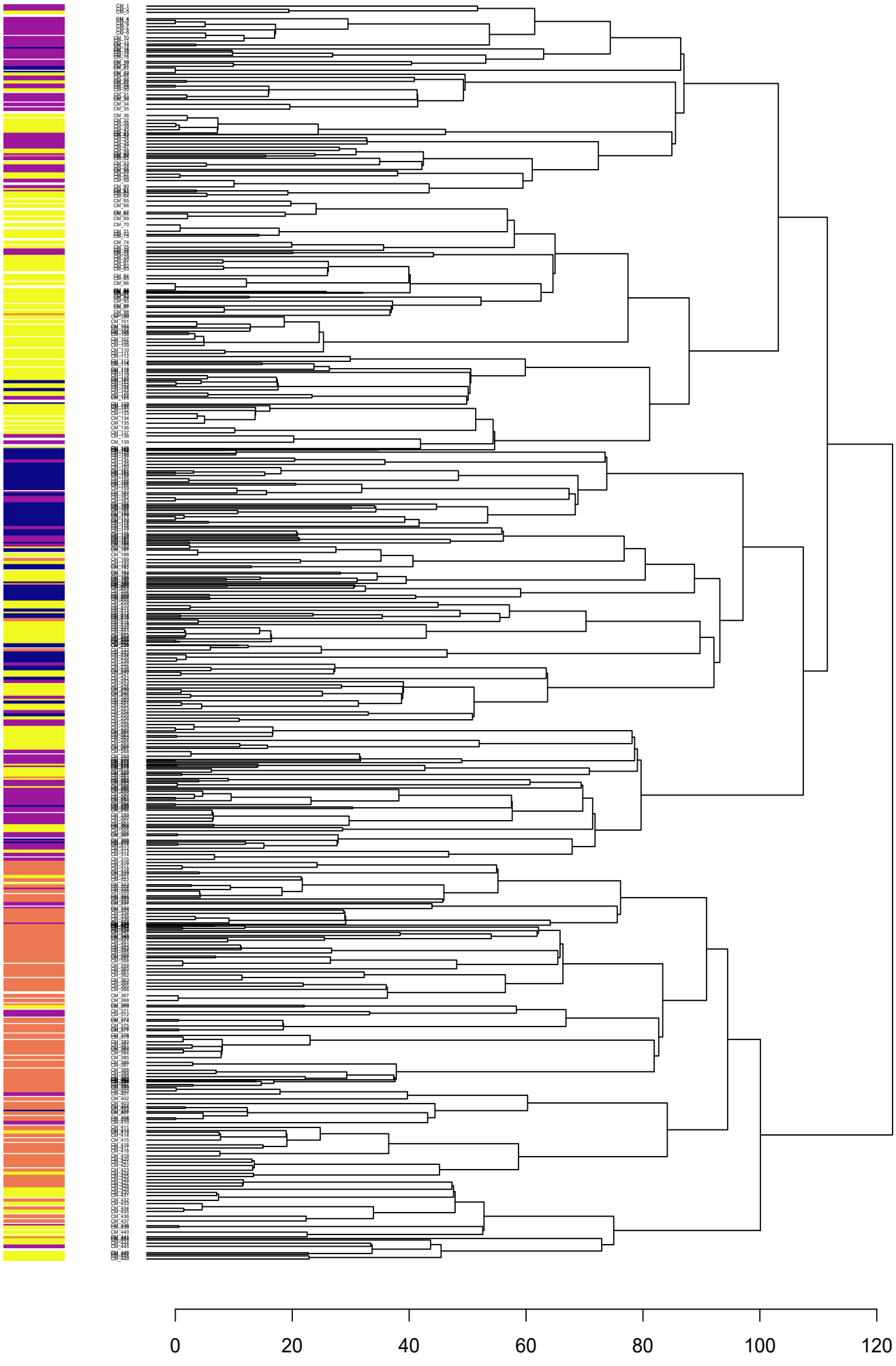

fviz_gap_stat: Gap Statistic
Gap statistic (k)
0.7
0.6
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75
Number of clusters k


The Silhouette Plot
Average silhouette width
0.15
0.10
0.05
0.00
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
Number of clusters k

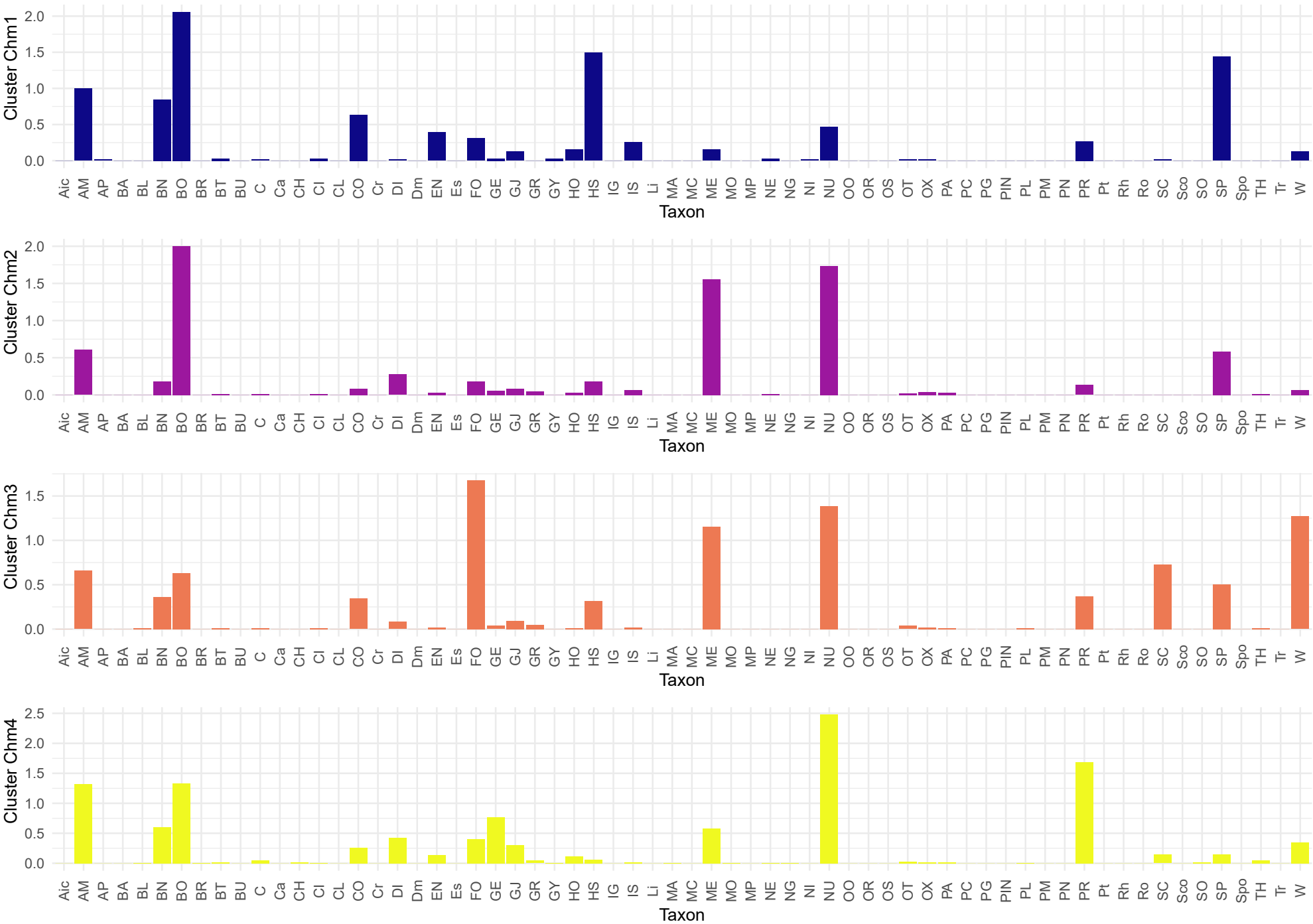

SC
W FO
CO
HS
ME
BN
SP
NU
PR
GJ
GE
AP
BO
DI
DCA2
DCA1
2
1
0
−1
−2
−2
−1
0
1
2
CM11 Cluster
Chm1
Chm2
Chm3
Chm4

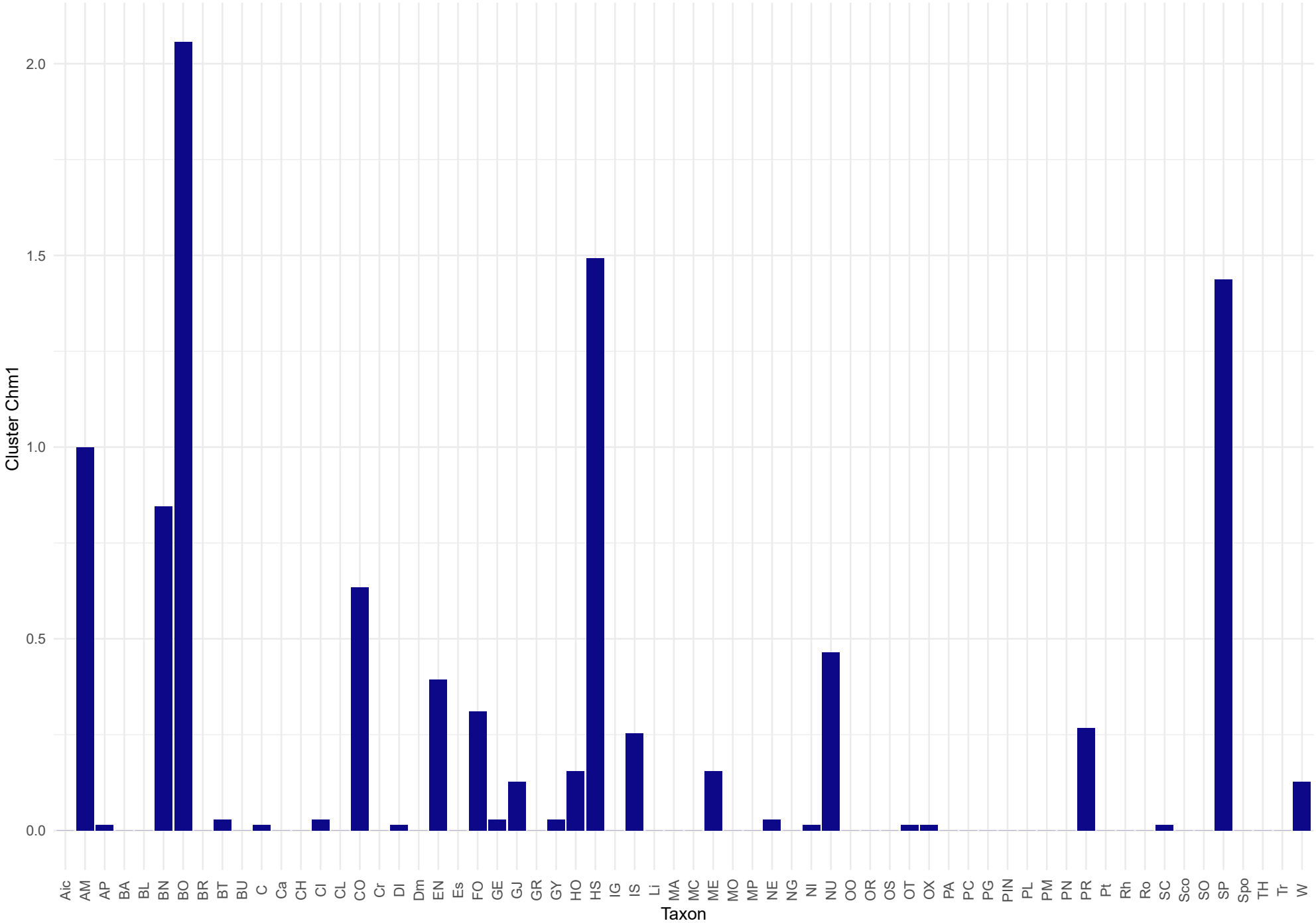

DCA2
DCA1
1
0
−1
−1
0
1
CM11 Cluster
Chm1
Chm2
Chm3
Chm4

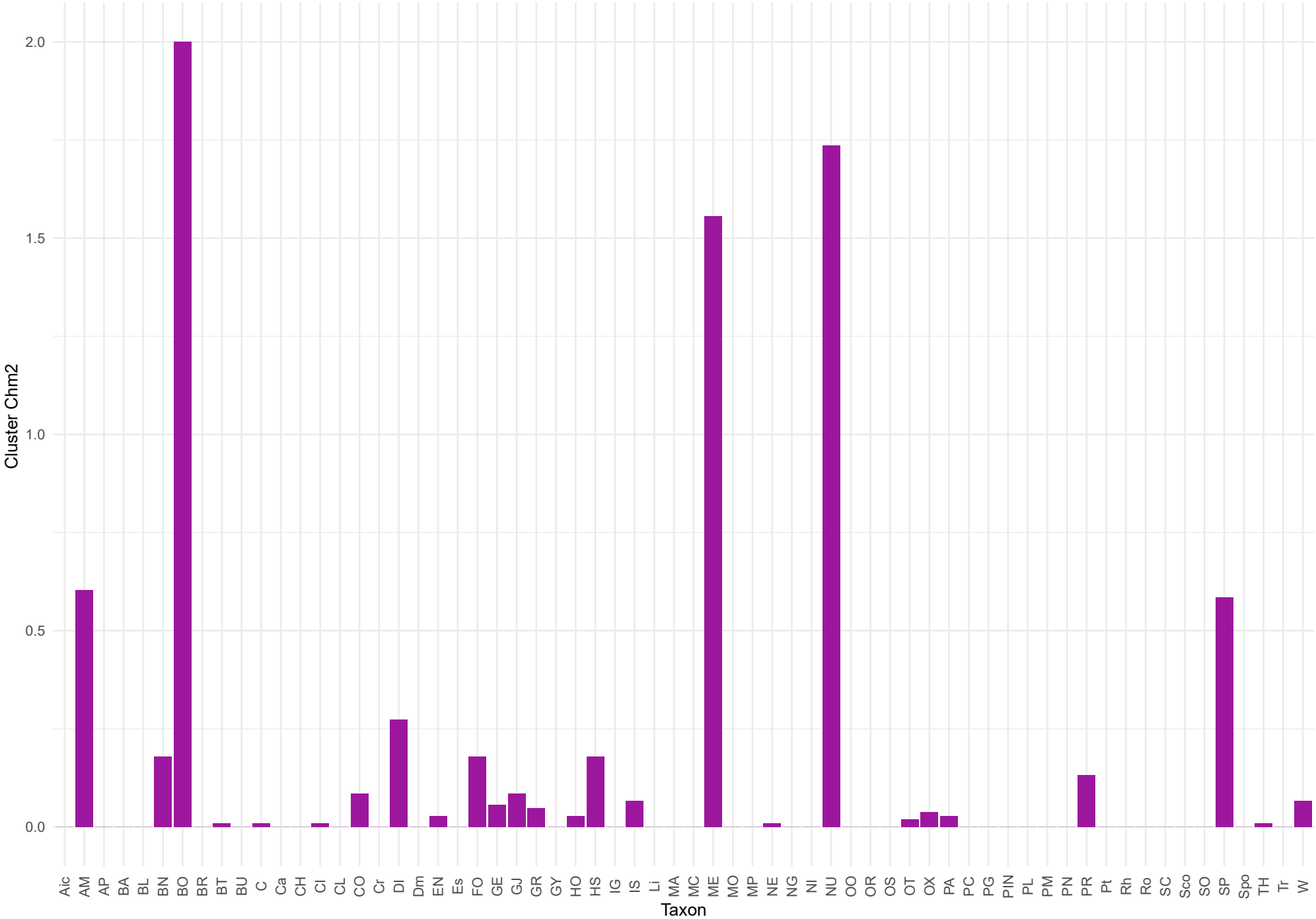

120
100
80
60
40
20
0
NERO

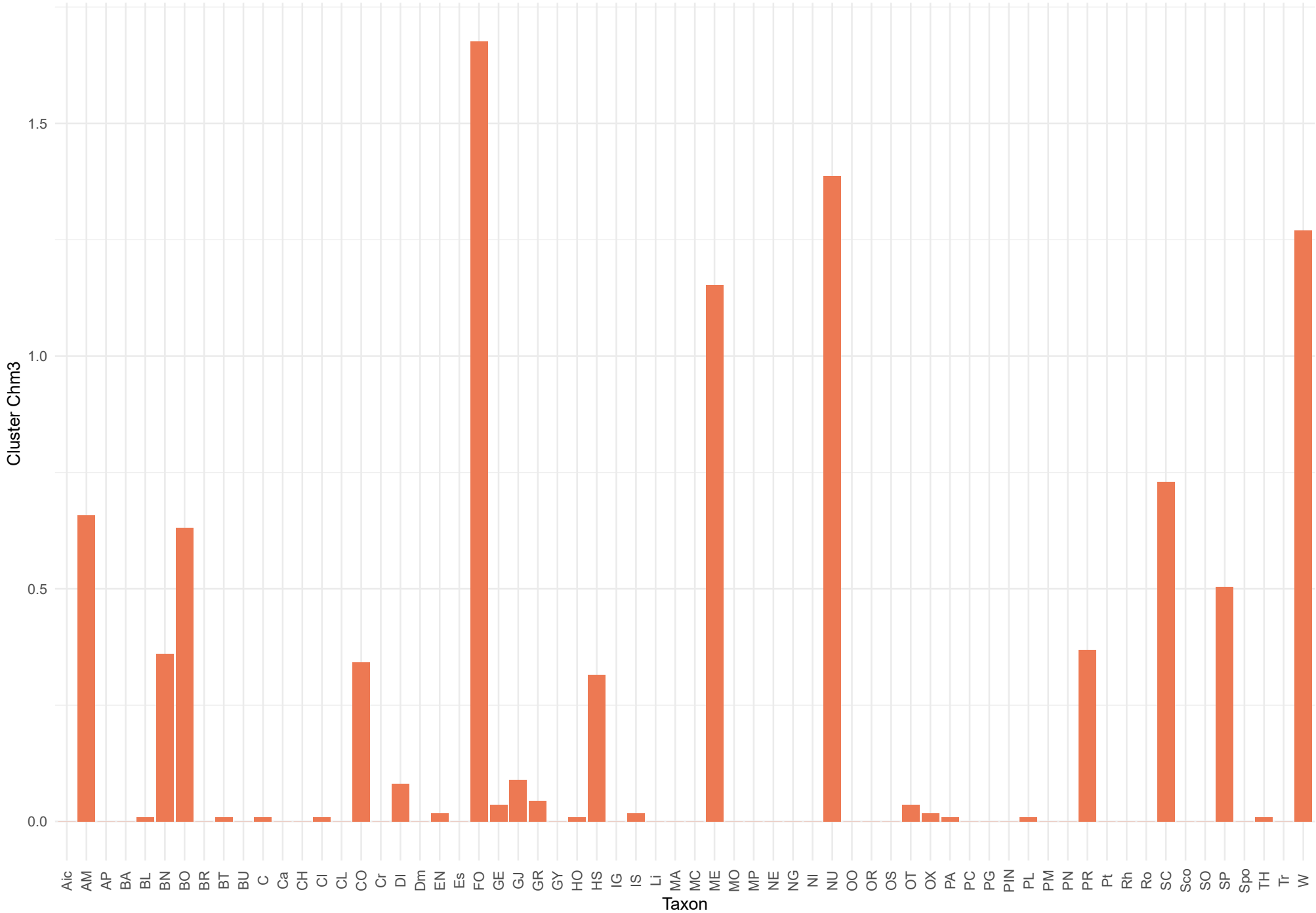


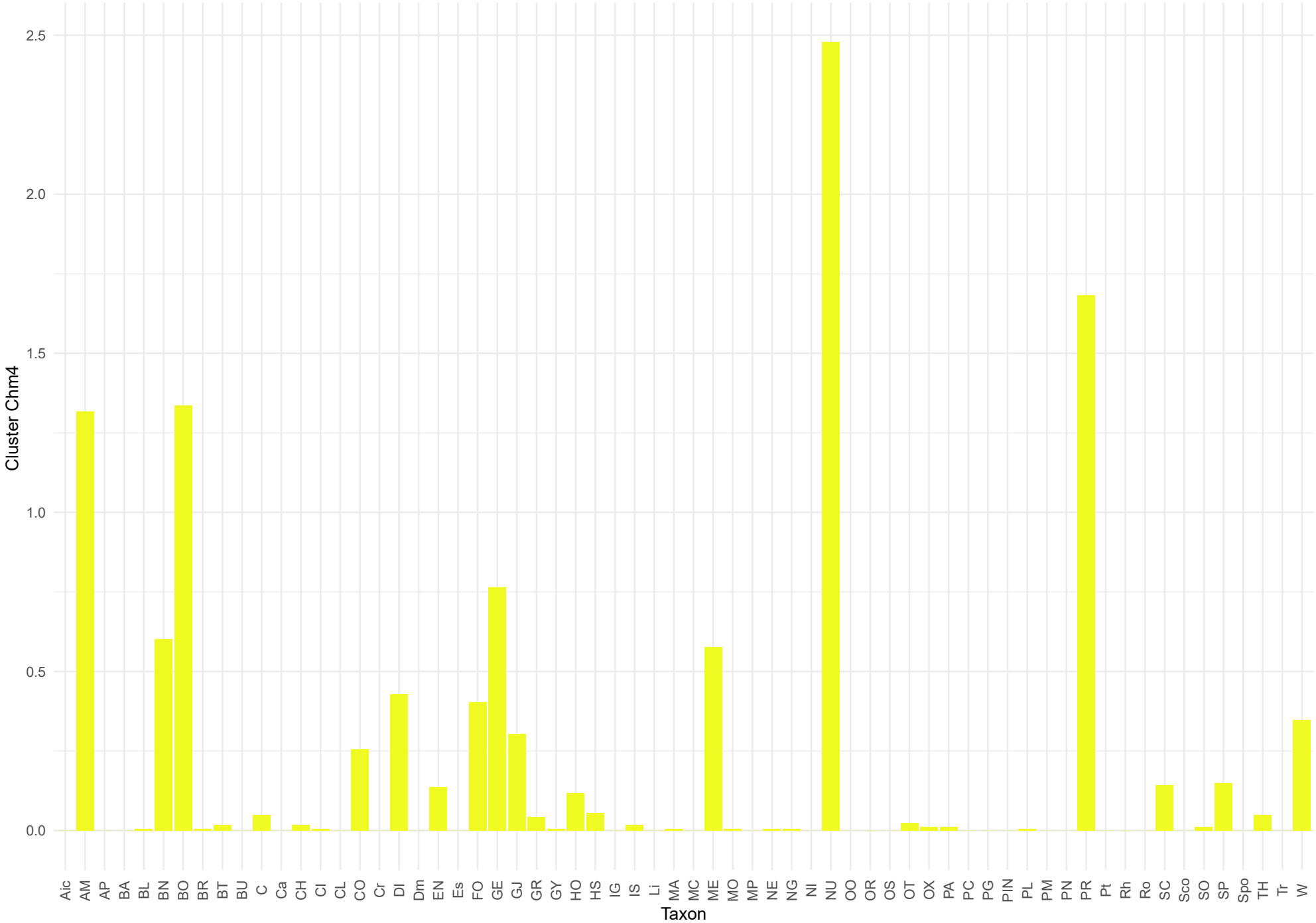
ChristianMalford11(CM11)

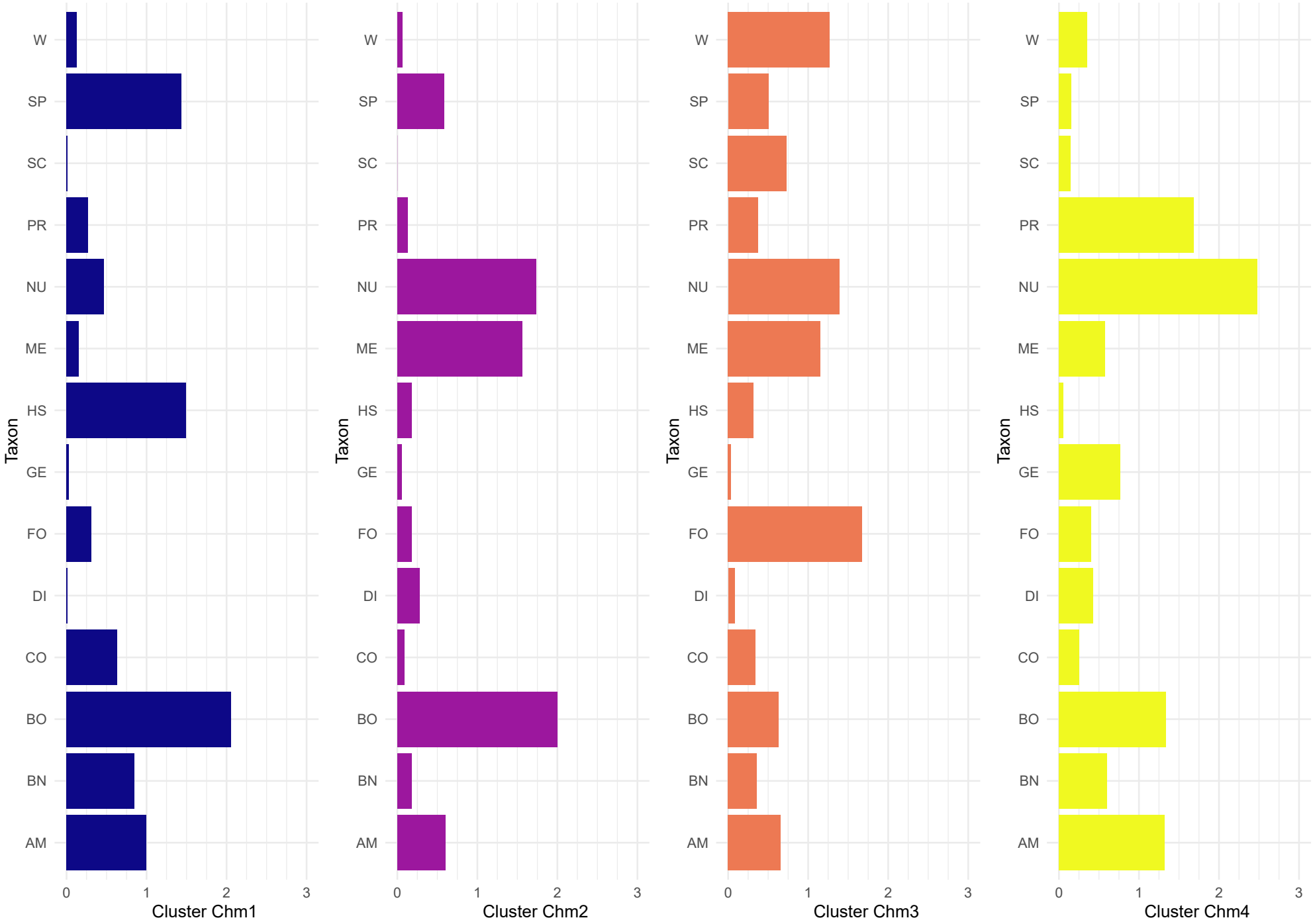

Cluster Chm1
Cluster Chm2
Cluster Chm3
Cluster Chm4
Taxon
Aic AM AP BA BL BN BO BR BT BU C Ca CH Cl CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W


Cluster Chm1
2.0
1.5
1.0
0.5
0.0
Aic
AM
AP
BA
BL
BN
BO
BR
BT
BU
C
Ca
CH
CI
CL
CO
Cr
DI
Dm
EN
Es
FO
GE
GJ
GR
GY
HO
HS
IG
IS
Li
MA
MC
ME
MO
MP
NE
NG
NI
NU
OO
OR
OS
OT
OX
PA
PC
PG
PIN
PL
PM
PN
PR
Pt
Rh
Ro
SC
Sco
SO
SP
Spo
TH
Tr
W
Taxon

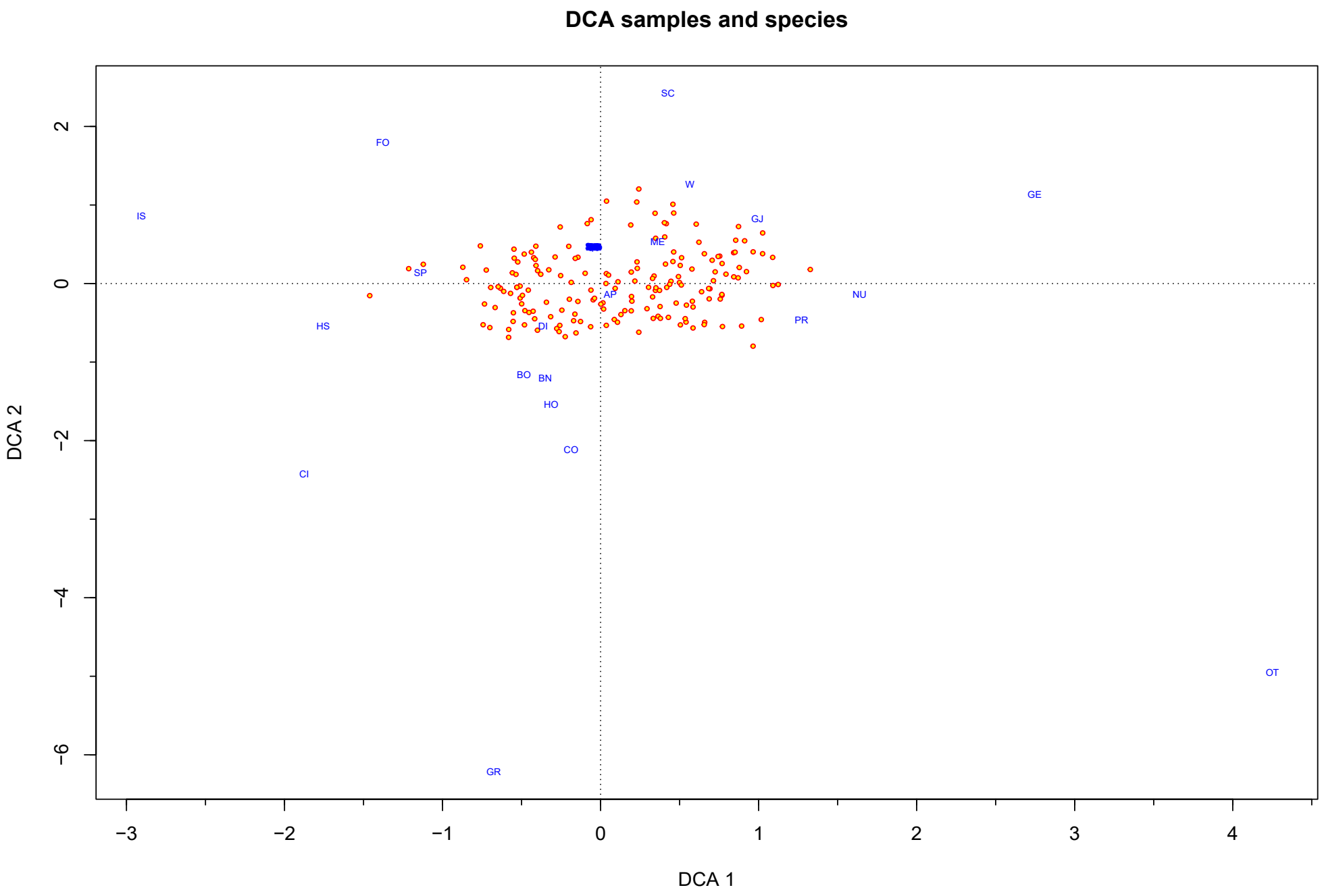

Cluster Chm2
2.0
1.5
1.0
0.5
0.0
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon

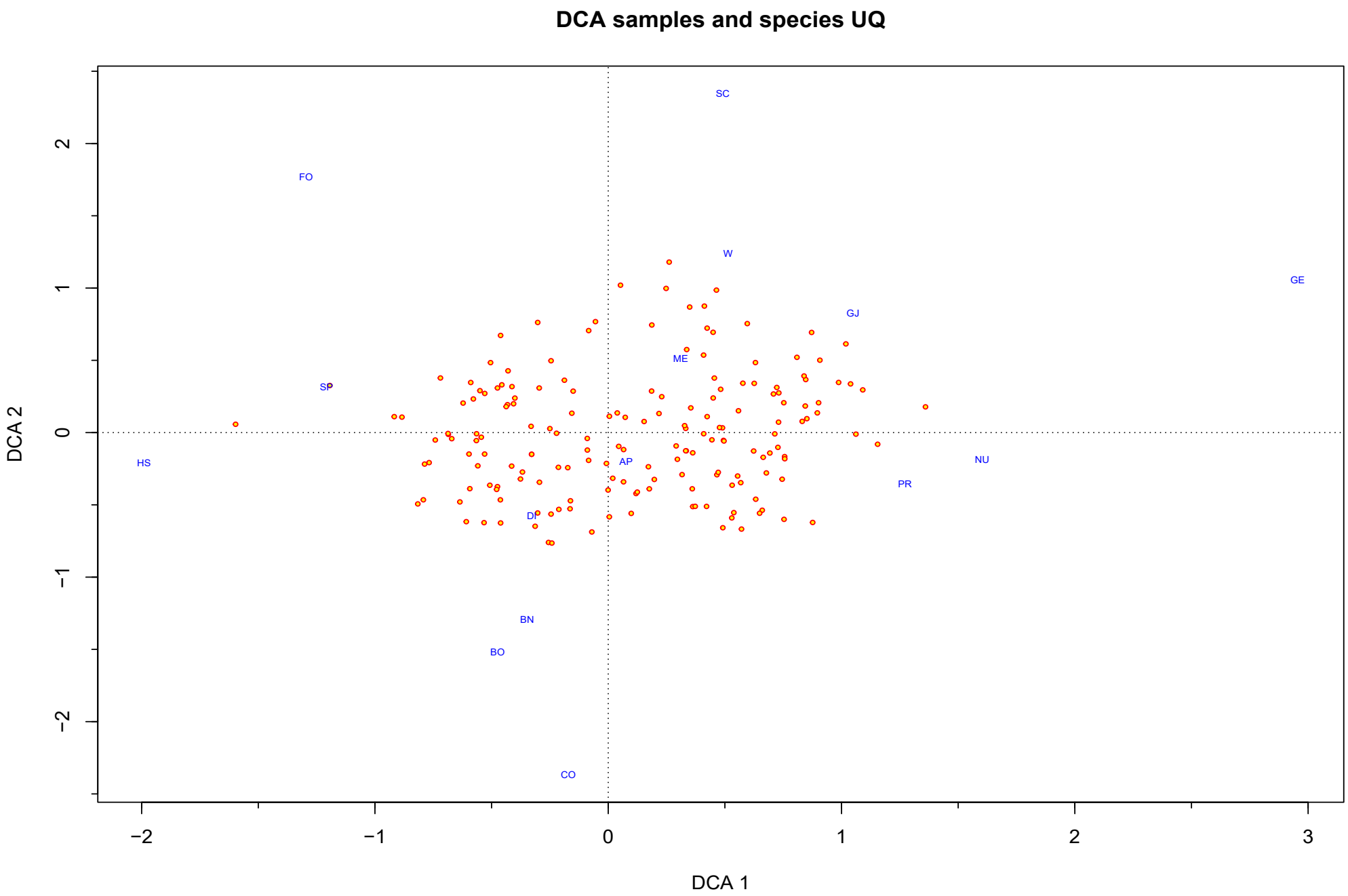

Cluster Chm3
1.5
1.0
0.5
0.0
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon

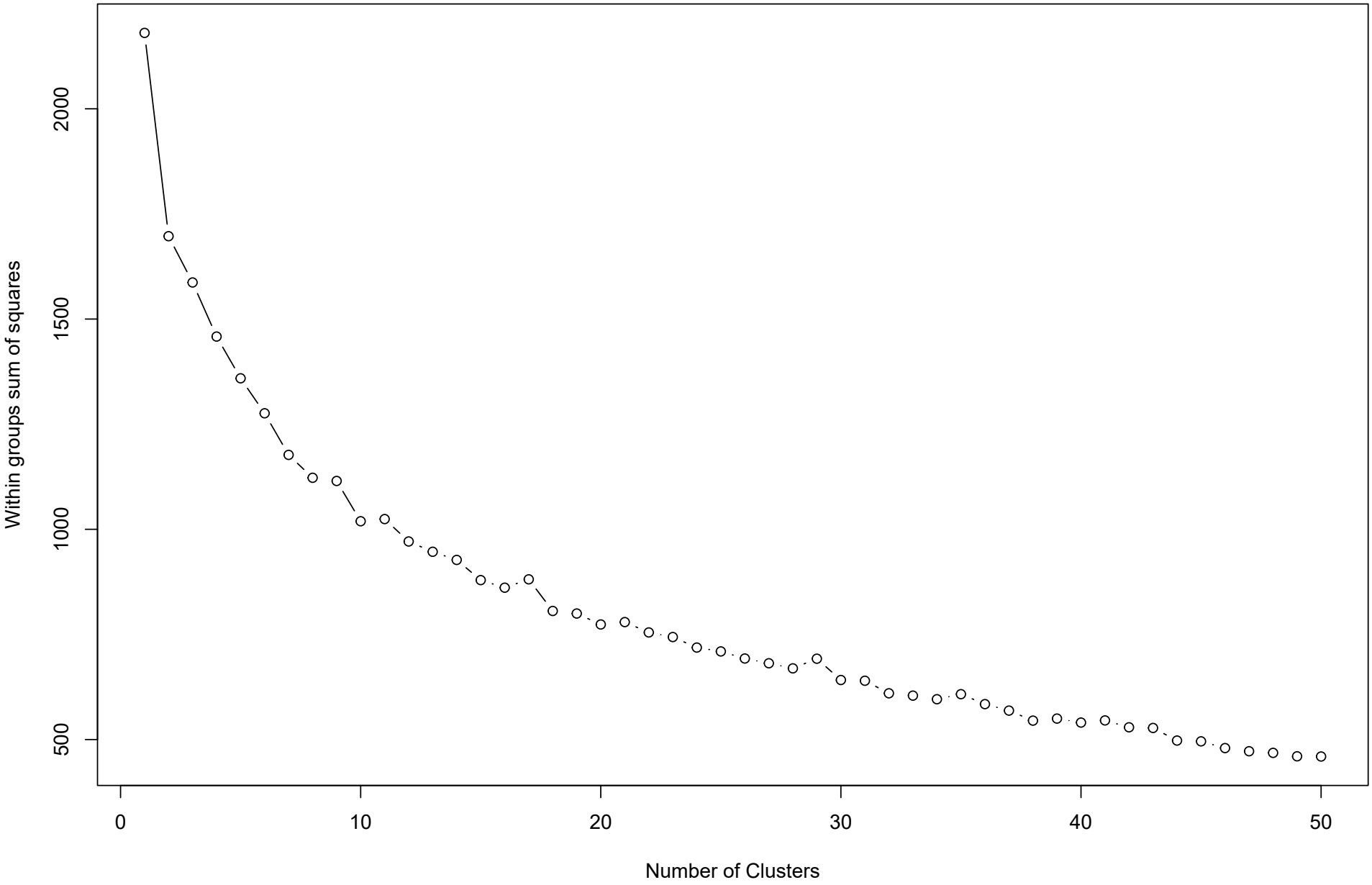

Cluster Chm4
2.5
2.0
1.5
1.0
0.5
0.0
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon

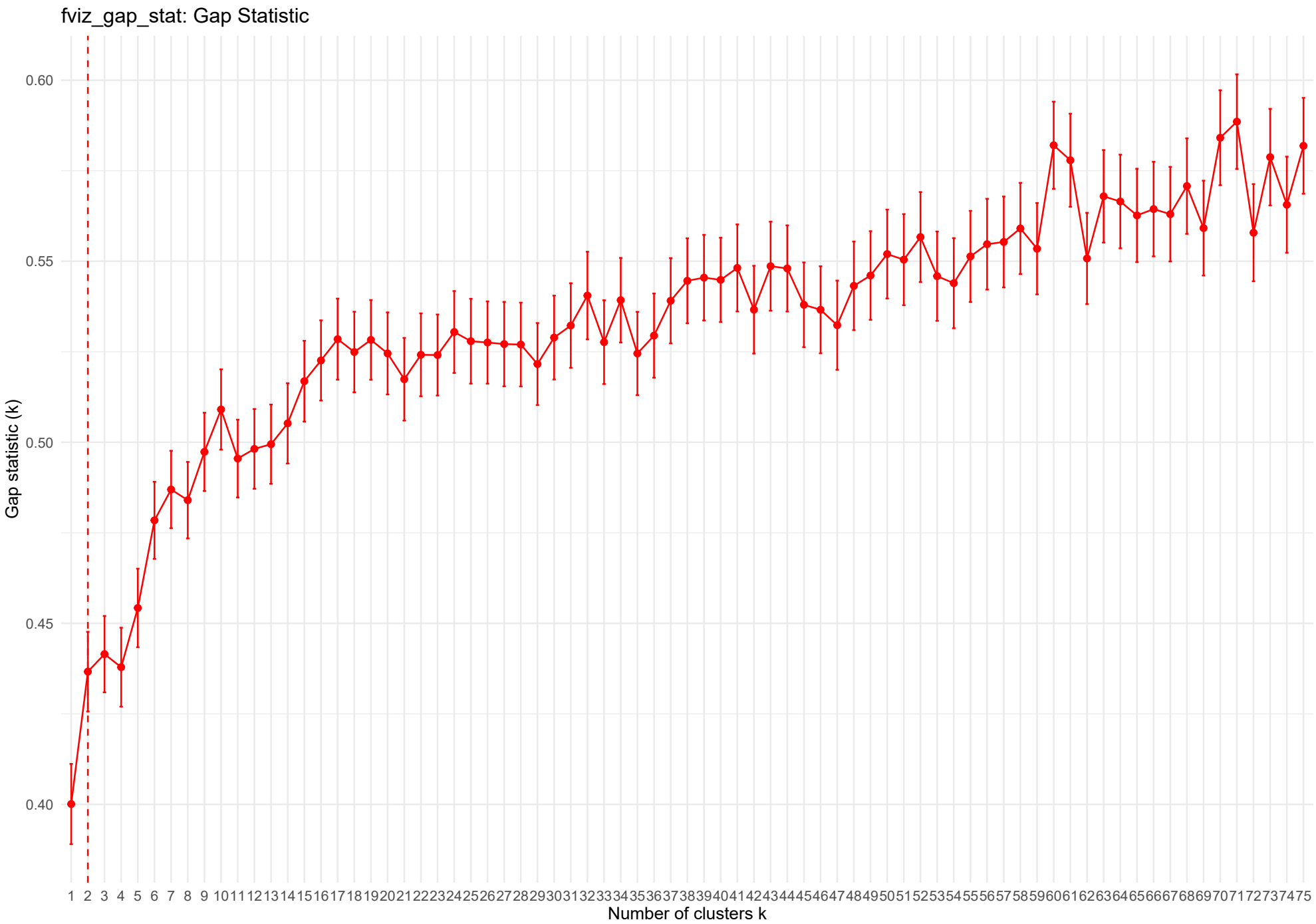

Taxon
W
SP
SC
PR
NU
ME
HS
GE
FO
DI
CO
BO
BN
AM
0
1
2
3
Cluster Chm1
Cluster Chm2
Cluster Chm3
Cluster Chm4

Christian Malford 9 (CM9)

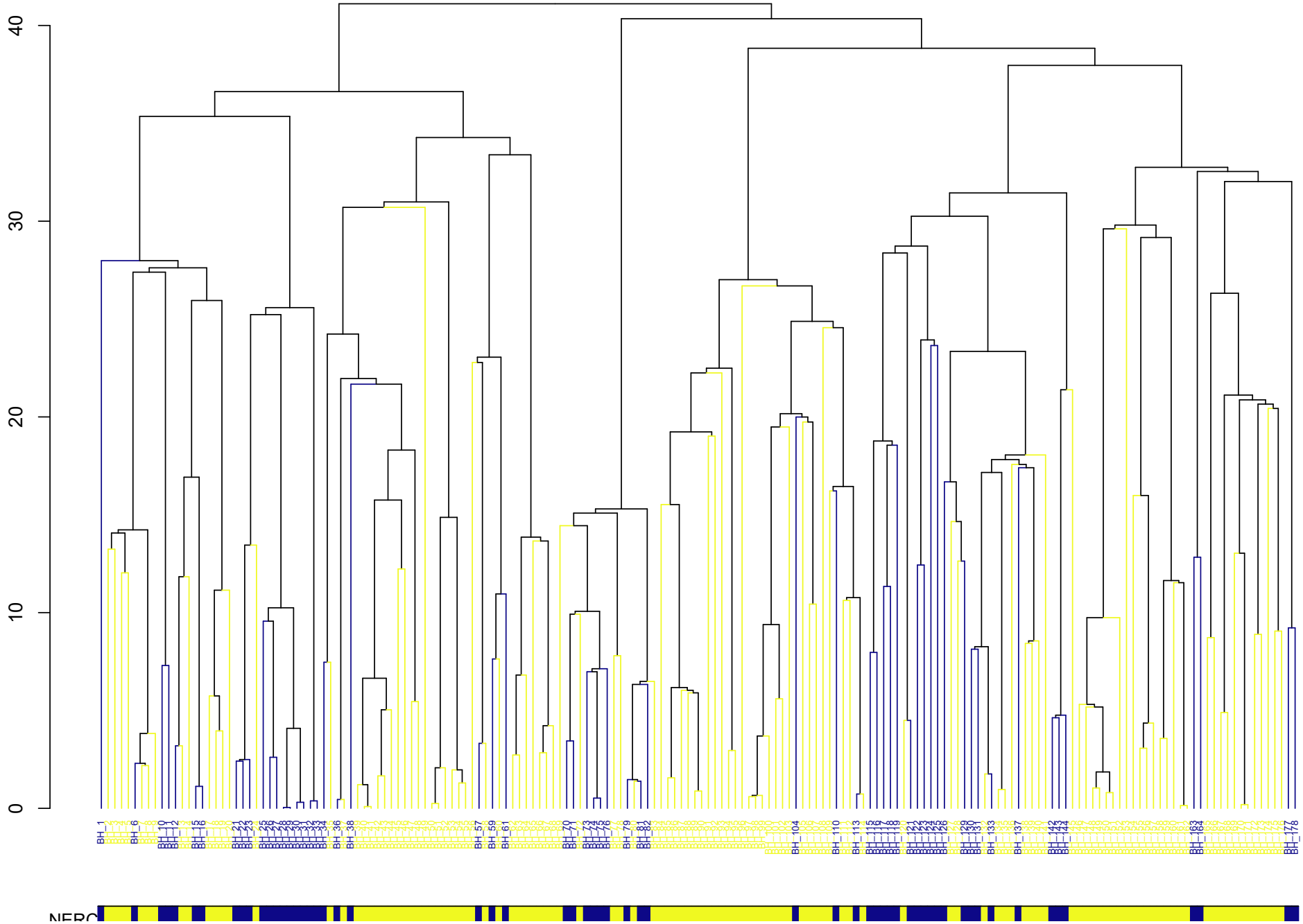

DCA samples and species
SC
FO
W
GE
IS
GJ
ME
SP
AP
NU
HS
DI
PR
BO
BN
HO
CO
CI
OT
GR
DCA 2
DCA 1
2
0
−2
−4
−6
−3
−2
−1
0
1
2
3
4

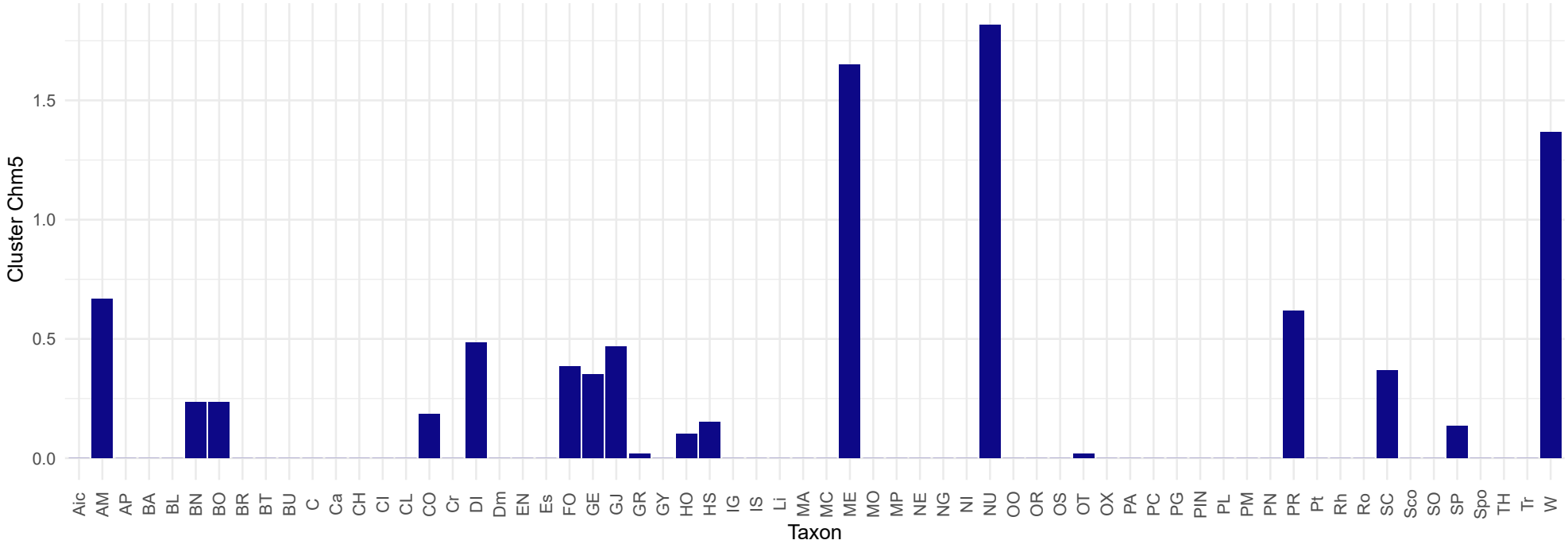

DCA samples and species UQ
SC
FO
W
GE
GJ
ME
SP
HS
AP
NU
PR
DI
BN
BO
CO
DCA 2
DCA 1
2
1
0
−1
−2
−2
−1
0
1
2
3

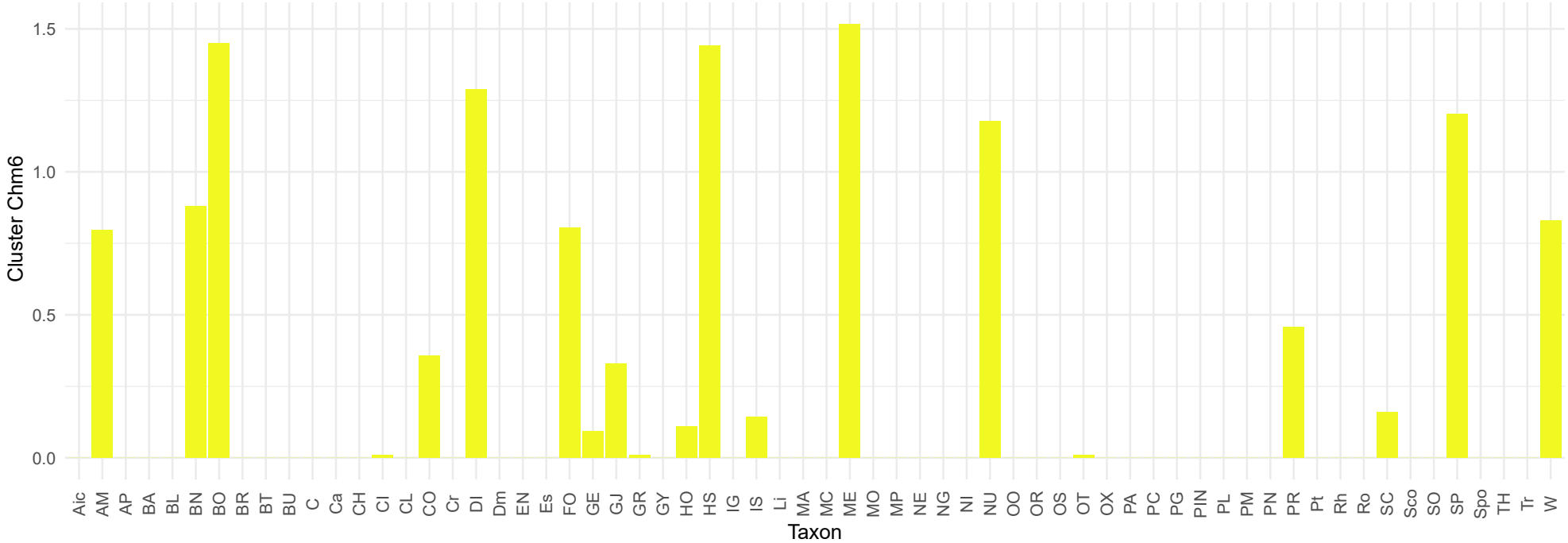

Within groups sum of squares
500
1000
1500
2000
0
10
20
30
40
50
Number of Clusters

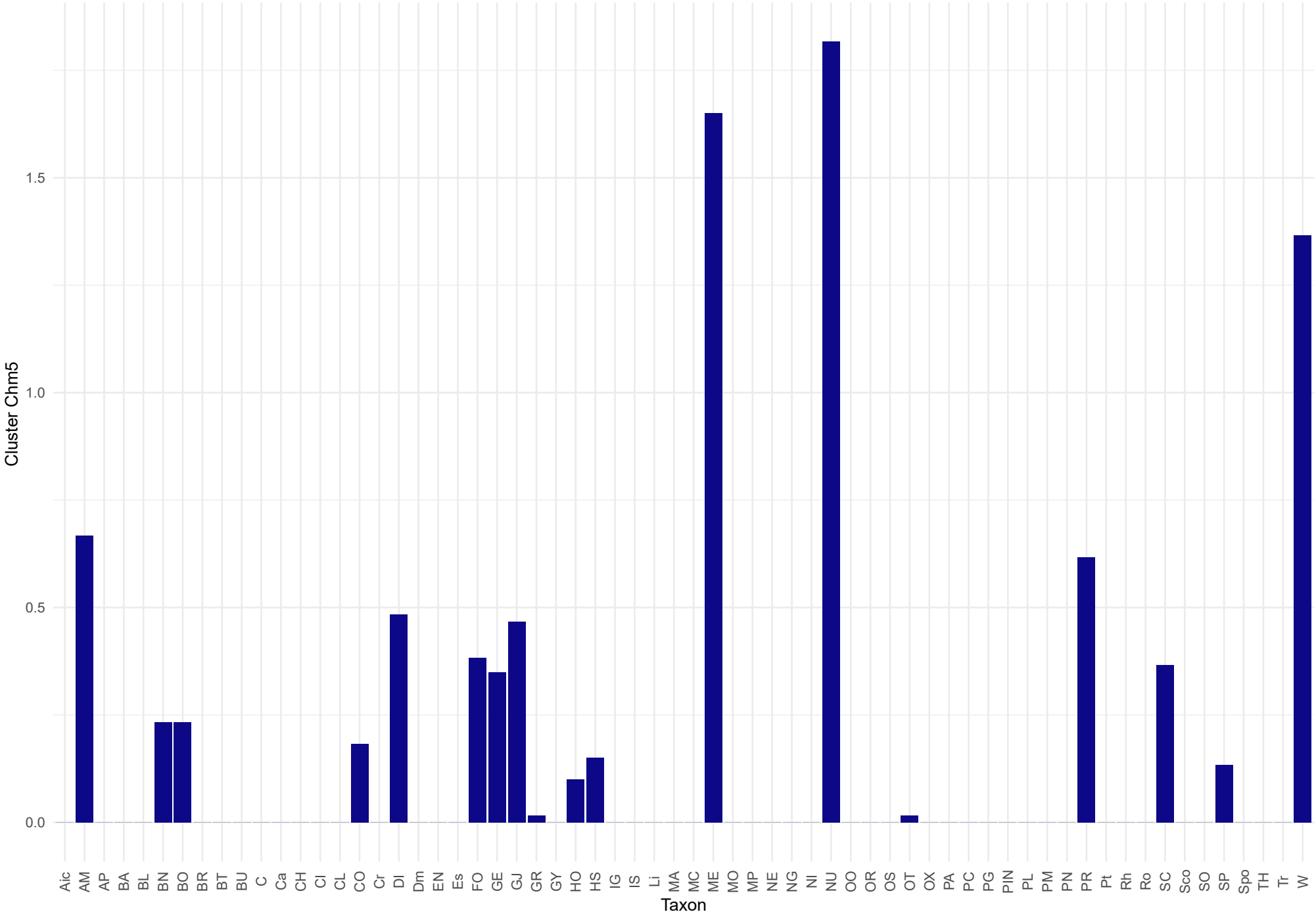

fviz_gap_stat: Gap Statistic
Gap statistic (k)
0.60
0.55
0.50
0.45
0.40
Number of clusters k

DCA2
DCA1
1.0
0.5
0.0
−0.5
−1
0
1
CM9 Cluster
a Chm5
a Chm6

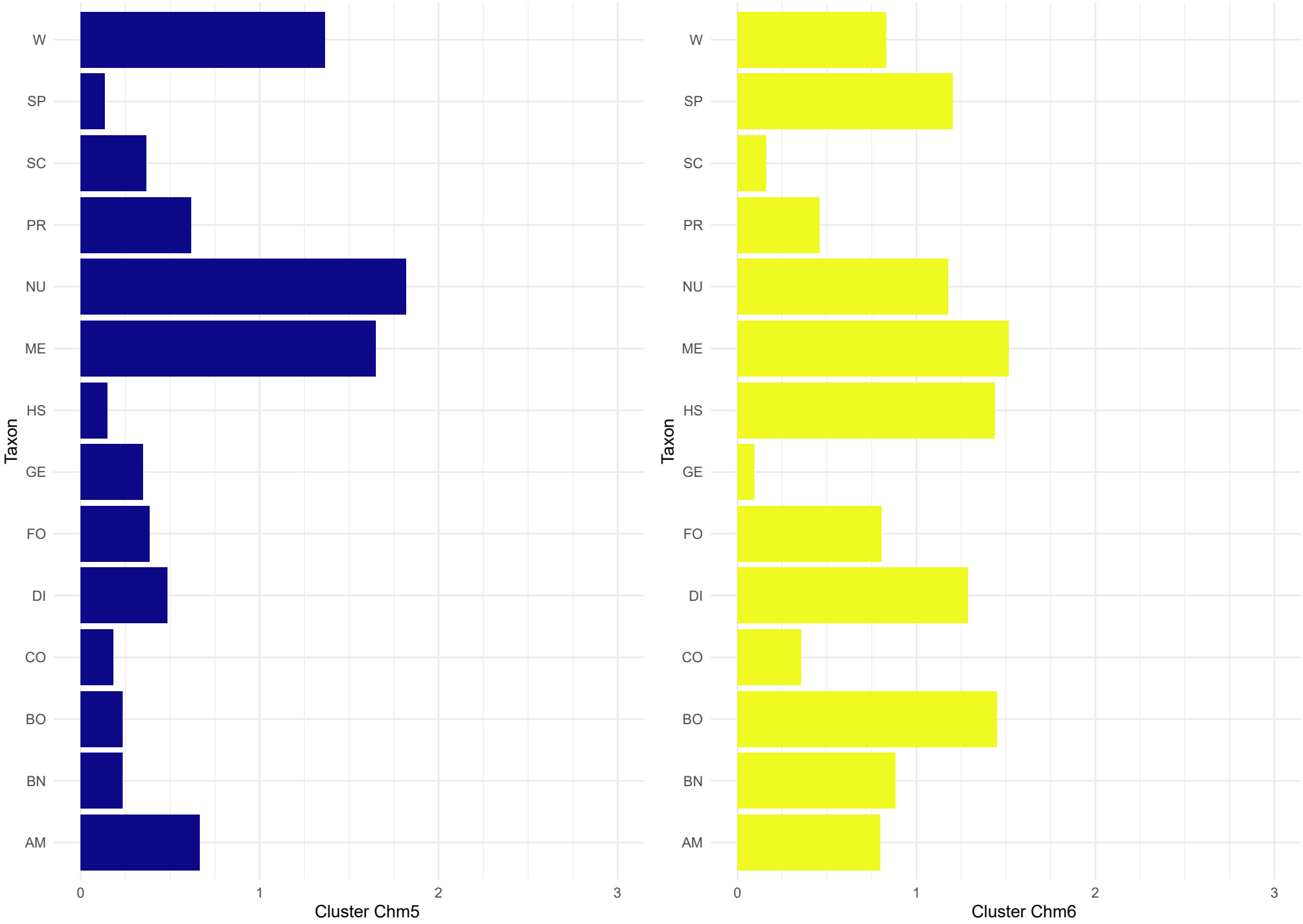

40
30
20
10
0
NERC


Cluster Chm5
1.5
1.0
0.5
0.0
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon

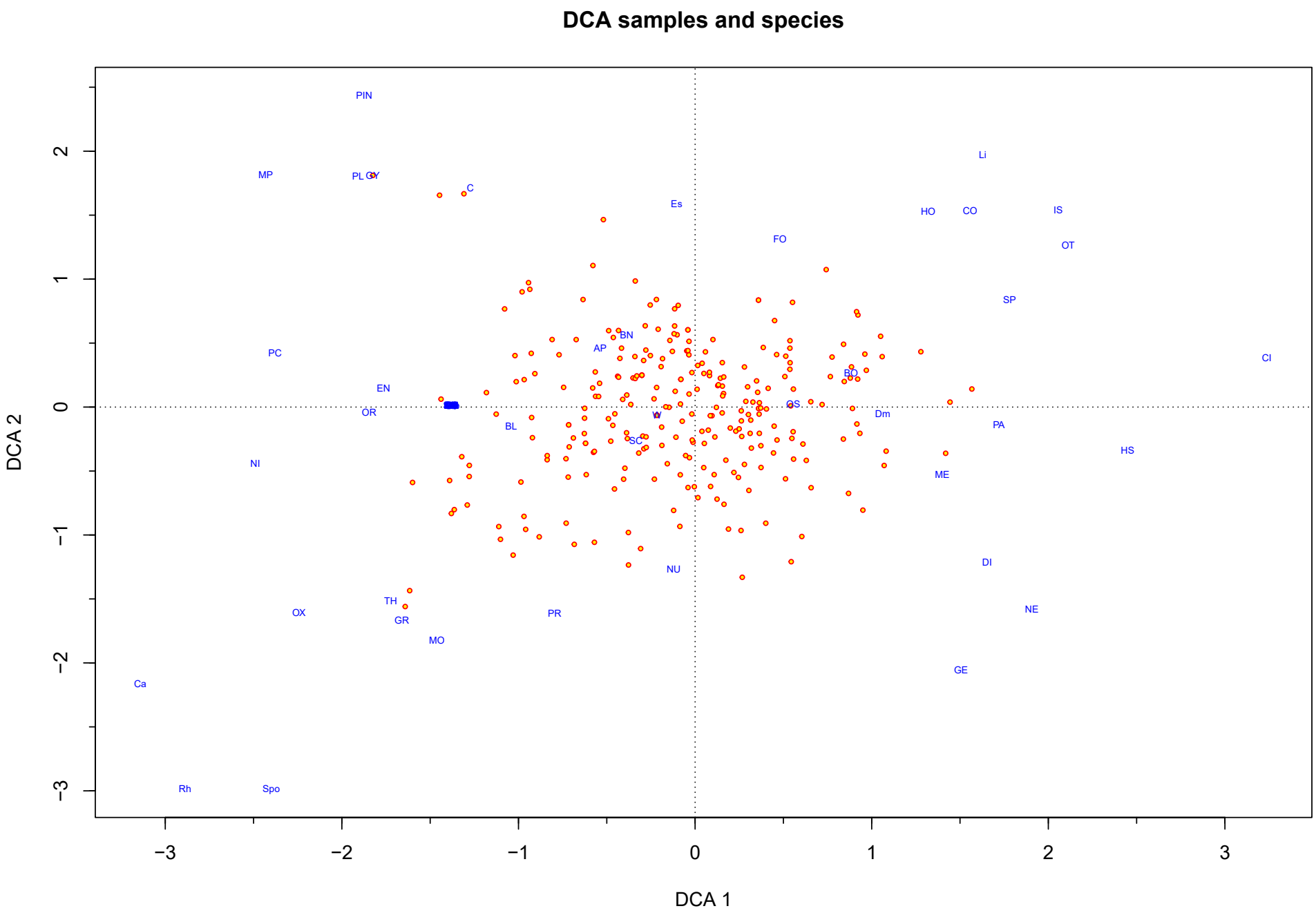

Cluster Chm6
1.5
1.0
0.5
0.0
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon


Cluster Chm5
1.5
1.0
0.5
0.0
Aic
AM
AP
BA
BL
BN
BO
BR
BT
BU
C
Ca
CH
CI
CL
CO
Cr
DI
Dm
EN
Es
FO
GE
GJ
GR
GY
HO
HS
IG
IS
Li
MA
MC
ME
MO
MP
NE
NG
NI
NU
OO
OR
OS
OT
OX
PA
PC
PG
PIN
PL
PM
PN
PR
Pt
Rh
Ro
SC
Sco
SO
SP
Spo
TH
Tr
W
Taxon

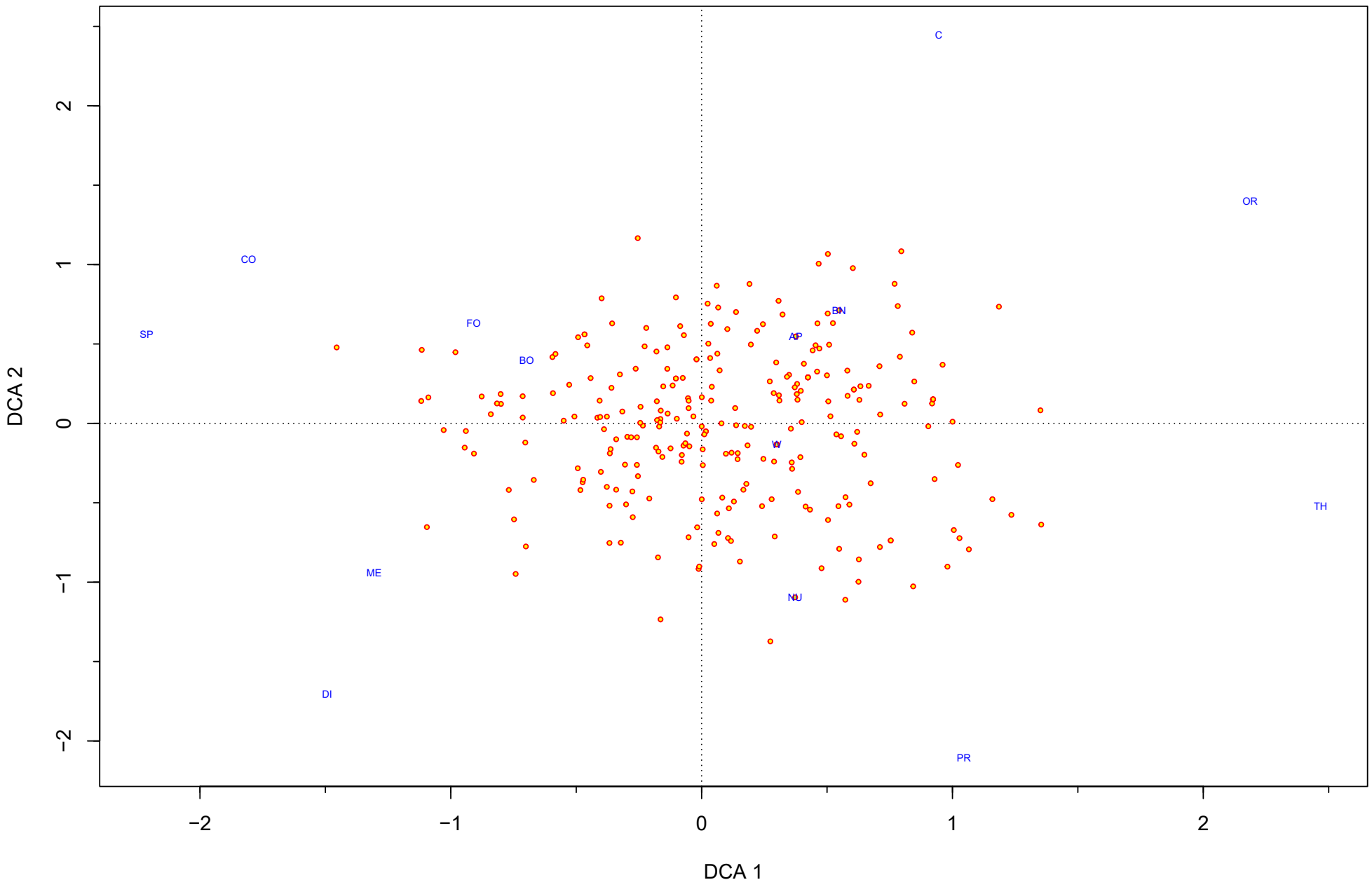
Cluster Chm6
1.5
1.0
0.5
0.0
Aic
AM
AP
BA
BL
BN
BO
BR
BT
BU
C
Ca
CH
CI
CL
CO
Cr
DI
Dm
EN
Es
FO
GE
GJ
GR
GY
HO
HS
IG
IS
Li
MA
MC
ME
MO
MP
NE
NG
NI
NU
OO
OR
OS
OT
OX
PA
PC
PG
PIN
PL
PM
PN
PR
Pt
Rh
Ro
SC
Sco
SO
SP
Spo
TH
Tr
W
Taxon

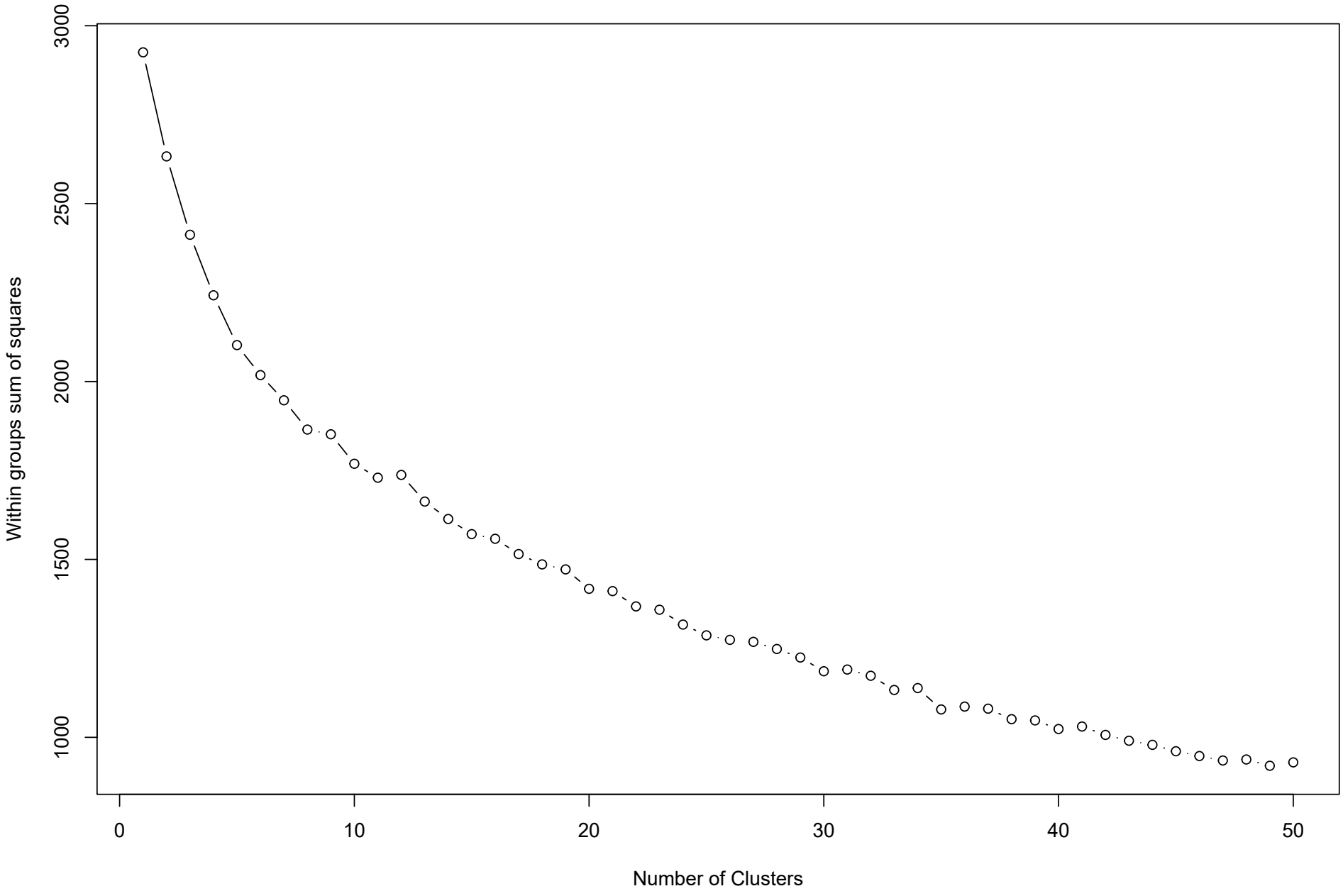

W
SP
SC
PR
NU
ME
HS
GE
FO
DI
CO
BO
BN
AM
Taxon
0
1
2
3
Cluster Chm5
Cluster Chm6

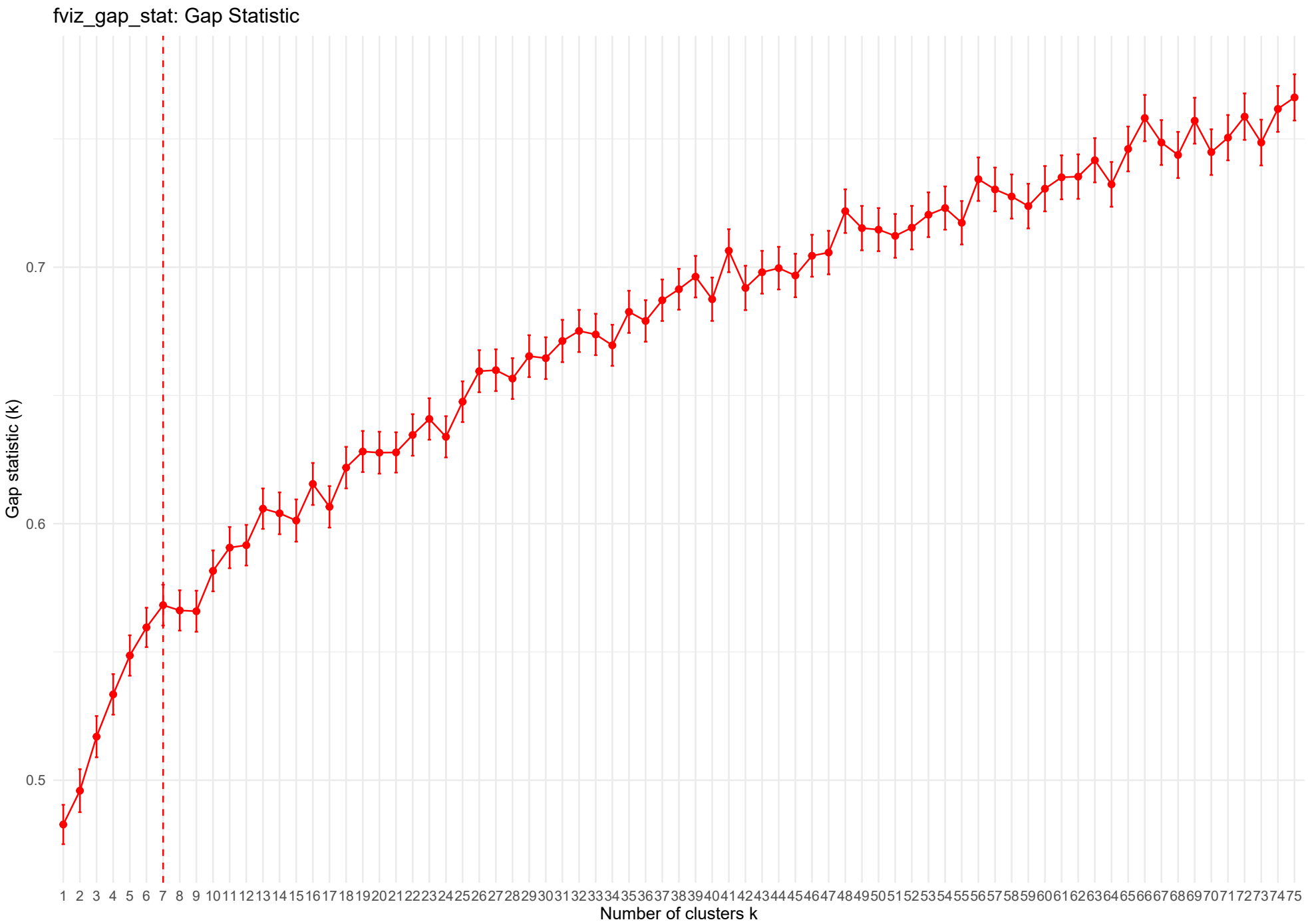
Combe Throop (CT)

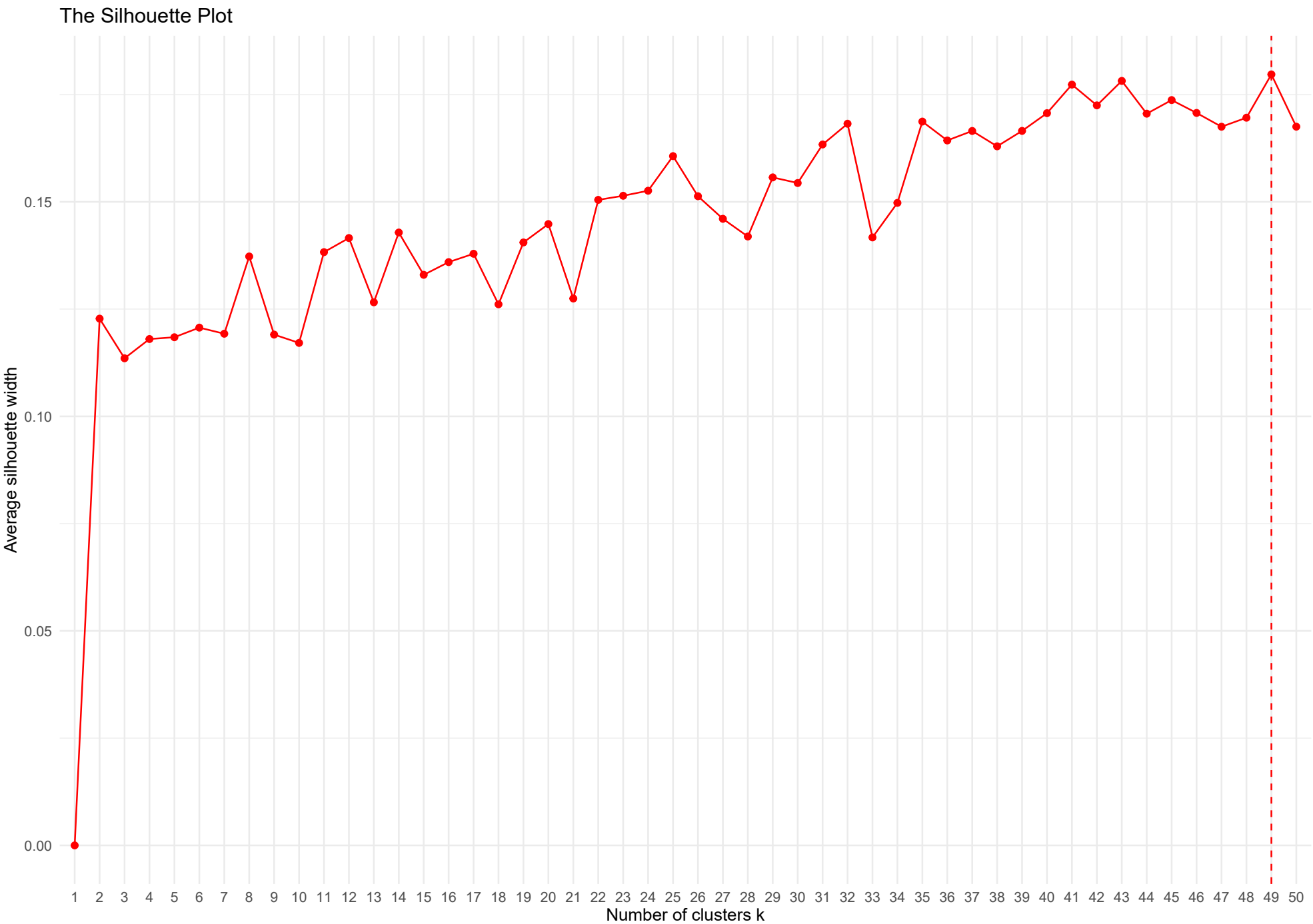

DCA samples and species
DCA 1
DCA 2
−3
−2
−1
0
1
2
3
PIN
MP
PL
GY
C
Es
Li
HO
CO
IS
OT
FO
SP
BN
AP
PC
EN
OR
BL
SC
W
OS
BO
Dm
PA
CI
HS
NI
ME
NU
DI
TH
OX
GR
PR
NE
MO
GE
Ca
Rh
Spo

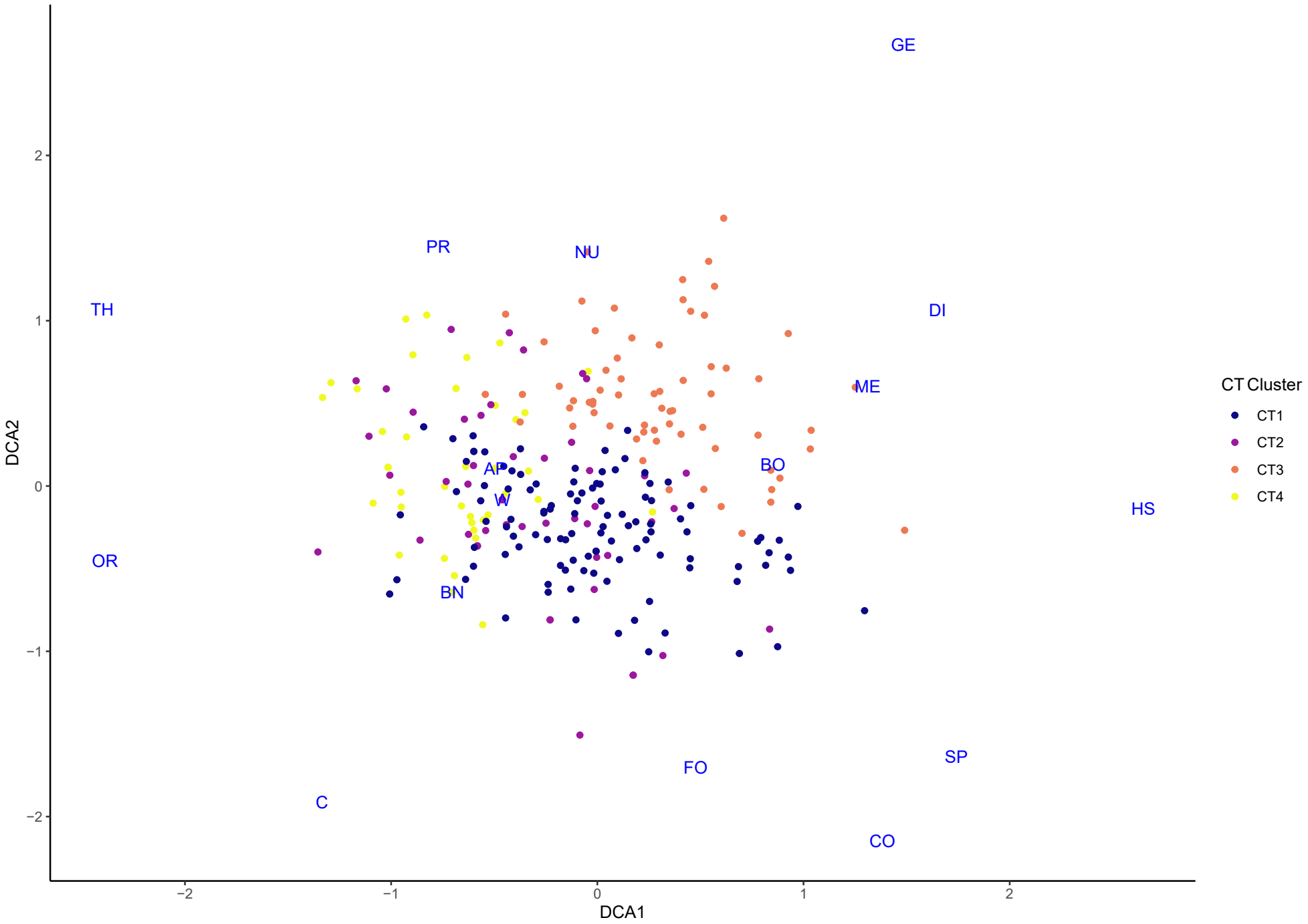
DCA samples and species UQ



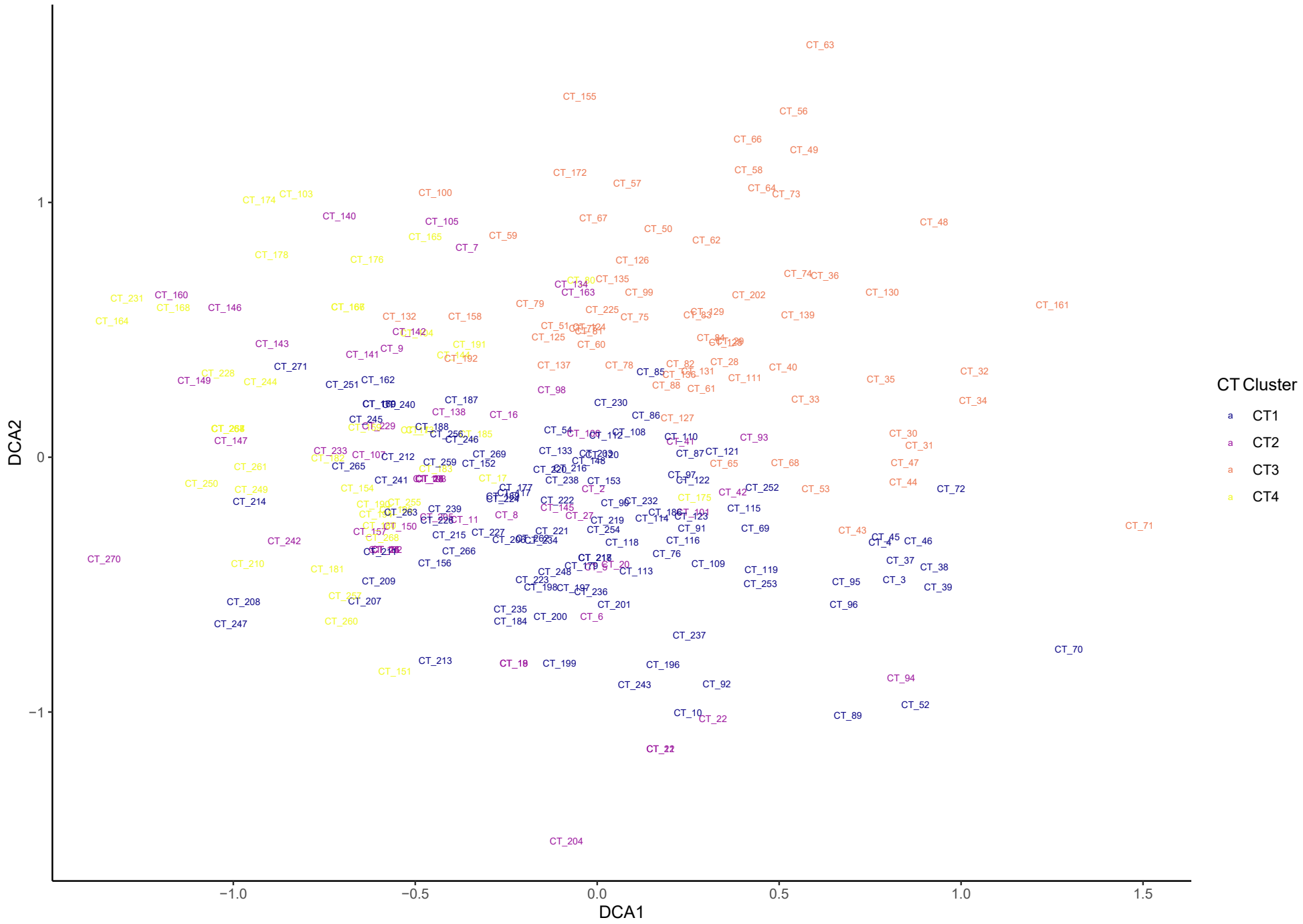

Within groups sum of squares
3000
2500
2000
1500
1000
0
10
20
30
40
50
Number of Clusters

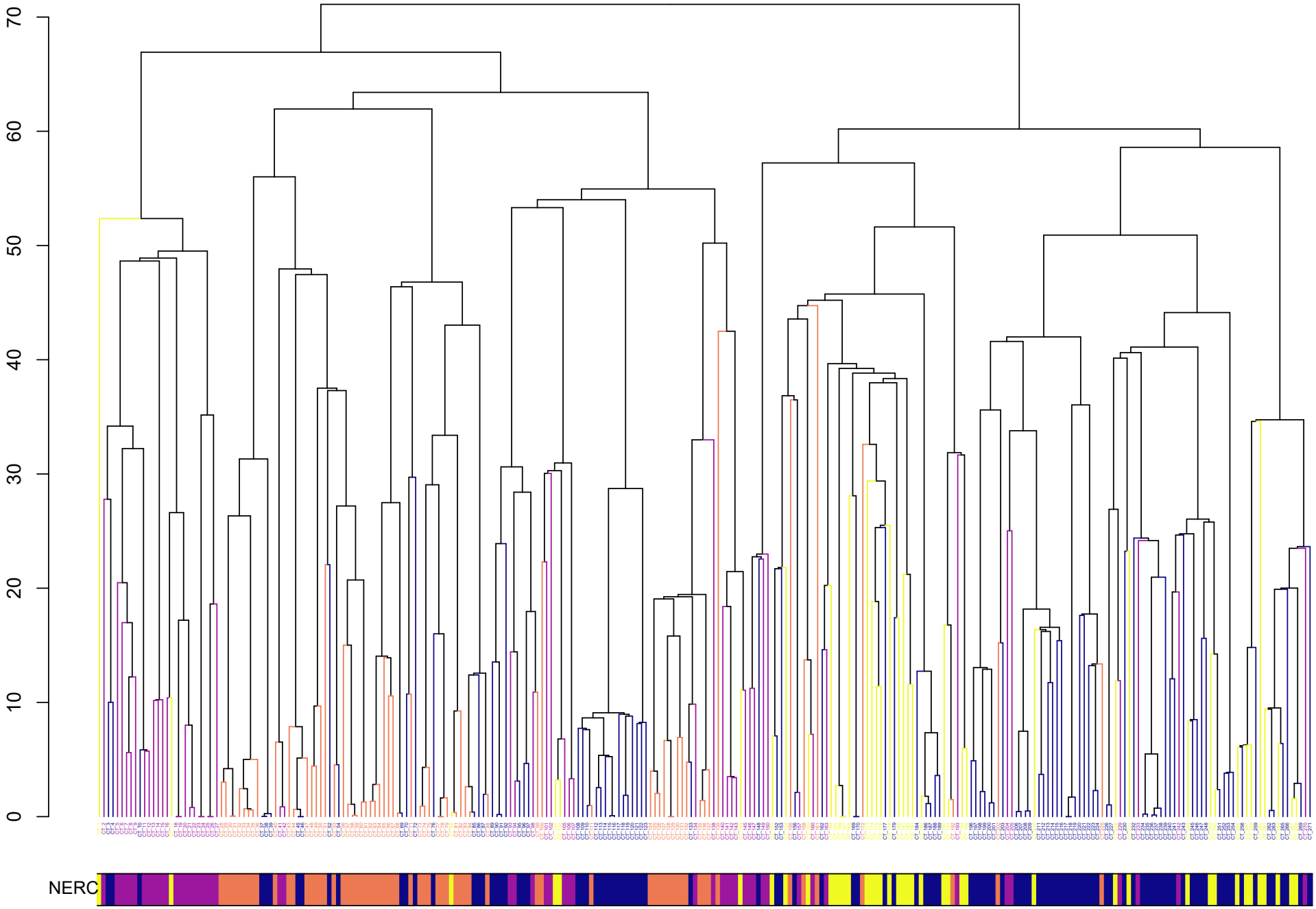

fviz_gap_stat: Gap Statistic
Gap statistic (k)
0.5
0.6
0.7
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75
Number of clusters k

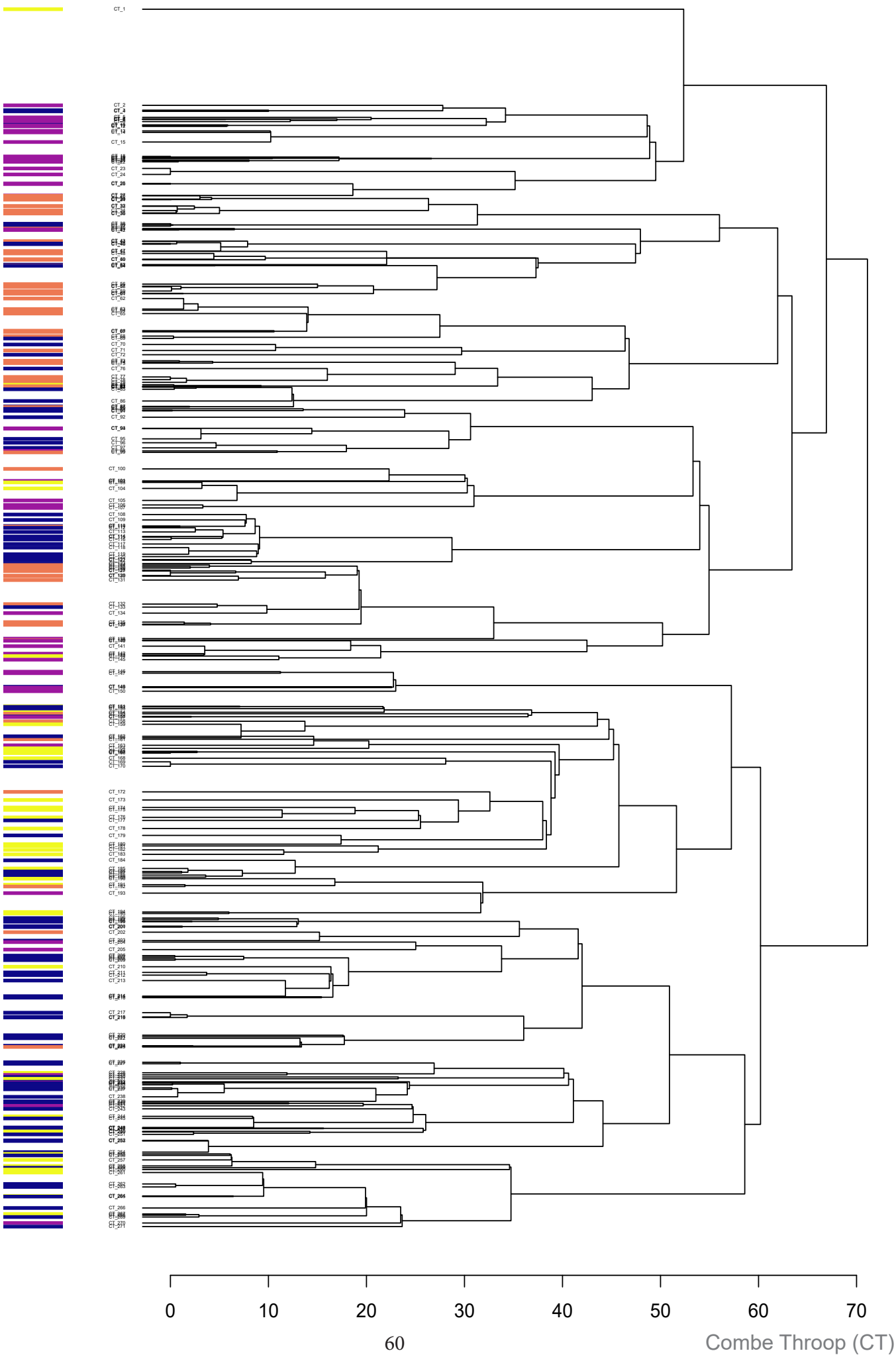

The Silhouette Plot
Average silhouette width
0.00
0.05
0.10
0.15
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50
Number of clusters k

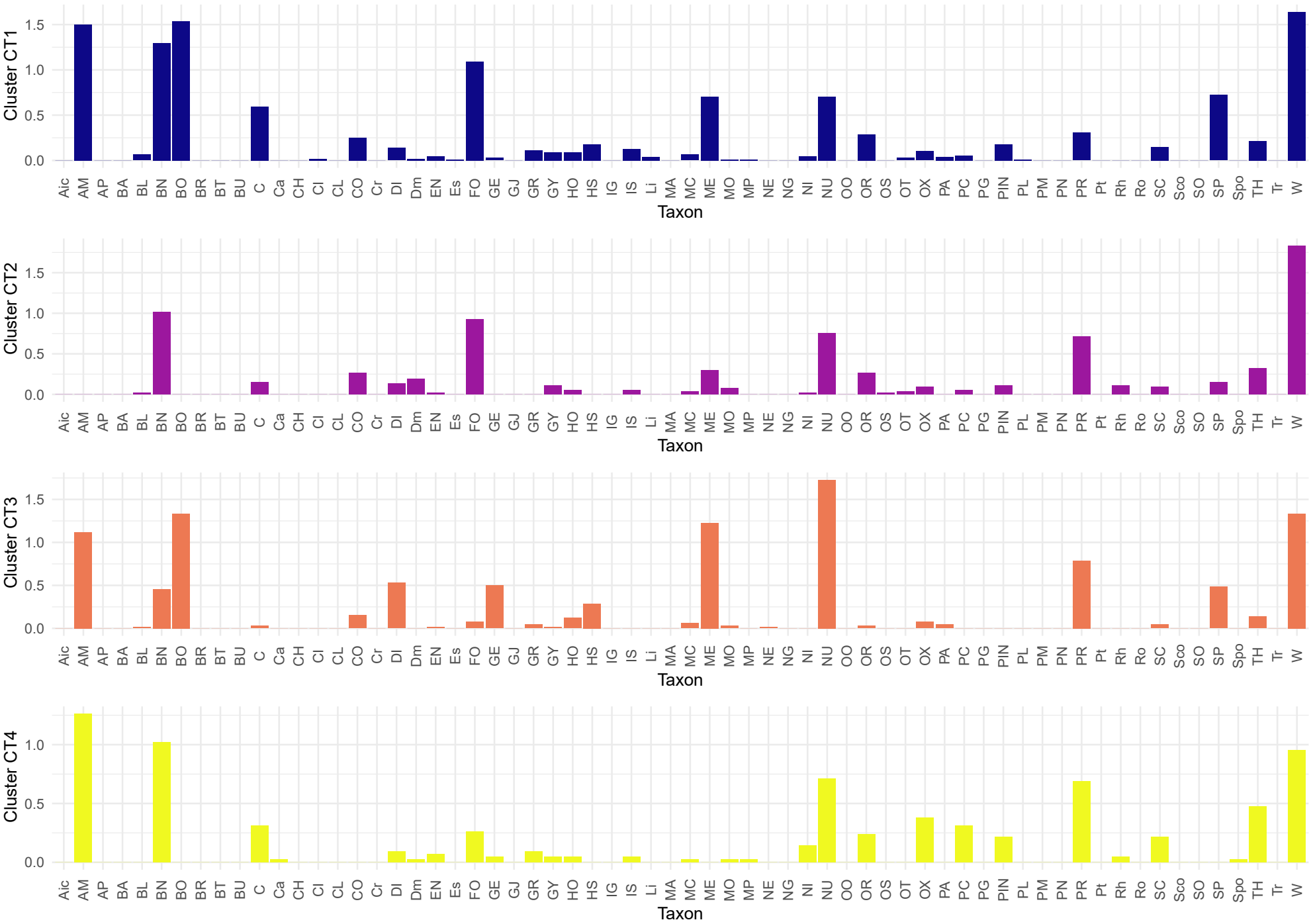


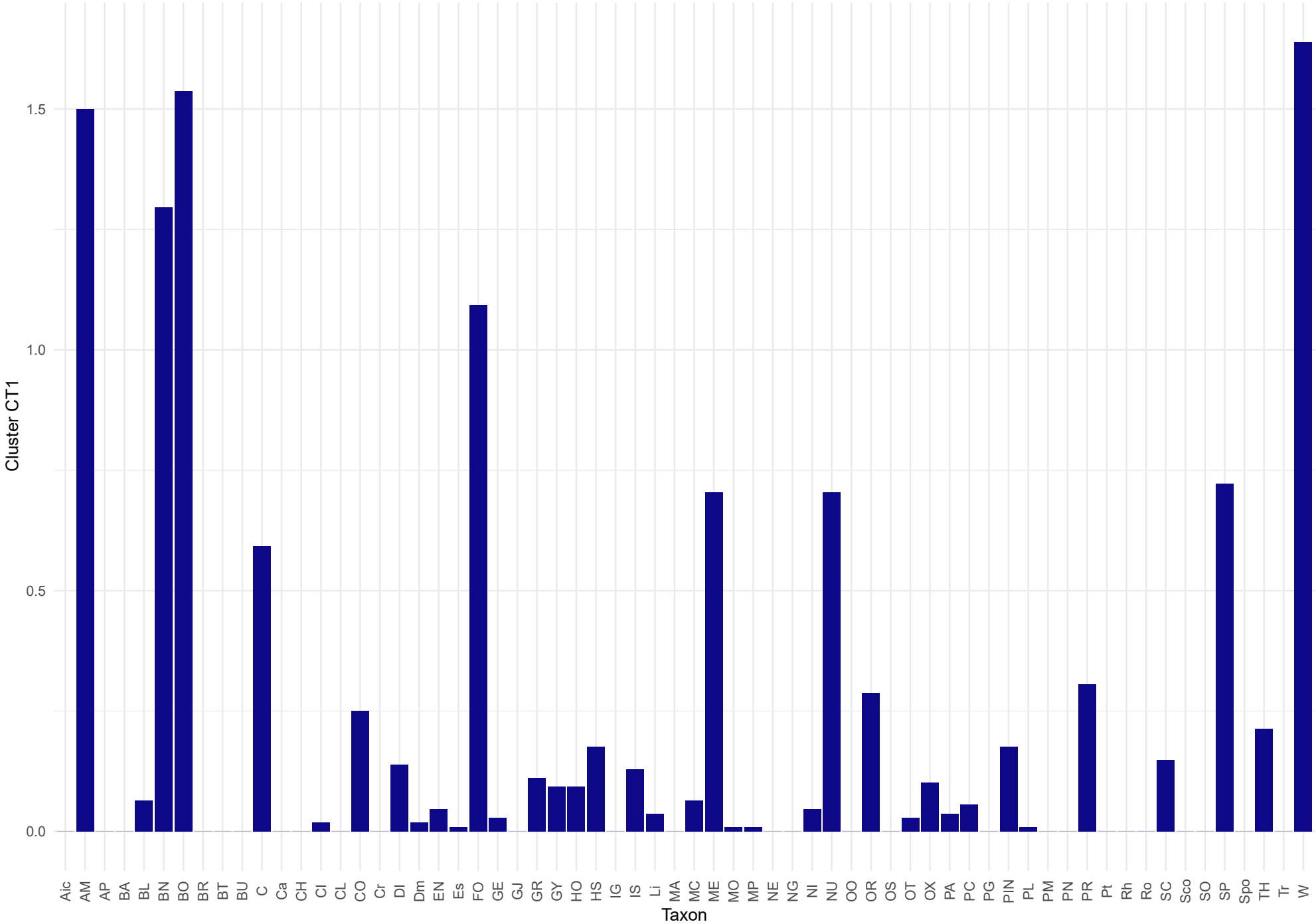
Combe Throop (CT)

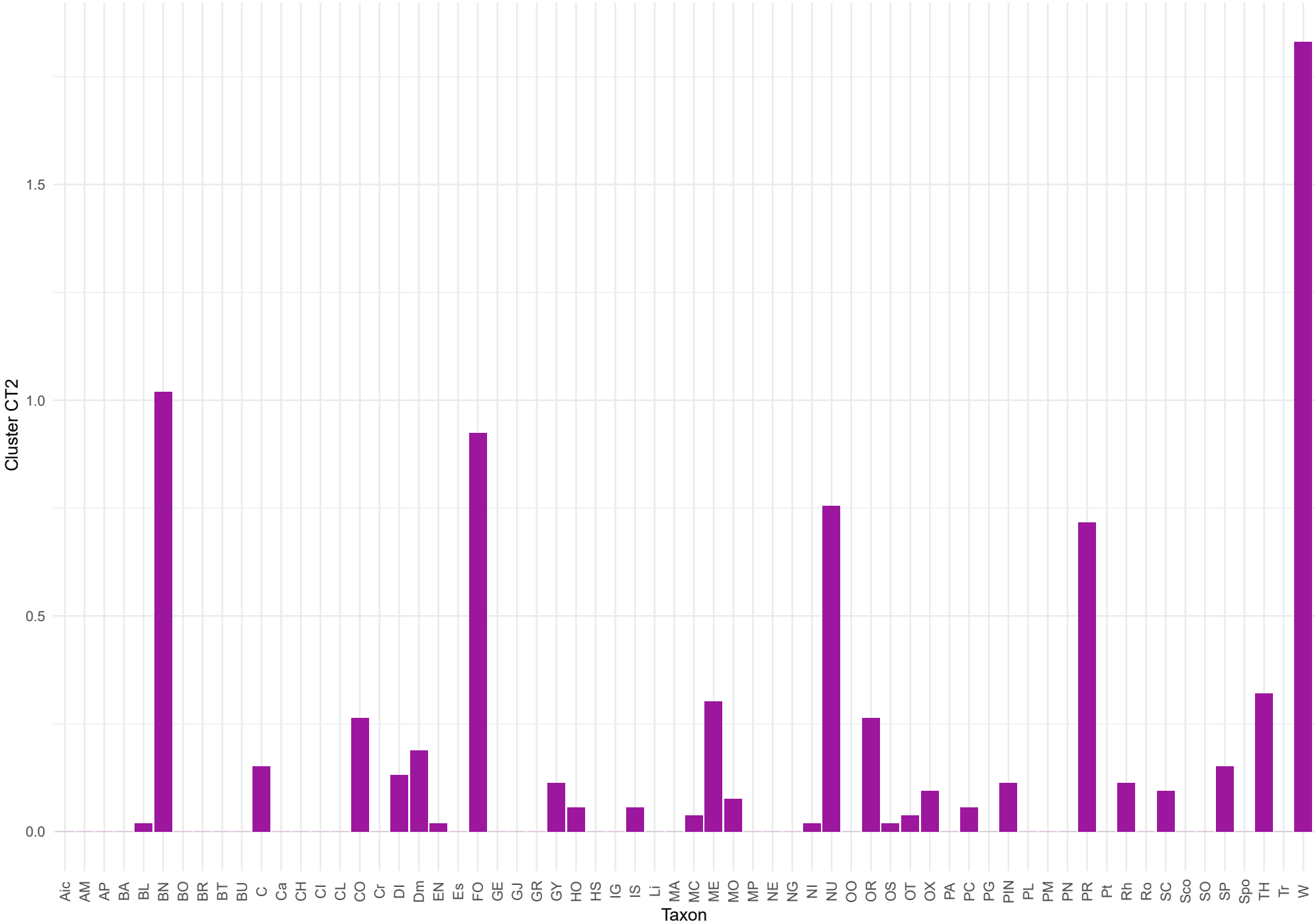

DCA2
DCA1
1
0
−1
−1.0
−0.5
0.0
0.5
1.0
1.5
CT Cluster
a CT1
a CT2
a CT3
a CT4

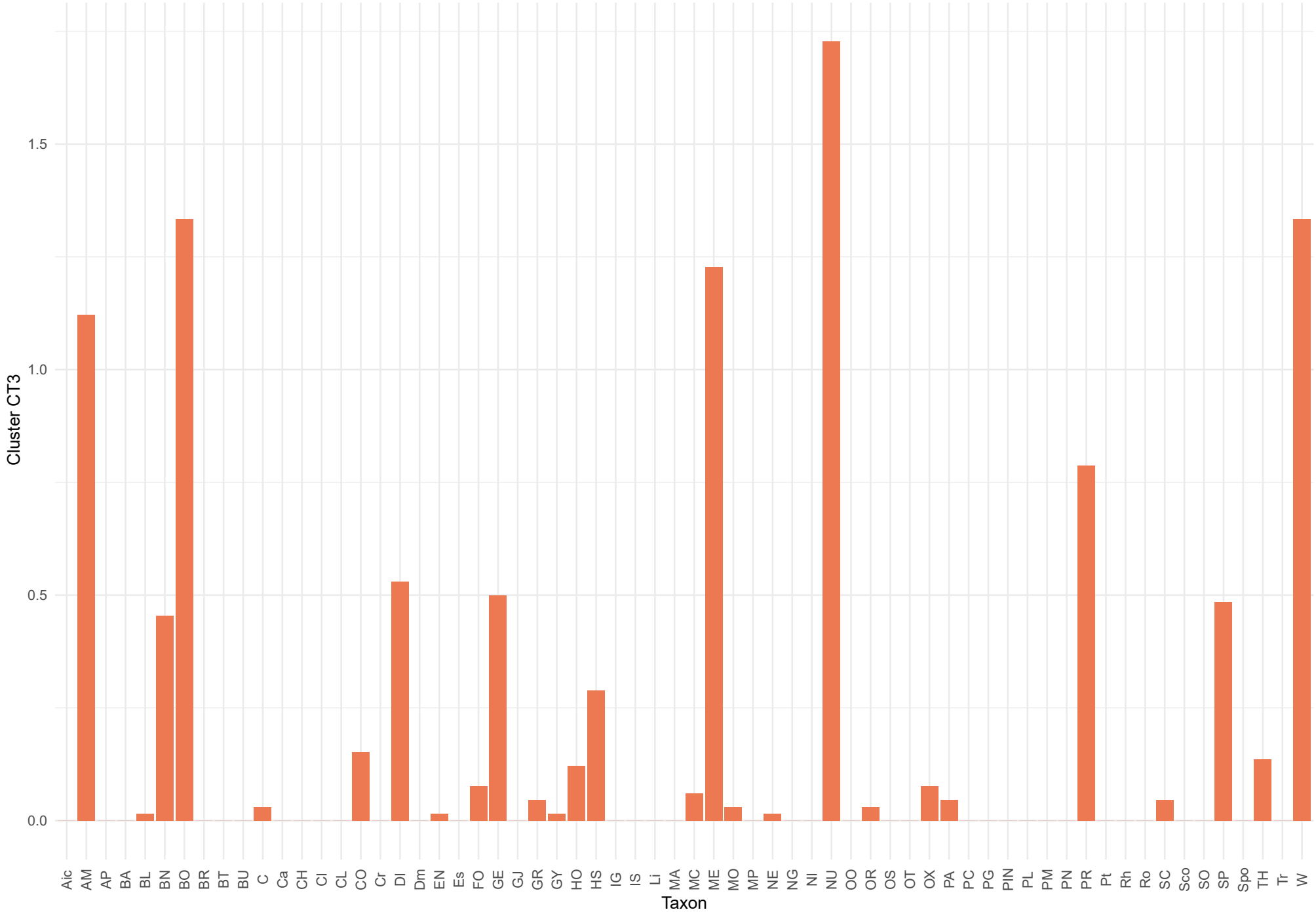

70
60
50
40
30
20
10
0
NERC

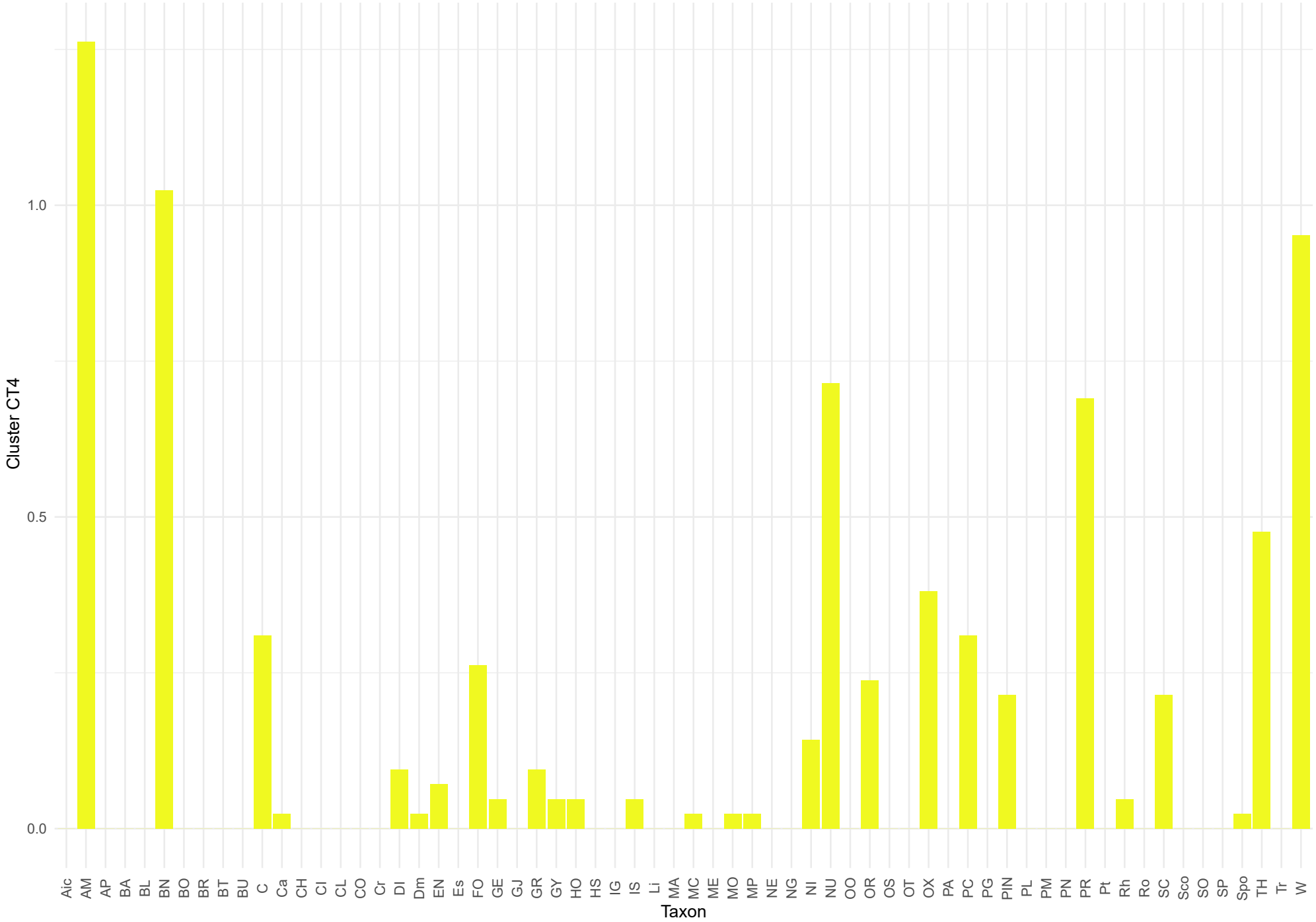

0
10
20
30
40
50
60
70
Combe Throop (CT)

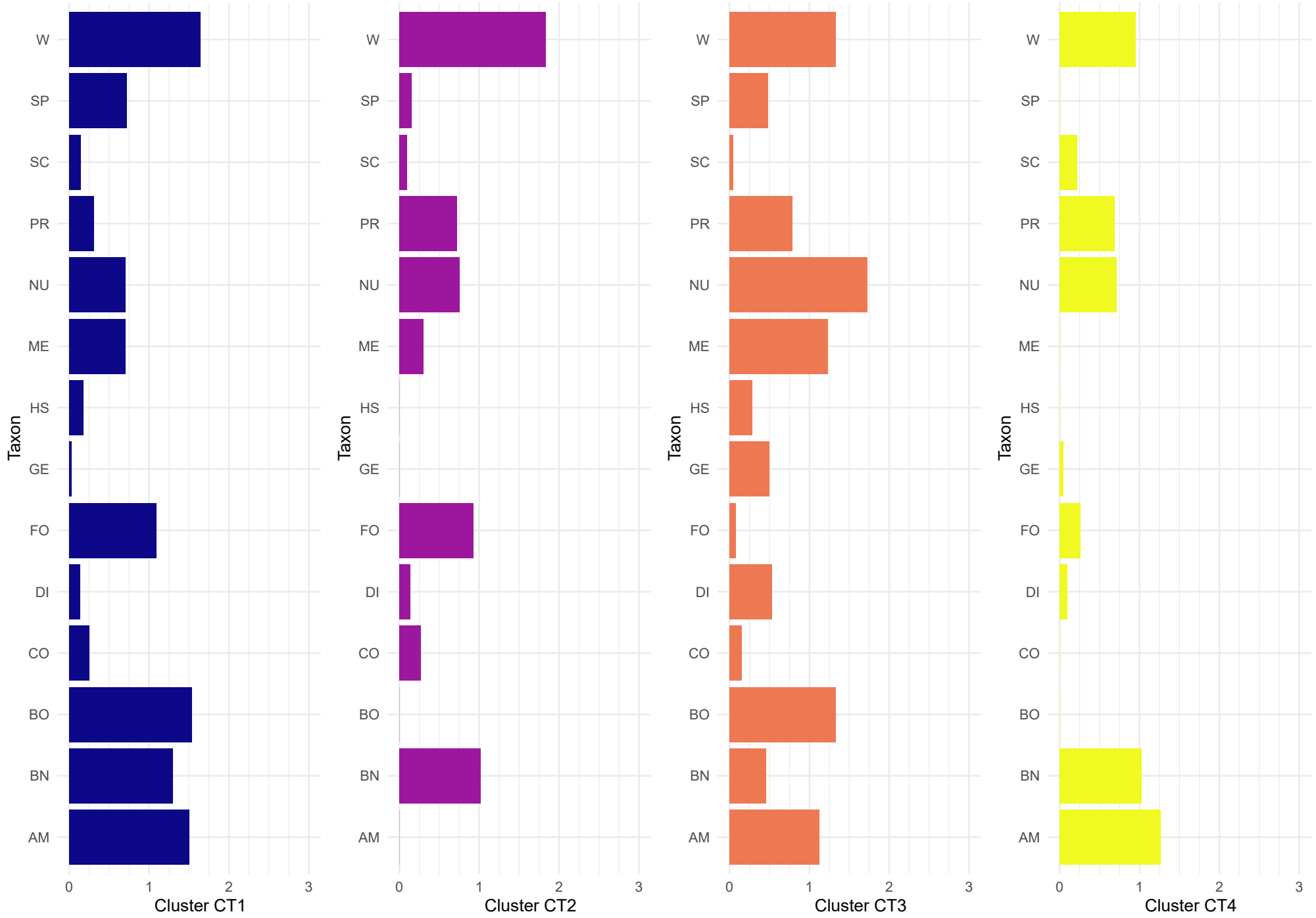

Cluster CT1
Cluster CT2
Cluster CT3
Cluster CT4
0.0
0.5
1.0
1.5
Aic AM AP BA BL BN BO BR BT BU C Ca CH Cl CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon


Cluster CT1
1.5
1.0
0.5
0.0
Aic
AM
AP
BA
BL
BN
BO
BR
BT
BU
C
Ca
CH
Cl
CL
CO
Cr
DI
Dm
EN
Es
FO
GE
GJ
GR
GY
HO
HS
IG
IS
Li
MA
MC
ME
MO
MP
NE
NG
NI
NU
OO
OR
OS
OT
OX
PA
PC
PG
PIN
PL
PM
PN
PR
Pt
Rh
Ro
SC
Sco
SO
SP
Spo
TH
Tr
W
Taxon


Cluster CT2
1.5
1.0
0.5
0.0
Aic
AM
AP
BA
BL
BN
BO
BR
BT
BU
C
Ca
CH
CI
CL
CO
Cr
DI
Dm
EN
Es
FO
GE
GJ
GR
GY
HO
HS
IG
IS
Li
MA
MC
ME
MO
MP
NE
NG
NI
NU
OO
OR
OS
OT
OX
PA
PC
PG
PIN
PL
PM
PN
PR
Pt
Rh
Ro
SC
Sco
SO
SP
Spo
TH
Tr
W
Taxon

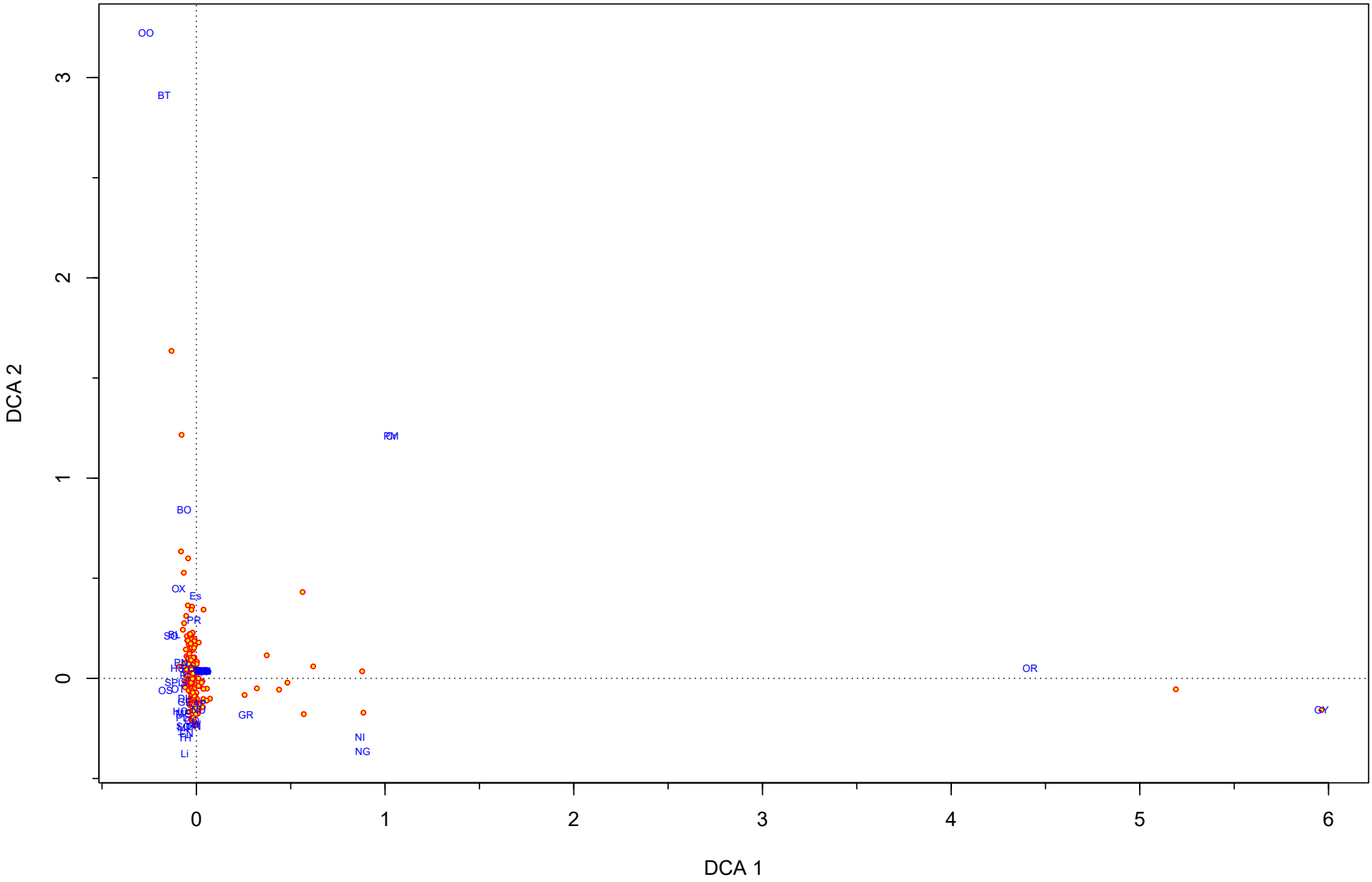

Cluster CT3
1.5
1.0
0.5
0.0
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon

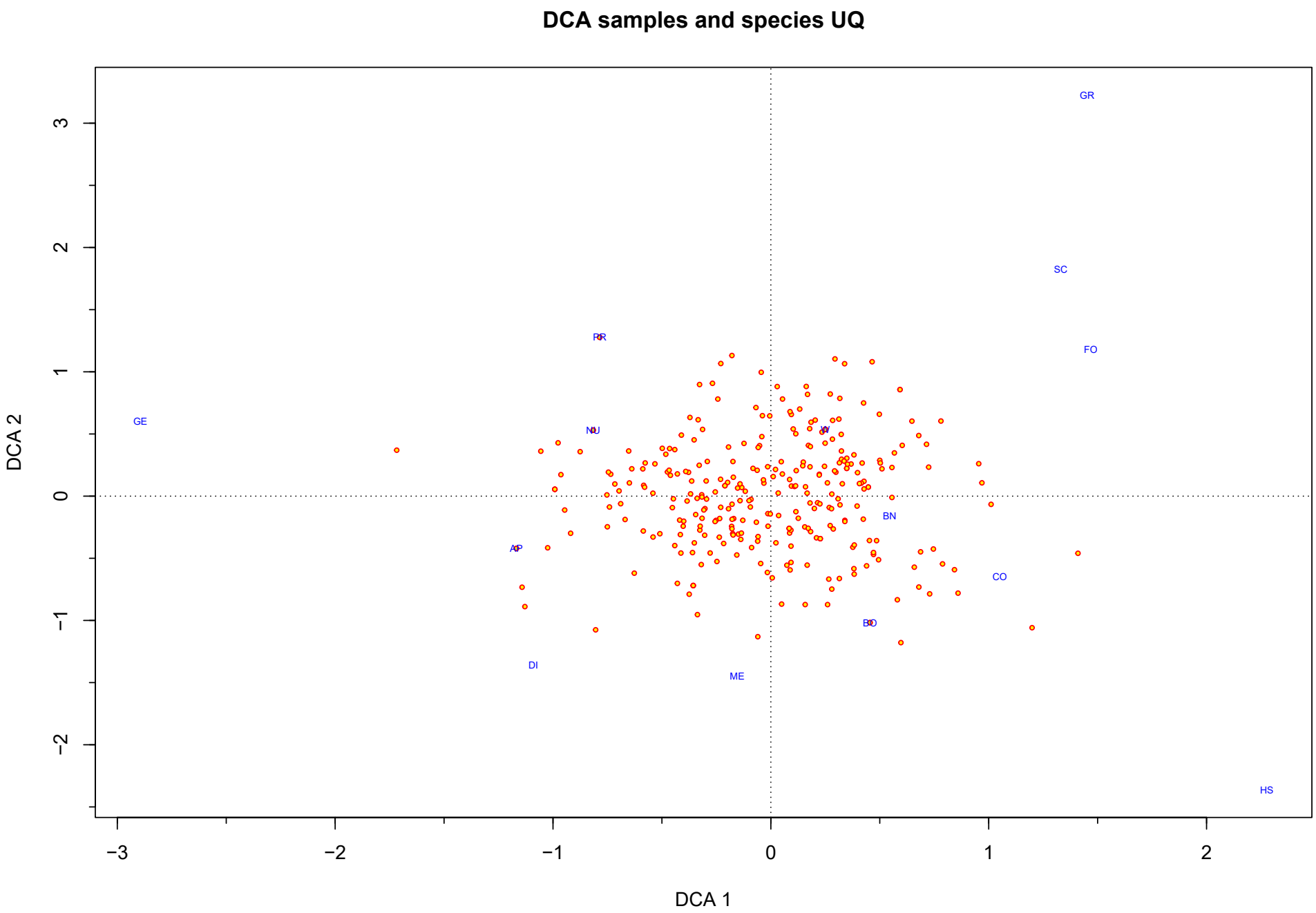

Cluster CT4
1.0
0.5
0.0
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon

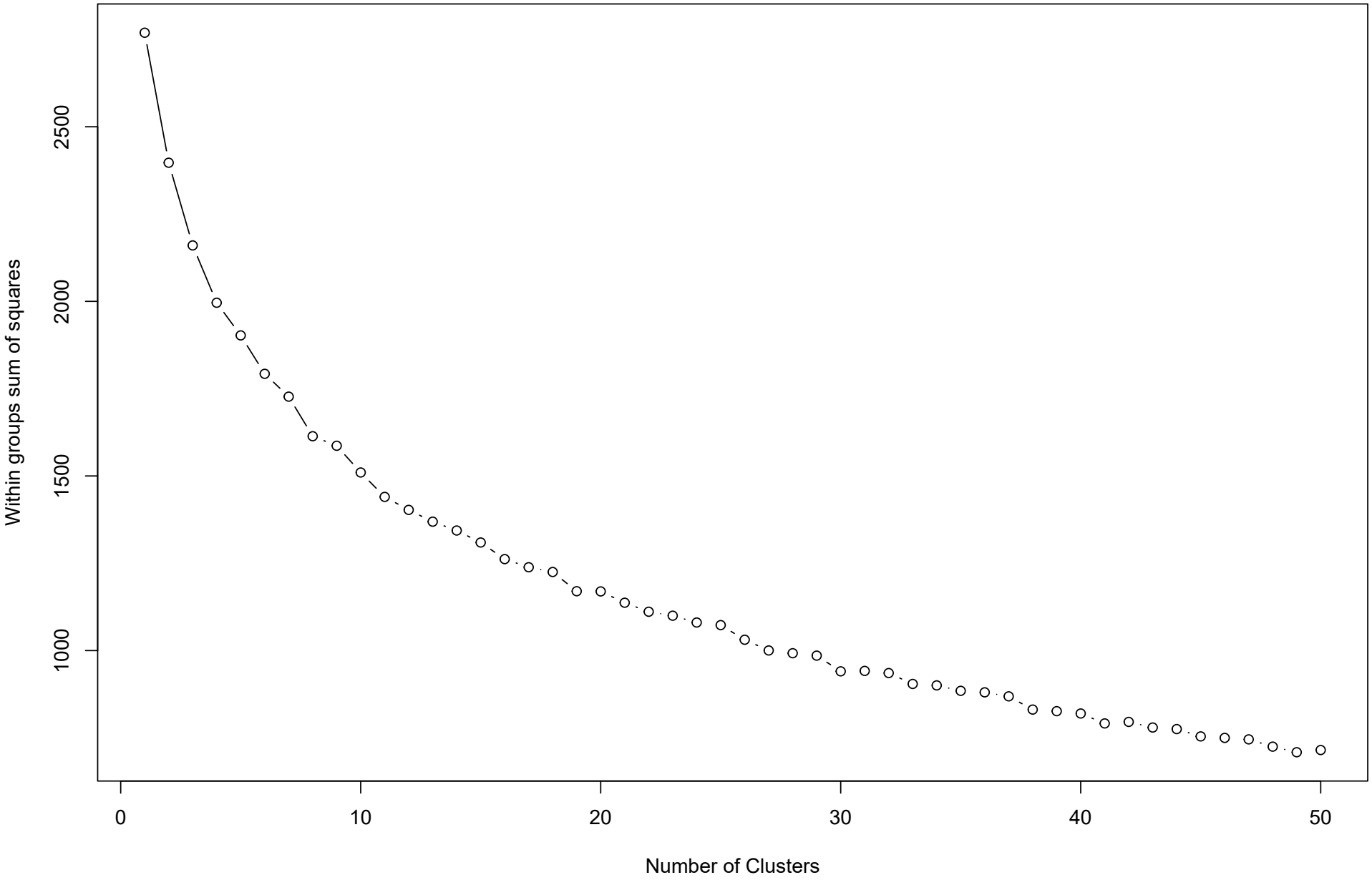

Taxon
W
SP
SC
PR
NU
ME
HS
GE
FO
DI
CO
BO
BN
AM
0
1
2
3
Cluster CT1
Cluster CT2
Cluster CT3
Cluster CT4

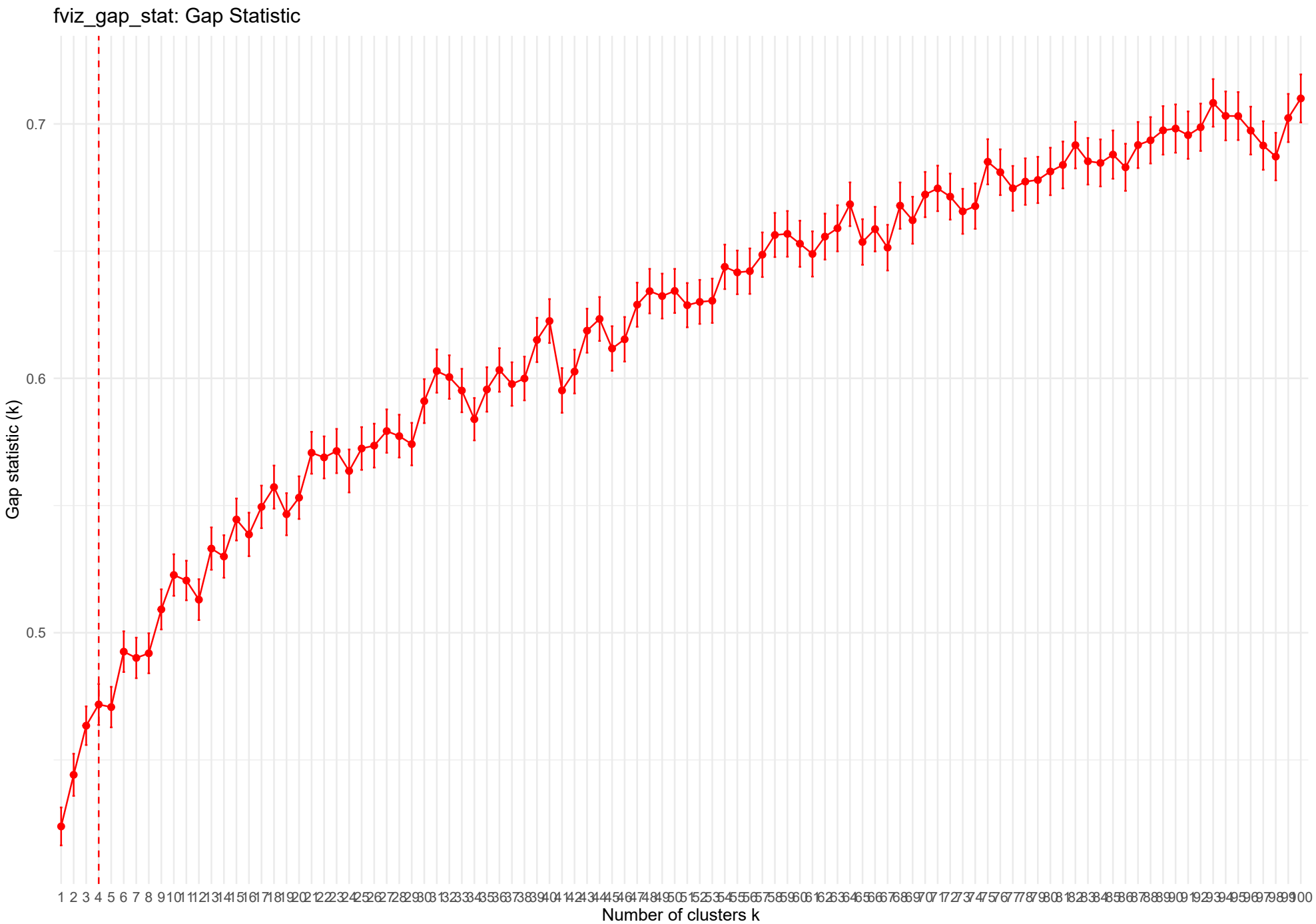
Down Ampney (DA)

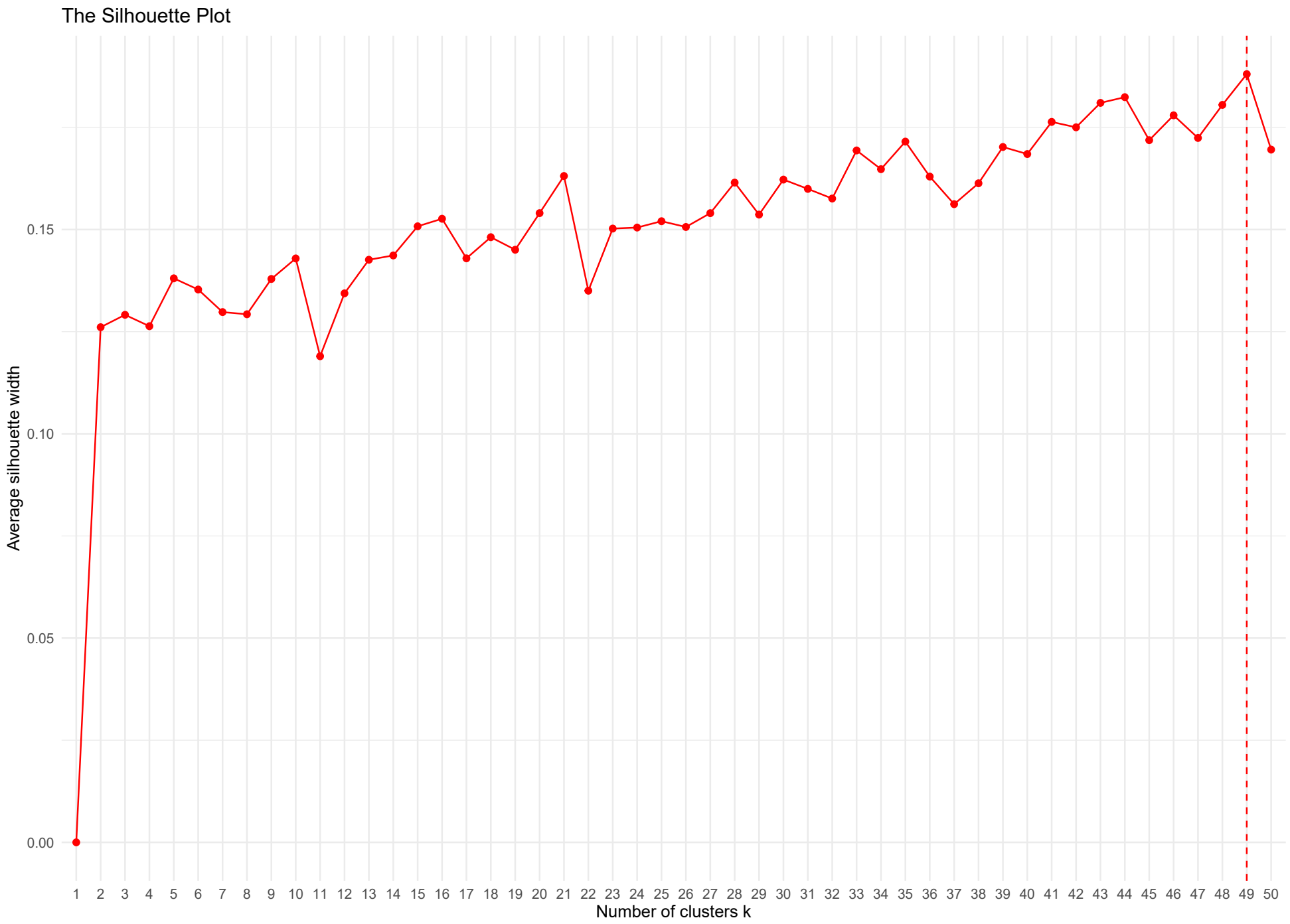
DCA samples and species

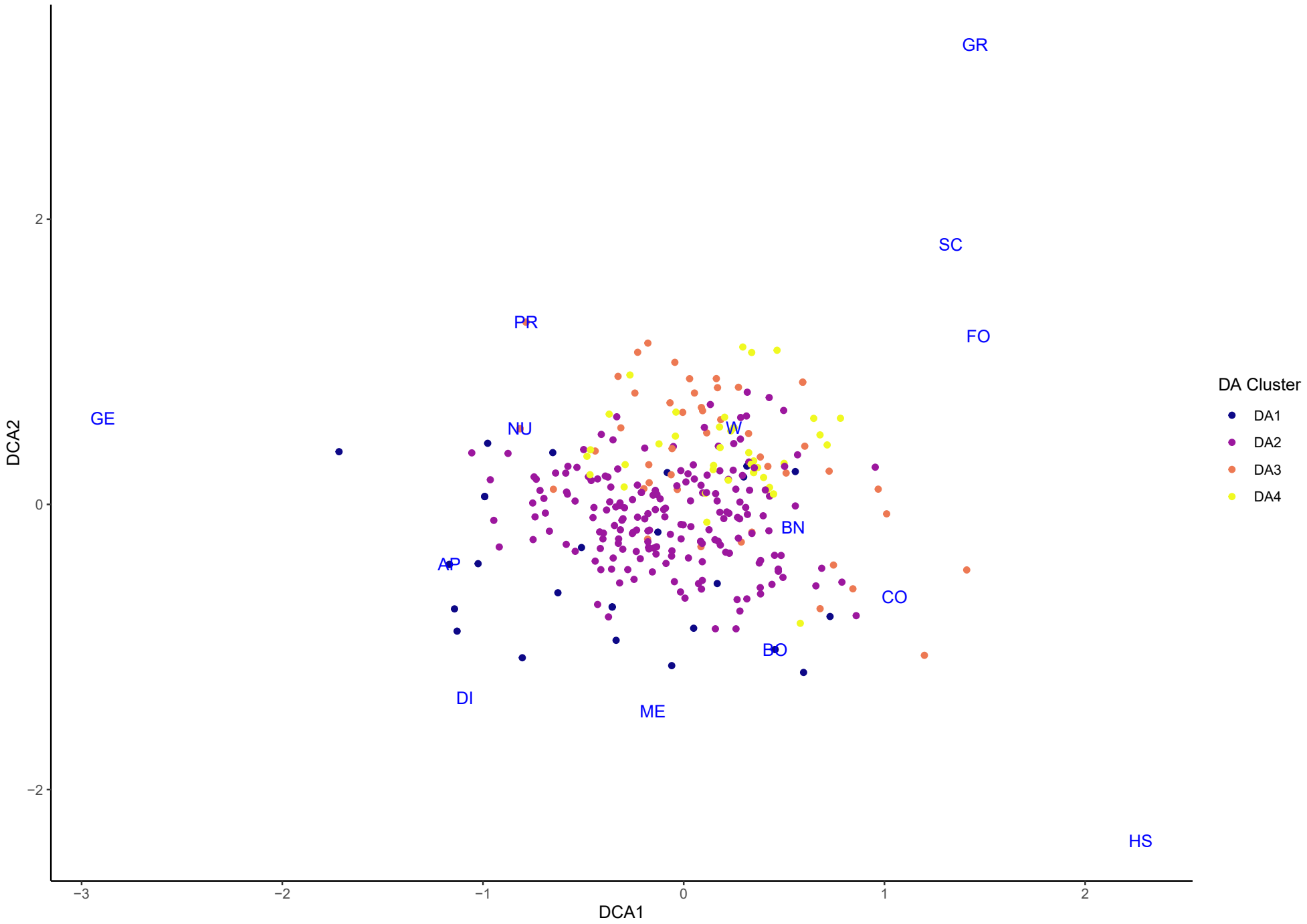


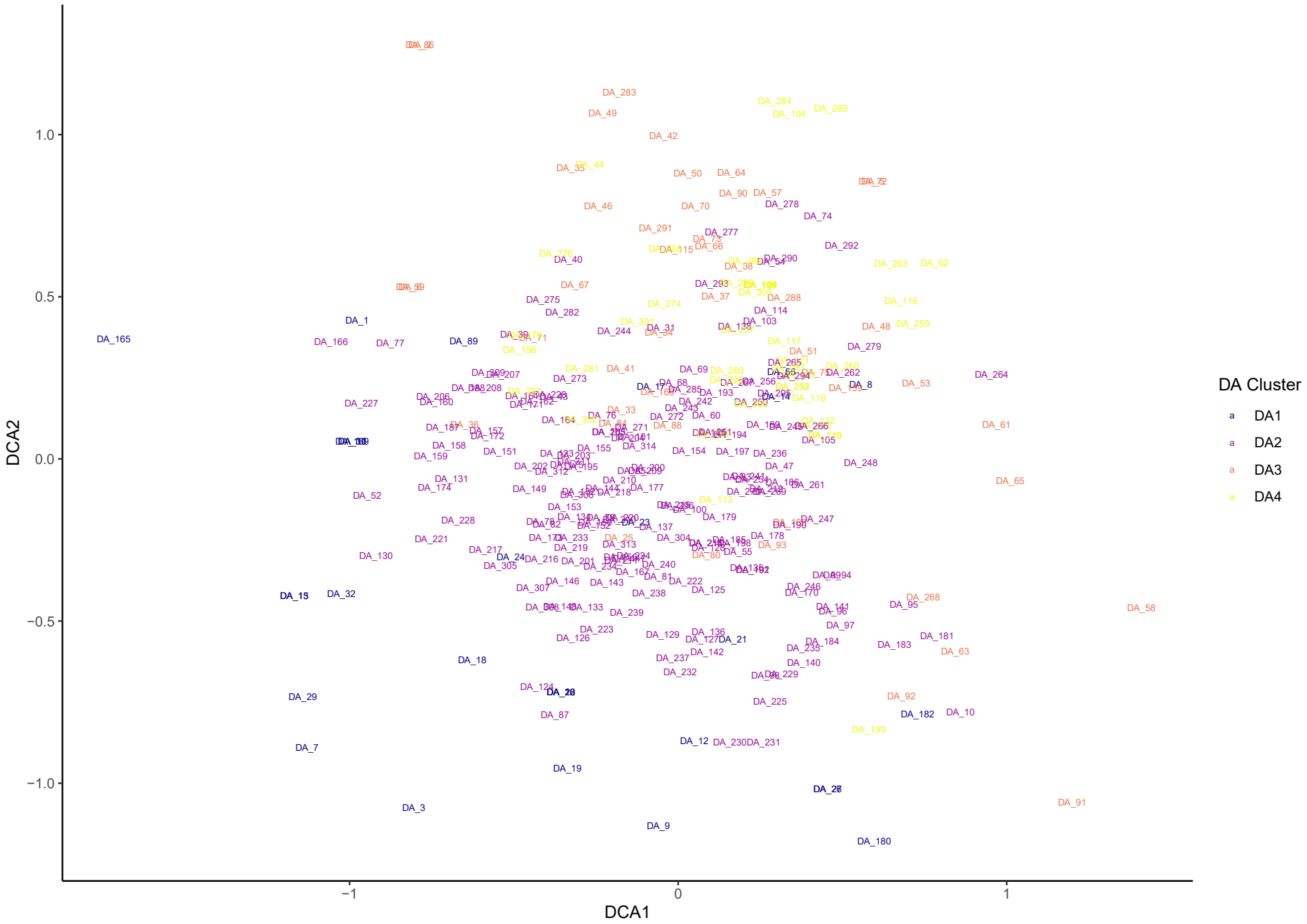

DCA samples and species UQ
GR
SC
FO
GE
BN
CO
DI
ME
HS
DCA 2
DCA 1
3
2
1
0
−1
−2
−3
−2
−1
0
1
2

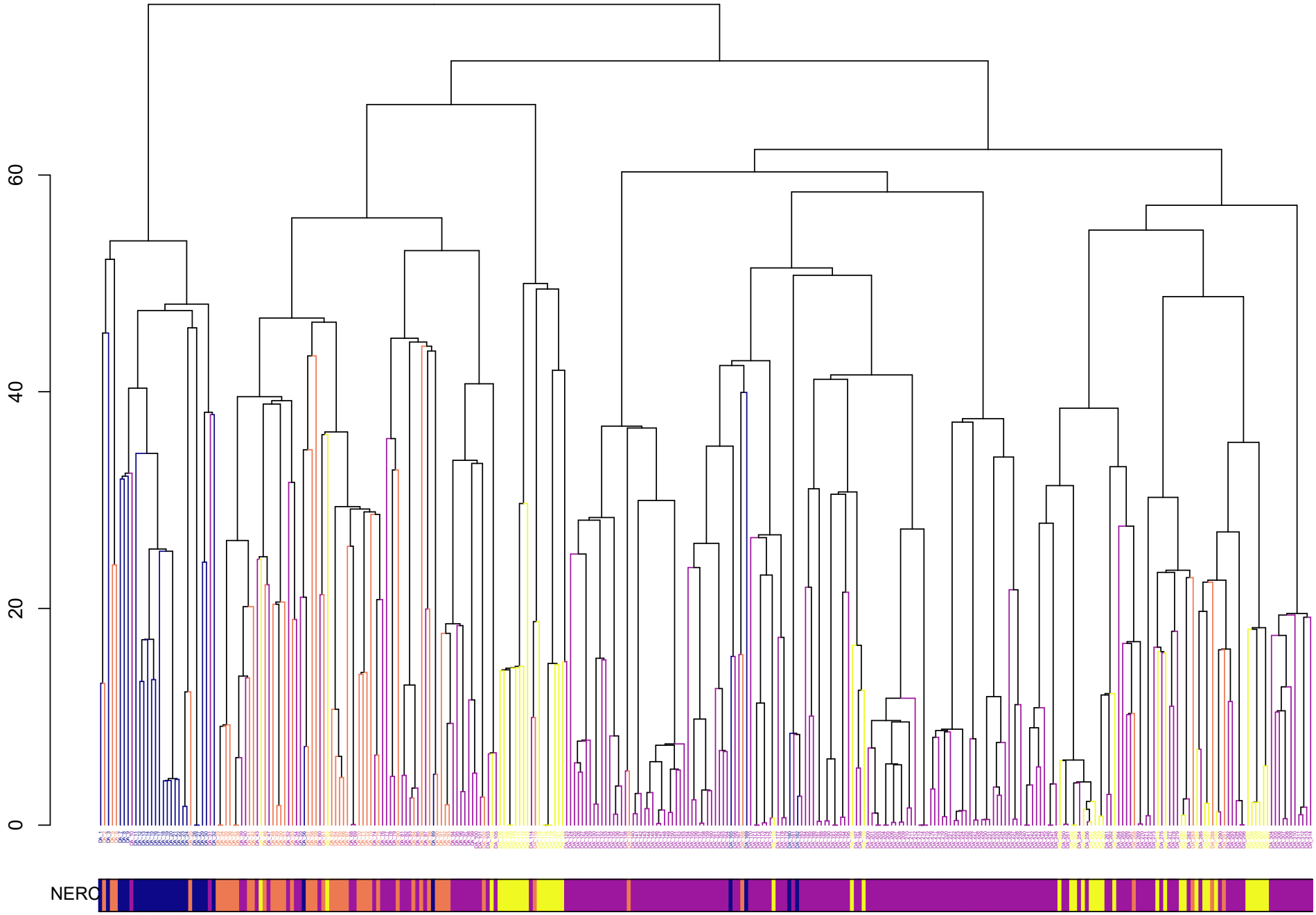

Within groups sum of squares
2500
2000
1500
1000
0
10
20
30
40
50
Number of Clusters

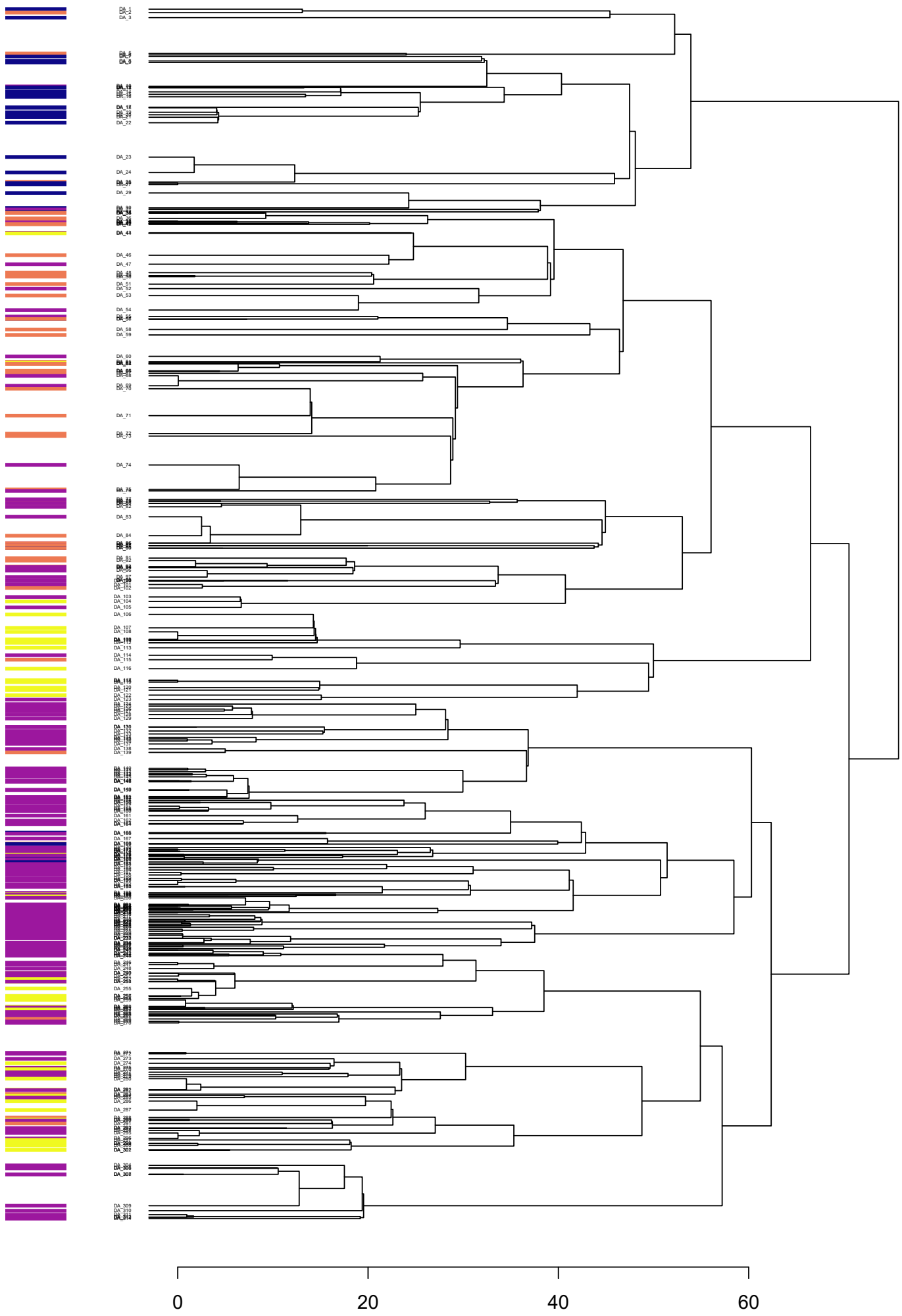

fviz_gap_stat: Gap Statistic
Gap statistic (k)
0.7
0.6
0.5
Number of clusters k

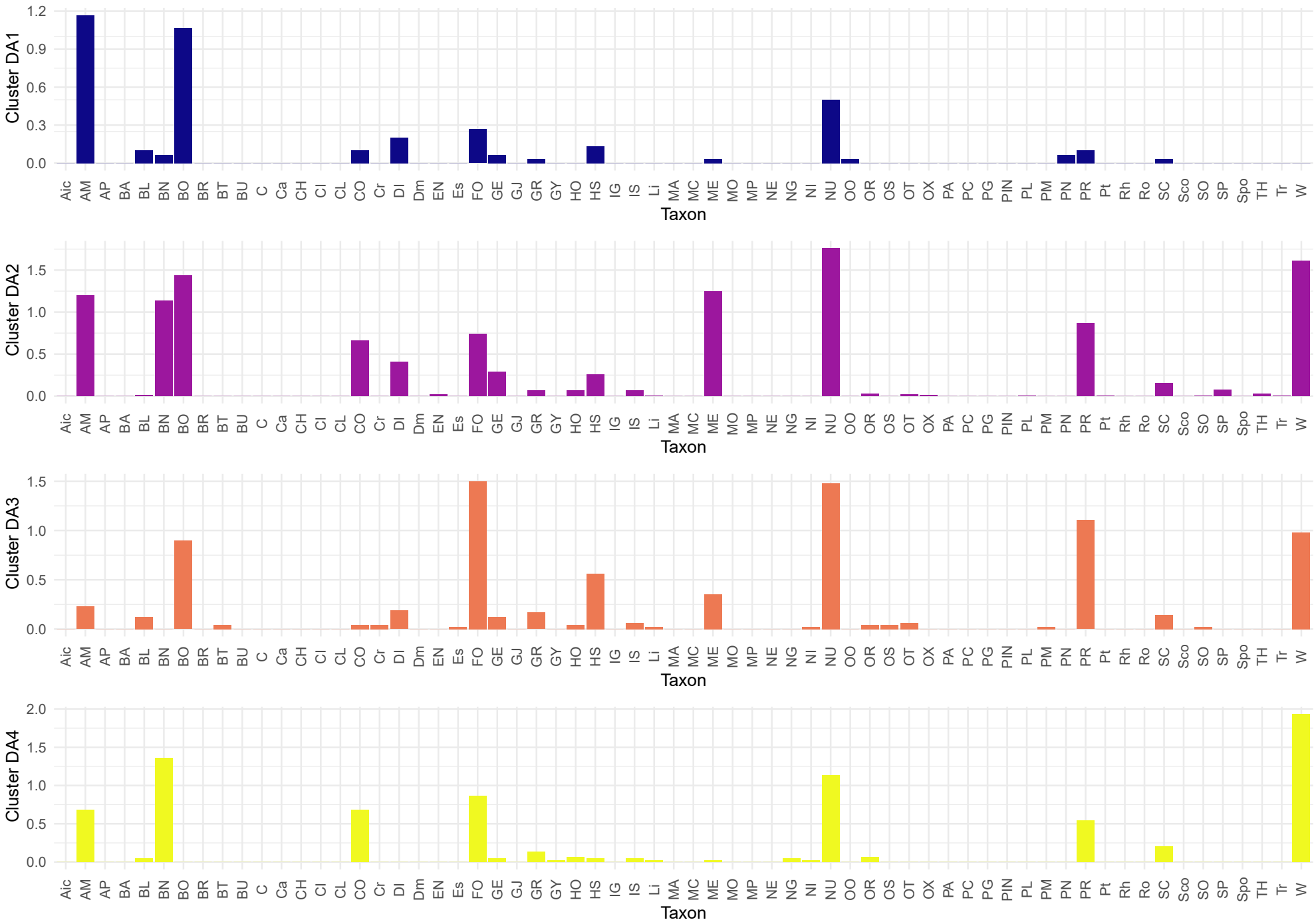

The Silhouette Plot
Average silhouette width
0.00
0.05
0.10
0.15
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50
Number of clusters k

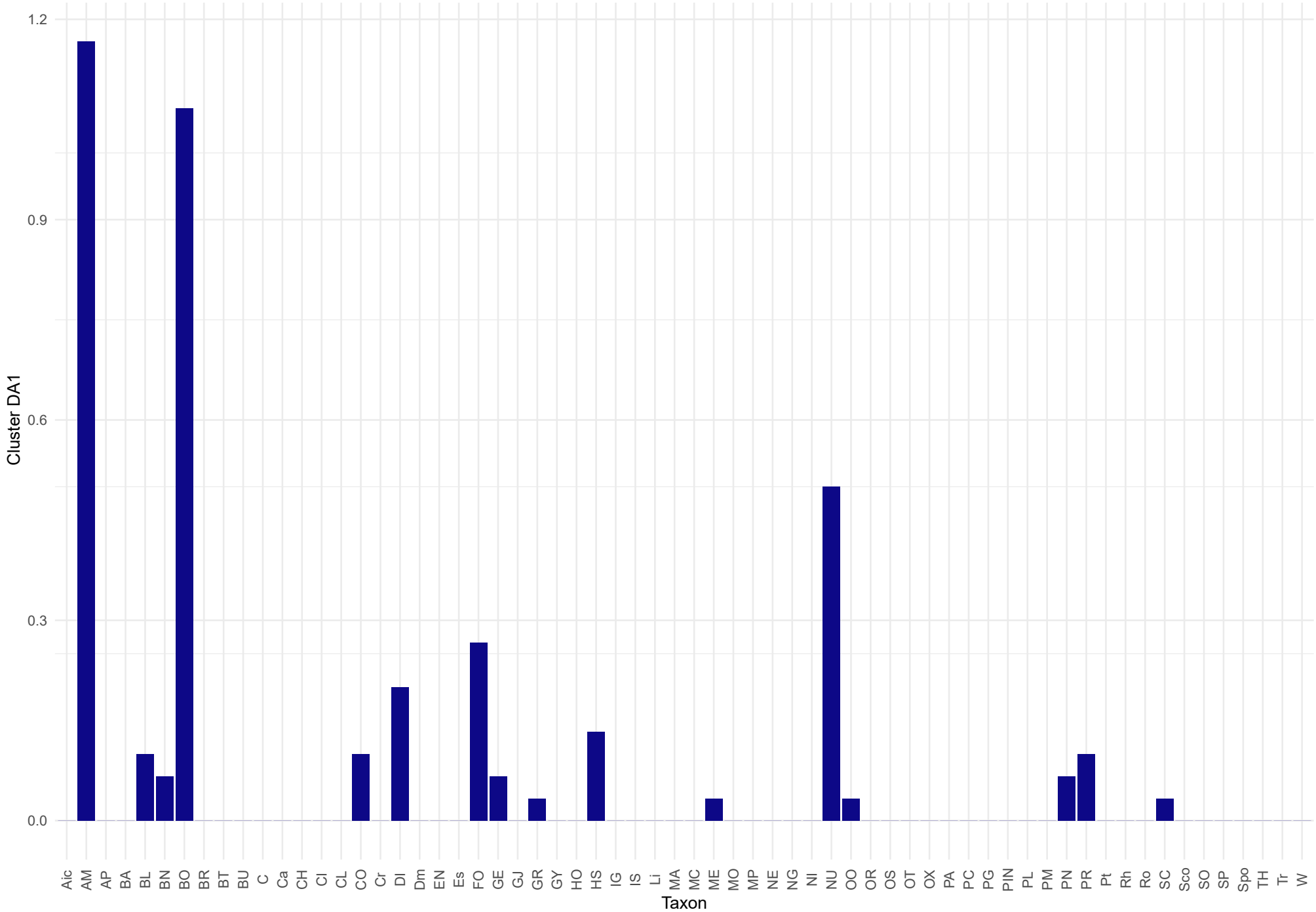

GR
SC
PR
FO
GE
NU
W
BN
AP
CO
BO
DI
ME
HS
DCA2
DCA1
2
0
−2
−3
−2
−1
0
1
2
DA Cluster
DA1
DA2
DA3
DA4

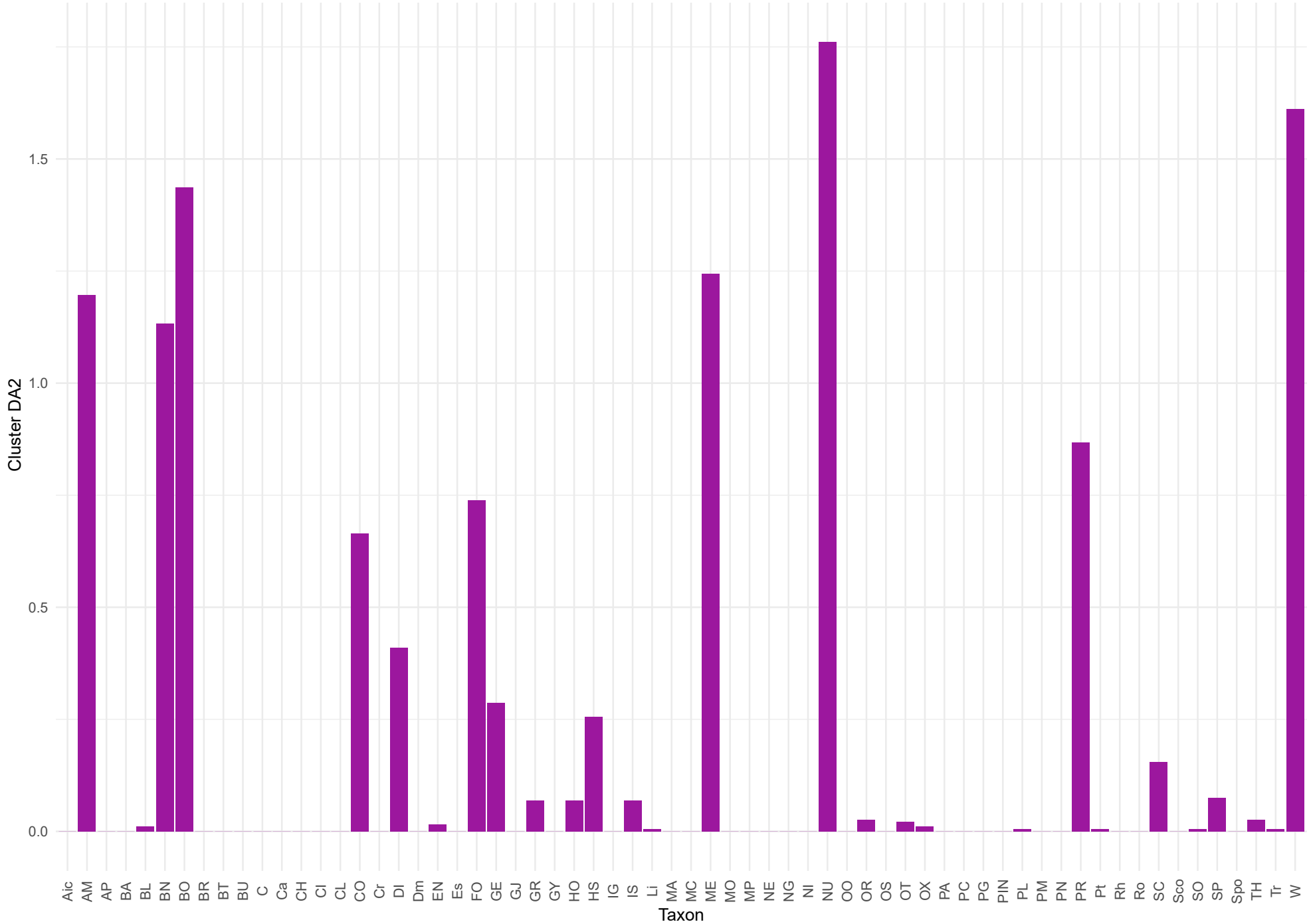

DCA2
DCA1
1.0
0.5
0.0
−0.5
−1.0
−1
0
1
DA Cluster
DA1
DA2
DA3
DA4

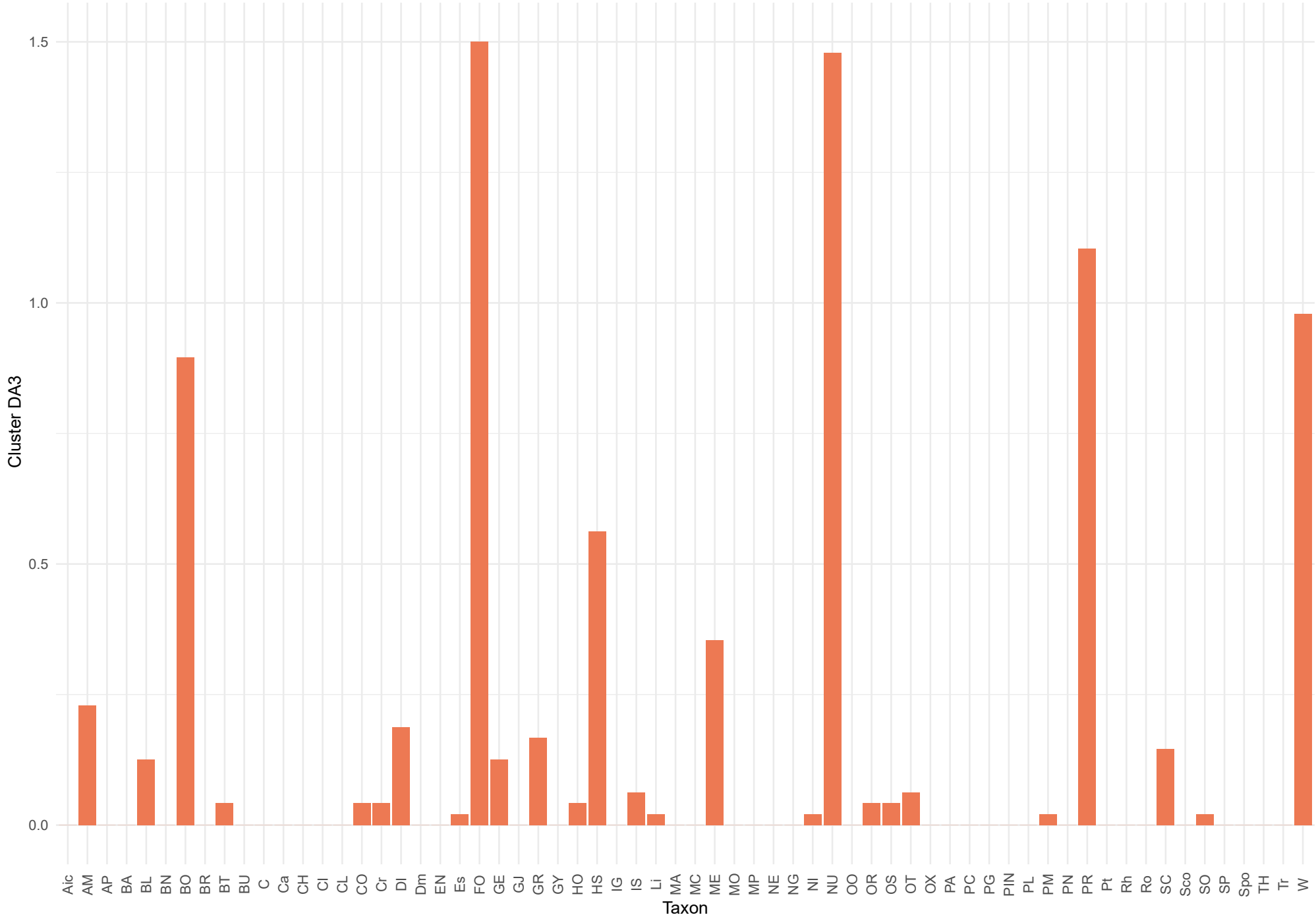

60
40
20
0
NERC

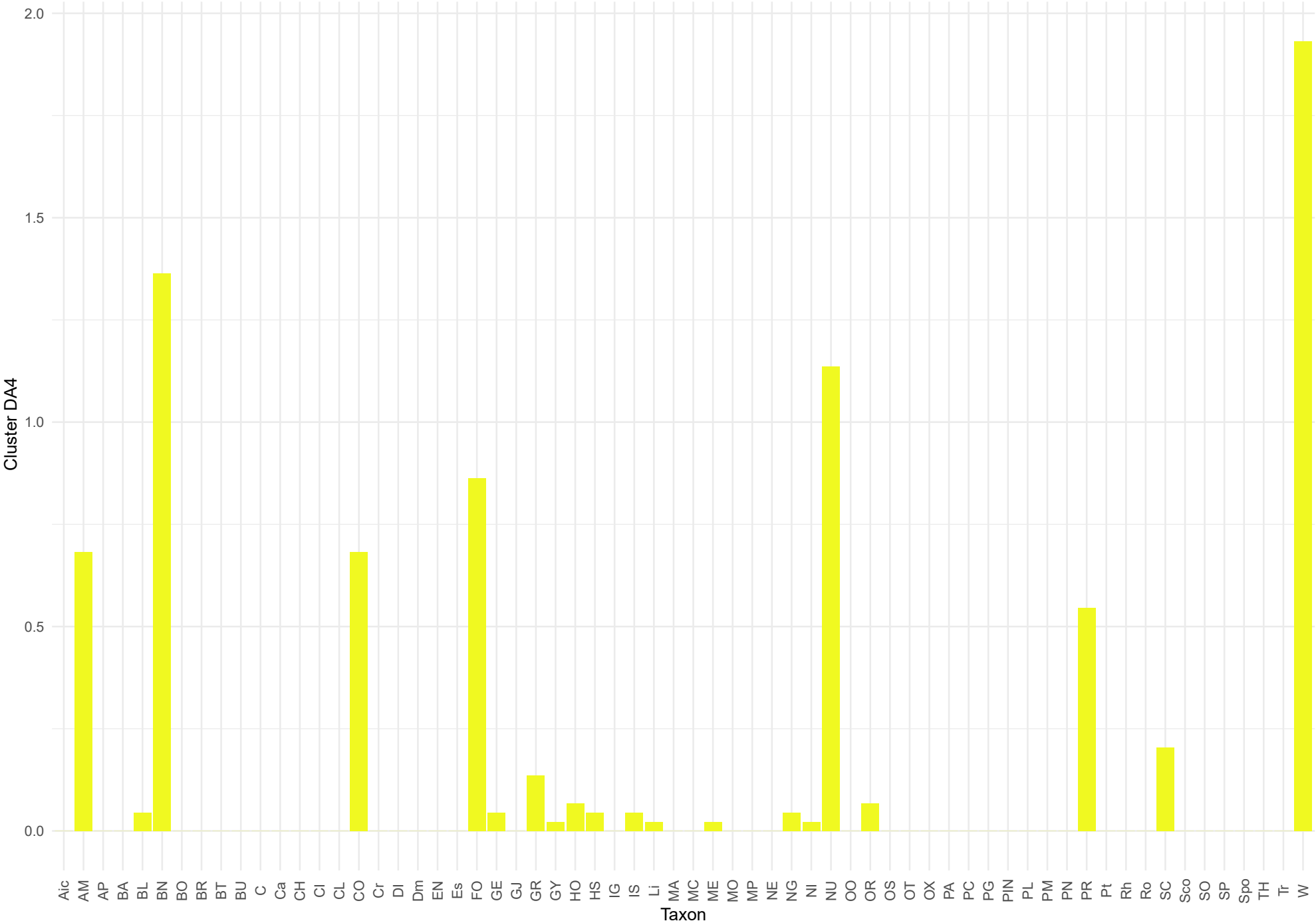

0
20
40
60

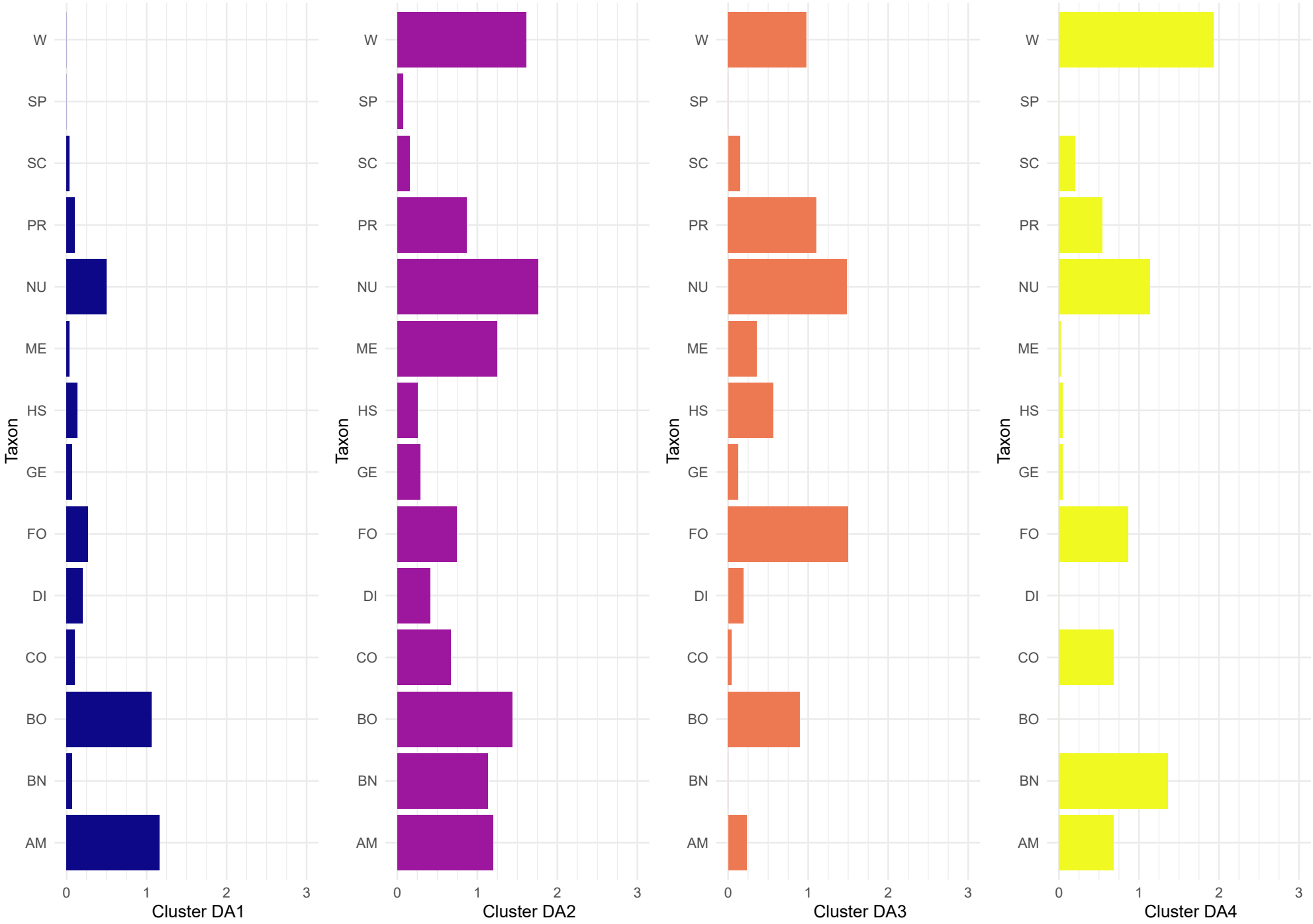

Cluster DA1
Cluster DA2
Cluster DA3
Cluster DA4
Taxon
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W


Cluster DA1
1.2
0.9
0.6
0.3
0.0
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon

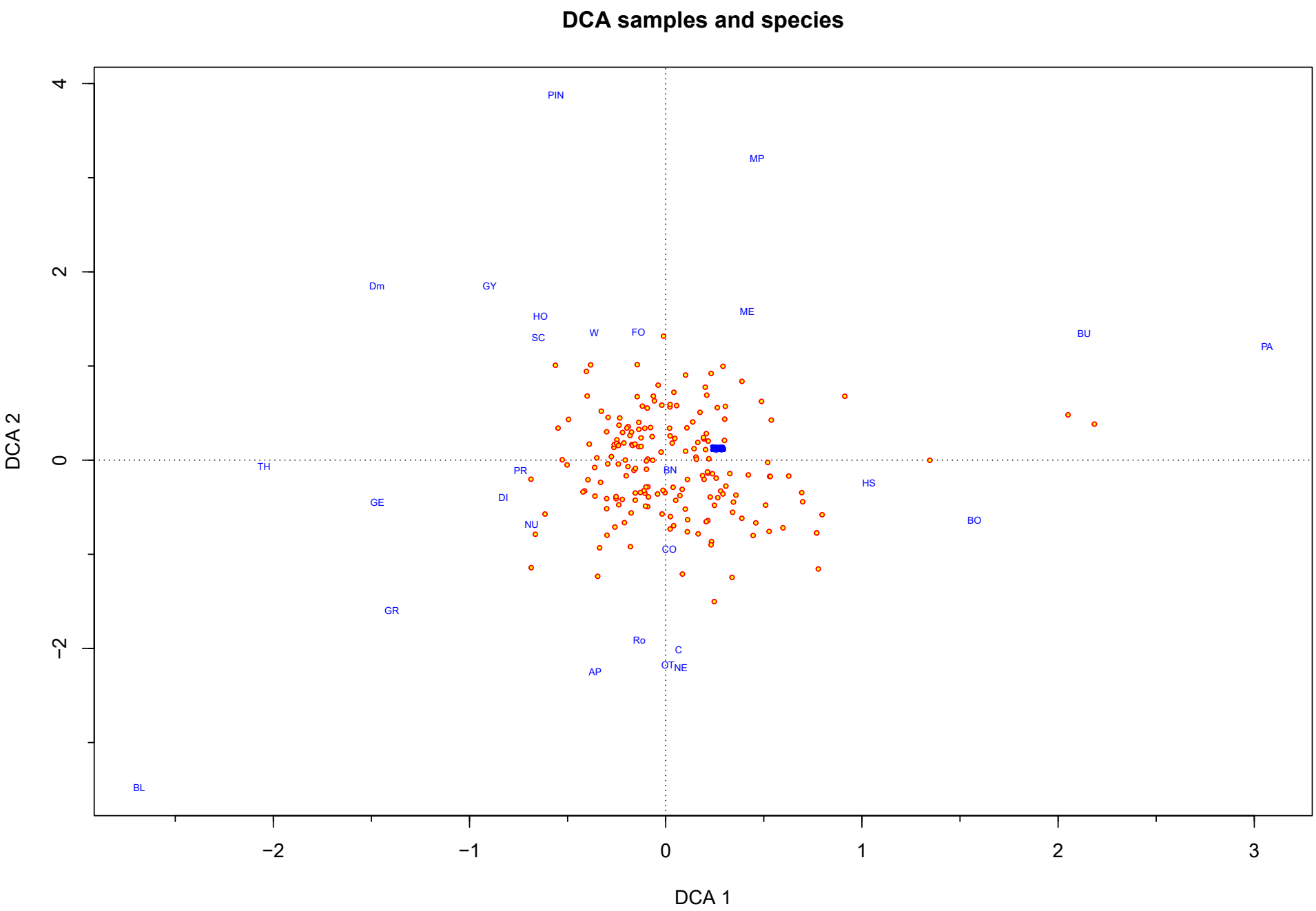

Cluster DA2
1.5
1.0
0.5
0.0
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon

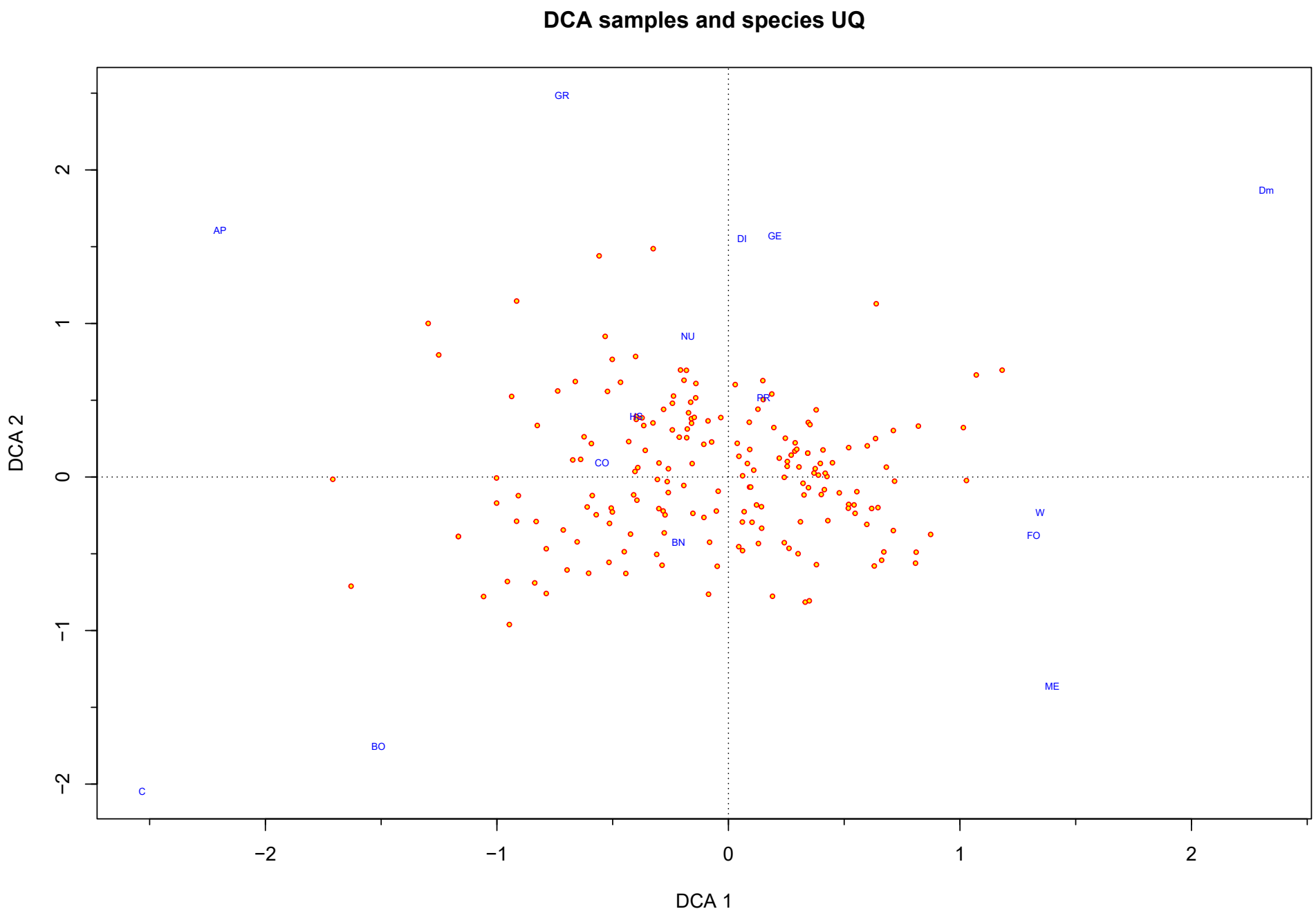

Cluster DA3
1.5
1.0
0.5
0.0
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon

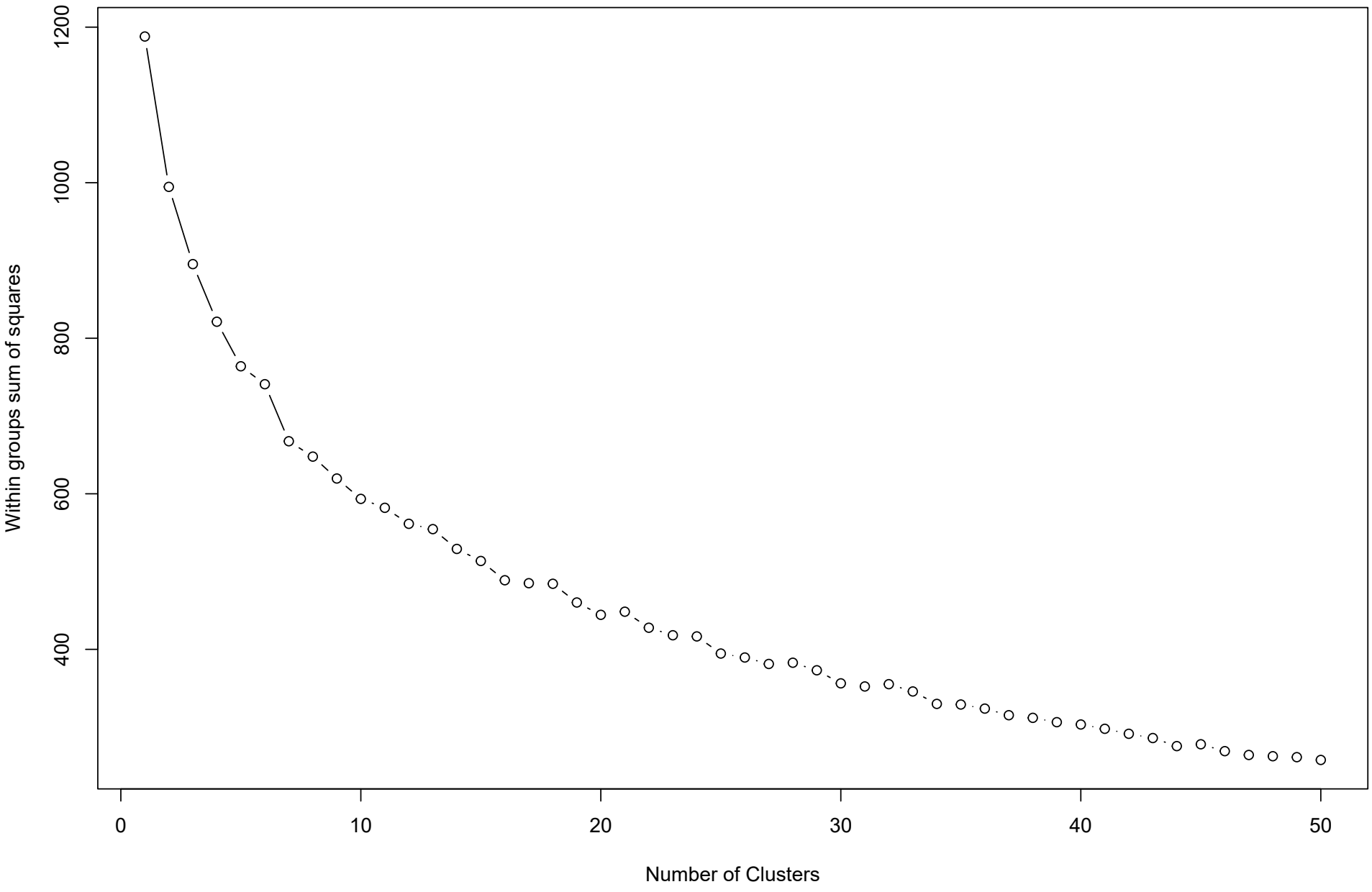

Cluster DA4
2.0
1.5
1.0
0.5
0.0
Aic AM AP BA BL BN BO BR BT BU C Ca CH Cl CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon

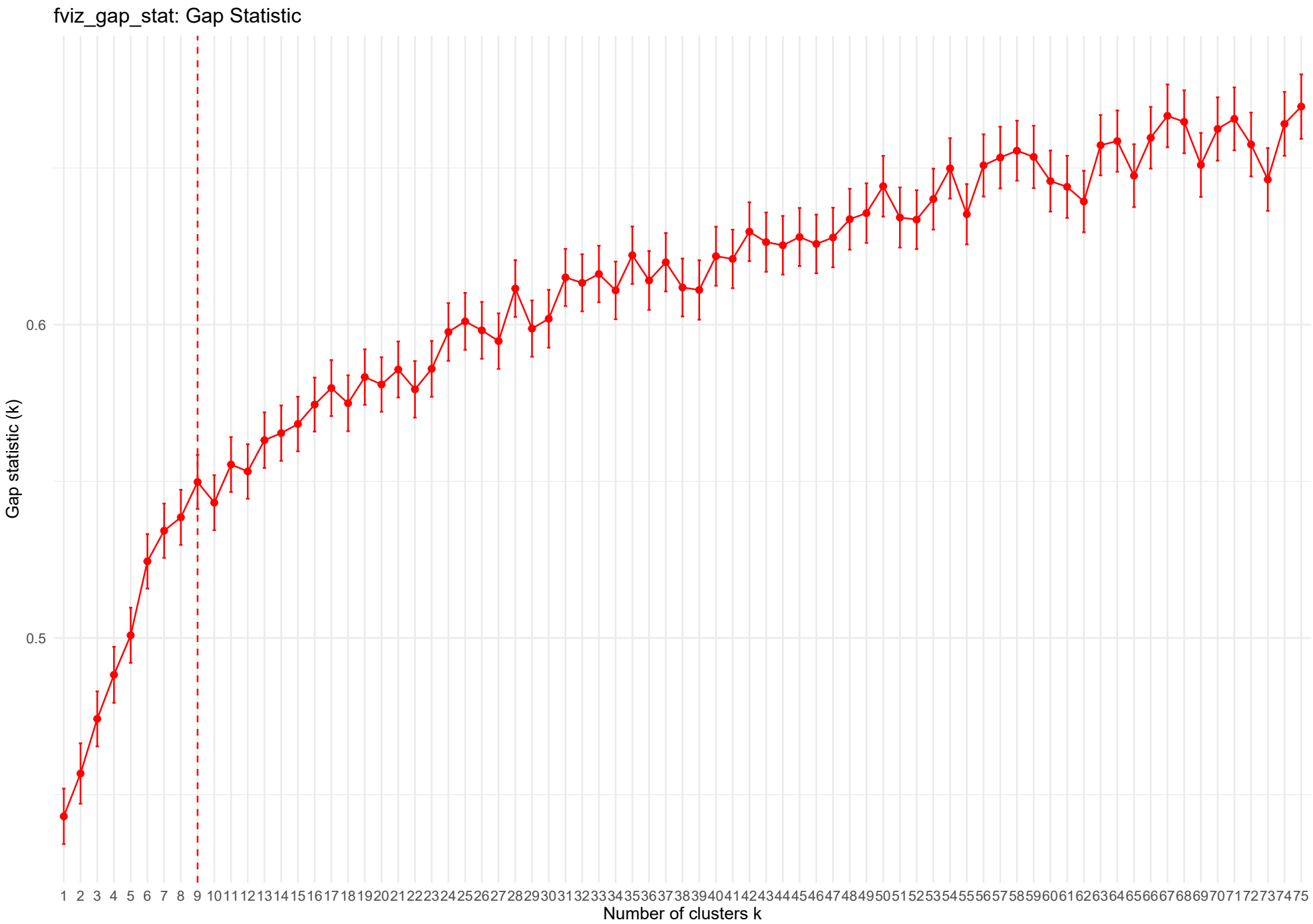

Taxon
W
SP
SC
PR
NU
ME
HS
GE
FO
DI
CO
BO
BN
AM
0
1
2
3
Cluster DA1
Cluster DA2
Cluster DA3
Cluster DA4

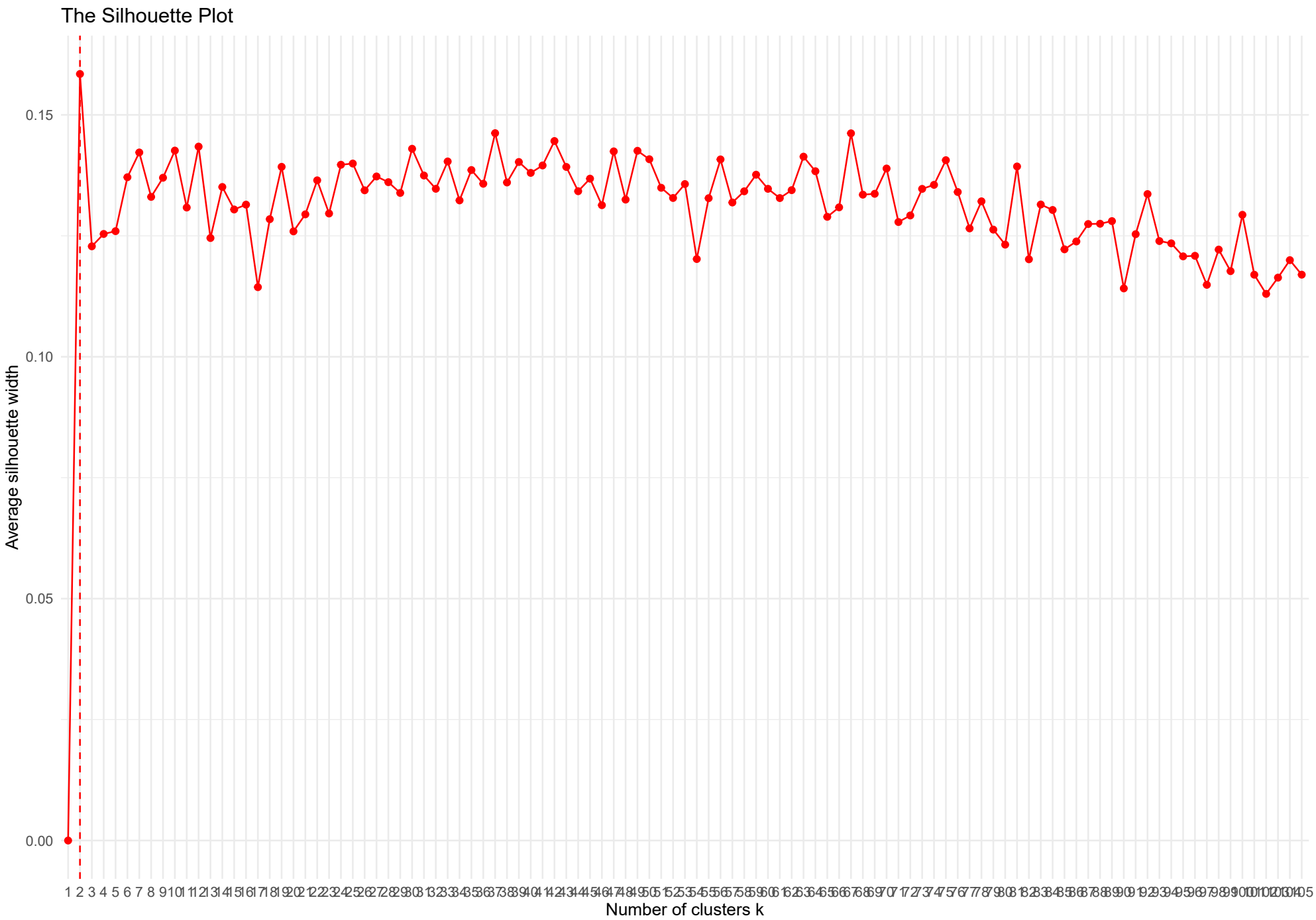
Eriswell (EW)

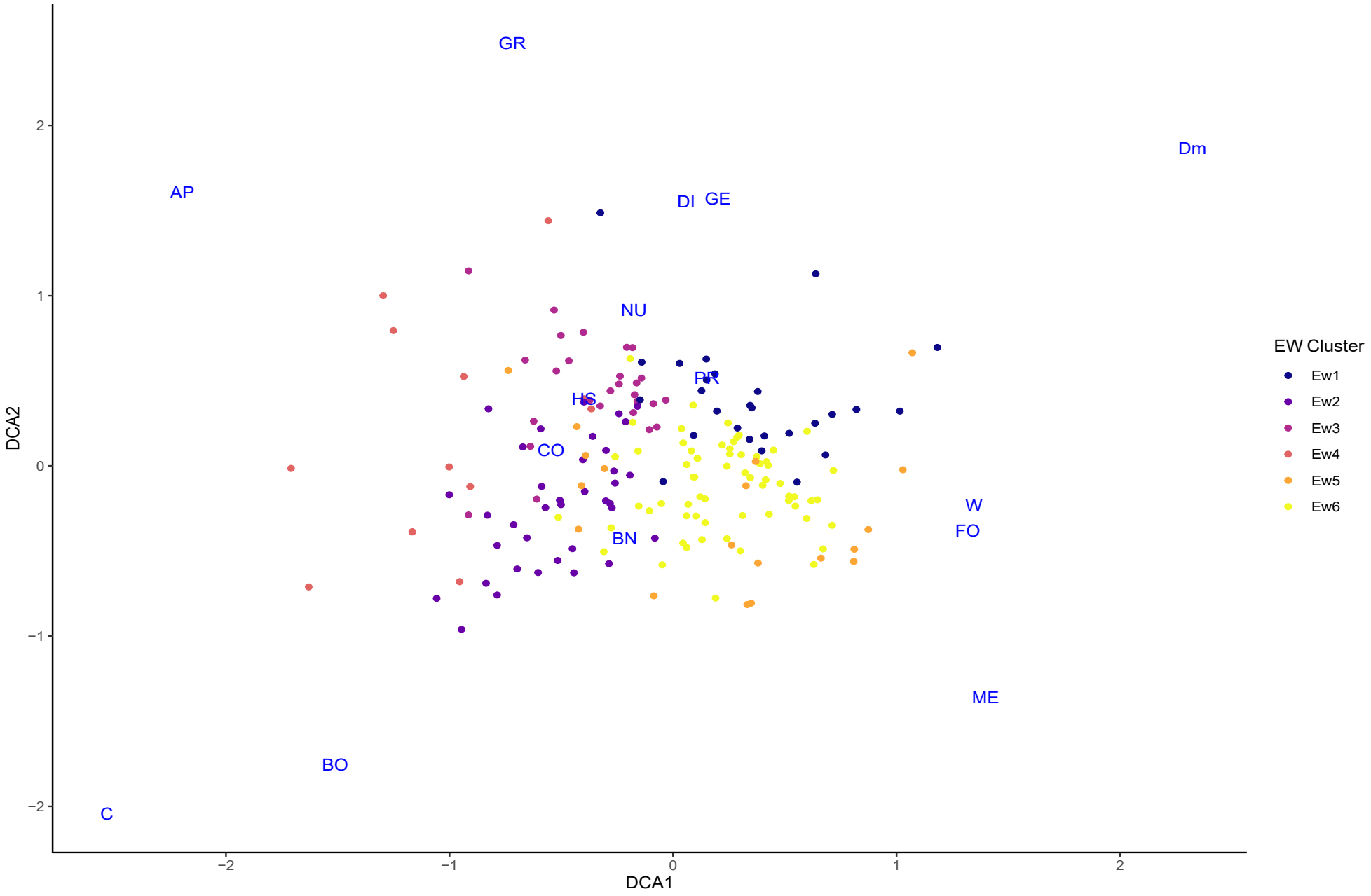

DCA samples and species
PIN
MP
Dm
GY
HO
SC
W
FO
ME
BU
PA
TH
PR
BN
HS
GE
DI
NU
BO
CO
GR
Ro
C
OT
NE
AP
BL
DCA 2
DCA 1
4
2
0
−2
−2
−1
0
1
2
3

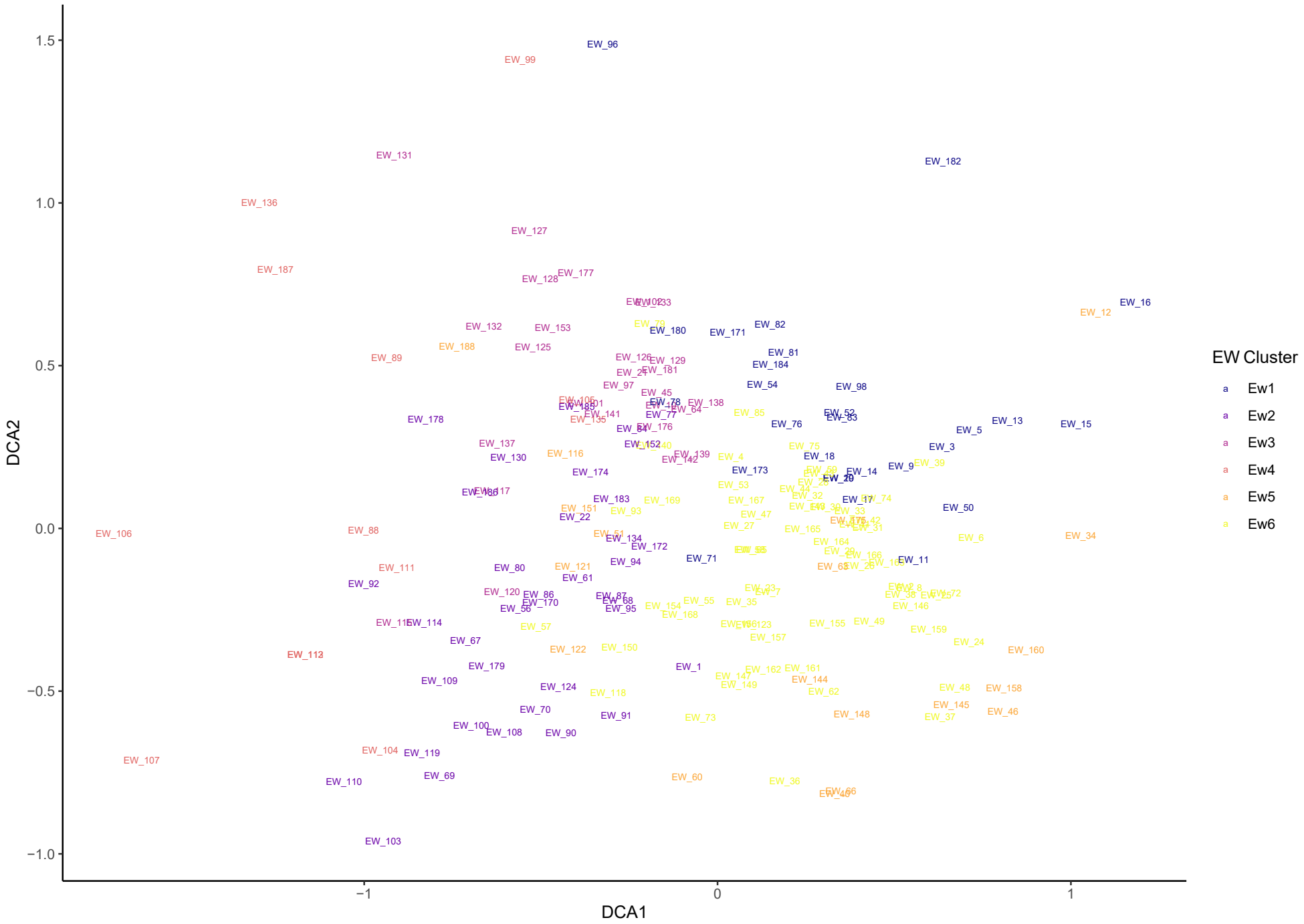

DCA samples and species UQ
GR
Dm
AP
DI
GE
NU
RR
HS
CO
W
FO
BN
ME
BO
C
DCA 2
DCA 1
2
1
0
−1
−2
−2
−1
0
1
2

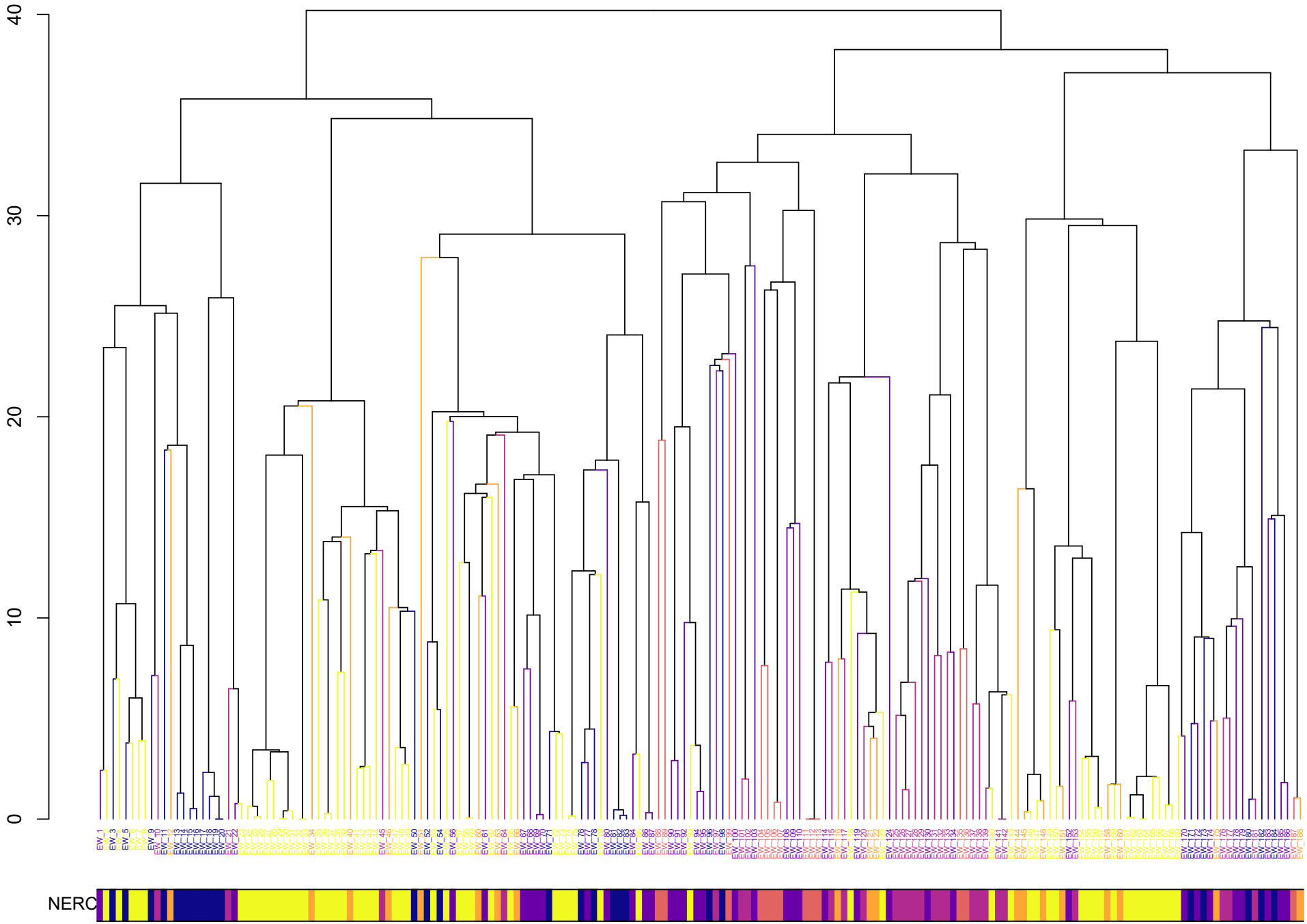

Within groups sum of squares
1200
1000
800
600
400
0
10
20
30
40
50
Number of Clusters

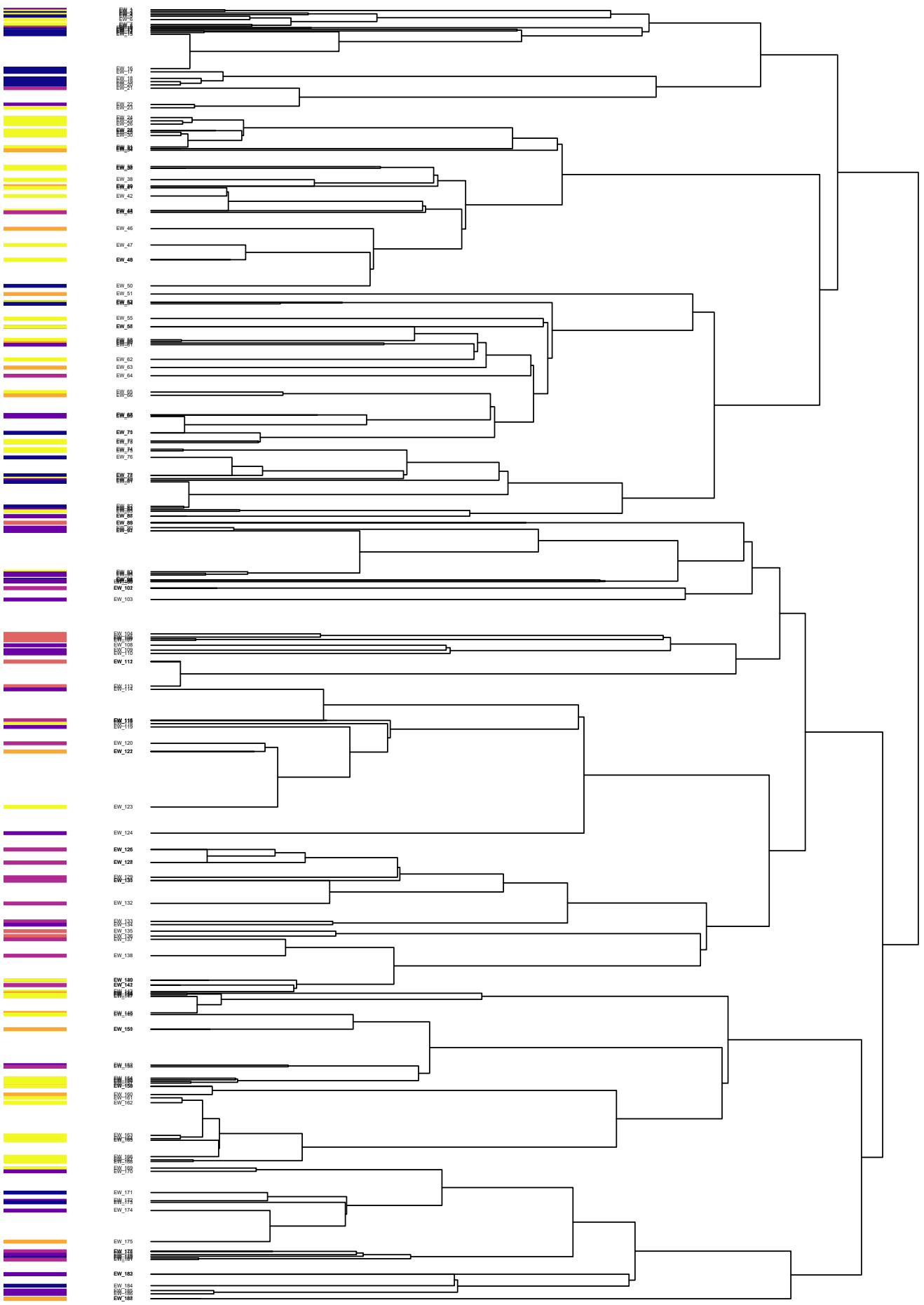

fviz_gap_stat: Gap Statistic
Gap statistic (k)
0.6
0.5
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75
Number of clusters k


The Silhouette Plot
Average silhouette width
0.15
0.10
0.05
0.00
Number of clusters k

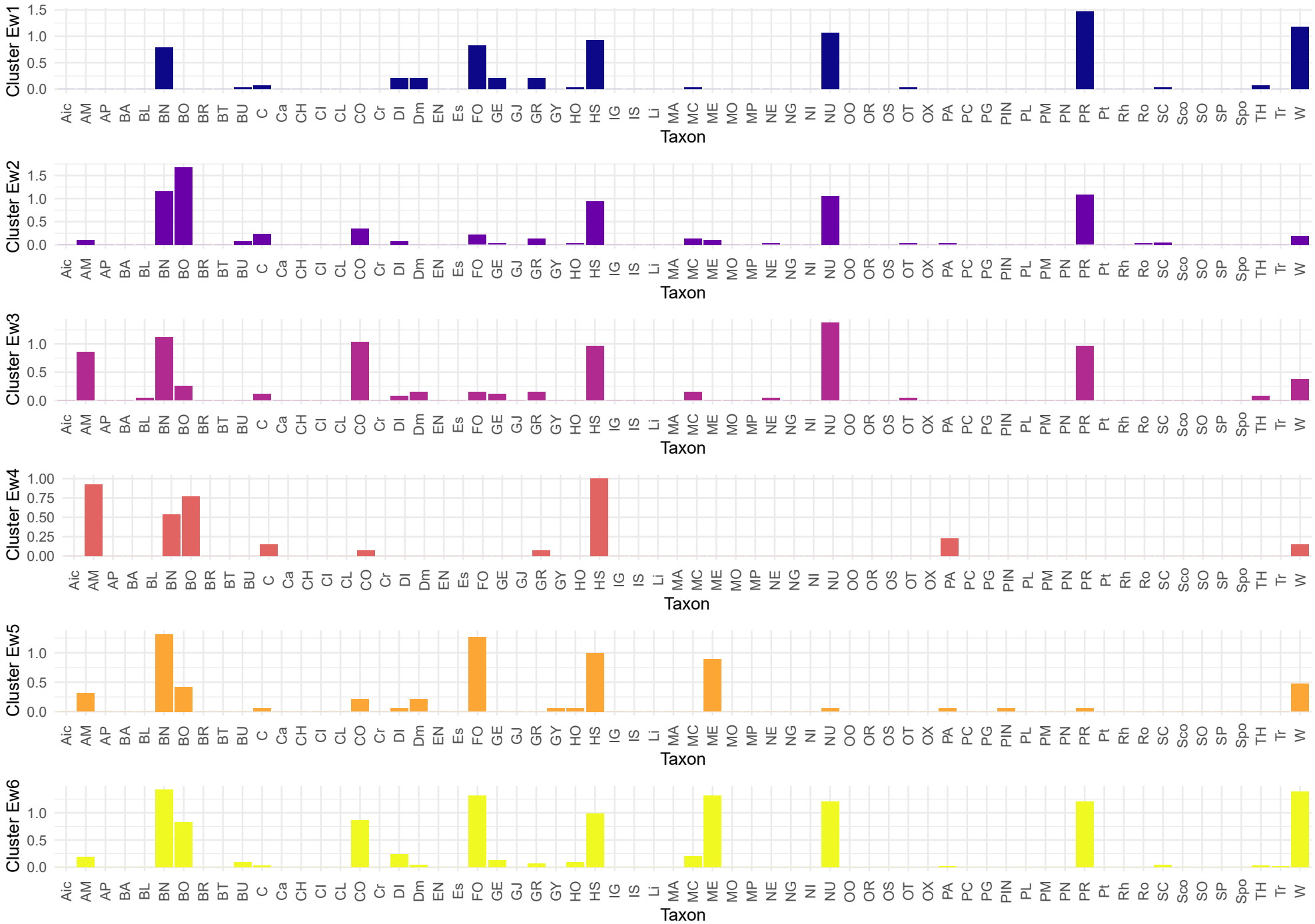

GR
Dm
AP
DI
GE
NU
PR
HS
CO
W
FO
BN
ME
BO
C
DCA2
DCA1
2
1
0
−1
−2
EW Cluster
Ew1
Ew2
Ew3
Ew4
Ew5
Ew6

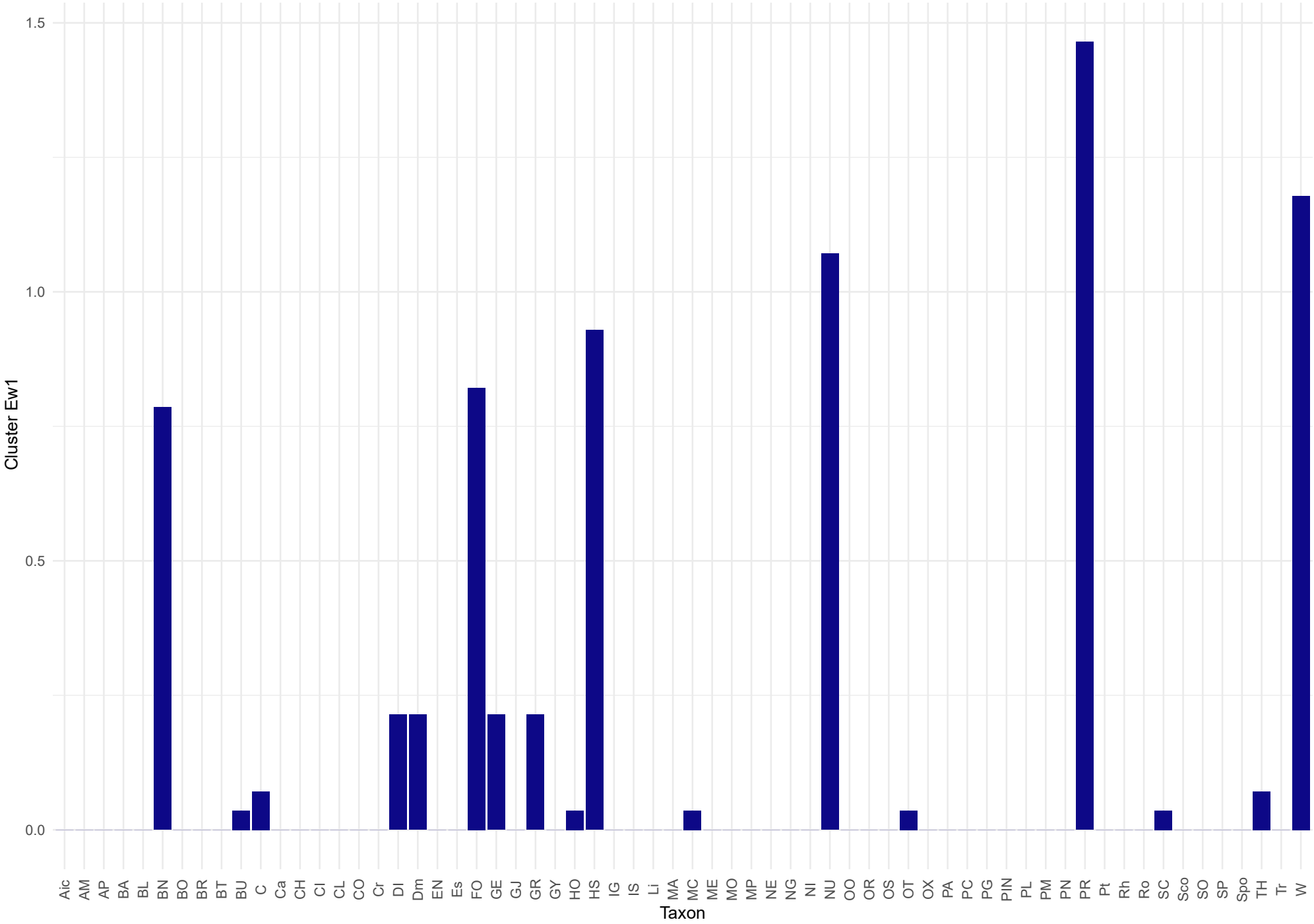

DCA2
DCA1
1.5
1.0
0.5
0.0
−0.5
−1.0
−1
0
1
EW Cluster
Ew1
Ew2
Ew3
Ew4
Ew5
Ew6

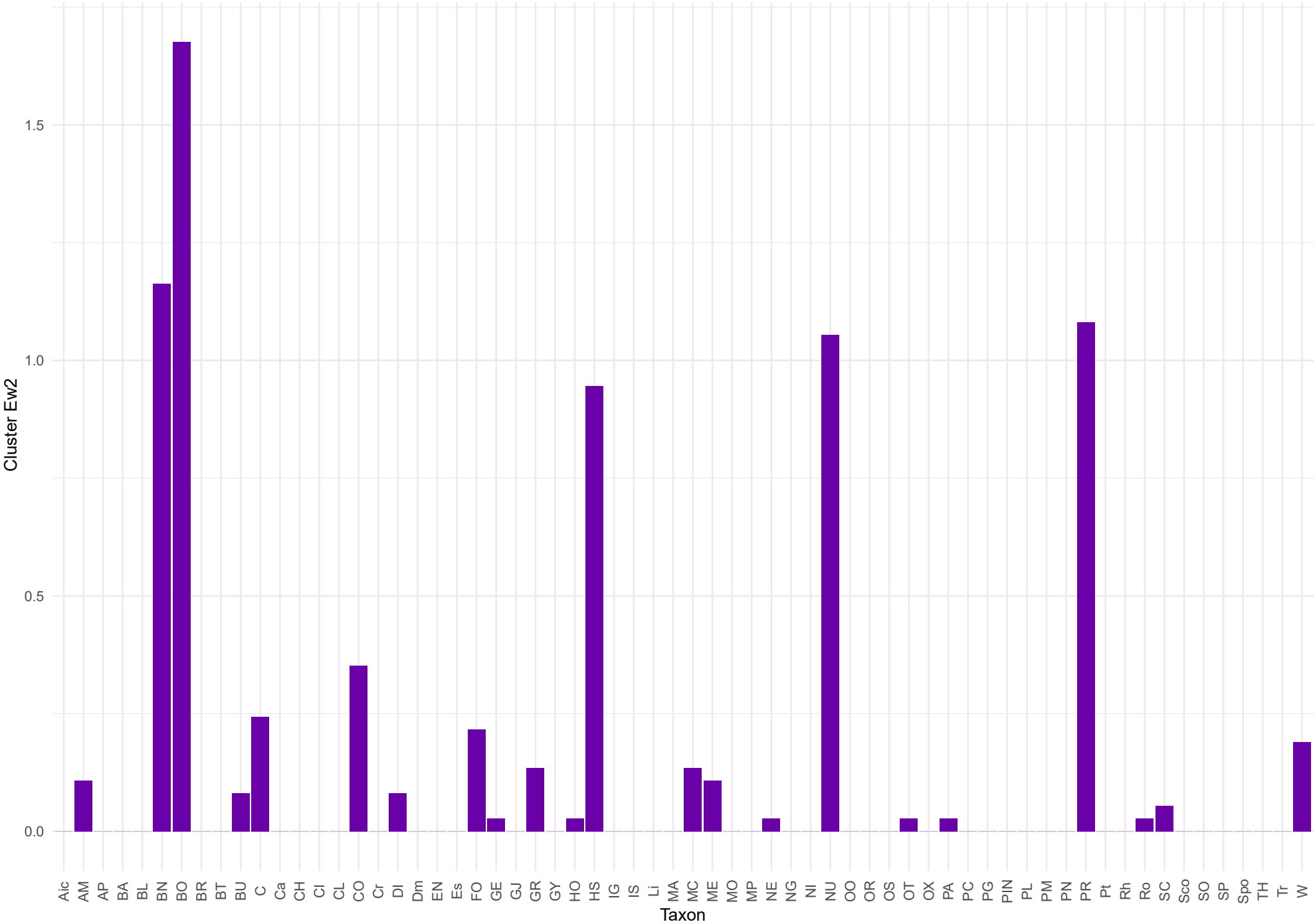

40
30
20
10
0
NERC

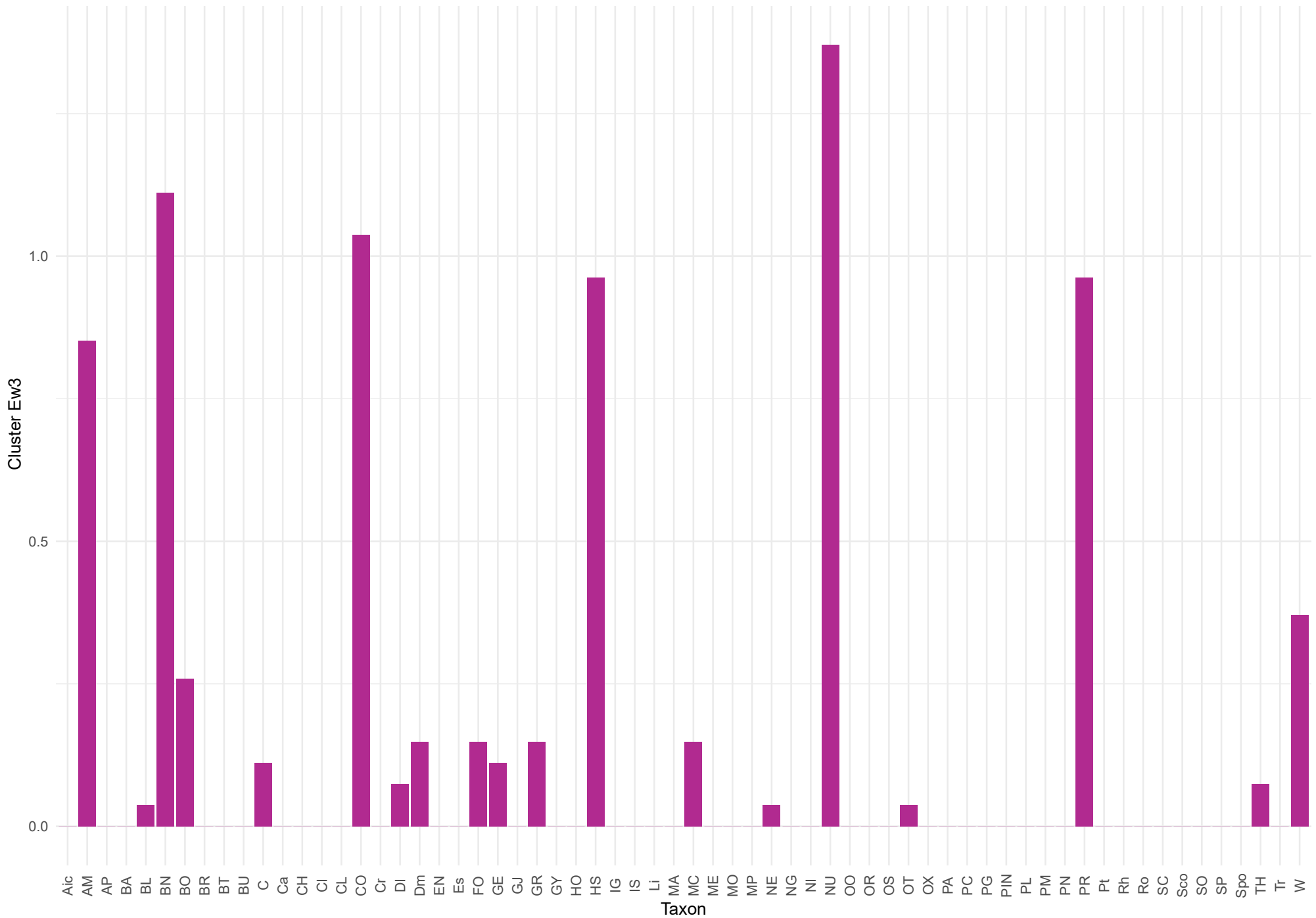


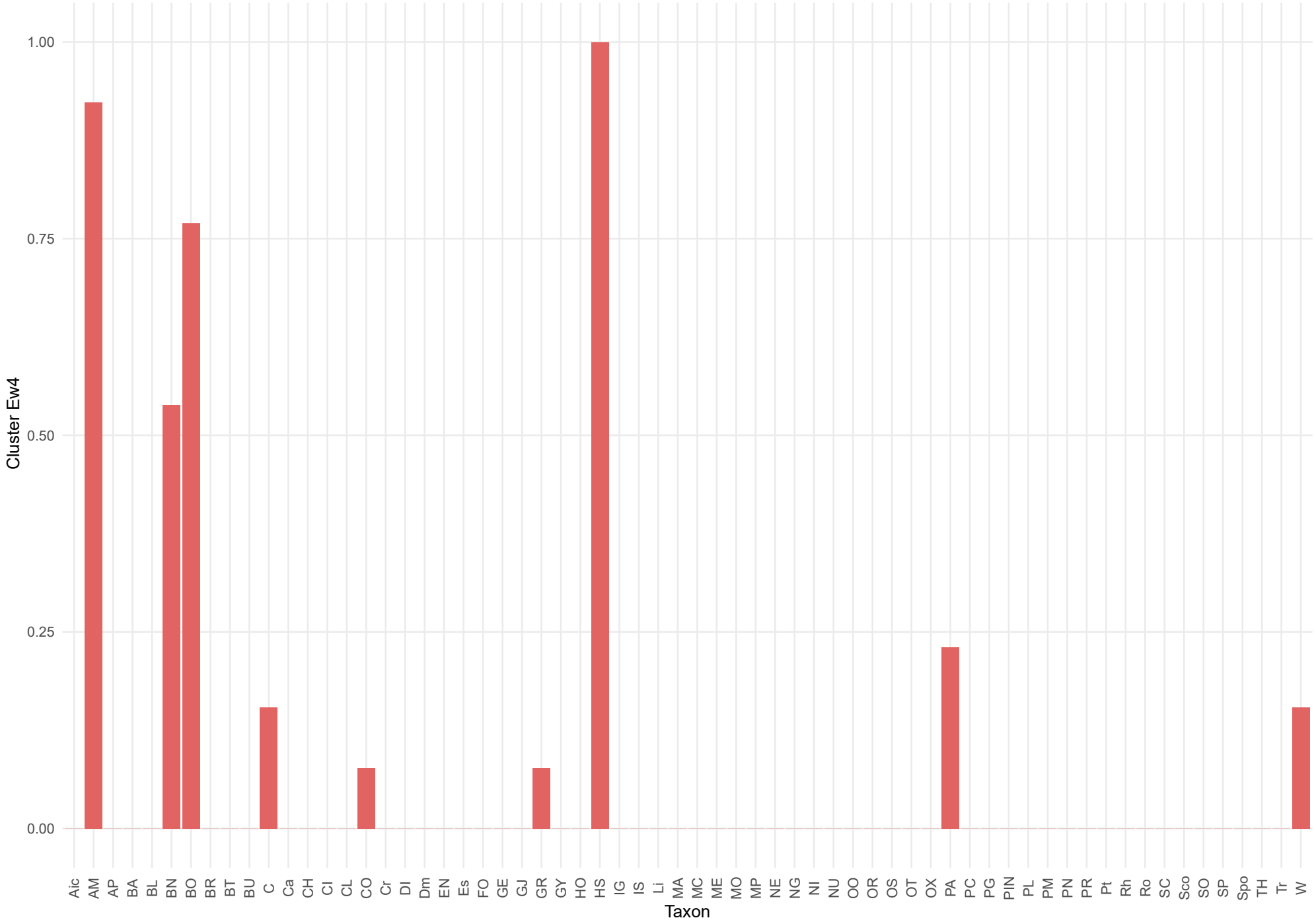
Eriswell (EW)

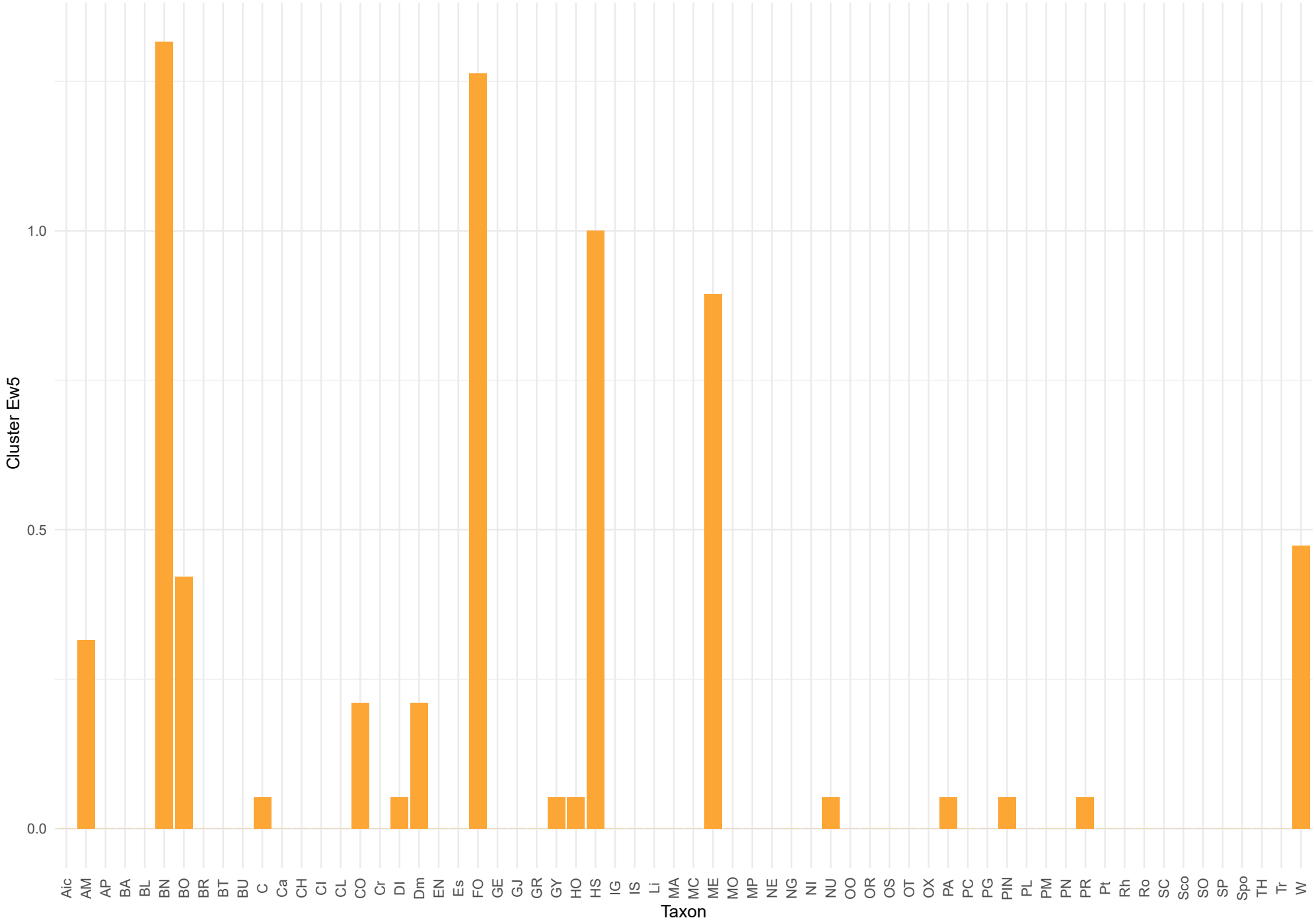

Cluster Ew1
Cluster Ew2
Cluster Ew3
Cluster Ew4
Cluster Ew5
Cluster Ew6
Taxon
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W

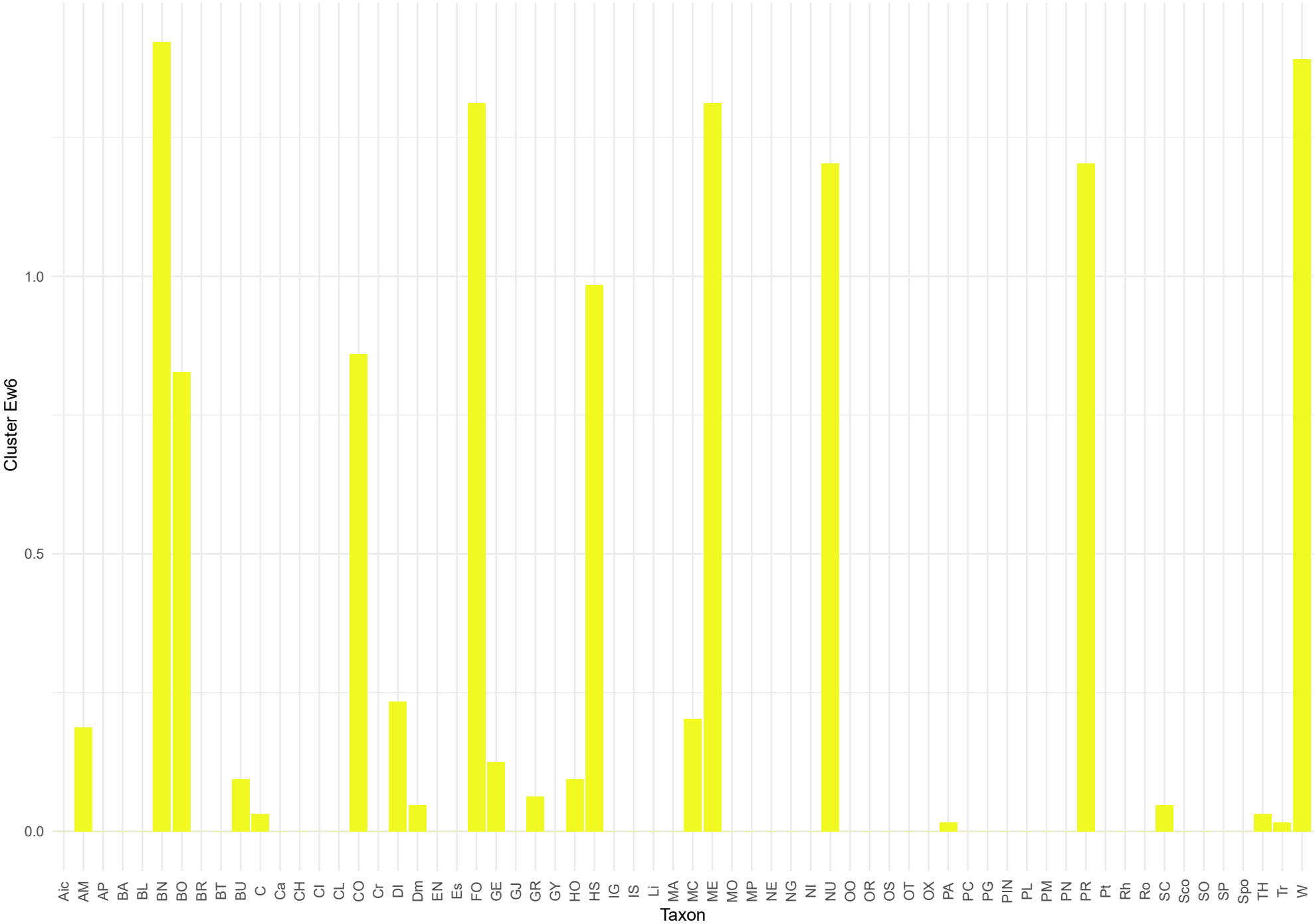

1.5
1.0
0.5
0.0
Cluster Ew1
Aic
AM
AP
BA
BL
BN
BO
BR
BT
BU
C
Ca
CH
CI
CL
CO
Cr
DI
Dm
EN
Es
FO
GE
GJ
GR
GY
HO
HS
IG
IS
Li
MA
MC
ME
MO
MP
NE
NG
NI
NU
OO
OR
OS
OT
OX
PA
PC
PG
PIN
PL
PM
PN
PR
Pt
Rh
Ro
SC
Sco
SO
SP
Spo
TH
Tr
W
Taxon

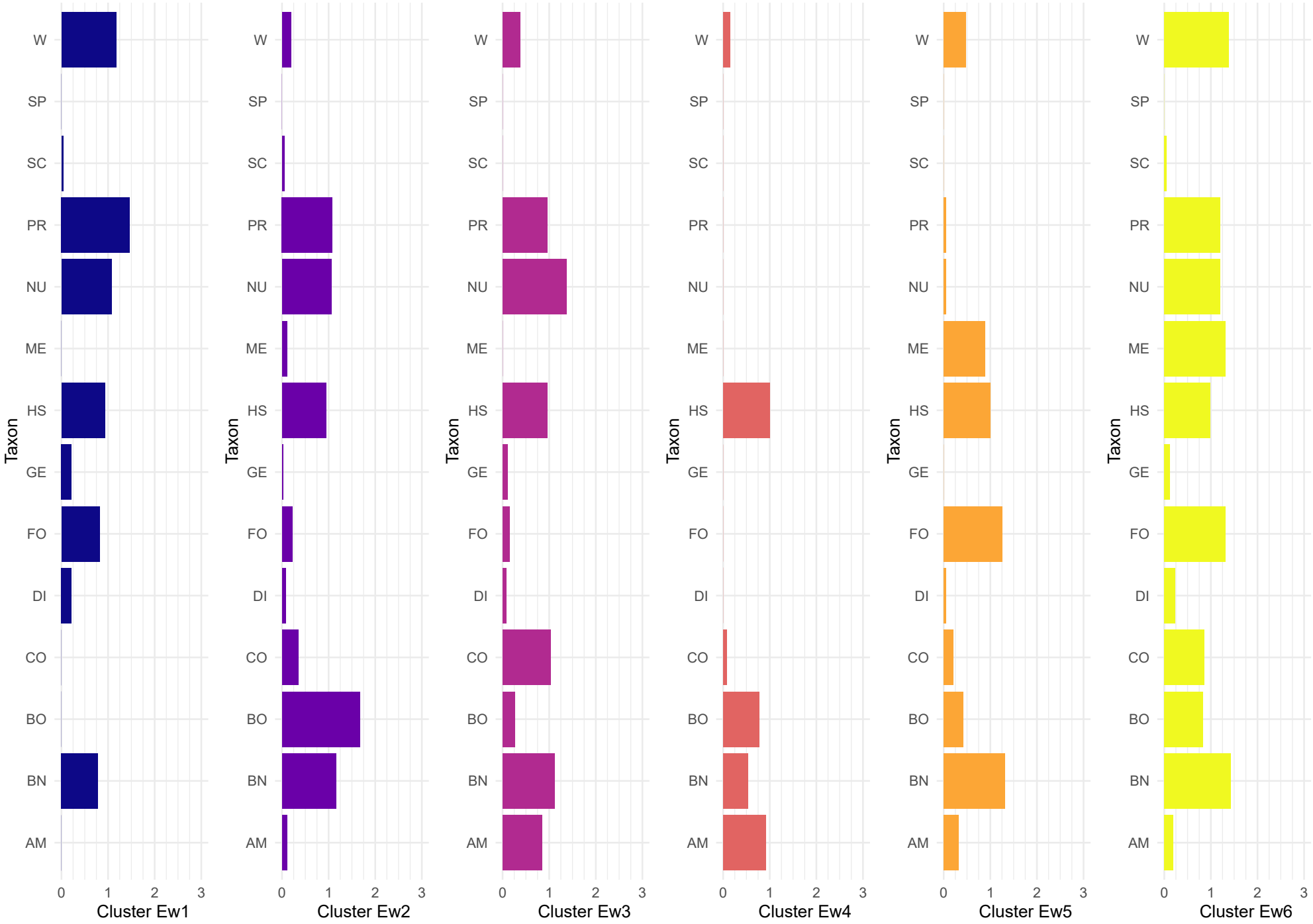

Cluster Ew2
1.5
1.0
0.5
0.0
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon


Cluster Ew3
1.0
0.5
0.0
Aic
AM
AP
BA
BL
BN
BO
BR
BT
BU
C
Ca
CH
CI
CL
CO
Cr
DI
Dm
EN
Es
FO
GE
GJ
GR
GY
HO
HS
IG
IS
Li
MA
MC
ME
MO
MP
NE
NG
NI
NU
OO
OR
OS
OT
OX
PA
PC
PG
PIN
PL
PM
PN
PR
Pt
Rh
Ro
SC
Sco
SO
SP
Spo
TH
Tr
W
Taxon

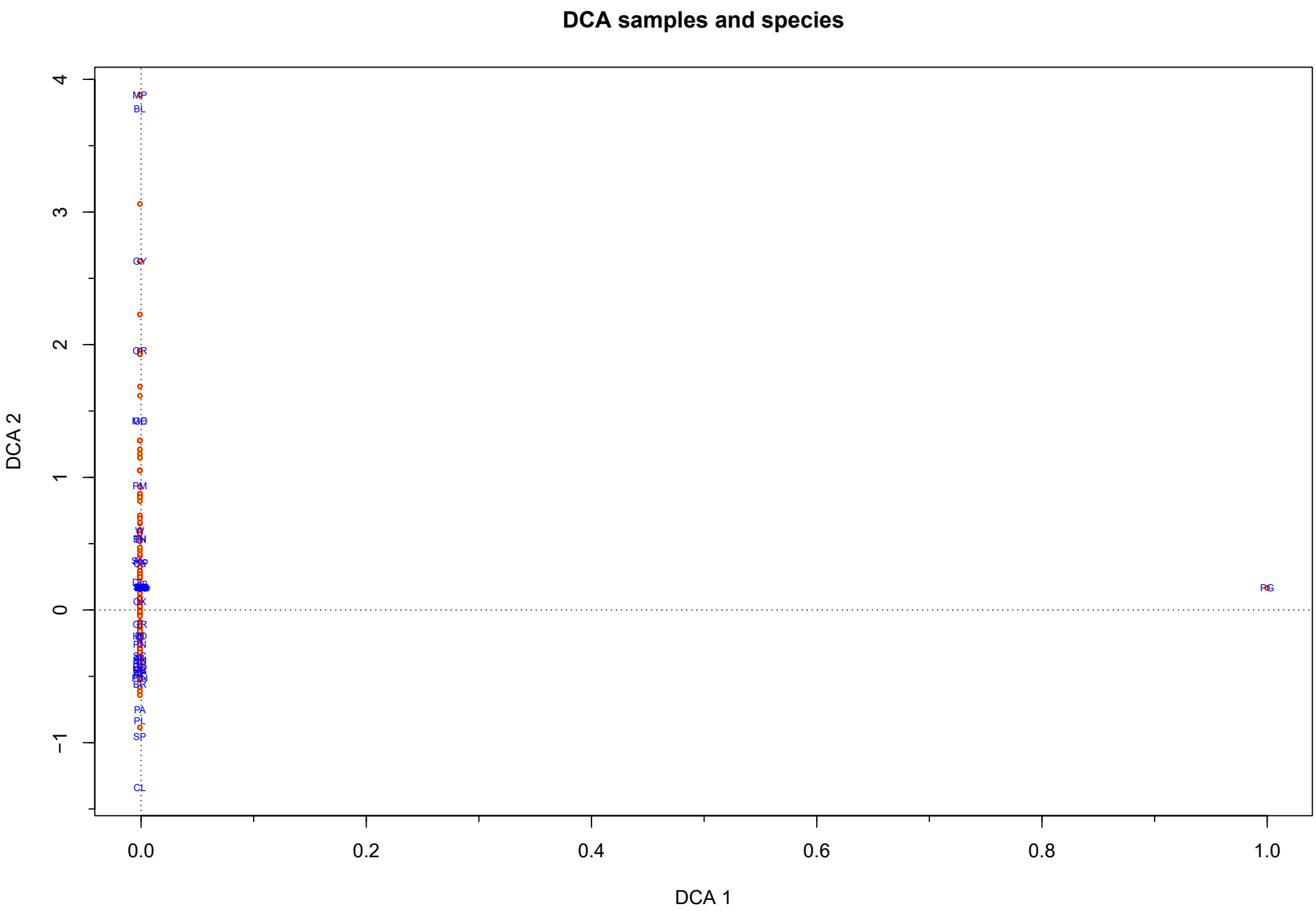

Cluster Ew4
1.00
0.75
0.50
0.25
0.00
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon


Cluster Ew5
1.0
0.5
0.0
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon

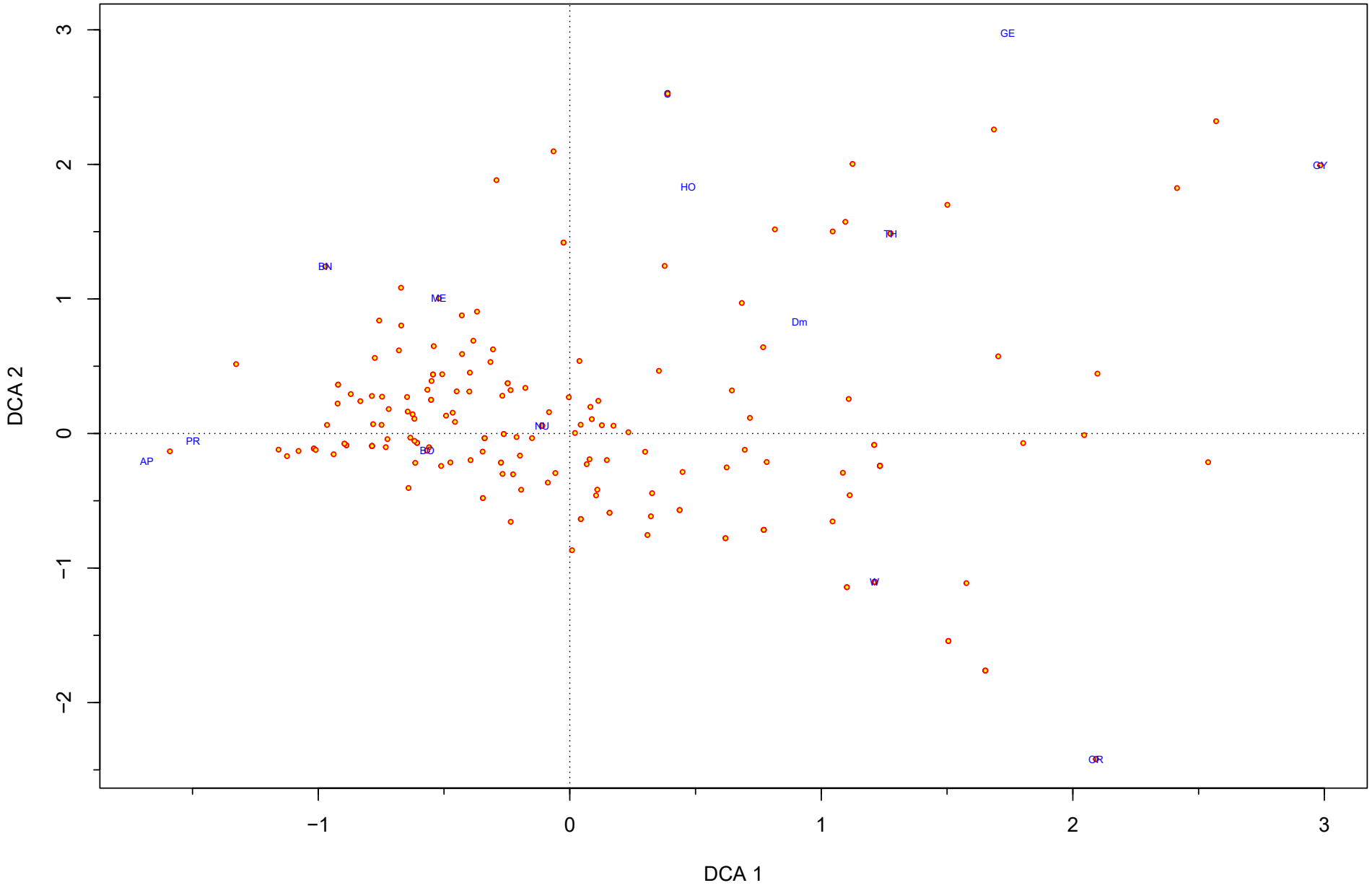

Cluster Ew6
1.0
0.5
0.0
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon

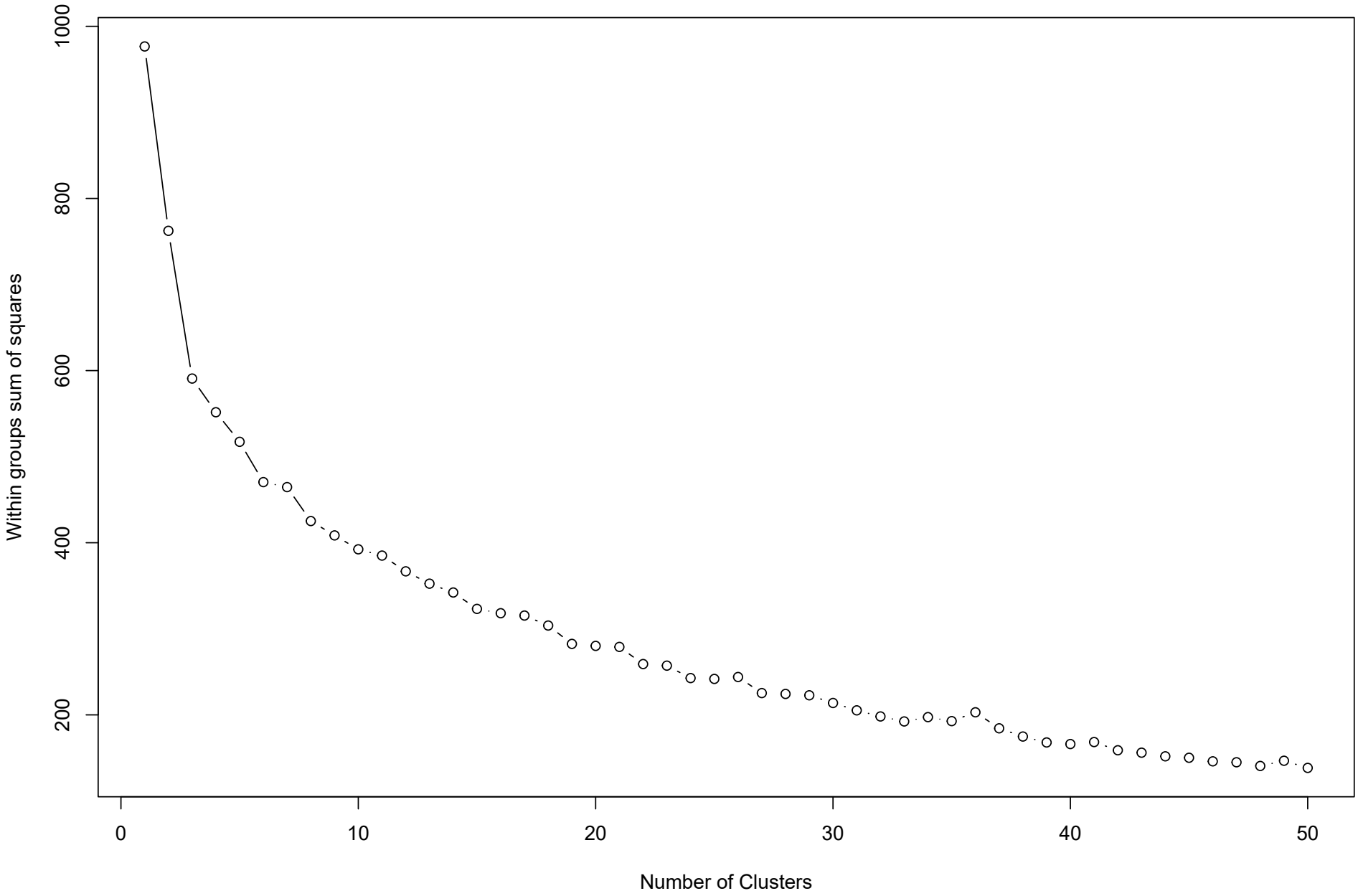

Taxon
W
SP
SC
PR
NU
ME
HS
GE
FO
DI
CO
BO
BN
AM
0
1
2
3
Cluster Ew1
Cluster Ew2
Cluster Ew3
Cluster Ew4
Cluster Ew5
Cluster Ew6

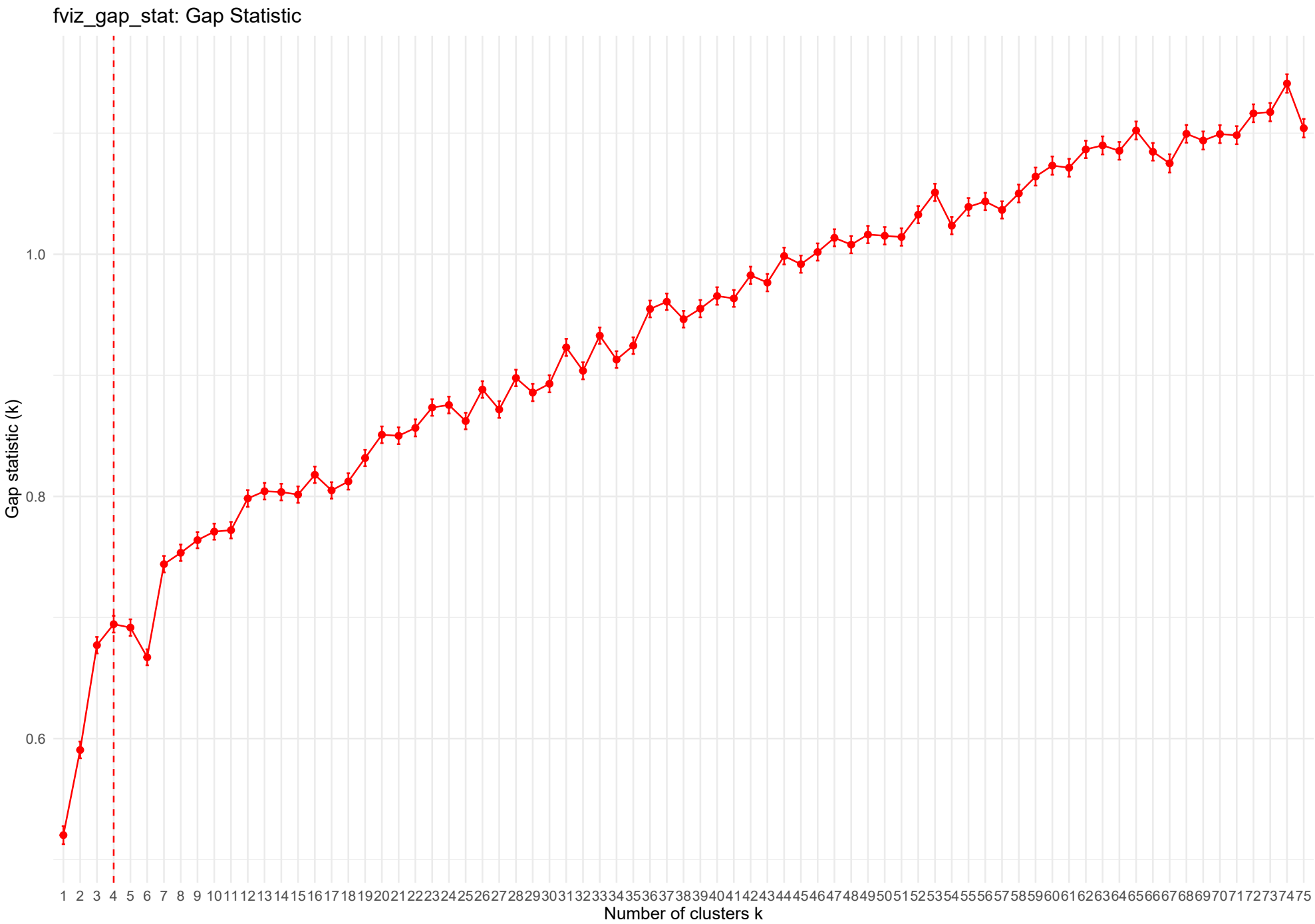
Kimmeridge 2 (KR)

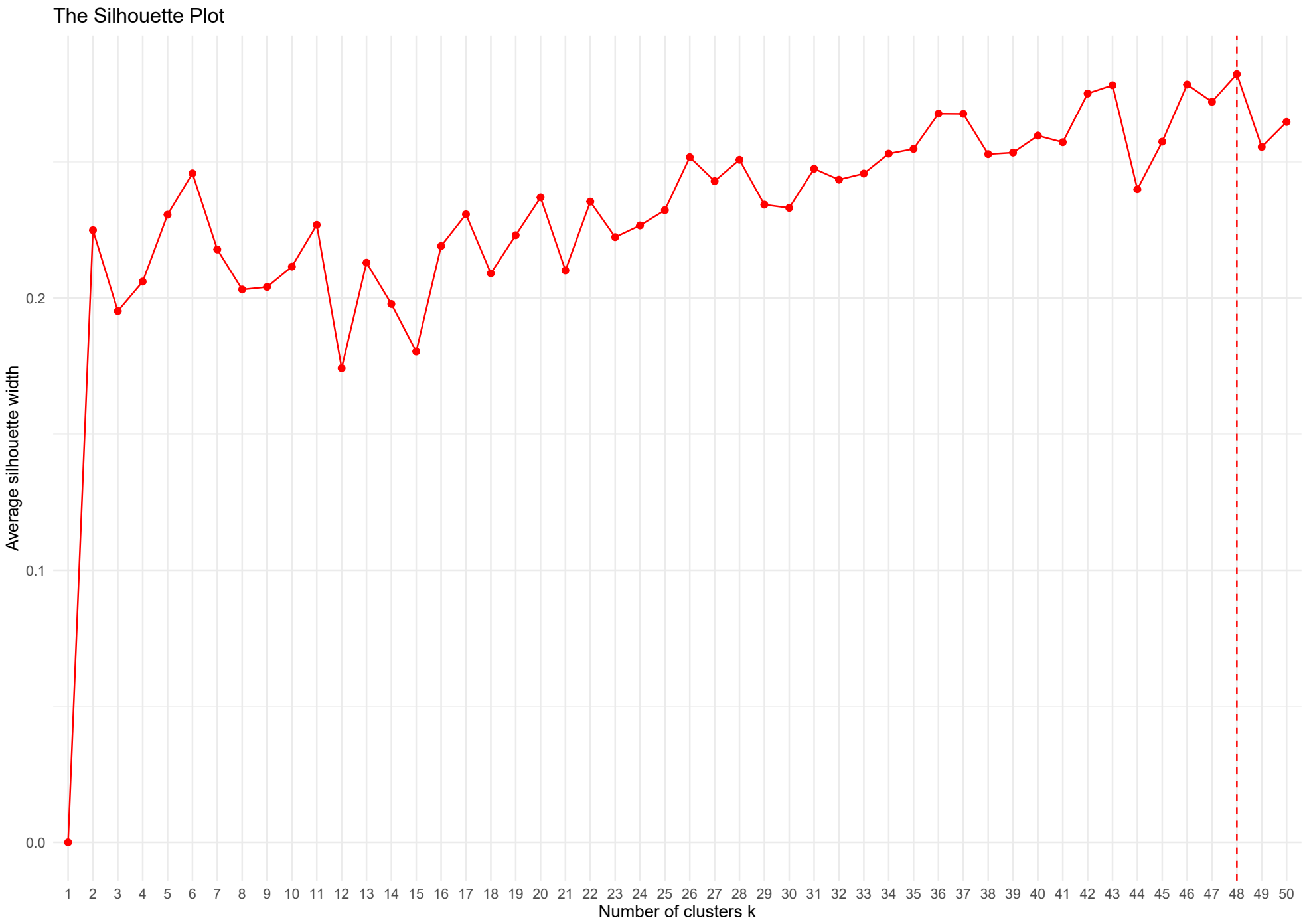

DCA samples and species
DCA 2
DCA 1
4
3
2
1
0
−1
0.0
0.2
0.4
0.6
0.8
1.0
MP
BL
GY
QR
PM
PA
PL
SP
CL
RG

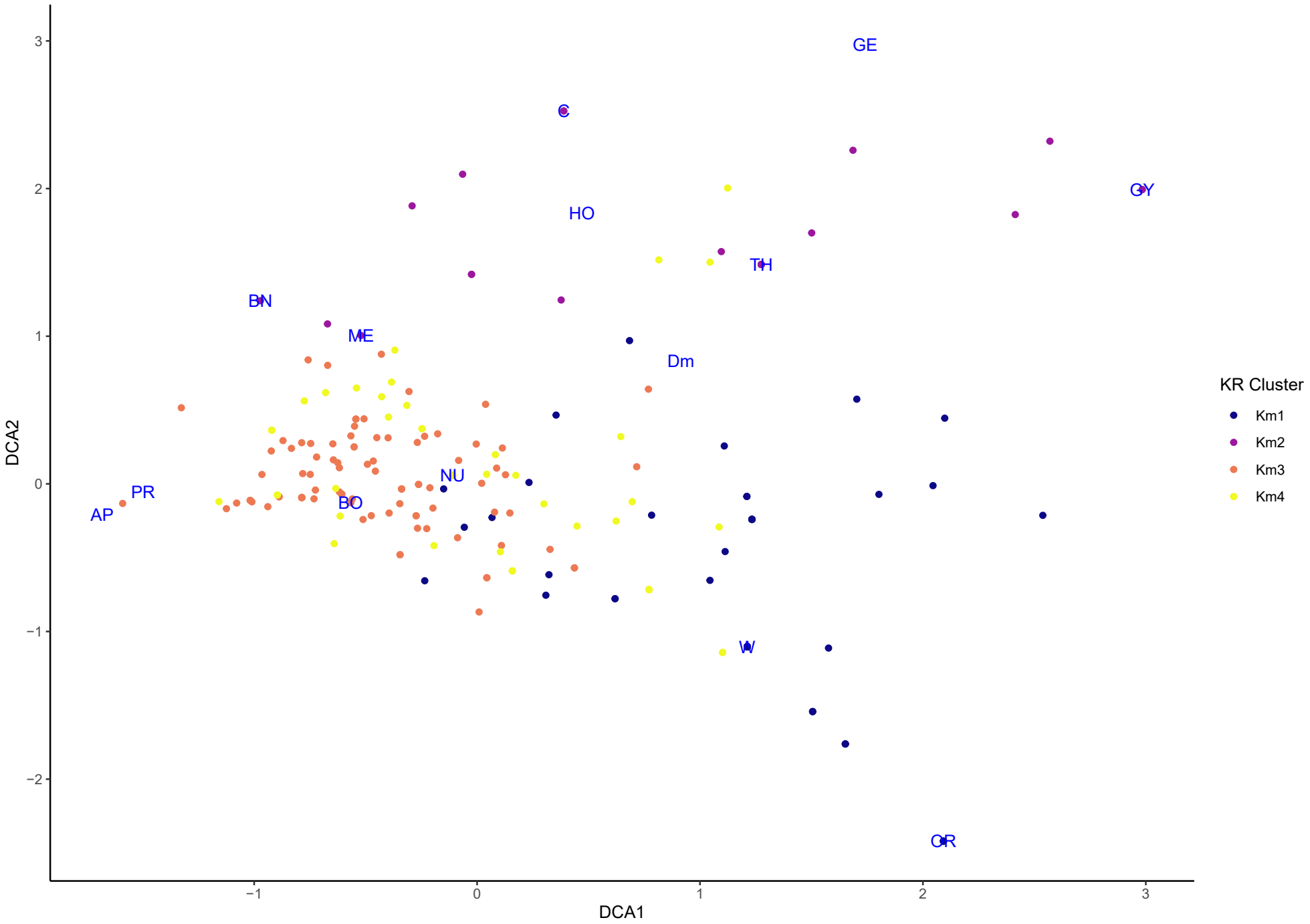
DCA samples and species UQ



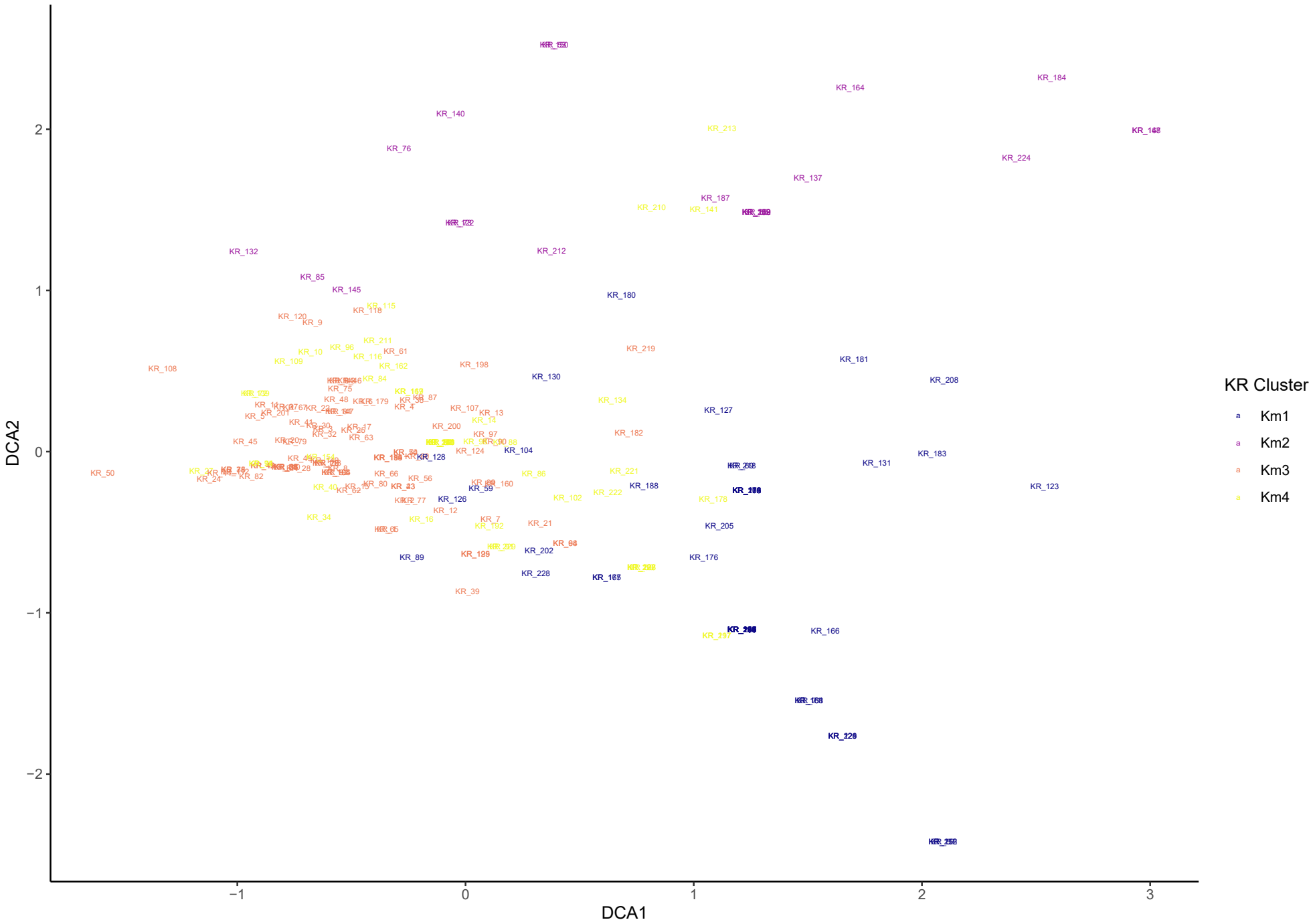

Within groups sum of squares
1000
800
600
400
200
0
10
20
30
40
50
Number of Clusters

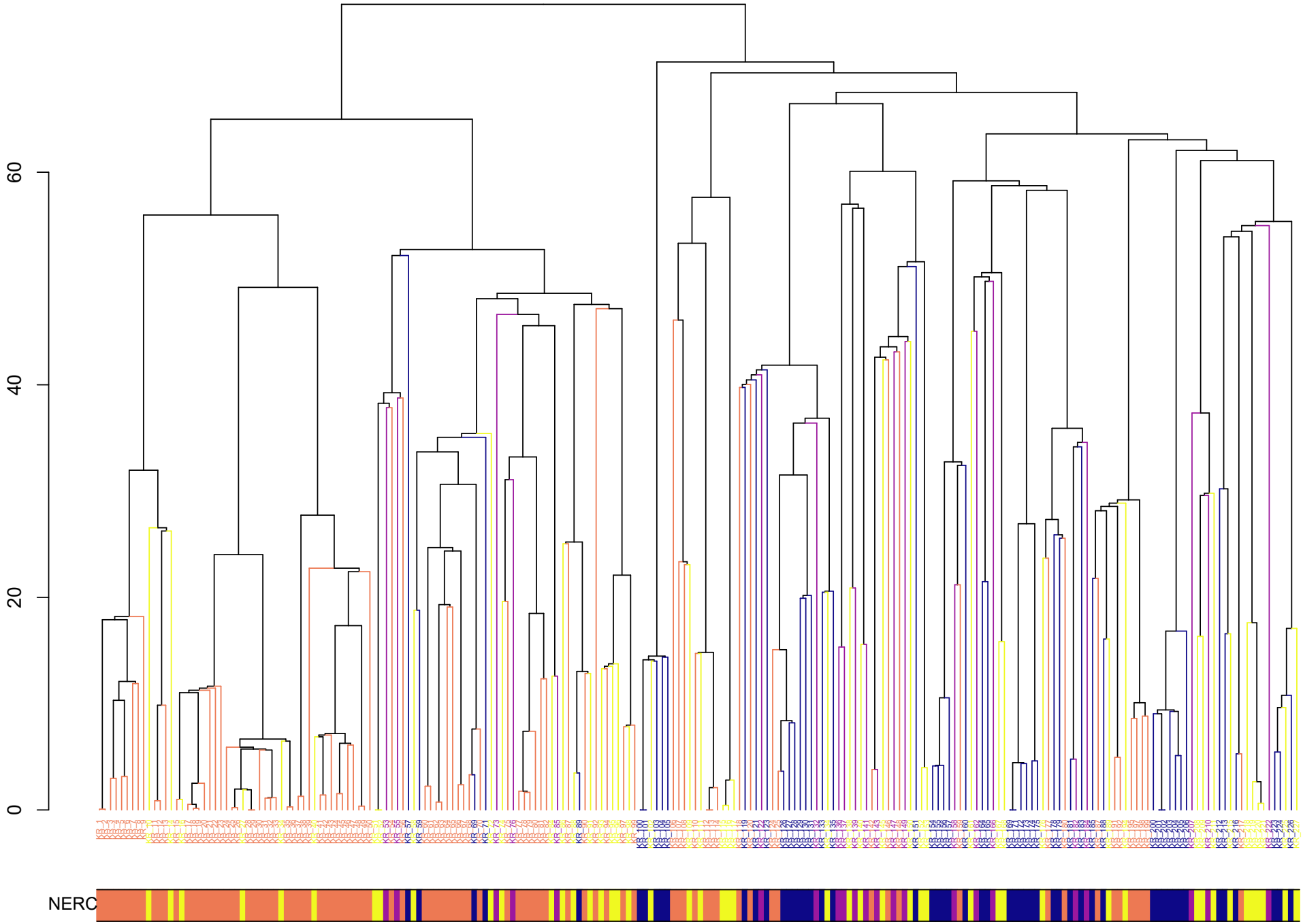

fviz_gap_stat: Gap Statistic
Gap statistic (k)
1.0
0.8
0.6
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75
Number of clusters k


The Silhouette Plot
Average silhouette width
0.0
0.1
0.2
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50
Number of clusters k

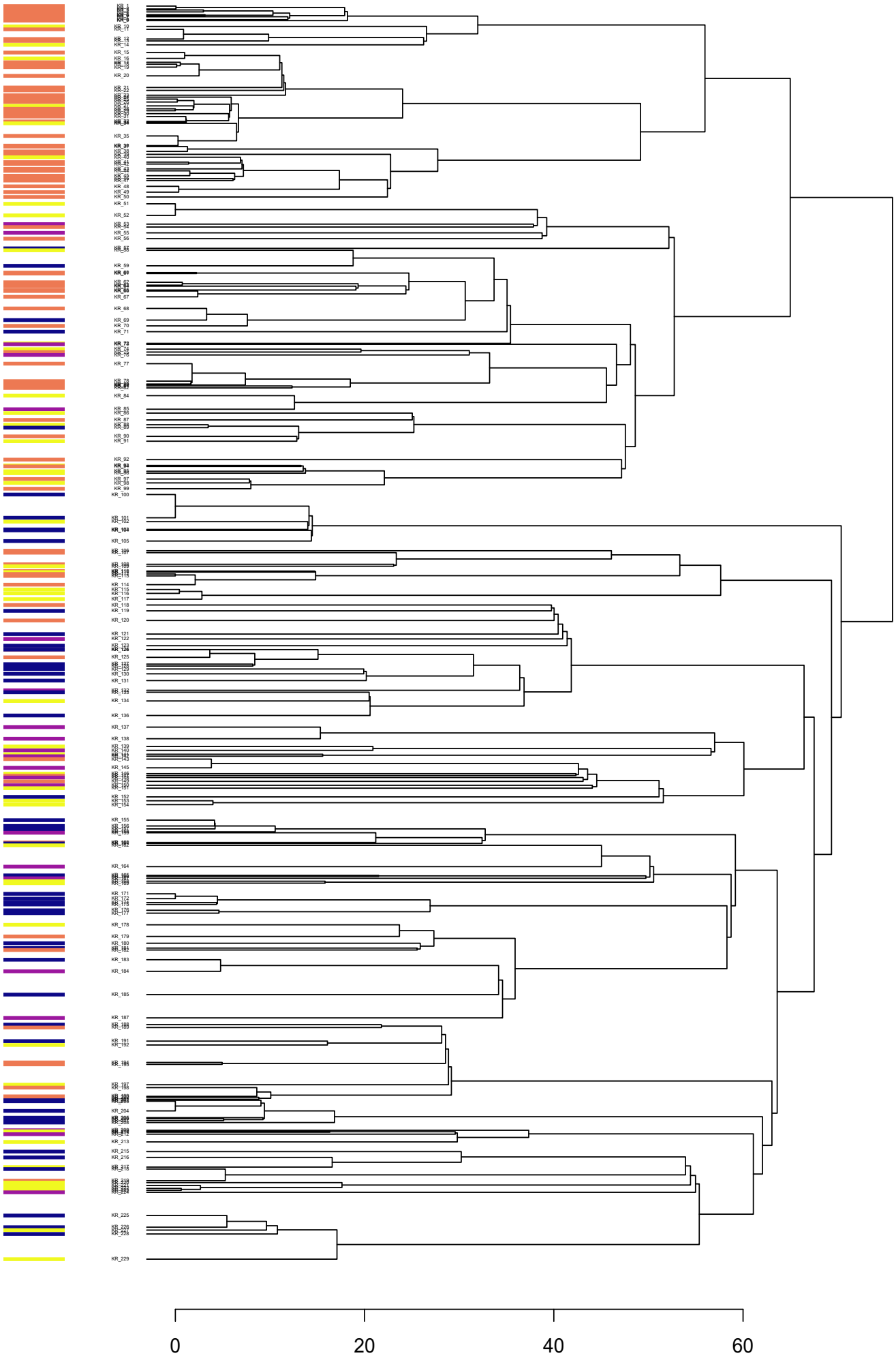


Kimmeridge 2 (KR)

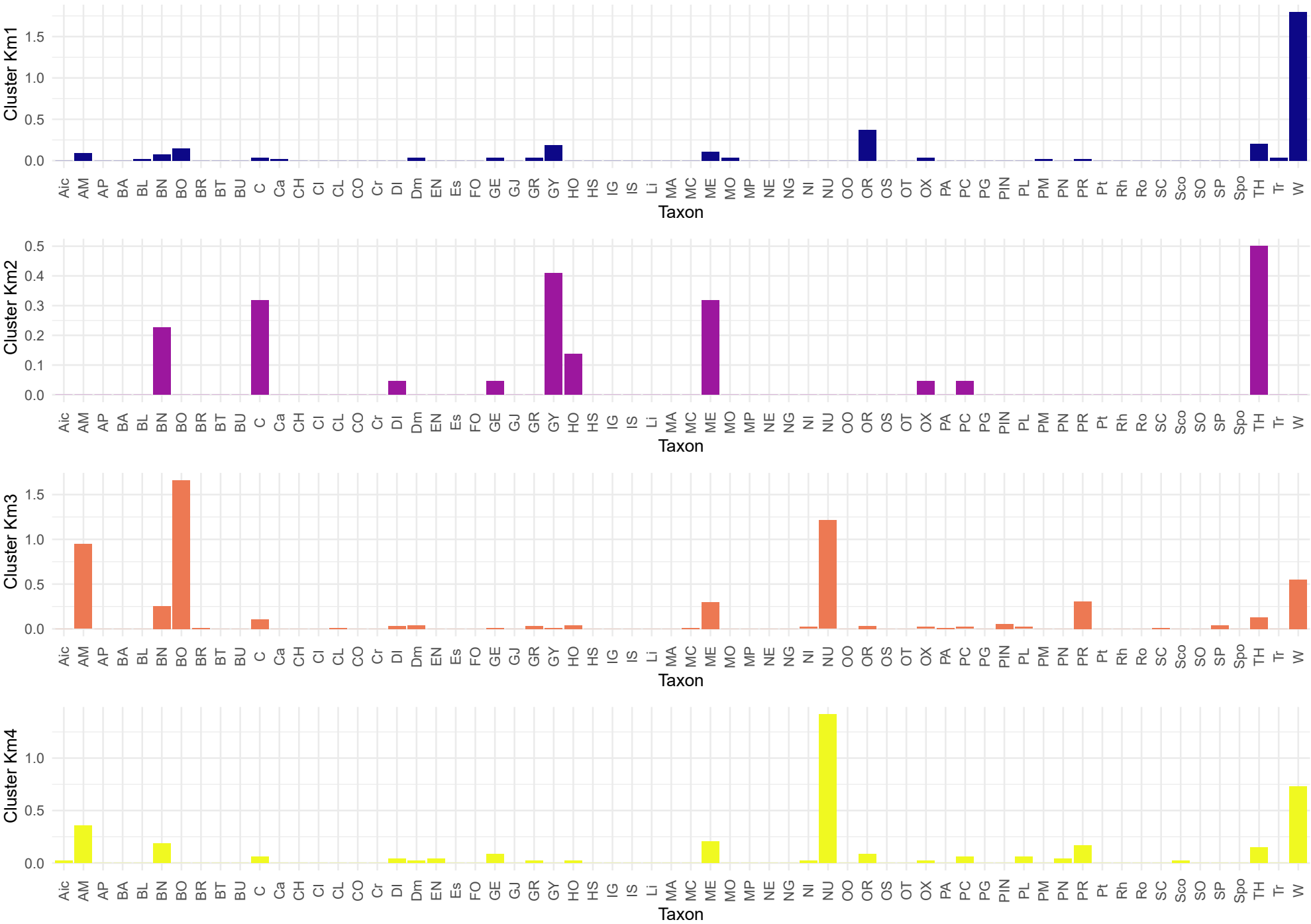

DCA2
DCA1
KR Cluster
Km1
Km2
Km3
Km4

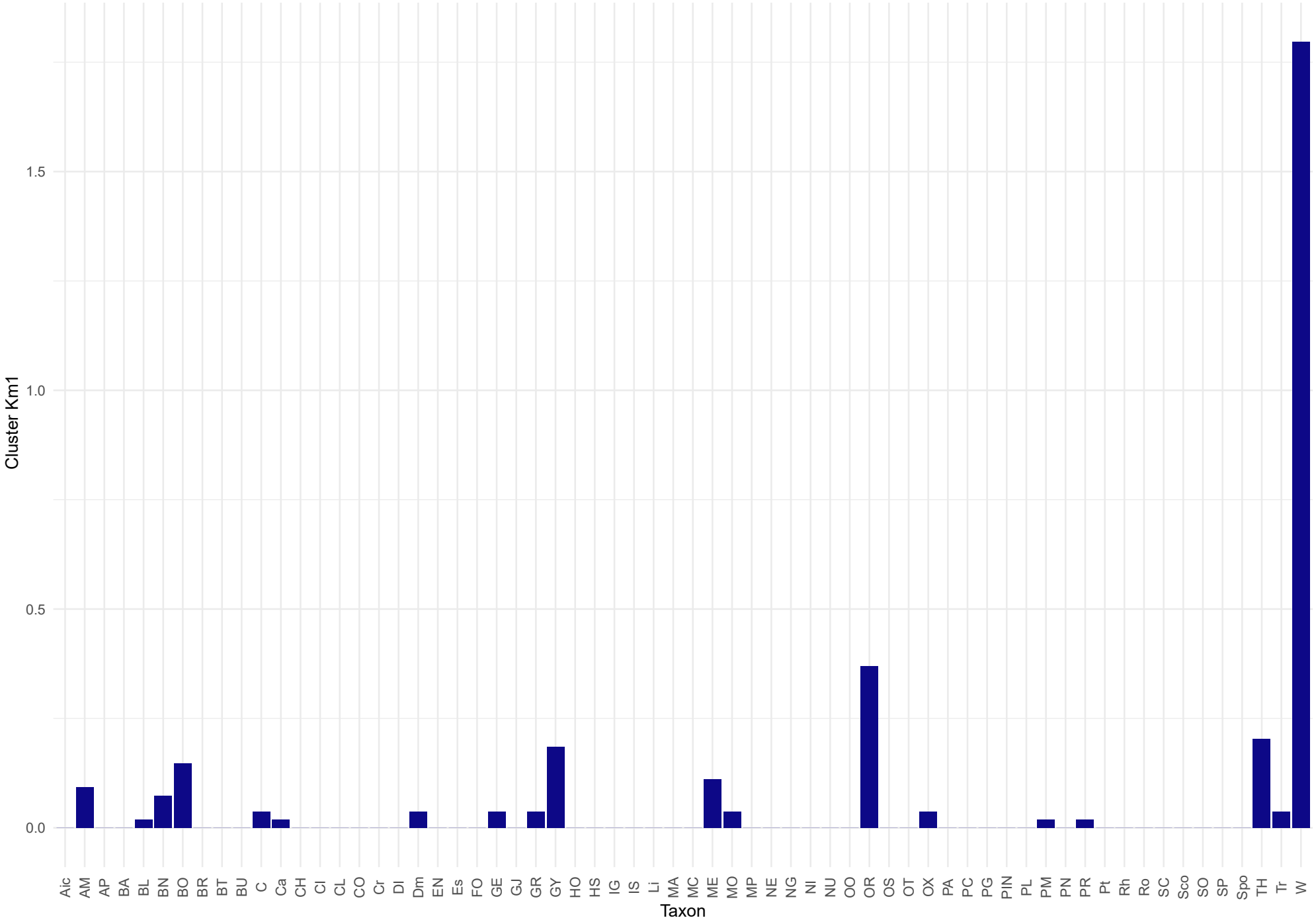


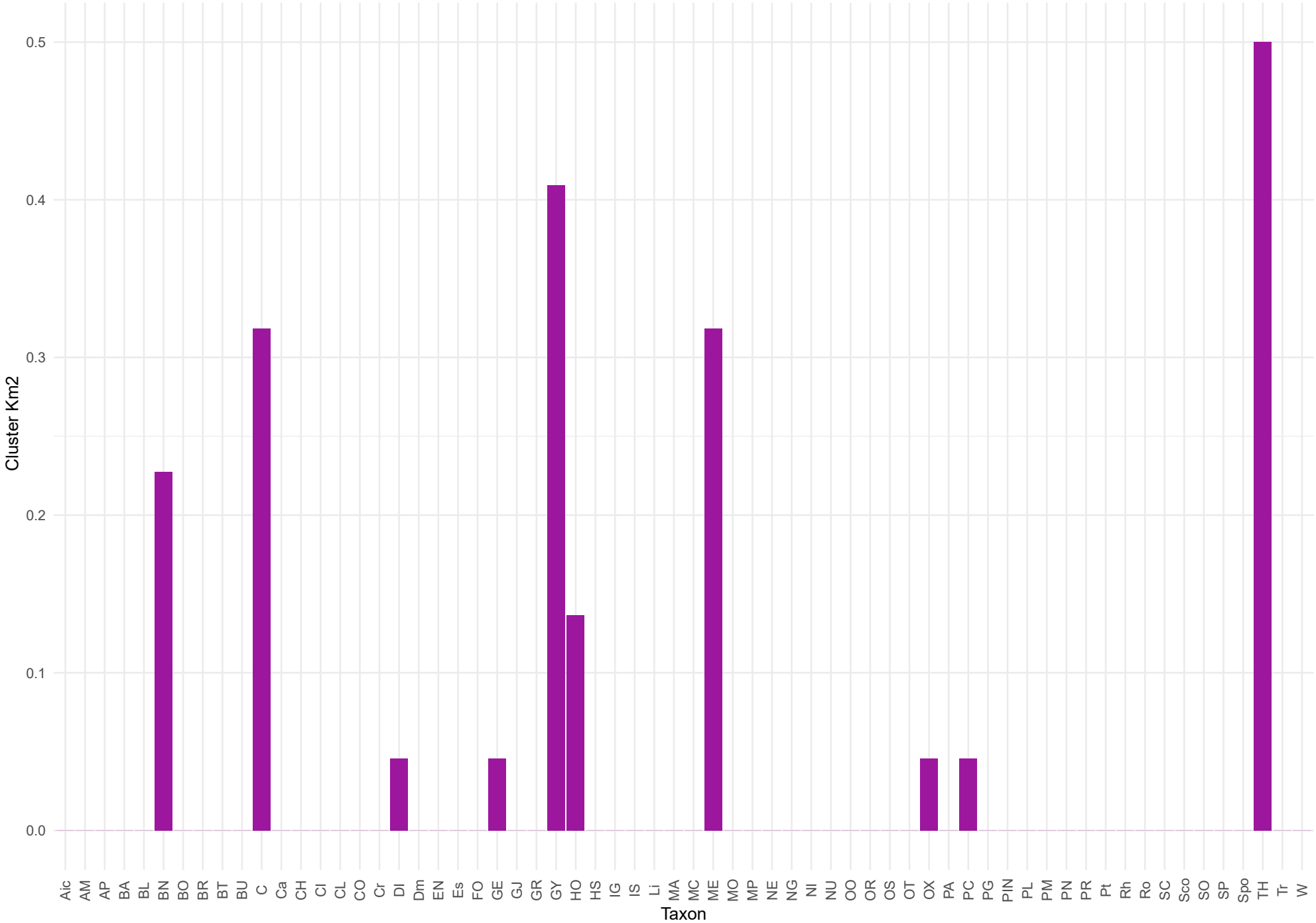
Kimmeridge 2 (KR)

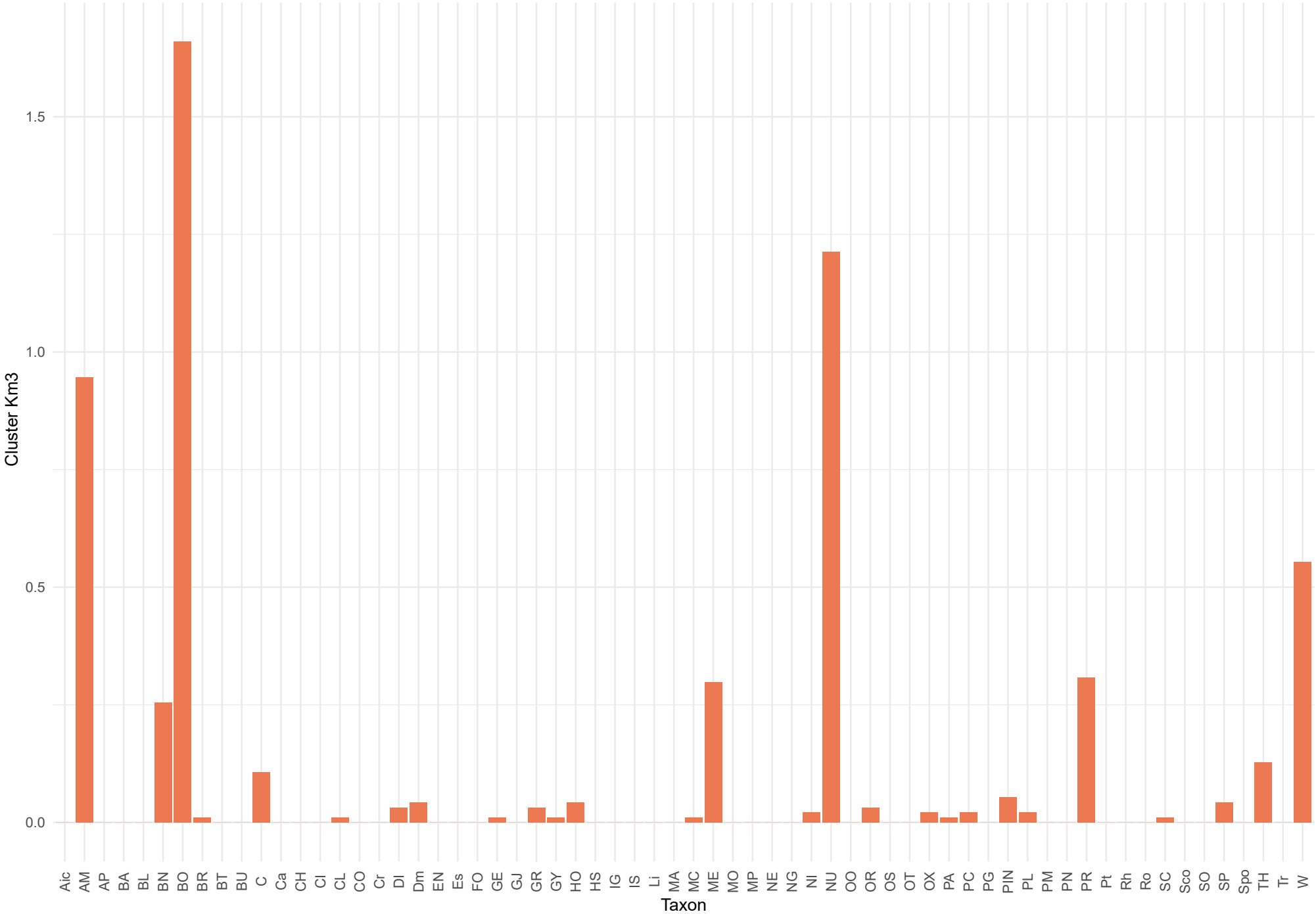


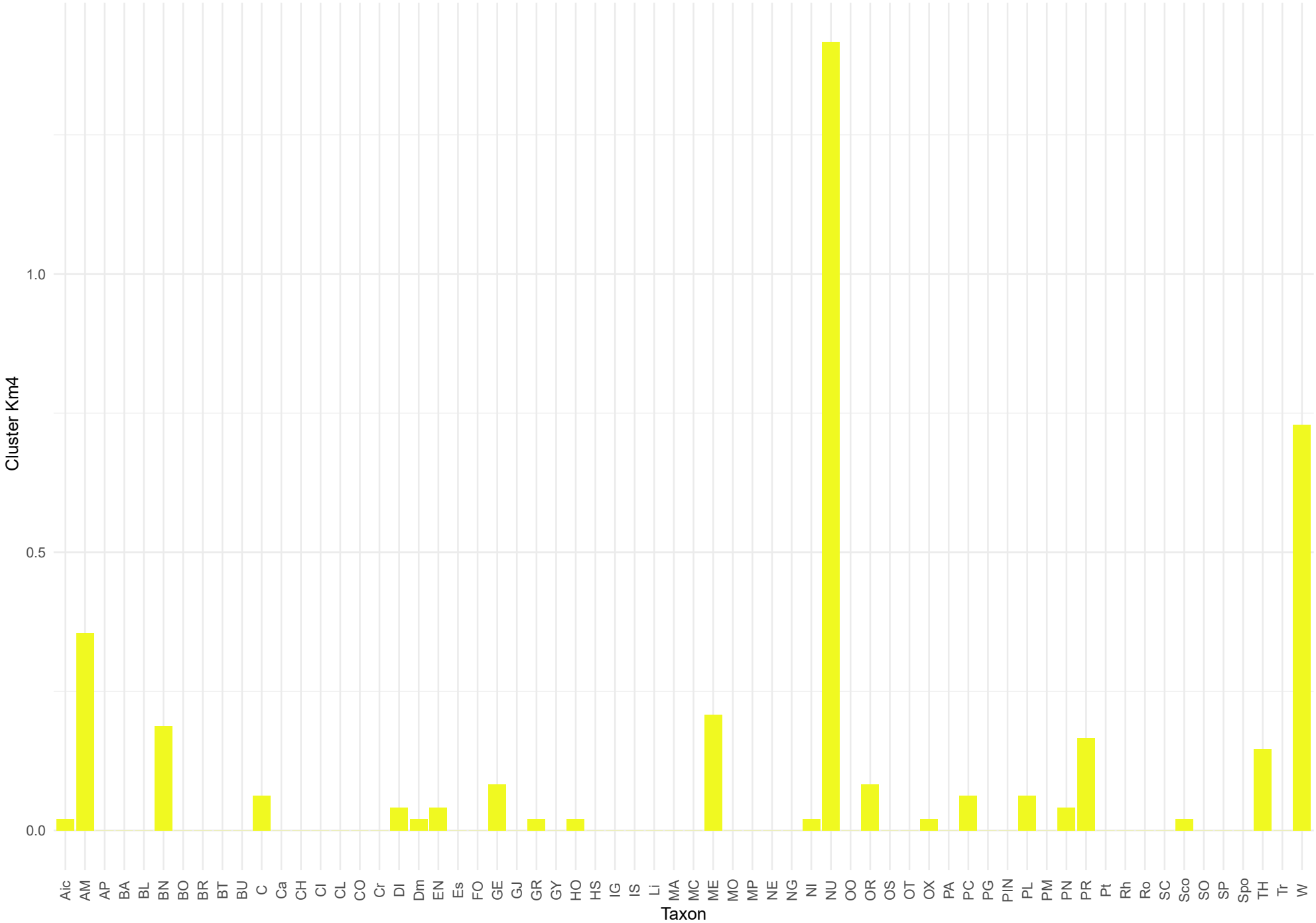
Kimmeridge 2 (KR)

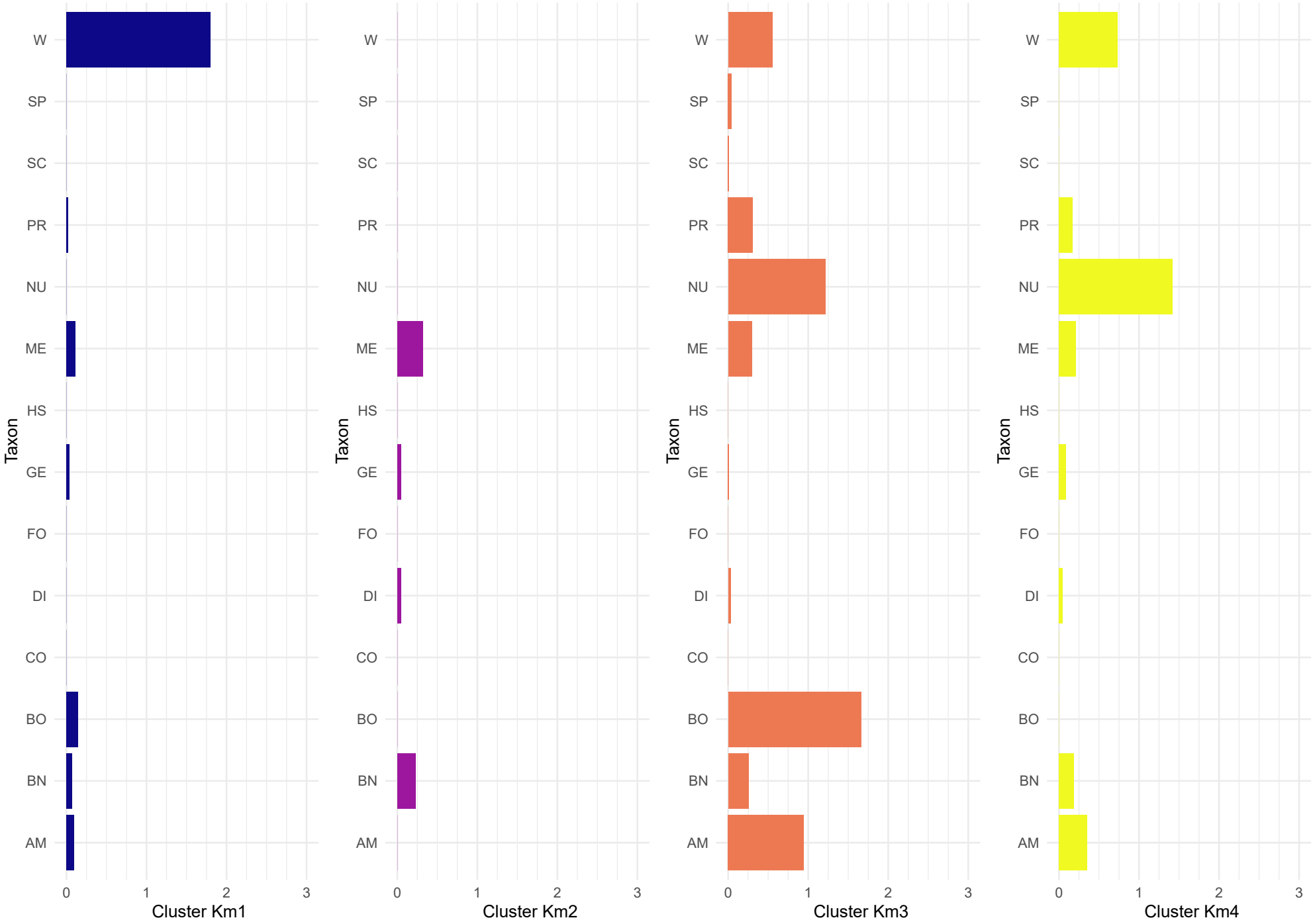

Cluster Km1
Cluster Km2
Cluster Km3
Cluster Km4
Taxon
Aic AM AP BA BL BN BO BR BT BU C Ca CH Cl CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W


Cluster Km1
1.5
1.0
0.5
0.0
Aic
AM
AP
BA
BL
BN
BO
BR
BT
BU
C
Ca
CH
Cl
CL
CO
Cr
DI
Dm
EN
Es
FO
GE
GJ
GR
GY
HO
HS
IG
IS
Li
MA
MC
ME
MO
MP
NE
NG
NI
NU
OO
OR
OS
OT
OX
PA
PC
PG
PIN
PL
PM
PN
PR
Pt
Rh
Ro
SC
Sco
SO
SP
Spo
TH
Tr
W
Taxon


Cluster Km2
0.0
0.1
0.2
0.3
0.4
0.5
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon

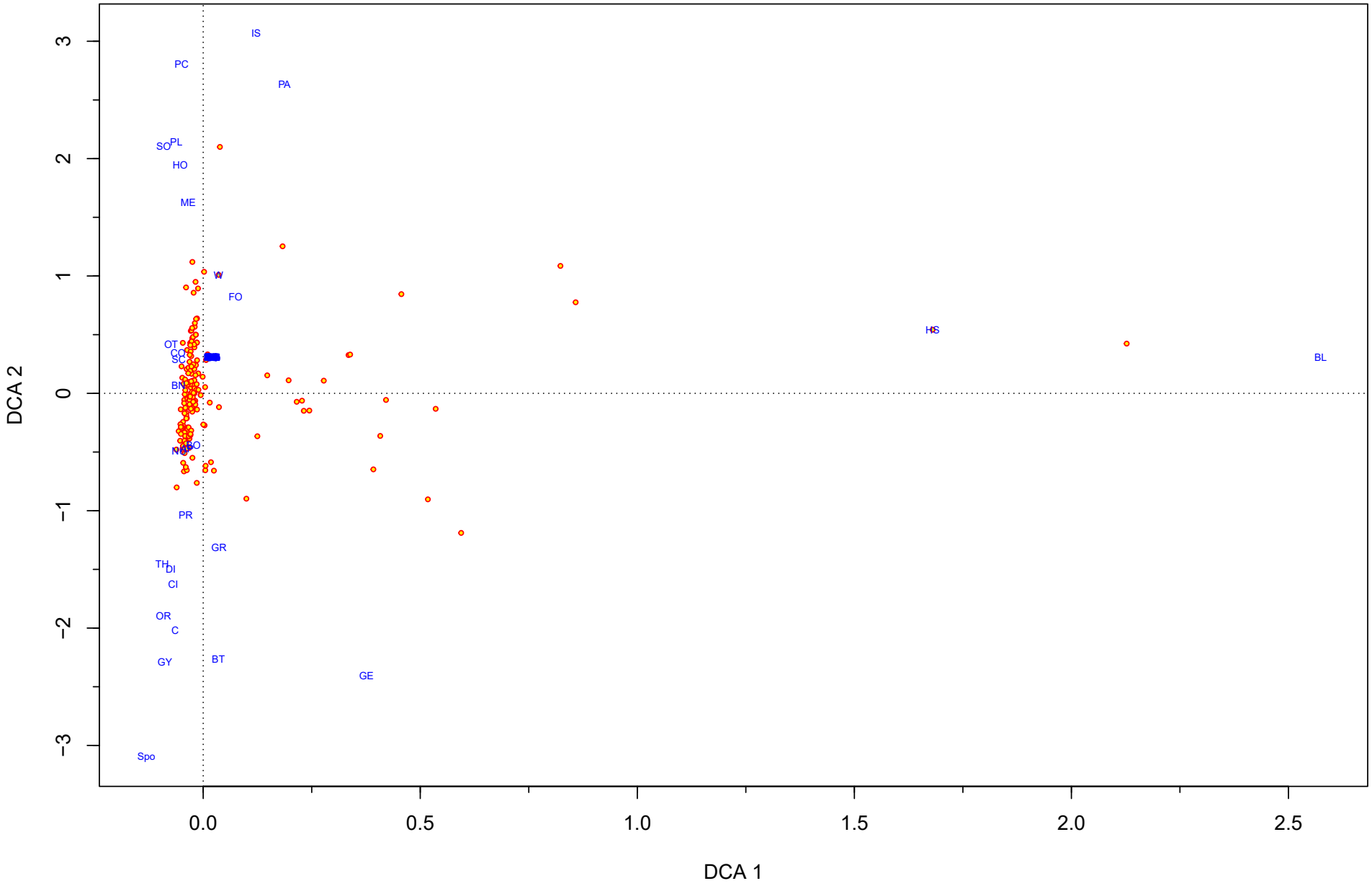

Cluster Km3
1.5
1.0
0.5
0.0
Aic
AM
AP
BA
BL
BN
BO
BR
BT
BU
C
Ca
CH
CI
CL
CO
Cr
DI
Dm
EN
Es
FO
GE
GJ
GR
GY
HO
HS
IG
IS
Li
MA
MC
ME
MO
MP
NE
NG
NI
NU
OO
OR
OS
OT
OX
PA
PC
PG
PIN
PL
PM
PN
PR
Pt
Rh
Ro
SC
Sco
SO
SP
Spo
TH
Tr
W
Taxon

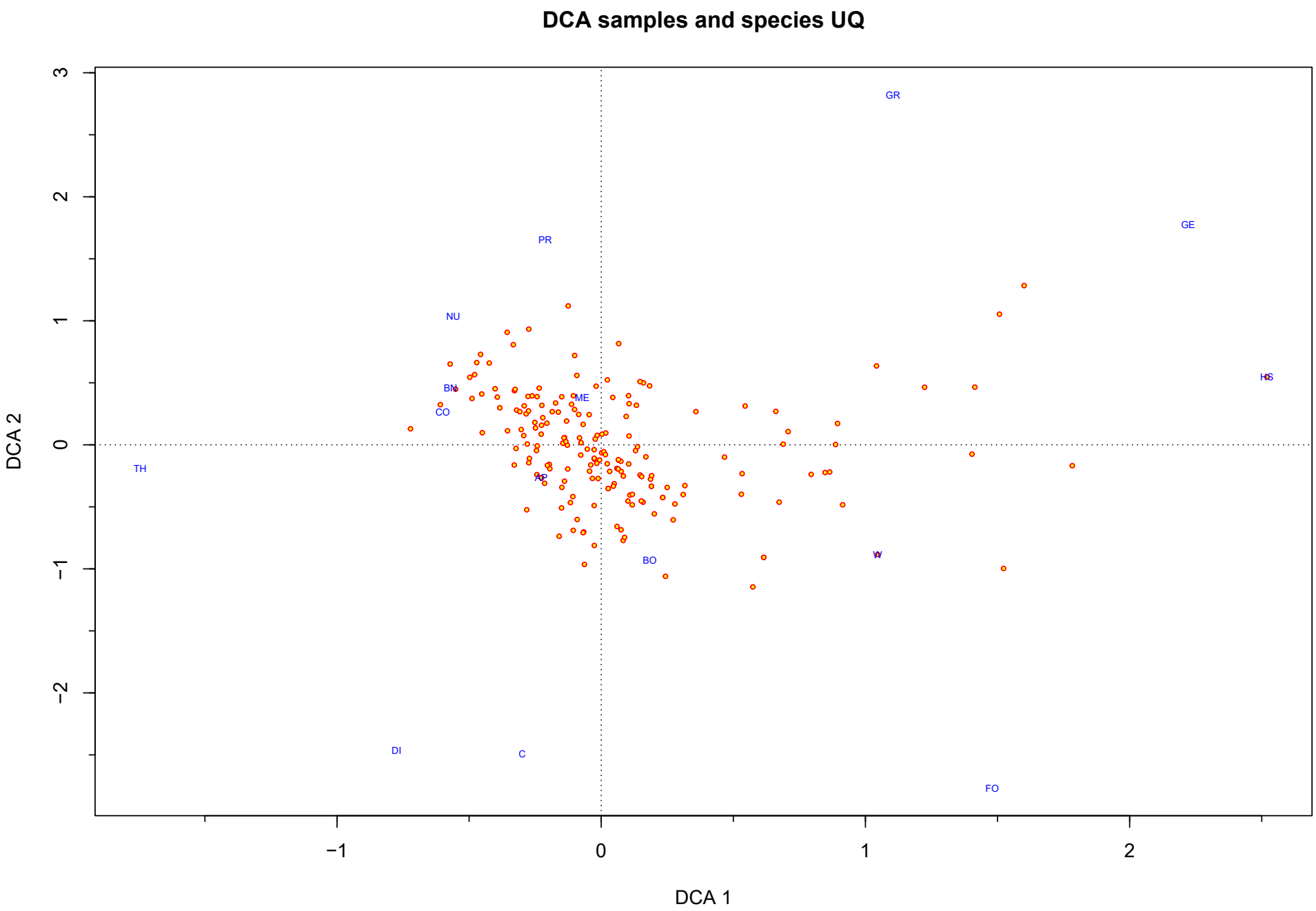

Cluster Km4
1.0
0.5
0.0
Aic
AM
AP
BA
BL
BN
BO
BR
BT
BU
C
Ca
CH
CI
CL
CO
Cr
DI
Dm
EN
Es
FO
GE
GJ
GR
GY
HO
HS
IG
IS
Li
MA
MC
ME
MO
MP
NE
NG
NI
NU
OO
OR
OS
OT
OX
PA
PC
PG
PIN
PL
PM
PN
PR
Pt
Rh
Ro
SC
Sco
SO
SP
Spo
TH
Tr
W
Taxon

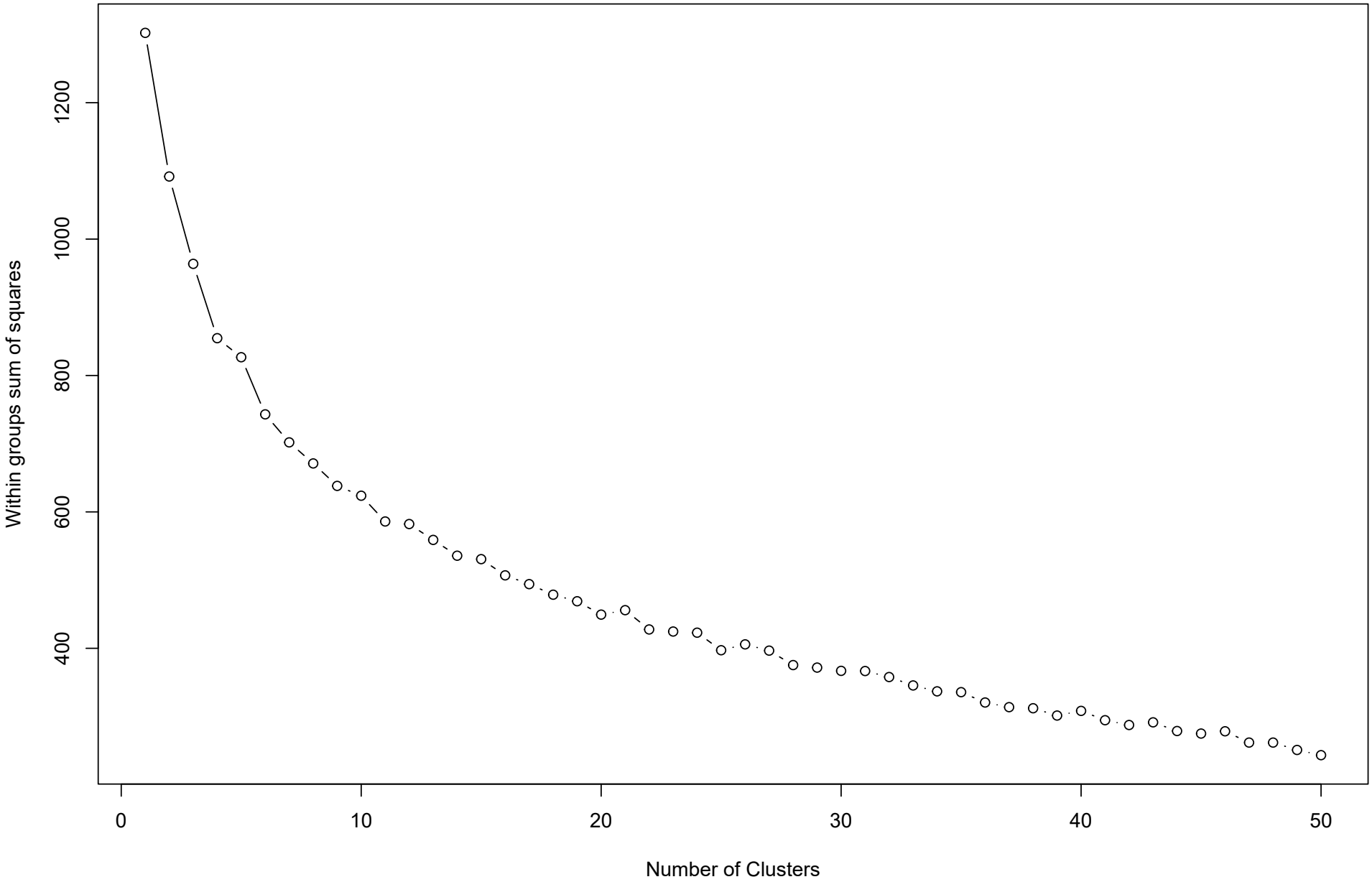

Taxon
W
SP
SC
PR
NU
ME
HS
GE
FO
DI
CO
BO
BN
AM
0
1
2
3
Cluster Km1
Cluster Km2
Cluster Km3
Cluster Km4

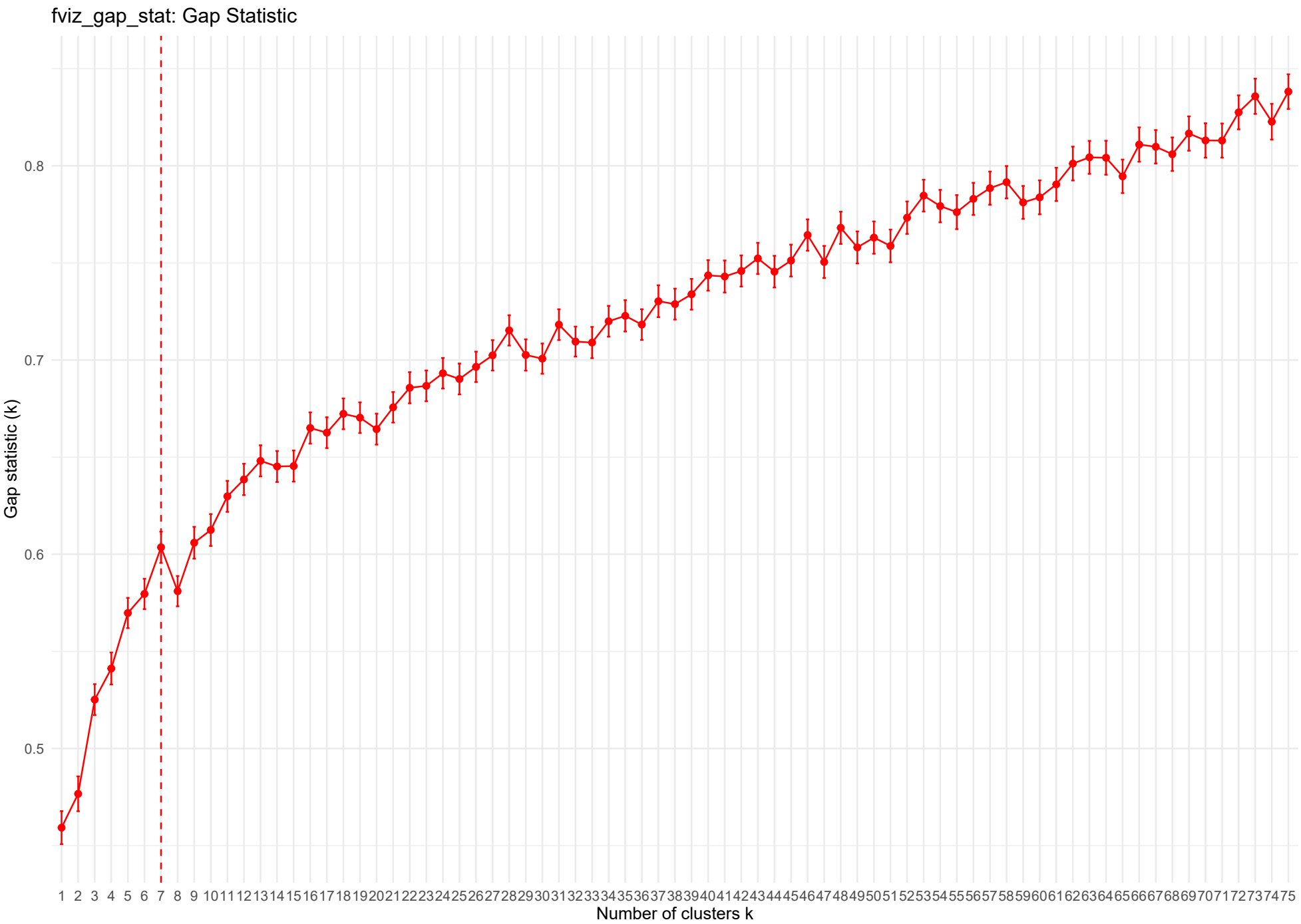
Parson Drove (PD)

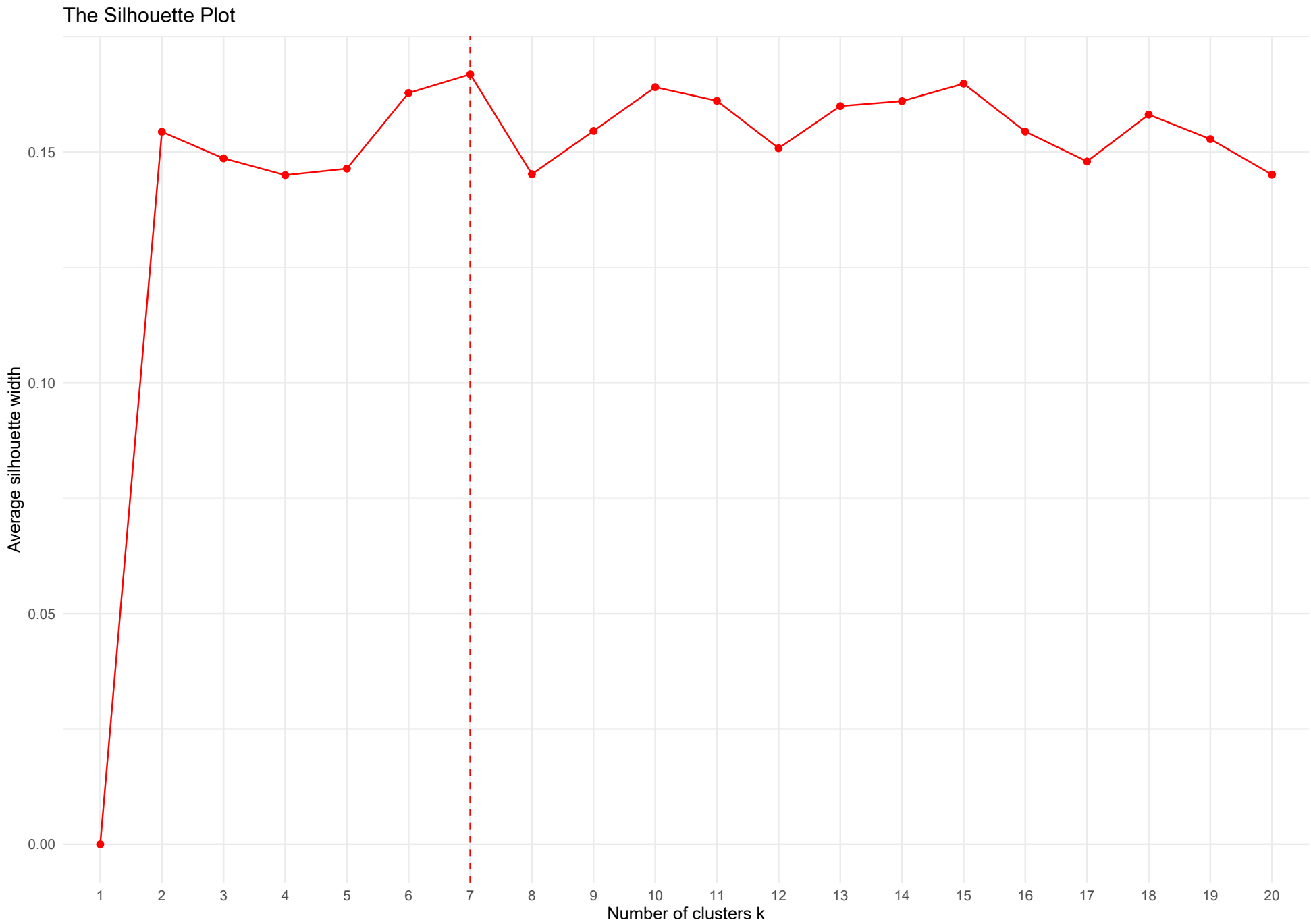
DCA samples and species

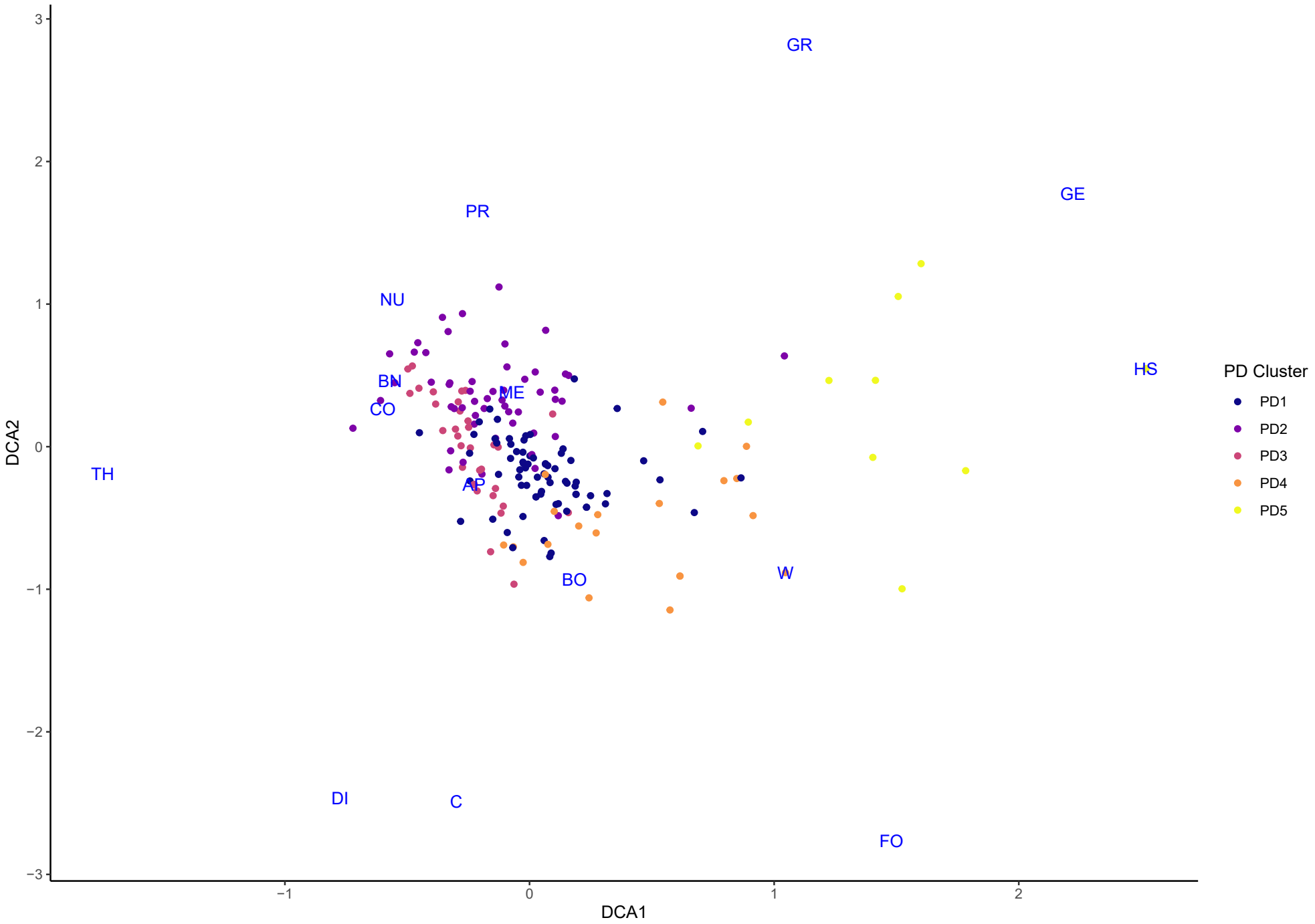



DCA samples and species UQ
DCA 2
DCA 1
3
2
1
0
−1
−2
−1
0
1
2
GR
GE
PR
NU
BN
CO
ME
TH
AP
BO
W
HS
DI
C
FO

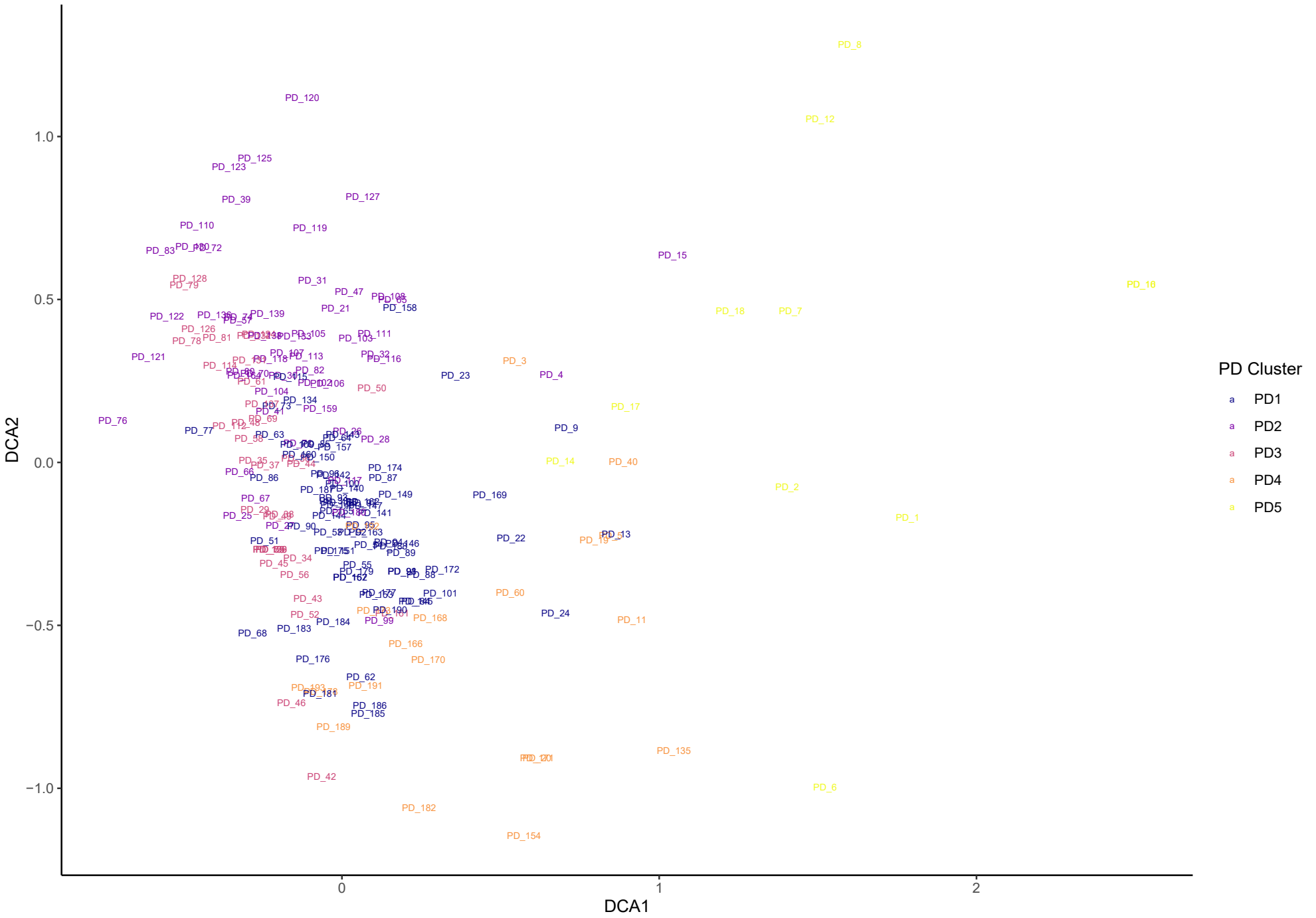

Within groups sum of squares
400
600
800
1000
1200
0
10
20
30
40
50
Number of Clusters

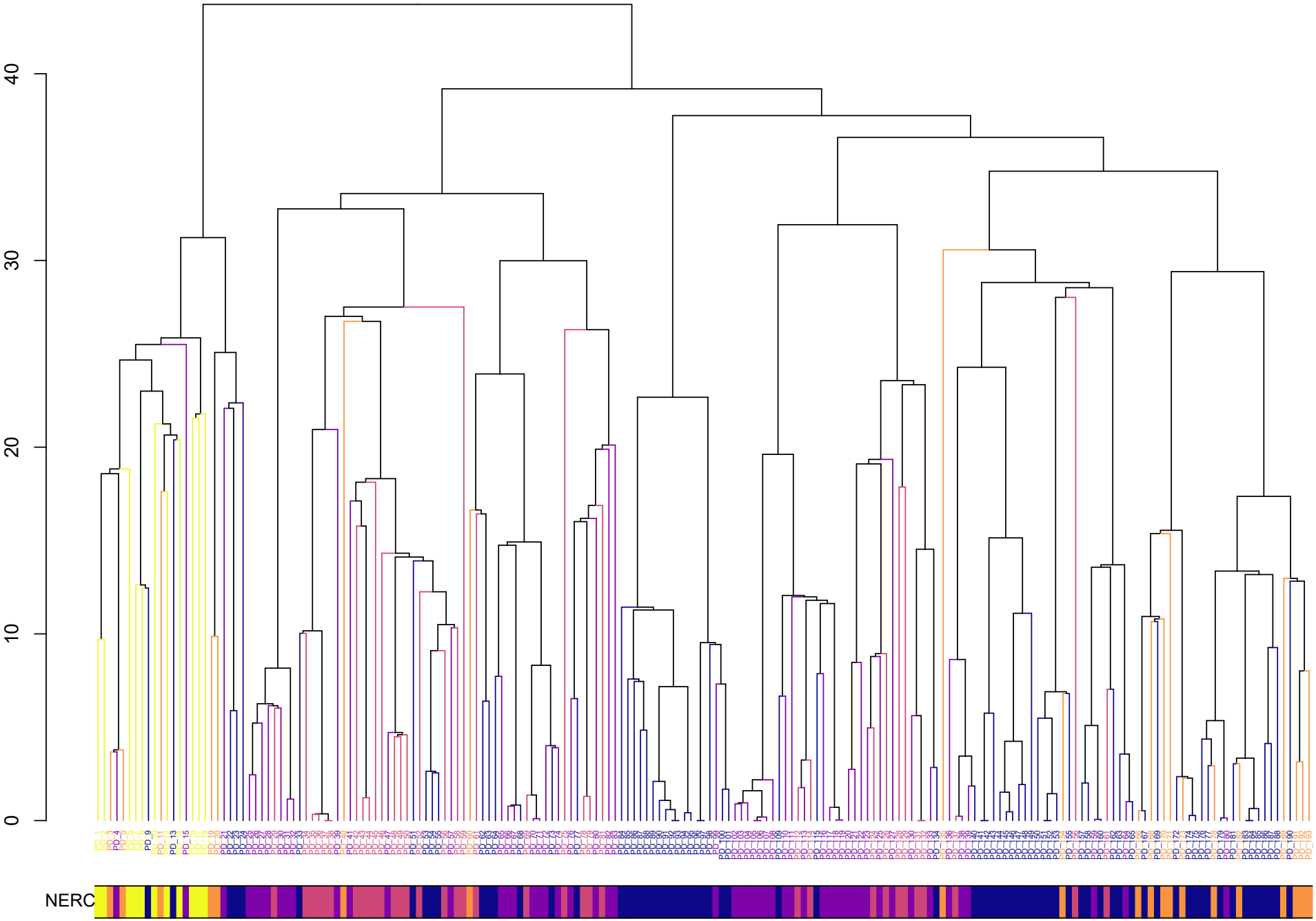

fviz_gap_stat: Gap Statistic
Gap statistic (k)
0.5
0.6
0.7
0.8
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75
Number of clusters k

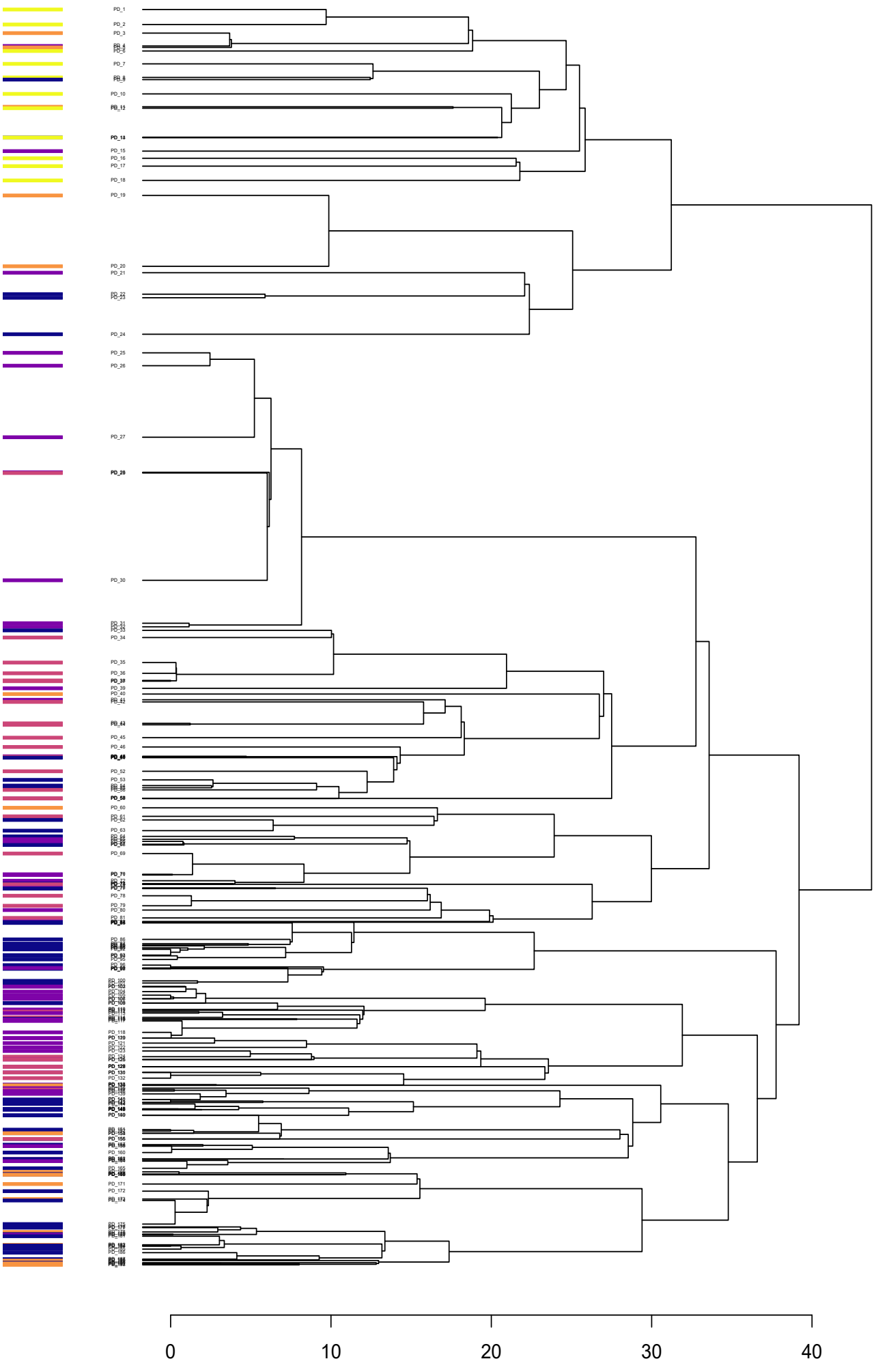

The Silhouette Plot
Average silhouette width
0.00
0.05
0.10
0.15
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
Number of clusters k



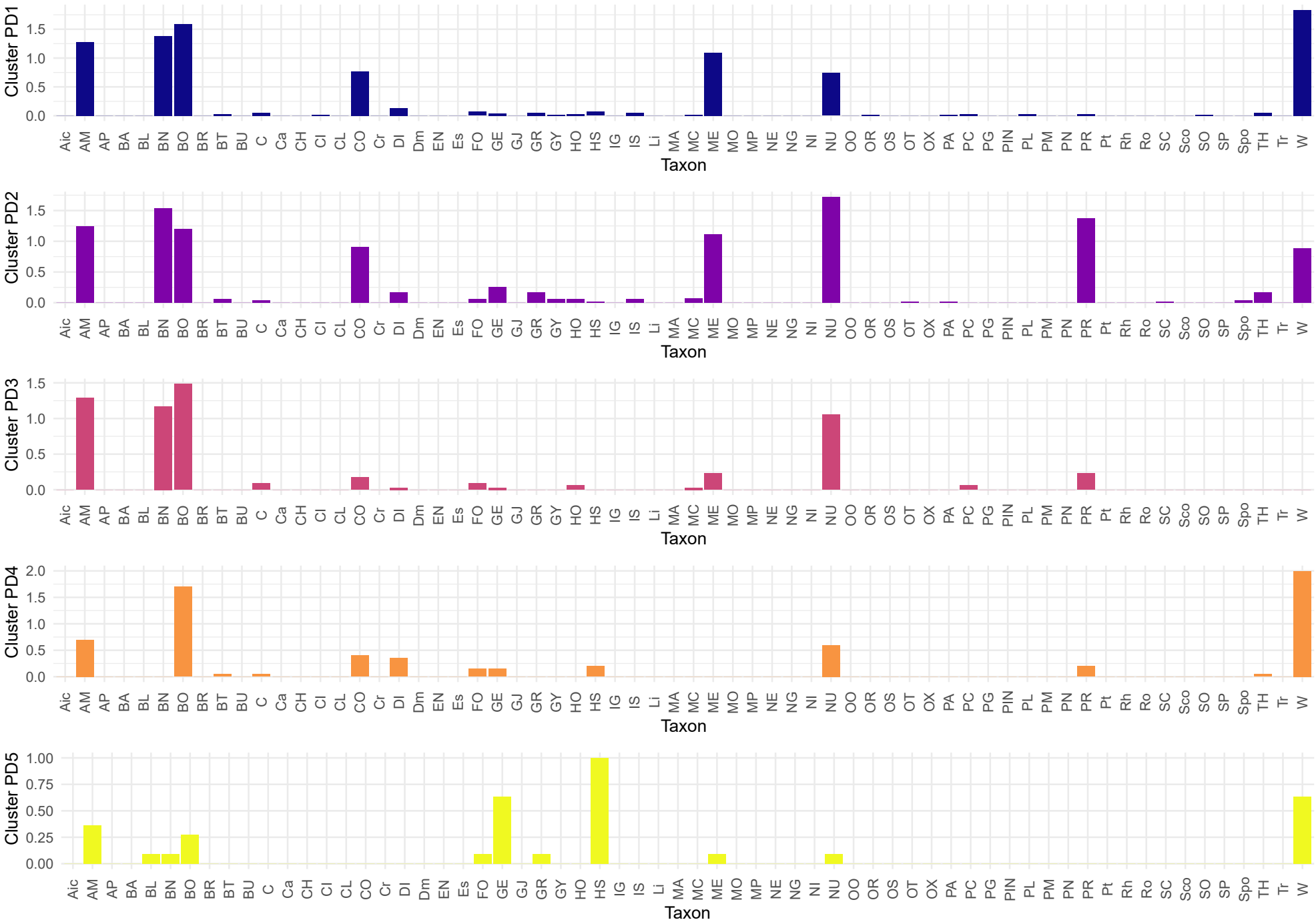
Parson Drove (PD)

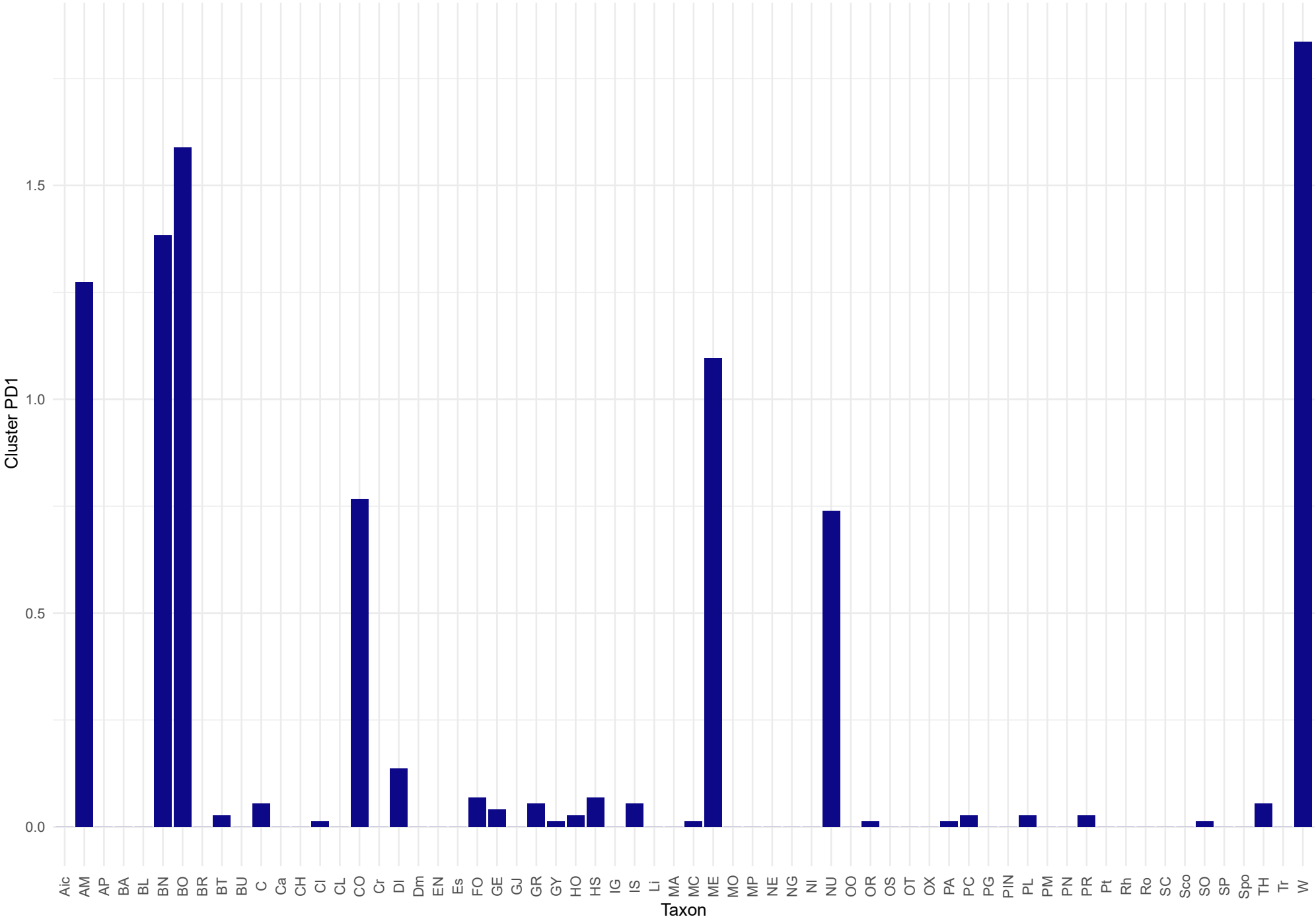

DCA2
DCA1
1.0
0.5
0.0
−0.5
−1.0
0
1
2
PD Cluster
PD1
PD2
PD3
PD4
PD5

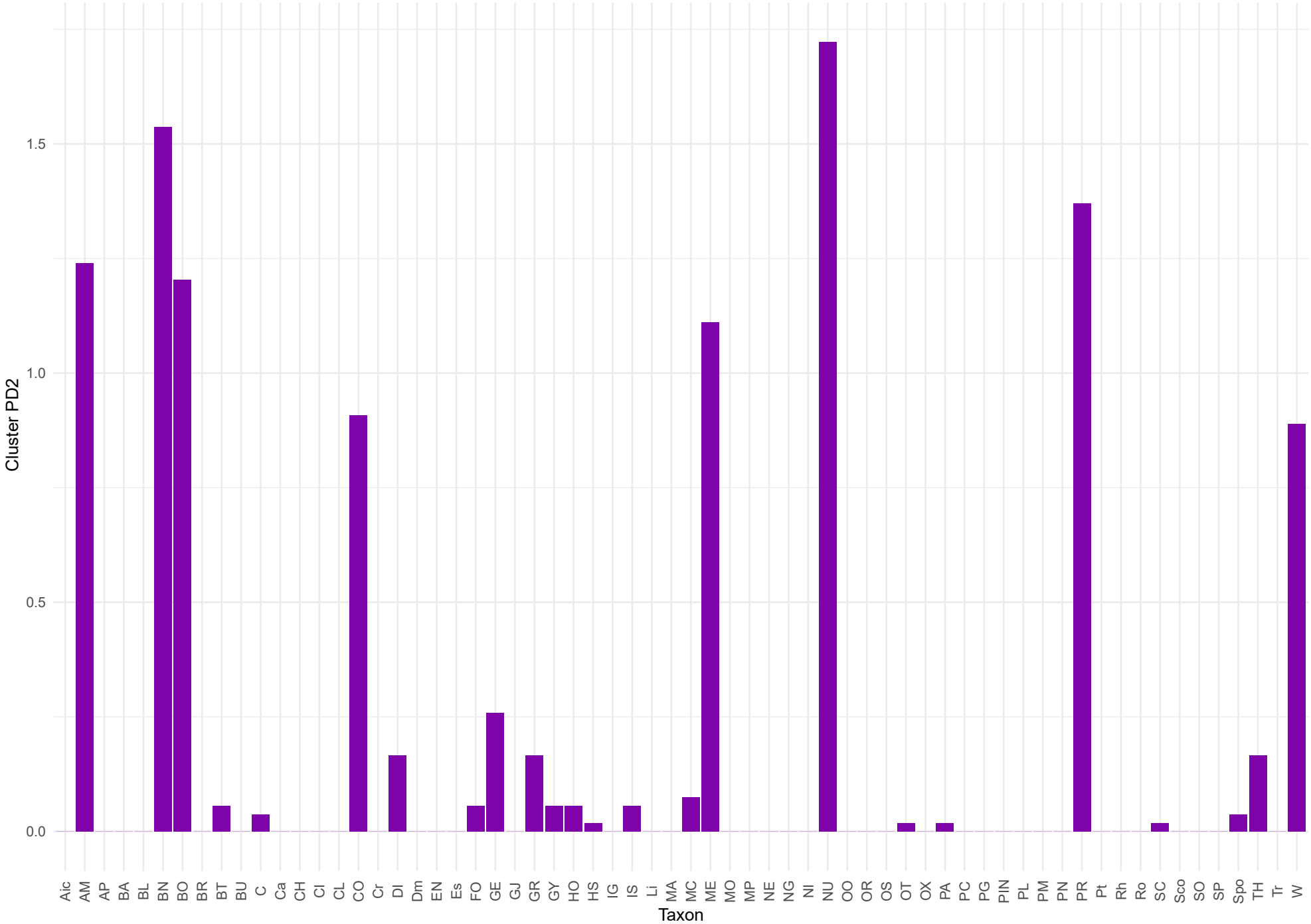

40
30
20
10
0
NERC

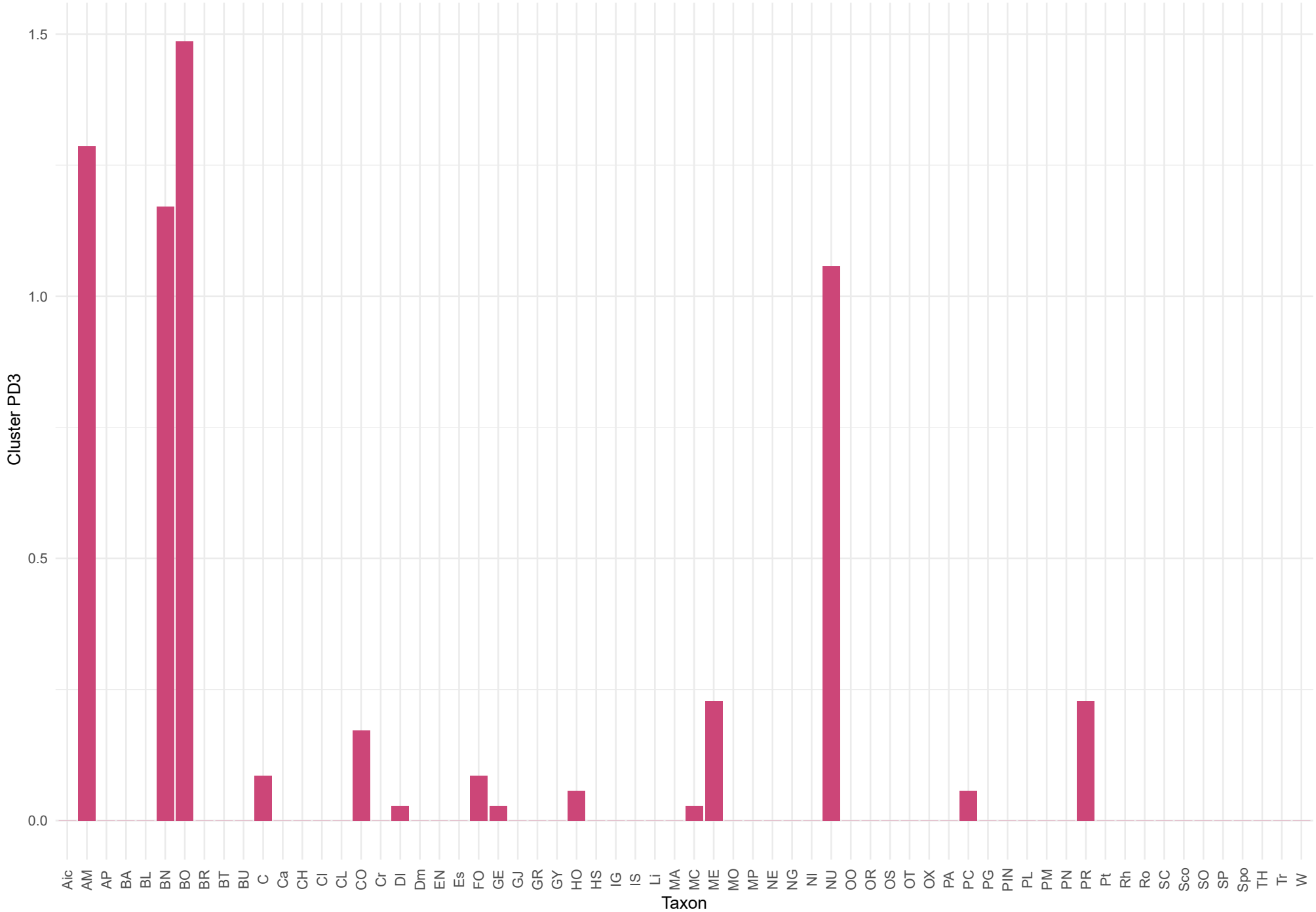


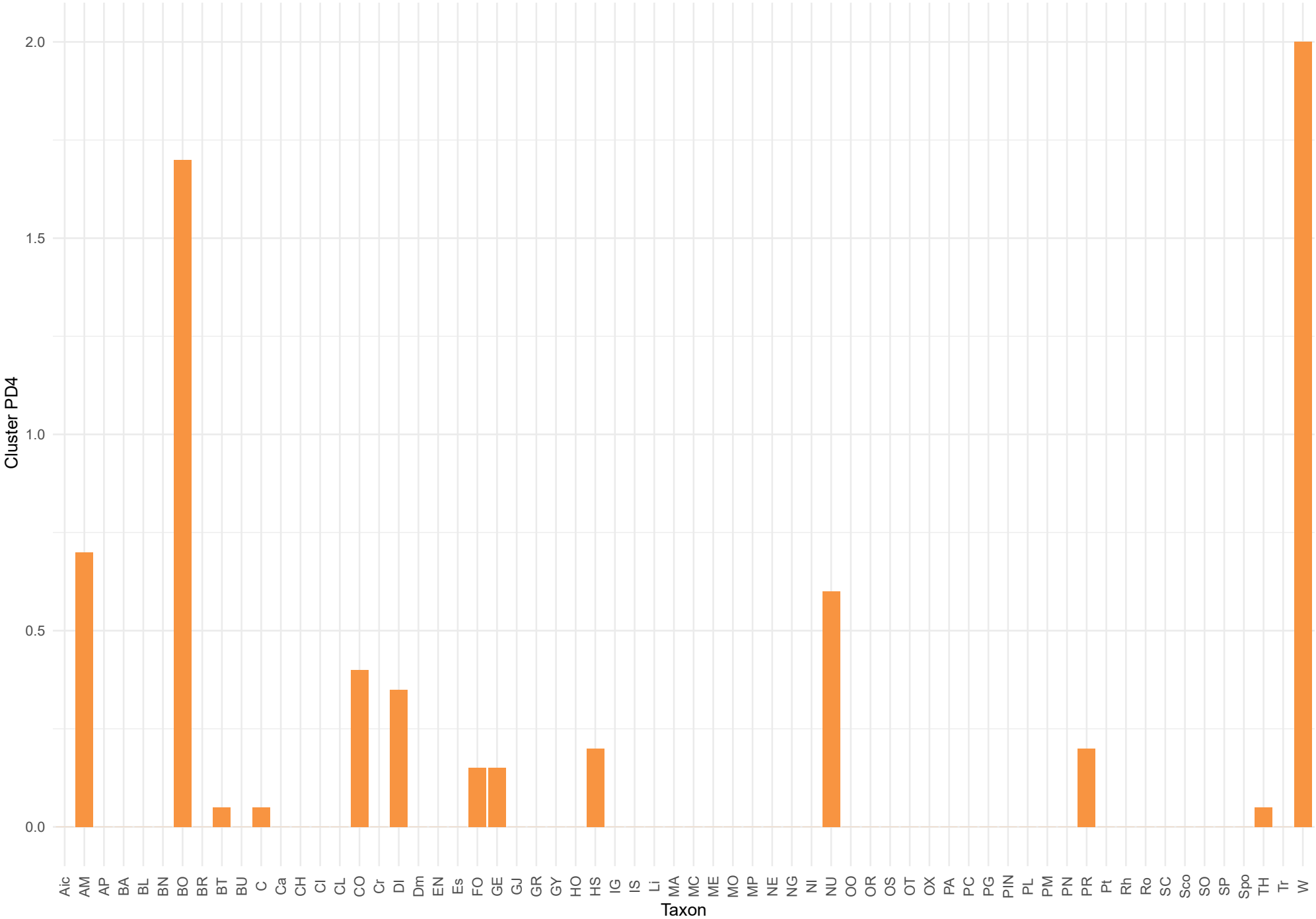
Parson Drove (PD)


Cluster PD1
Cluster PD2
Cluster PD3
Cluster PD4
Cluster PD5
Taxon
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W


Cluster PD1
1.5
1.0
0.5
0.0
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon


Cluster PD2
1.5
1.0
0.5
0.0
Aic
AM
AP
BA
BL
BN
BO
BR
BT
BU
C
Ca
CH
CI
CL
CO
Cr
DI
Dm
EN
Es
FO
GE
GJ
GR
GY
HO
HS
IG
IS
Li
MA
MC
ME
MO
MP
NE
NG
NI
NU
OO
OR
OS
OT
OX
PA
PC
PG
PIN
PL
PM
PN
PR
Pt
Rh
Ro
SC
Sco
SO
SP
Spo
TH
Tr
W
Taxon


Cluster PD3
1.5
1.0
0.5
0.0
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon


Cluster PD4
2.0
1.5
1.0
0.5
0.0
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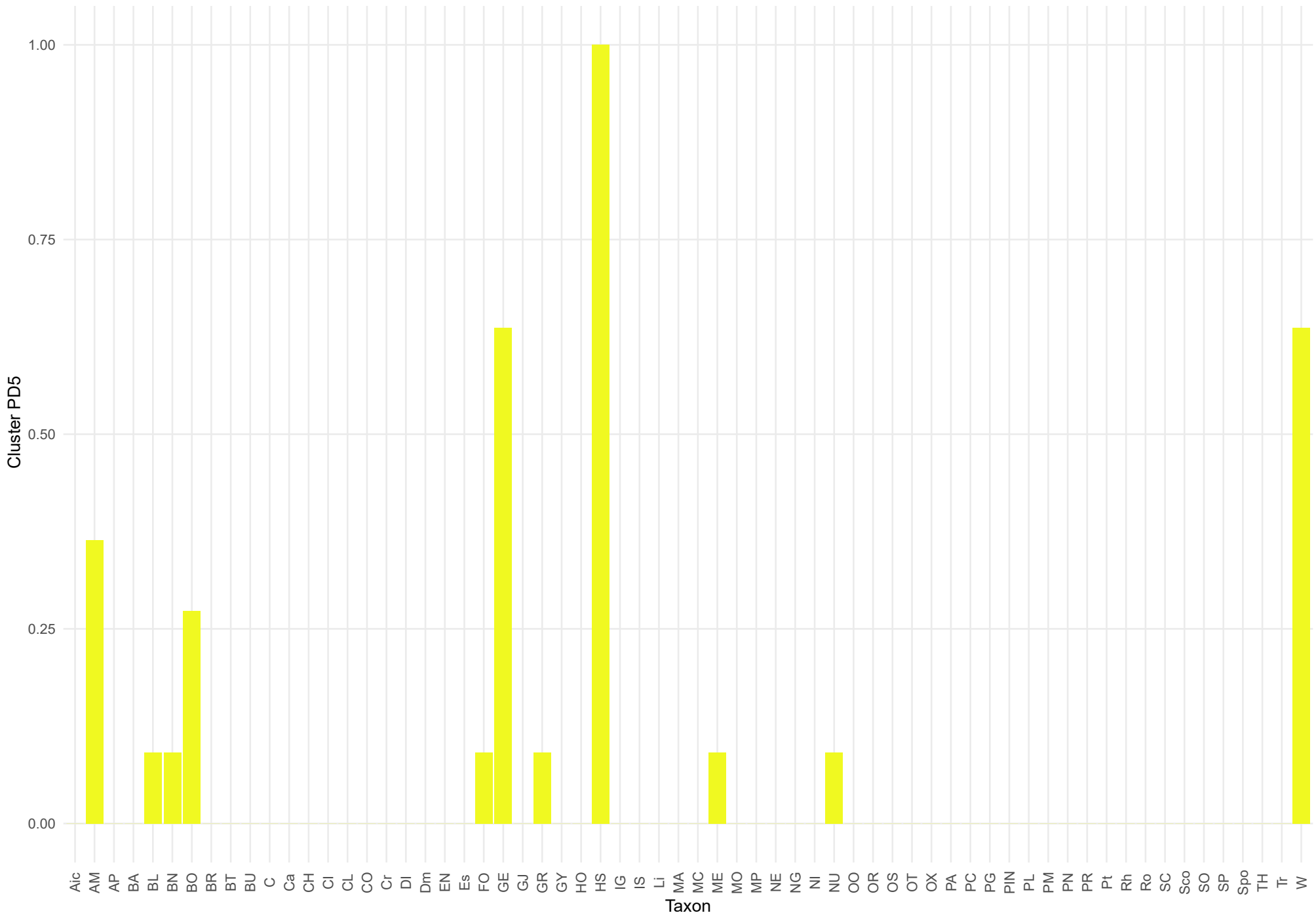
Taxon


Cluster PD5
1.00
0.75
0.50
0.25
0.00
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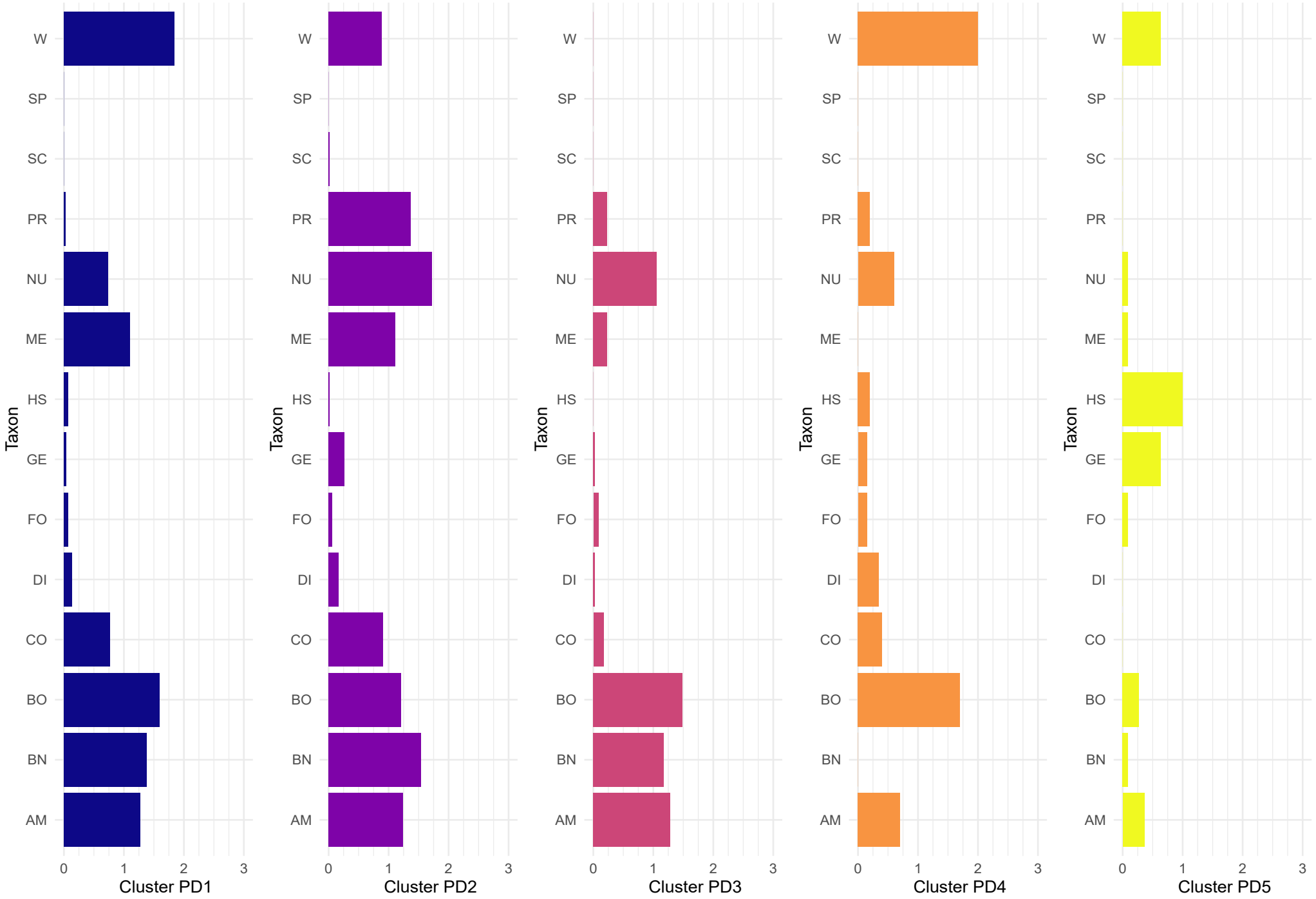
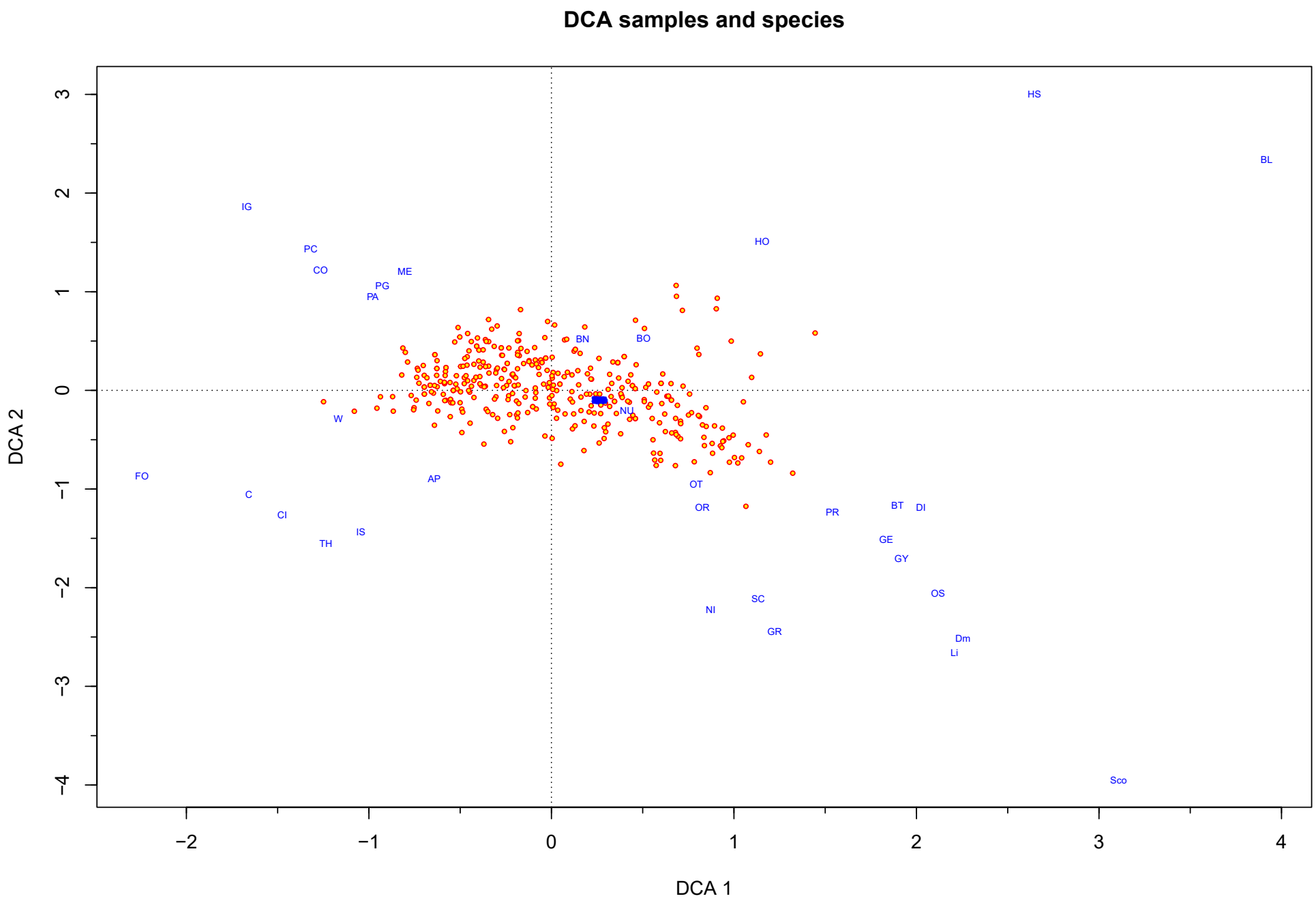
Taxon


Taxon
W
SP
SC
PR
NU
ME
HS
GE
FO
DI
CO
BO
BN
AM
0
1
2
3
Cluster PD1
Cluster PD2
Cluster PD3
Cluster PD4
Cluster PD5

Warlingham (WH)


DCA samples and species
DCA 1
DCA 2
HS
BL
IG
HO
PC
CO
ME
PG
PA
BN
BO
NU
W
FO
AP
OT
C
OR
PR
BT
DI
CI
IS
TH
GE
GY
OS
SC
NI
GR
Dm
Li
Sco
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−1
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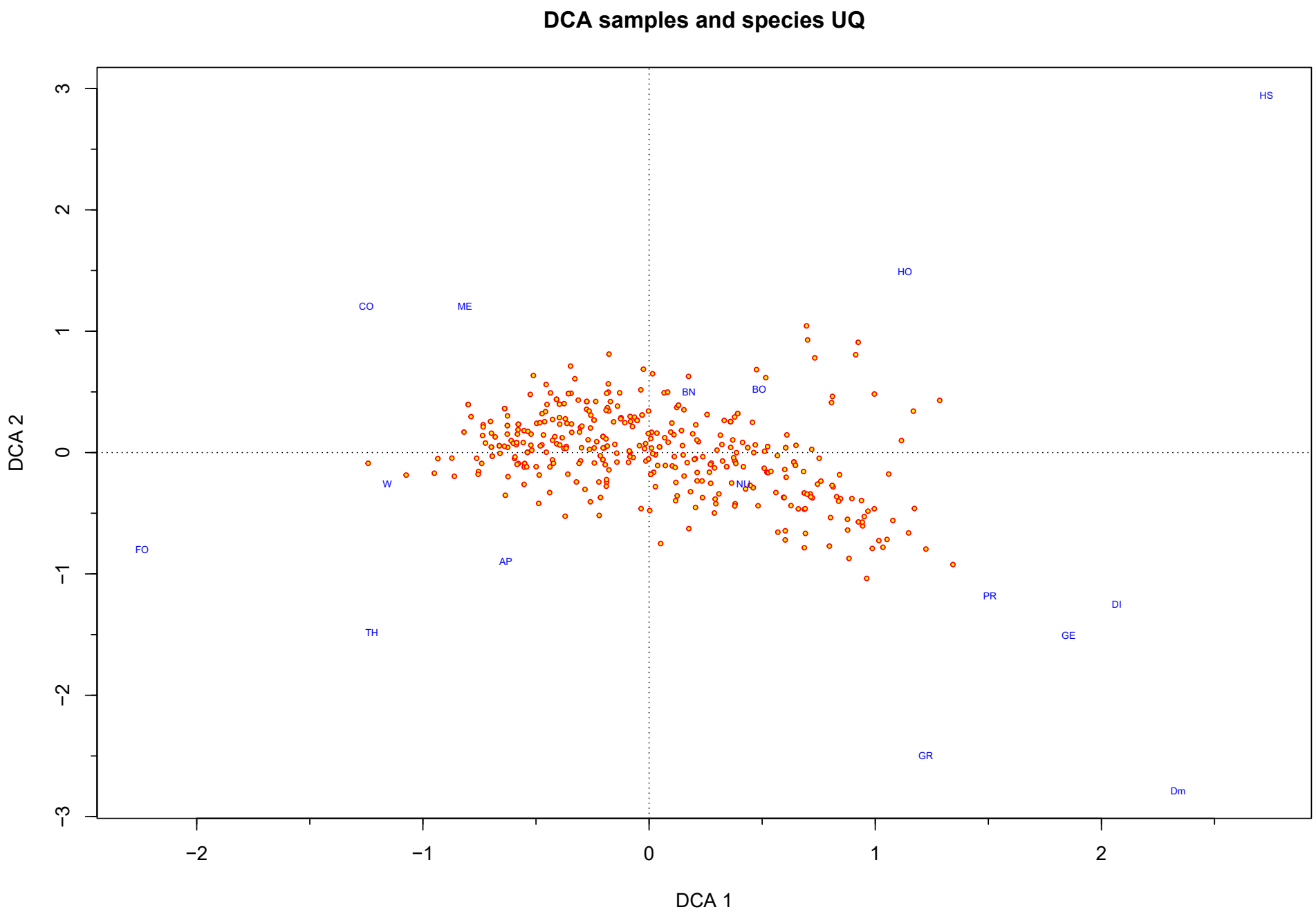
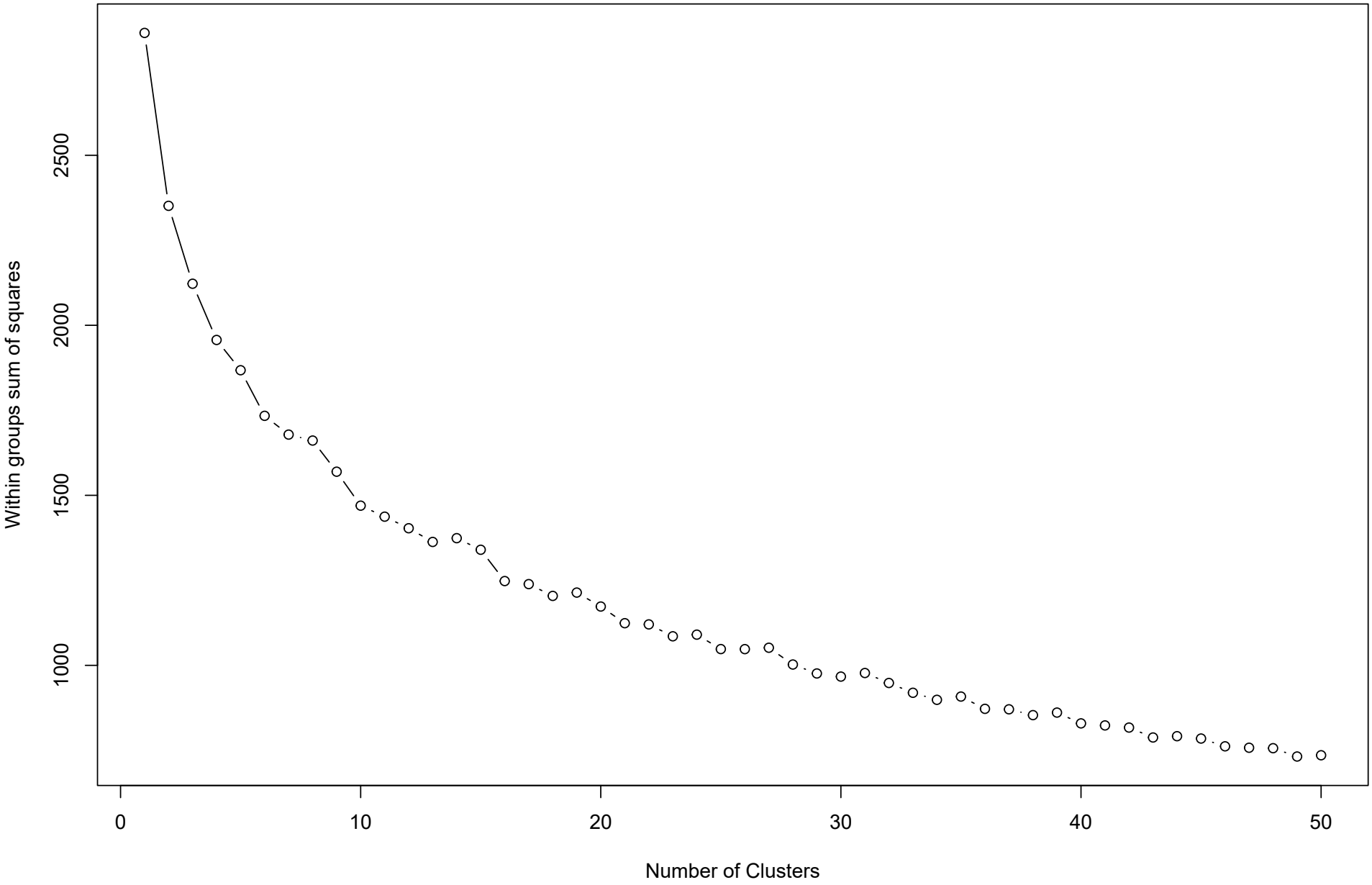
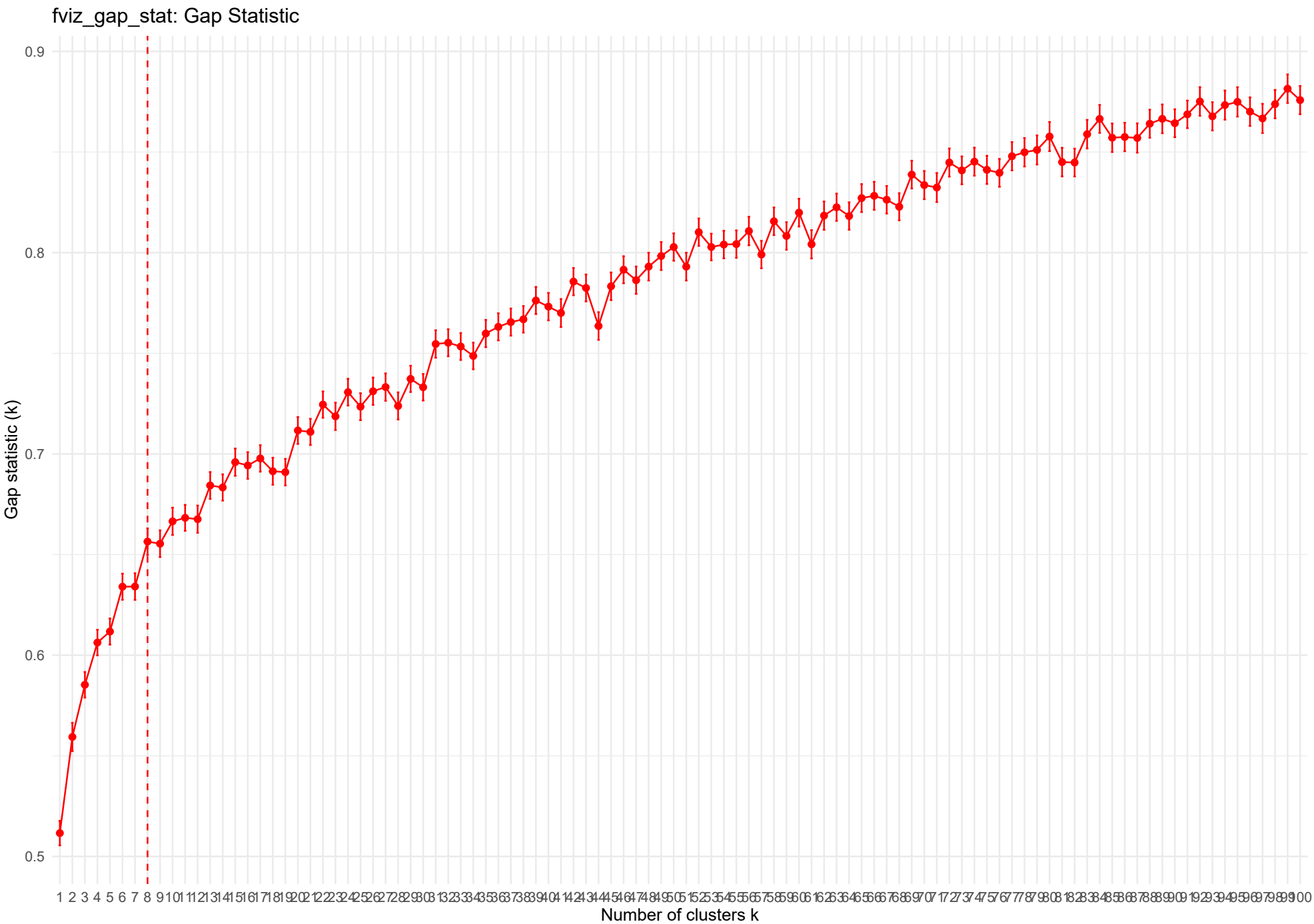
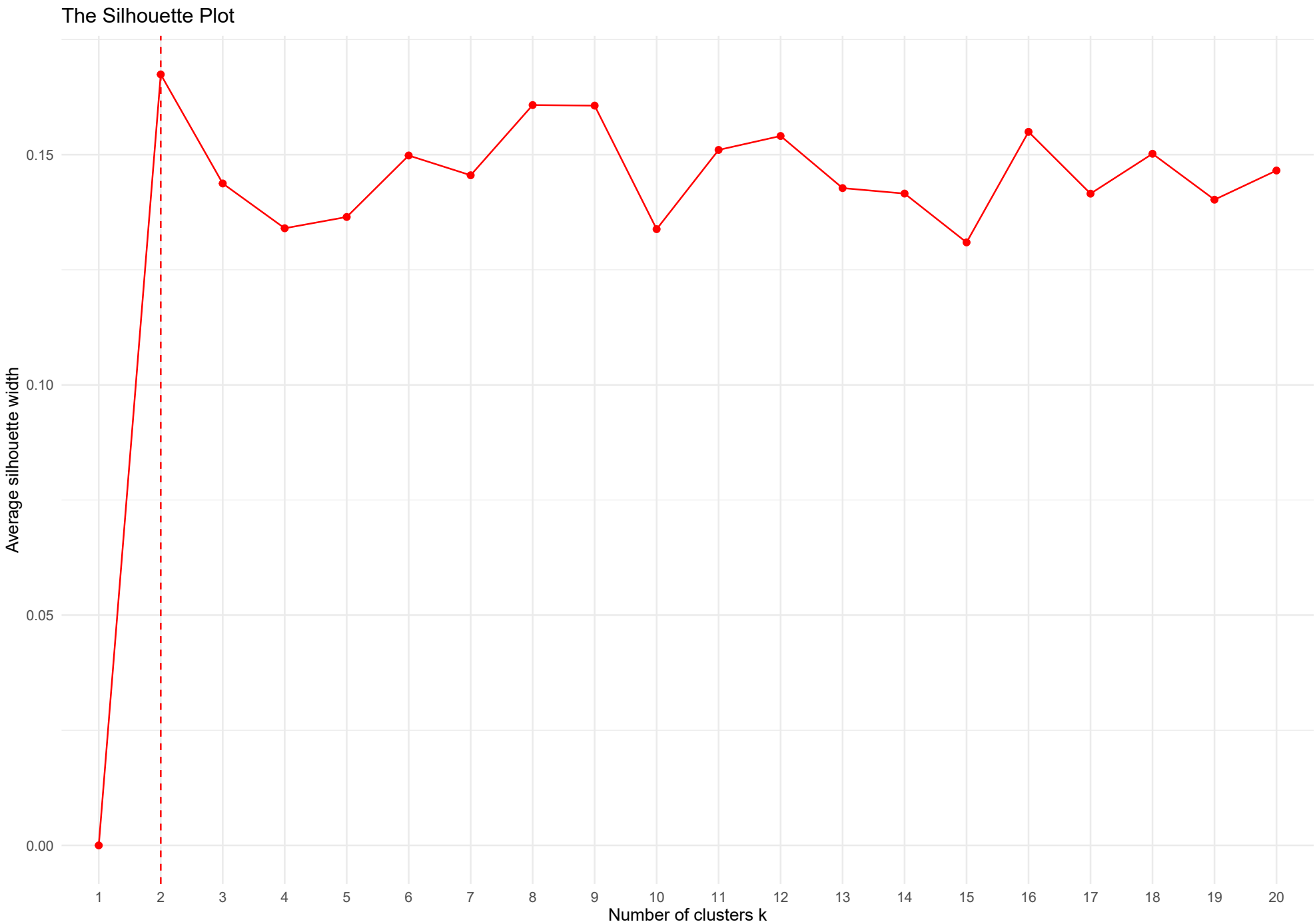
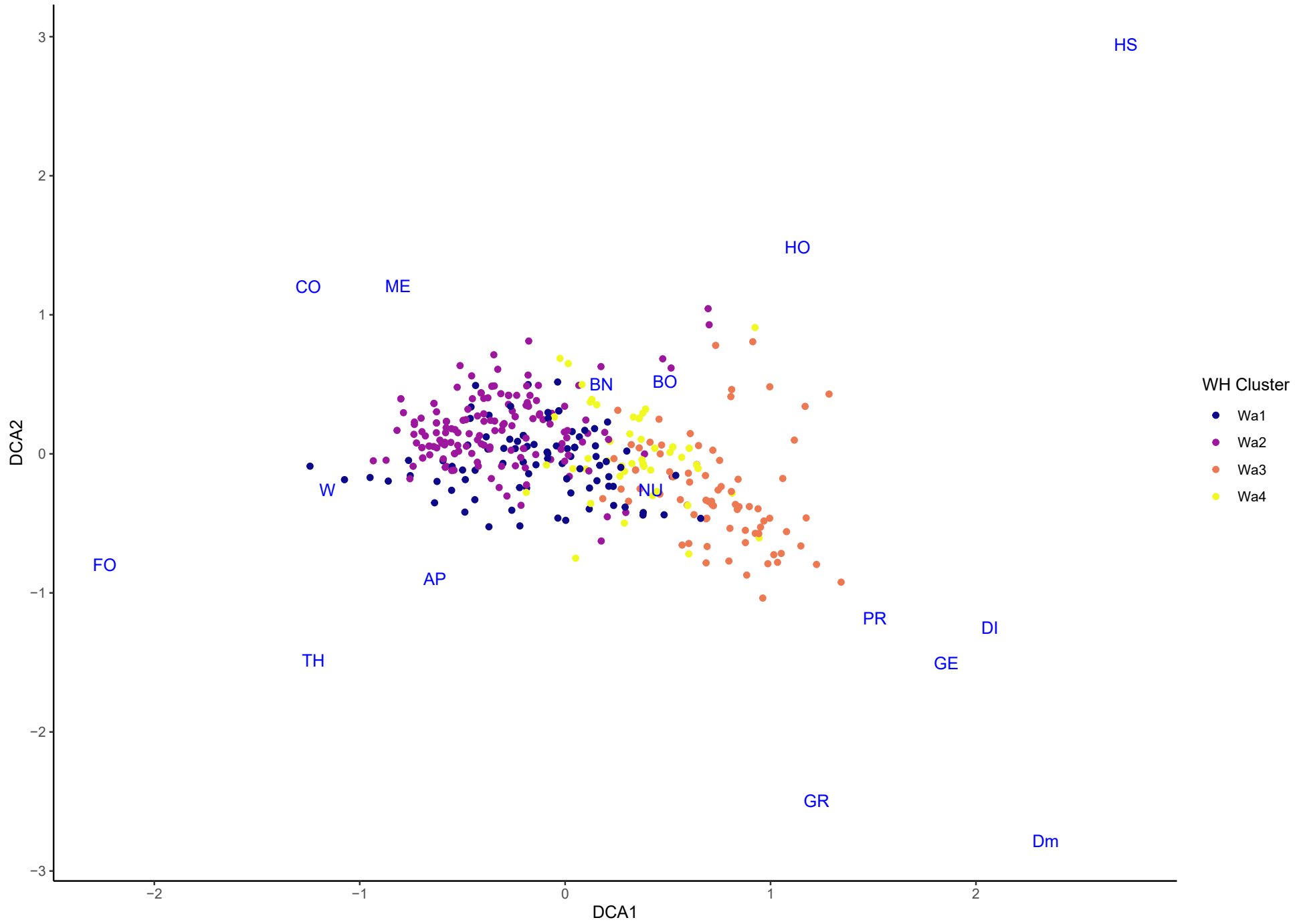
1
2
3
4
−4
−3
−2
−1
0
1
2
3


DCA samples and species UQ
HS
HO
CO
ME
BN
BO
W
NU
FO
AP
PR
DI
TH
GE
GR
Dm
DCA 2
DCA 1
3
2
1
0
−1
−2
−3
−2
−1
0
1
2

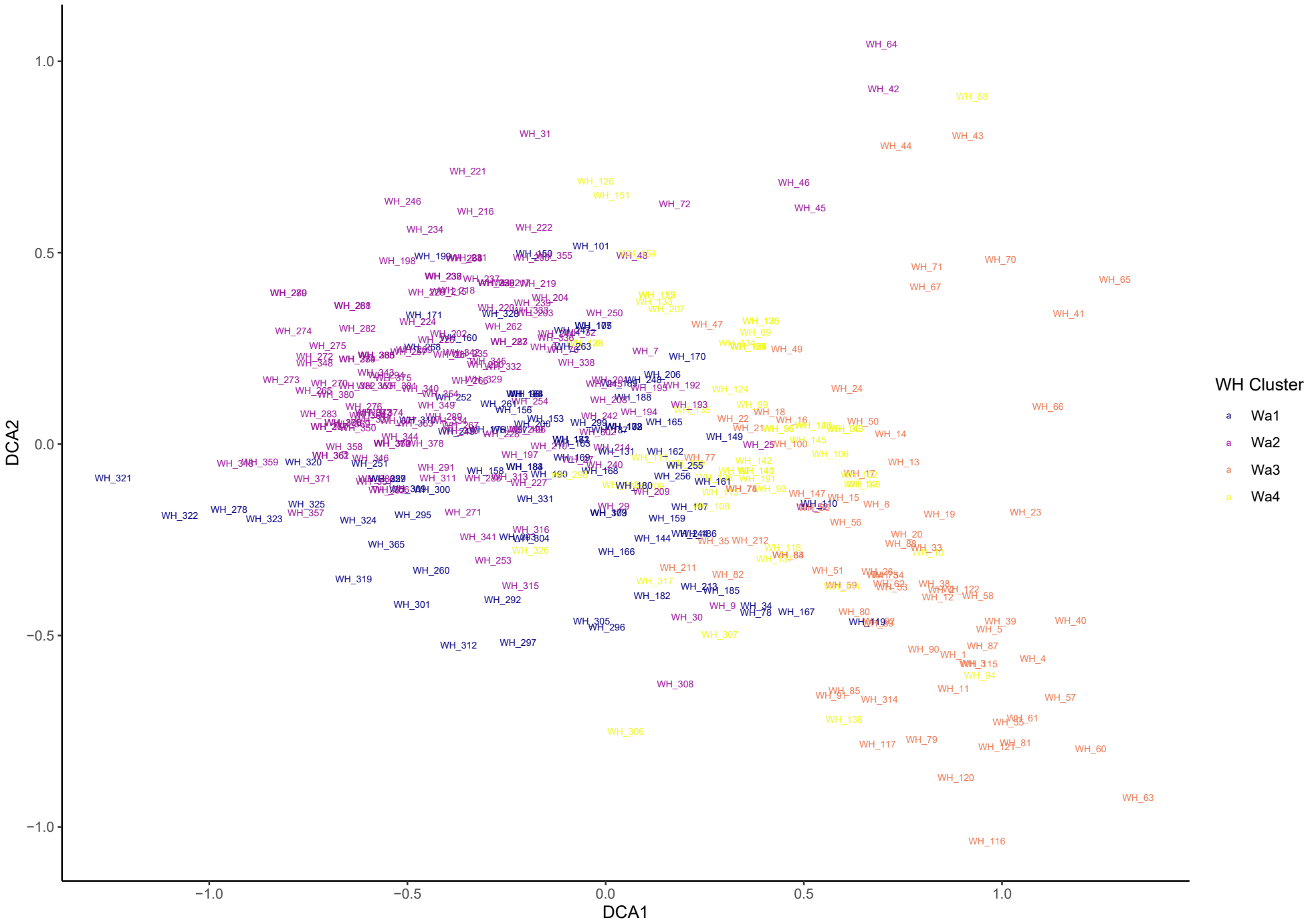

Within groups sum of squares
1000
1500
2000
2500
0
10
20
30
40
50
Number of Clusters


fviz_gap_stat: Gap Statistic
Gap statistic (k)
0.9
0.8
0.7
0.6
0.5
Number of clusters k


The Silhouette Plot
Average silhouette width
0.00
0.05
0.10
0.15
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
Number of clusters k



Warlingham (WH)


DCA2
DCA1
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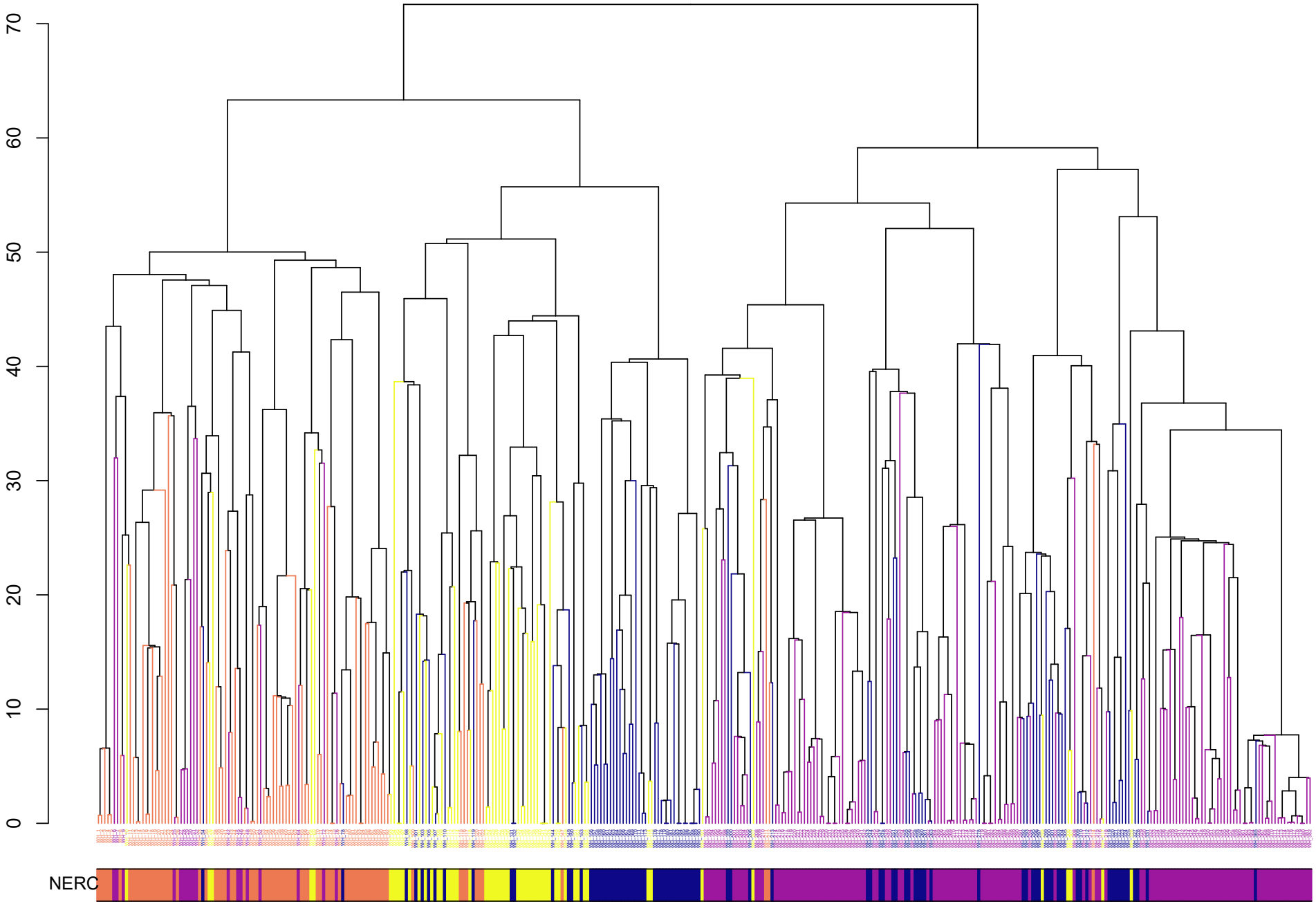
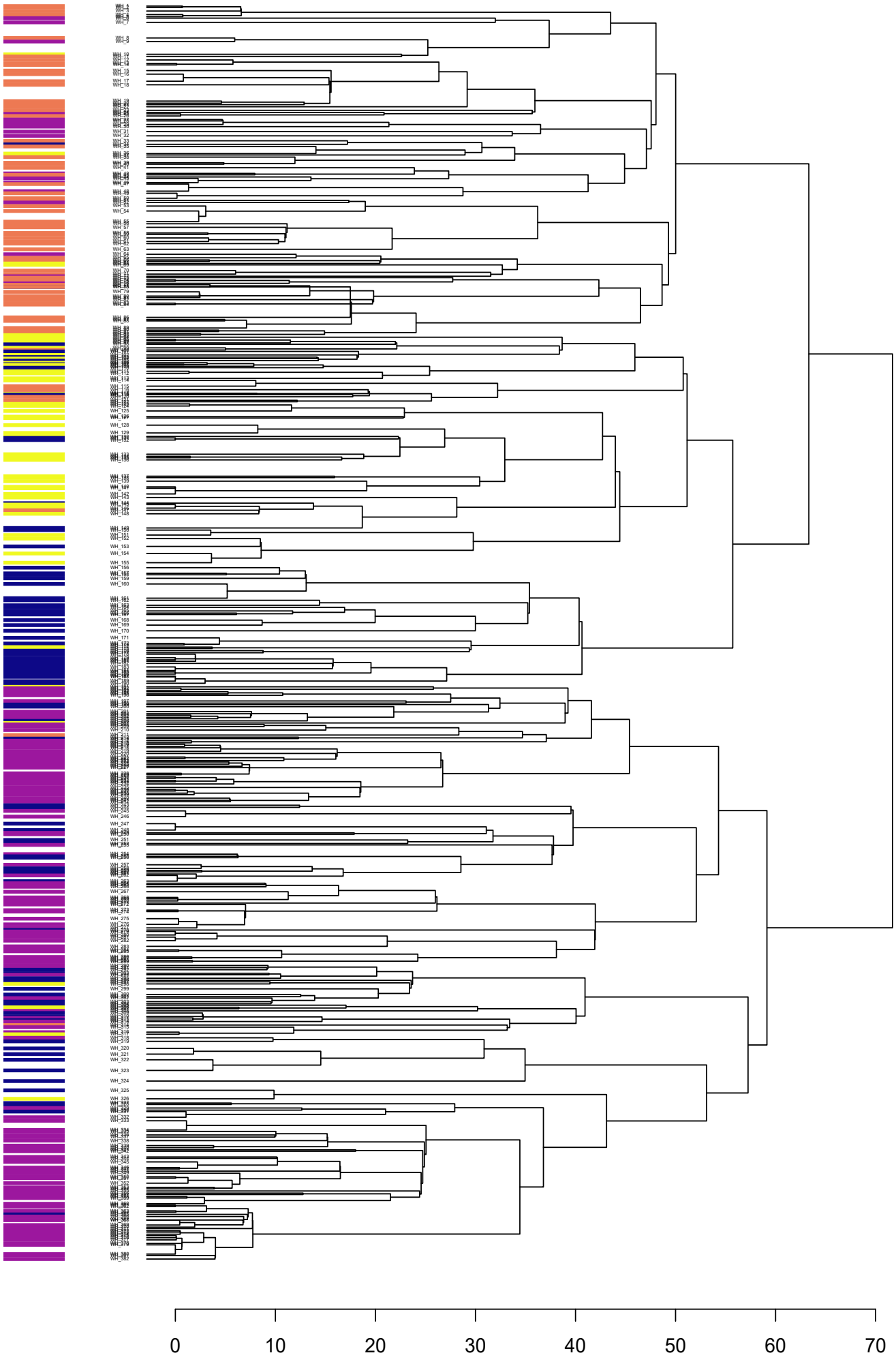
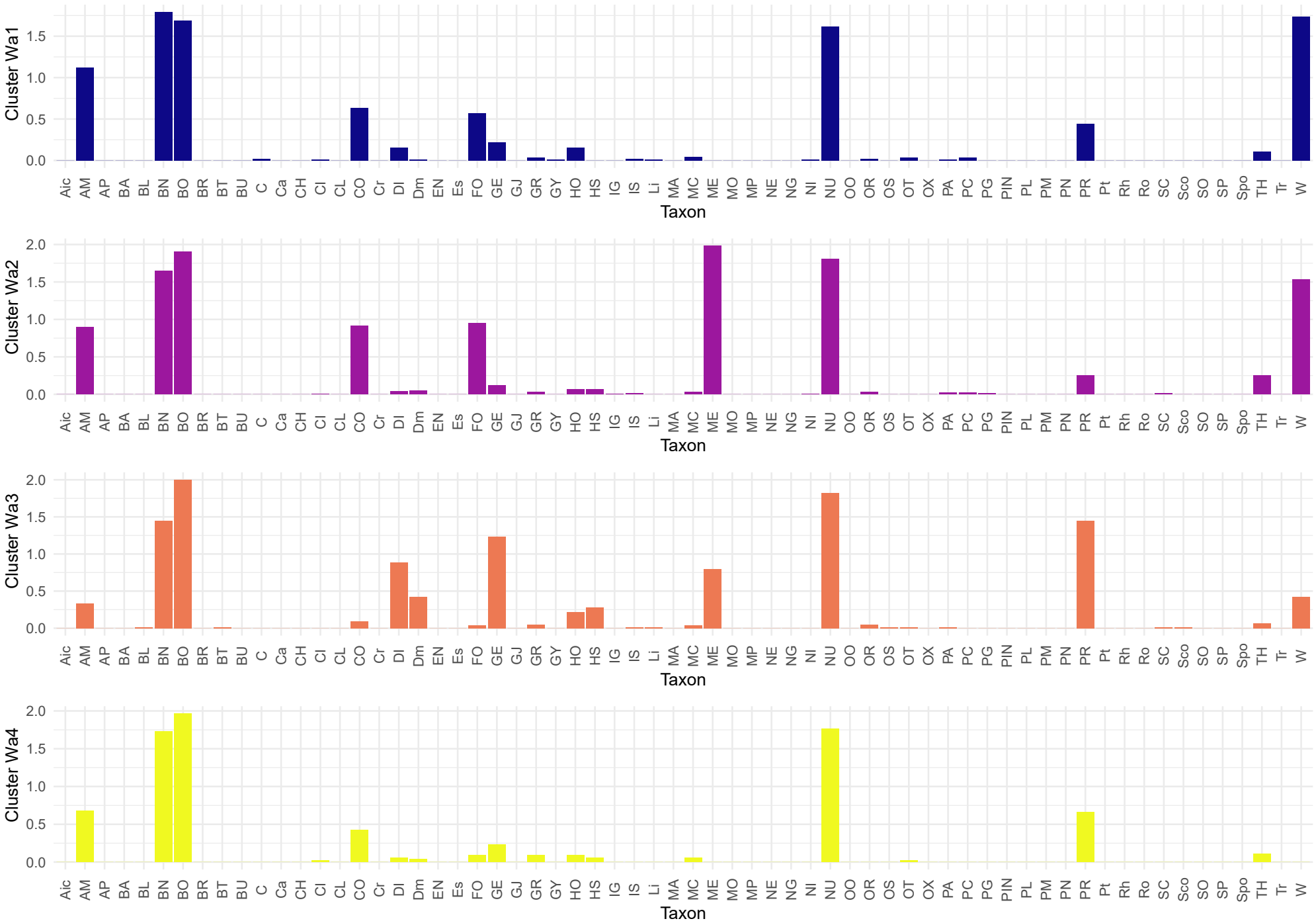
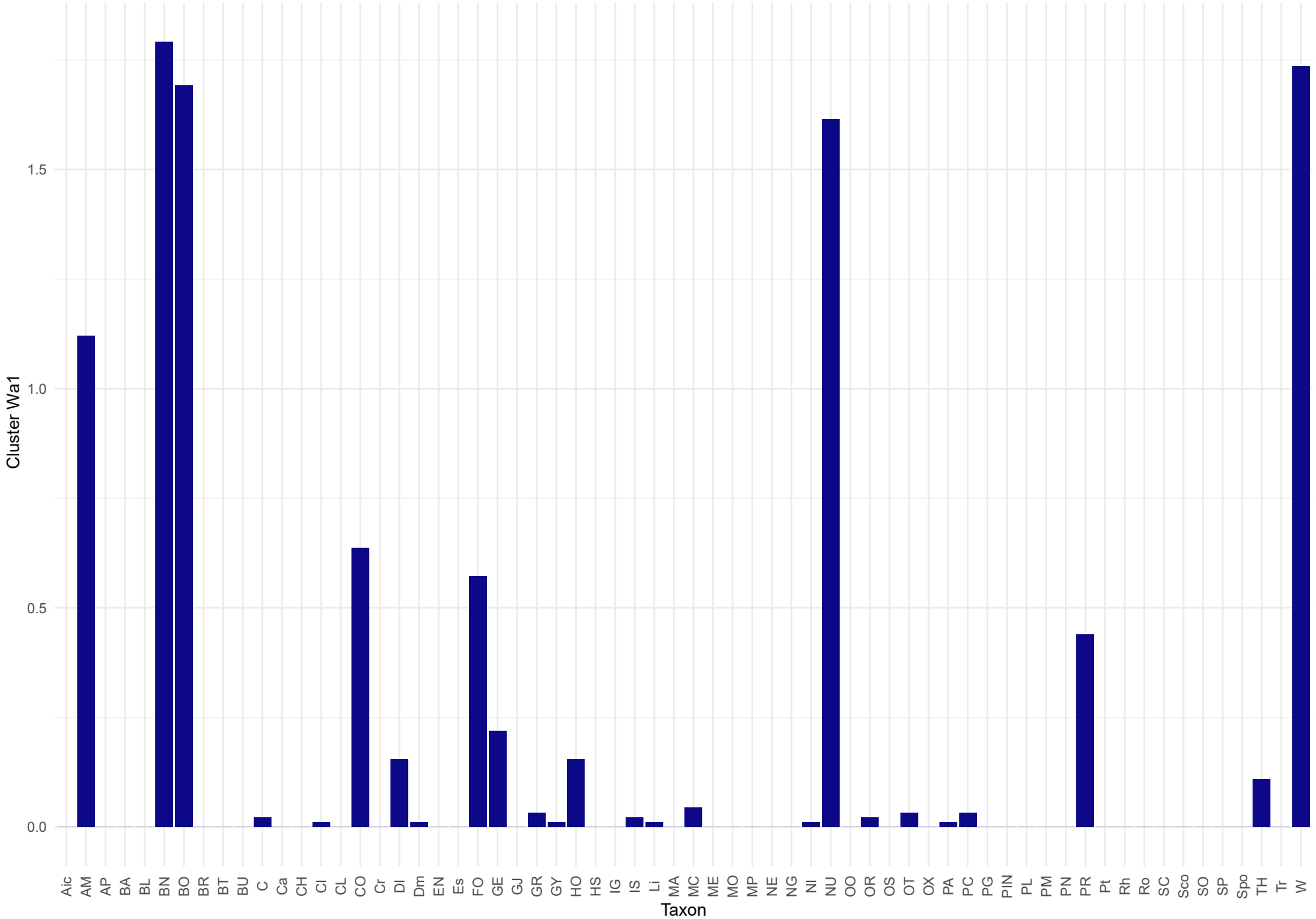
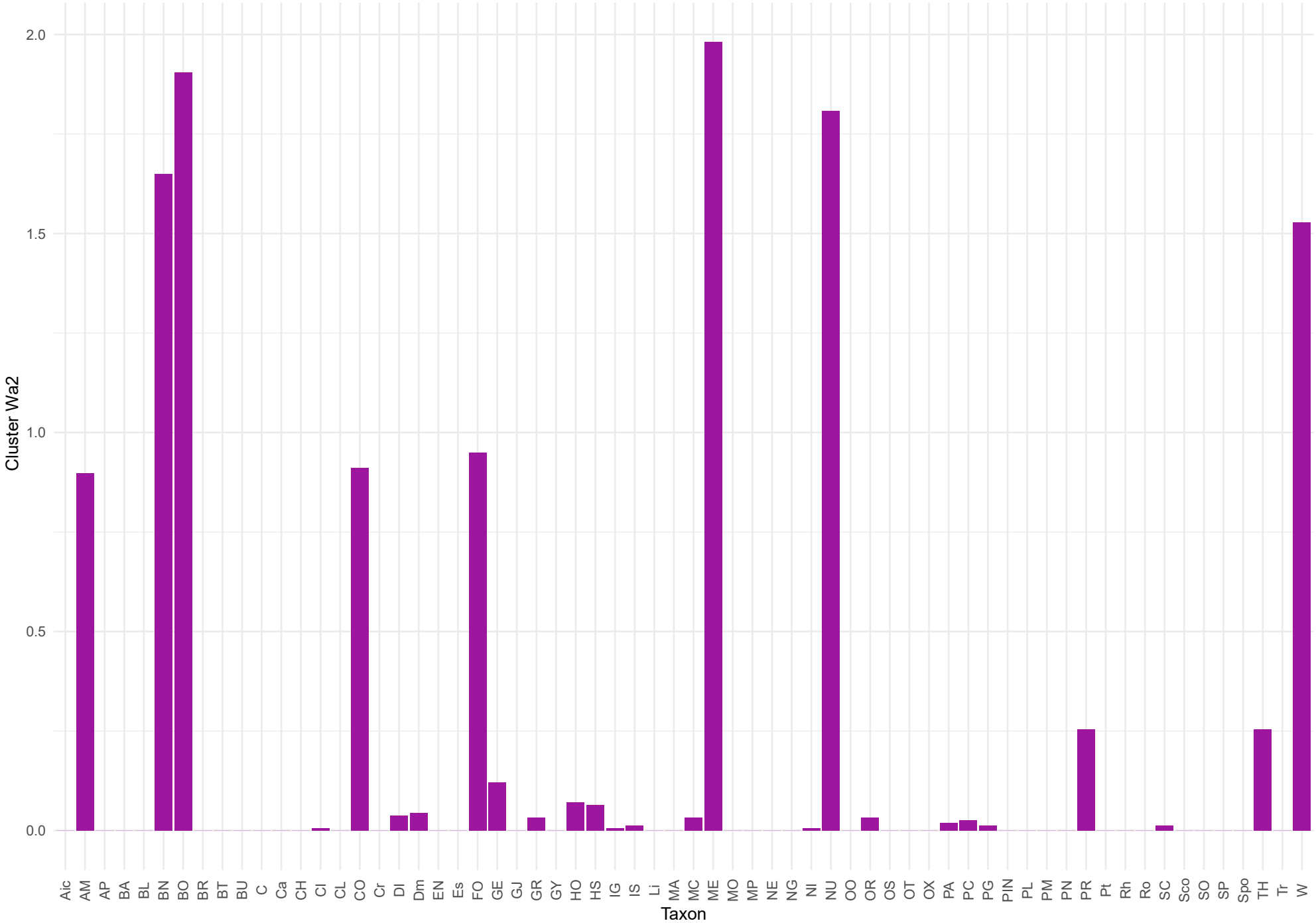
0.5
0.0
−0.5
−1.0
WH Cluster
Wa1
Wa2
Wa3
Wa4

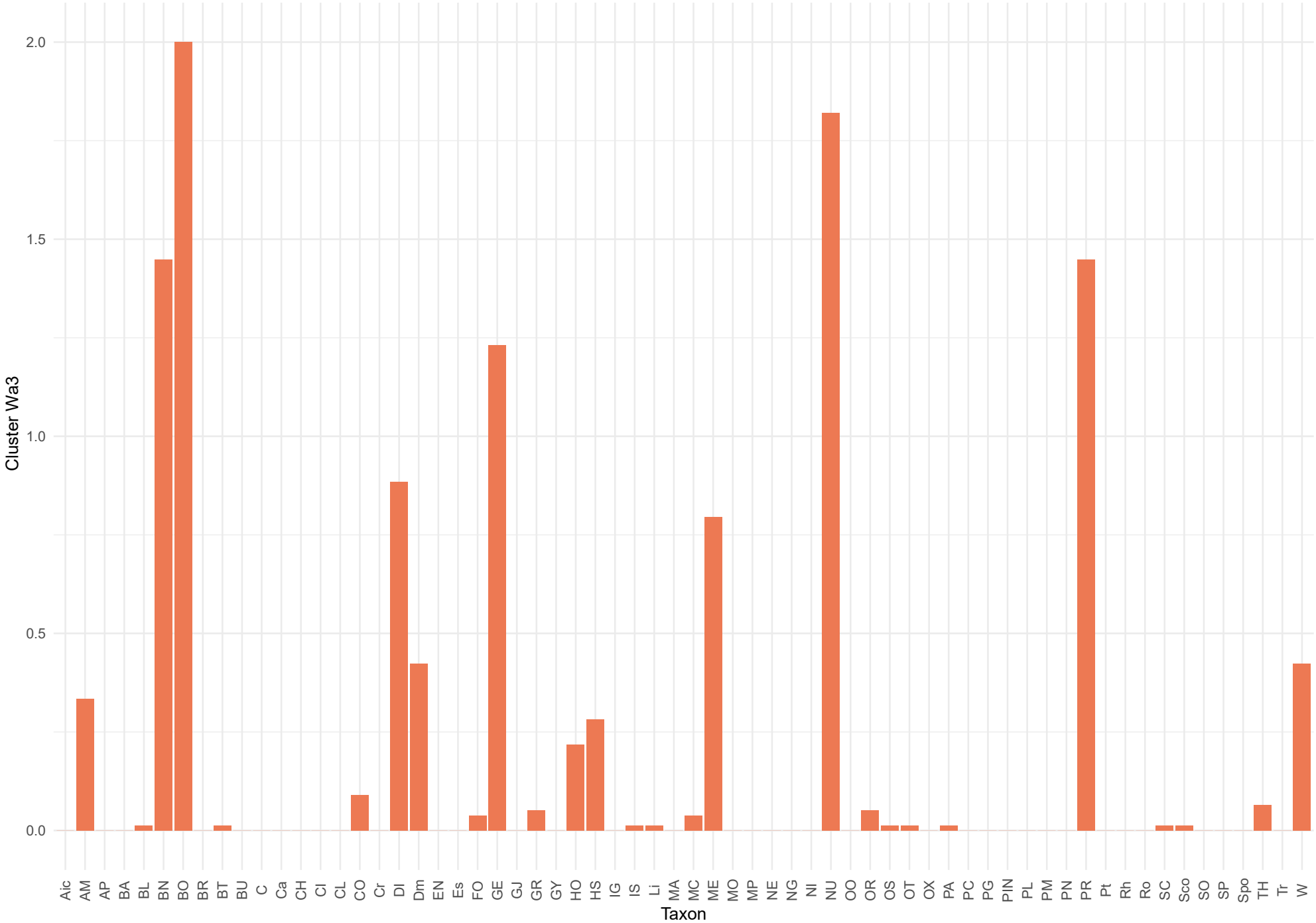

70
60
50
40
30
20
10
0
NERC

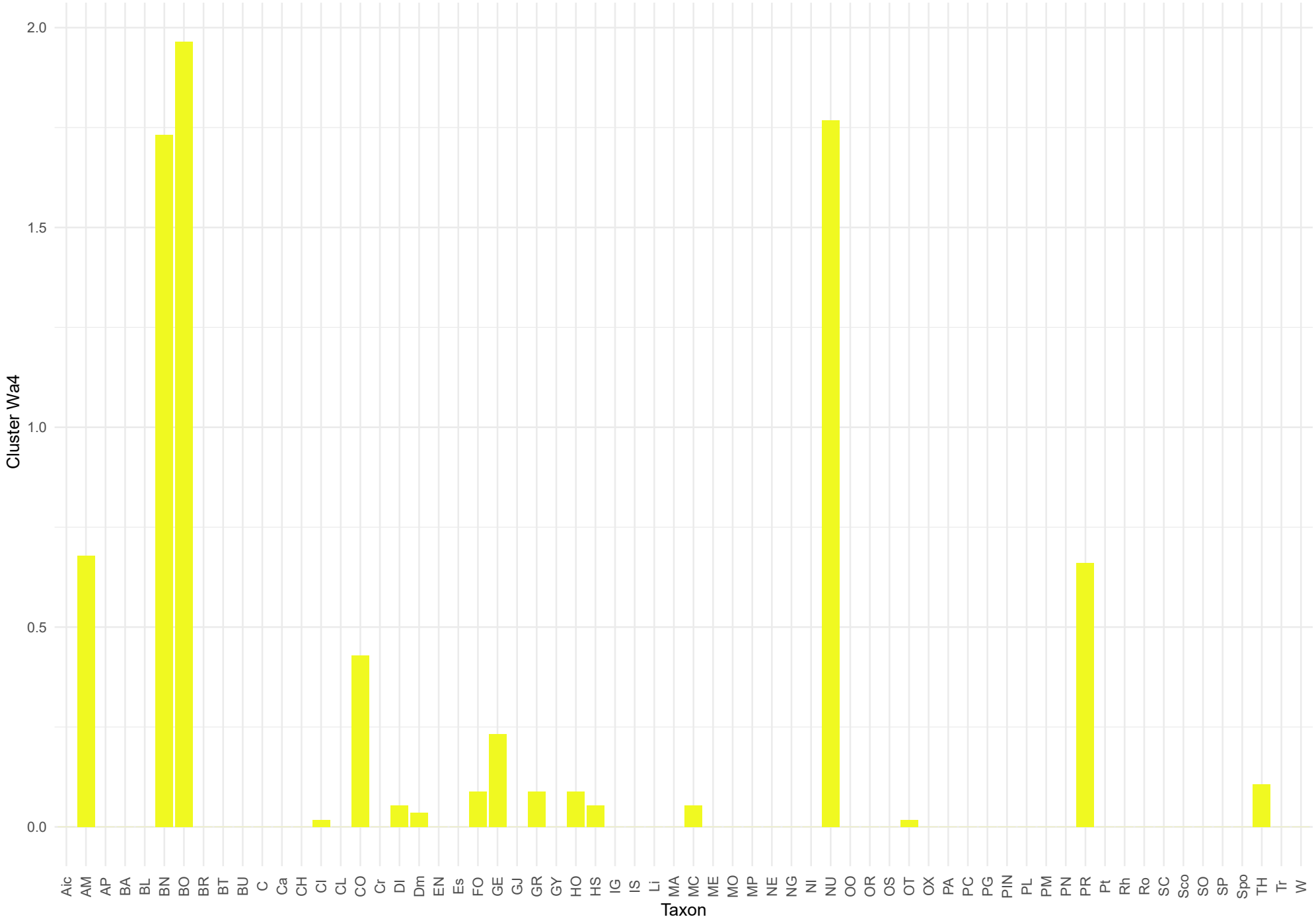

0
10
20
30
40
50
60
70

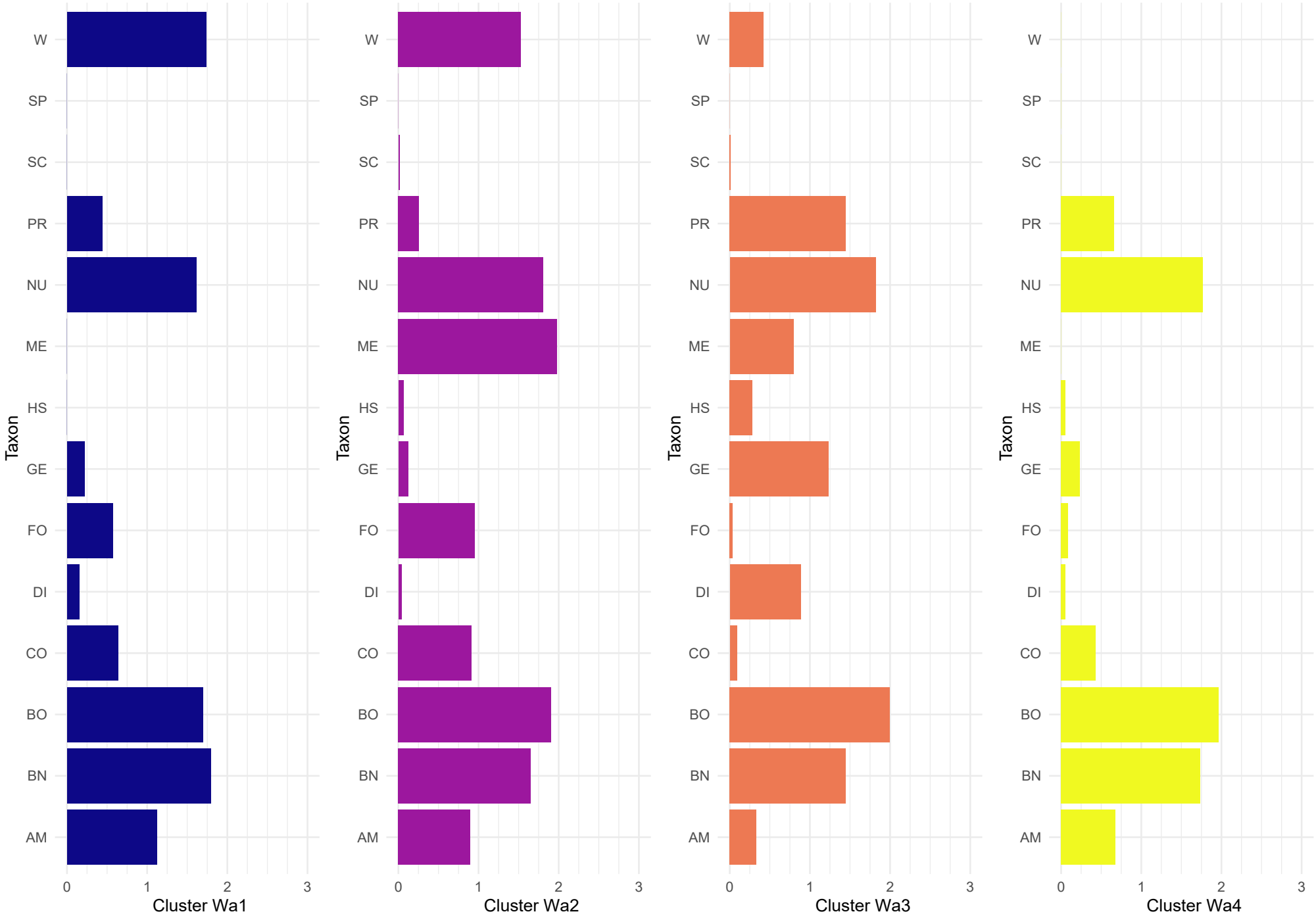

Cluster Wa1
Cluster Wa2
Cluster Wa3
Cluster Wa4
0.0
0.5
1.0
1.5
2.0
Aic AM AP BA BL BN BO BR BT BU C Ca CH Cl CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon


Cluster Wa1
0.0
0.5
1.0
1.5
Aic
AM
AP
BA
BL
BN
BO
BR
BT
BU
C
Ca
CH
Cl
CL
CO
Cr
DI
Dm
EN
Es
FO
GE
GJ
GR
GY
HO
HS
IG
IS
Li
MA
MC
ME
MO
MP
NE
NG
NI
NU
OO
OR
OS
OT
OX
PA
PC
PG
PIN
PL
PM
PN
PR
Pt
Rh
Ro
SC
Sco
SO
SP
Spo
TH
Tr
W
Taxon


Cluster Wa2
2.0
1.5
1.0
0.5
0.0
Aic AM AP BA BL BN BO BR BT BU C Ca CH Cl CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon


Cluster Wa3
2.0
1.5
1.0
0.5
0.0
Aic AM AP BA BL BN BO BR BT BU C Ca CH CI CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon


Cluster Wa4
2.0
1.5
1.0
0.5
0.0
Aic AM AP BA BL BN BO BR BT BU C Ca CH Cl CL CO Cr DI Dm EN Es FO GE GJ GR GY HO HS IG IS Li MA MC ME MO MP NE NG NI NU OO OR OS OT OX PA PC PG PIN PL PM PN PR Pt Rh Ro SC Sco SO SP Spo TH Tr W
Taxon


Taxon
W
SP
SC
PR
NU
ME
HS
GE
FO
DI
CO
BO
BN
AM
0
1
2
3
Cluster Wa1
Cluster Wa2
Cluster Wa3
Cluster Wa4

Appendix 3 for ‘Rolling back the ‘mudstone blanket’: complex geometric and facies responses to basin architecture in the epicontinental Oxford Clay Formation (Jurassic, UK)’

Statistical analysis of the Duff (1975) dataset on samples from four outcrops of the Oxford Clay Formation.

Contents

Locations 3
Palaeontological Data 3
Statistical analysis: procedure 3
Data Analysis 4

Script 1: Duff_EDA 4
Script 2: Duff_DCA_Local 4
Script 3: Duff_Number of clusters 5

Data manipulation 5

Script 4: Duff_NERC_UQ 5
Script 5: DCA analysis using the upper quartile taxa 6
Script 6 hierarchical clustering 6

Results 6
References 7

Bletchley (BL) 8
Calvert (CA) 25
Norman Cross (NC) 42
Stewartby (ST) 60

Locations

The four sample locations of Duff (1975) are listed in Table S.1 alongside their code used throughout this document.

Table S.1: Location codes

Borehole	Code
Bletchley	BL
Calvert	CA
Norman Cross	NC
Stewartby	ST

Palaeontological Data

Duff (1975) provided relative abundance data of some 44 taxa. The faunal codes for the taxa recognized by Duff (1975) and the codes for the zones and subzones are described in Appendix 1. Note that we coordinated the faunal codes with the data from the nine newly studied boreholes.

Other notes on the palaeontological data:

1. AP and AM were combined and listed as “AM” (= AP +AM).
2. Data sheets were separated on the basis of locality: Stewartby, Norman Cross, Calvert and Bletchley
3. Almost none of the relative abundances in the original data added up to 100.0/sample
4. Four samples in Stewartby with only P/A data were removed (4, 5, 6D and 11)
5. P’s often occurred in merged cells. These were unmerged and P’s placed in all of them
6. P? was replaced with P
7. All P’s were replaced with 0.01 (order of magnitude smaller than lowest recorded occurrence)
8. Merged both species of *Dicroloma* together. Same for *Pleuromya*
9. PRa = ?*Praecoria*; QU = *Quenstedtia*; SE = Serpulid; OP = Ophiuroid
10. GR = *Cucullaea clathrate* + *Grammatodon concinnum*
11. MS = *Mecochirus* ; TE = Terebratulid
12. AM = Kosmoceratids + Hecticoceratids + *Erymnoceras* + Perisphinctids + *Longaeviceras* + *Choffatia* + Reineckeids + carinate ammonite
13. AR = Arcid (in Bletchley only).
14. Samples with exclusively P/A data were removed from the dataset

There were a number of samples with a ‘plaster’ denomination, mostly for *Meleagrinella*. In the nine newly investigated cores, plastered surfaces were given a score of 3, which is 25% over the second most abundant score. The same rule was applied to the Duff samples. For samples that contained a ‘plaster’ of a species, 25% was added to the highest relative abundance. In the subsequent statistical analyses, all scores are recalculated to 100%. The samples with ‘plaster’ are:

1. Stewartby: 14B, 14D, 14F and 14H for *Meleagrinella*.
2. Norman Cross: 26, 28, 31, 34
3. Calvert: 10L, 10N, 10R for ME
4. Bletchley: NU and MC in 14; ME in 17D and 17F

Statistical analysis: procedure

All the statistical analyses were performed in the open source environment R (R Development Core

Team, 2020). Six scripts were written to perform the necessary transformations to produce the figures following this introduction. These six scripts use functions from the following R packages: *Hmisc* (v4.4-1; Harrell, 2020), *vegan* (v2.5-6; Oksanen et al., 2020), *rioja* (v0.9-21; Juggins, 2017), *tidyverse* (Wickham et al., 2019), *fossil* (v0.4.0; Vavrek, 2011), *ecodist* (v2.0.7; Goslee and Urban, 2007), *cluster* (v2.1.0; Maechler et al., 2019), *NbClust* (v3.0; Charrad et al., 2014), *dendextend* (v1.14.0; Galili, 2015), and *factoextra* (v1.0.7; Kassambra and Mundt, 2020).

The six scripts perform specific tasks in the statistical workflow. The ultimate aim of the statistical analysis in the current study is twofold:

1. Understand the pattern of biofacies for each borehole (and the extent to which biofacies successions for individual boreholes can be merged into a unified set of biofacies for all the boreholes).
2. Understand how zones / subzones vary or are similar between borehole locations – this is reflected in the biofacies patterns for those zones / ubzones.

The workflow is divided into three stages: data acquisition, data manipulation and interpretation. Appendix 1 focuses on the first two stages for the nine UK boreholes where extra data was acquired which lay the foundation for the interpretation discussed in the main text. We are focusing on each borehole separately to fulfil goal 1: visualizing and interpreting the changes in biofacies in each borehole to understand the palaeo-ecological changes.

Data Analysis

For the analysis of the Duff (1975) data, we used 7 different scripts in the R environment, summarized below.

Script 1: Duff_EDA

This script performs the pre-processing analysis of the data (EDA = exploratory data analysis) and can be summarized as follows:

1. The pre-screened (see above) data for the four localities was loaded and combined into one table.
2. All generated NA's (not available) were replaced with zeros ('missing taxa' should be replaced with zeros for subsequent calculation).
3. All data was recalculated as relative abundances (to account for the conversion of plastered surfaces etc., see above).
4. Nuculaceans and Mesosacellas were combined: NU = NU + MC
5. AM groups all the ammonites
6. Biozonation data was loaded and added
7. All data was exported per location

Script 2: Duff_DCA_Local

The script performs an initial DCA to determine the upper quartile taxa that will steer the clustering.
1. Raw counts for a location were loaded.
2. DCA was run for that location.
3. The DCA taxon scores were extracted.
4. The DCA sample scores were extracted.
5. Results were plotted.
6. Eigenvalues were extracted.
7. The upper quartile taxa were determined

Script 3: Duff_Number of clusters

To determine the number of clusters to be utilised in each borehole, we use the NbClust (v3.0; Charrad et al., 2014) package. It draws on >20 methods to perform cluster analysis. The function NbClust performs tests all methods and reaches a conclusion informing the most suggested number of clusters. As an input, this function requires a minimum and maximum number of clusters to consider. We use the 'Elbow' plot in combination with the initial DCA plot to provide that information. The two other methods we relied on for the current analysis are the gap statistic (function clusGap) and the silhouette plot (function fviz_nbclust). Based on these four lines of evidence, we choose an appropriate number of clusters for each borehole.

Data manipulation

Clustering which assumes discontinuities to exist in the dataset which form the basis to recognise discrete groups. This technique is desirable in heterogeneous datasets. The outcome of cluster analysis is a two-dimensional dendrogram. No relationships between the clusters and underlying environmental gradients can be discerned directly, although the clusters may be interpreted as representing communities, biofacies, or faunal provinces.

Ecological **ordination**: the ordering or arrangement of samples and/or variables (taxa) in an ecological space in relation to environmental gradients. Ordination extracts major directions of variation from the original data by rearranging the data points in a multidimensional space so that they are concentrated on the first few, preferably two, principal axes. No assumption of a grouping structure is made, instead, ordinations assume continuity in the data. The outcome is a two-dimensional scatter plot in which the samples and/or variables are located relative to on another according to their variations on these axes. Natural groupings of samples and/or variables are revealed in this way.

We employed three multivariate techniques: two clustering techniques: (Non-Euclidian Relational Clustering (NERC) and hierarchical clustering) and one ordination technique (detrended correspondence analysis (DCA)). NERC is considered to be the most reliable clustering method for palaeontology and palaeobiology datasets because it scores better on incomplete datasets (Vavrek, 2016). However, in the current study we exclusively use borehole data which introduces an inescapable relationship between the samples: a stratigraphical ordering, which assuming the absence of faulting or folding, means an ordering by age. This is typically more easily visualized by dendrograms and therefore we have utilised a combination of both clustering techniques: a dendrogram coloured using the NERC clustering. To better understand the clustering results, we use the same NERC colours for the DCA plots to allow downhole interpretations of palaeoecological changes.

Script 4: Duff_NERC_UQ

Most functions for multivariate analysis require an ecological distance matrix as input, constructed by applying a formula to the raw counts or the semiquantitative scores. We used the Sørenson dissimilarity index (or Dice or coincidence index, Dice, 1945). It is one of the most commonly used indices and is regarded as one of the most effective presence/absence dissimilarity measures (Southwood & Henderson, 2000; Magurran, 2004) and is the recommended input for NERC (Vavrek, 2011).

In the strategy for the nine boreholes described in Appendix 1, we employed the Sørenson index because it is recommended (Legendre and Legendre, 2012) for a dataset consisting of species abundances that are not raw counts without probability levels and it is the recommended index for input in the NERC function of the fossil package (Vavrek, 2011, 2016). For consistency and to allow easy comparison with the results of the nine boreholes, we maintain this strategy for the Duff (1975) dataset.

In R, the Sørenson index is given by the ecol.dist function of the ecodist package. The resulting distance matrix was then used for the rclust function of the fossil package, with the specified number of clusters to be recognized (script 3) to perform the NERC analysis.

1. The raw data for the upper quartile dataset was used.
2. An ecological distance matrix using the Sorenson equation was calculated
3. A NERC function with the number of clusters determined by script 4 was performed.

Script 5: DCA analysis using the upper quartile taxa

Script 1 resulted in an initial DCA plot based on the full dataset for each borehole. However, in many cases interpretations will be made almost impossible because the presence of rare taxa forces the isolation of a few samples, while the majority of samples is packed in one tight cluster. A common technique to avoid skewing the DCA plots, is to consider only the taxa with an upper quartile statistical weight. Using script 1, we subset the original dataset to isolate the upper quartile taxa and ran a DCA analysis using the decorana function of the vegan package. We then coloured the datapoints using the NERC clusters. For each borehole, a figure with only the samples and a figure with samples and taxa is provided.

Script 6 hierarchical clustering

To perform hierarchical clustering, we utilised the hclust function of the rioja package. A dendrogram where the samples are in order and coloured using the NERC clustering with a NERC colour bar is provided.

Results

The following pages, following the references, show the results of the statistical analysis of all the boreholes. The figures provided are:

1. DCA of samples and all taxa.
2. DCA of samples and only upper quartile (UQ) taxa.
3. Elbow plot to determine optimal amount of clusters.
4. Gap statistic plot to help determine the optimal amount of clusters.
5. A silhouette plot to help determine the optimal amount of clusters.
6. A DCA plot of NERC coloured samples and (UQ) taxa.
7. A DCA plot of NERC coloured samples.
8. Dendrogram (hierarchical clustering) with NERC colour bar.
9. Bar chart showing the average cluster compositions.
10. Bar charts of the average cluster composition per cluster.
11. Bar charts of the cluster composition of selected taxa.

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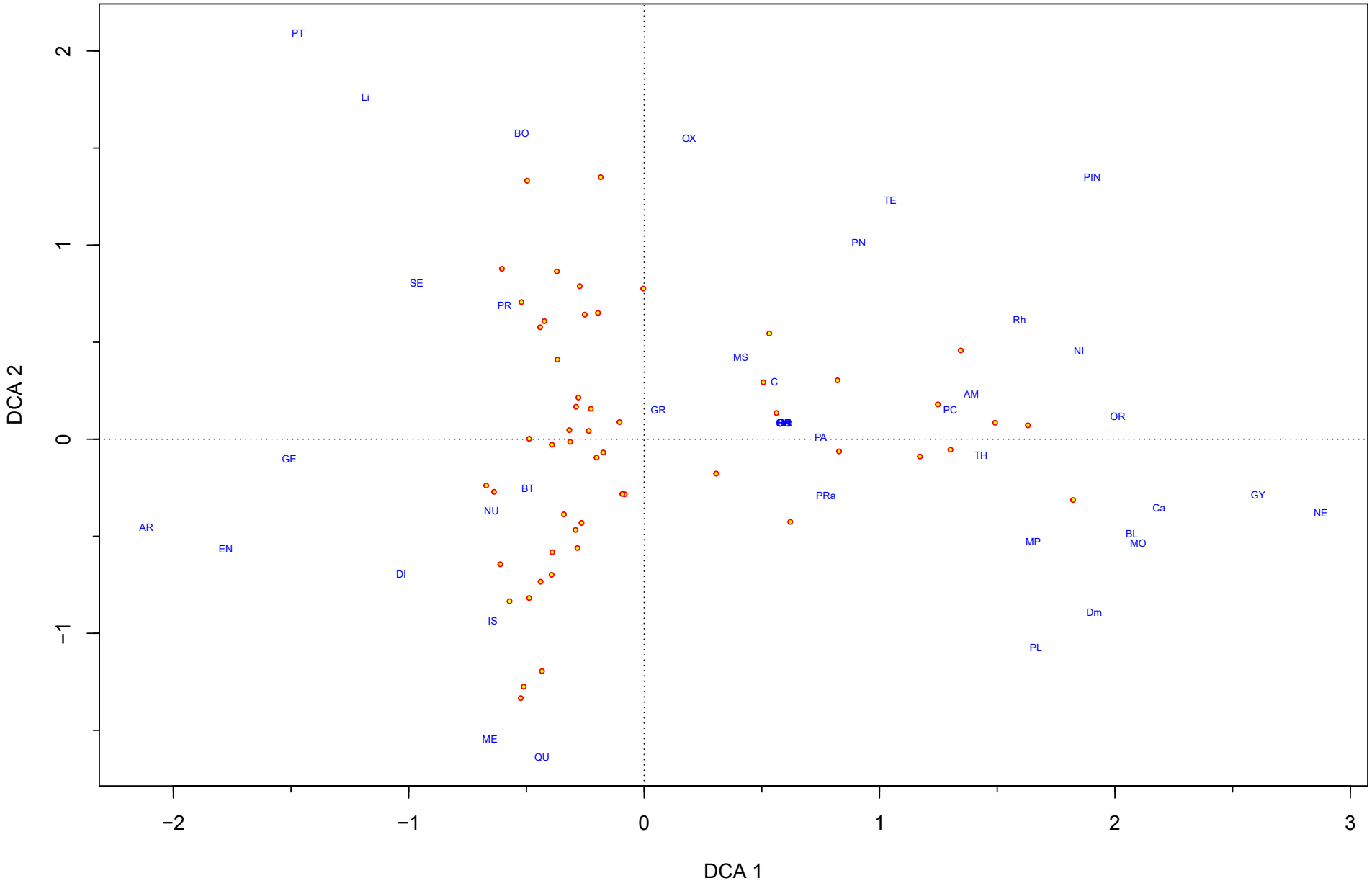
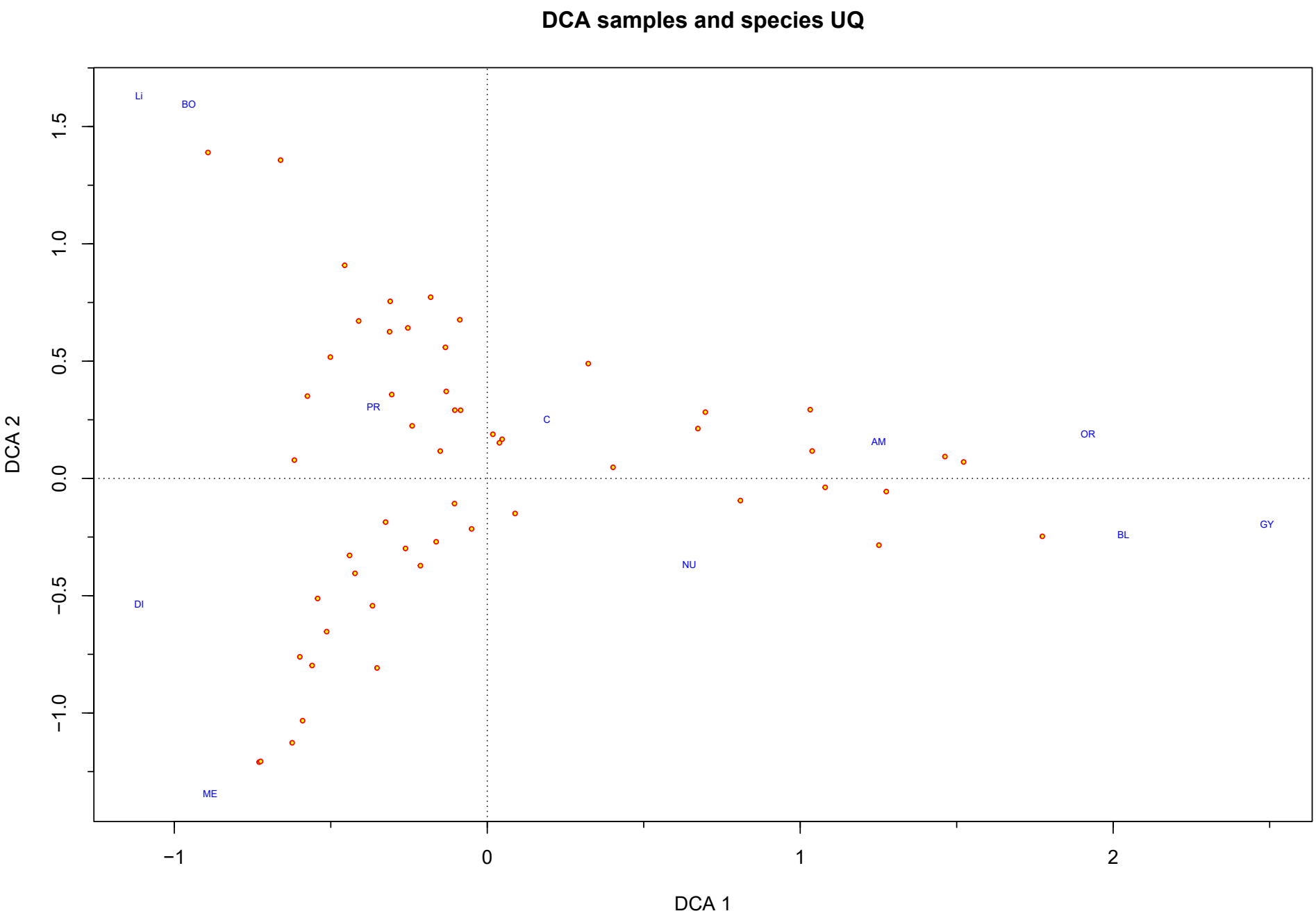
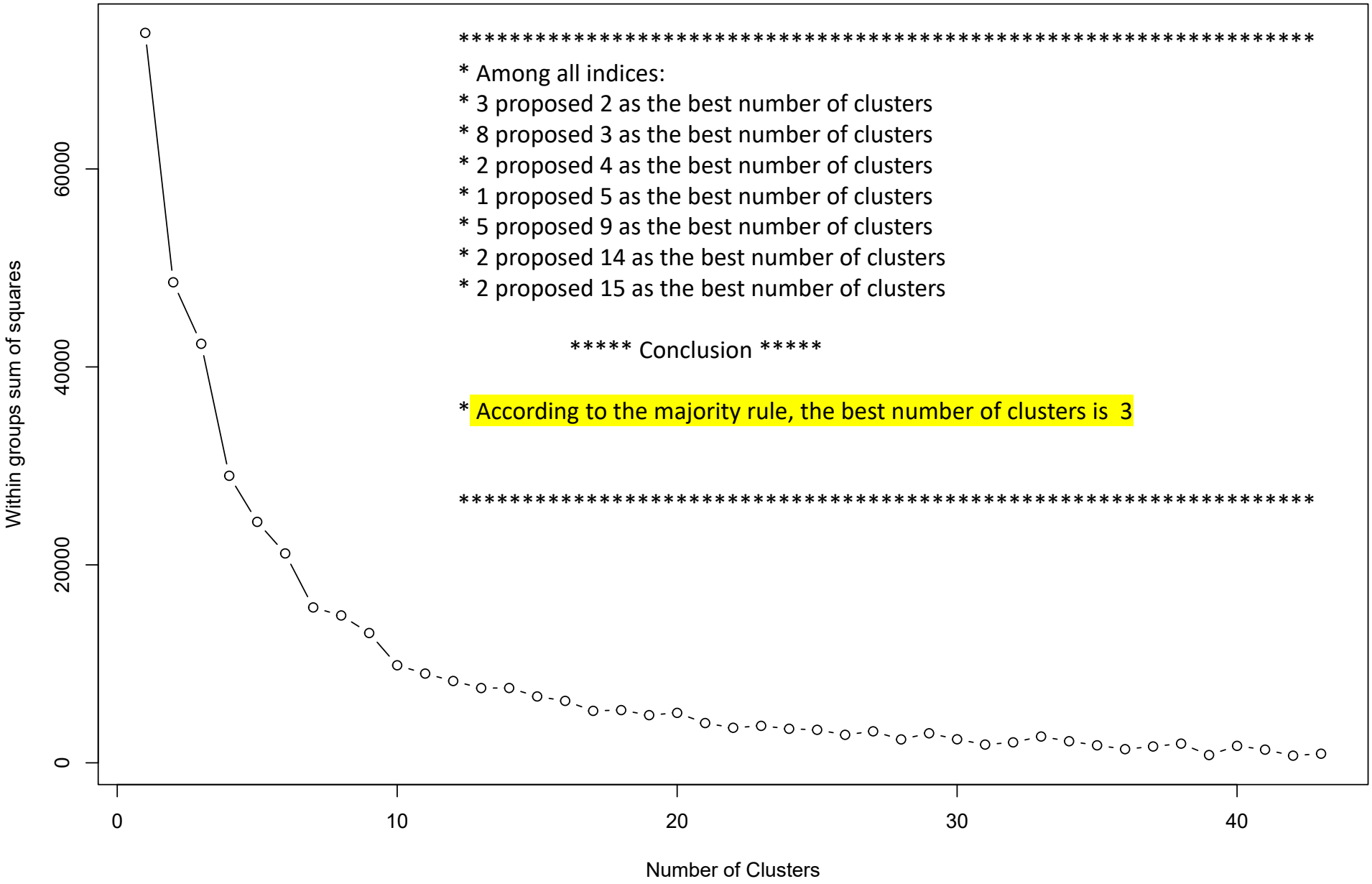
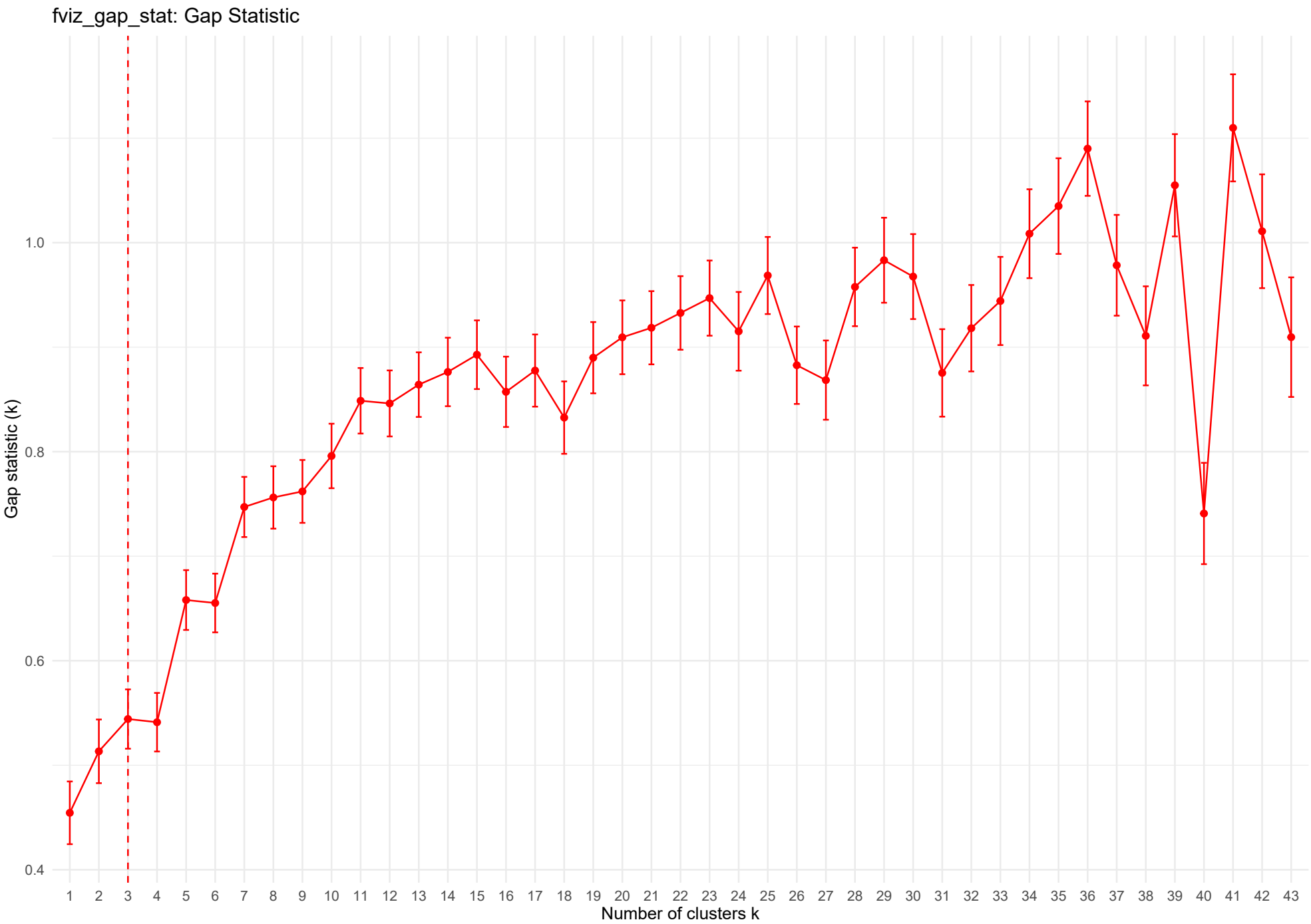
Bletchley (BL)

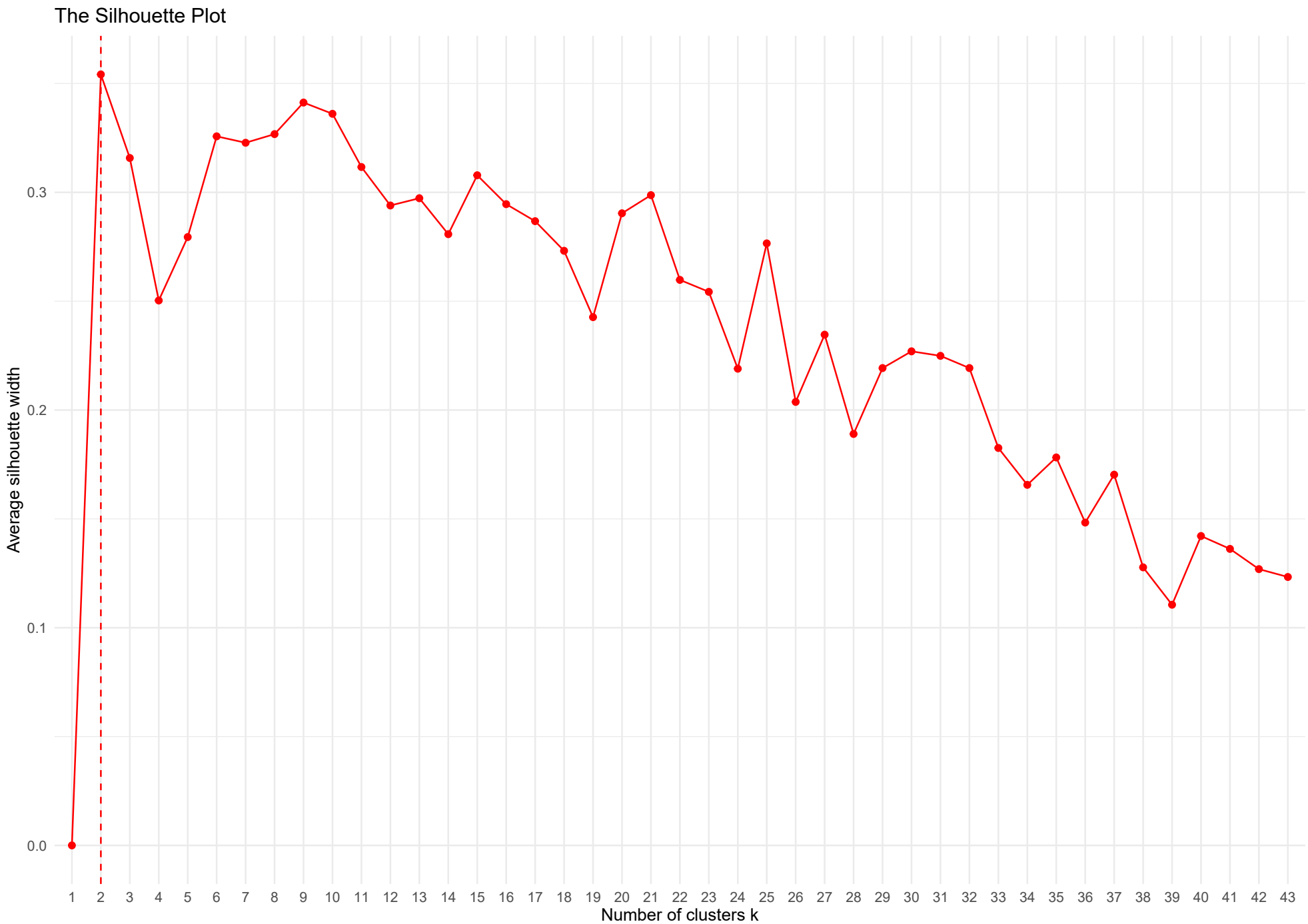
DCA samples and species

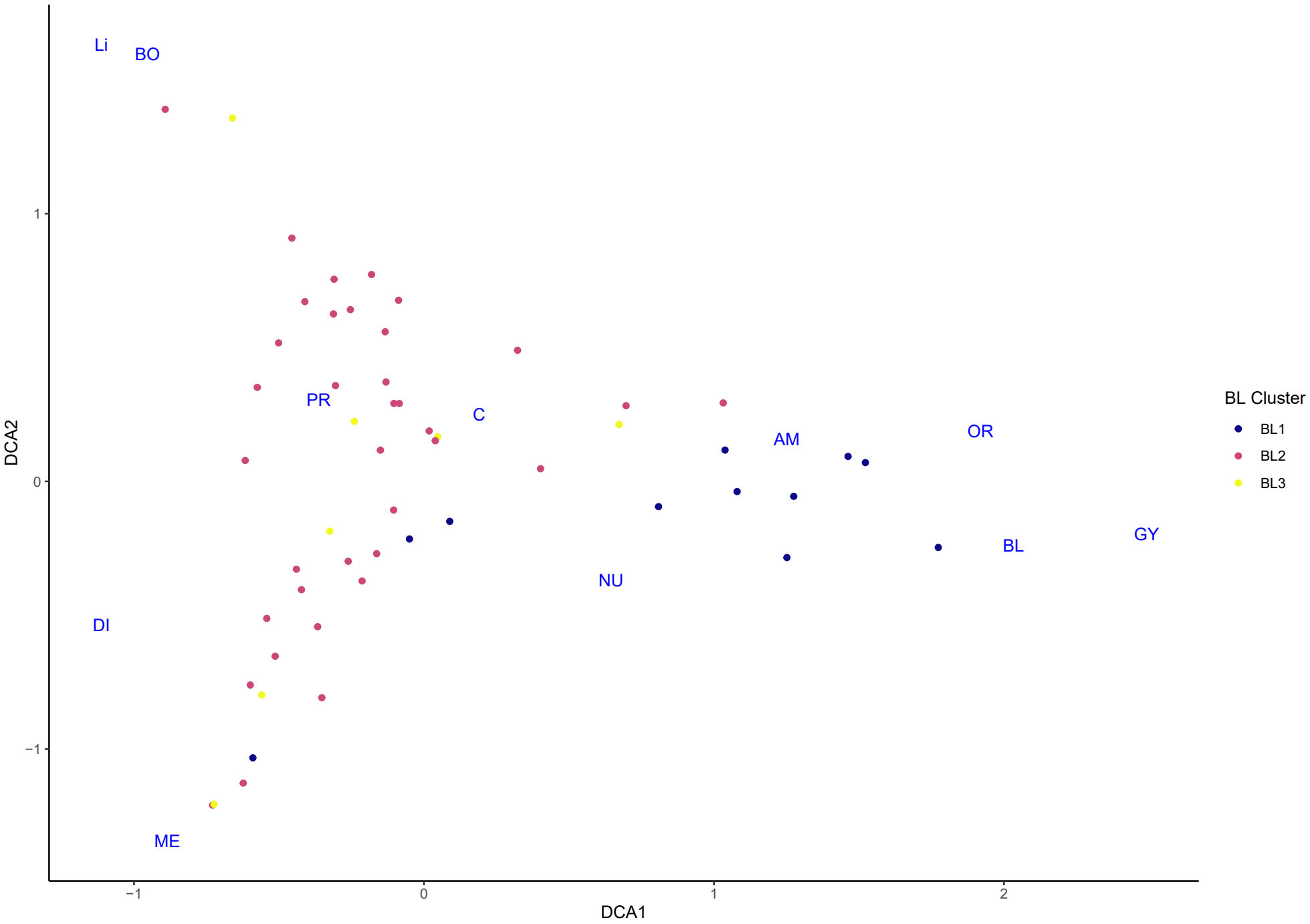



DCA samples and species UQ
Li
BO
PR
C
AM
OR
BL
GY
NU
DI
ME
DCA 2
DCA 1
1.5
1.0
0.5
0.0
−0.5
−1.0
−1
0
1
2

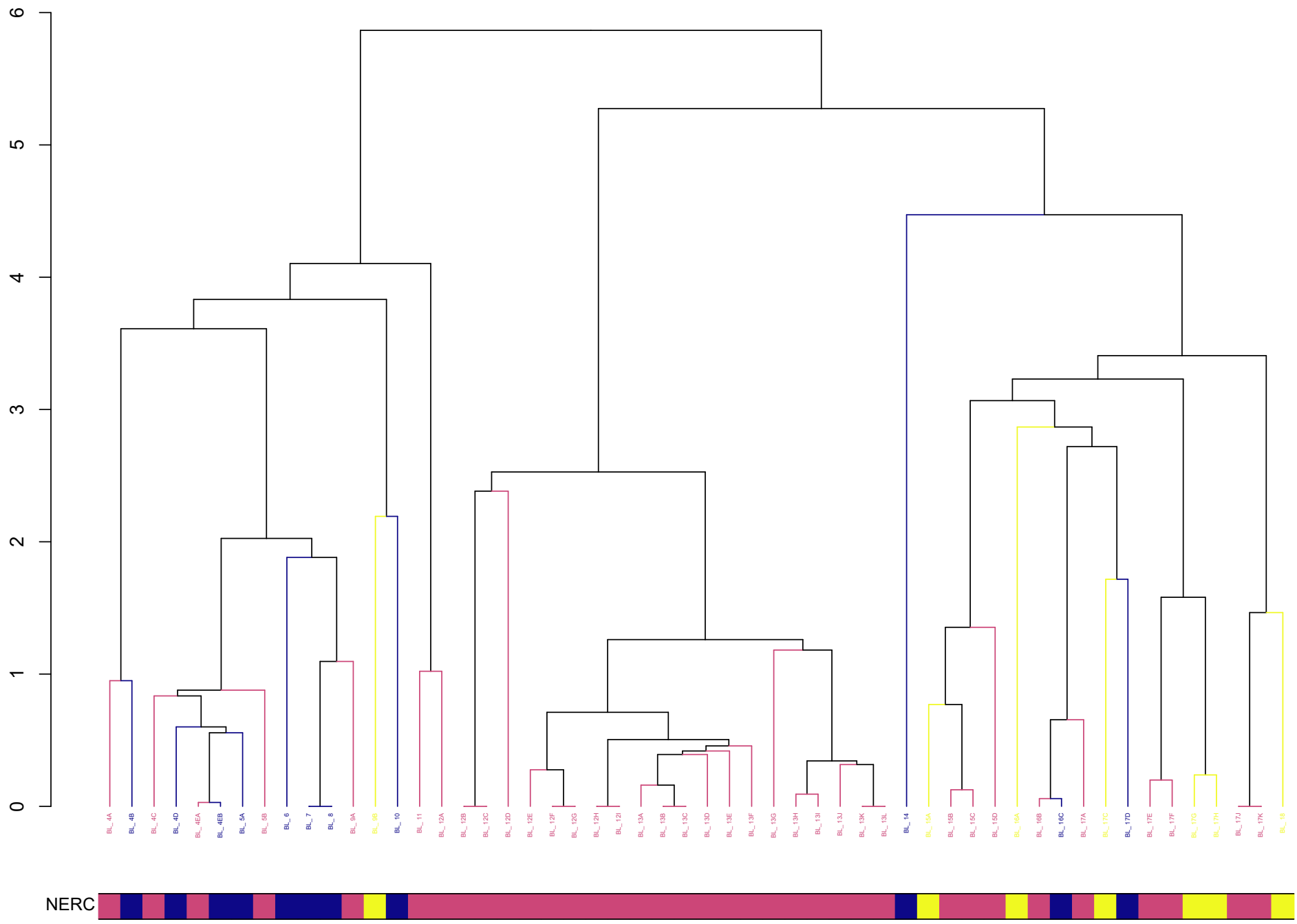

Within groups sum of squares
0
20000
40000
60000
0
10
20
30
40
Number of Clusters
****
* Among all indices:
* 3 proposed 2 as the best number of clusters
* 8 proposed 3 as the best number of clusters
* 2 proposed 4 as the best number of clusters
* 1 proposed 5 as the best number of clusters
* 5 proposed 9 as the best number of clusters
* 2 proposed 14 as the best number of clusters
* 2 proposed 15 as the best number of clusters
***** Conclusion *****
* According to the majority rule, the best number of clusters is 3
****

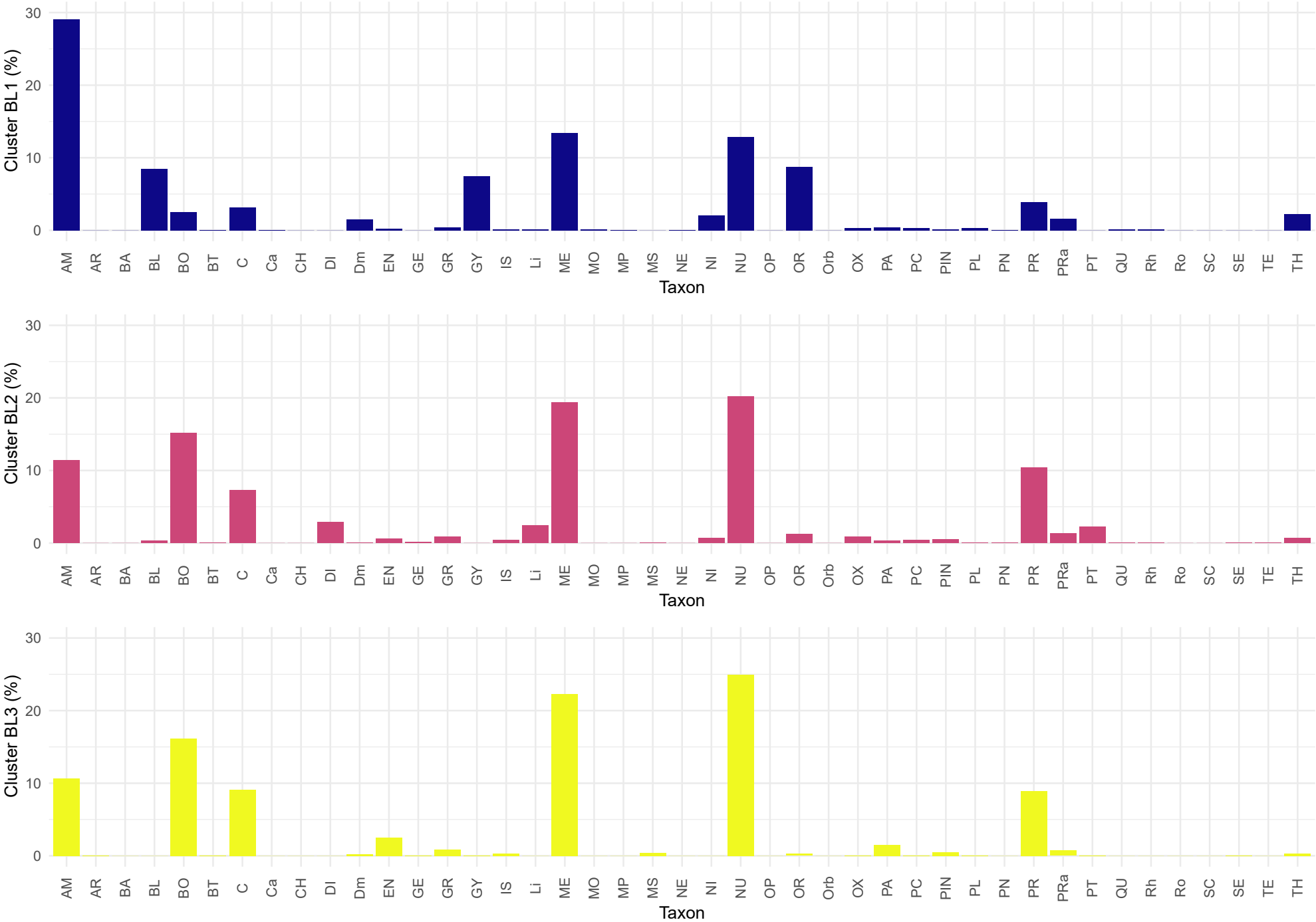

fviz_gap_stat: Gap Statistic
Gap statistic (k)
1.0
0.8
0.6
0.4
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43
Number of clusters k

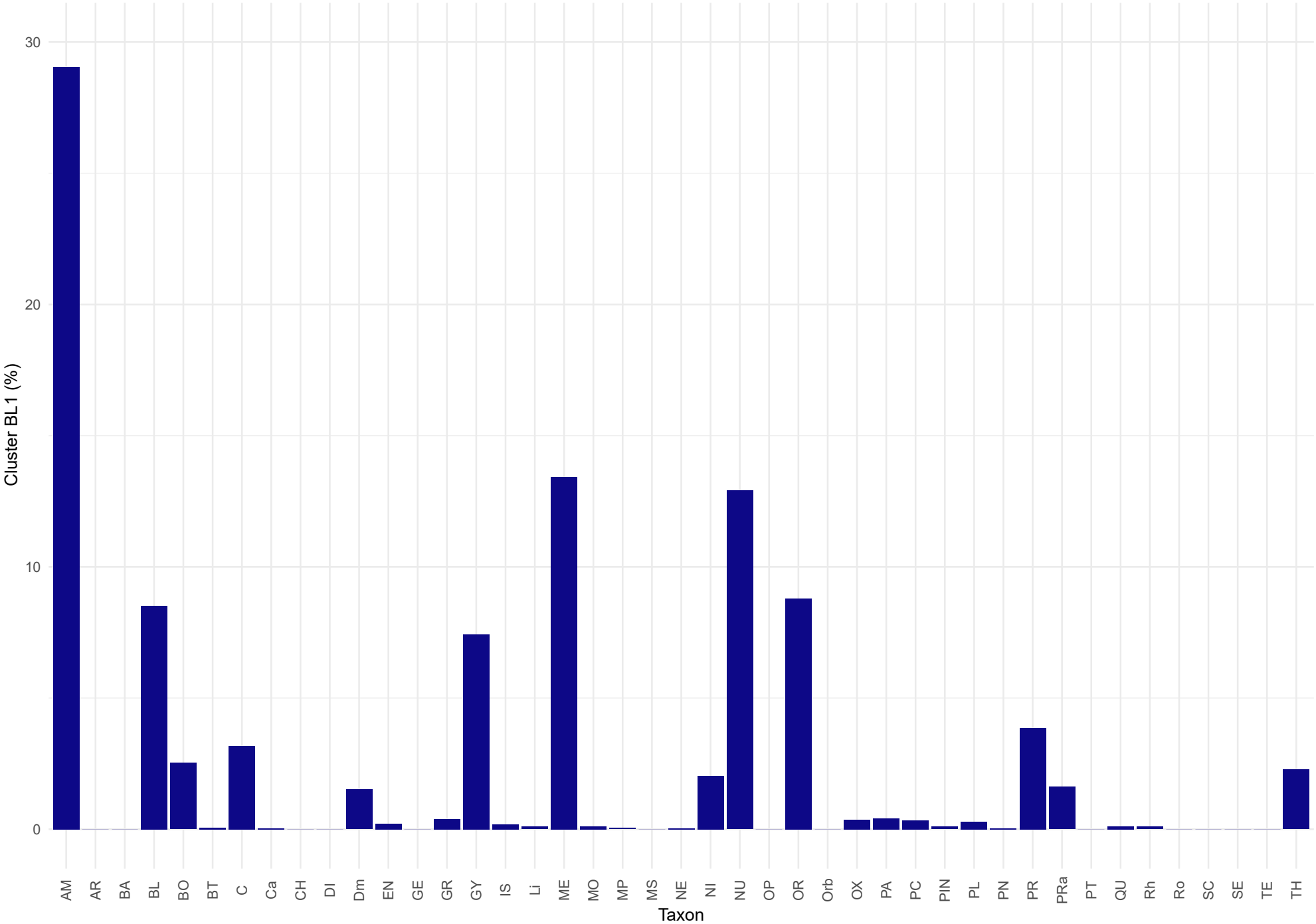

The Silhouette Plot
Average silhouette width
0.0
0.1
0.2
0.3
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43
Number of clusters k

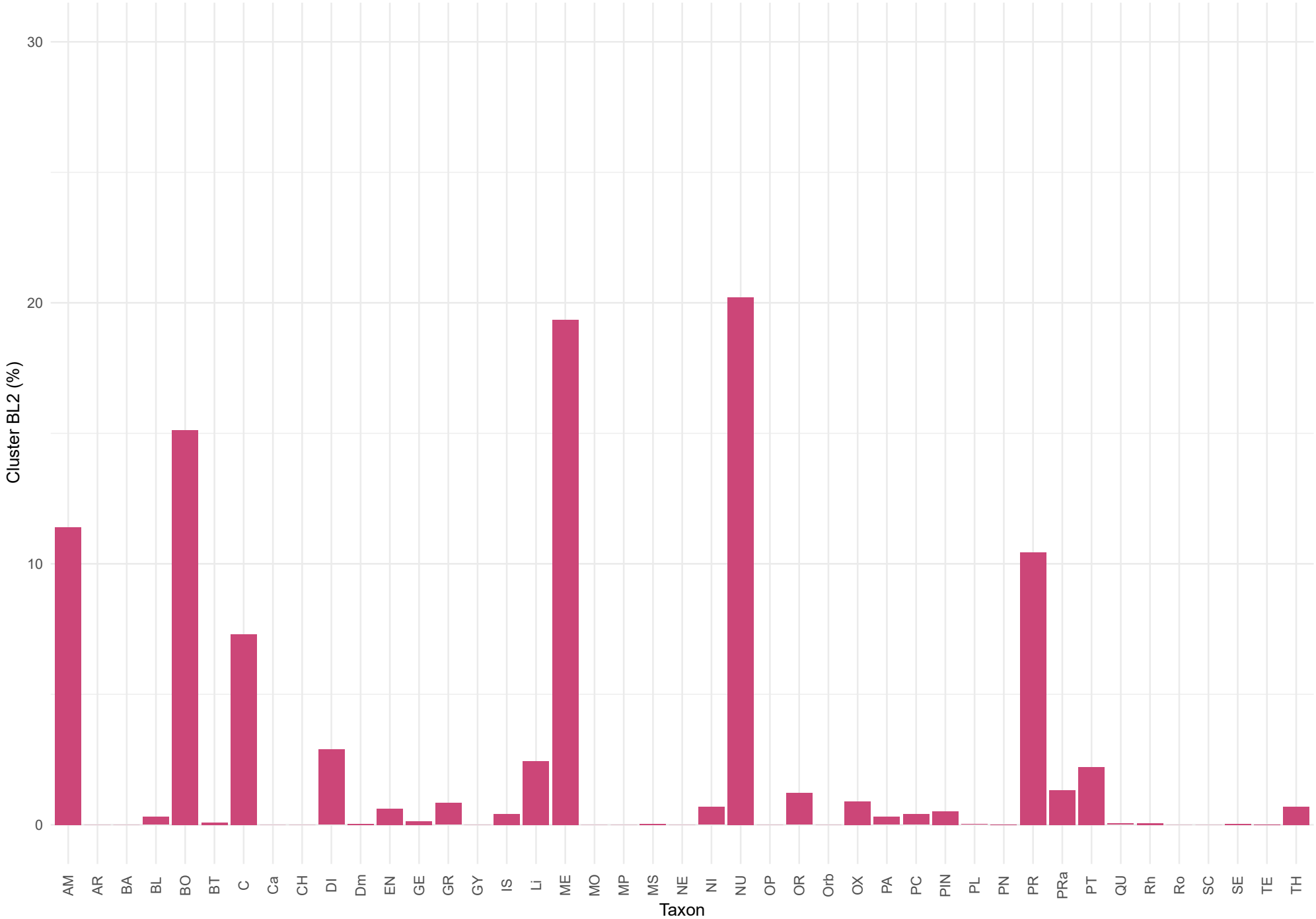

Li
BO
PR
C
AM
OR
BL
GY
NU
DI
ME
DCA2
DCA1
1
0
−1
−1
0
1
2
BL Cluster
BL1
BL2
BL3

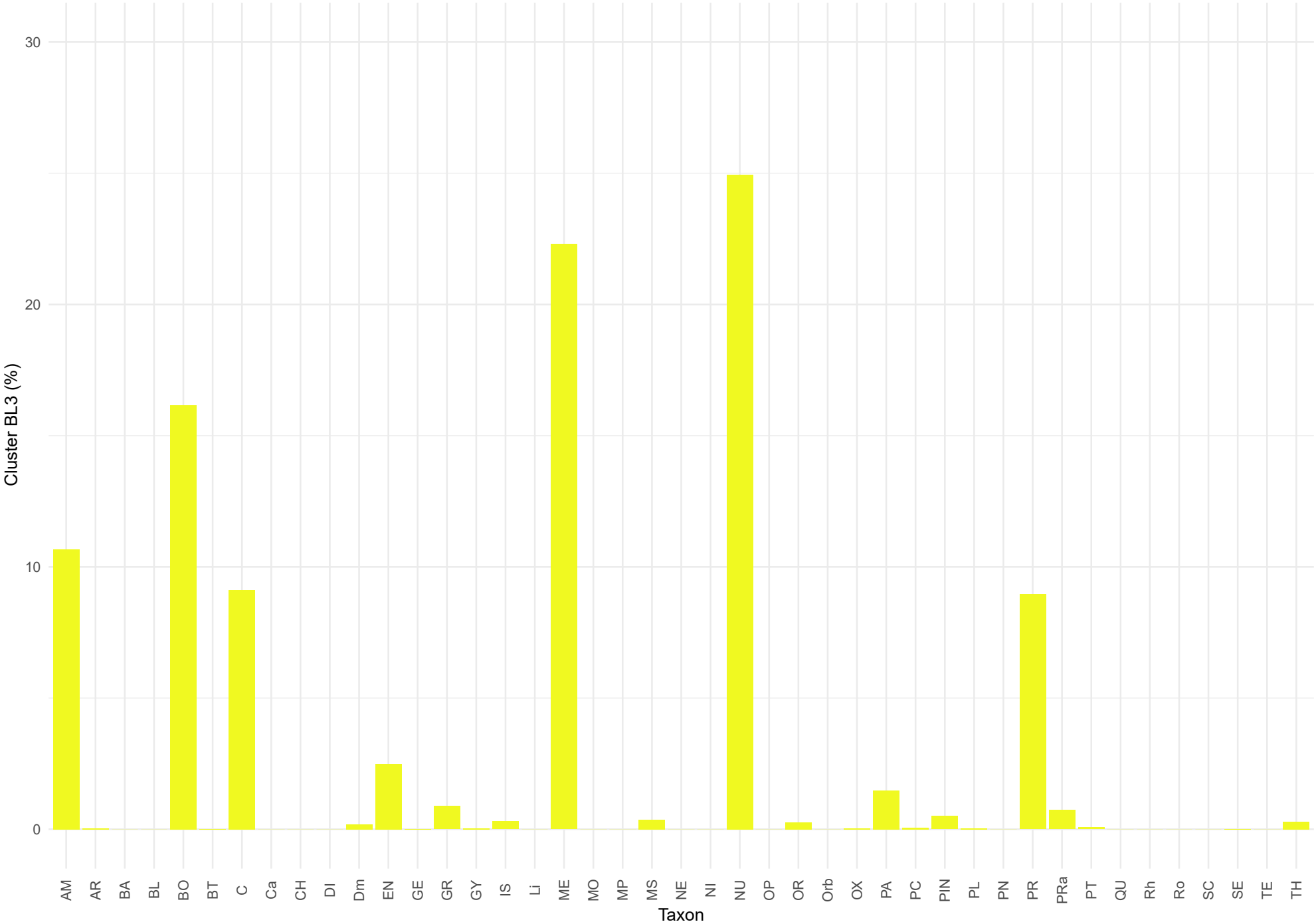
DCA2
DCA1
1.5
1.0
0.5
0.0
−0.5
−1.0
−1
0
1
BL_ 12D
BL_ 9B
BL_ 12E
BL_ 13B
BL_ 4EA
BL_ 12I
BL_ 12G
BL_ 13C
BL_ 12F
BL_ 13A
BL_ 9A
BL_ 12C
BL_ 13D
BL_ 15D
BL_ 5B
BL_ 4A
BL_ 17G
BL_ 18
BL_ 15B
BL_ 17K
BL_ 17J
BL_ 4B
BL_ 12B
BL_ 17E
BL_ 5A
BL_ 10
BL_ 8
BL_ 4D
BL_ 4EB
BL_ 13G
BL_ 7
BL_ 17C
BL_ 16C
BL_ 6
BL_ 13H
BL_ 17A
BL_ 14
BL_ 13J
BL_ 16B
BL_ 13E
BL_ 13F
BL_ 13I
BL_ 13L
BL_ 13K
BL_ 17H
BL_ 17F
BL_ 17D
BL_ 12A
BL Cluster
BL1
BL2
BL3

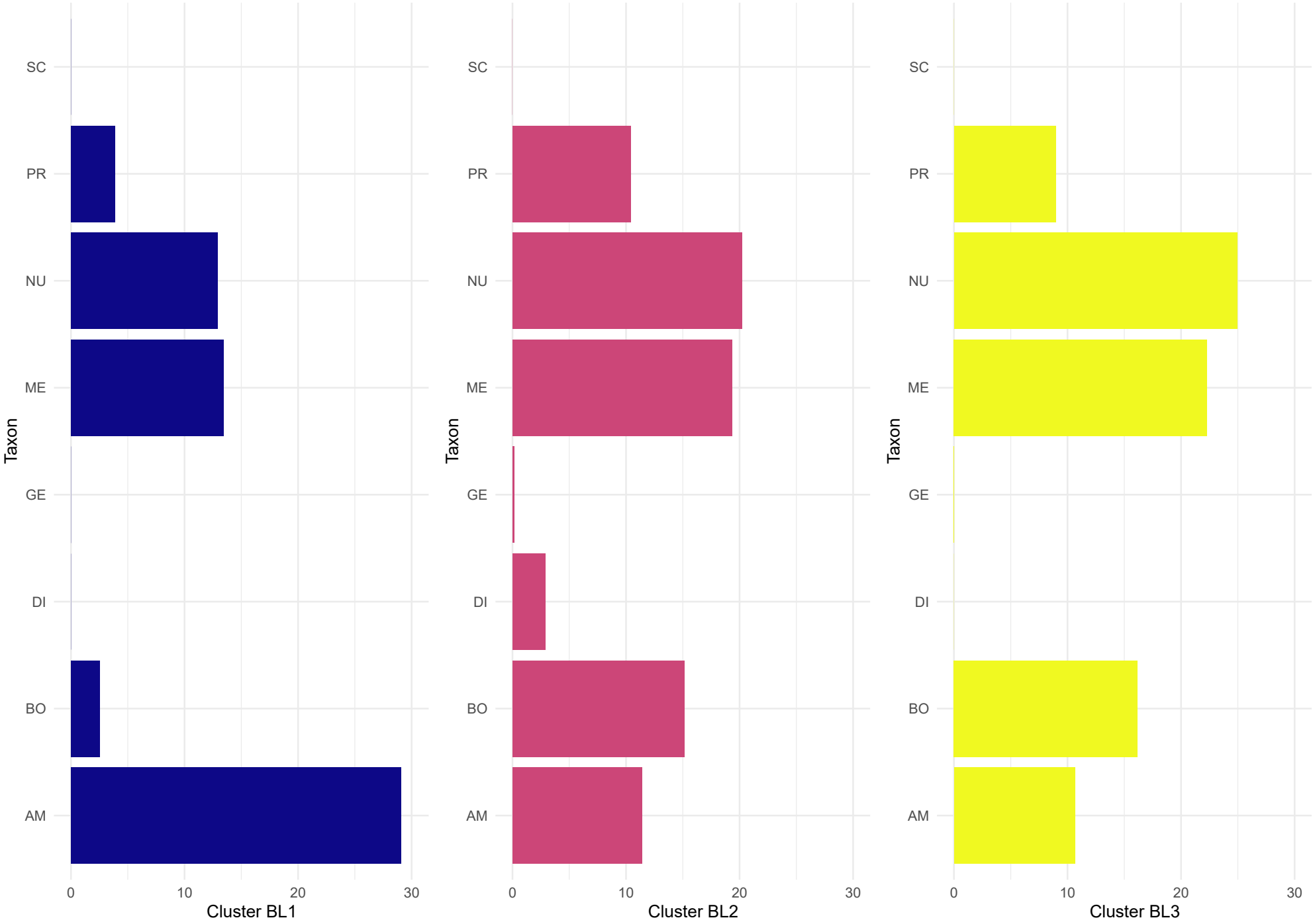

0
1
2
3
4
5
6
BL_4A
BL_4B
BL_4C
BL_4D
BL_4EA
BL_4EB
BL_5A
BL_5B
BL_6
BL_7
BL_8
BL_9A
BL_9B
BL_10
BL_11
BL_12A
BL_12B
BL_12C
BL_12D
BL_12E
BL_12F
BL_12G
BL_12H
BL_12I
BL_13A
BL_13B
BL_13C
BL_13D
BL_13E
BL_13F
BL_13G
BL_13H
BL_13I
BL_13J
BL_13K
BL_13L
BL_14
BL_15A
BL_15B
BL_15C
BL_15D
BL_16A
BL_16B
BL_16C
BL_17A
BL_17C
BL_17D
BL_17E
BL_17F
BL_17G
BL_17H
BL_17J
BL_17K
BL_18
NERC


Cluster BL1 (%)
Cluster BL2 (%)
Cluster BL3 (%)
0
10
20
30
AM AR BA BL BO BT C Ca CH DI Dm EN GE GR GY IS Li ME MO MP MS NE NI NU OP OR Orb OX PA PC PIN PL PN PR PRa PT QU Rh Ro SC SE TE TH
Taxon

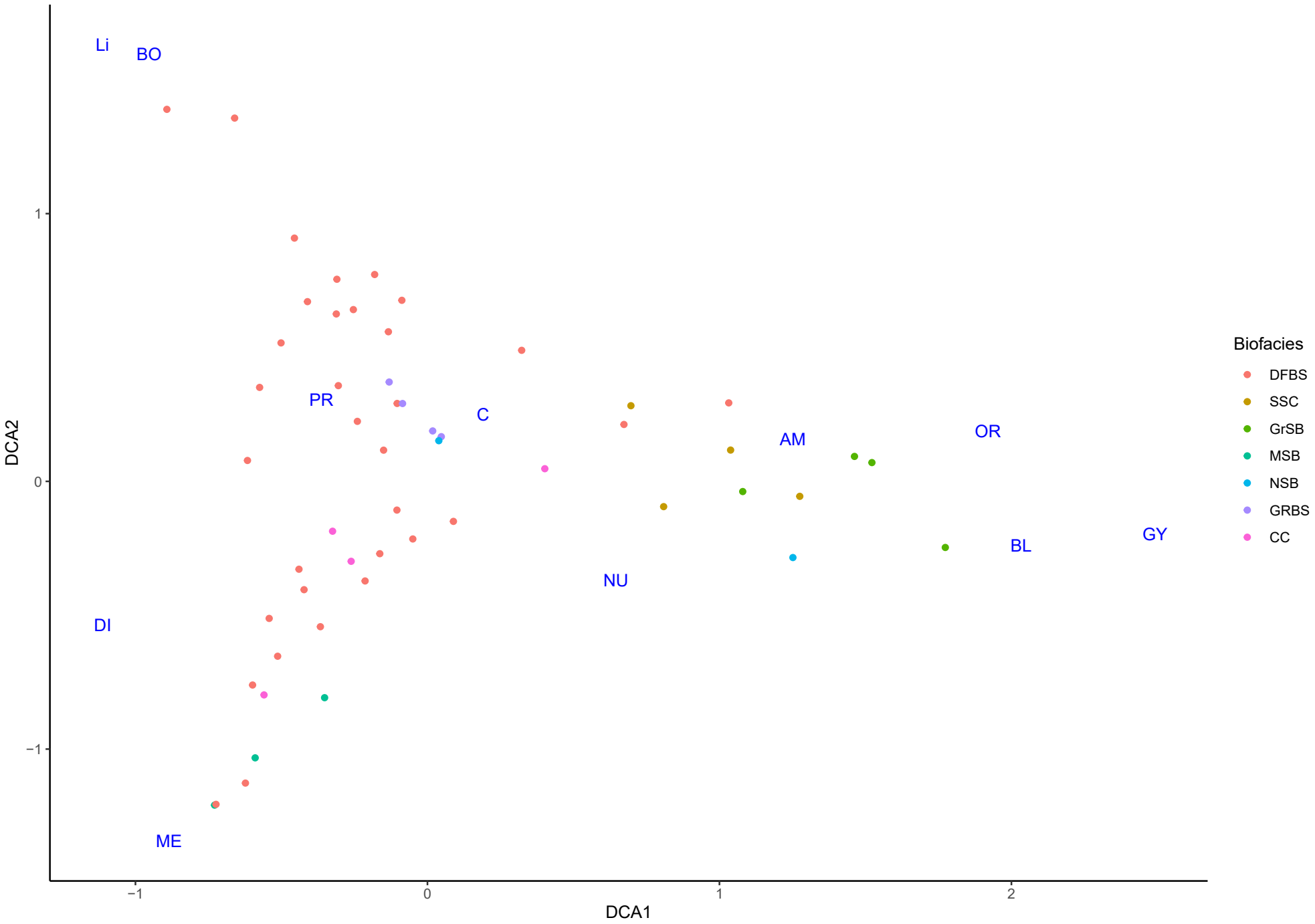

Cluster BL1 (%)
30
20
10
0
AM
AR
BA
BL
BO
BT
C
Ca
CH
DI
Dm
EN
GE
GR
GY
IS
Li
ME
MO
MP
MS
NE
NI
NU
OP
OR
Orb
OX
PA
PC
PIN
PL
PN
PR
PRa
PT
QU
Rh
Ro
SC
SE
TE
TH
Taxon


Cluster BL2 (%)
30
20
10
0
AM
AR
BA
BL
BO
BT
C
Ca
CH
DI
Dm
EN
GE
GR
GY
IS
Li
ME
MO
MP
MS
NE
NI
NU
OP
OR
Orb
OX
PA
PC
PIN
PL
PN
PR
PRa
PT
QU
Rh
Ro
SC
SE
TE
TH
Taxon

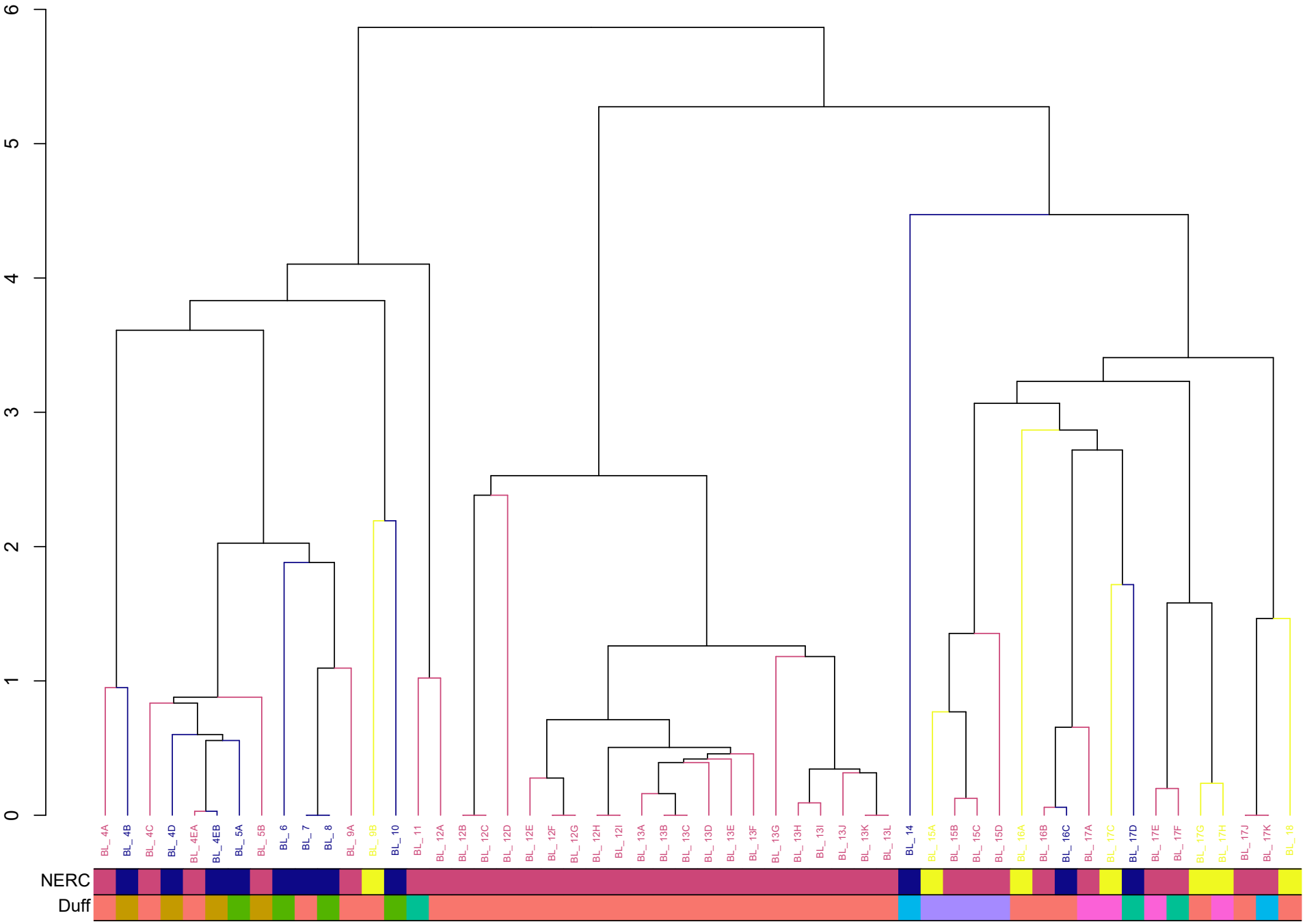

Cluster BL3 (%)
30
20
10
0
AM
AR
BA
BL
BO
BT
C
Ca
CH
DI
Dm
EN
GE
GR
GY
IS
Li
ME
MO
MP
MS
NE
NI
NU
OP
OR
Orb
OX
PA
PC
PIN
PL
PN
PR
PRa
PT
QU
Rh
Ro
SC
SE
TE
TH
Taxon



Bletchley (BL)

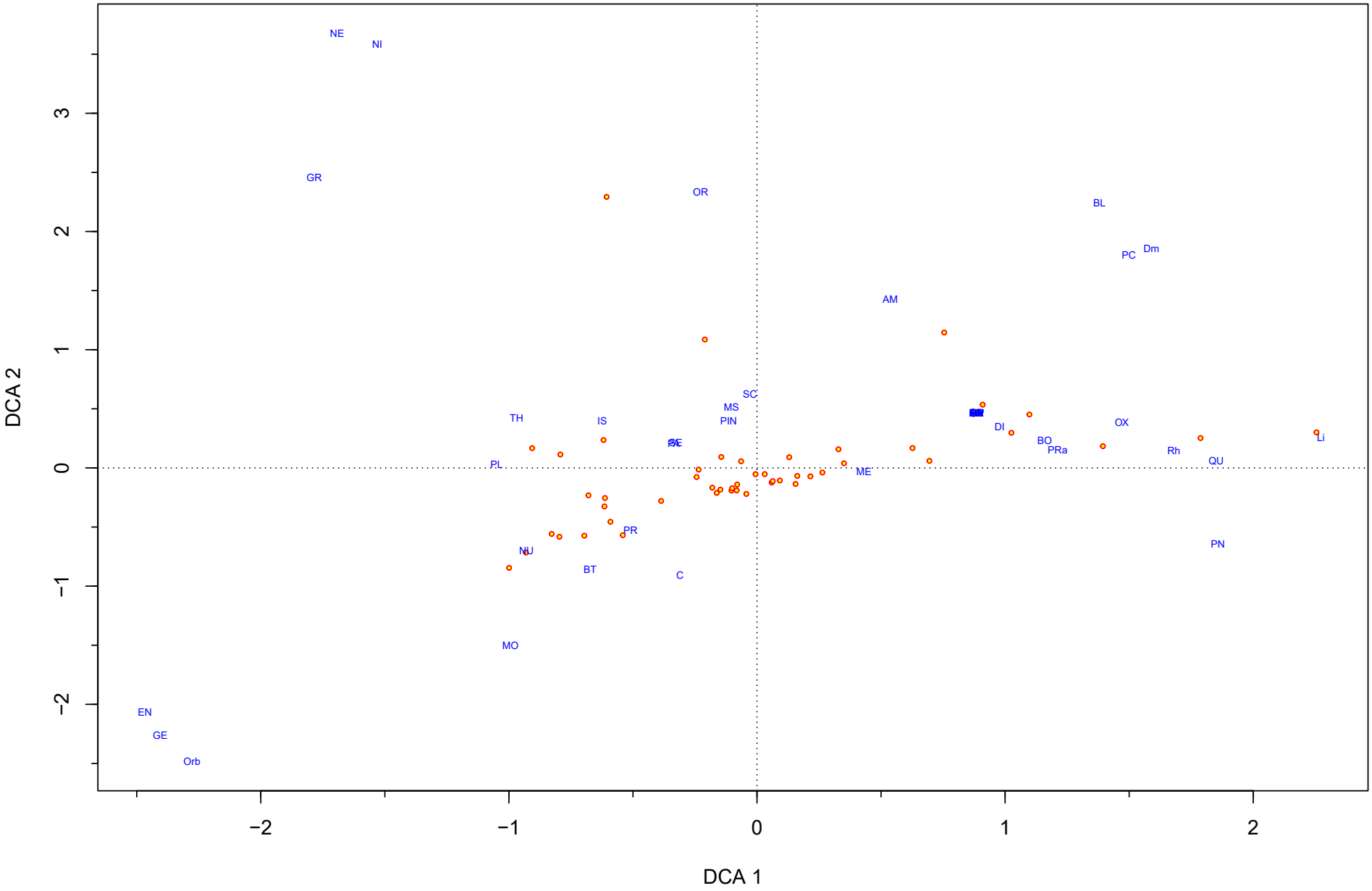

Li
BO
PR
C
AM
OR
BL
GY
NU
DI
ME
DCA2
DCA1
1
0
−1
−1
0
1
2
Biofacies
DFBS
SSC
GrSB
MSB
NSB
GRBS
CC

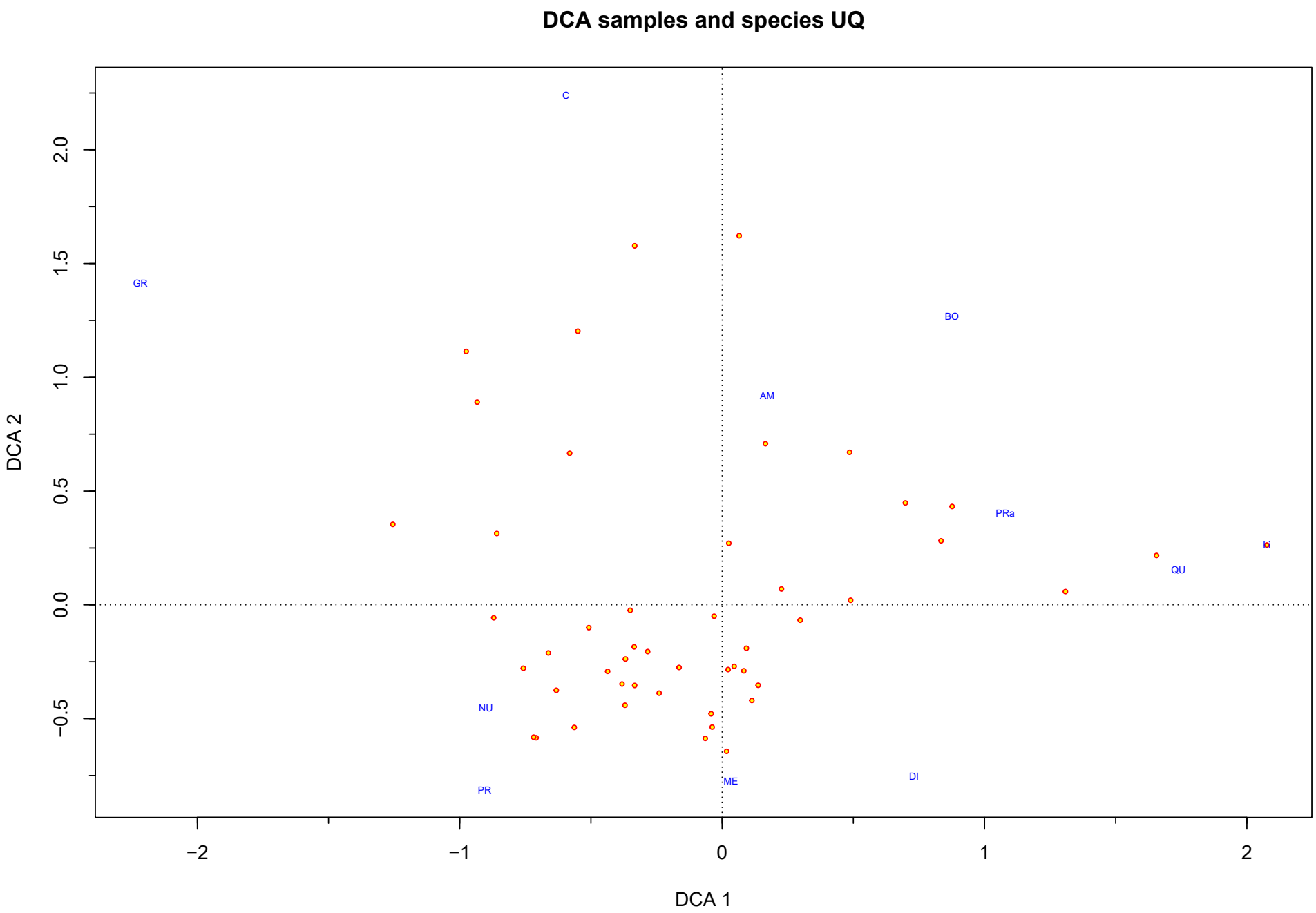
DCA2
DCA1
1.5
1.0
0.5
0.0
−0.5
−1.0
−1
0
1
BL_ 12D
BL_ 9B
BL_ 12E
BL_ 13B
BL_ 4EA
BL_ 12I
BL_ 12G
BL_ 13C
BL_ 12H
BL_ 12F
BL_ 13A
BL_ 9A
BL_ 12C
BL_ 13D
BL_ 15D
BL_ 5B
BL_ 4A
BL_ 17G
BL_ 18
BL_ 15B
BL_ 17K
BL_ 17J
BL_ 4B
BL_ 5A
BL_ 10
BL_ 12B
BL_ 17E
BL_ 8
BL_ 4D
BL_ 4EB
BL_ 13G
BL_ 7
BL_ 17C
BL_ 16C
BL_ 6
BL_ 13H
BL_ 17A
BL_ 14
BL_ 13J
BL_ 16B
BL_ 13E
BL_ 13F
BL_ 13I
BL_ 13L
BL_ 13K
BL_ 17H
BL_ 17F
BL_ 17D
BL_ 12A
Biofacies
DFBS
SSC
GrSB
MSB
NSB
GRBS
CC

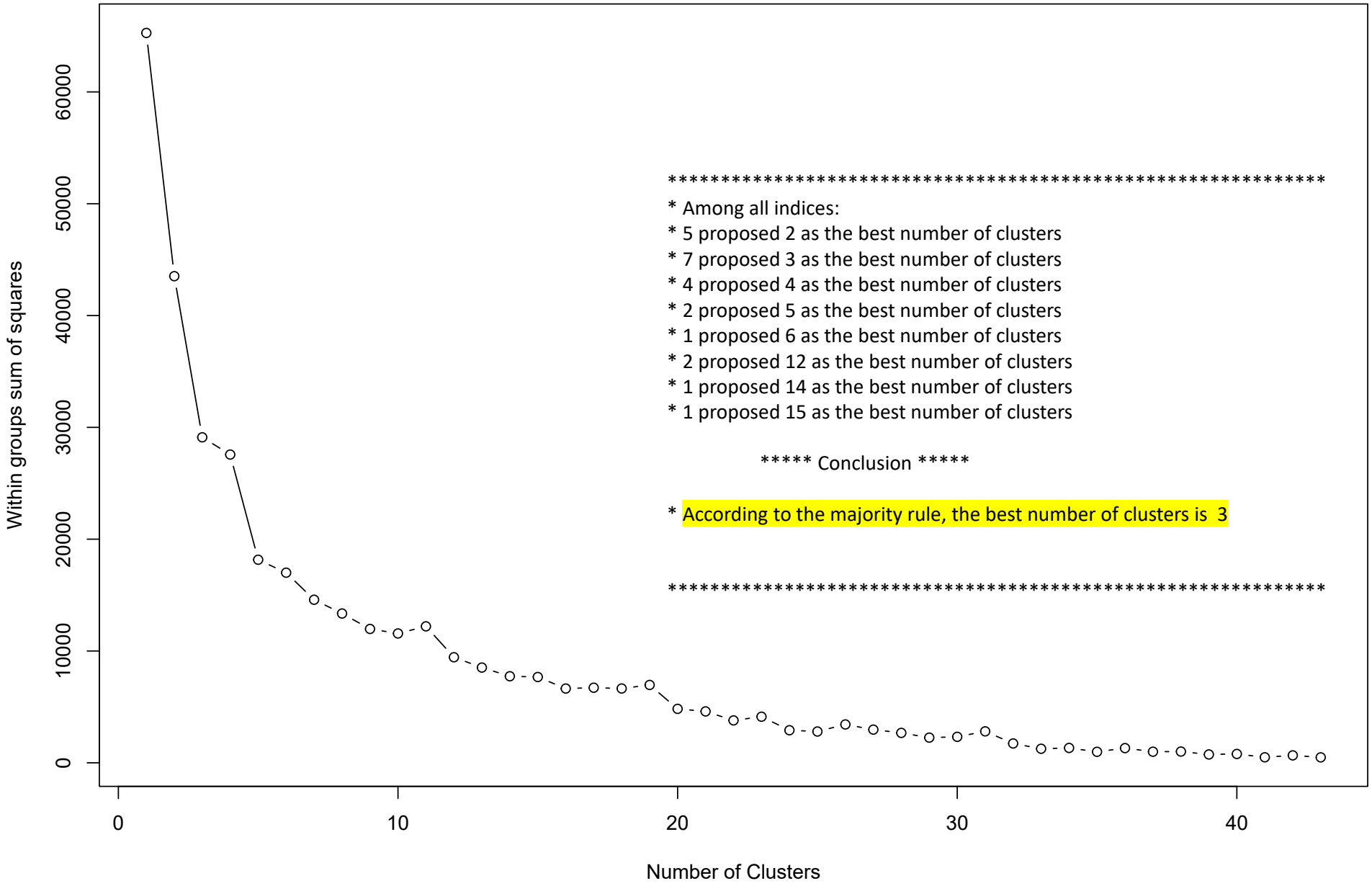

0
1
2
3
4
5
6
BL_ 4A
BL_ 4B
BL_ 4C
BL_ 4D
BL_ 4EA
BL_ 4EB
BL_ 5A
BL_ 5B
BL_ 6
BL_ 7
BL_ 8
BL_ 9A
BL_ 9B
BL_ 10
BL_ 11
BL_ 12A
BL_ 12B
BL_ 12C
BL_ 12D
BL_ 12E
BL_ 12F
BL_ 12G
BL_ 12H
BL_ 12I
BL_ 13A
BL_ 13B
BL_ 13C
BL_ 13D
BL_ 13E
BL_ 13F
BL_ 13G
BL_ 13H
BL_ 13I
BL_ 13J
BL_ 13K
BL_ 13L
BL_ 14
BL_ 15A
BL_ 15B
BL_ 15C
BL_ 15D
BL_ 16A
BL_ 16B
BL_ 16C
BL_ 17A
BL_ 17C
BL_ 17D
BL_ 17E
BL_ 17F
BL_ 17G
BL_ 17H
BL_ 17J
BL_ 17K
BL_ 18
NERC
Duff

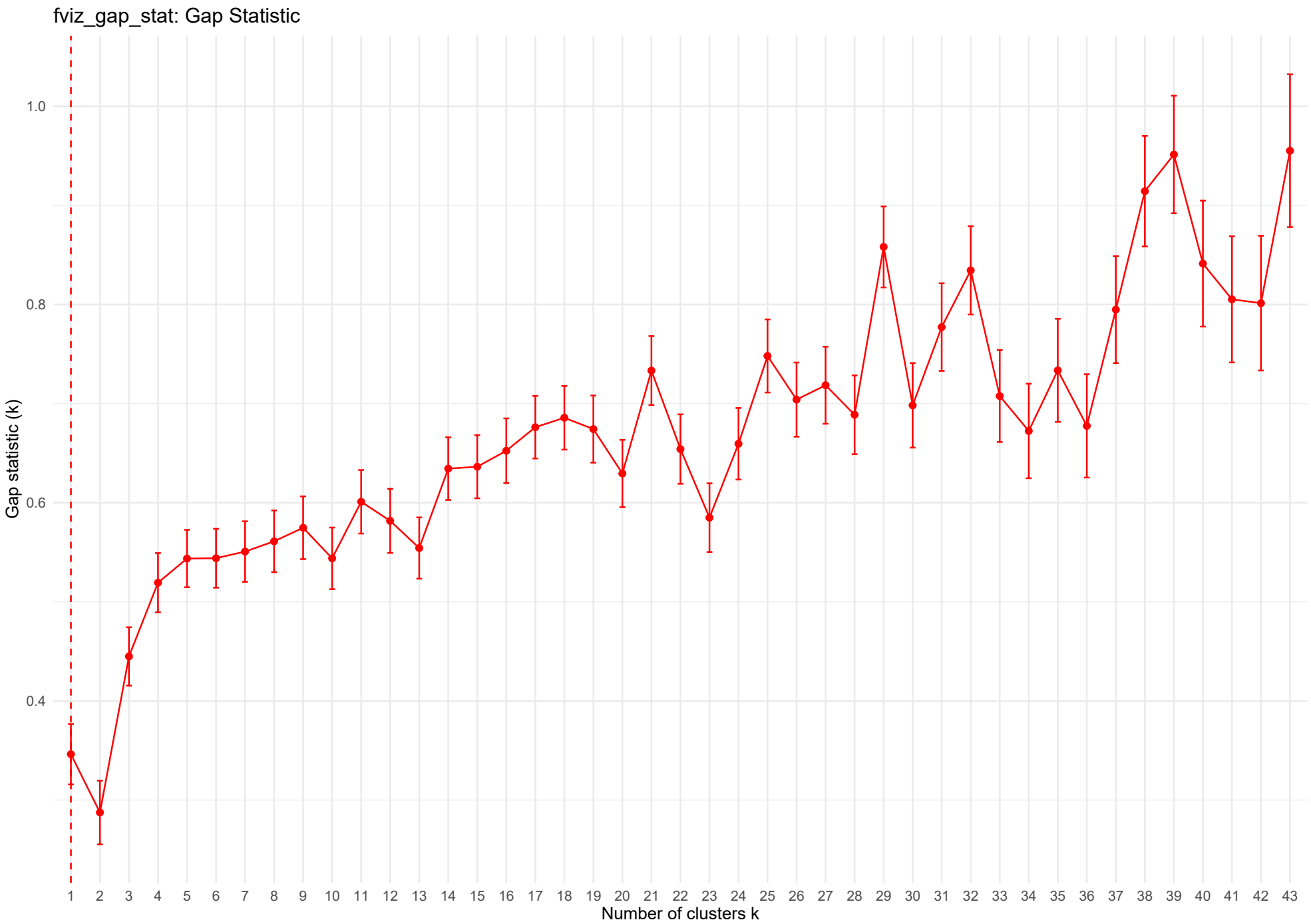
Calvert (CA)

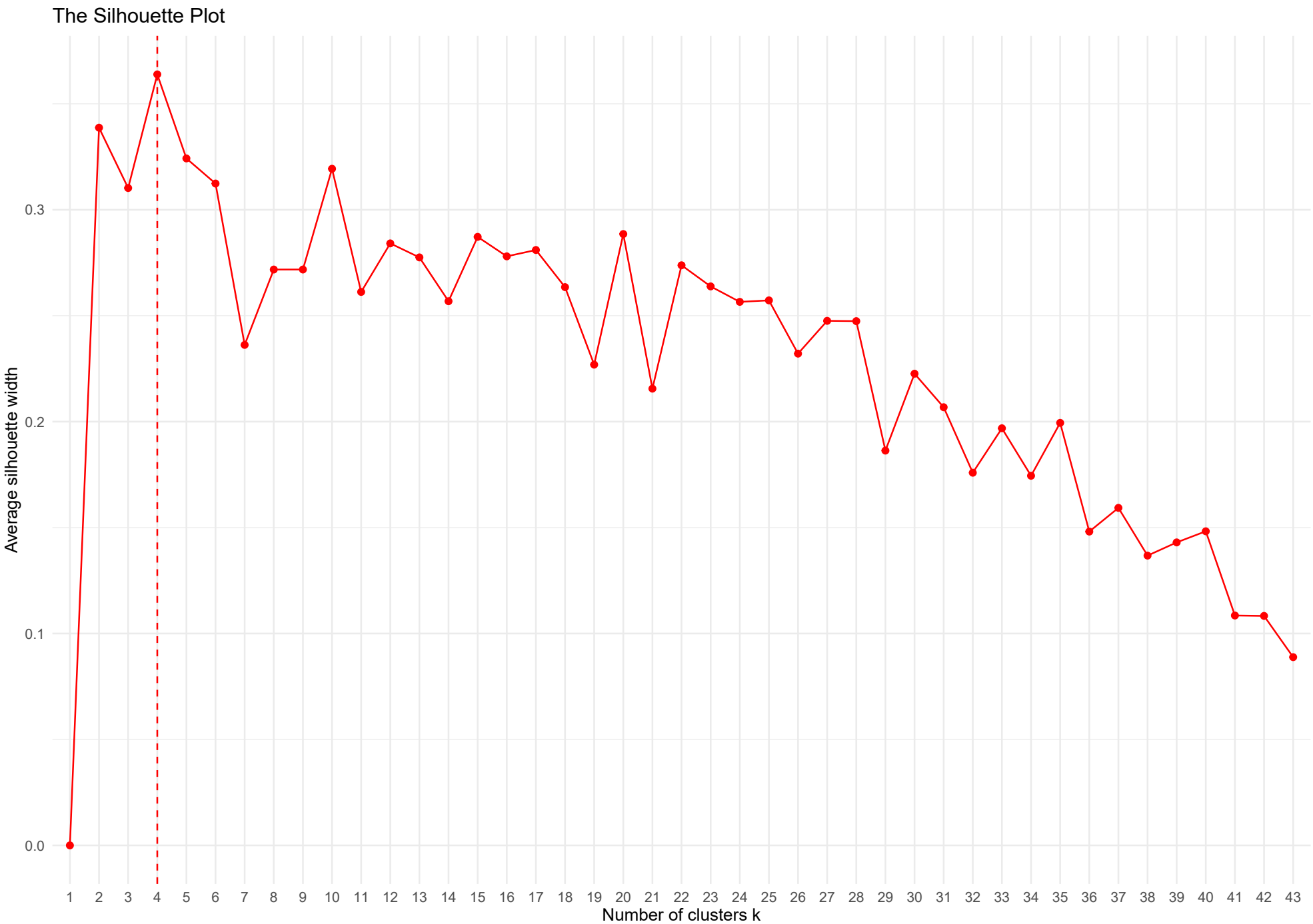
DCA samples and species

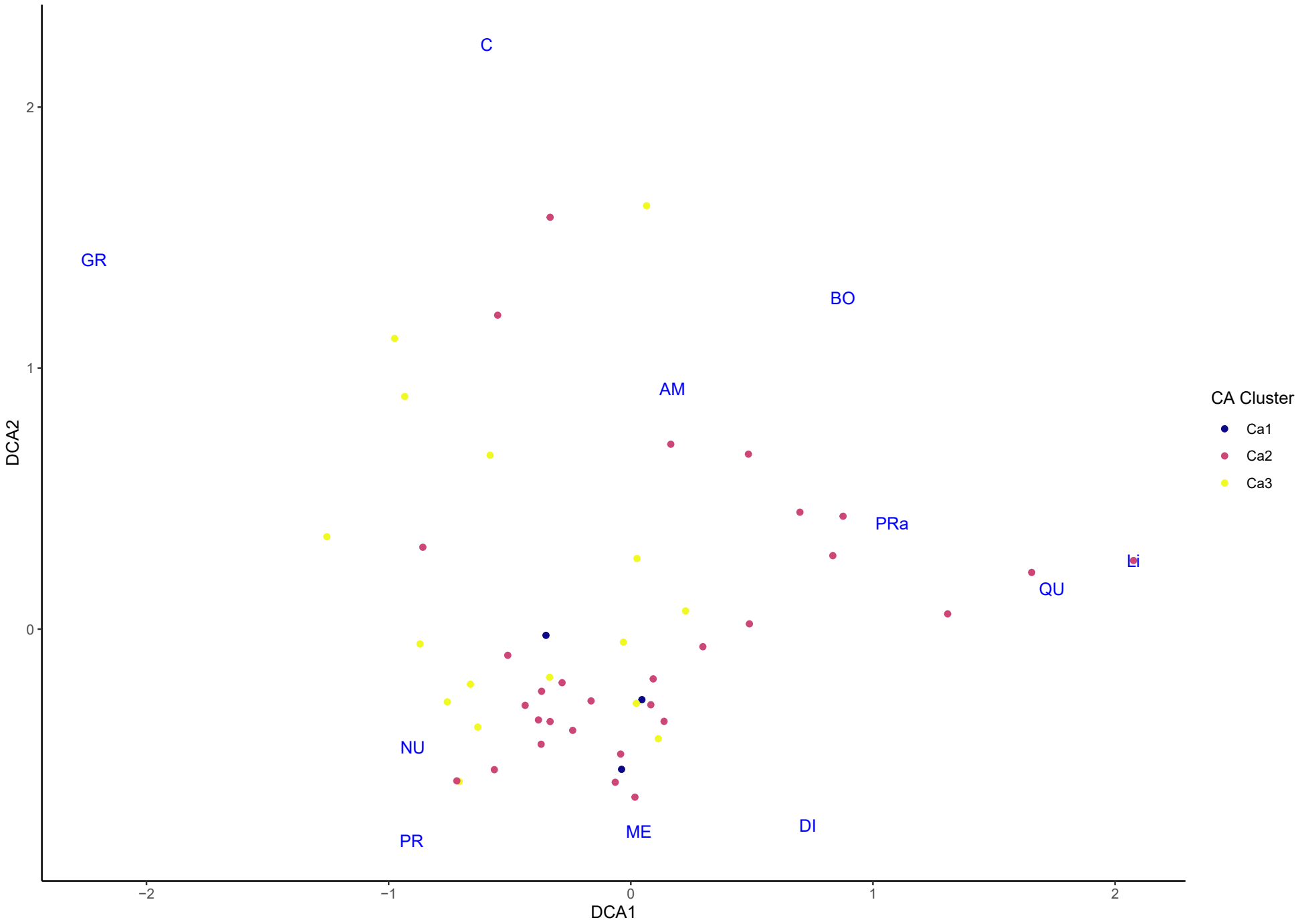



DCA samples and species UQ
C
GR
BO
AM
PRa
QU
NU
PR
ME
DI
DCA 2
DCA 1
2.0
1.5
1.0
0.5
0.0
−0.5
−2
−1
0
1
2

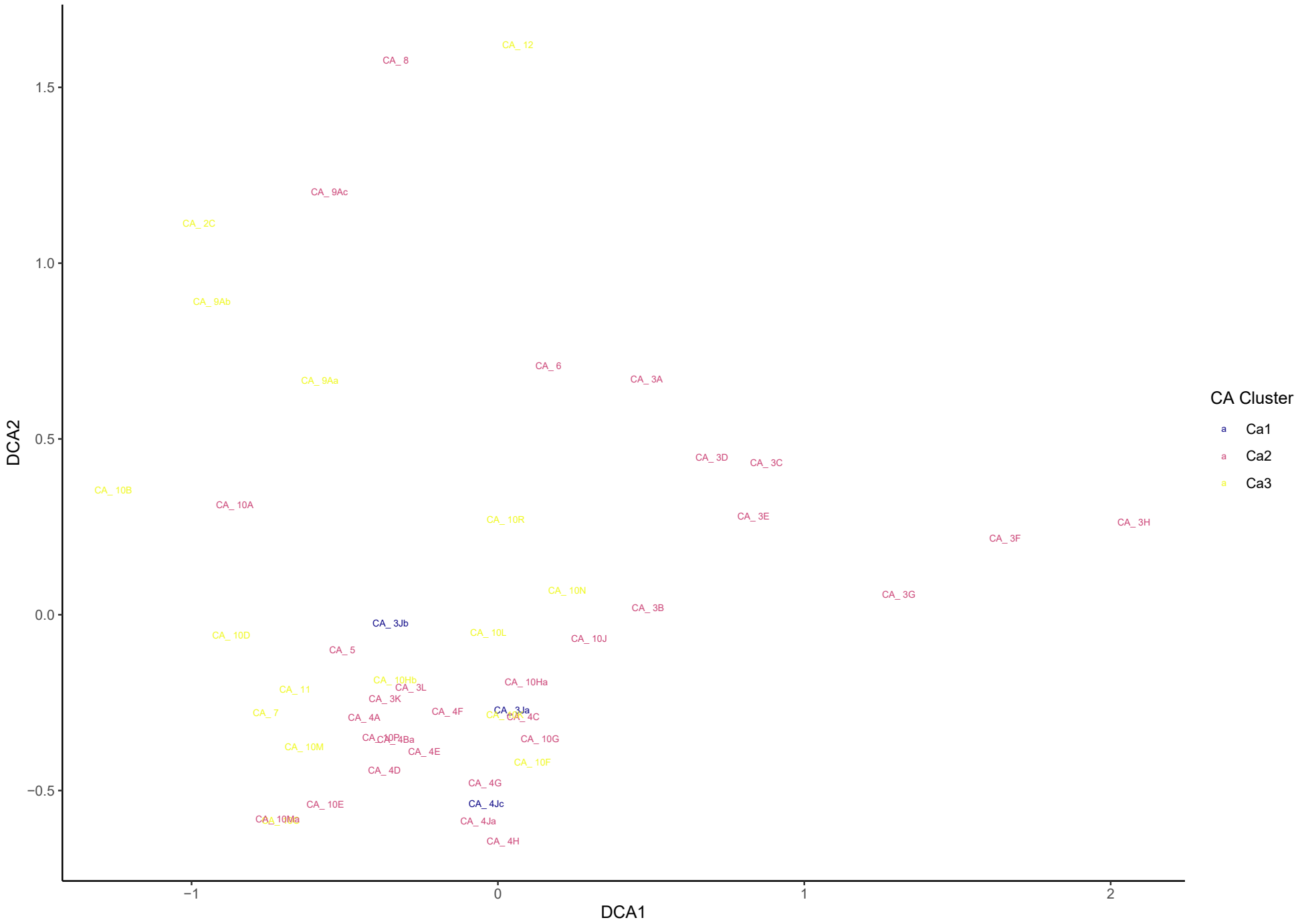

Within groups sum of squares
0
10000
20000
30000
40000
50000
60000
0
10
20
30
40
Number of Clusters
****
* Among all indices:
* 5 proposed 2 as the best number of clusters
* 7 proposed 3 as the best number of clusters
* 4 proposed 4 as the best number of clusters
* 2 proposed 5 as the best number of clusters
* 1 proposed 6 as the best number of clusters
* 2 proposed 12 as the best number of clusters
* 1 proposed 14 as the best number of clusters
* 1 proposed 15 as the best number of clusters
***** Conclusion *****
* According to the majority rule, the best number of clusters is 3
****

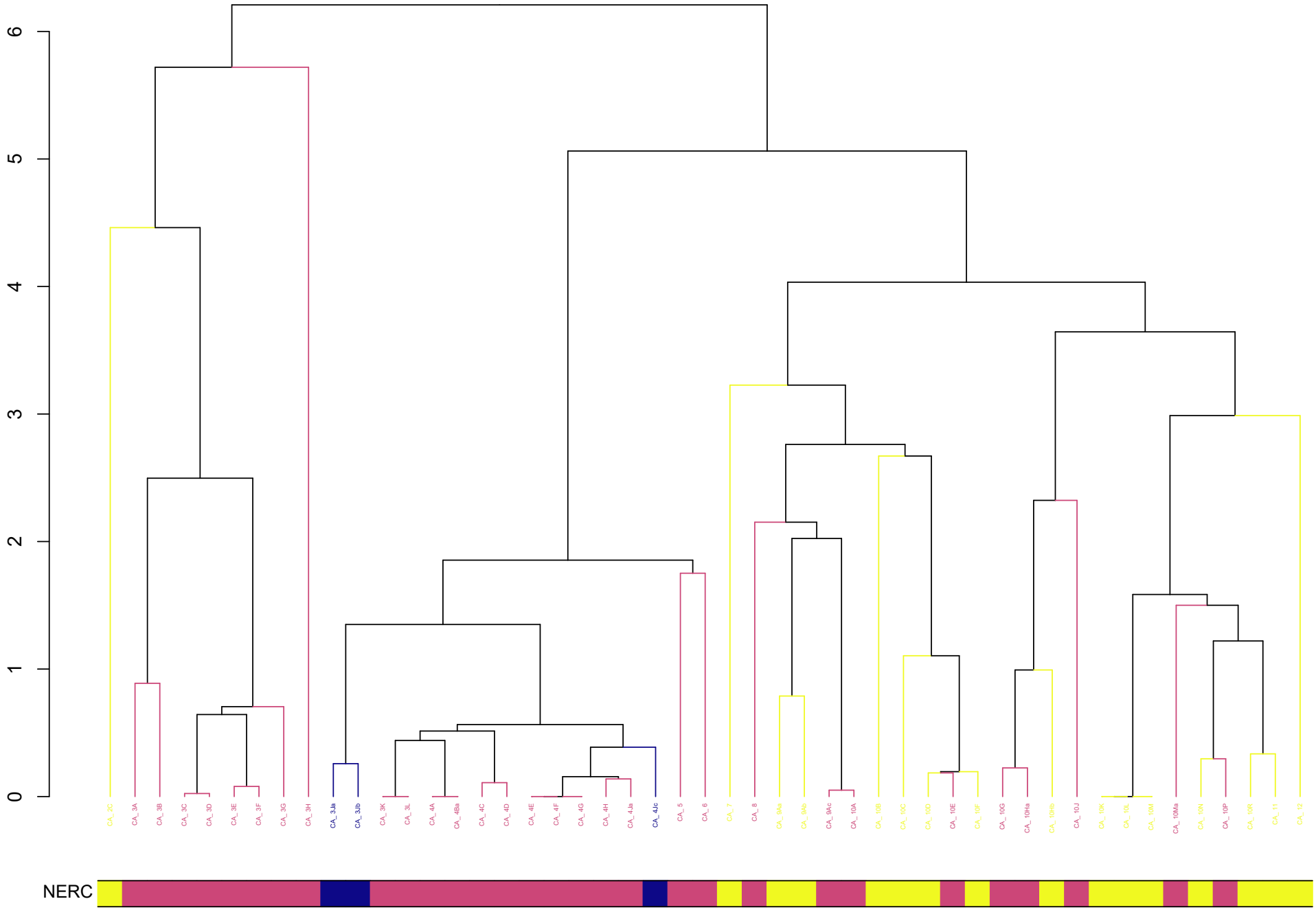

fviz_gap_stat: Gap Statistic
Gap statistic (k)
1.0
0.8
0.6
0.4
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43
Number of clusters k

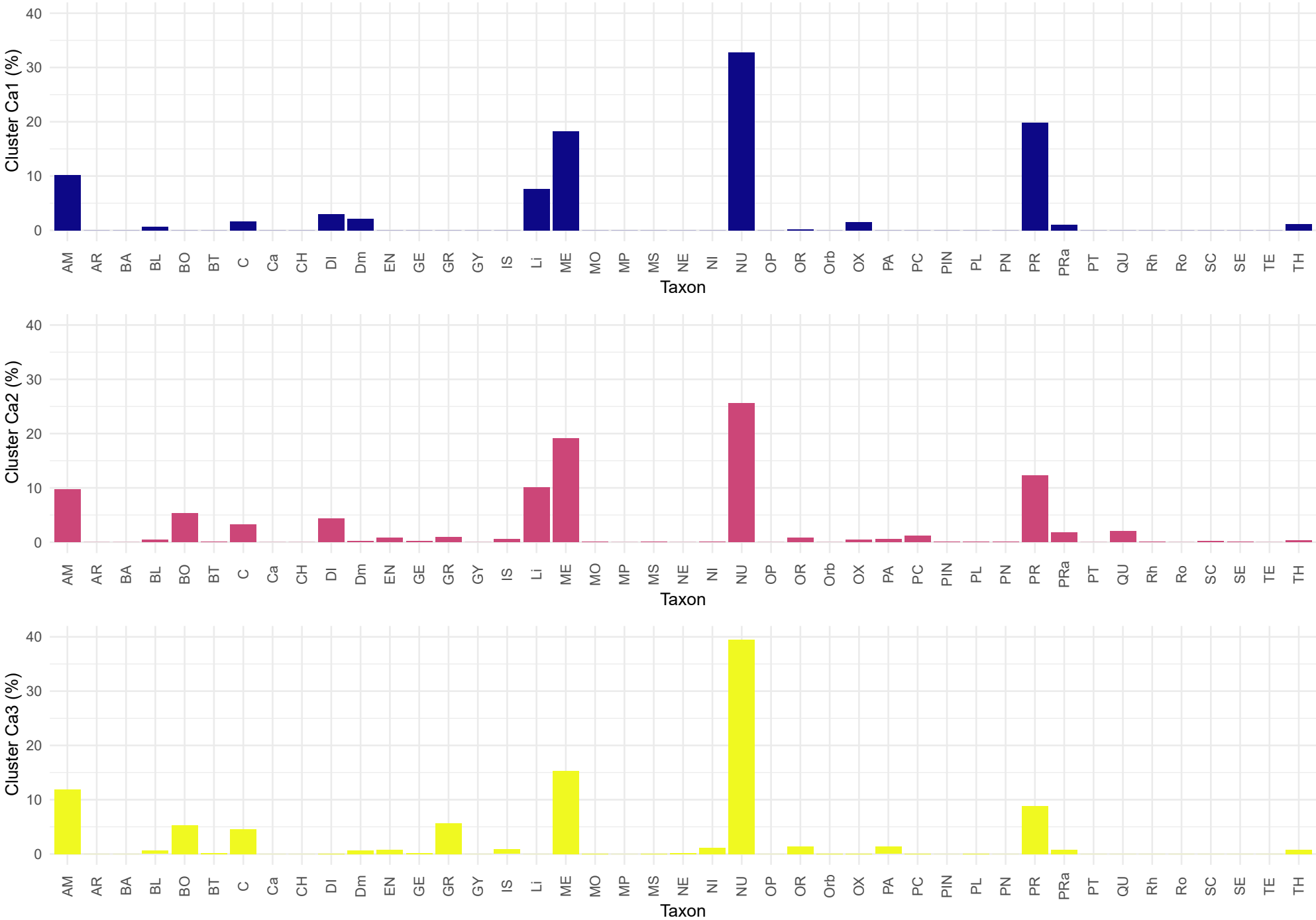

The Silhouette Plot
Average silhouette width
0.0
0.1
0.2
0.3
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43
Number of clusters k

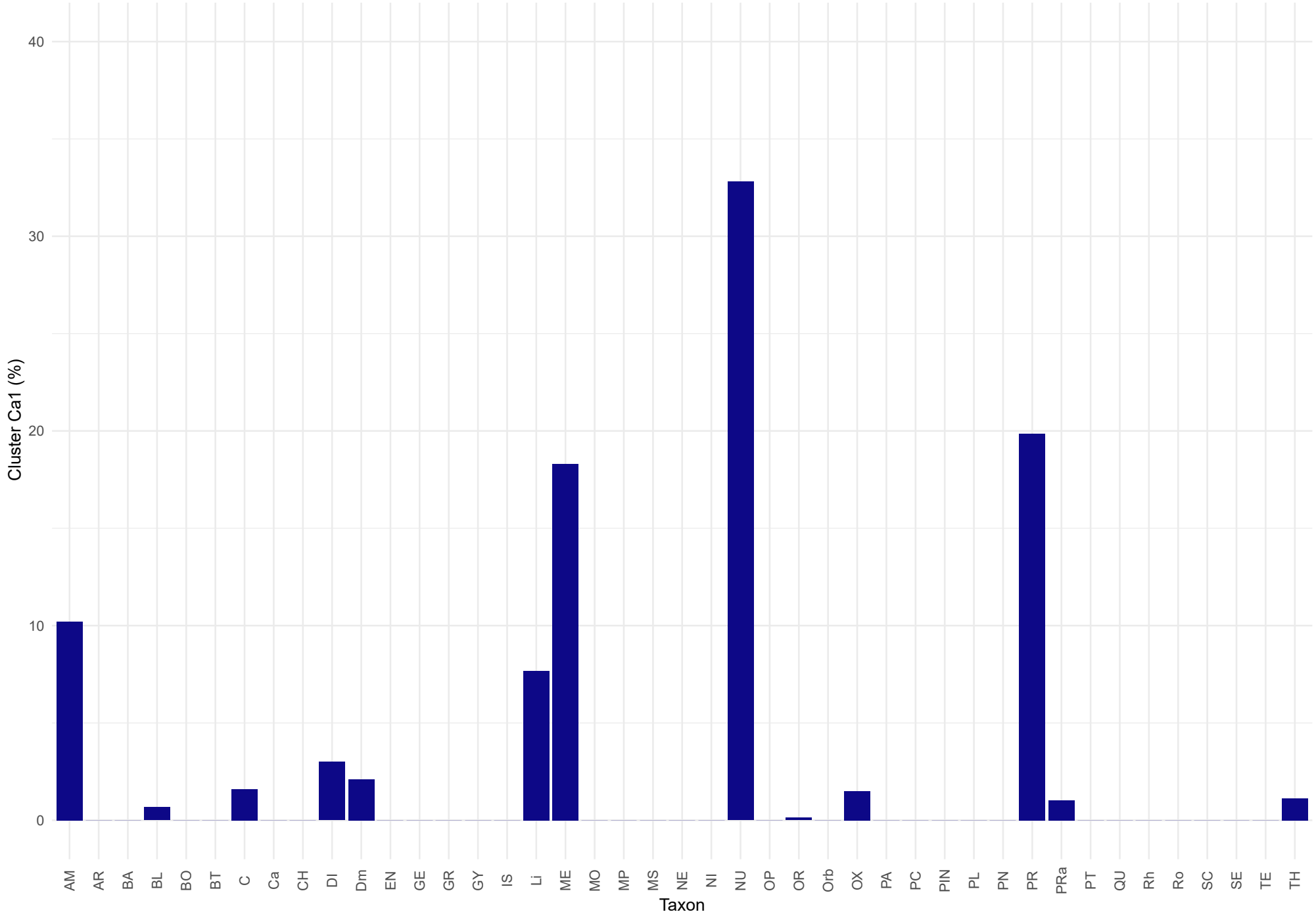

C
GR
BO
AM
PRa
Li
QU
NU
PR
ME
DI
DCA2
DCA1
2
1
0
−2
−1
0
1
2
CA Cluster
Ca1
Ca2
Ca3

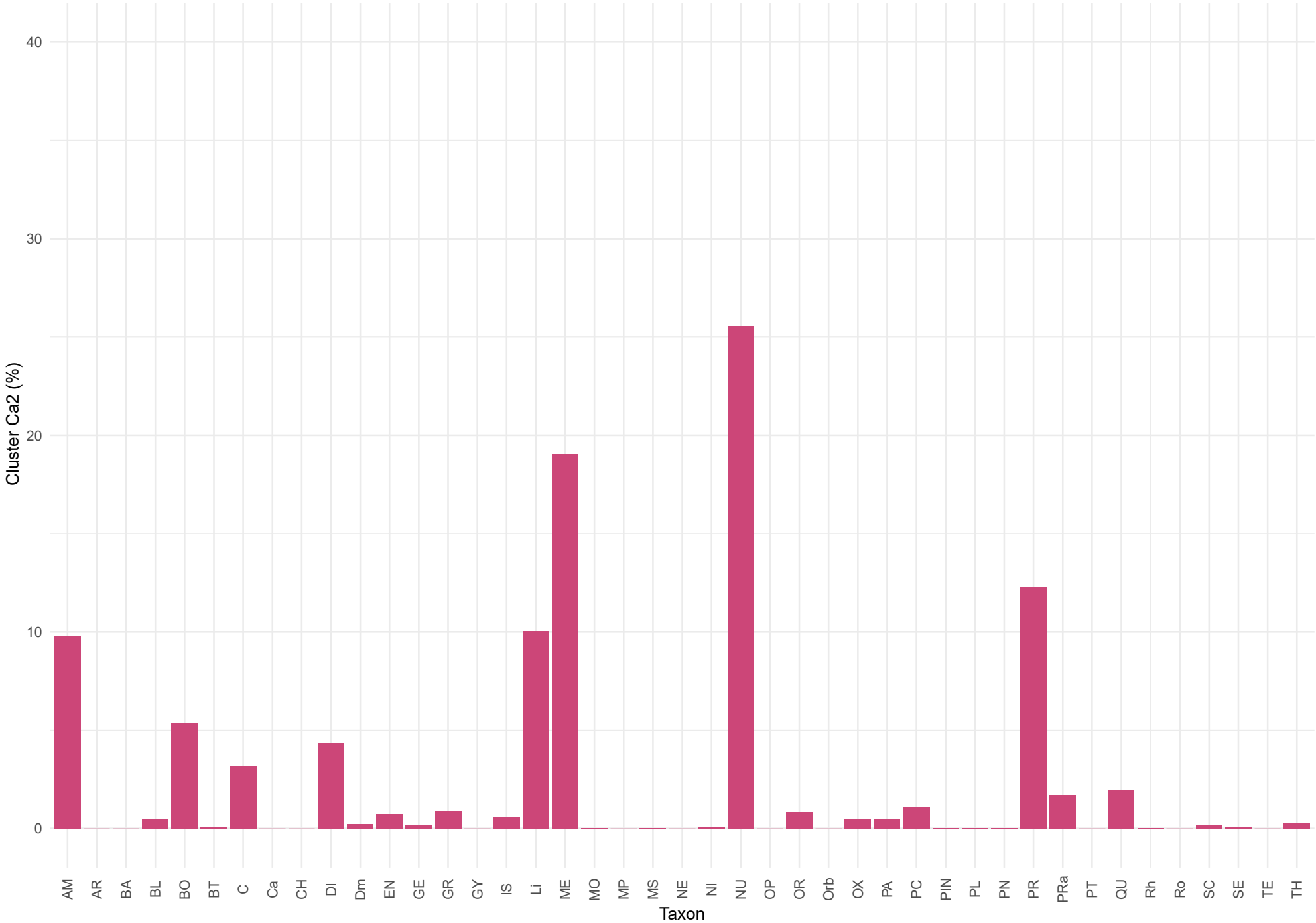
Calvert (CA)

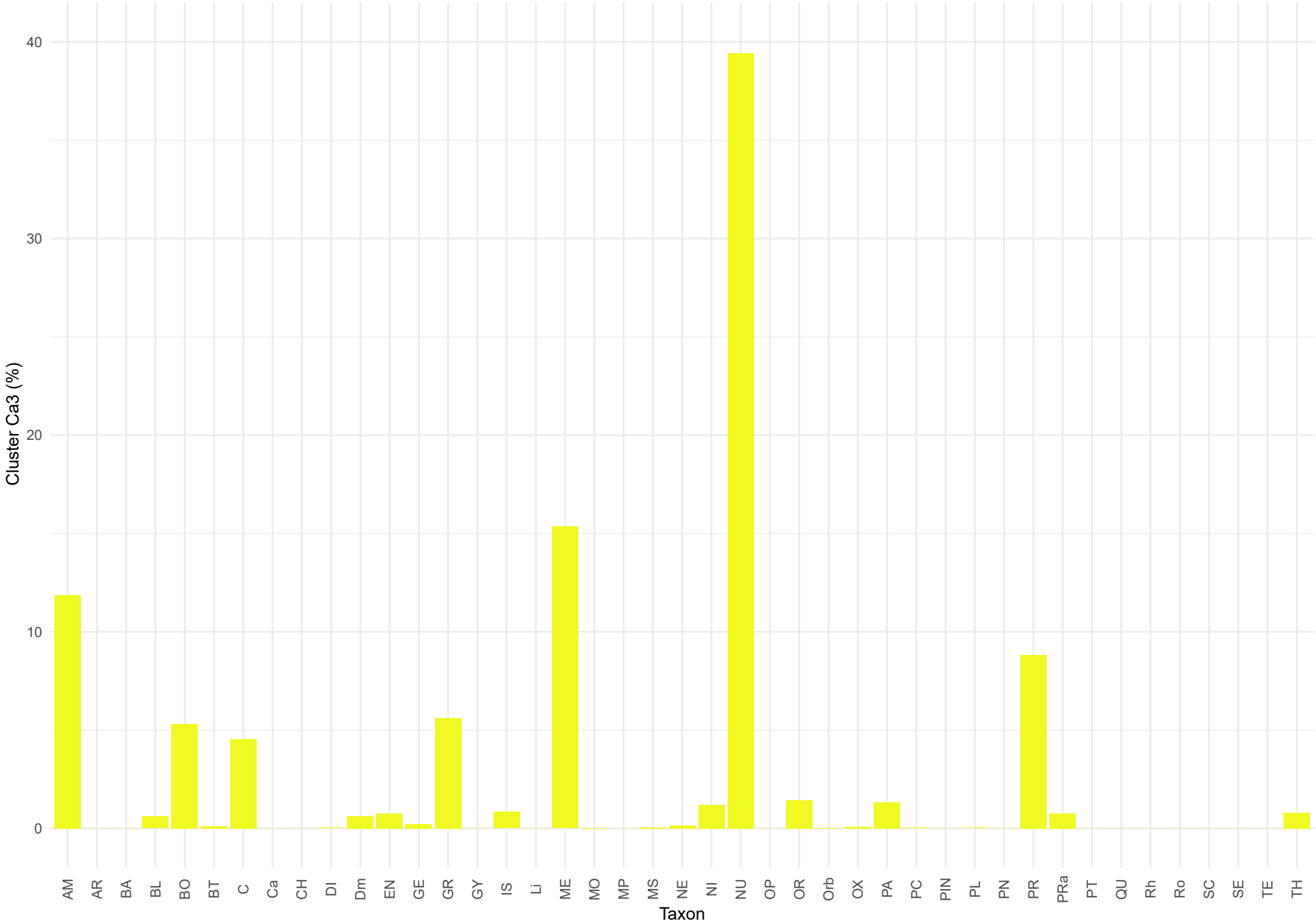

CA_ 12
CA_ 8
CA_ 9Ac
CA_ 2C
CA_ 9Ab
CA_ 6
CA_ 9Aa
CA_ 3A
CA_ 3D
CA_ 3C
CA_ 10B
CA_ 10A
CA_ 10R
CA_ 3E
CA_ 3H
CA_ 3F
CA_ 10N
CA_ 3G
CA_ 3B
CA_ 3Jb
CA_ 10D
CA_ 10L
CA_ 10J
CA_ 5
CA_ 10Hb
CA_ 10Ha
CA_ 11
CA_ 3L
CA_ 3K
CA_ 7
CA_ 4A
CA_ 4F
CA_ 3Ja
CA_ 4C
CA_ 10G
CA_ 10M
CA_ 4Ba
CA_ 4E
CA_ 10F
CA_ 4D
CA_ 4G
CA_ 10E
CA_ 4Jc
CA_ 10Ma
CA_ 4Ja
CA_ 4H
DCA2
DCA1
1.5
1.0
0.5
0.0
−0.5
−1
0
1
2
CA Cluster
Ca1
Ca2
Ca3

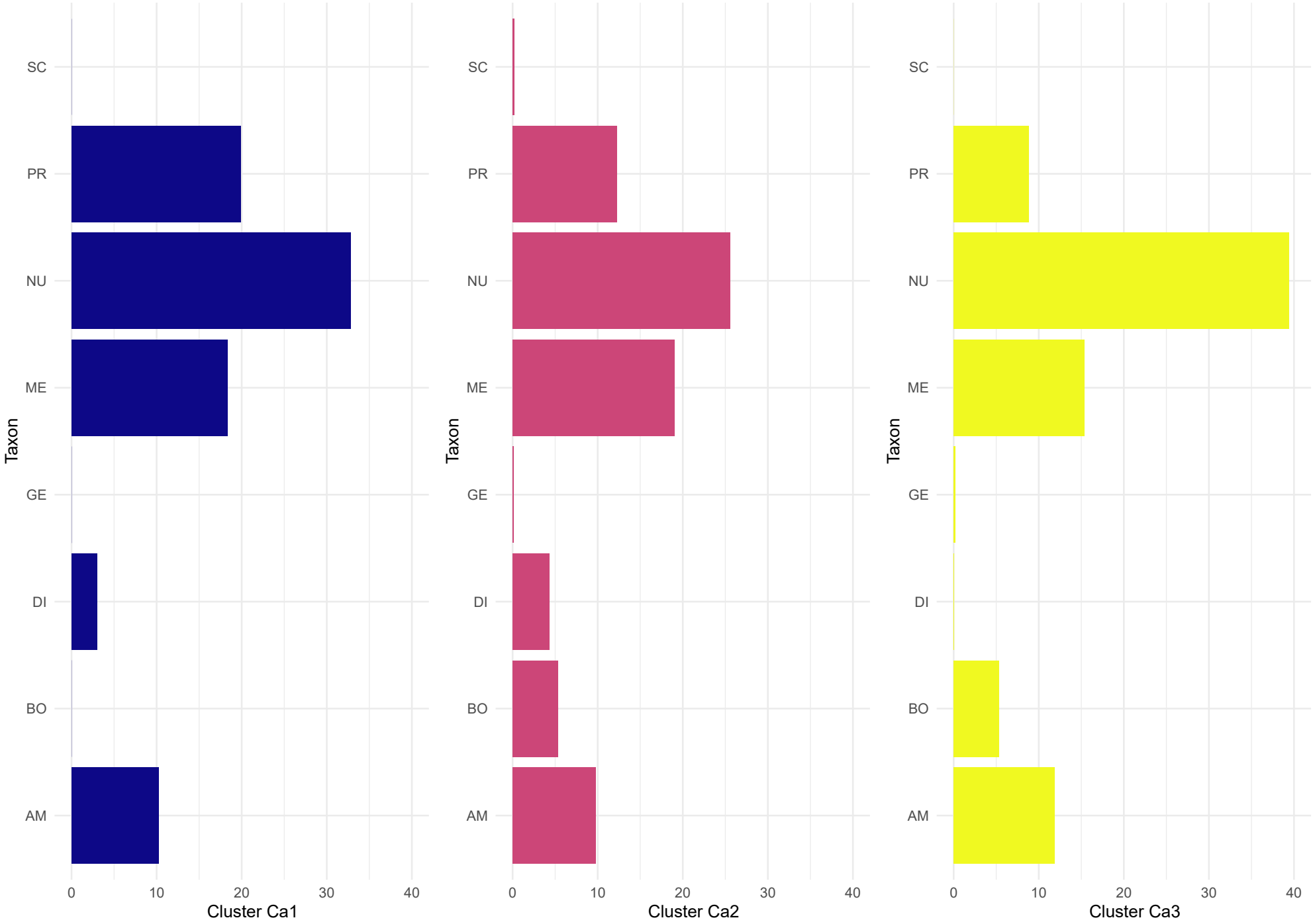

0
1
2
3
4
5
6
CA_2C
CA_3A
CA_3B
CA_3C
CA_3D
CA_3E
CA_3F
CA_3G
CA_3H
CA_3Ja
CA_3Jb
CA_3K
CA_3L
CA_4A
CA_4Ba
CA_4C
CA_4D
CA_4E
CA_4F
CA_4G
CA_4H
CA_4Ja
CA_4Jc
CA_5
CA_6
CA_7
CA_8
CA_9Ka
CA_9Kb
CA_9Kc
CA_10A
CA_10B
CA_10C
CA_10D
CA_10E
CA_10F
CA_10G
CA_10Ha
CA_10Hb
CA_10J
CA_10K
CA_10L
CA_10M
CA_10Ma
CA_10N
CA_10P
CA_10R
CA_11
CA_12
NERC

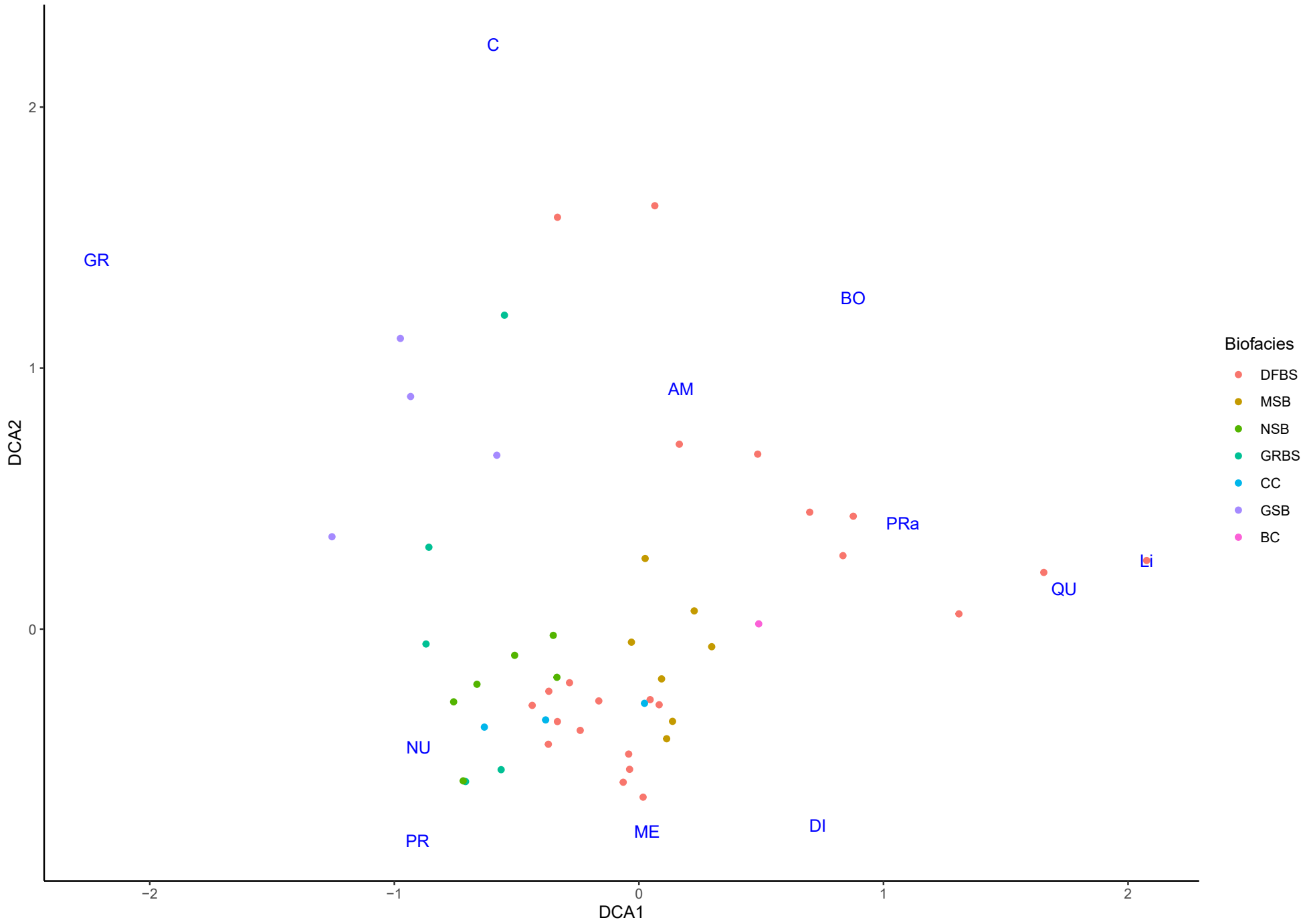

Cluster Ca1 (%)
Cluster Ca2 (%)
Cluster Ca3 (%)
0
10
20
30
40
AM AR BA BL BO BT C Ca CH DI Dm EN GE GR GY IS Li ME MO MP MS NE NI NU OP OR Orb OX PA PC PIN PL PN PR PRa PT QU Rh Ro SC SE TE TH
Taxon

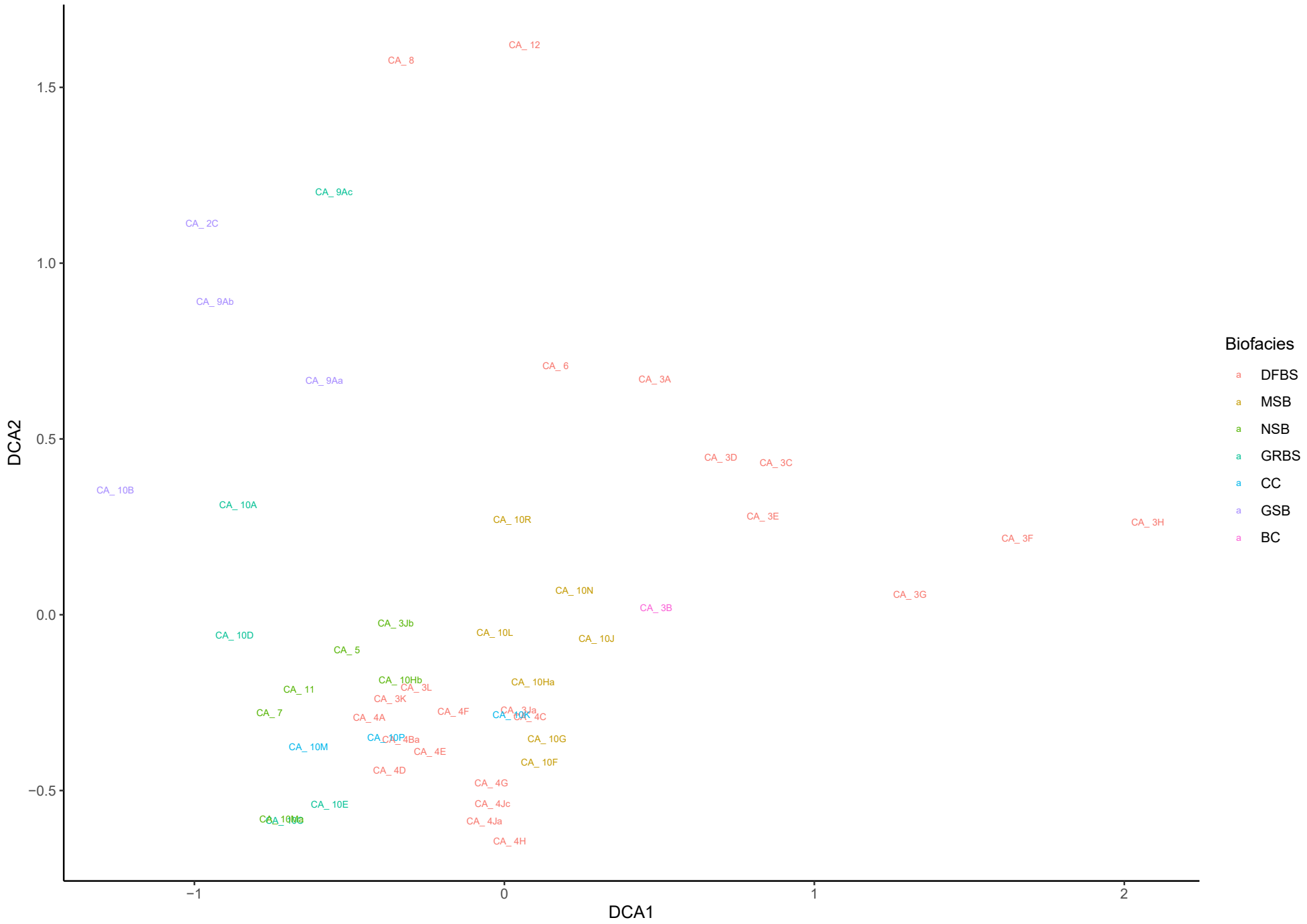

Cluster Ca1 (%)
40
30
20
10
0
AM
AR
BA
BL
BO
BT
C
Ca
CH
DI
Dm
EN
GE
GR
GY
IS
Li
ME
MO
MP
MS
NE
NI
NU
OP
OR
Orb
OX
PA
PC
PIN
PL
PN
PR
PRa
PT
QU
Rh
Ro
SC
SE
TE
TH
Taxon


Cluster Ca2 (%)
40
30
20
10
0
AM
AR
BA
BL
BO
BT
C
Ca
CH
DI
Dm
EN
GE
GR
GY
IS
Li
ME
MO
MP
MS
NE
NI
NU
OP
OR
Orb
OX
PA
PC
PIN
PL
PN
PR
PRa
PT
QU
Rh
Ro
SC
SE
TE
TH
Taxon

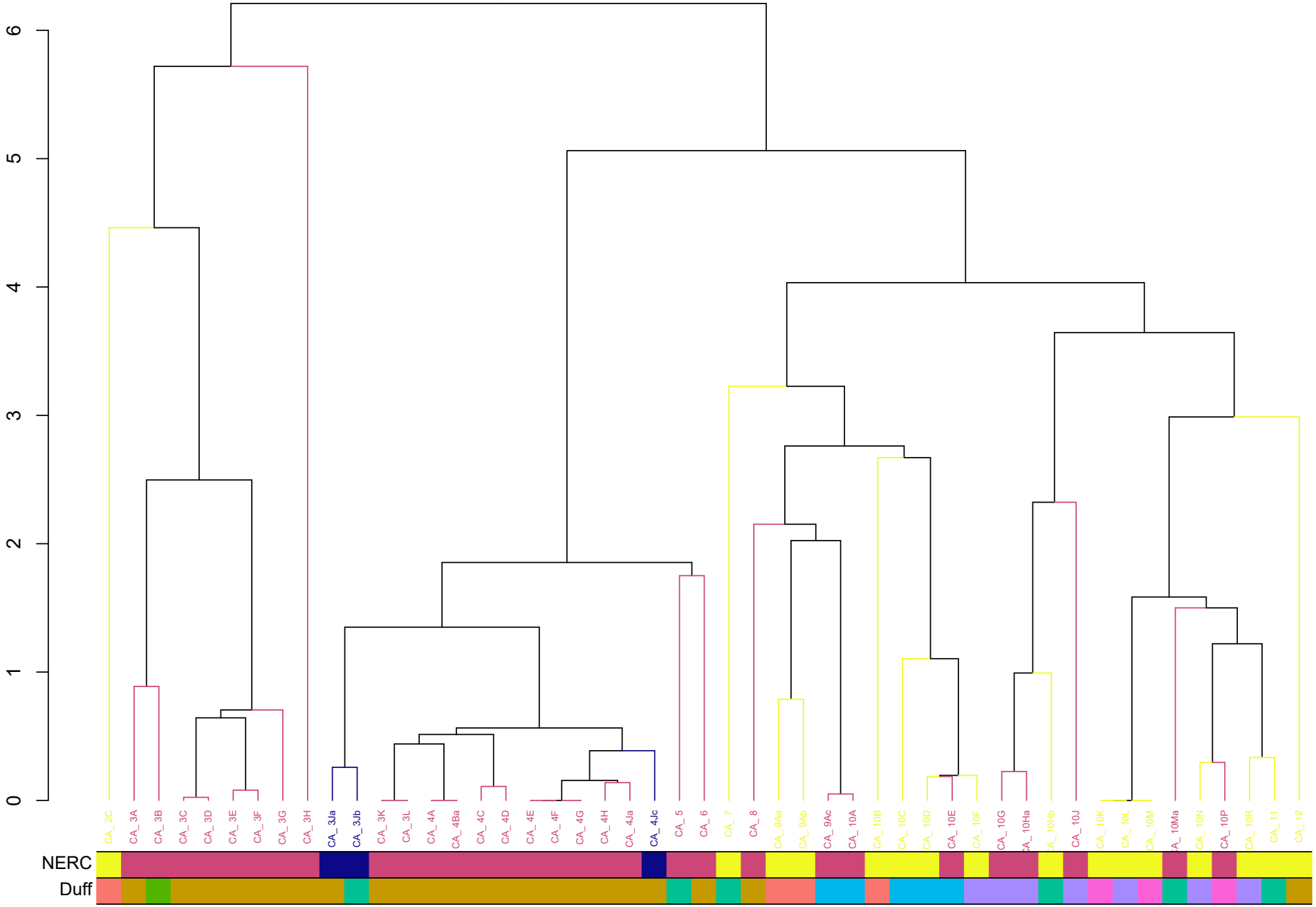

Cluster Ca3 (%)
40
30
20
10
0
AM
AR
BA
BL
BO
BT
C
Ca
CH
DI
Dm
EN
GE
GR
GY
IS
Li
ME
MO
MP
MS
NE
NI
NU
OP
OR
Orb
OX
PA
PC
PIN
PL
PN
PR
PRa
PT
QU
Rh
Ro
SC
SE
TE
TH
Taxon


SC
PR
NU
ME
GE
DI
BO
AM
Taxon
0
10
20
30
40
Cluster Ca1
Cluster Ca2
Cluster Ca3

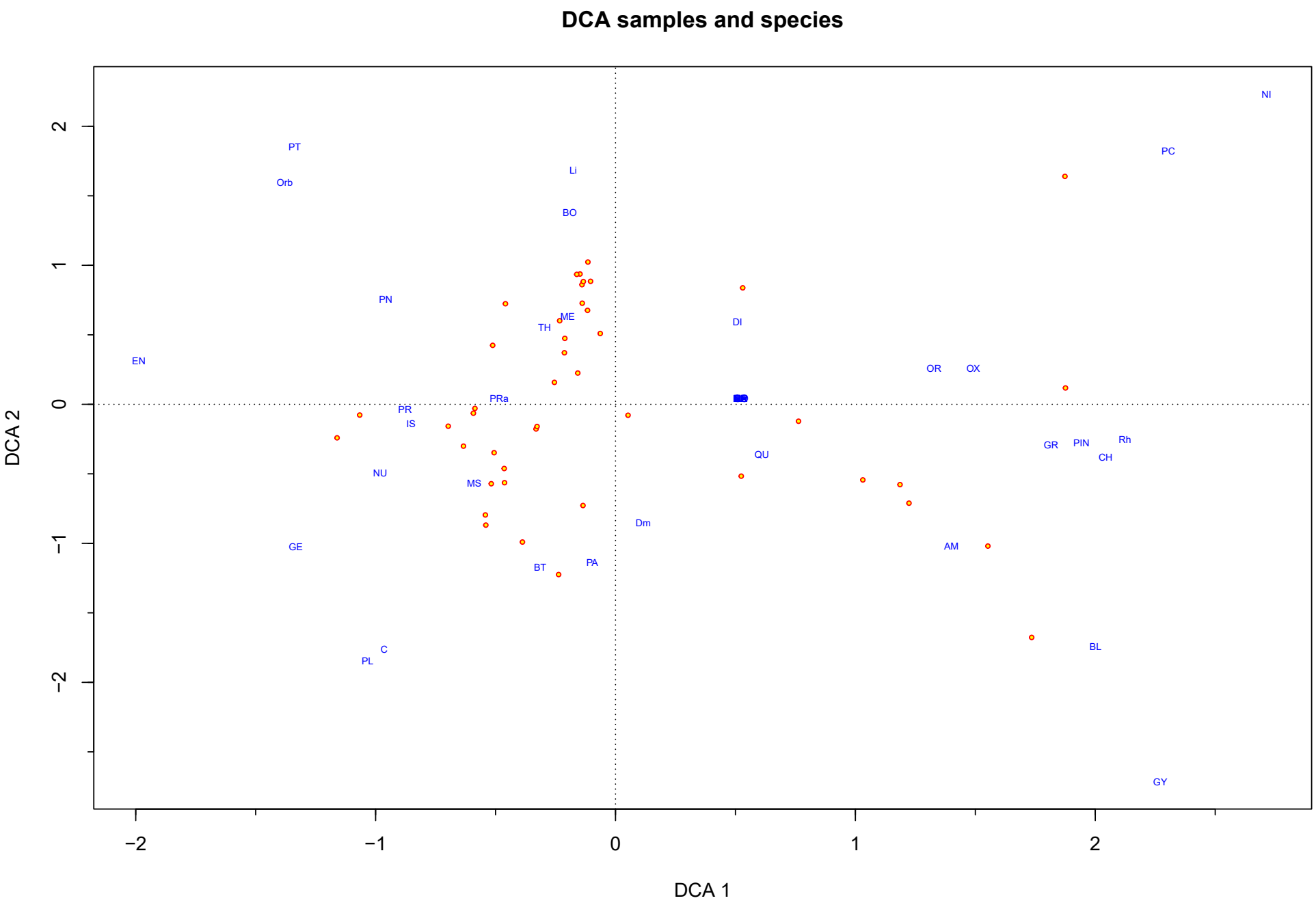

C
GR
BO
AM
PRa
Li
QU
NU
PR
ME
DI
DCA2
DCA1
2
1
0
−2
−1
0
1
2
Biofacies
DFBS
MSB
NSB
GRBS
CC
GSB
BC

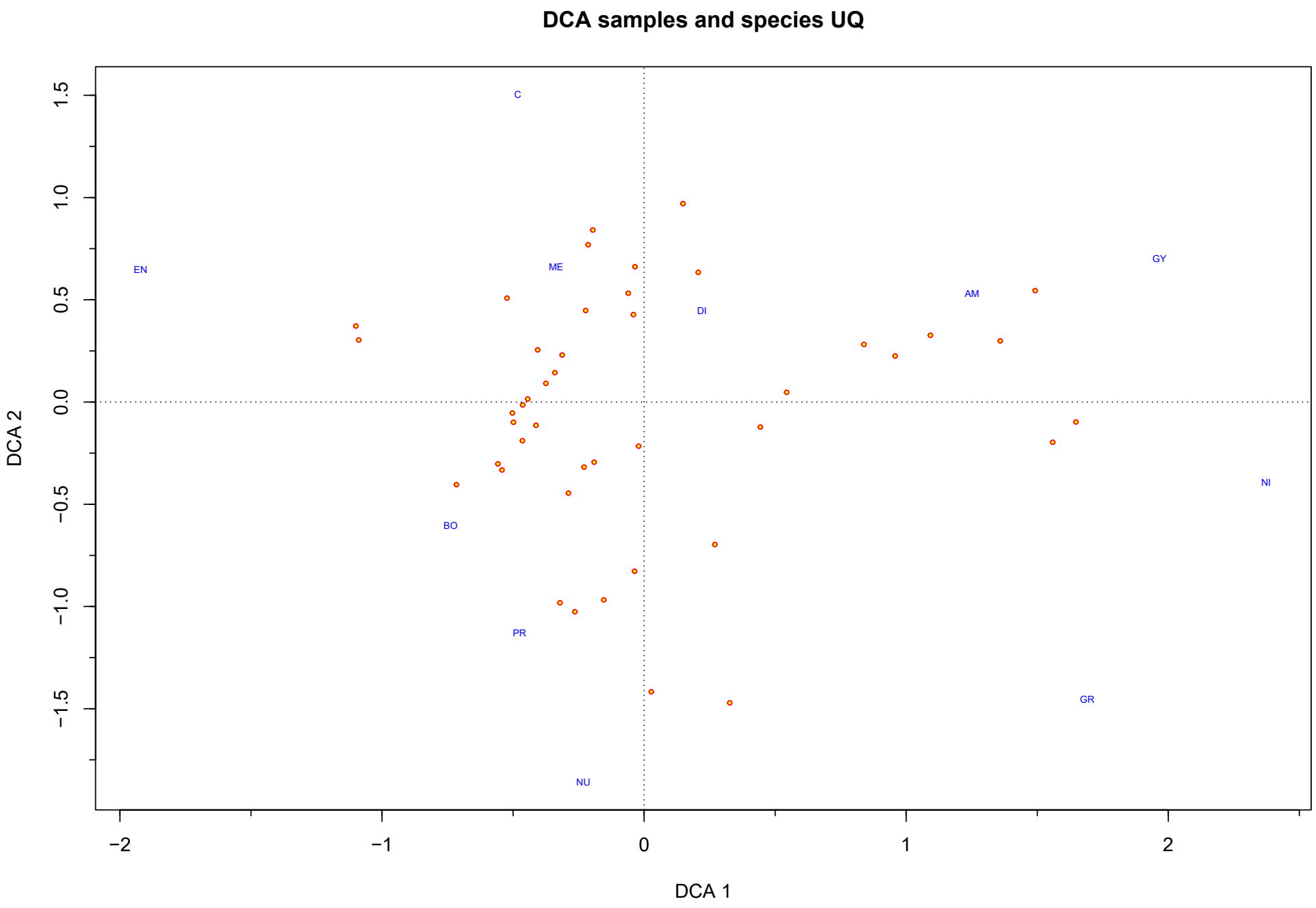

DCA2
DCA1
1.5
1.0
0.5
0.0
−0.5
−1
0
1
2
CA_ 12
CA_ 8
CA_ 9Ac
CA_ 2C
CA_ 9Ab
CA_ 6
CA_ 9Aa
CA_ 3A
CA_ 3D
CA_ 3C
CA_ 10B
CA_ 10A
CA_ 10R
CA_ 3E
CA_ 3H
CA_ 3F
CA_ 10N
CA_ 3G
CA_ 3B
CA_ 3Jb
CA_ 10L
CA_ 10D
CA_ 10J
CA_ 5
CA_ 10Hb
CA_ 10Ha
CA_ 11
CA_ 3L
CA_ 3K
CA_ 7
CA_ 4A
CA_ 4F
CA_ 3Ja
CA_ 4C
CA_ 10G
CA_ 10M
CA_ 4Ba
CA_ 4E
CA_ 10F
CA_ 4D
CA_ 4G
CA_ 10E
CA_ 4Jc
CA_ 4Ja
CA_ 4H
Biofacies
DFBS
MSB
NSB
GRBS
CC
GSB
BC

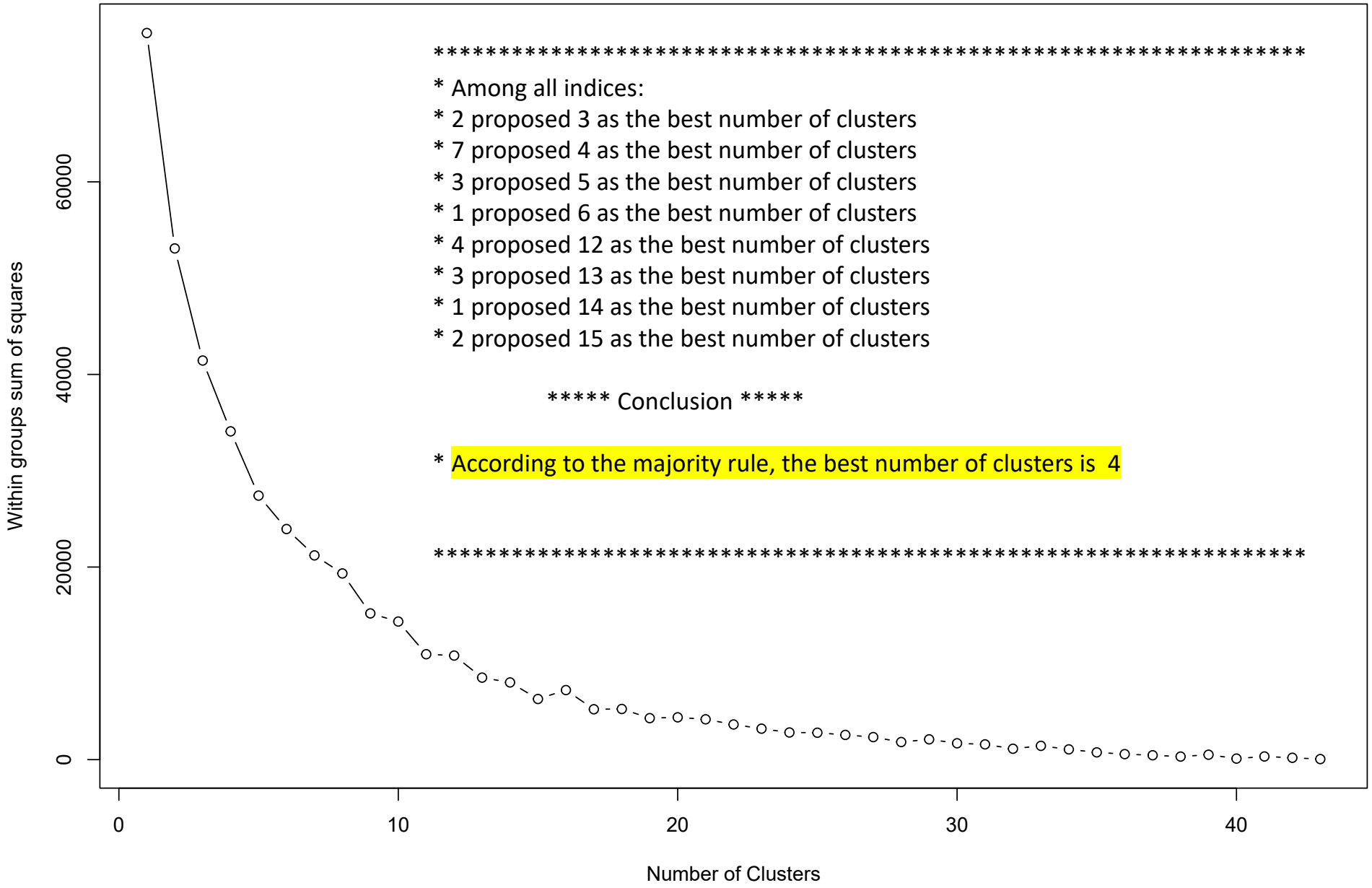
Calvert (CA)


0
1
2
3
4
5
6
CA_2C
CA_3A
CA_3B
CA_3C
CA_3D
CA_3E
CA_3F
CA_3G
CA_3H
CA_3Ia
CA_3Ib
CA_3K
CA_3L
CA_4A
CA_4Ba
CA_4C
CA_4D
CA_4E
CA_4F
CA_4G
CA_4H
CA_4Ia
CA_4Ic
CA_5
CA_6
CA_7
CA_8
CA_9Aa
CA_9Ab
CA_9Ac
CA_10A
CA_10B
CA_10C
CA_10D
CA_10E
CA_10F
CA_10G
CA_10Ha
CA_10Hb
CA_10J
CA_10K
CA_10L
CA_10M
CA_10Ma
CA_10N
CA_10P
CA_10R
CA_11
CA_12
NERC
Duff

Norman Cross (NC)


DCA samples and species
DCA 1
DCA 2
−2
−1
0
1
2
NI
PC
PT
Orb
Li
BO
PN
ME
TH
DI
EN
OR
OX
PRa
PR
IS
QU
GR
PIN
Rh
CH
NU
MS
Dm
GE
AM
BT
PA
C
PL
BL
GY


DCA samples and species UQ
C
EN
ME
DI
AM
GY
NI
BO
PR
GR
NU
DCA 2
DCA 1
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−2
−1
0
1
2

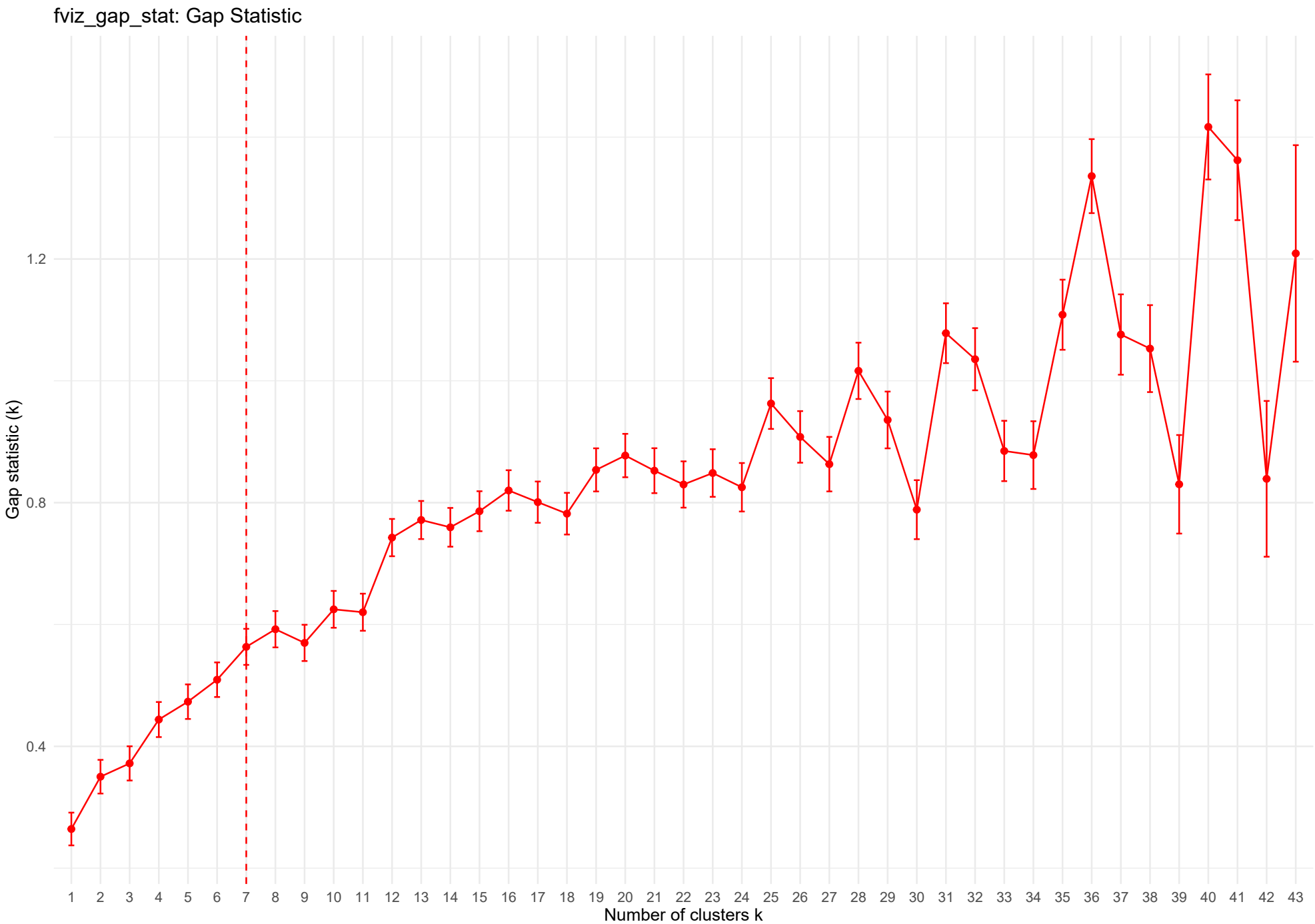


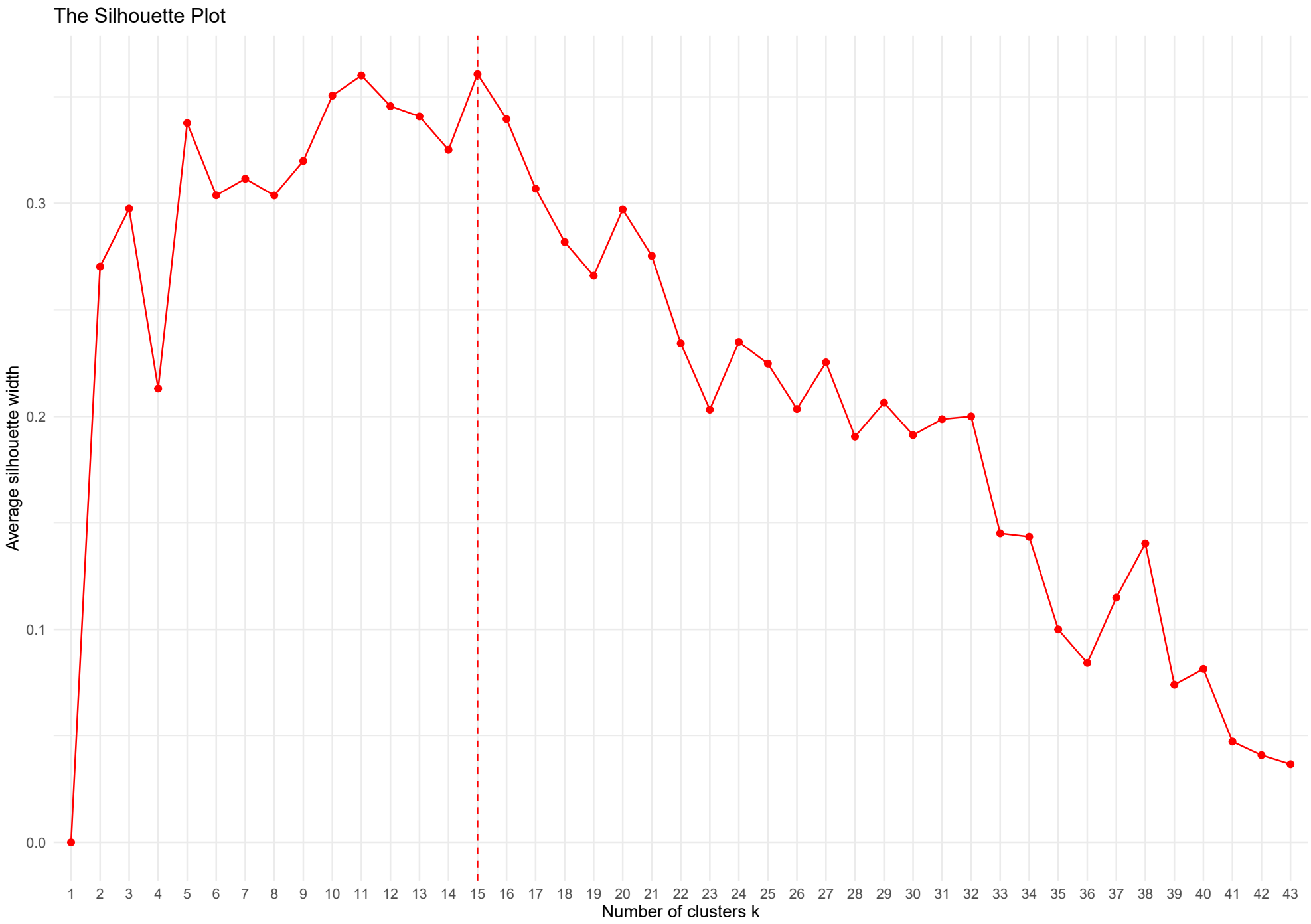
****
* Among all indices:
* 2 proposed 3 as the best number of clusters
* 7 proposed 4 as the best number of clusters
* 3 proposed 5 as the best number of clusters
* 1 proposed 6 as the best number of clusters
* 4 proposed 12 as the best number of clusters
* 3 proposed 13 as the best number of clusters
* 1 proposed 14 as the best number of clusters
* 2 proposed 15 as the best number of clusters

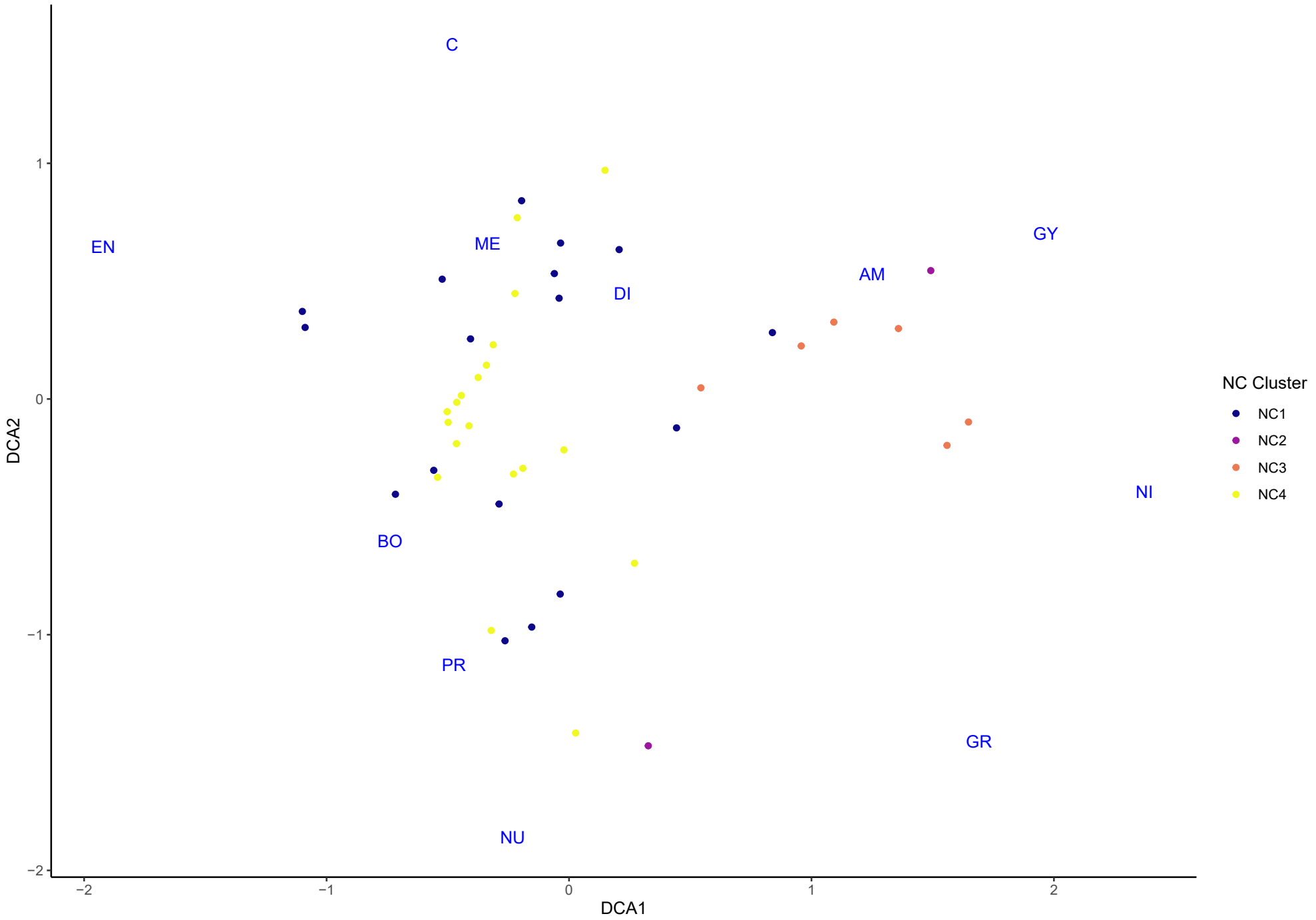
***** Conclusion *****

* According to the majority rule, the best number of clusters is 4

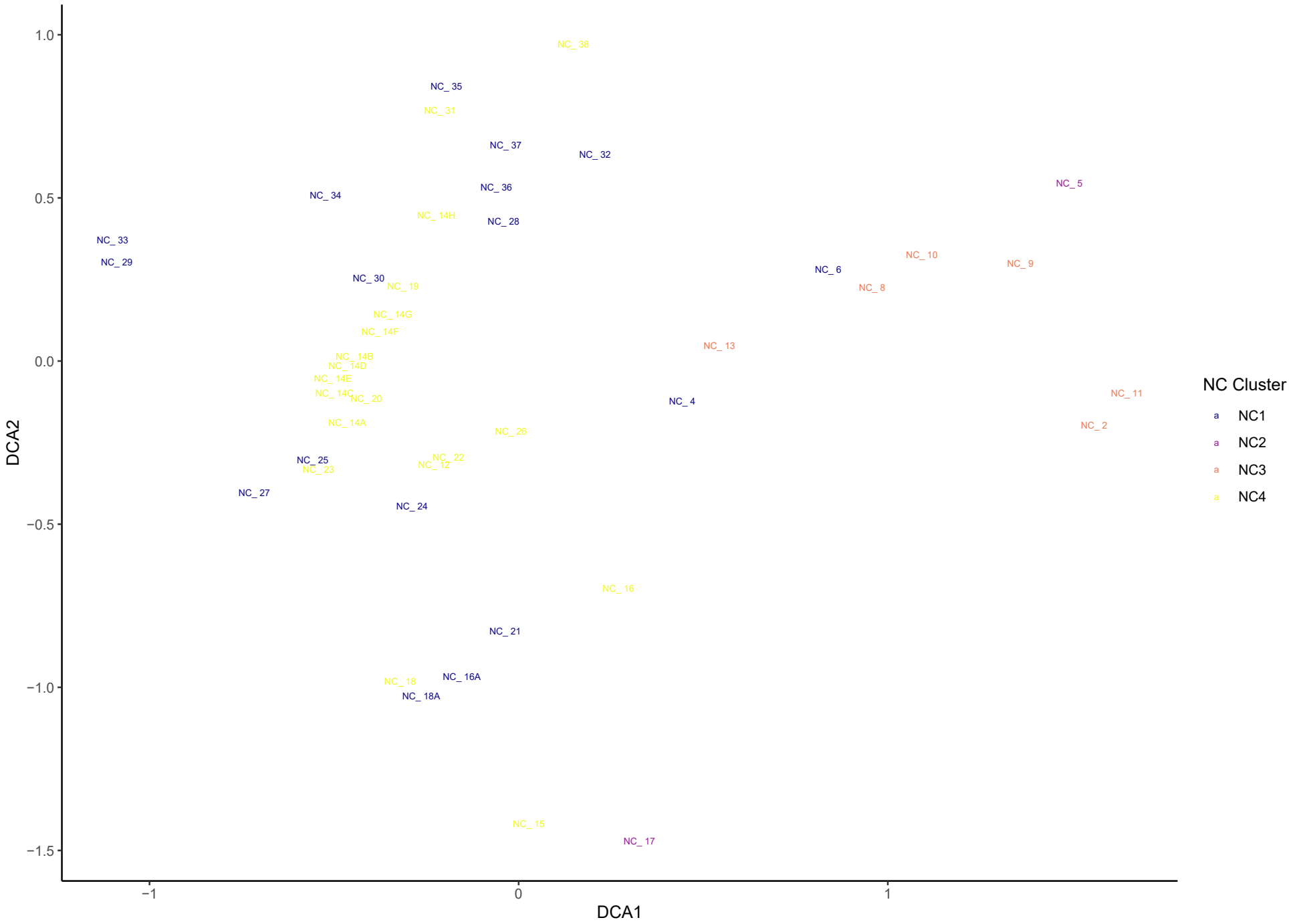
****

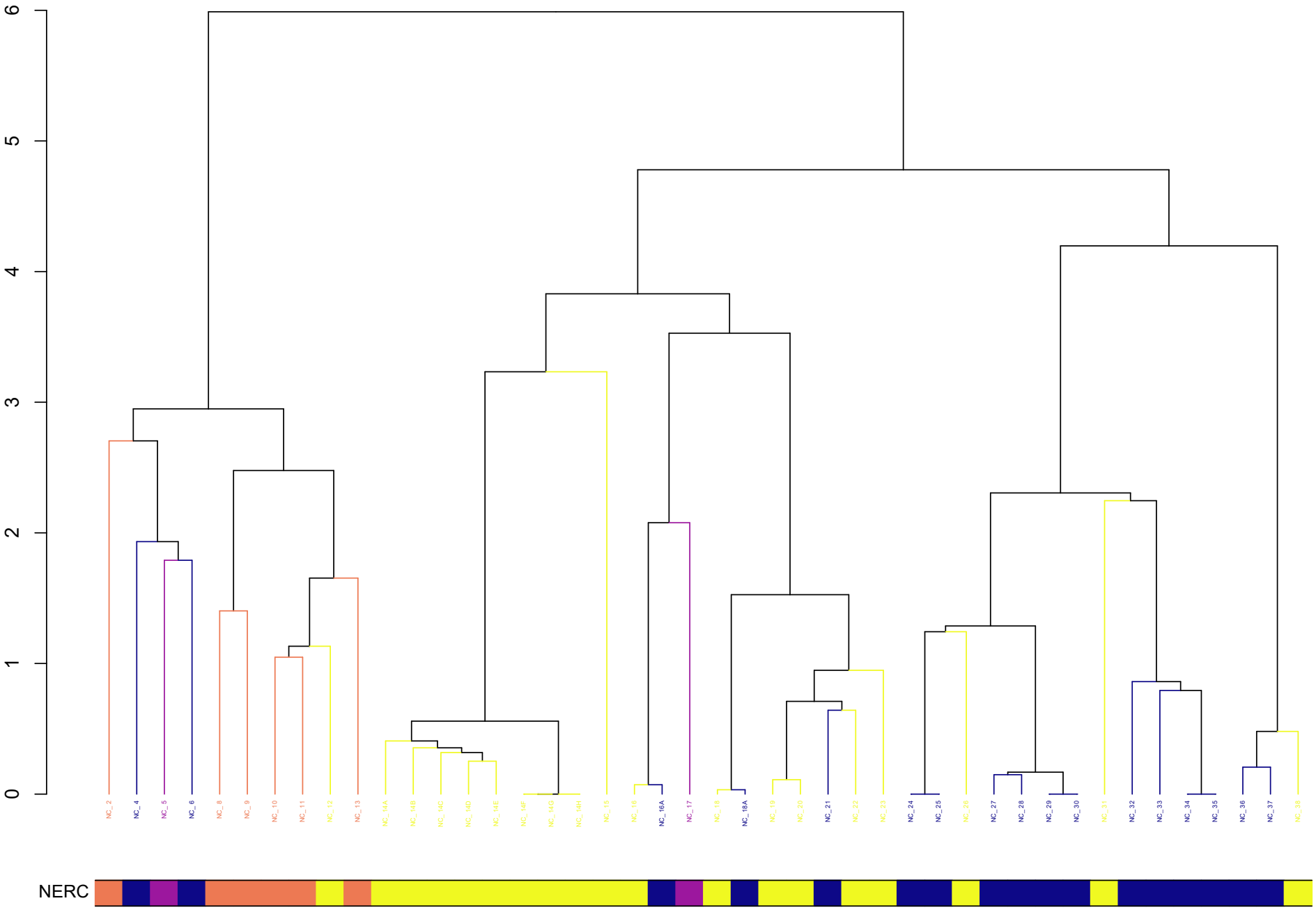

fviz_gap_stat: Gap Statistic
Gap statistic (k)
0.4
0.8
1.2
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43
Number of clusters k

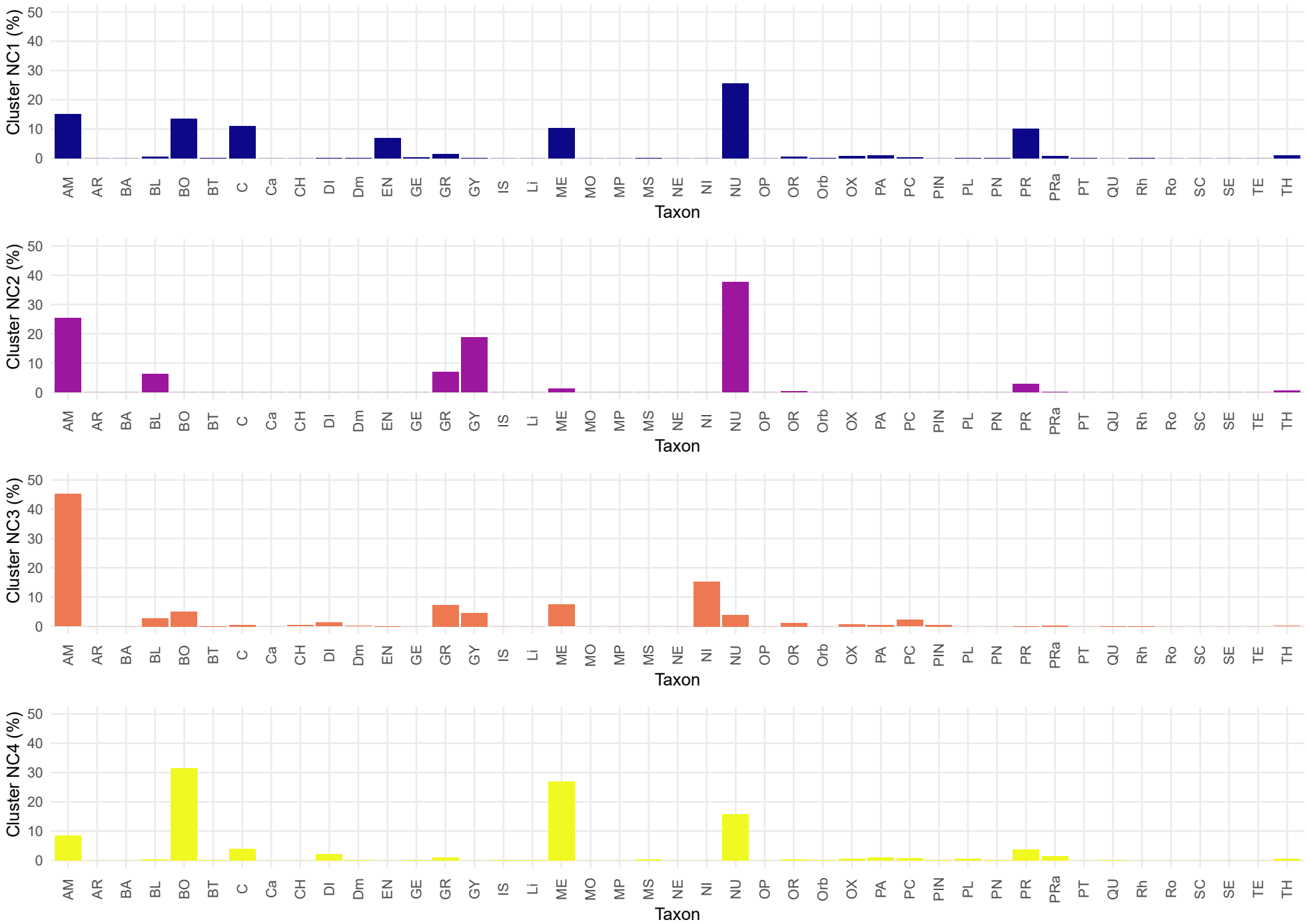

The Silhouette Plot
Average silhouette width
0.0
0.1
0.2
0.3
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43
Number of clusters k

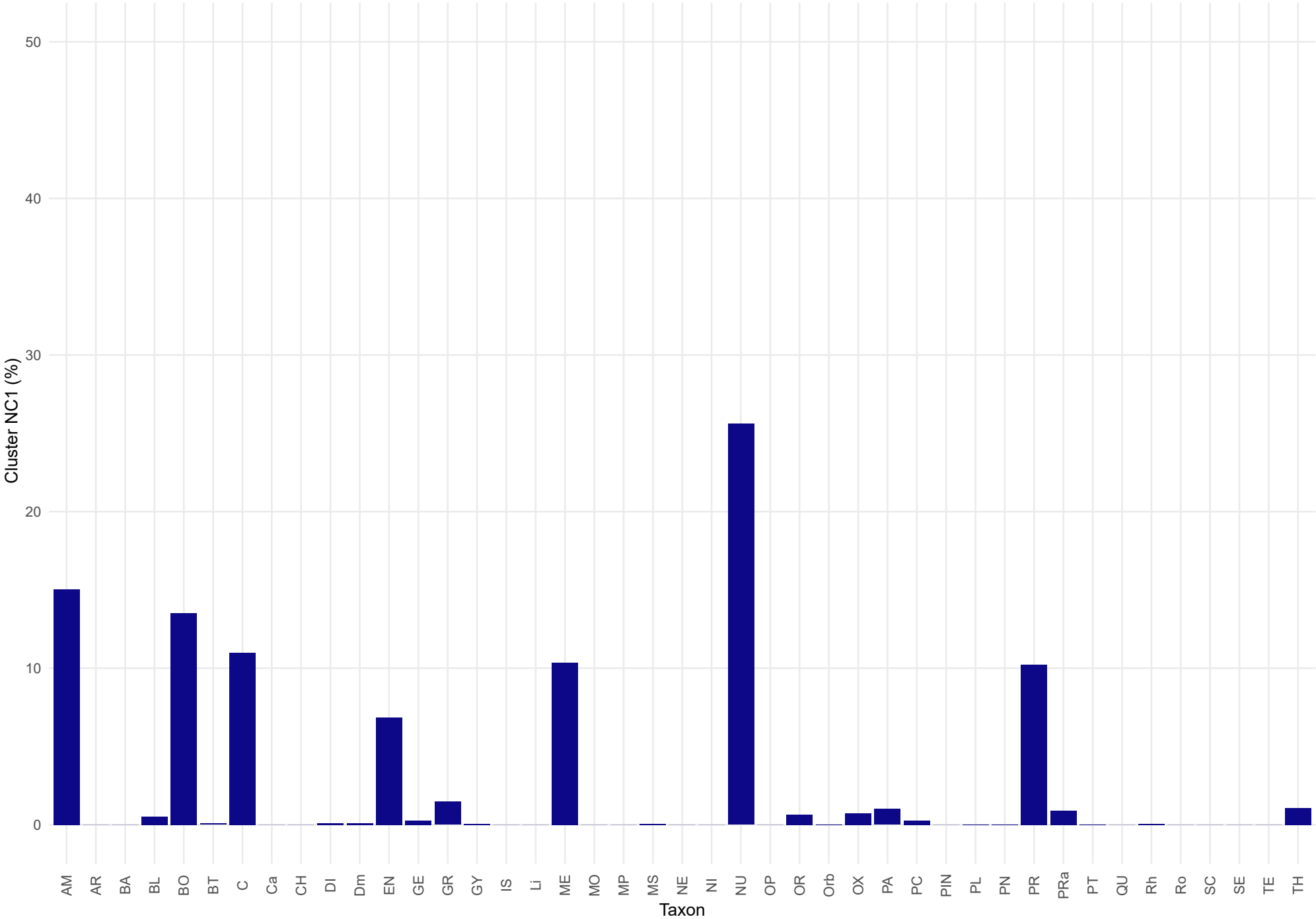


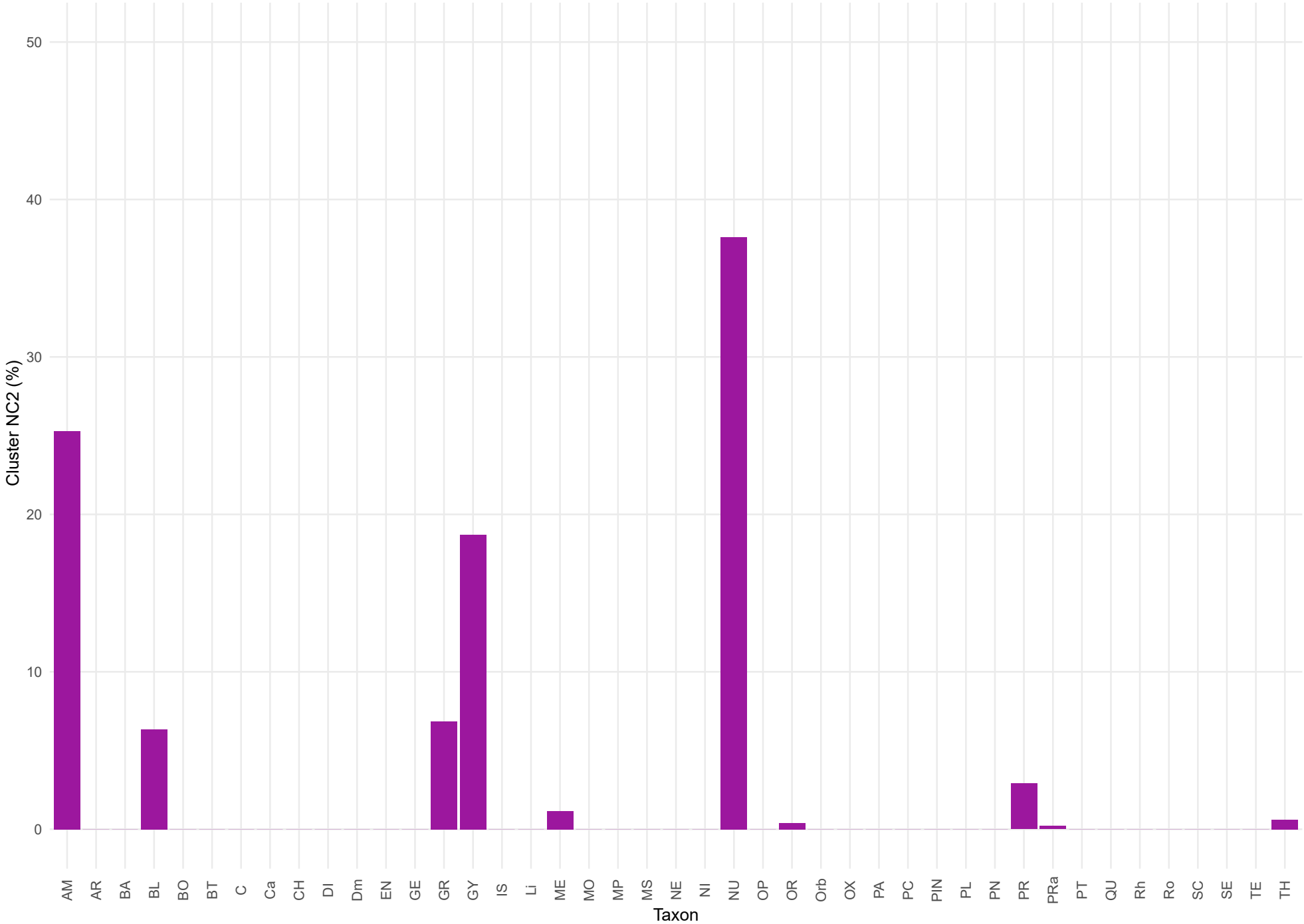
Norman Cross (NC)

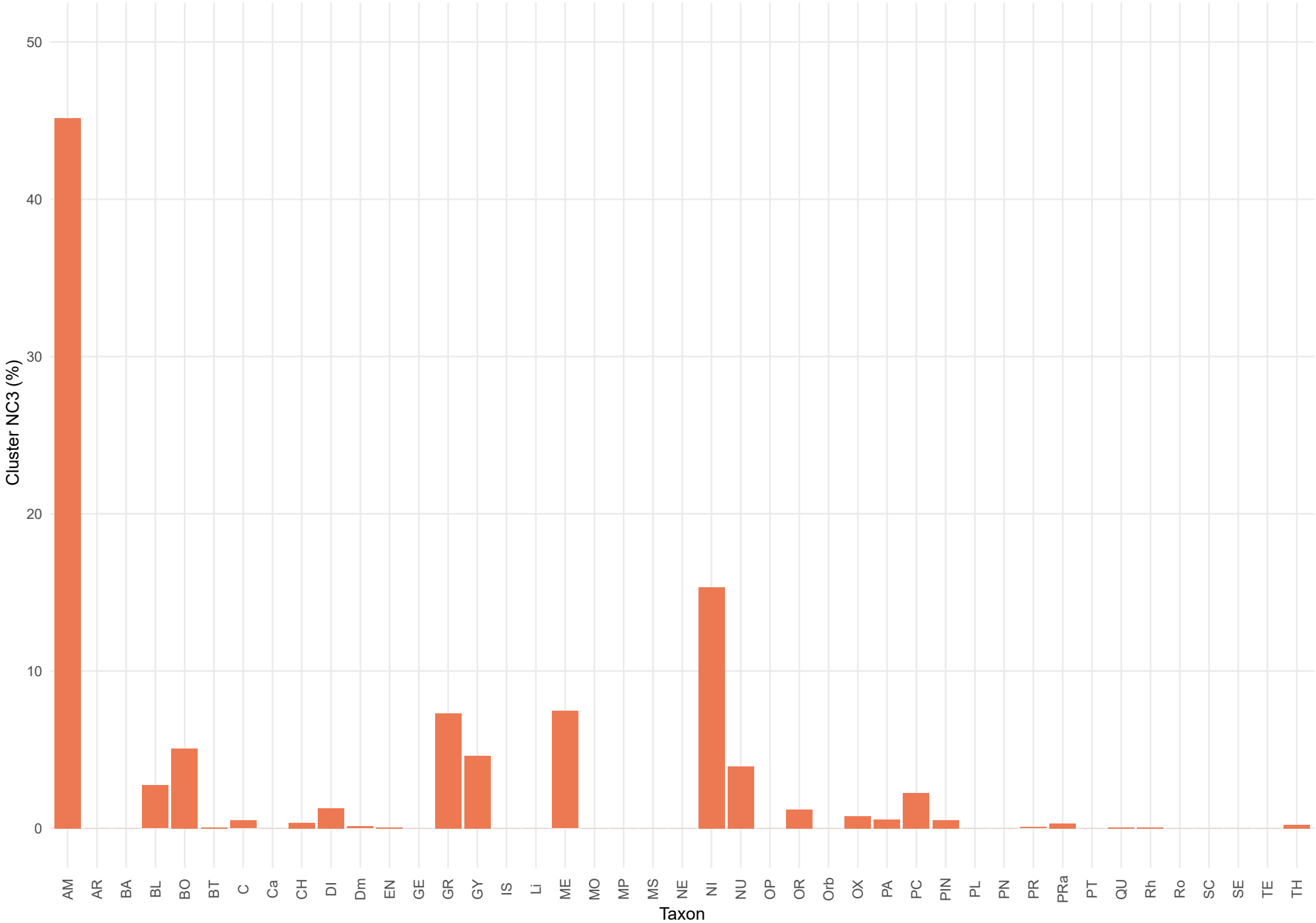

1.0
0.5
0.0
−0.5
−1.0
−1.5
DCA2
−1
0
1
DCA1
NC_ 38
NC_ 35
NC_ 31
NC_ 37
NC_ 32
NC_ 5
NC_ 34
NC_ 36
NC_ 14H
NC_ 28
NC_ 33
NC_ 29
NC_ 10
NC_ 9
NC_ 6
NC_ 30
NC_ 19
NC_ 8
NC_ 14G
NC_ 14F
NC_ 13
NC_ 14B
NC_ 14D
NC_ 14E
NC_ 14C
NC_ 20
NC_ 11
NC_ 4
NC_ 14A
NC_ 26
NC_ 2
NC_ 25
NC_ 22
NC_ 23
NC_ 12
NC_ 27
NC_ 24
NC_ 16
NC_ 21
NC_ 16A
NC_ 18
NC_ 18A
NC_ 15
NC_ 17
NC Cluster
NC1
NC2
NC3
NC4

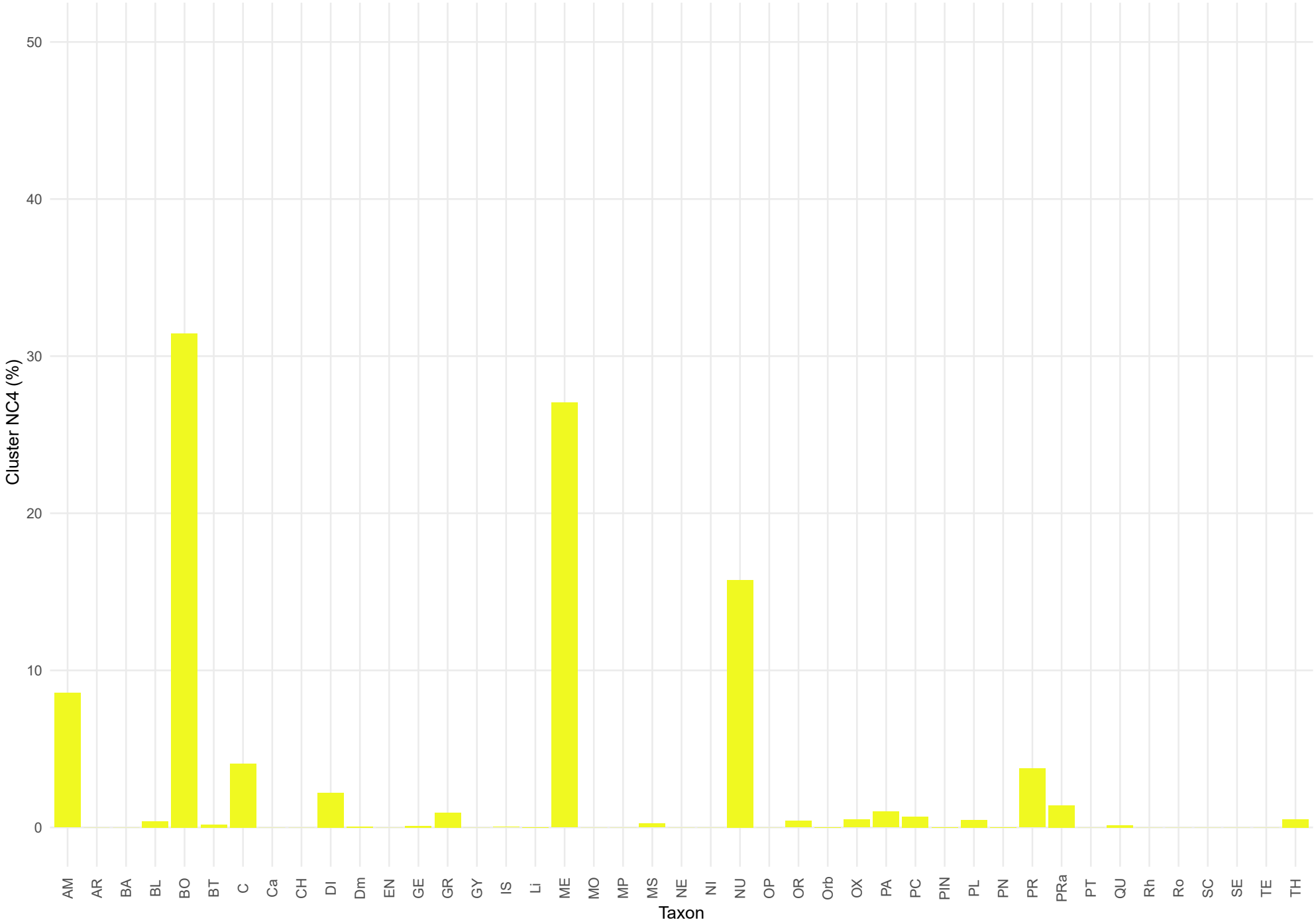

0
1
2
3
4
5
6
NC_2
NC_4
NC_5
NC_6
NC_8
NC_9
NC_10
NC_11
NC_12
NC_13
NC_14A
NC_14B
NC_14C
NC_14D
NC_14E
NC_14F
NC_14G
NC_14H
NC_15
NC_16
NC_16A
NC_17
NC_18
NC_18A
NC_19
NC_20
NC_21
NC_22
NC_23
NC_24
NC_25
NC_26
NC_27
NC_28
NC_29
NC_30
NC_31
NC_32
NC_33
NC_34
NC_35
NC_36
NC_37
NC_38
NERC

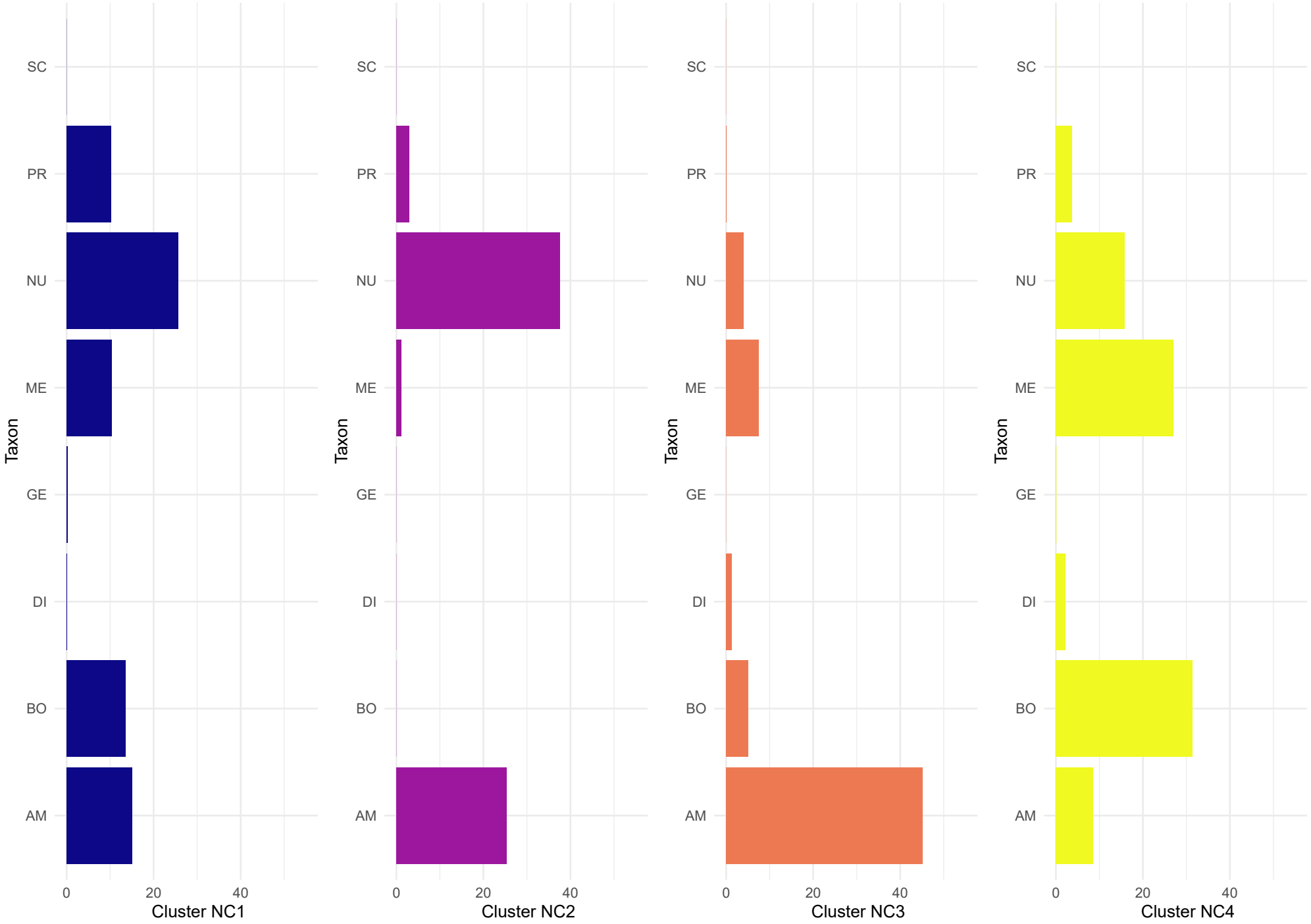

Cluster NC1 (%)
Cluster NC2 (%)
Cluster NC3 (%)
Cluster NC4 (%)
0
10
20
30
40
50
AM AR BA BL BO BT C Ca CH DI Dm EN GE GR GY IS Li ME MO MP MS NE NI NU OP OR Orb OX PA PC PIN PL PN PR PRa PT QU Rh Ro SC SE TE TH
Taxon


Cluster NC1 (%)
50
40
30
20
10
0
AM
AR
BA
BL
BO
BT
C
Ca
CH
DI
Dm
EN
GE
GR
GY
IS
Li
ME
MO
MP
MS
NE
NI
NU
OP
OR
Orb
OX
PA
PC
PIN
PL
PN
PR
PRa
PT
QU
Rh
Ro
SC
SE
TE
TH
Taxon

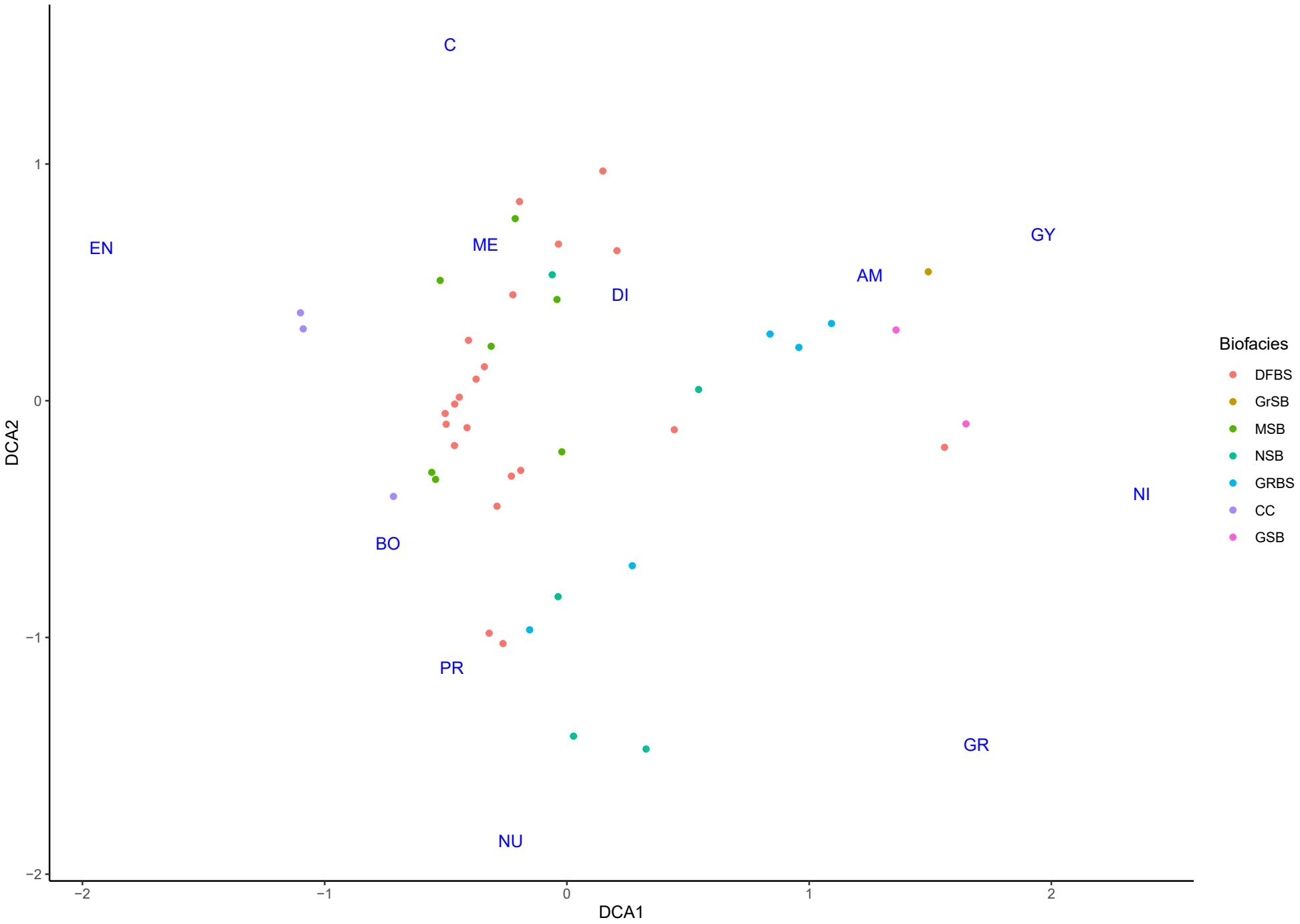

Cluster NC2 (%)
50
40
30
20
10
0
AM
AR
BA
BL
BO
BT
C
Ca
CH
DI
Dm
EN
GE
GR
GY
IS
Li
ME
MO
MP
MS
NE
NI
NU
OP
OR
Orb
OX
PA
PC
PIN
PL
PN
PR
PRa
PT
QU
Rh
Ro
SC
SE
TE
TH
Taxon


Cluster NC3 (%)
50
40
30
20
10
0
AM
AR
BA
BL
BO
BT
C
Ca
CH
DI
Dm
EN
GE
GR
GY
IS
Li
ME
MO
MP
MS
NE
NI
NU
OP
OR
Orb
OX
PA
PC
PIN
PL
PN
PR
PRa
PT
QU
Rh
Ro
SC
SE
TE
TH
Taxon

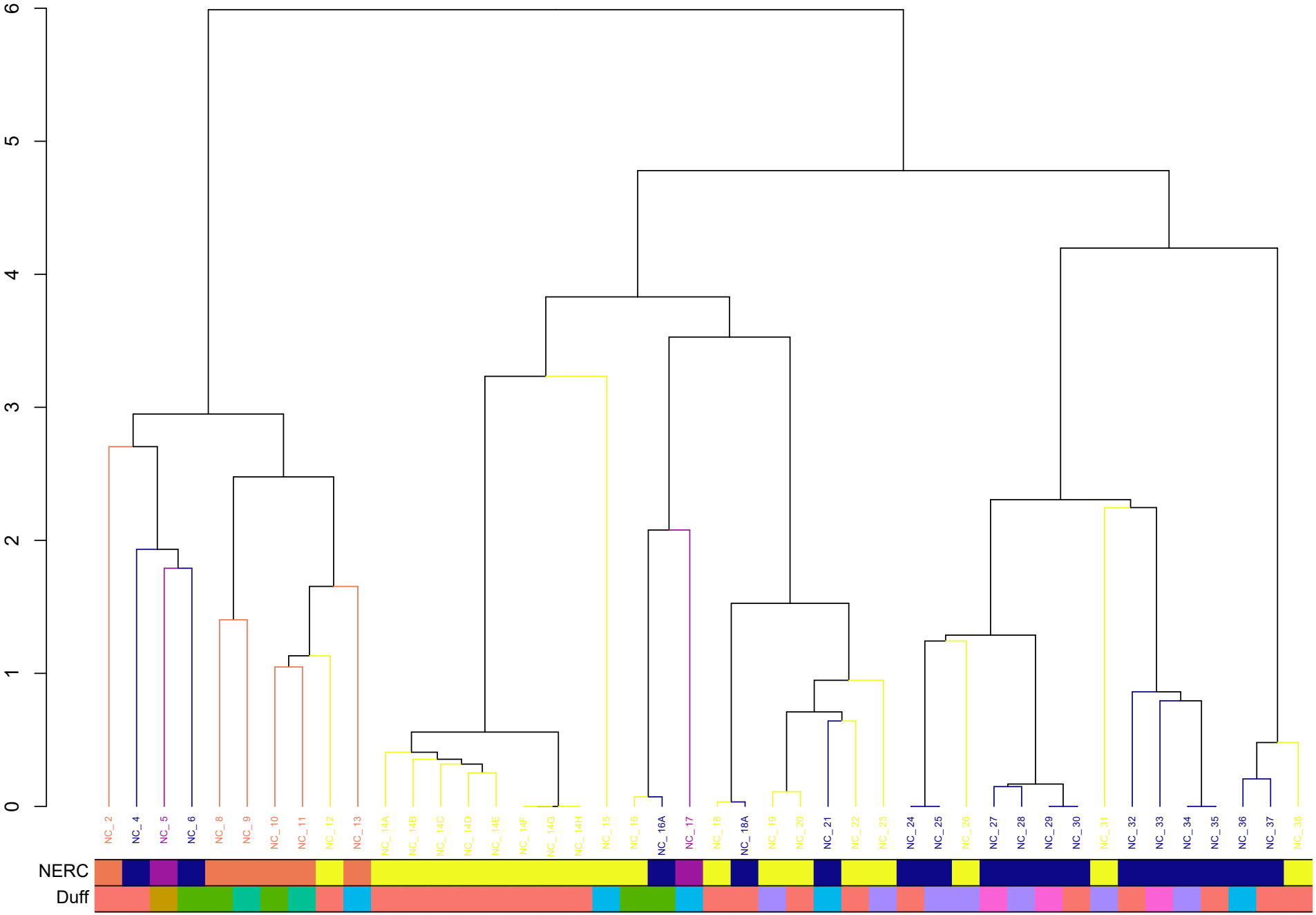

Cluster NC4 (%)
50
40
30
20
10
0
AM
AR
BA
BL
BO
BT
C
Ca
CH
DI
Dm
EN
GE
GR
GY
IS
Li
ME
MO
MP
MS
NE
NI
NU
OP
OR
Orb
OX
PA
PC
PIN
PL
PN
PR
PRa
PT
QU
Rh
Ro
SC
SE
TE
TH
Taxon



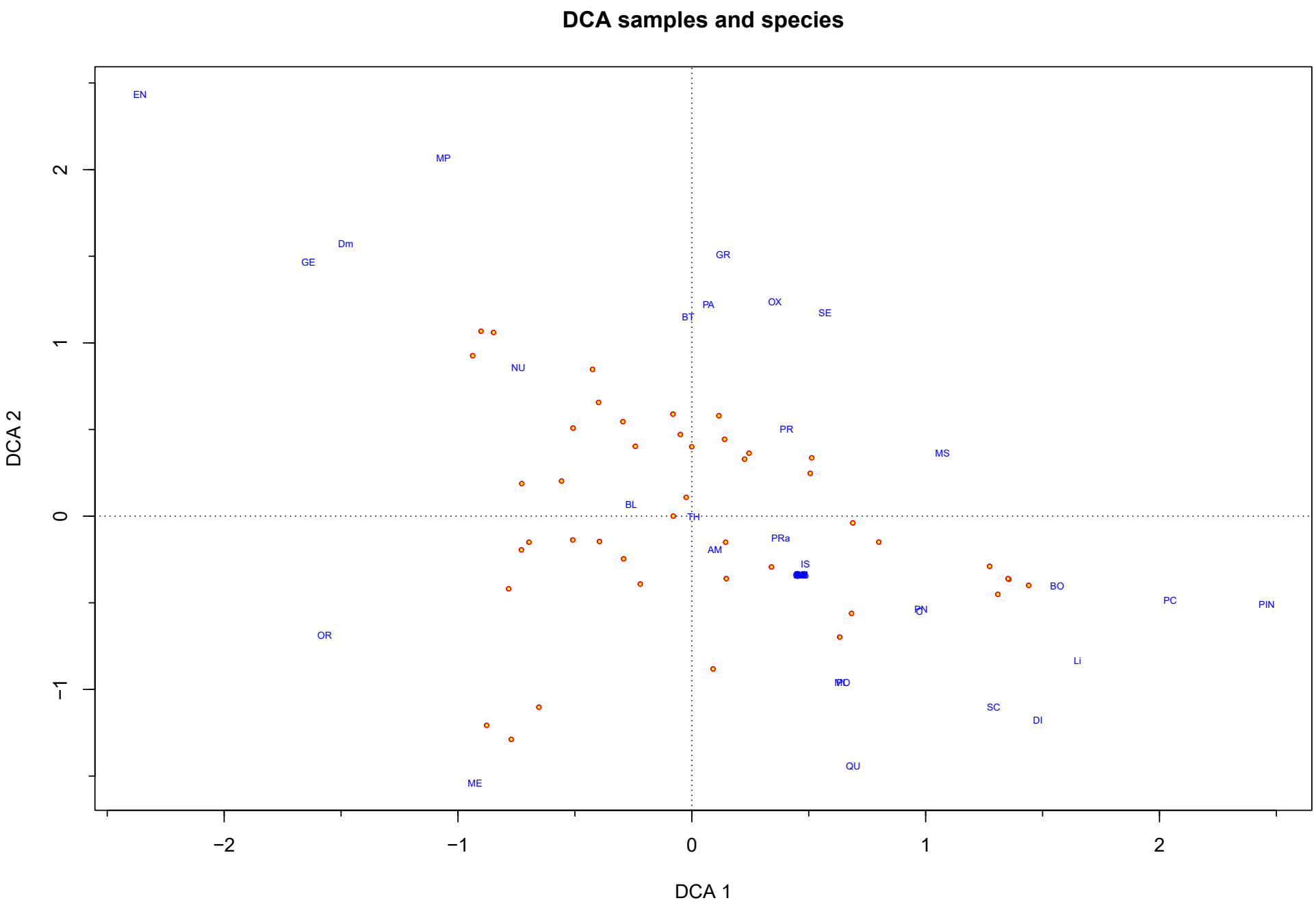
Norman Cross (NC)

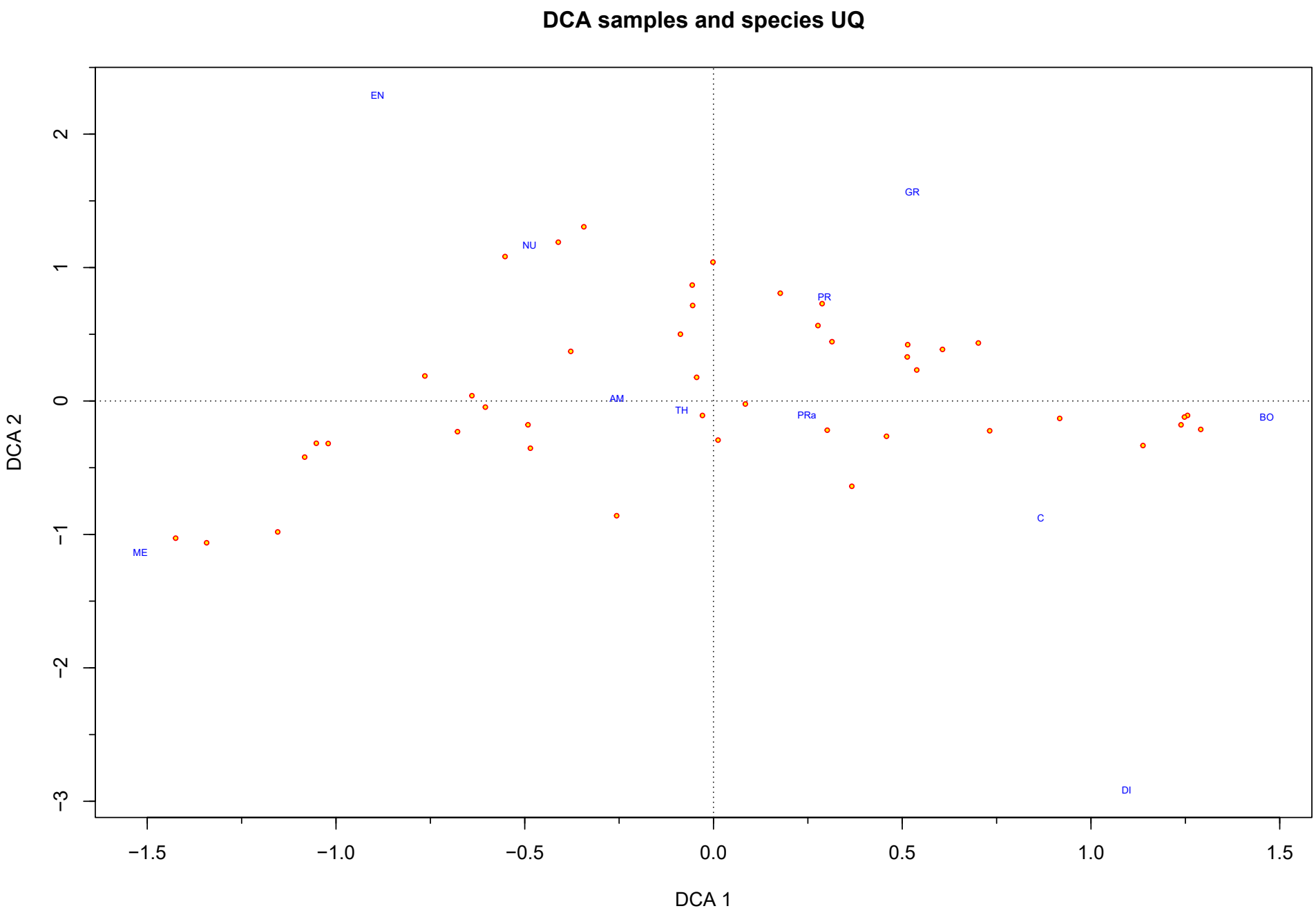

C
EN
ME
DI
AM
GY
NI
BO
PR
GR
NU
DCA2
DCA1
1
0
−1
−2
−2
−1
0
1
2
Biofacies
DFBS
GrSB
MSB
NSB
GRBS
CC
GSB

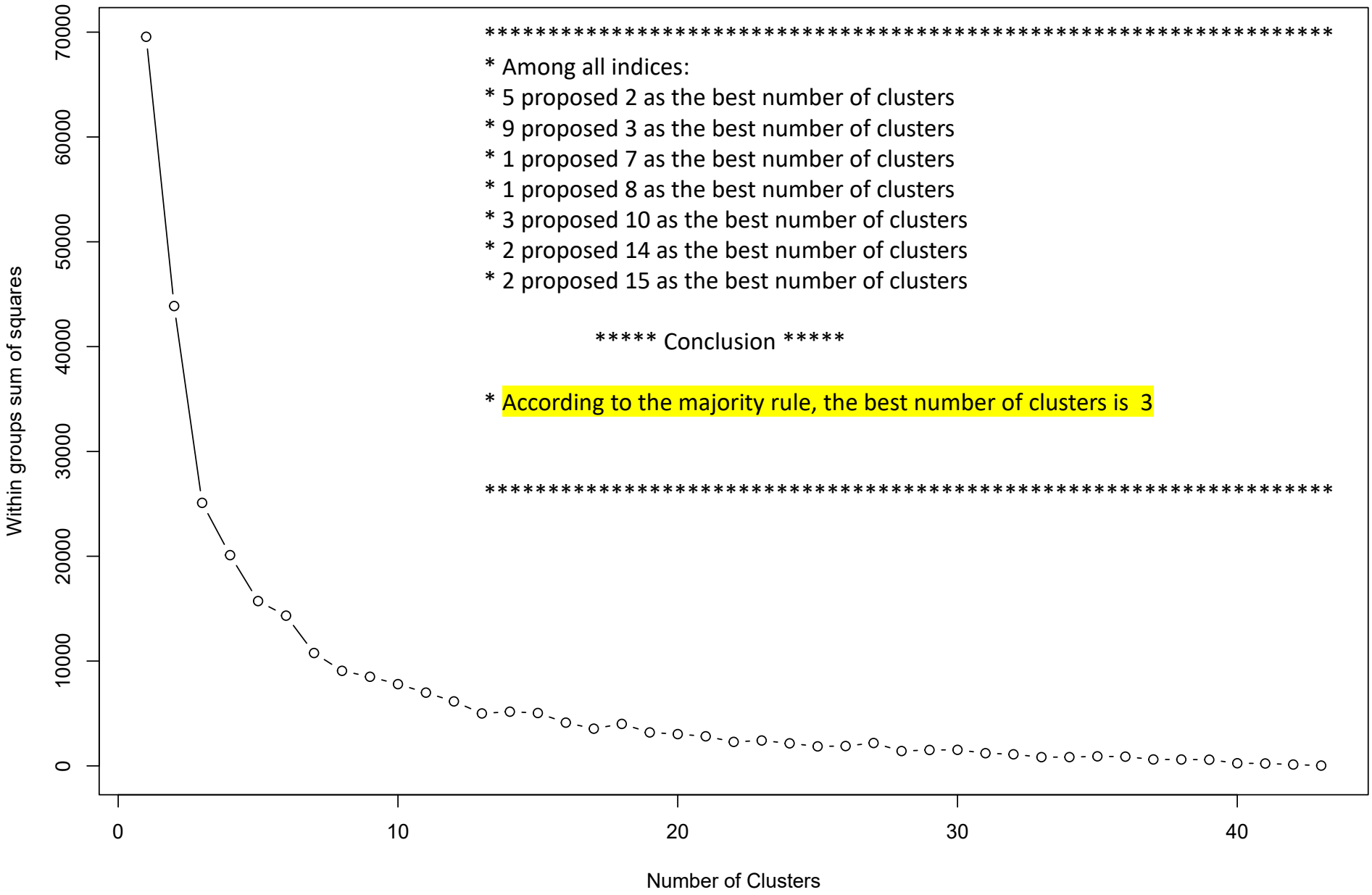
Norman Cross (NC)

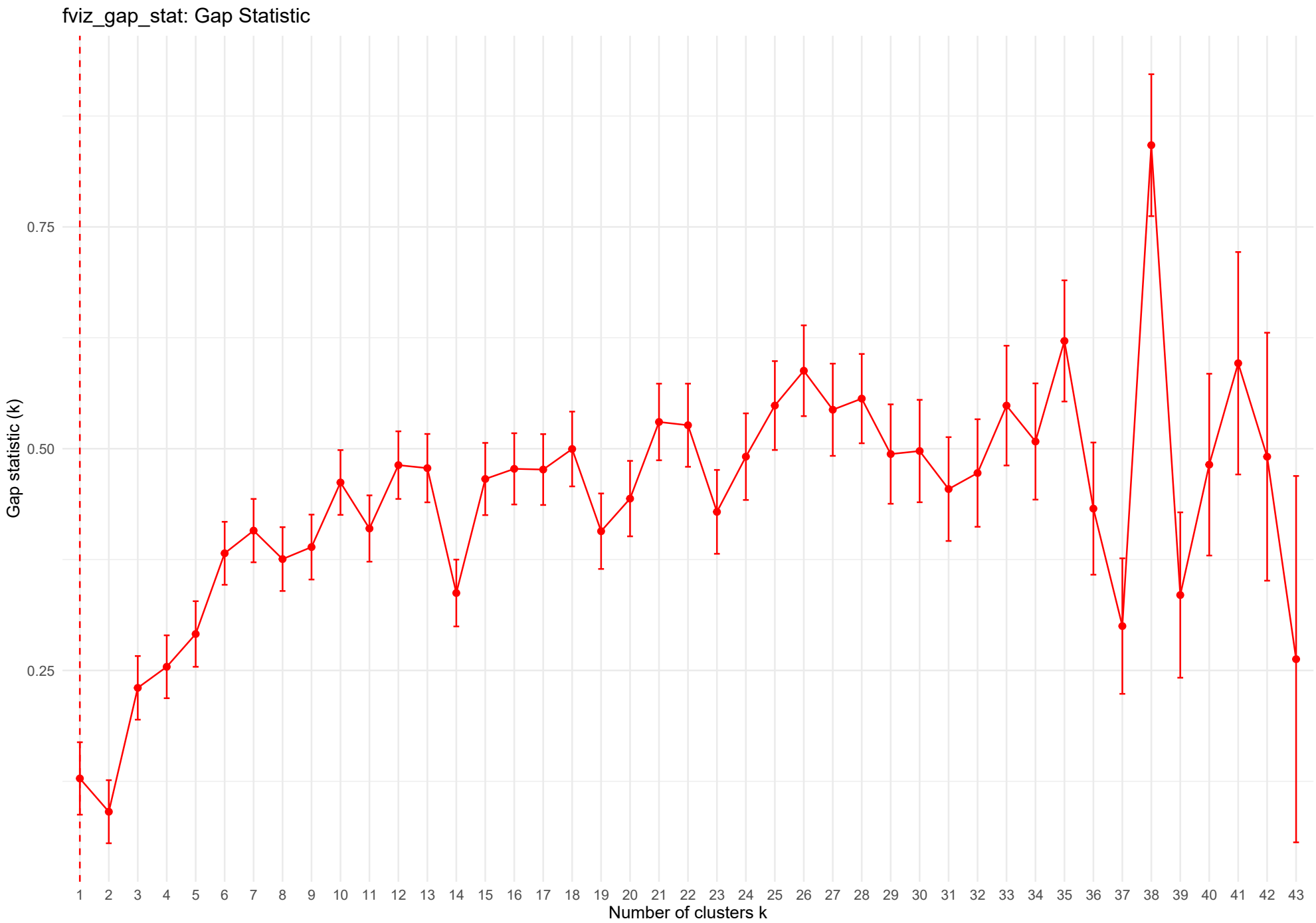

0
1
2
3
4
5
6
NC_2
NC_4
NC_5
NC_6
NC_8
NC_9
NC_10
NC_11
NC_12
NC_13
NC_14A
NC_14B
NC_14C
NC_14D
NC_14E
NC_14F
NC_14G
NC_14H
NC_15
NC_16
NC_16A
NC_17
NC_18
NC_18A
NC_19
NC_20
NC_21
NC_22
NC_23
NC_24
NC_25
NC_26
NC_27
NC_28
NC_29
NC_30
NC_31
NC_32
NC_33
NC_34
NC_35
NC_36
NC_37
NC_38
NERC
Duff

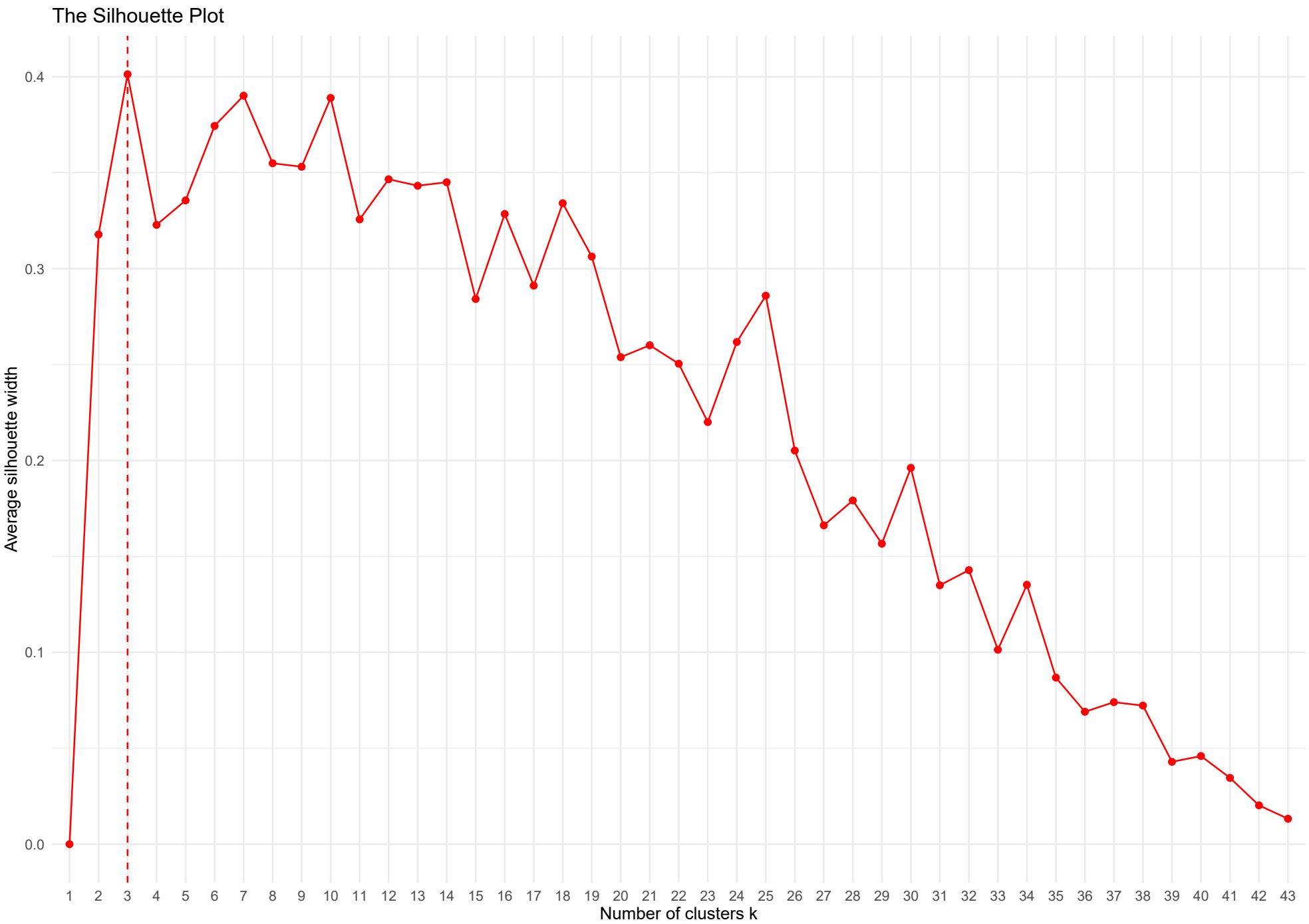
Stewartby (ST)

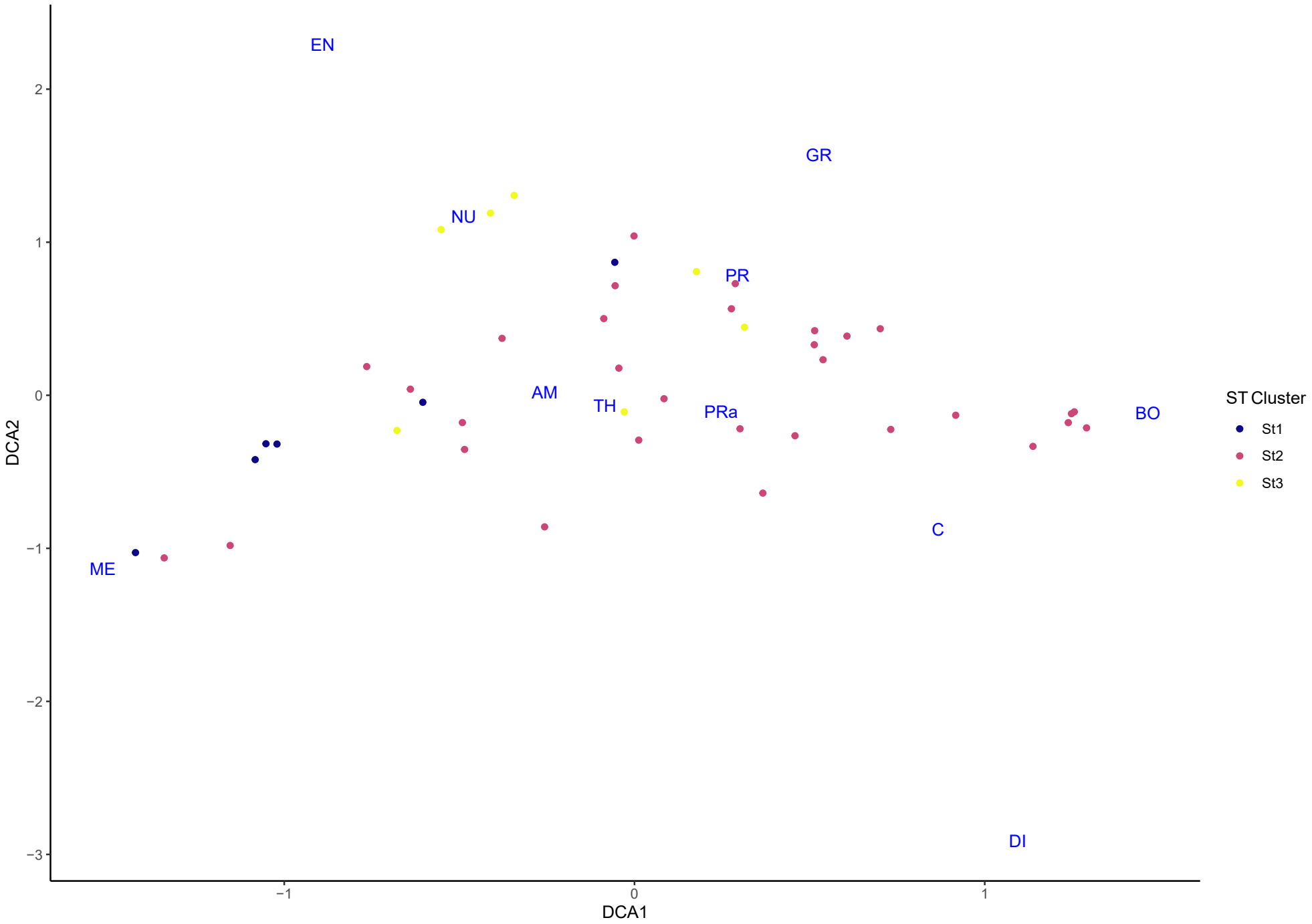

DCA samples and species
EN
MP
Dm
GE
GR
PA
OX
SE
BT
NU
PR
MS
BL
TH
PRa
AM
IS
BO
PC
PIN
OR
Li
SC
DI
QU
ME
DCA 2
DCA 1
−2
−1
0
1
2


DCA samples and species UQ
EN
GR
NU
PR
AM
TH
PRa
BO
C
ME
DI
DCA 2
DCA 1
2
1
0
−1
−2
−3
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5

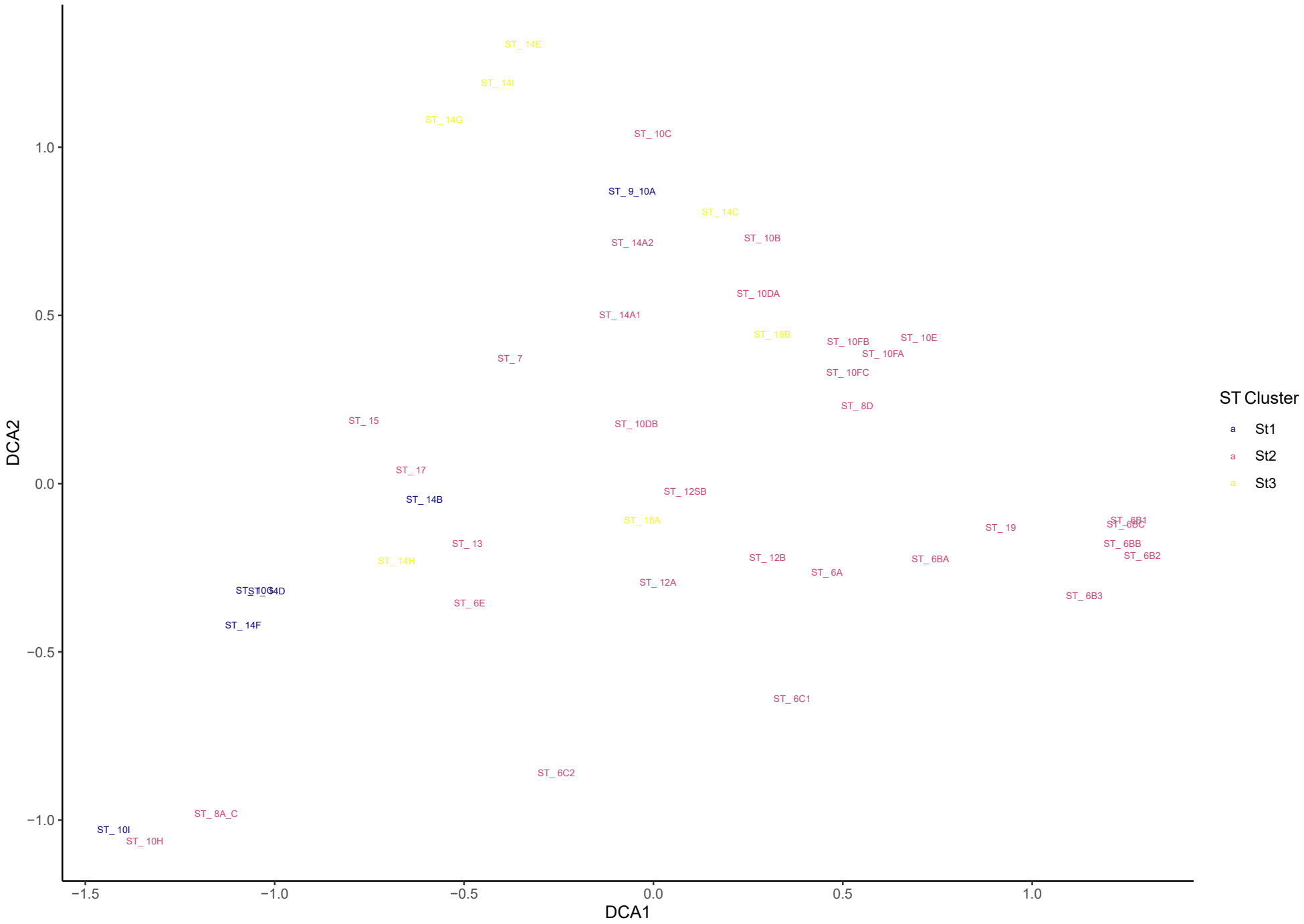

Within groups sum of squares
0
10000
20000
30000
40000
50000
60000
70000
0
10
20
30
40
Number of Clusters
****
* Among all indices:
* 5 proposed 2 as the best number of clusters
* 9 proposed 3 as the best number of clusters
* 1 proposed 7 as the best number of clusters
* 1 proposed 8 as the best number of clusters
* 3 proposed 10 as the best number of clusters
* 2 proposed 14 as the best number of clusters
* 2 proposed 15 as the best number of clusters
***** Conclusion *****
* According to the majority rule, the best number of clusters is 3
****

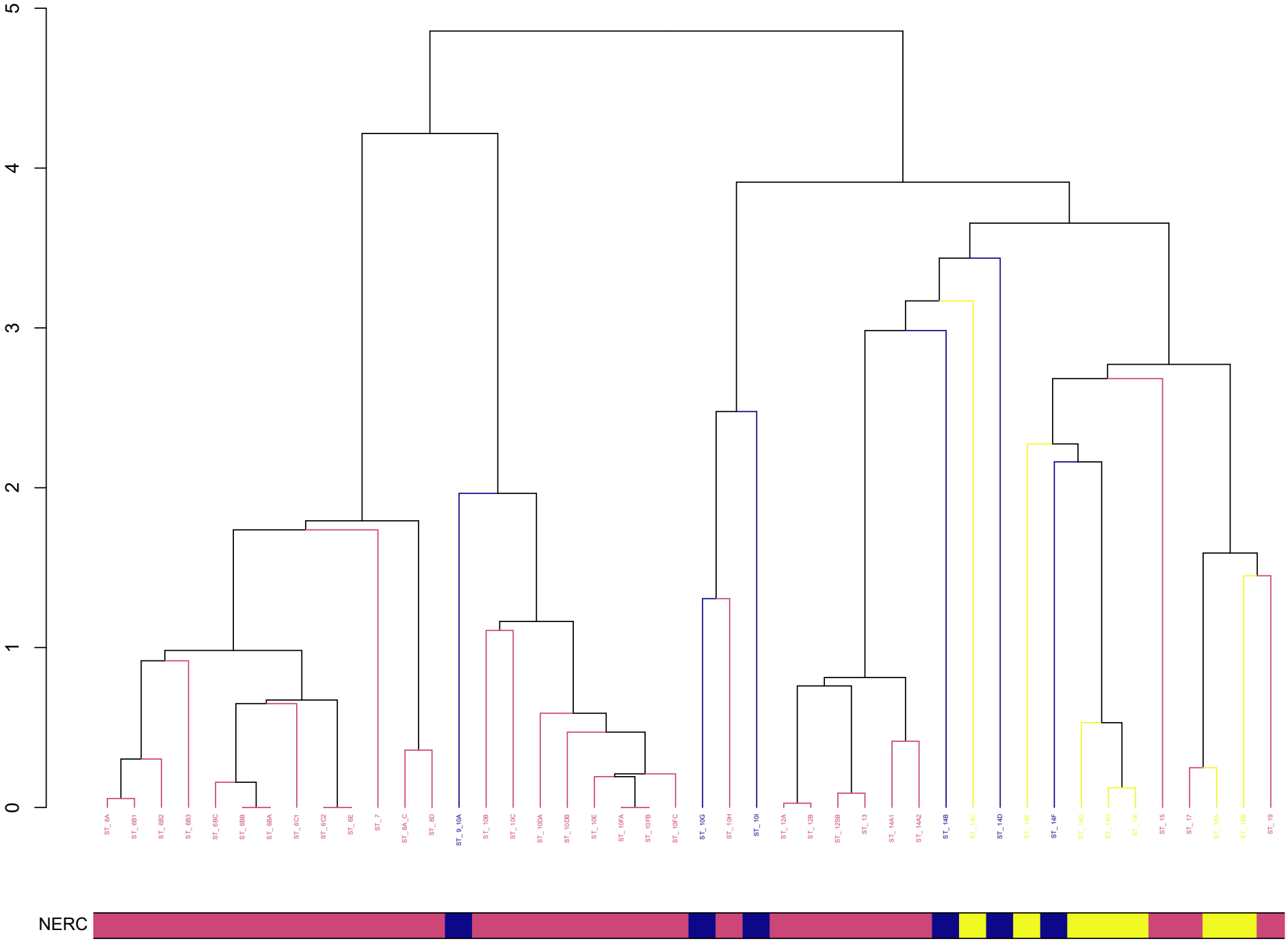

fviz_gap_stat: Gap Statistic
Gap statistic (k)
0.25
0.50
0.75
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43
Number of clusters k

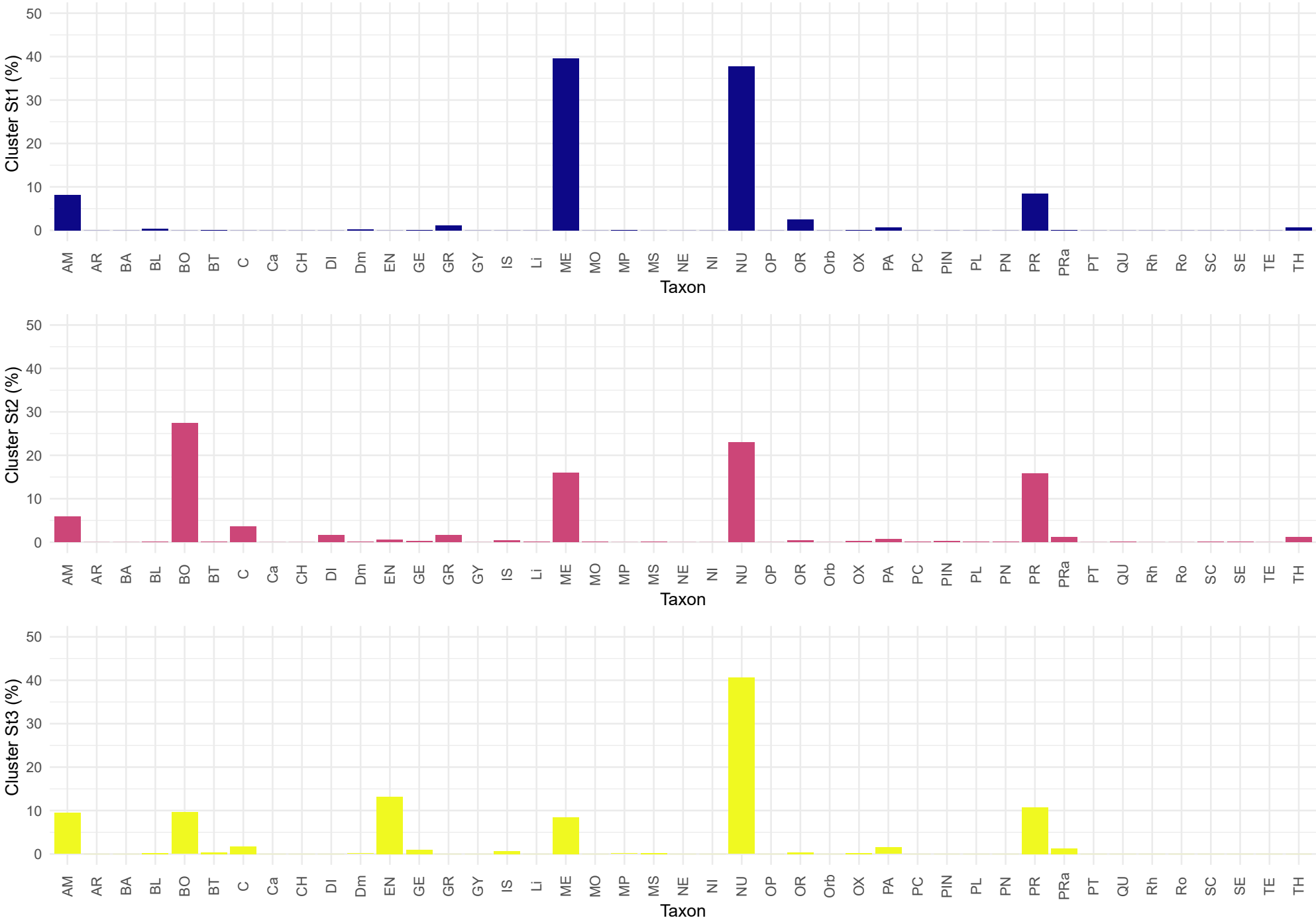

The Silhouette Plot
Average silhouette width
0.0
0.1
0.2
0.3
0.4
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43
Number of clusters k

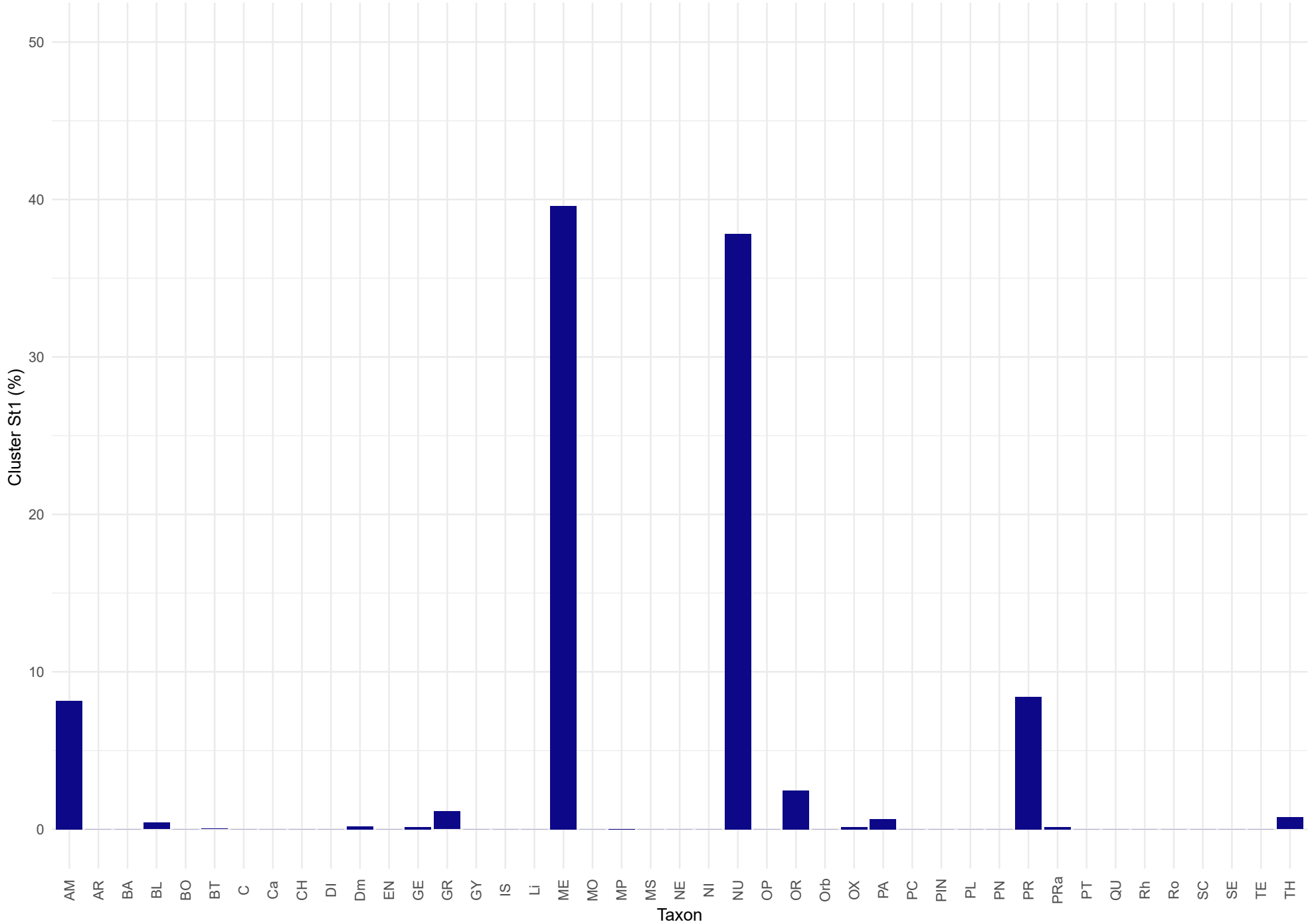


Stewartby (ST)

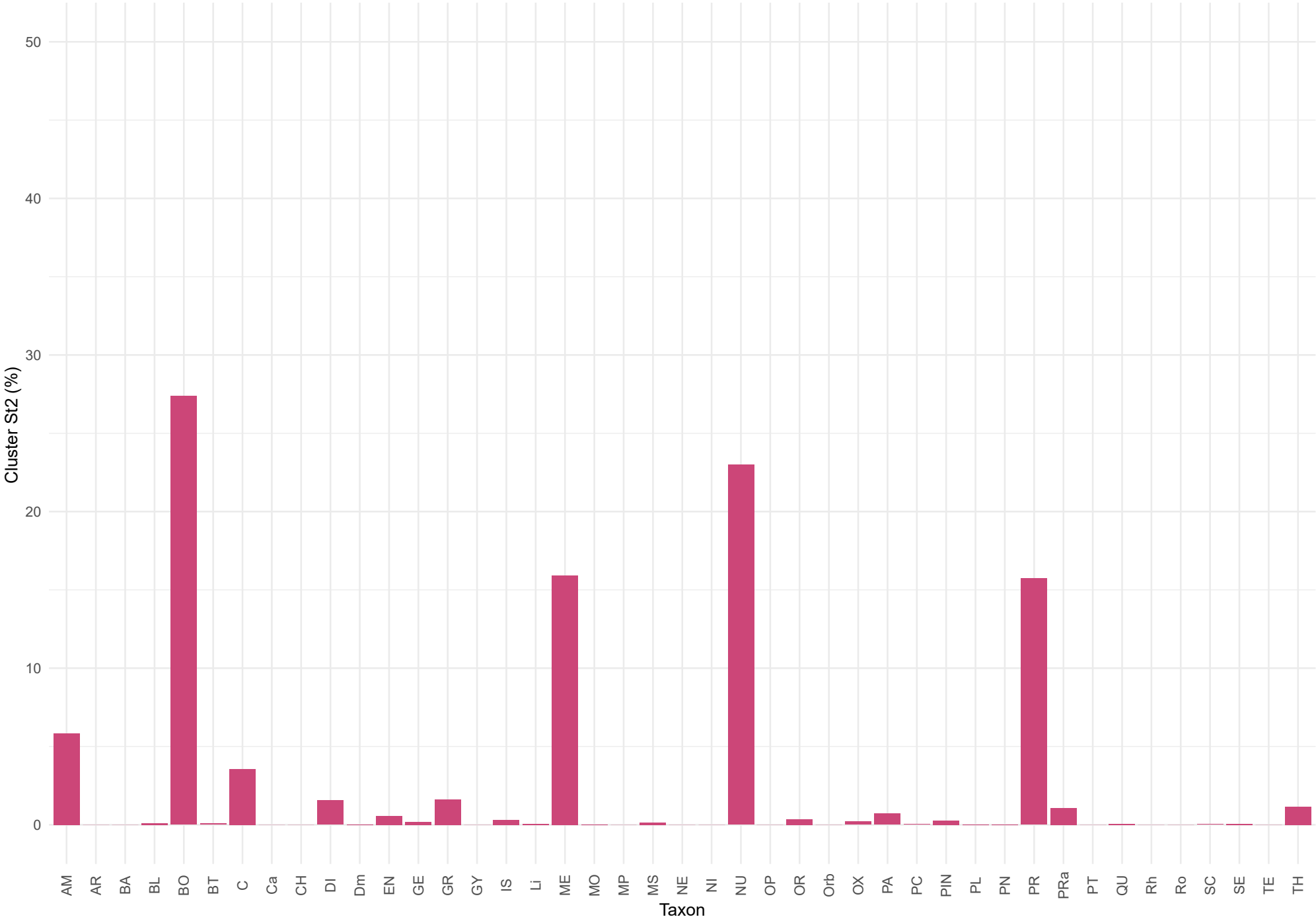

ST_ 14E
ST_ 14I
ST_ 14G
ST_ 10C
ST_ 9_10A
ST_ 14C
ST_ 14A2
ST_ 10B
ST_ 10DA
ST_ 14A1
ST_ 18B
ST_ 10FB
ST_ 10E
ST_ 10FA
ST_ 7
ST_ 10FC
ST_ 8D
ST_ 15
ST_ 10DB
ST_ 17
ST_ 12SB
ST_ 14B
ST_ 18A
ST_ 19
ST_ 6B4
ST_ 6BC
ST_ 13
ST_ 6BB
ST_ 14H
ST_ 12B
ST_ 6BA
ST_ 6B2
ST_ 6A
ST_ 12A
ST_ 6B3
ST_ 6E
ST_ 14F
ST_ 6C1
ST_ 6C2
ST_ 8A_C
ST_ 10I
ST_ 10H
DCA2
DCA1
1.0
0.5
0.0
−0.5
−1.0
−1.5
ST Cluster
St1
St2
St3

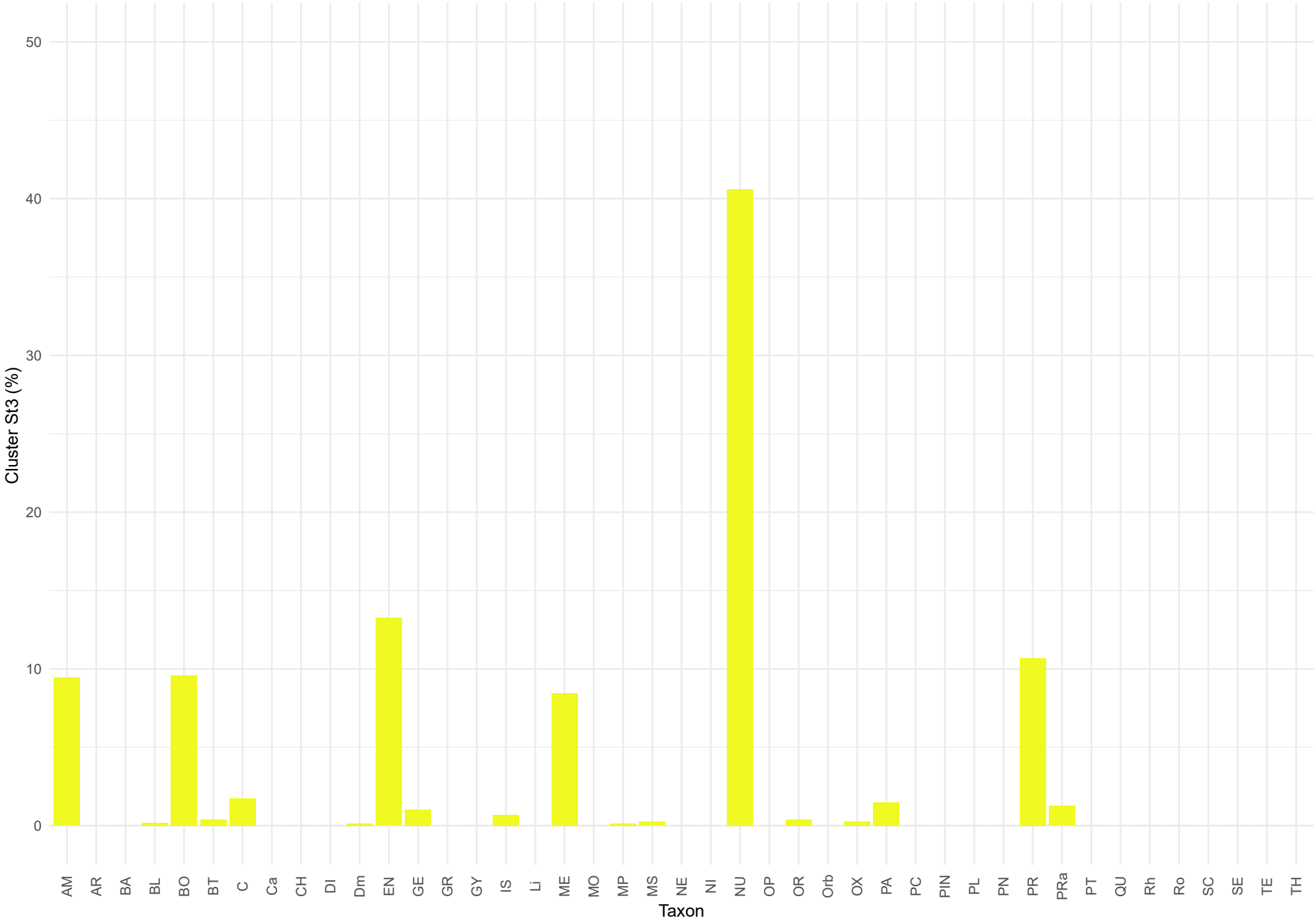

0
1
2
3
4
5
ST_6A
ST_6B1
ST_6B2
ST_6B3
ST_6BC
ST_6BB
ST_6BA
ST_6C1
ST_6C2
ST_6E
ST_7
ST_8A_C
ST_8D
ST_9_10A
ST_10B
ST_10C
ST_10DA
ST_10DB
ST_10E
ST_10FA
ST_10FB
ST_10FC
ST_10G
ST_10H
ST_10I
ST_12A
ST_12B
ST_12SB
ST_13
ST_14A1
ST_14A2
ST_14B
ST_14C
ST_14D
ST_14E
ST_14F
ST_14G
ST_14H
ST_14I
ST_15
ST_17
ST_18A
ST_18B
ST_19
NERC

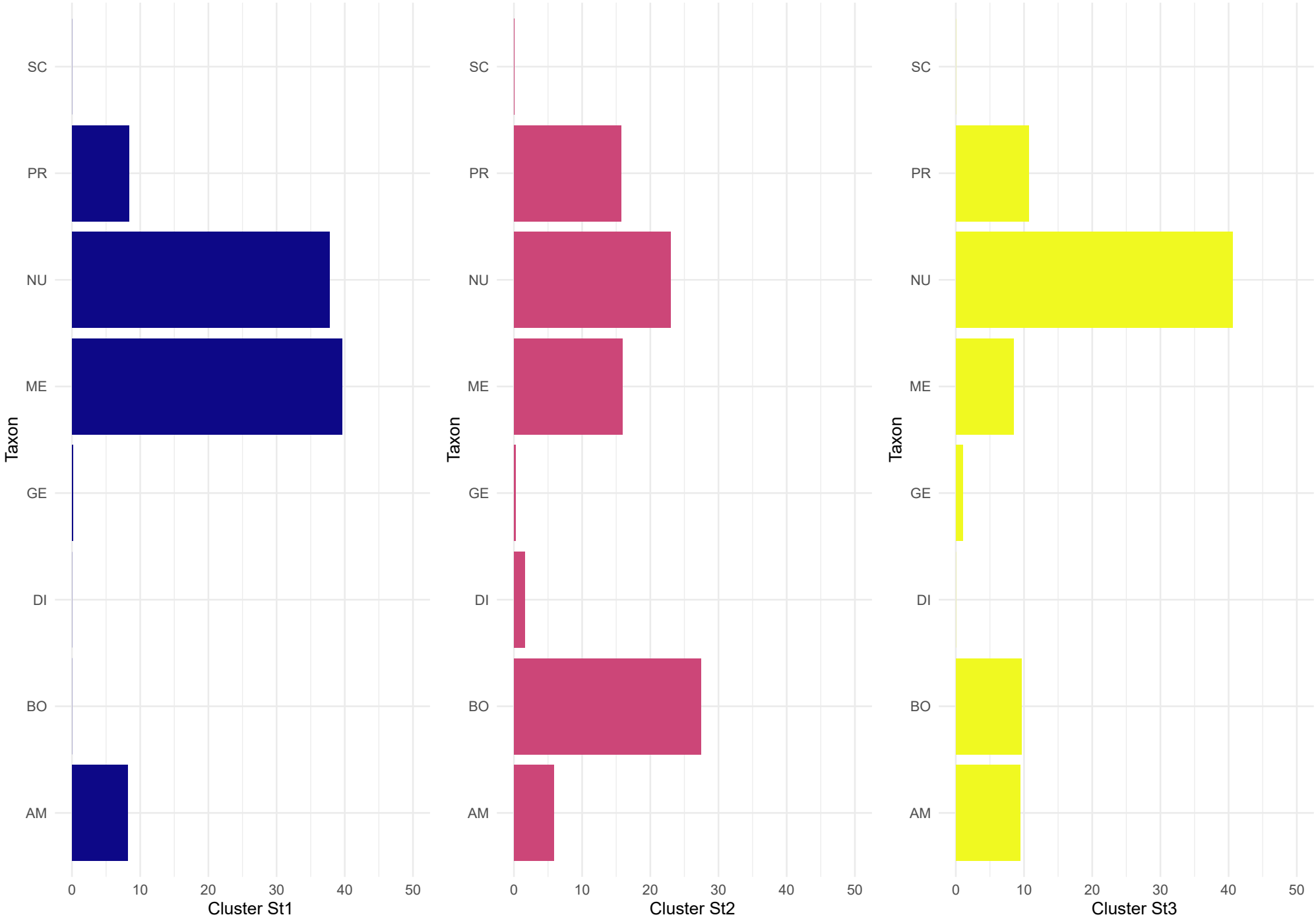

Cluster St1 (%)
Cluster St2 (%)
Cluster St3 (%)
0
10
20
30
40
50
AM AR BA BL BO BT C Ca CH DI Dm EN GE GR GY IS Li ME MO MP MS NE NI NU OP OR Orb OX PA PC PIN PL PN PR PRa PT QU Rh Ro SC SE TE TH
Taxon

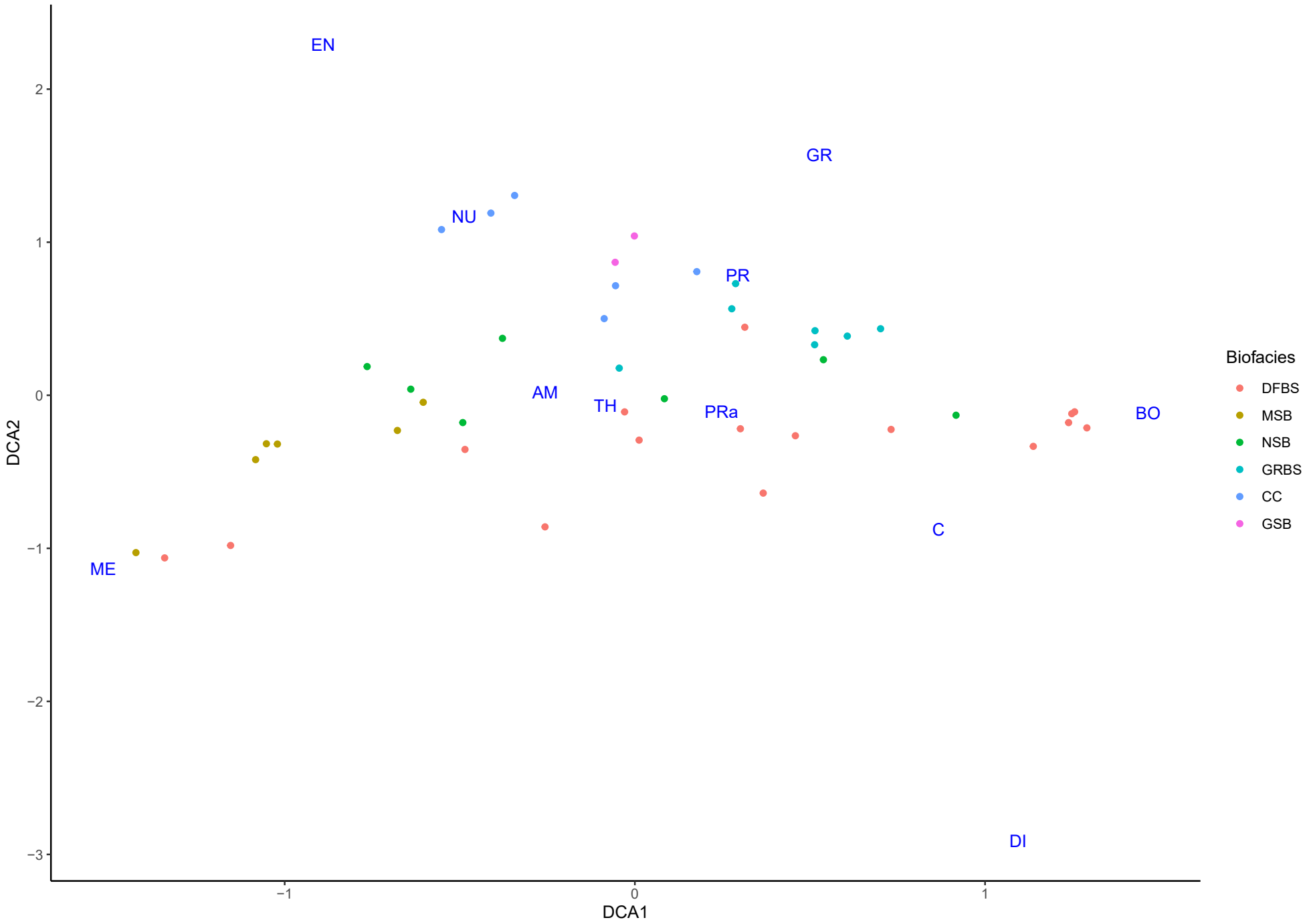


Stewartby (ST)

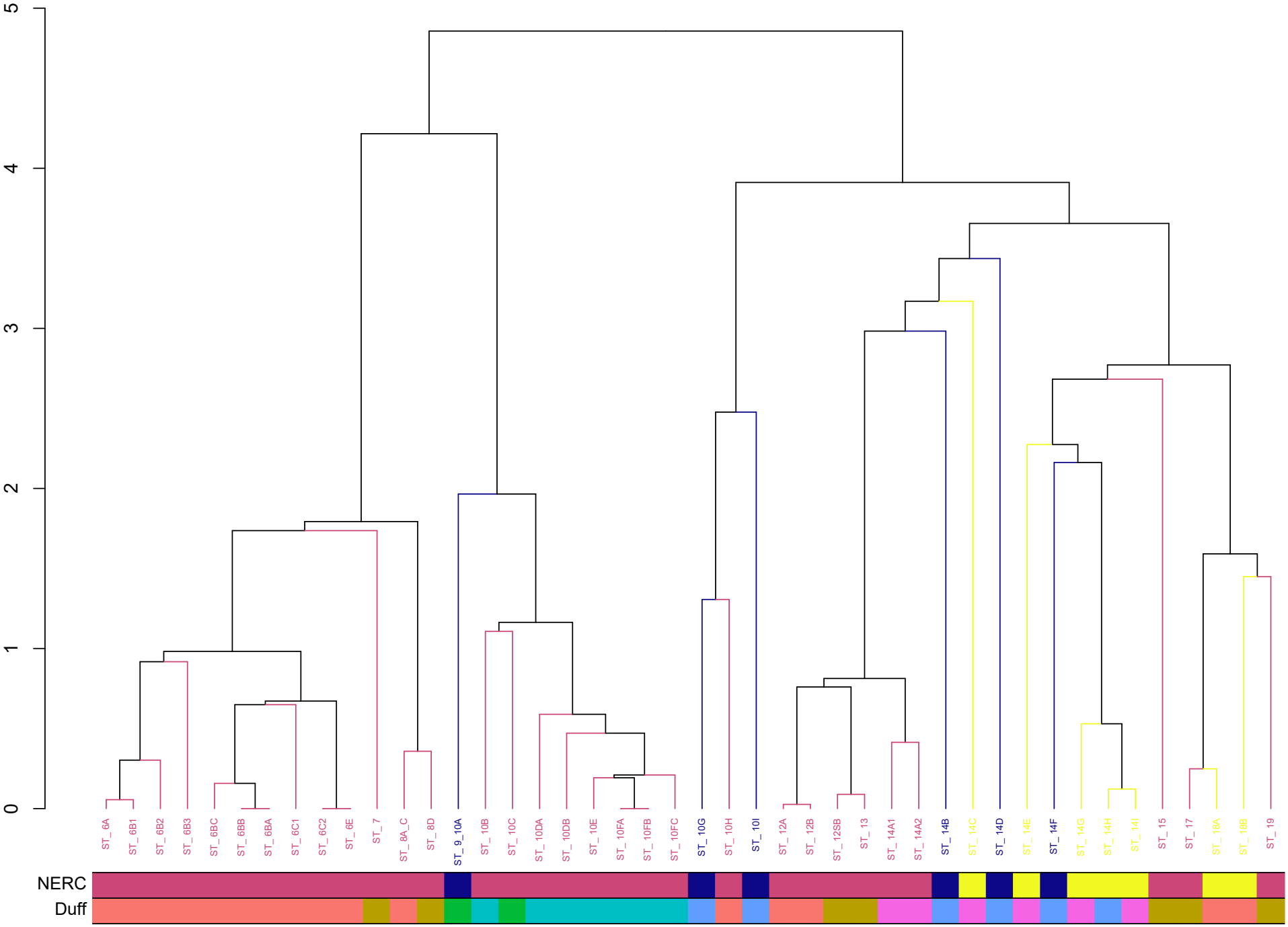

Cluster St2 (%)
50
40
30
20
10
0
AM
AR
BA
BL
BO
BT
C
Ca
CH
DI
Dm
EN
GE
GR
GY
IS
Li
ME
MO
MP
MS
NE
NI
NU
OP
OR
Orb
OX
PA
PC
PIN
PL
PN
PR
PRa
PT
QU
Rh
Ro
SC
SE
TE
TH
Taxon


Cluster St3 (%)
50
40
30
20
10
0
AM
AR
BA
BL
BO
BT
C
Ca
CH
DI
Dm
EN
GE
GR
GY
IS
Li
ME
MO
MP
MS
NE
NI
NU
OP
OR
Orb
OX
PA
PC
PIN
PL
PN
PR
PRa
PT
QU
Rh
Ro
SC
SE
TE
TH
Taxon


SC
PR
NU
ME
GE
DI
BO
AM
Taxon
0
10
20
30
40
50
Cluster St1
Cluster St2
Cluster St3


EN
GR
NU
PR
AM
TH
PRa
BO
C
ME
DI
2
1
0
−1
−2
−3
DCA2
−1
0
1
DCA1
Biofacies
DFBS
MSB
NSB
GRBS
CC
GSB

Stewartby (ST)


0
1
2
3
4
5
ST_6A
ST_6B1
ST_6B2
ST_6B3
ST_6BC
ST_6BB
ST_6BA
ST_6C1
ST_6C2
ST_6E
ST_7
ST_8A_C
ST_8D
ST_9_10A
ST_10B
ST_10C
ST_10DA
ST_10DB
ST_10E
ST_10FA
ST_10FB
ST_10FC
ST_10G
ST_10H
ST_10I
ST_12A
ST_12B
ST_12SB
ST_13
ST_14A1
ST_14A2
ST_14B
ST_14C
ST_14D
ST_14E
ST_14F
ST_14G
ST_14H
ST_14I
ST_15
ST_17
ST_18A
ST_18B
ST_19
NERC
Duff