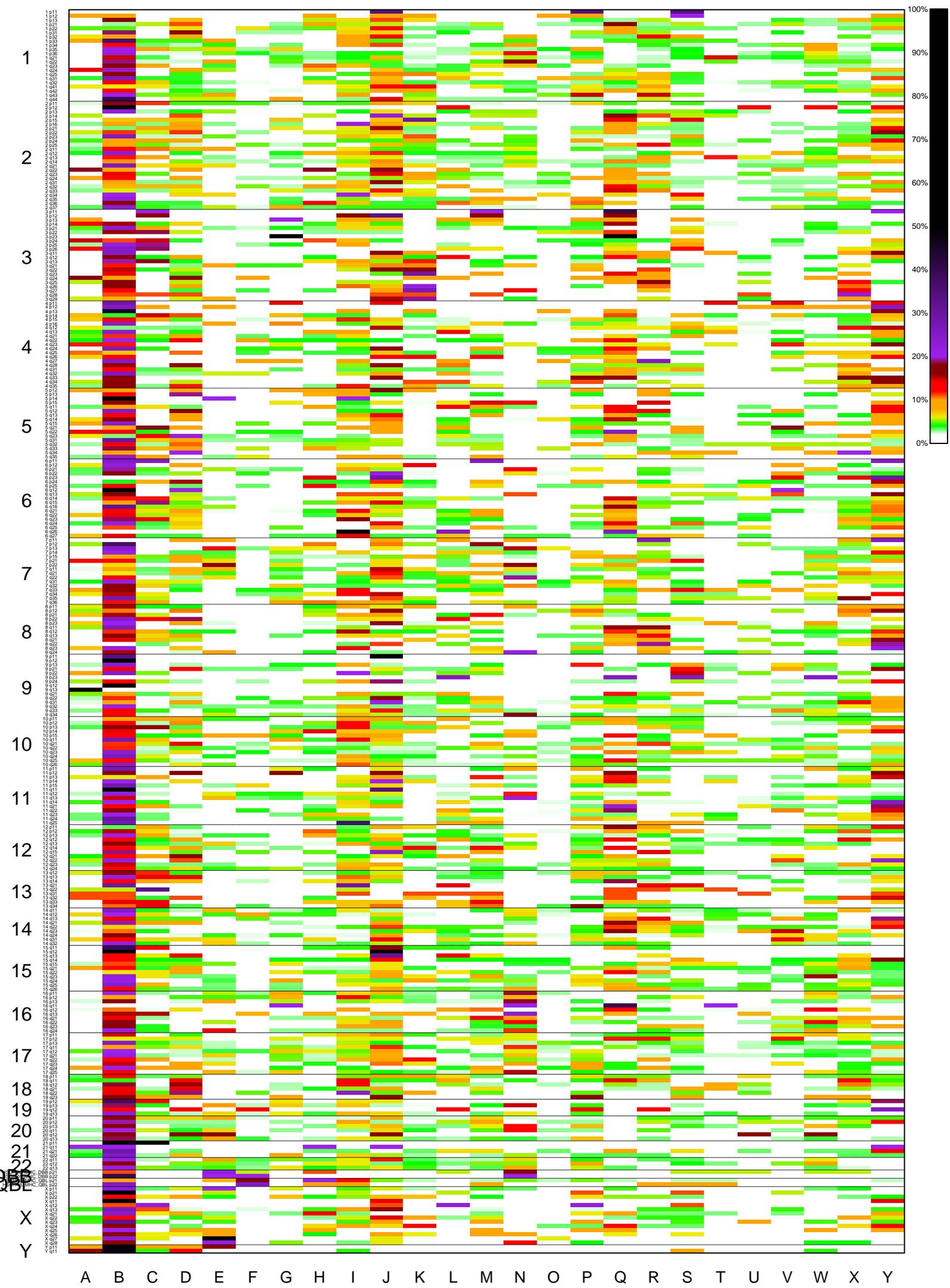


K-Means Cluster Chromosome Map



Spot A

genes in spot = 394 (383 with loci information)

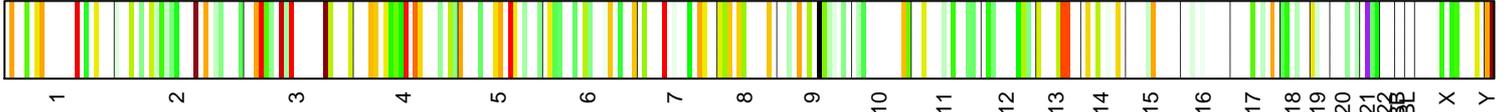
samples with spot = 42 (15.3 %)

Atypical : 19 (25.7 %)

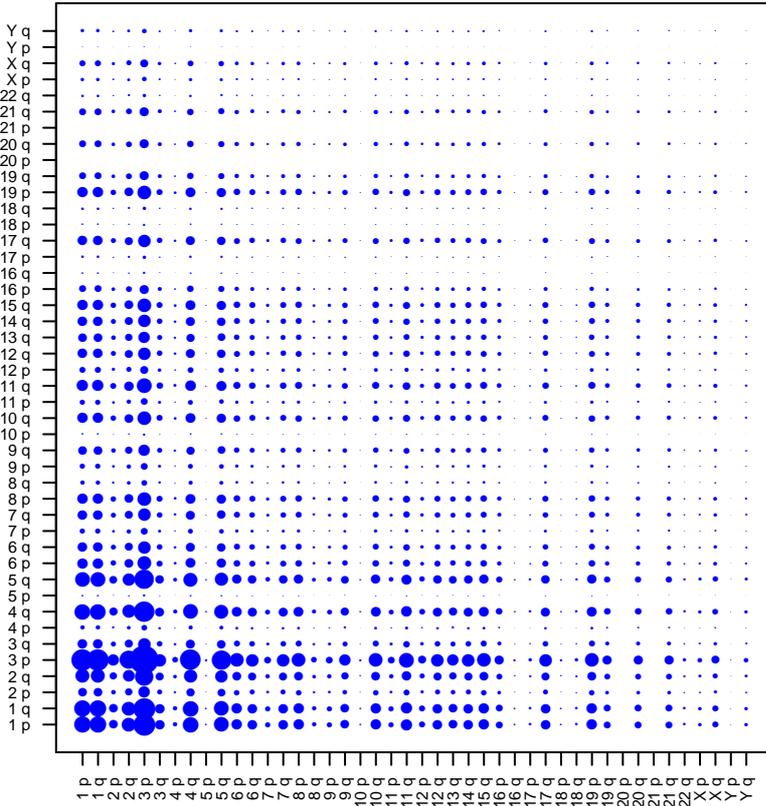
Classical : 4 (12.5 %)

Mesenchymal : 5 (5.9 %)

Basal : 14 (16.7 %)



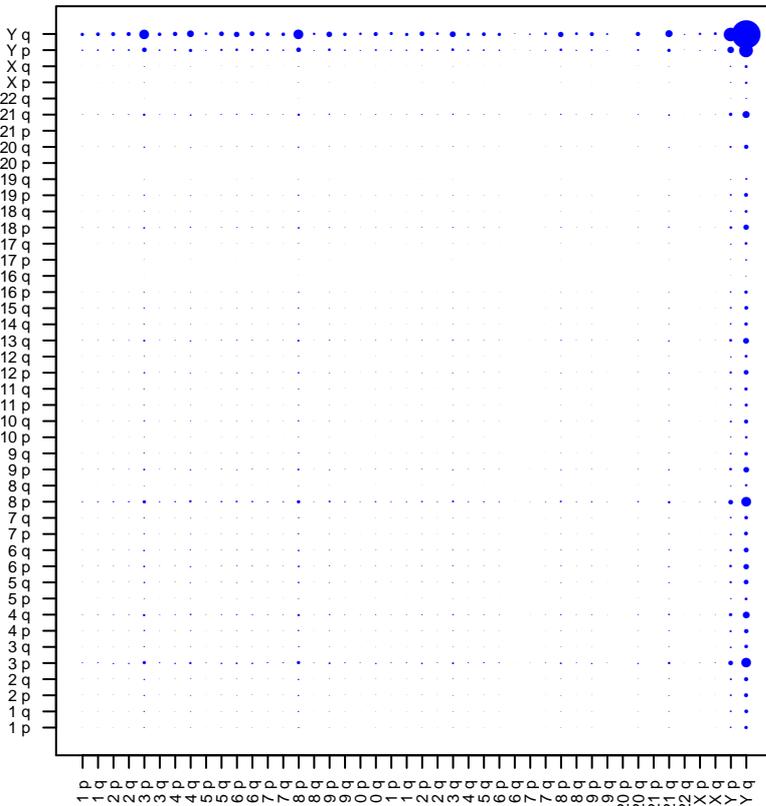
Absolute numbers



Rank	locus	# genes	%	p-value
1	3 p	25	5.9	4e-05
2	1 p	19	2.2	0.8
3	1 q	19	2.2	0.6
4	4 a	18	4.2	0.02
5	4 q	17	2.9	0.3
6	2 q	16	5	0.08
7	11 q	13	2.7	0.3
8	8 p	11	3.3	0.04
9	8 p	11	3.3	0.04
10	10 q	11	2.5	0.5
11	15 q	11	2.3	0.5
12	19 p	11	2.4	0.5
13	3 q	11	2.2	0.7
14	16 q	11	3	0.3
15	7 q	11	2.2	0.7
16	12 q	11	1.8	0.9
17	14 a	11	2.1	0.7
18	17 q	11	1.7	0.9
19	2 p	10	2.5	0.5
20	9 q	10	2.2	0.7
21	13 q	10	3.6	0.1
22	16 p	10	2.2	0.7
23	19 q	10	1.2	1
24	20 q	10	2.4	0.5
25	12 q	10	3.6	0.08
26	21 q	10	2.4	0.5
27	X q	7	1.8	0.4
28	7 p	6	3.4	0.06
29	9 p	6	3.4	0.06
30	11 p	6	1.9	0.8
31	4 p	5	2.7	0.5
32	8 q	5	1.5	0.9
33	X p	5	1.5	0.9
34	Y q	4	17.4	0.002
35	17 p	3	1	1
36	18 q	3	1.8	0.8
37	22 a	3	0.8	1
38	5 p	2	1.7	0.8
39	10 p	2	1.6	0.8
40	16 q	2	0	1
41	18 p	2	0	0.4
42	Y p	1	0	0.3
43	20 p	0	0	1
44	21 p	0	0	1

H3CHR6-MHC-DBP

Relative numbers

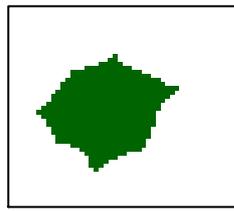


Rank	locus	# genes	%	p-value
1	Y q	4	17.4	0.002
2	Y p	1	8.3	0.3
3	8 p	2	6	0.004
4	3 p	2	5.9	4e-05
5	21 q	8	4.3	0.08
6	4 q	18	4.2	0.02
7	13 q	10	3.6	0.1
8	9 p	6	3.4	0.3
9	6 p	12	3.3	0.2
10	18 p	2	3.3	0.4
11	6 q	11	3.3	0.3
12	12 p	7	3.3	0.4
13	5 q	11	3.3	0.3
14	4 p	5	3.3	0.4
15	20 q	8	3.3	0.3
16	10 q	5	3.3	0.5
17	20 q	5	3.3	0.5
18	2 p	10	2.5	0.5
19	19 p	12	2.4	0.5
20	7 p	6	2.4	0.6
21	15 q	12	2.3	0.6
22	1 q	19	2.3	0.6
23	3 q	11	2.2	0.7
24	7 q	11	2.2	0.7
25	9 q	10	2.2	0.7
26	14 q	11	2	0.7
27	1 p	2	1	0.8
28	16 p	8	2	0.7
29	11 q	13	2	0.8
30	11 p	6	1	0.8
31	X q	7	1	0.8
32	12 q	1	1	0.8
33	18 q	1	1	0.8
34	5 p	2	1	0.8
35	17 q	1	1.7	0.9
36	10 p	2	1.6	0.8
37	8 q	5	1.5	0.9
38	X p	4	1.5	0.9
39	19 q	8	1.2	1
40	17 p	3	1	1
41	22 q	3	0.8	1
42	16 q	2	0.6	1
43	20 p	0	0	1
44	21 p	0	0	1

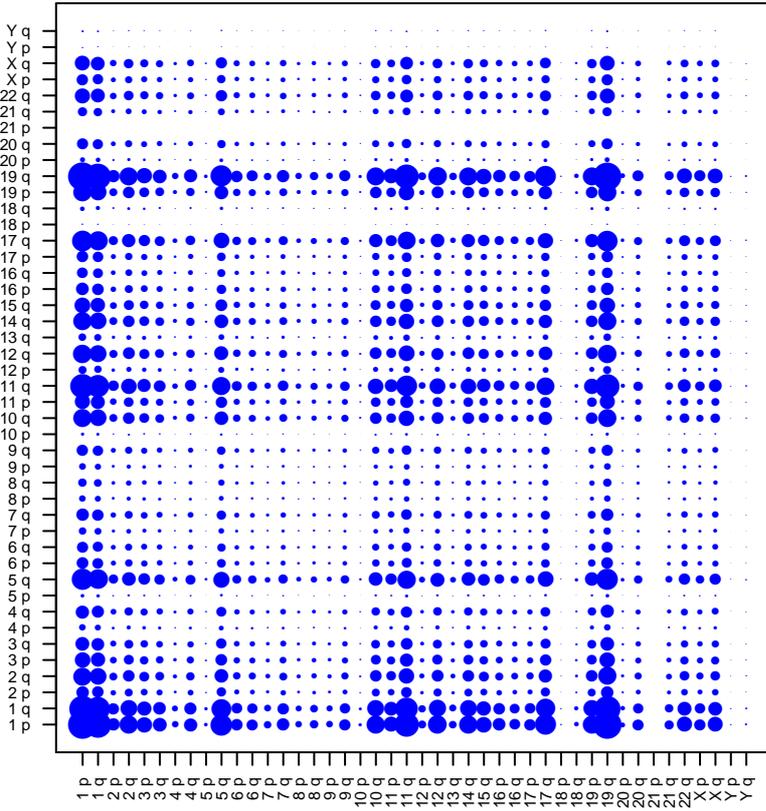
Spot B

genes in spot = 3085 (2835 with loci information)

samples with spot = 0 (0 %)



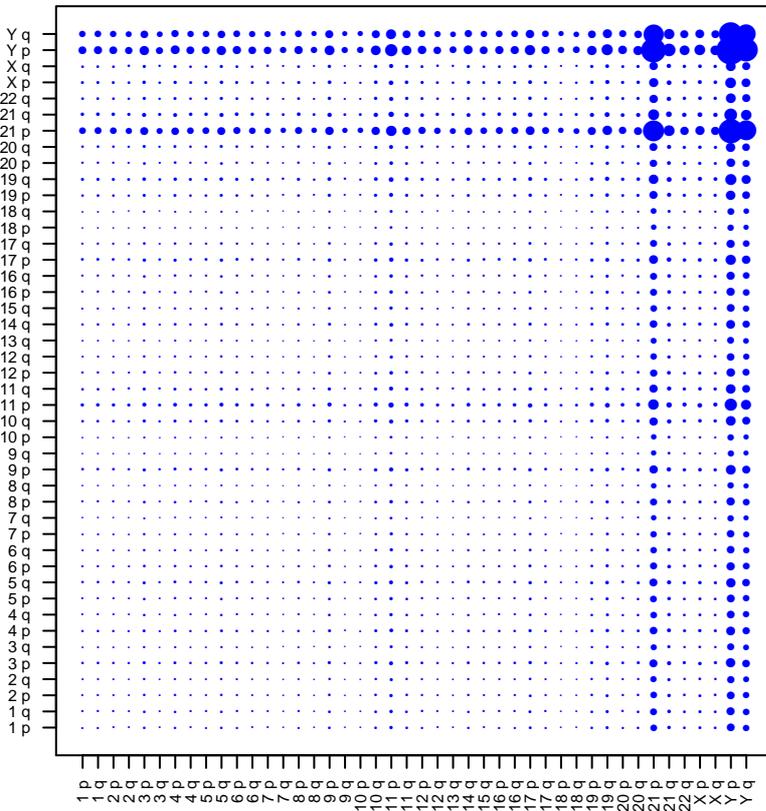
Absolute numbers



Rank	locus	# genes	%	p-value
1	1 p	149	16.1	1
2	19 q	148	22.7	0.01
3	1 q	137	16.6	1
4	11 q	127	19.6	0.4
5	5 q	112	0.5	0.5
6	17 q	109	5.8	0.9
7	12 q	97	1	1
8	2 q	95	1	1
9	10 q	95	0.3	0.3
10	14 q	95	0.7	0.7
11	19 q	95	0.4	0.4
12	15 q	82	1	1
13	3 p	81	1	0.5
14	11 p	79	2.5	0.005
15	22 q	79	20.1	0.3
16	X q	78	19.9	0.3
17	3 q	72	14.5	1
18	4 q	69	15.9	1
19	16 p	66	8	0.9
20	2 p	65	16.8	1
21	7 q	65	13	1
22	6 p	61	9	0.9
23	17 p	60	2.1	0.2
24	9 q	59	1	1
25	X p	59	5.8	0.1
26	6 q	58	1	1
27	20 q	58	0.5	0.5
28	16 q	56	0.8	0.9
29	21 q	48	2.5	0.01
30	8 q	44	13.3	1
31	12 p	42	17.4	0.8
32	13 q	40	14.2	1
33	7 p	39	15.4	0.9
34	9 p	35	20	0.4
35	4 p	34	18.2	0.6
36	8 p	34	16.9	0.8
37	20 p	26	17.7	0.7
38	18 q	24	14	1
39	5 p	19	16.2	0.8
40	10 p	17	13.2	1
41	Y q	11	4.7	0.002
42	18 p	8	15.5	0.9
43	Y p	7	58.3	0.003
44	21 p	1	50	0.3

H3CHR6-MHC-QBB

Relative numbers



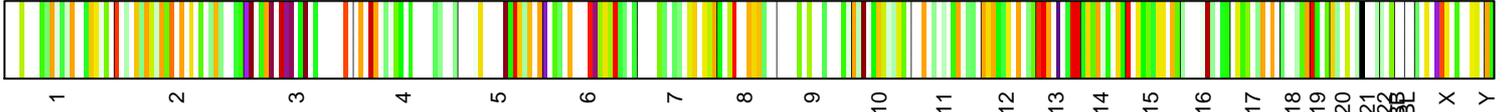
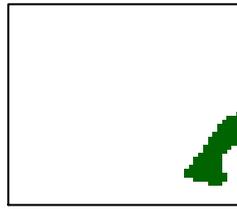
Rank	locus	# genes	%	p-value
1	Y p	7	58.3	0.003
2	21 p	1	50	0.3
3	Y q	11	47.8	0.002
4	21 q	48	25.9	0.01
5	11 p	79	2.5	0.005
6	19 q	148	22.7	0.01
7	X p	59	21.9	0.1
8	17 p	60	21	0.2
9	22 q	79	20.1	0.3
10	9 p	35	20	0.4
11	X q	78	19.9	0.3
12	10 q	95	19.9	0.3
13	11 q	127	19.6	0.4
14	19 p	95	19.6	0.4
15	3 p	81	1	0.5
16	20 q	58	1	0.5
17	5 q	112	1	0.5
18	4 p	34	18.2	0.6
19	14 q	95	18.2	0.7
20	20 p	26	17.7	0.7
21	12 p	42	17.4	0.8
22	6 p	61	16.9	0.9
23	8 p	34	16.9	0.8
24	16 p	66	16.8	0.9
25	16 q	56	16.8	0.9
26	17 q	109	16.8	0.9
27	1 q	137	16.6	1
28	5 p	19	16.2	0.8
29	1 p	149	1	1
30	15 q	82	1	1
31	11 p	65	1	1
32	4 q	65	1	1
33	6 q	58	1	1
34	12 q	97	1	1
35	7 p	39	1	0.9
36	2 q	95	1	1
37	3 q	72	1	1
38	13 q	40	1	1
39	18 q	24	1	1
40	10 p	17	1	1
41	18 p	8	1	1
42	8 q	44	1	0.9
43	7 q	65	1	1
44	9 q	59	1	1

Spot C

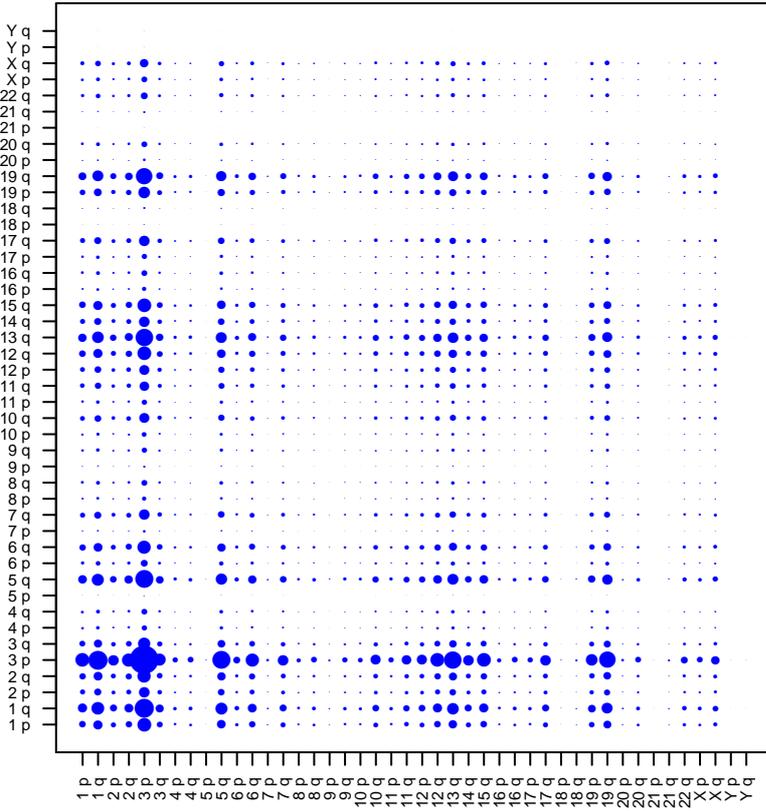
genes in spot = 715 (688 with loci information)

samples with spot = 23 (8.4 %)

Atypical : 23 (31.1 %)



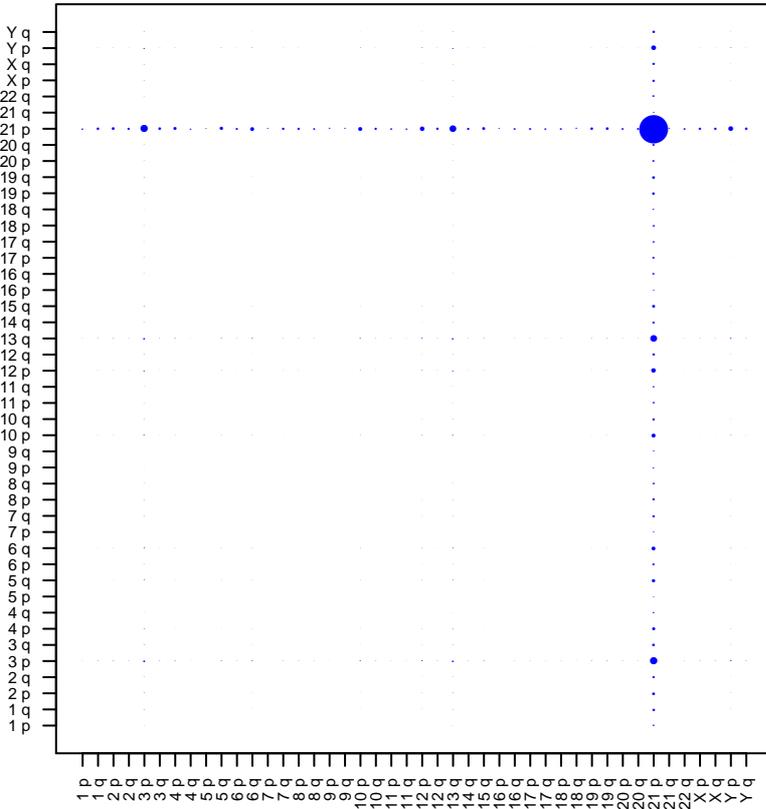
Absolute numbers



Rank	locus	# genes	%	p-value
1	3 p	54	12.7	2e-12
2	1 q	36	4.4	0.6
3	5 q	34	5.8	0.07
4	13 q	33	11.7	3e-07
5	19 q	31	4.8	0.4
6	12 p	26	2.8	1
7	10 p	26	4.2	0.7
8	15 q	26	5.1	0.3
9	6 q	25	6.7	0.02
10	4 p	25	3.8	0.4
11	3 q	23	4.6	0.4
12	19 p	23	4.5	0.5
13	2 p	20	4.9	0.3
14	7 q	20	4	0.7
15	14 q	20	3.8	0.8
16	17 q	20	3.1	1
17	10 q	19	4	0.7
18	12 p	19	7.9	0.01
19	11 q	18	2.8	1
20	X q	16	4.1	0.7
21	6 p	13	3.6	0.8
22	22 q	13	3.3	0.9
23	4 q	11	2.5	1
24	8 q	11	3.3	0.9
25	16 q	11	3.3	0.9
26	20 q	11	3.6	0.8
27	X p	11	4.1	0.6
28	4 p	10	5.3	0.3
29	9 q	10	2.2	1
30	11 p	10	3.3	0.9
31	17 p	10	3.5	0.8
32	10 p	9	7	0.1
33	8 p	8	4	0.7
34	16 p	8	2	1
35	7 p	5	2	1
36	20 p	5	3.4	0.8
37	9 p	4	2.3	1
38	18 q	4	2.3	0.9
39	21 q	4	2.2	1
40	5 p	2	1.7	1
41	18 p	2	3.3	0.8
42	21 p	2	2	0.9
43	Y q	1	8.3	0.4
44	Y q	1	4.3	0.6

H3CHR6-MHC-QBB

Relative numbers



Rank	locus	# genes	%	p-value
1	21 p	1	50	0.09
2	3 p	54	12.7	2e-12
3	13 q	33	11.7	3e-07
4	Y p	1	8.3	0.4
5	12 p	19	7.9	0.01
6	10 p	7	1	0.1
7	6 q	25	6.7	0.02
8	5 q	34	5.8	0.07
9	4 p	10	5.3	0.3
10	15 q	26	5.1	0.3
11	2 p	20	4.9	0.3
12	19 q	31	4.8	0.4
13	3 q	23	4.6	0.4
14	19 p	22	4.5	0.5
15	1 q	36	4.4	0.6
16	Y q	1	4.3	0.6
17	12 q	26	4.2	0.7
18	X q	16	4.1	0.7
19	X p	11	4.1	0.6
20	7 q	20	4	0.7
21	10 q	19	4	0.7
22	8 p	8	4	0.7
23	2 q	25	3.9	0.8
24	14 q	20	3.8	0.8
25	20 q	11	3.6	0.8
26	6 p	13	3.6	0.8
27	17 p	10	3.5	0.8
28	20 p	5	3.4	0.8
29	22 q	13	3.3	0.8
30	16 q	11	3.3	0.9
31	18 p	2	3.3	0.9
32	8 q	11	3.3	0.9
33	11 p	10	3.2	0.9
34	17 q	20	3.1	0.9
35	1 p	26	3.1	1
36	11 q	18	2.8	1
37	4 q	11	2.5	1
38	18 q	4	2.3	0.9
39	9 p	4	2.3	1
40	9 q	10	2.2	1
41	21 q	4	2.2	1
42	16 p	8	2	1
43	7 p	5	2	1
44	5 p	2	1.7	1

Spot D

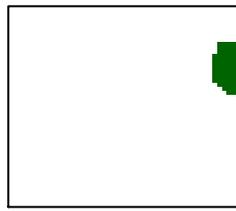
genes in spot = 699 (684 with loci information)

samples with spot = 4 (1.5 %)

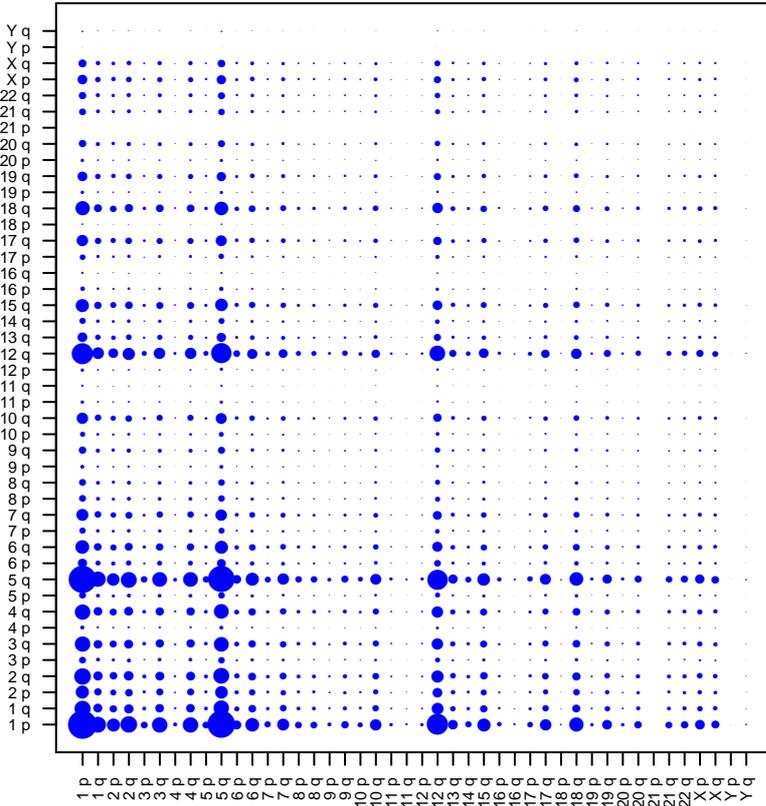
Atypical : 2 (2.7 %)

Classical : 1 (3.1 %)

Mesenchymal : 1 (1.2 %)



Absolute numbers

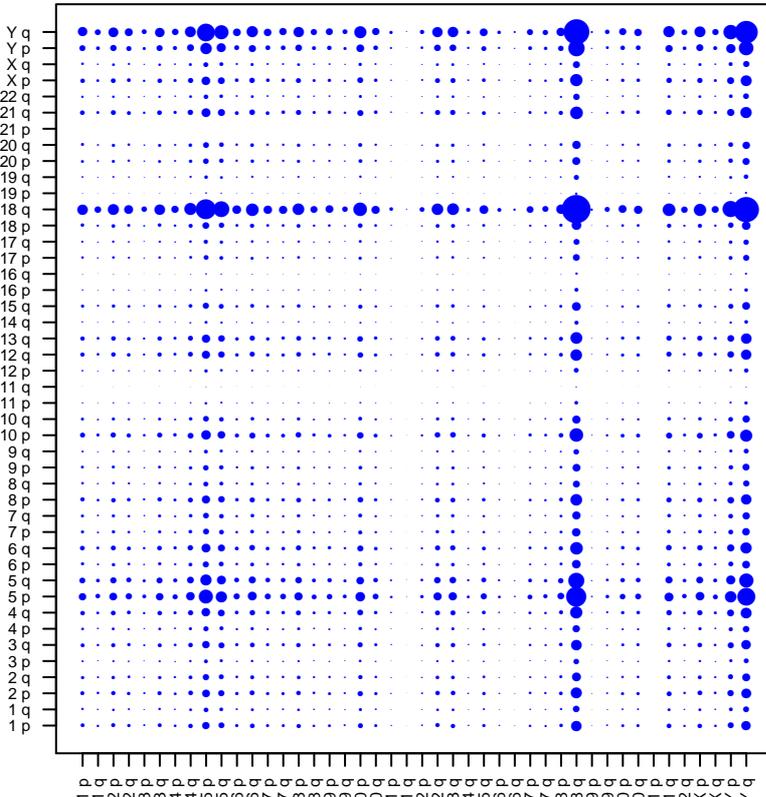


Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	1 p	50	5.4	0.06
2	5 q	48	8.2	2e-05
3	12 q	37	5.9	0.03
4	2 q	29	4.6	0.4
5	1 q	28	3.4	0.9
6	3 q	27	5.5	0.1
7	4 q	27	6.2	0.04
8	18 q	25	14.6	9e-08
9	6 q	25	6.5	0.03
10	2 q	23	5.7	0.1
11	15 q	23	4.5	0.5
12	7 q	21	4.2	0.6
13	10 q	20	4.2	0.6
14	17 q	20	3.1	1
15	13 q	17	6	0.1
16	19 q	17	2.6	1
17	X p	17	6.3	0.08
18	6 p	16	4.4	0.5
19	X q	14	3.6	0.8
20	9 q	13	2.8	1
21	20 q	13	4.3	0.6
22	22 q	13	3.3	0.9
23	3 p	12	2.8	1
24	5 p	12	10.3	0.005
25	8 p	12	6	0.2
26	9 p	12	3.6	0.8
27	21 q	12	6.5	0.1
28	7 p	11	4.3	0.5
29	14 q	11	2.1	1
30	17 p	10	3.5	0.8
31	10 p	9	7	0.1
32	16 p	8	2	1
33	4 p	7	3.7	0.7
34	9 p	7	4	0.6
35	11 p	6	1.9	1
36	12 p	6	2.5	1
37	19 p	6	1.2	1
38	20 p	6	4.1	0.6
39	11 q	4	0.6	1
40	16 q	4	1.2	1
41	18 p	3	1.9	0.5
42	Y q	3	4.9	0.07
43	Y p	3	1.3	0.4
44	21 p	0	8.3	1

HSCHR6-MHC-DQB1

Relative numbers



Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	18 q	25	14.6	9e-08
2	Y q	3	13	0.07
3	5 p	12	10.3	0.005
4	Y p	1	8.3	0.4
5	5 q	48	8.2	2e-05
6	10 p	9	7	0.1
7	21 q	12	6.5	0.1
8	6 q	24	6.5	0.03
9	X p	17	6.3	0.08
10	4 q	27	6.2	0.04
11	13 q	17	6	0.1
12	8 p	12	6	0.2
13	12 q	37	5.9	0.03
14	2 p	23	5.7	0.1
15	3 q	27	5.5	0.1
16	1 q	25	5.4	0.06
17	18 p	50	4.9	0.5
18	2 q	29	4.6	0.4
19	15 q	23	4.5	0.5
20	6 p	16	4.4	0.5
21	7 p	11	4.3	0.5
22	20 q	13	4.3	0.6
23	7 q	21	4.2	0.6
24	10 q	20	4.2	0.6
25	20 p	6	4.1	0.6
26	9 p	7	4	0.6
27	4 p	7	3.7	0.7
28	X q	14	3.6	0.8
29	8 q	12	3.6	0.8
30	17 p	10	3.5	0.8
31	1 q	28	3.4	0.9
32	2 q	13	3.3	0.9
33	17 q	20	3.1	1
34	3 p	12	2.8	1
35	9 q	13	2.8	1
36	19 q	17	2.6	1
37	12 p	6	2.5	1
38	14 q	11	2.1	1
39	16 p	8	2	1
40	11 p	6	1.9	1
41	19 p	6	1.2	1
42	16 q	4	1.2	1
43	11 q	4	0.6	1
44	21 p	0	0	1

Spot E

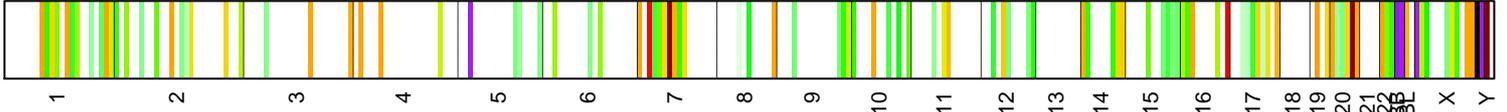
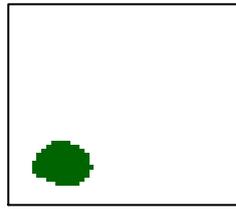
genes in spot = 682 (649 with loci information)

samples with spot = 19 (6.9 %)

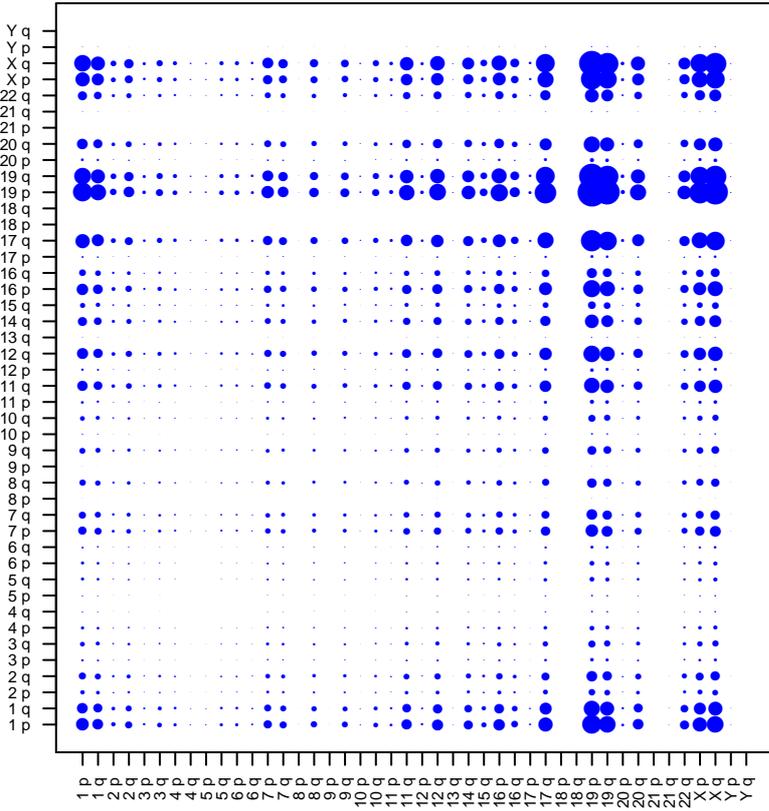
Atypical : 8 (10.8 %)

Mesenchymal : 7 (8.2 %)

Basal : 4 (4.8 %)



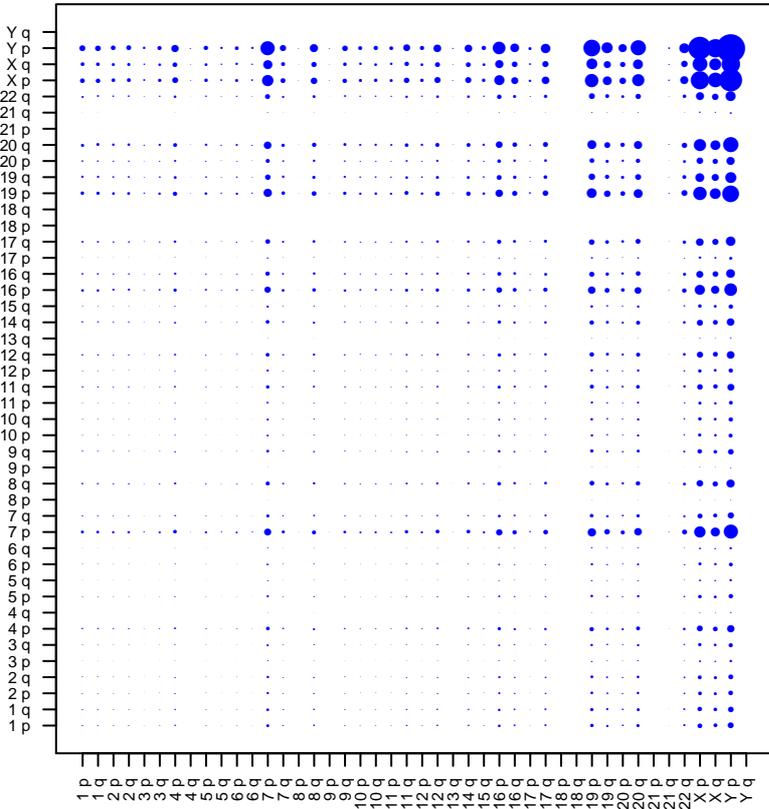
Absolute numbers



Rank	locus	# genes	%	p-value
1	19 p	48	9.8	5e-08
2	19 q	42	6.4	0.004
3	X q	42	10.7	2e-08
4	17 q	36	5.5	0.06
5	X p	36	13.3	9e-10
6	1 p	33	3.5	0.9
7	16 p	29	7.4	0.002
8	12 q	28	4.5	0.4
9	1 q	28	4.5	0.9
10	20 q	27	8.9	2e-04
11	11 q	26	4	0.6
12	14 q	23	5.9	0.4
13	22 q	23	5.9	0.07
14	7 p	21	8.3	0.003
15	2 q	18	2.8	1
16	7 q	18	3.6	0.8
17	16 q	17	5.1	0.2
18	8 q	16	4.8	0.3
19	9 q	15	3.3	0.9
20	15 q	13	2.5	1
21	3 q	12	2.4	1
22	10 q	12	2.5	1
23	2 p	11	2.7	1
24	4 p	11	4.3	0.5
25	5 q	8	1.4	1
26	6 p	8	2.2	1
27	1 p	7	2.2	1
28	20 p	7	4.8	0.4
29	3 p	6	1.4	1
30	12 p	6	2.5	0.9
31	6 q	5	1.3	1
32	17 p	5	1.7	1
33	4 q	5	0.7	1
34	5 p	3	2.6	0.9
35	10 p	3	2.3	0.9
36	13 q	2	0.7	1
37	21 q	2	1.1	1
38	Y p	2	16.7	0.09
39	8 p	1	0.5	1
40	9 p	1	0.6	1
41	18 p	0	0	1
42	18 q	0	0	1
43	21 p	0	0	1
44	Y q	0	0	1

H3CHR6-MHC-QBB

Relative numbers



Rank	locus	# genes	%	p-value
1	Y p	2	16.7	0.09
2	X p	36	13.3	9e-10
3	X q	42	10.7	2e-08
4	19 p	48	9.8	5e-08
5	20 q	27	8.9	2e-04
6	7 p	21	8.3	0.003
7	16 p	29	7.4	0.002
8	19 q	42	6.4	0.004
9	22 q	23	5.9	0.07
10	17 q	36	5.5	0.06
11	16 q	17	5.1	0.2
12	8 q	16	4.8	0.3
13	20 p	7	4.8	0.4
14	12 q	28	4.5	0.4
15	14 q	23	4.4	0.4
16	4 p	8	4.3	0.5
17	11 q	8	4	0.6
18	7 q	18	3.6	0.8
19	1 p	32	3.5	0.9
20	1 q	27	3.3	0.9
21	9 q	15	3.3	0.9
22	2 q	18	2.8	1
23	2 p	11	2.7	1
24	5 p	3	2.6	0.9
25	15 q	13	2.5	1
26	10 q	12	2.5	1
27	12 p	6	2.5	0.9
28	3 q	12	2.4	1
29	10 p	3	2.3	0.9
30	6 p	8	2.2	1
31	11 p	7	2.2	1
32	17 p	5	1.7	1
33	5 p	6	1.4	1
34	5 q	8	1.4	1
35	6 q	8	1.4	1
36	21 q	2	1.3	1
37	13 q	2	1.1	1
38	4 q	3	0.7	1
39	9 p	1	0.6	1
40	8 p	1	0.5	1
41	18 p	0	0	1
42	18 q	0	0	1
43	21 p	0	0	1
44	Y q	0	0	1

Spot F

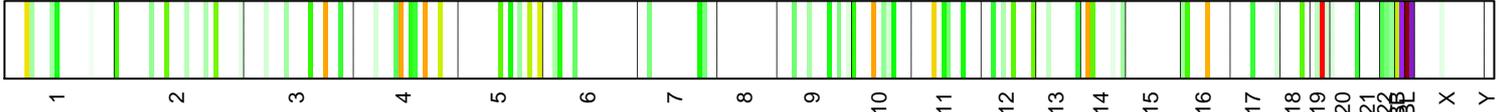
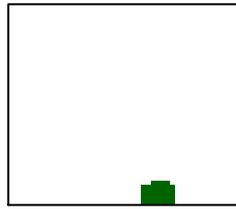
genes in spot = 300 (277 with loci information)

samples with spot = 37 (13.5 %)

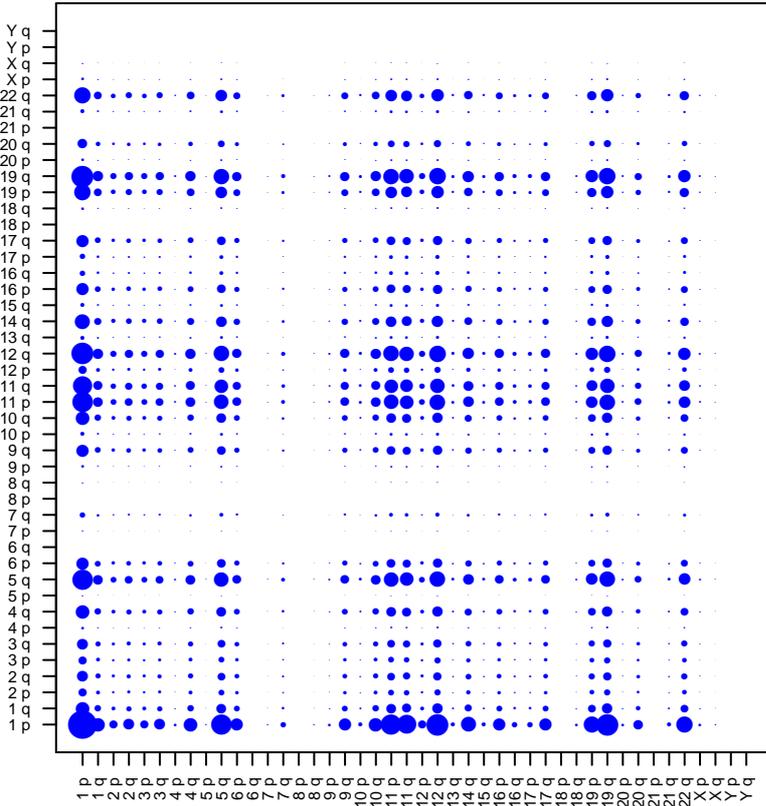
Atypical : 14 (18.9 %)

Mesenchymal : 16 (18.8 %)

Basal : 7 (8.3 %)



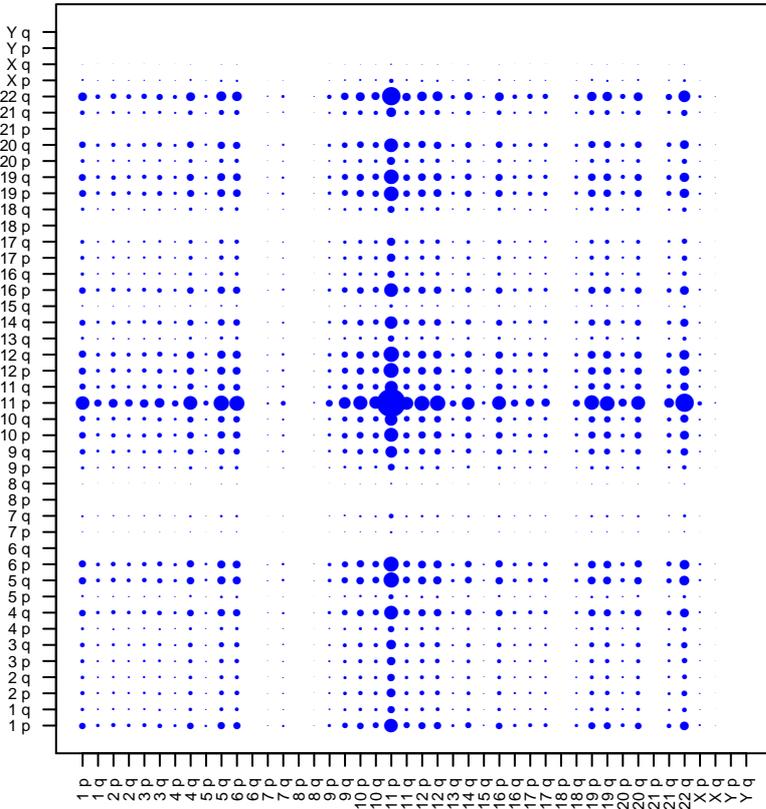
Absolute numbers



Rank	locus	# genes	%	p-value
1	1 p	21	2.3	0.2
2	12 p	16	2.6	0.1
3	19 q	16	2.5	0.2
4	5 q	15	2.6	0.1
5	11 p	15	2.7	0.1
6	11 q	14	2.2	0.3
7	19 p	12	2.4	0.2
8	14 q	11	2.1	0.3
9	10 p	11	2.2	0.3
10	1 q	10	2.2	0.4
11	4 q	10	2.3	0.3
12	10 q	10	2.3	0.4
13	6 p	9	2.5	0.2
14	9 q	9	2.5	0.5
15	16 p	9	2.3	0.3
16	17 q	9	1.4	0.9
17	2 q	8	1.3	0.9
18	3 q	8	1.6	0.7
19	20 q	7	2.3	0.3
20	2 p	6	1.5	0.8
21	3 p	6	1.4	0.8
22	12 p	6	2.5	0.3
23	7 q	4	0.8	1.1
24	16 p	4	0.8	0.9
25	17 p	4	1.4	0.8
26	10 q	4	1.1	0.9
27	13 q	3	2.3	0.4
28	15 q	3	1.1	1.1
29	21 q	3	1.6	0.7
30	4 p	2	1.1	0.9
31	9 p	2	1.1	0.8
32	18 p	2	1.2	0.8
33	20 p	2	1.4	0.8
34	X p	2	0.7	1.1
35	5 p	1	0.9	0.9
36	7 p	1	0.4	1.1
37	8 q	1	0.3	1.1
38	X q	1	0.3	1.1
39	6 q	0	0	1.1
40	8 p	0	0	1.1
41	18 p	0	0	1.1
42	21 p	0	0	1.1
43	Y p	0	0	1.1
44	Y q	0	0	1.1

H3CHR6-MHC-QBB

Relative numbers



Rank	locus	# genes	%	p-value
1	11 p	15	4.7	8e-04
2	22 q	15	3.1	0.06
3	12 q	16	2.6	0.1
4	5 q	15	2.6	0.1
5	6 p	9	2.5	0.2
6	12 p	6	2.5	0.3
7	19 q	16	2.5	0.2
8	19 p	12	2.4	0.2
9	10 p	3	2.3	0.4
10	4 q	10	2.3	0.3
11	20 q	7	2.3	0.3
12	16 p	9	2.3	0.3
13	1 p	11	2.1	0.3
14	11 q	11	1.1	0.4
15	14 q	11	1.1	0.4
16	10 q	10	1.1	0.4
17	9 q	9	1.1	0.4
18	2 q	8	1.6	0.5
19	3 q	8	1.6	0.7
20	2 p	6	1.5	0.8
21	3 p	6	1.4	0.8
22	17 p	4	1.4	0.8
23	17 q	9	1.4	0.9
24	20 p	2	1.4	0.8
25	2 q	8	1.3	0.8
26	1 q	10	1.1	0.9
27	16 q	4	1.1	0.9
28	18 q	2	1.2	0.8
29	9 p	2	1.1	0.9
30	4 p	2	1.1	0.9
31	13 q	1	1.1	0.9
32	5 q	1	0.9	0.9
33	7 q	1	0.9	0.9
34	X q	2	0.7	1.1
35	15 q	3	0.6	1.1
36	7 p	1	0.4	1.1
37	8 q	1	0.3	1.1
38	X q	1	0.3	1.1
39	6 q	0	0	1.1
40	8 p	0	0	1.1
41	18 p	0	0	1.1
42	21 p	0	0	1.1
43	Y p	0	0	1.1
44	Y q	0	0	1.1

Spot G

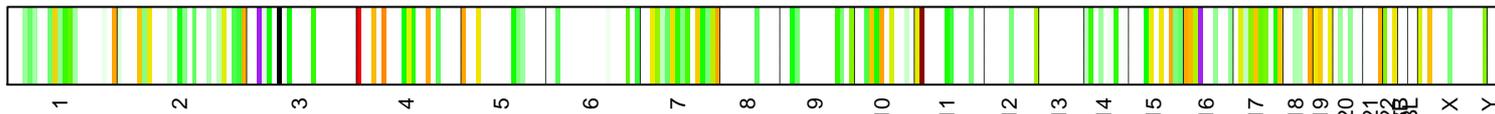
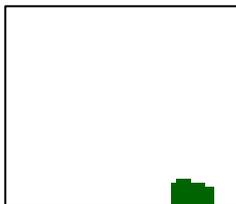
genes in spot = 537 (503 with loci information)

samples with spot = 35 (12.7 %)

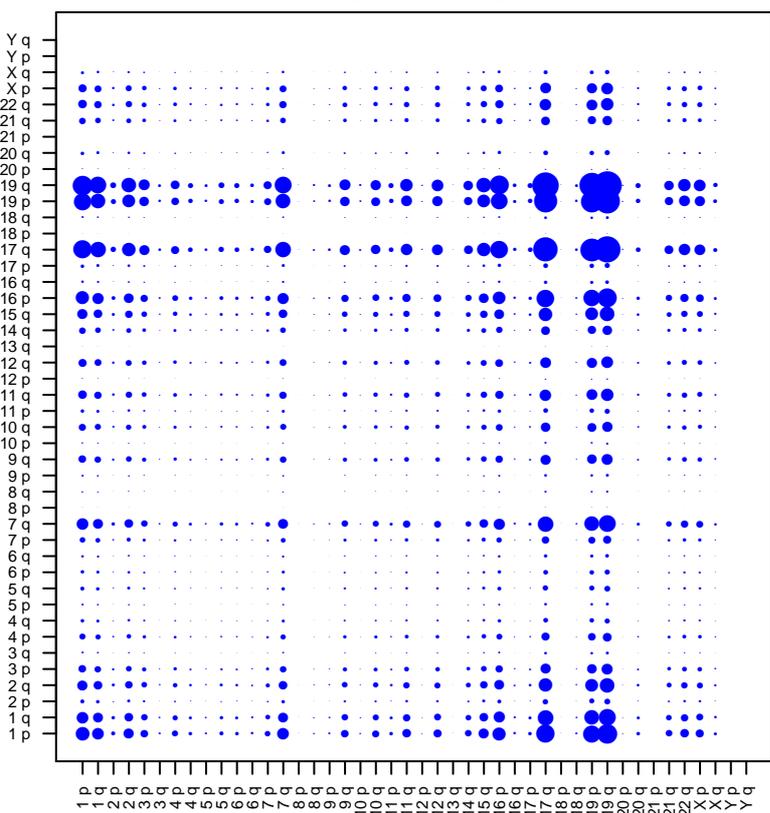
Atypical : 27 (36.5 %)

Mesenchymal : 6 (7.1 %)

Basal : 2 (2.4 %)



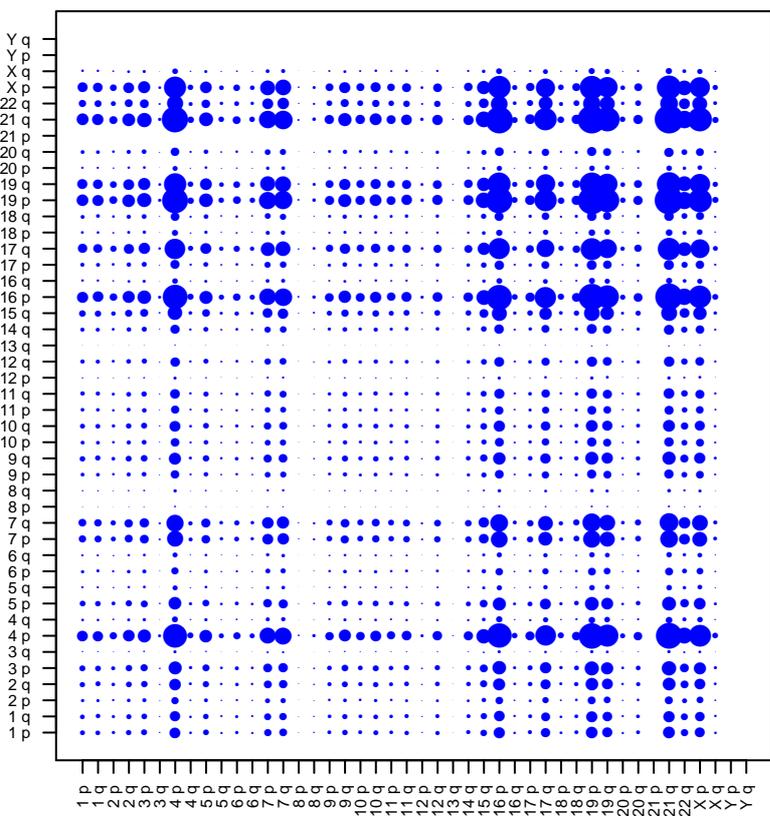
Absolute numbers



Rank	locus	# genes	%	p-value
1	19q	39	6	3e-04
2	17q	36	5	0.002
3	19p	34	6	4e-05
4	1p	27	6	0.8
5	16p	26	6	6e-04
6	1q	23	4	0.8
7	7q	23	4	0.007
8	2q	20	3	0.003
9	15q	20	3	0.003
10	11q	20	3	0.003
11	22q	17	2	0.003
12	12q	17	2	0.003
13	Xp	16	2	0.002
14	3p	15	2	0.4
15	9q	15	2	0.6
16	10q	14	2	0.7
17	14q	13	2	0.9
18	21q	7	0	0.009
19	4p	12	6	0.02
20	7p	11	4	0.2
21	2p	8	2	1
22	5q	8	1	1
23	4q	7	1	1
24	6p	7	1	1
25	11p	7	2	0.009
26	17p	7	2	0.009
27	20q	7	2	0.009
28	Xq	6	1	1
29	6q	5	1	1
30	16q	5	1	1
31	3q	4	0	1
32	5p	4	3	0.5
33	9p	4	2	0.8
34	18q	4	2	0.8
35	8q	3	1	1
36	10p	3	2	0.8
37	12p	2	0	1
38	20p	2	1	1
39	8p	1	0	1
40	13q	1	0	1
41	18p	1	0	1
42	21p	0	0	1
43	Yq	0	0	1
44	Yq	0	0	1

HSCHR6-MHC-DBP

Relative numbers



Rank	locus	# genes	%	p-value
1	21q	13	7	0.009
2	34p	13	6	4e-05
3	16p	26	6	6e-04
4	4p	12	6	0.02
5	19q	39	6	3e-04
6	Xp	16	5	0.002
7	17q	36	4	0.007
8	7q	23	4	0.2
9	7p	11	4	0.2
10	22q	17	4	0.2
11	15q	20	3	0.3
12	3p	15	3	0.4
13	5p	4	3	0.5
14	9q	15	3	0.6
15	2q	20	1	0.6
16	10q	14	1	0.6
17	1p	27	2	0.7
18	11q	23	2	0.8
19	11p	17	2	0.8
20	12q	16	2	0.9
21	14q	13	2	0.9
22	17p	7	2	0.8
23	18q	4	2	0.8
24	10p	3	2	0.8
25	20q	7	2	0.9
26	9p	4	2	0.8
27	11p	7	2	0.9
28	2p	8	2	1
29	6p	7	1	1
30	18p	1	1	0.9
31	4q	7	1	1
32	Xq	6	1	1
33	16q	5	1	1
34	5q	8	1	1
35	20p	2	1	1
36	6q	5	1	1
37	8q	3	0	1
38	12p	2	0	1
39	3q	4	0	1
40	8p	1	0	1
41	13q	1	0	1
42	21p	0	0	1
43	Yq	0	0	1
44	Yq	0	0	1

Spot H

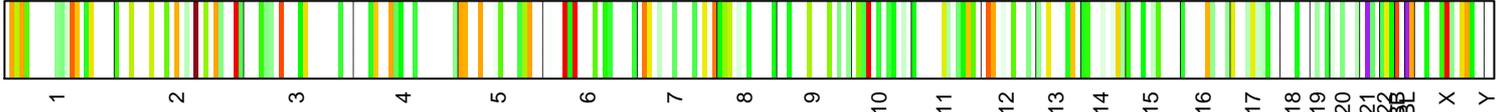
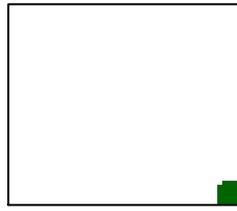
genes in spot = 482 (457 with loci information)

samples with spot = 66 (24 %)

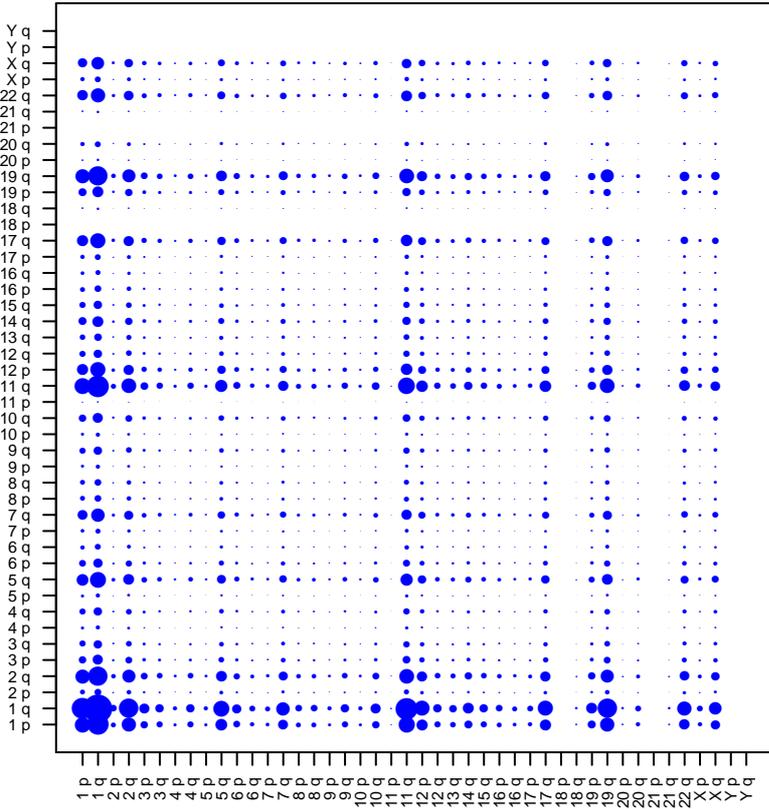
Atypical : 47 (63.5 %)

Mesenchymal : 12 (14.1 %)

Basal : 7 (8.3 %)



Absolute numbers

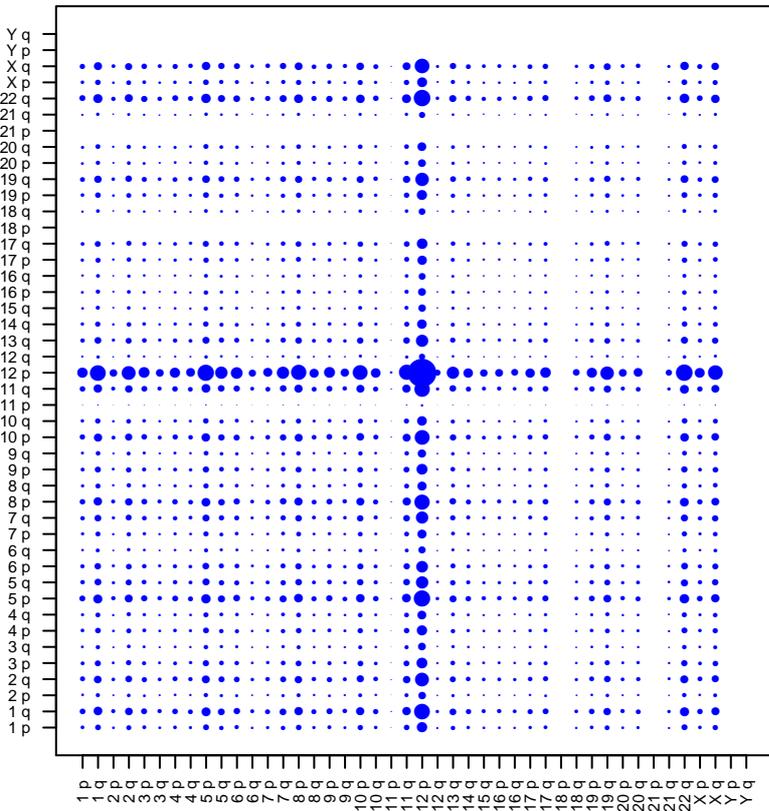


Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	1 q	34	4.1	0.03
2	11 q	26	4	0.08
3	1 p	25	2.7	0.7
4	2 q	23	3.6	0.2
5	19 q	23	3.5	0.2
6	5 q	19	3.2	0.4
7	12 p	18	3.8	3e-04
8	17 q	18	3.5	0.07
9	11 q	18	3.5	0.08
10	7 q	16	4.4	0.04
11	X q	15	3.1	0.2
12	14 q	13	3.5	0.08
13	19 p	13	3.6	0.7
14	3 p	12	2.6	0.6
15	10 q	12	2.5	0.8
16	6 p	11	2.1	0.5
17	3 q	10	2	0.9
18	4 q	10	2.3	0.8
19	9 q	10	2.2	0.9
20	12 q	10	1.6	0.9
21	15 q	10	2	0.9
22	13 q	9	2.2	0.5
23	2 p	8	2.4	0.09
24	8 p	8	2.4	0.09
25	16 p	7	1.9	0.09
26	17 q	7	1.9	0.09
27	20 q	7	2.3	0.8
28	X p	7	2.4	0.8
29	20 q	7	2.4	0.8
30	X p	6	2.6	0.7
31	7 p	6	2.4	0.8
32	16 q	6	1.8	0.9
33	4 p	5	2.7	0.7
34	5 p	5	4.3	0.3
35	9 p	5	3.9	0.6
36	10 p	5	3.9	0.3
37	18 q	5	1.8	0.9
38	20 p	2	2	0.8
39	21 q	2	1.6	0.9
40	11 p	0	0	0.9
41	18 p	0	0	1
42	21 p	0	0	1
43	Y p	0	0	1
44	Y q	0	0	1

H3CHR6-MHC-QBB

Relative numbers



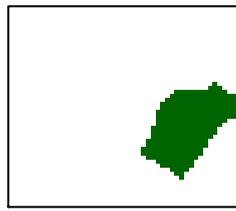
Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	12 p	18	7.5	3e-04
2	22 q	17	4.3	0.08
3	5 p	5	4.3	0.3
4	1 q	34	4.1	0.03
5	11 q	26	4	0.08
6	8 p	8	4	0.2
7	10 p	5	3.9	0.3
8	X q	15	3.8	0.2
9	2 q	23	3.6	0.2
10	19 q	23	3.5	0.2
11	5 q	19	3.2	0.4
12	7 q	16	3.8	0.4
13	13 q	9	2.7	0.5
14	6 p	11	2.1	0.5
15	3 p	5	2	0.6
16	9 p	10	2.3	0.6
17	17 q	7	1.9	0.7
18	4 p	5	2.5	0.7
19	19 p	7	2.7	0.7
20	X p	13	2.6	0.7
21	X q	7	2	0.7
22	10 q	12	2.5	0.8
23	14 q	13	2.5	0.8
24	17 p	7	2.4	0.8
25	8 q	8	2.4	0.8
26	7 p	6	2.4	0.8
27	4 q	10	2.3	0.8
28	20 q	7	2.3	0.8
29	9 q	10	2.2	0.8
30	16 p	8	2	0.8
31	20 p	2	1.6	0.9
32	3 q	10	2	0.9
33	2 q	8	2	0.9
34	15 q	10	2	0.9
35	6 q	7	1.1	0.9
36	16 q	6	1.1	0.9
37	18 q	3	1.1	0.9
38	21 q	3	1.6	0.9
39	12 q	10	1.6	0.9
40	11 p	2	0	1
41	18 p	0	0	1
42	21 p	0	0	1
43	Y p	0	0	1
44	Y q	0	0	1

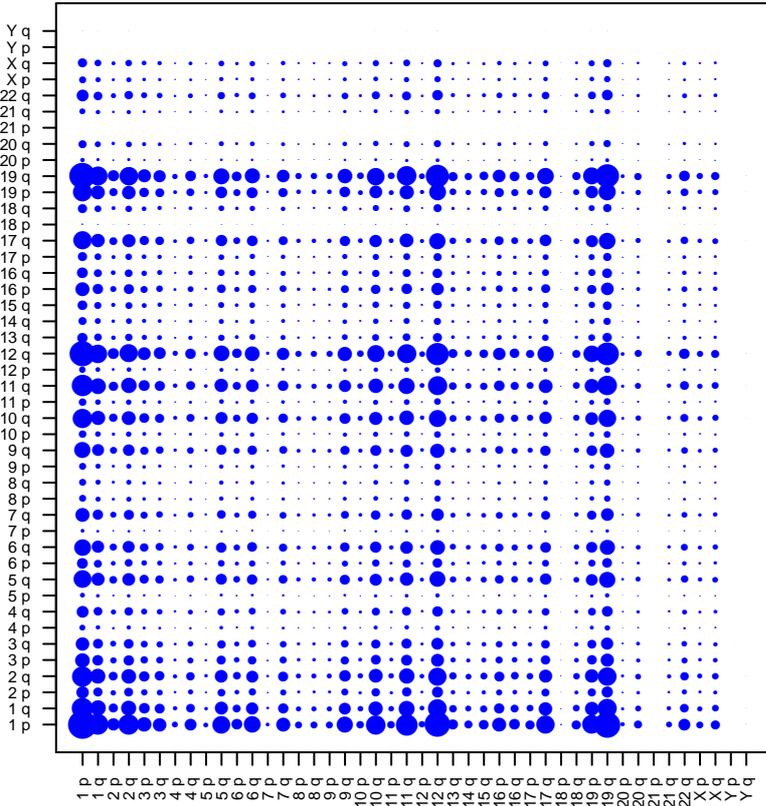
Spot I

genes in spot = 977 (935 with loci information)

samples with spot = 0 (0 %)



Absolute numbers

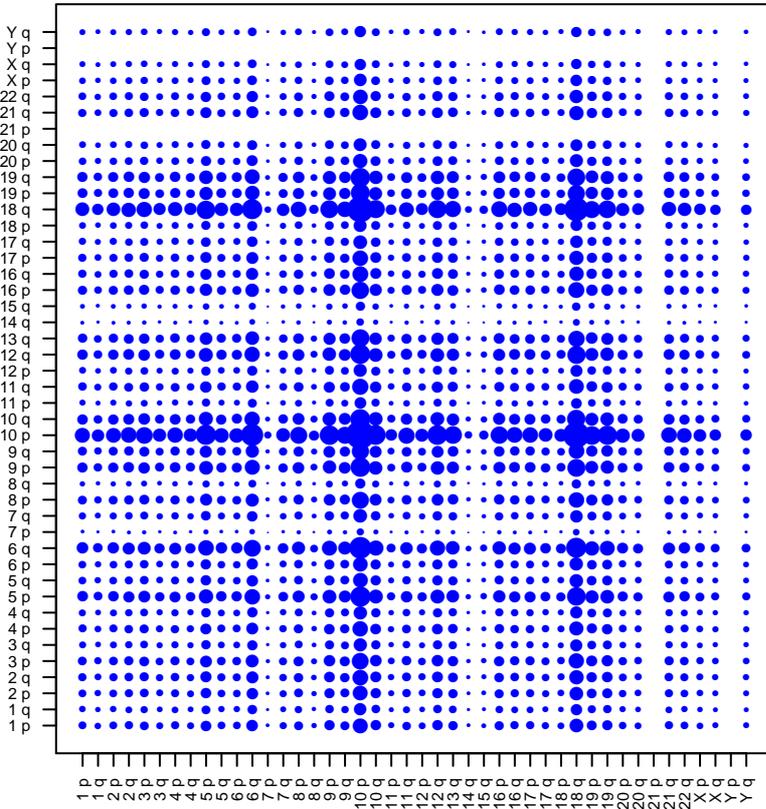


Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	1 p	53	5.7	0.7
2	19 p	48	7.4	0.09
3	12 q	47	7.5	0.07
4	11 q	40	6.2	0.57
5	1 q	39	4.7	1
6	2 q	38	6	0.5
7	10 q	36	7.5	0.1
8	19 p	35	7.1	0.2
9	17 p	35	7.1	0.2
10	5 q	33	5.2	0.8
11	6 q	33	5.2	0.8
12	9 q	30	6.4	0.4
13	3 p	27	6.4	0.4
14	7 q	26	5.2	0.8
15	16 p	26	6.6	0.3
16	3 q	25	5.1	0.8
17	2 p	23	5.7	0.7
18	4 q	22	5.1	0.8
19	22 q	22	5.6	0.7
20	6 p	20	5.6	0.7
21	16 q	20	6.6	0.5
22	13 q	19	6.8	0.3
23	15 q	18	5.5	0.9
24	17 p	17	9.9	1
25	18 q	17	9.9	0.03
26	X q	17	4.3	0.9
27	14 q	15	2.9	1
28	20 p	15	4.9	0.8
29	10 p	14	10.9	0.02
30	11 p	14	4.4	0.9
31	8 p	13	6.5	0.4
32	8 q	13	3.9	1
33	9 p	13	7.4	0.3
34	X p	13	4.8	0.8
35	12 p	12	5	0.8
36	4 p	11	5.9	0.6
37	21 q	11	5.9	0.6
38	5 p	9	7.7	0.3
39	20 p	8	5.4	0.7
40	7 p	7	2.8	1
41	18 p	3	4.4	0.7
42	Y q	1	4.3	0.8
43	21 p	0	0	1
44	Y p	0	0	1

HSCHR6-MHC-DAB

Relative numbers



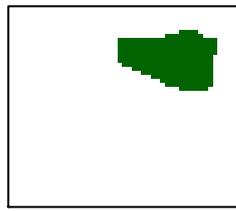
Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	10 p	14	10.9	0.02
2	18 q	17	9.9	0.03
3	6 q	31	8.4	0.04
4	5 p	9	7.7	0.3
5	10 q	36	7.5	0.1
6	12 q	47	7.5	0.07
7	9 p	13	7.4	0.3
8	19 q	48	7.4	0.09
9	19 p	35	7.1	0.2
10	13 q	19	6.8	0.3
11	16 p	26	6.6	0.3
12	9 q	30	6.5	0.4
13	8 p	13	6.5	0.4
14	3 p	27	6.4	0.4
15	11 q	40	6.2	0.57
16	16 q	20	5.6	0.7
17	2 q	38	6.6	0.5
18	21 q	17	5.9	0.6
19	17 p	17	5.9	0.6
20	4 p	11	5.9	0.6
21	1 p	53	5.7	0.7
22	2 p	23	5.7	0.7
23	5 q	33	5.6	0.7
24	22 q	22	5.6	0.7
25	6 p	20	5.6	0.7
26	20 p	8	5.4	0.7
27	17 q	34	5.2	0.8
28	7 q	26	5.2	0.8
29	4 q	22	5.1	0.8
30	3 q	25	5.1	0.8
31	12 p	12	5	0.8
32	20 q	15	4.9	0.8
33	18 p	3	4.9	0.7
34	X p	13	4.8	0.8
35	1 q	39	4.7	1
36	11 p	14	4.4	0.9
37	X q	17	4.3	0.9
38	Y q	1	4.3	0.8
39	8 q	13	3.9	1
40	15 q	18	3.5	1
41	14 q	15	2.9	1
42	7 p	7	2.8	1
43	21 p	0	0	1
44	Y p	0	0	1

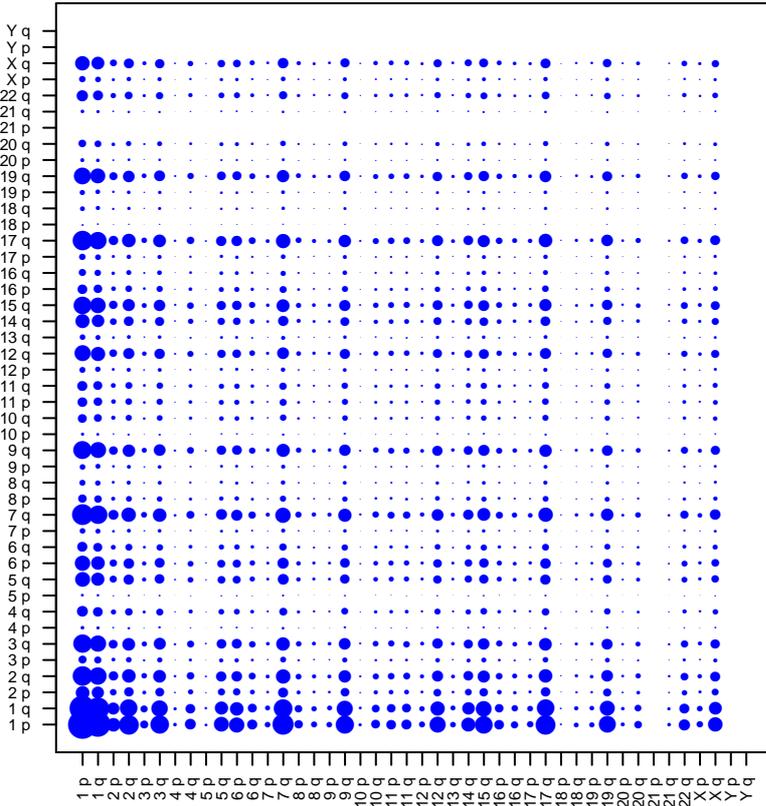
Spot J

genes in spot = 1175 (1111 with loci information)

samples with spot = 0 (0 %)



Absolute numbers

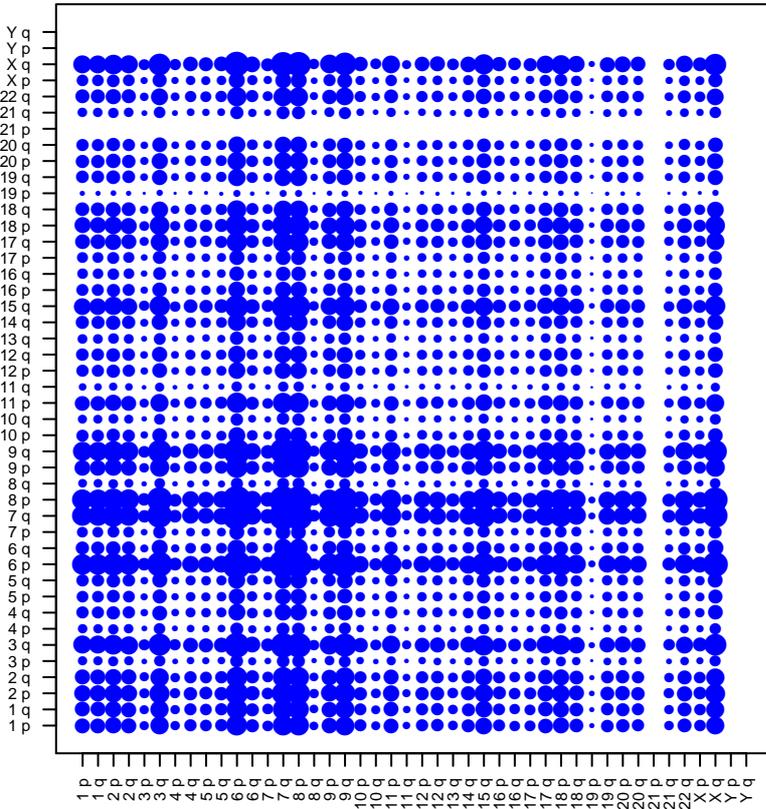


Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	1 p	71	7.7	0.3
2	1 q	63	7.6	0.4
3	7 q	52	10.4	0.005
4	2 q	49	7.7	0.3
5	17 q	49	7.5	0.4
6	3 q	46	9.3	0.05
7	9 q	45	8.8	0.03
8	15 q	44	8.6	0.1
9	19 q	42	6.4	0.8
10	12 q	40	6.4	0.8
11	6 p	38	10.6	0.01
12	5 q	37	6.3	0.8
13	X q	36	9.2	0.08
14	14 q	35	6.7	0.7
15	2 p	34	8.4	0.2
16	22 q	28	7.1	0.6
17	4 q	27	6.2	0.8
18	6 q	25	6.7	0.7
19	11 q	25	3.9	1
20	11 p	24	7.6	0.4
21	16 p	24	6.1	0.8
22	10 q	22	4.6	1
23	8 p	21	10.4	0.06
24	3 p	20	4.7	1
25	20 q	19	6.2	0.8
26	16 q	18	5.4	0.9
27	17 p	16	5.6	0.9
28	X p	16	5.9	0.8
29	8 q	15	4.5	1
30	12 p	15	6.2	0.8
31	7 p	14	5.5	0.9
32	9 p	14	8	0.4
33	13 q	14	5	1
34	19 p	13	2.6	1
35	18 q	12	7	0.6
36	20 p	10	6.8	0.6
37	4 p	9	4.8	0.9
38	21 q	9	4.9	0.9
39	10 p	8	6.2	0.7
40	5 p	7	6.8	0.8
41	18 p	5	8.2	0.5
42	21 p	0	0	1
43	Y p	0	0	1
44	Y q	0	0	1

HSCHR6-MHC-DQB1

Relative numbers



Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	6 p	38	10.6	0.01
2	8 p	21	10.4	0.06
3	7 q	52	10.4	0.005
4	9 q	45	9.8	0.03
5	3 q	46	9.3	0.05
6	X q	36	9.2	0.08
7	15 q	44	8.6	0.1
8	2 p	34	8.4	0.2
9	18 p	5	8.2	0.5
10	9 p	14	8	0.4
11	2 q	49	7.7	0.3
12	1 p	71	7.7	0.3
13	1 q	63	7.6	0.4
14	11 p	24	7.6	0.4
15	17 q	49	7.5	0.4
16	22 q	28	7.1	0.6
17	18 q	12	7.1	0.6
18	20 p	25	6.8	0.6
19	6 q	25	6.7	0.7
20	14 q	35	6.7	0.7
21	19 q	42	6.4	0.8
22	12 q	40	6.4	0.8
23	5 q	37	6.3	0.8
24	20 q	19	6.2	0.8
25	4 q	27	6.2	0.8
26	12 p	15	6.2	0.8
27	10 p	8	6.2	0.7
28	16 p	24	6.1	0.8
29	5 p	7	6	0.8
30	X p	16	5.9	0.8
31	17 p	16	5.6	0.8
32	7 p	14	5.5	0.9
33	16 q	18	5.4	0.9
34	13 q	14	5	1
35	21 q	9	4.9	0.9
36	4 p	9	4.8	0.9
37	3 p	20	4.7	1
38	10 q	22	4.6	1
39	8 q	15	4.5	1
40	11 q	25	3.9	1
41	19 p	13	2.6	1
42	21 p	0	0	1
43	Y p	0	0	1
44	Y q	0	0	1

Spot K

genes in spot = 513 (503 with loci information)

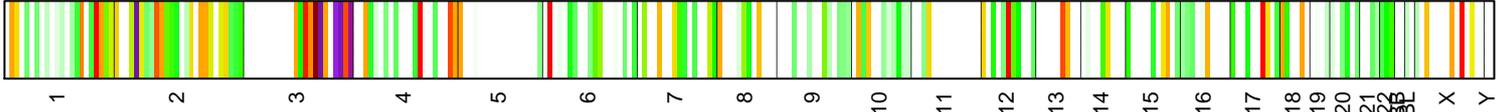
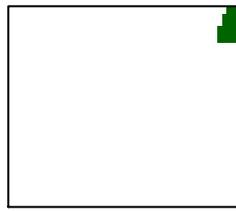
samples with spot = 36 (13.1 %)

Atypical : 14 (18.9 %)

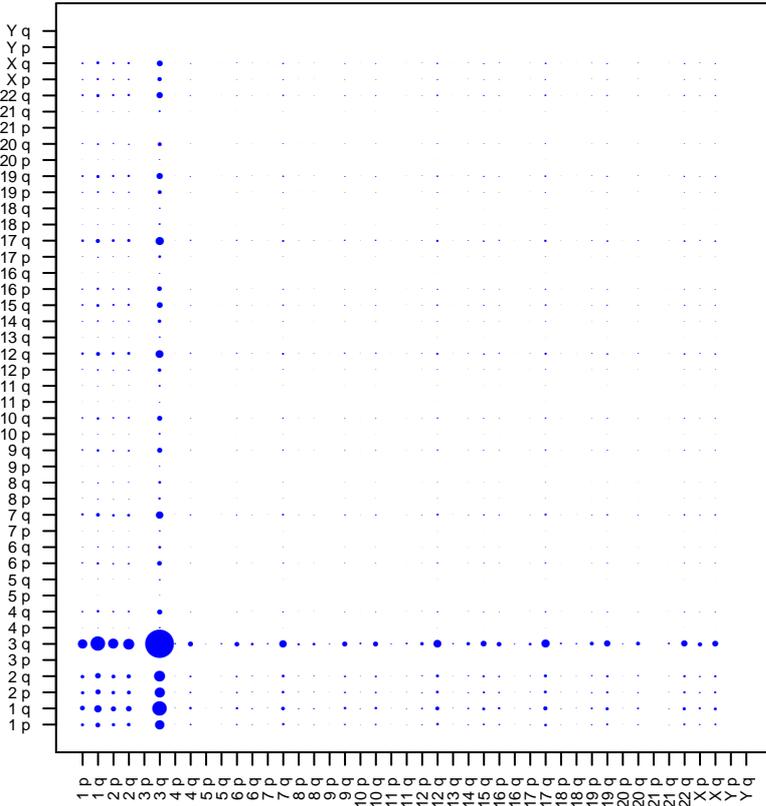
Classical : 14 (43.8 %)

Mesenchymal : 3 (3.5 %)

Basal : 5 (6 %)



Absolute numbers

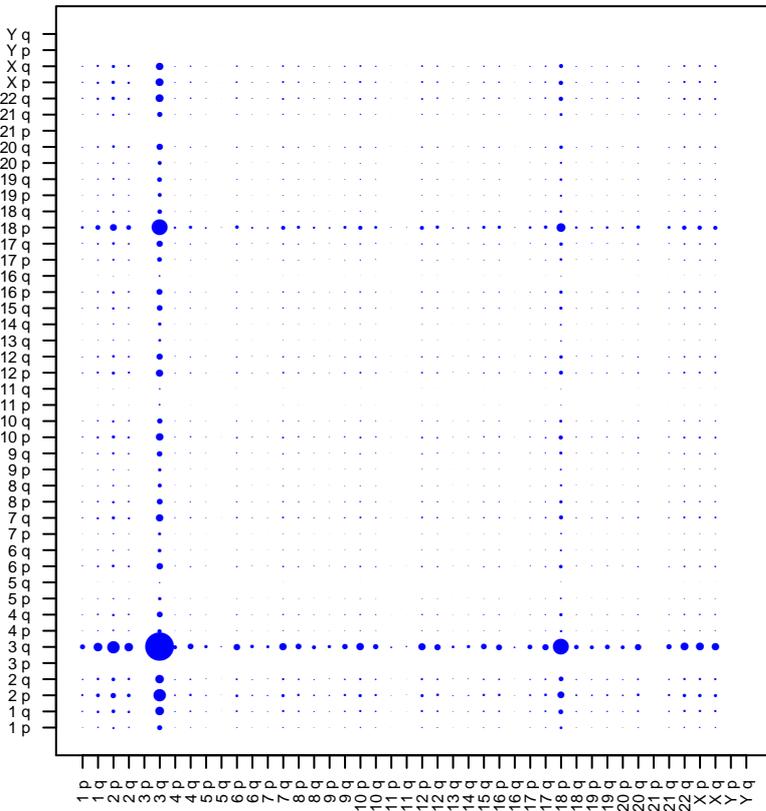


Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	3 q	73	14.7	<2e-16
2	1 q	37	4.5	0.02
3	2 q	28	4.4	0.05
4	2 p	26	6.4	6e-04
5	1 p	24	2.6	0.09
6	17 q	21	3.2	0.00
7	12 q	20	3.2	0.00
8	7 q	19	3.8	0.00
9	19 q	19	4.1	0.00
10	22 q	15	2.5	0.00
11	15 q	11	3.9	0.00
12	X q	11	2.9	0.03
13	4 q	8	2.9	0.7
14	9 q	8	3.3	0.6
15	10 q	7	2.8	0.7
16	6 p	6	3.3	0.5
17	16 p	6	2.7	0.6
18	X p	5	4.1	0.2
19	19 p	5	2.2	1
20	20 q	5	3.3	0.5
21	12 p	5	3.7	0.4
22	14 q	4	1.7	1
23	6 q	4	1.9	1
24	8 q	4	2.1	0.9
25	17 p	4	2.4	0.8
26	8 p	4	3.9	0.6
27	10 p	4	3.9	0.4
28	11 q	4	3.9	1
29	18 p	4	8.2	0.04
30	21 q	4	2.7	0.7
31	4 p	4	2.1	0.8
32	5 q	4	0.7	1
33	7 p	4	1.6	1
34	13 q	4	1.4	1
35	18 q	4	2.3	0.8
36	9 p	3	1.7	0.9
37	11 p	3	0.9	1
38	16 q	3	2	1
39	20 p	3	0.9	0.8
40	5 p	3	1.7	0.9
41	3 p	3	0	1
42	21 p	0	0	1
43	Y q	0	0	1
44	Y q	0	0	1

H3CHR6-MHC-QBB

Relative numbers



Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	3 q	73	14.7	<2e-16
2	18 p	5	8.2	0.04
3	2 p	26	6.4	6e-04
4	1 q	37	4.5	0.02
5	2 q	28	4.4	0.05
6	X p	11	4.1	0.2
7	22 q	16	4.1	0.2
8	10 p	5	3.9	0.4
9	X q	15	3.8	0.3
10	7 q	19	3.8	0.2
11	12 p	9	3.7	0.4
12	6 p	12	3.3	0.5
13	20 q	10	3.3	0.5
14	17 q	21	3.3	0.00
15	12 q	20	3.3	0.00
16	16 p	15	2.2	0.5
17	4 q	13	1.1	0.6
18	8 p	6	0.6	0.6
19	15 q	15	2.9	0.16
20	9 q	13	2.9	0.9
21	10 q	13	2.8	0.7
22	21 q	5	2.7	0.7
23	1 p	24	2.6	0.9
24	19 q	16	2.5	0.9
25	17 p	7	2.4	0.8
26	18 q	4	2.3	0.8
27	4 p	4	2.1	0.8
28	8 q	7	2.1	1
29	20 p	3	2.1	0.9
30	19 p	3	2.1	0.8
31	6 q	10	2	1
32	14 q	9	1.9	1
33	9 p	9	1.7	1
34	5 p	2	1.7	0.9
35	7 p	2	1.7	0.9
36	13 q	4	1.6	1
37	11 p	4	1.4	1
38	16 q	3	0.9	1
39	11 q	5	0.8	1
40	5 q	4	0.7	1
41	3 p	0	0	1
42	21 p	0	0	1
43	Y p	0	0	1
44	Y q	0	0	1

Spot L

genes in spot = 418 (412 with loci information)

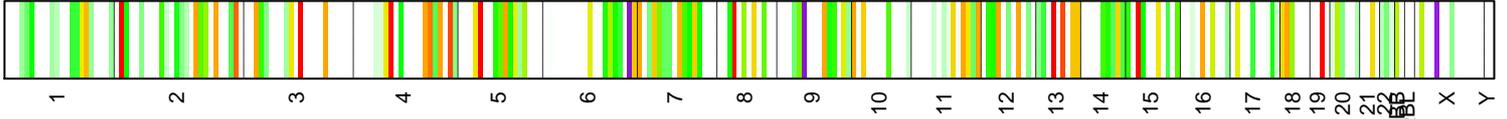
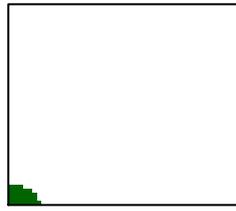
samples with spot = 60 (21.8 %)

Atypical : 8 (10.8 %)

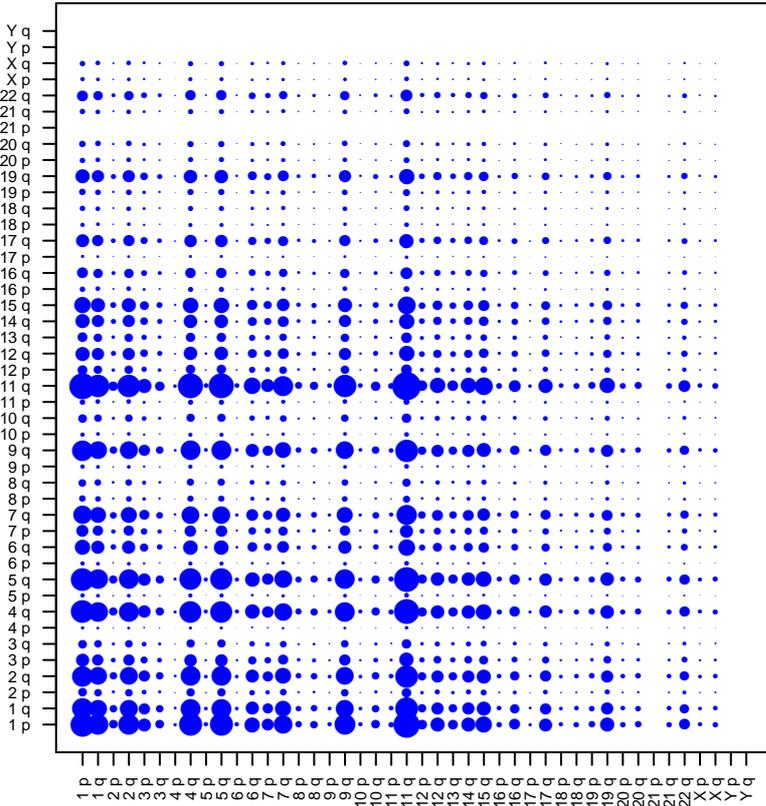
Classical : 2 (6.2 %)

Mesenchymal : 46 (54.1 %)

Basal : 4 (4.8 %)



Absolute numbers

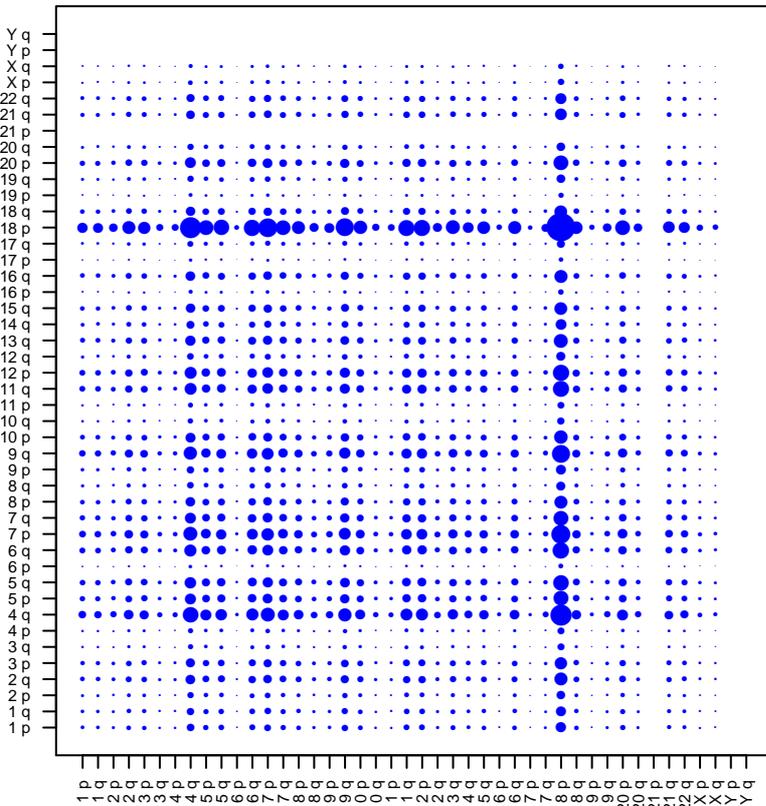


Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	11 q	24	3.7	0.05
2	1 p	22	2.4	0.7
3	4 q	21	4.8	0.004
4	5 q	21	3.6	0.08
5	1 q	19	2.3	0.7
6	2 q	19	3.1	0.3
7	9 q	19	4.1	0.03
8	7 q	17	3.4	0.1
9	15 q	15	3.9	0.03
10	6 q	14	3.8	0.1
11	12 q	13	3.1	0.8
12	14 q	13	3.8	0.06
13	19 q	13	2.1	0.9
14	3 p	12	2.8	0.4
15	17 q	12	1.8	0.9
16	7 p	11	4.3	0.07
17	16 q	10	3	0.4
18	22 q	10	2.5	0.6
19	12 p	9	3.7	0.2
20	13 q	9	3.2	0.3
21	2 p	8	2	0.8
22	3 q	8	1.6	0.9
23	10 q	7	1.7	0.9
24	8 q	7	2.1	0.8
25	8 p	5	3	0.4
26	19 p	5	1.2	1
27	20 q	5	2	0.8
28	11 p	5	1.6	0.9
29	16 p	5	1.3	1
30	18 q	5	2.9	0.5
31	20 q	5	3.4	0.3
32	21 q	5	2.7	0.5
33	X q	5	1.3	1
34	5 p	4	3.4	0.4
35	6 p	4	1.1	1
36	9 p	4	2.3	0.7
37	10 p	4	3.1	0.4
38	18 p	4	6.6	0.07
39	X p	4	6.6	0.07
40	4 p	3	1.1	0.9
41	17 p	3	1.1	0.9
42	21 p	0	0	1
43	Y q	0	0	1
44	Y q	0	0	1

H3CHR6-MHC-QBB

Relative numbers



Rank locus # genes % p-value

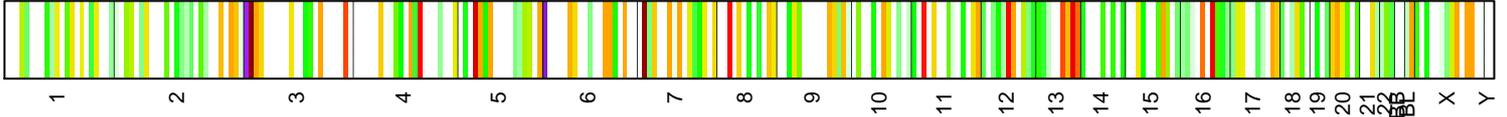
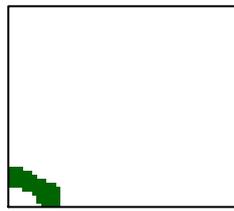
Rank	locus	# genes	%	p-value
1	18 p	4	6.6	0.07
2	4 q	21	4.8	0.004
3	11 p	19	4.3	0.07
4	9 q	19	4.1	0.03
5	6 q	14	3.8	0.1
6	12 p	9	3.7	0.2
7	11 q	24	3.7	0.05
8	5 q	21	3.6	0.08
9	5 p	4	3.4	0.4
10	7 q	17	3.4	0.1
11	20 p	5	3.4	0.3
12	13 q	9	3.4	0.3
13	10 p	4	1	0.4
14	16 q	10	3	0.4
15	2 q	19	3.3	0.3
16	8 p	6	3	0.4
17	15 q	15	3.3	0.3
18	18 q	5	2.9	0.5
19	3 p	12	2.8	0.4
20	21 q	5	2.7	0.5
21	22 q	10	2.5	0.6
22	14 q	13	2.5	0.6
23	1 p	22	2.4	0.7
24	1 q	19	2.3	0.7
25	9 p	4	2.3	0.7
26	8 q	7	2.1	0.8
27	12 q	13	2.1	0.8
28	19 q	13	2	0.9
29	20 q	6	2	0.9
30	2 p	8	2	0.8
31	17 q	1	1.8	0.9
32	10 q	2	1.7	0.9
33	3 q	8	1.6	0.9
34	4 p	5	1.6	0.9
35	11 p	5	1.6	0.9
36	X p	4	1.5	0.9
37	X q	5	1.3	1
38	16 p	5	1.3	1
39	19 p	5	1.2	1
40	6 p	4	1.1	1
41	17 p	3	1	1
42	21 p	0	0	1
43	Y p	0	0	1
44	Y q	0	0	1

Spot M

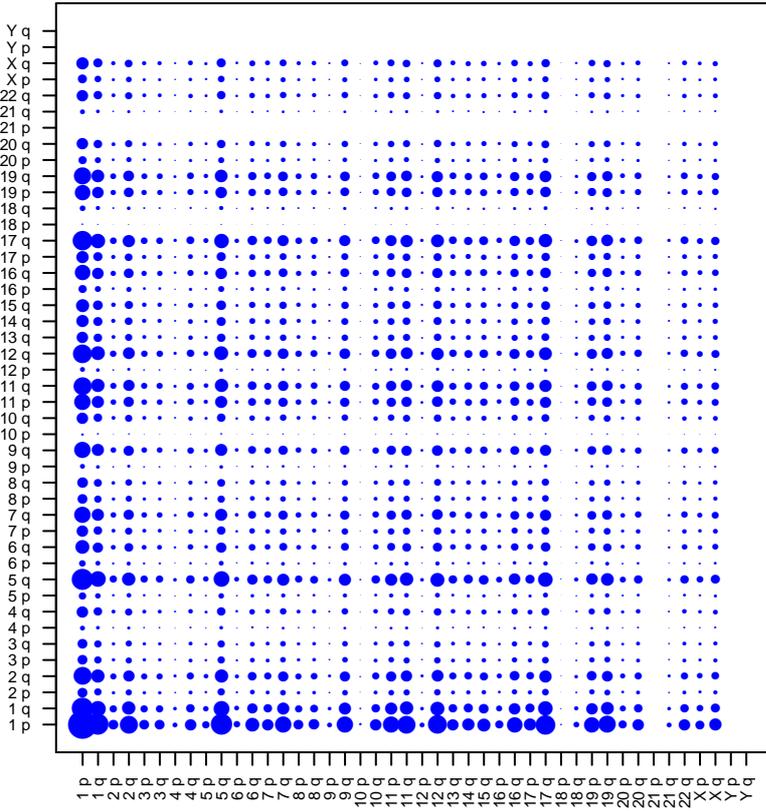
genes in spot = 619 (604 with loci information)

samples with spot = 18 (6.5 %)

Mesenchymal : 18 (21.2 %)



Absolute numbers

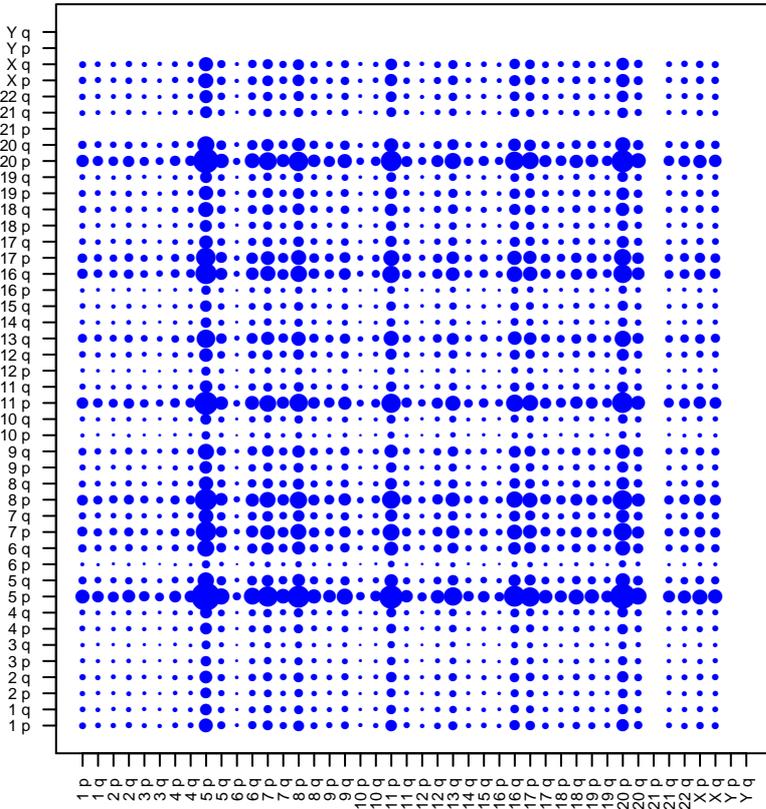


Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	1 p	35	3.8	0.6
2	1 q	26	3.1	0.9
3	5 q	26	4.4	0.2
4	17 q	24	3.7	0.6
5	12 q	23	3.7	0.6
6	2 q	22	3.5	0.7
7	11 q	22	4.4	0.7
8	19 q	21	2.2	0.8
9	7 q	20	4.4	0.4
10	9 q	20	3.3	0.5
11	11 p	20	3.3	0.5
12	16 q	19	3.3	0.5
13	19 p	19	4.6	0.3
14	6 q	17	3.1	0.8
15	15 q	16	2.9	0.9
16	14 q	15	5.2	0.1
17	17 p	15	3.8	0.5
18	X q	14	3.2	0.8
19	4 q	14	5.5	0.1
20	7 p	14	5.9	0.9
21	10 q	14	5.9	0.9
22	13 q	14	5.9	0.9
23	20 q	14	4.6	0.5
24	22 q	14	3.3	0.6
25	8 q	13	3.3	0.6
26	3 q	13	3.3	0.6
27	3 p	12	3.3	0.6
28	3 q	12	3.3	0.6
29	8 p	12	4.4	1
30	X p	11	4.1	0.5
31	16 p	10	6.8	0.9
32	20 p	10	6.8	0.06
33	5 p	9	7.7	0.04
34	6 p	8	2.2	1
35	18 q	7	4.1	0.5
36	4 p	6	3.2	0.7
37	9 p	6	3.4	0.7
38	12 p	6	3.5	0.9
39	21 q	6	3.5	0.7
40	10 p	5	3.5	0.9
41	18 p	5	3.5	0.7
42	21 p	0	0	1
43	Y q	0	0	1
44	Y q	0	0	1

H3CHR6-MHC-QBB

Relative numbers



Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	5 p	9	7.7	0.04
2	20 p	10	6.8	0.06
3	11 p	20	6.3	0.02
4	8 p	12	6	0.08
5	16 q	19	5.7	0.05
6	7 p	14	5.5	0.1
7	17 p	15	5.2	0.1
8	13 q	14	5	0.2
9	20 q	14	4.6	0.3
10	6 q	17	4.6	0.3
11	5 q	26	4.4	0.2
12	9 q	20	4.3	0.3
13	18 q	7	4.1	0.5
14	X p	11	4.1	0.5
15	7 q	20	4.4	0.4
16	19 p	9	3.9	0.5
17	8 q	13	3.9	0.5
18	X q	15	3.8	0.5
19	1 p	18	3.8	0.6
20	17 q	24	3.7	0.6
21	12 q	23	3.7	0.6
22	22 q	14	3.6	0.6
23	2 q	22	3.5	0.7
24	9 p	6	3.4	0.7
25	11 q	22	3.4	0.7
26	18 p	2	3.3	0.7
27	21 q	6	3.3	0.7
28	4 q	14	3.3	0.8
29	19 q	21	3.3	0.8
30	4 p	6	2.2	1
31	1 q	26	1.1	0.9
32	15 q	6	1.1	0.9
33	2 p	12	1.1	0.9
34	10 q	14	0.9	0.9
35	14 q	15	0.9	0.9
36	3 p	12	0.9	0.9
37	16 p	10	2.5	0.9
38	12 p	6	2.4	0.9
39	3 q	12	2.4	0.9
40	10 p	3	2.3	0.9
41	6 p	8	2.2	1
42	21 p	0	0	1
43	Y p	0	0	1
44	Y q	0	0	1

Spot N

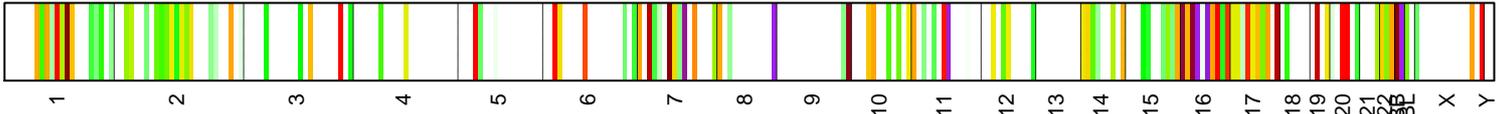
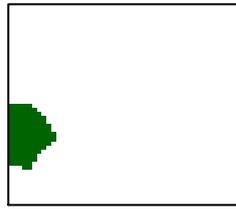
genes in spot = 908 (866 with loci information)

samples with spot = 9 (3.3 %)

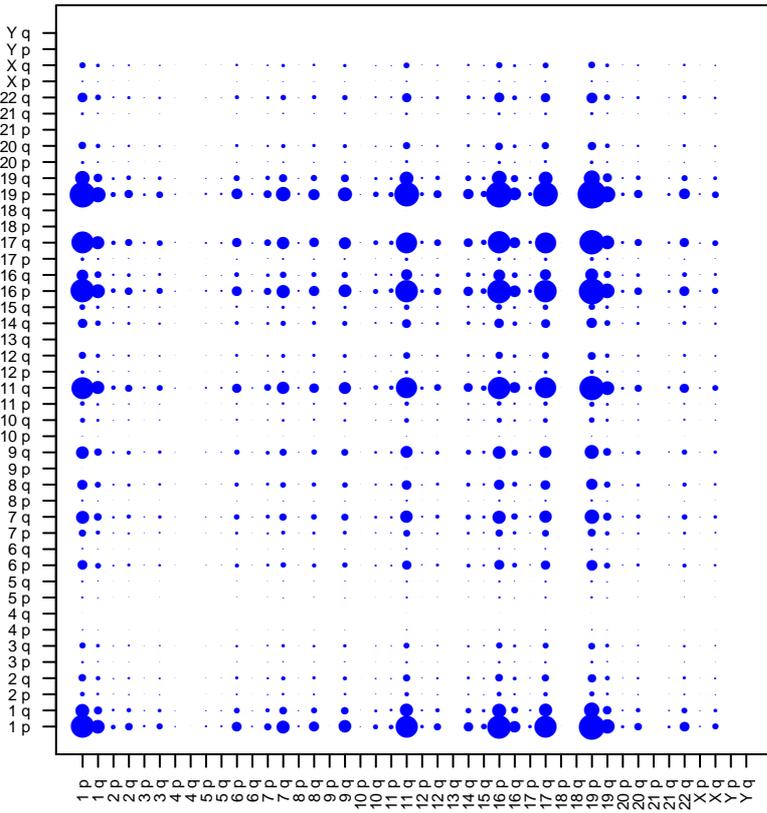
Atypical : 2 (2.7 %)

Mesenchymal : 6 (7.1 %)

Basal : 1 (1.2 %)



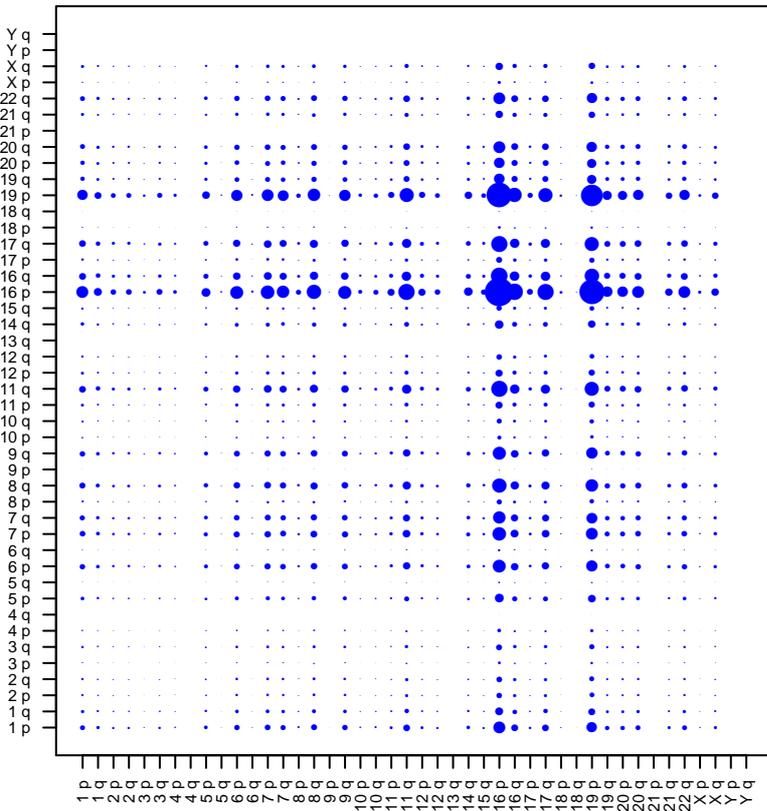
Absolute numbers



Rank	locus	# genes	%	p-value
1	19 p	71	14.5	1e-13
2	16 p	65	16.6	2e-15
3	1 p	64	6.9	0.05
4	11 q	61	9.4	5e-05
5	17 q	61	9.4	5e-05
6	19 q	40	6.1	0.03
7	1 q	38	4.6	0.09
8	7 q	36	7.7	0.07
9	9 q	36	6.6	0.04
10	16 q	33	9.9	0.002
11	8 q	28	8.3	0.02
12	6 p	27	7.5	0.08
13	22 q	27	9.9	0.2
14	14 q	26	5.5	0.8
15	2 q	21	3.3	1
16	20 q	21	6.9	0.2
17	7 p	20	7.9	0.08
18	12 q	20	3.2	1
19	3 q	17	3.4	1
20	X q	17	4.3	0.9
21	15 q	16	3.1	1
22	10 q	14	2.9	1
23	2 p	13	2.2	1
24	11 p	13	4.1	0.9
25	12 p	10	4.1	1
26	2 p	10	3.5	1
27	20 p	9	6.1	0.4
28	21 q	8	4.3	0.8
29	3 p	7	1.7	1
30	5 p	6	5.1	0.6
31	5 q	6	1.1	1
32	8 p	6	3	1
33	6 q	5	1.3	1
34	X p	5	1.9	1
35	4 p	4	2.1	1
36	10 p	3	2.3	1
37	4 q	1	0.2	1
38	9 p	1	0.6	1
39	18 p	1	1.6	1
40	18 q	1	0.6	1
41	13 q	0	0	1
42	21 p	0	0	1
43	Y p	0	0	1
44	Y q	0	0	1

H3CHR6-MHC-QBB

Relative numbers



Rank	locus	# genes	%	p-value
1	16 p	65	16.6	2e-15
2	19 q	71	14.5	1e-13
3	16 q	32	9.6	0.002
4	11 q	61	9.4	5e-05
5	17 q	61	9.4	5e-05
6	8 q	28	8.3	0.02
7	7 p	20	7.9	0.08
8	9 q	35	7.6	0.04
9	6 p	27	7.5	0.08
10	7 q	36	7.2	0.07
11	20 q	21	6.9	0.2
12	1 p	64	6.9	0.05
13	22 q	27	6.9	0.2
14	19 q	40	9.9	0.3
15	20 p	9	6.1	0.4
16	5 p	6	5.1	0.6
17	14 q	26	5.5	0.8
18	1 q	38	4.6	0.09
19	X q	17	4.3	0.9
20	21 q	8	4.3	0.8
21	12 p	10	4.1	0.9
22	11 p	13	4.1	1
23	17 p	10	3.5	1
24	3 q	17	3.4	1
25	2 q	21	3.3	1
26	2 p	13	3.2	1
27	12 q	20	3.3	1
28	15 q	16	3.3	1
29	8 p	6	3.3	1
30	10 q	14	3.3	1
31	10 p	3	3.3	1
32	4 p	3	2.1	1
33	X p	5	1.9	1
34	3 p	7	1.7	1
35	18 p	1	1.6	1
36	6 q	5	1.3	1
37	5 q	6	1	1
38	18 q	1	0.6	1
39	9 p	1	0.6	1
40	4 q	1	0.2	1
41	13 q	0	0	1
42	21 p	0	0	1
43	Y p	0	0	1
44	Y q	0	0	1

Spot O

genes in spot = 203 (197 with loci information)

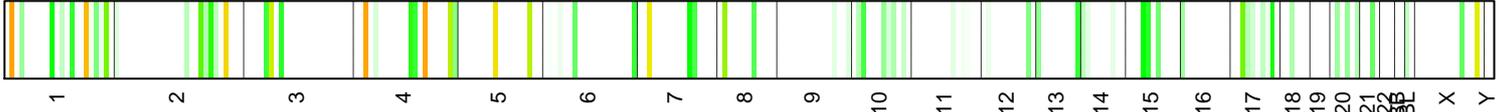
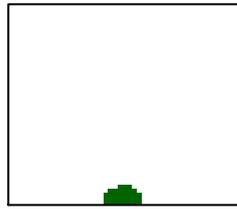
samples with spot = 37 (13.5 %)

Atypical : 9 (12.2 %)

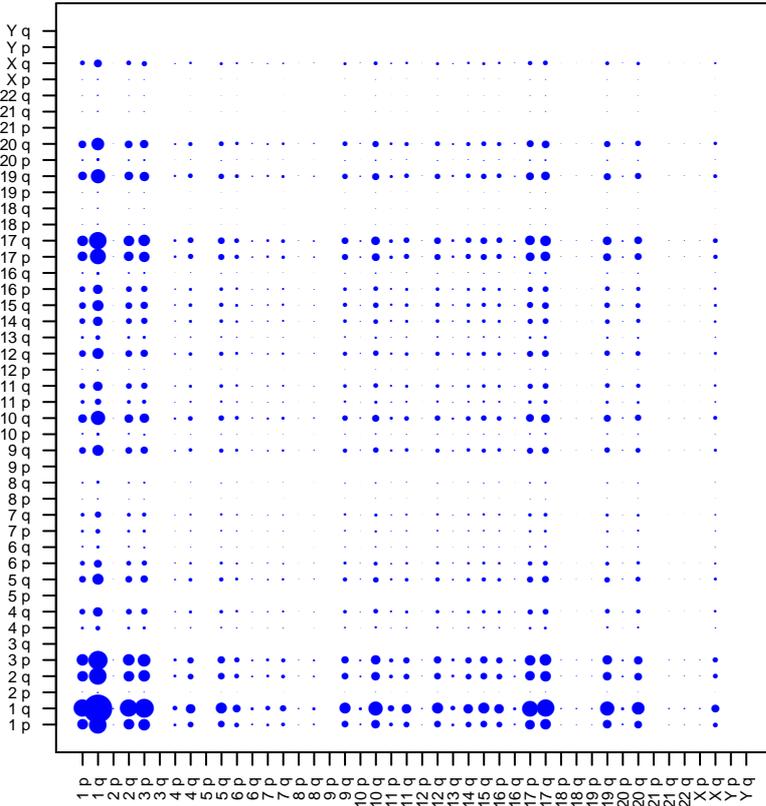
Classical : 4 (12.5 %)

Mesenchymal : 16 (18.8 %)

Basal : 8 (9.5 %)



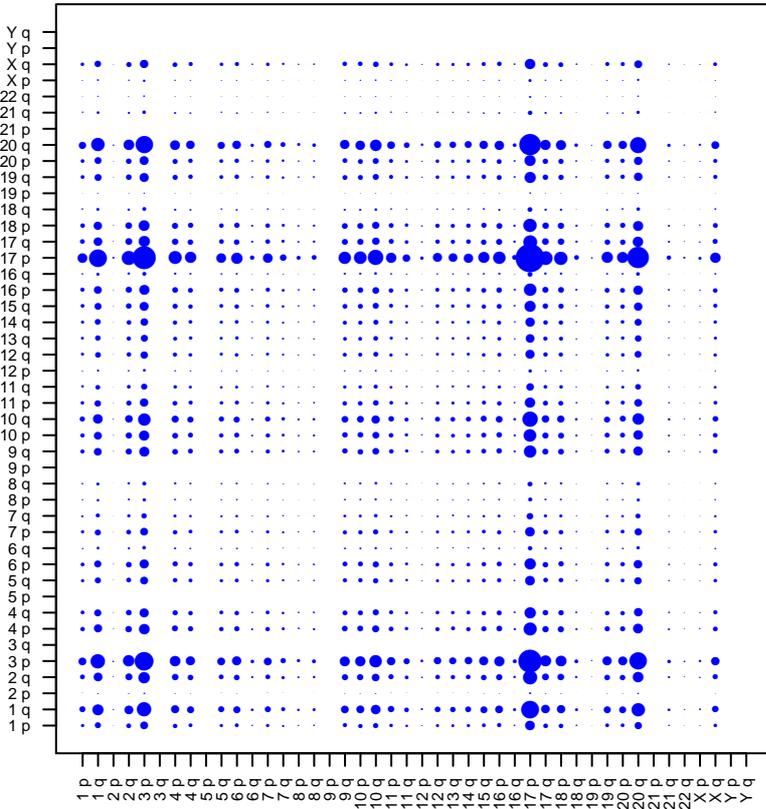
Absolute numbers



Rank	locus	# genes	%	p-value
1	1 q	18	2.2	0.02
2	3 p	12	2.8	0.007
3	1 p	11	1.2	0.6
4	2 q	11	1.7	0.2
5	17 q	11	1.7	0.2
6	17 p	11	1.7	0.2
7	10 q	10	3.5	0.003
8	19 q	9	1.9	0.1
9	20 q	9	1.4	0.4
10	5 q	8	2.2	0.04
11	9 q	7	1.5	0.6
12	12 q	7	1.1	0.4
13	15 q	7	1.4	0.7
14	4 q	6	1.4	0.5
15	11 q	6	0.9	0.8
16	14 q	6	1.1	0.6
17	16 p	6	1.5	0.4
18	6 p	5	1.4	0.5
19	X q	5	1.3	0.5
20	7 q	4	0.8	0.9
21	11 p	4	1.3	0.6
22	4 p	3	1.6	0.4
23	7 p	3	1.2	0.6
24	13 q	3	1.1	0.7
25	6 q	3	0.0	0.9
26	8 q	3	0.0	0.9
27	10 p	3	0.6	0.5
28	16 p	3	0.6	0.5
29	20 p	3	1.4	0.6
30	8 p	2	0.2	1
31	8 p	2	0.5	0.9
32	12 p	2	0.4	1
33	18 p	2	1.6	0.5
34	18 q	2	0.6	0.9
35	19 p	2	0.2	1
36	21 q	2	0.5	0.9
37	22 q	2	0.3	1
38	X q	0	0.0	1
39	3 q	0	0.0	1
40	5 p	0	0.0	1
41	9 p	0	0.0	1
42	21 p	0	0.0	1
43	Y p	0	0.0	1
44	Y q	0	0.0	1

H3CHR6-MHC-QBB

Relative numbers



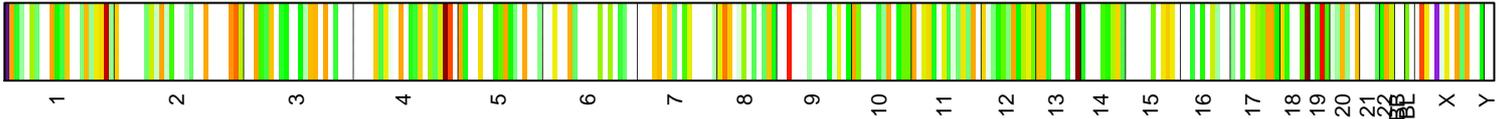
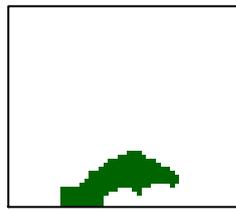
Rank	locus	# genes	%	p-value
1	17 p	10	3.5	0.003
2	3 p	12	2.8	0.007
3	20 q	8	2.6	0.04
4	1 q	18	2.2	0.02
5	10 q	9	1.9	0.1
6	2 q	11	1.7	0.2
7	17 q	11	1.7	0.2
8	18 p	11	1.6	0.5
9	4 p	3	1.6	0.4
10	10 p	2	1.6	0.5
11	16 p	6	1.5	0.4
12	9 q	7	1.5	0.4
13	6 p	5	1.4	0.5
14	4 q	6	1.4	0.5
15	19 q	7	1.4	0.4
16	15 q	7	1.4	0.5
17	20 p	5	1.4	0.5
18	X q	5	1.4	0.5
19	11 p	4	1.3	0.6
20	5 q	4	1.2	0.6
21	1 p	1	1.2	0.6
22	7 p	3	1.2	0.6
23	14 q	6	1.1	0.6
24	12 q	7	1.1	0.7
25	13 q	3	1.1	0.7
26	11 q	6	0.9	0.8
27	7 q	4	0.8	0.9
28	16 q	2	0.6	0.9
29	8 q	2	0.6	0.9
30	18 q	1	0.6	0.9
31	21 q	1	0.5	0.9
32	2 q	2	0.5	0.9
33	12 p	1	0.4	1
34	8 p	1	0.4	1
35	X p	1	0.4	1
36	22 p	1	0.3	1
37	2 p	1	0.2	1
38	19 p	1	0.2	1
39	3 q	0	0.0	1
40	5 p	0	0.0	1
41	9 p	0	0.0	1
42	21 p	0	0.0	1
43	Y p	0	0.0	1
44	Y q	0	0.0	1

Spot P

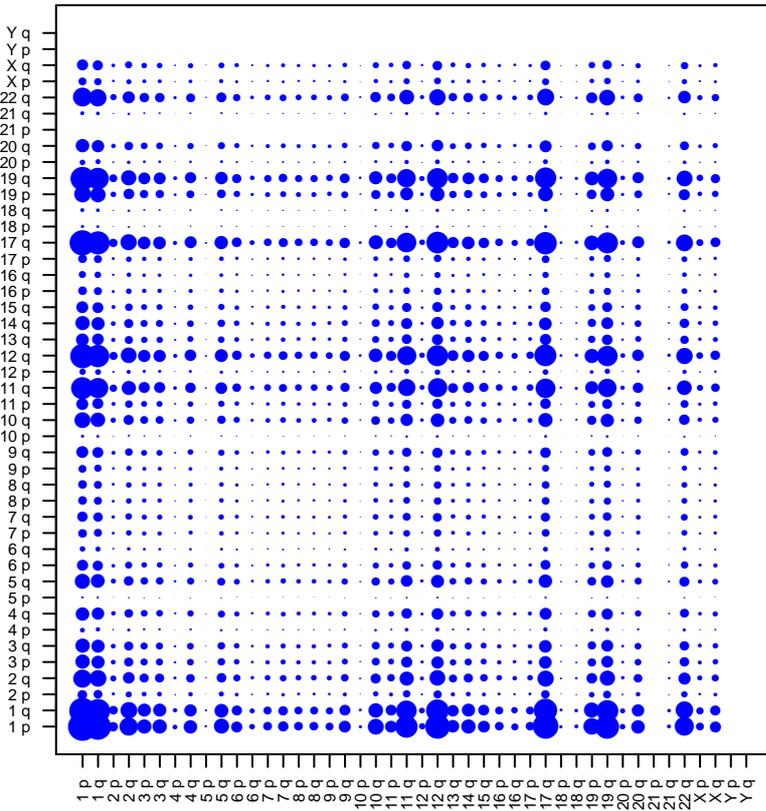
genes in spot = 651 (632 with loci information)

samples with spot = 2 (0.7 %)

Mesenchymal : 2 (2.4 %)



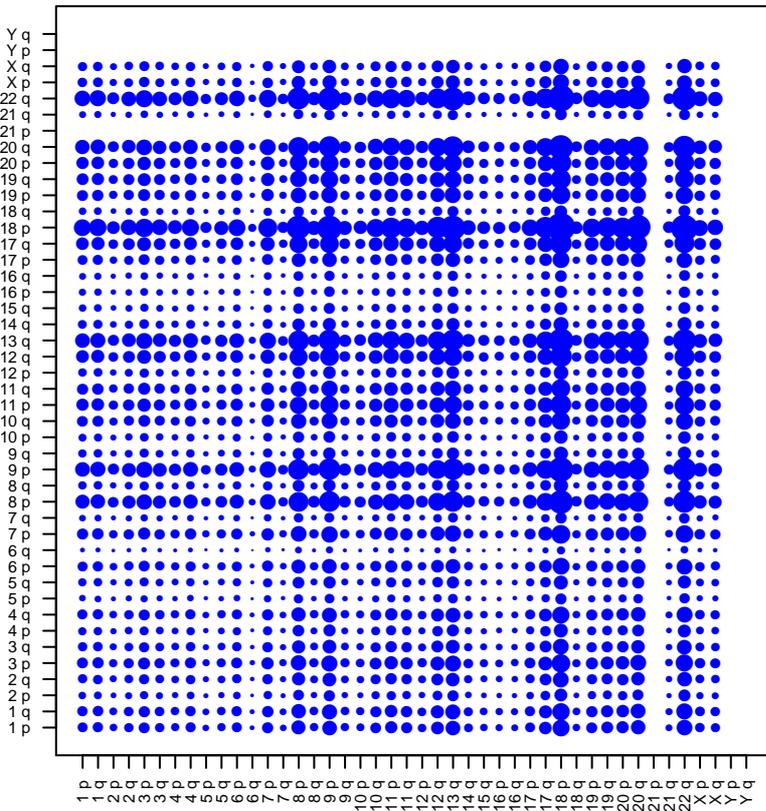
Absolute numbers



Rank	locus	# genes	%	p-value
1	1 p	36	3.9	0.6
2	1 q	33	4	0.5
3	17 q	32	4.9	0.1
4	12 q	31	5	0.1
5	19 q	30	4.6	0.2
6	11 q	28	4.3	0.4
7	22 q	24	6.1	0.03
8	2 q	23	3.6	0.7
9	19 p	23	4.4	0.4
10	10 q	20	4.4	0.5
11	5 q	19	3.3	0.9
12	3 q	18	4.2	0.4
13	3 q	18	3.6	0.7
14	14 q	18	3.4	0.8
15	4 q	17	3.9	0.6
16	20 q	17	5.9	0.1
17	13 q	16	5.7	0.1
18	9 q	15	3.3	0.8
19	11 p	15	4.7	0.3
20	15 q	15	2.9	0.9
21	6 p	14	3.9	0.6
22	X q	14	3.6	0.7
23	7 q	13	6	1
24	2 p	12	6	0.9
25	7 p	11	4.3	0.4
26	8 q	11	3.3	0.8
27	8 q	11	3.3	0.8
28	16 p	11	8	0.9
29	17 p	11	8	0.6
30	9 p	10	7	0.2
31	X p	10	7.7	0.6
32	16 q	9	2.7	0.9
33	12 p	8	3.3	0.8
34	6 q	7	1.9	1
35	20 p	7	4.8	0.4
36	4 p	6	3.2	0.8
37	18 q	5	2.9	0.8
38	21 q	5	2.7	0.9
39	10 p	4	3.1	0.8
40	18 p	4	6	0.9
41	5 p	3	6	0.9
42	21 p	0	0	1
43	Y q	0	0	1
44	Y q	0	0	1

H3CHR6-MHC-QBB

Relative numbers

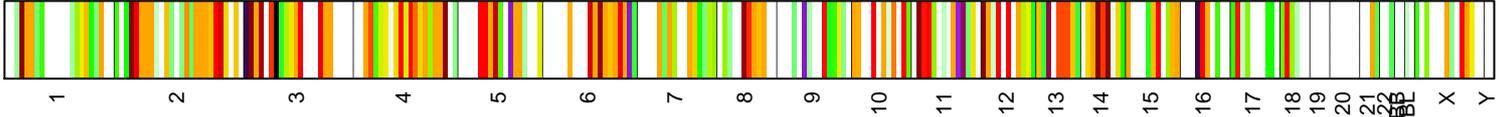
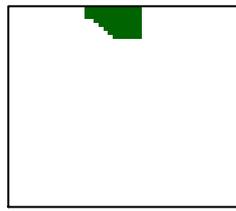


Rank	locus	# genes	%	p-value
1	18 p	4	6.6	0.2
2	22 q	4	6.1	0.03
3	9 p	10	5.7	0.2
4	13 q	16	5.7	0.1
5	20 q	17	5.6	0.1
6	8 p	11	5.5	0.2
7	12 q	31	5	0.1
8	17 q	32	4.9	0.1
9	20 p	7	4.8	0.4
10	11 p	15	4.7	0.3
11	19 q	30	4.6	0.2
12	7 p	11	4.3	0.4
13	11 q	28	4.3	0.4
14	19 p	21	4.3	0.4
15	3 p	18	4.3	0.4
16	10 q	20	4.2	0.5
17	1 q	33	4	0.5
18	4 q	17	3.9	0.6
19	6 p	14	3.9	0.6
20	1 p	36	3.8	0.6
21	17 p	11	3.8	0.6
22	X p	10	3.7	0.6
23	3 q	18	3.6	0.7
24	2 q	23	3.6	0.7
25	X q	14	3.6	0.7
26	14 q	18	3.4	0.8
27	12 p	8	3.3	0.8
28	8 q	11	3.3	0.8
29	9 q	15	3.3	0.8
30	5 q	19	3.3	0.8
31	4 p	6	2.2	1
32	10 p	4	1.1	0.8
33	2 p	15	2.9	0.9
34	15 q	5	2.9	0.8
35	18 q	5	2.9	0.8
36	16 p	11	2.8	0.9
37	16 q	9	2.7	0.9
38	21 q	5	2.7	0.9
39	7 q	13	2.6	1
40	5 p	3	2.6	0.9
41	6 q	7	1.9	1
42	21 p	0	0	1
43	Y p	0	0	1
44	Y q	0	0	1

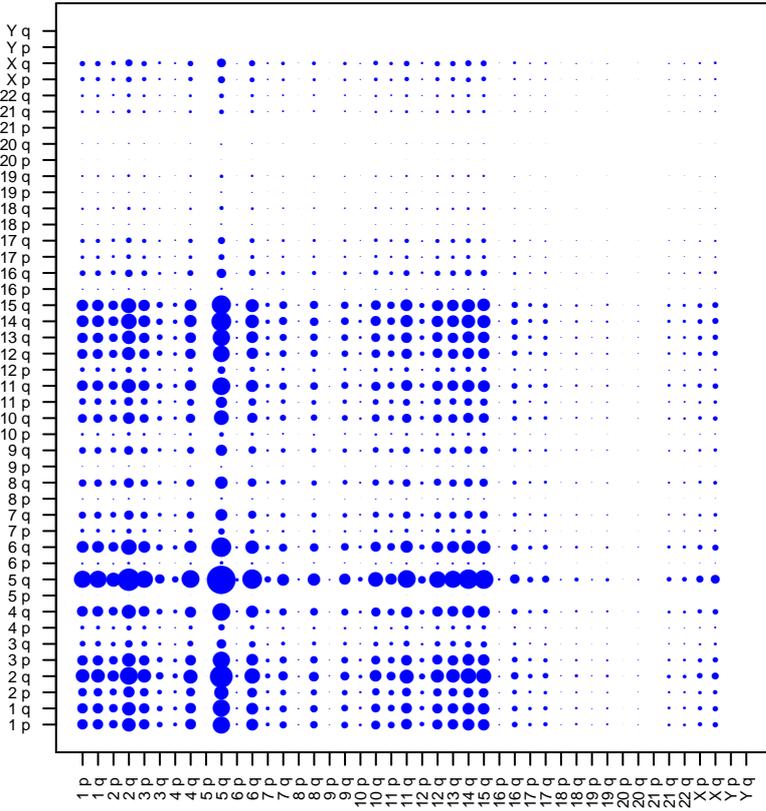
Spot Q

genes in spot = 710 (697 with loci information)

samples with spot = 0 (0 %)



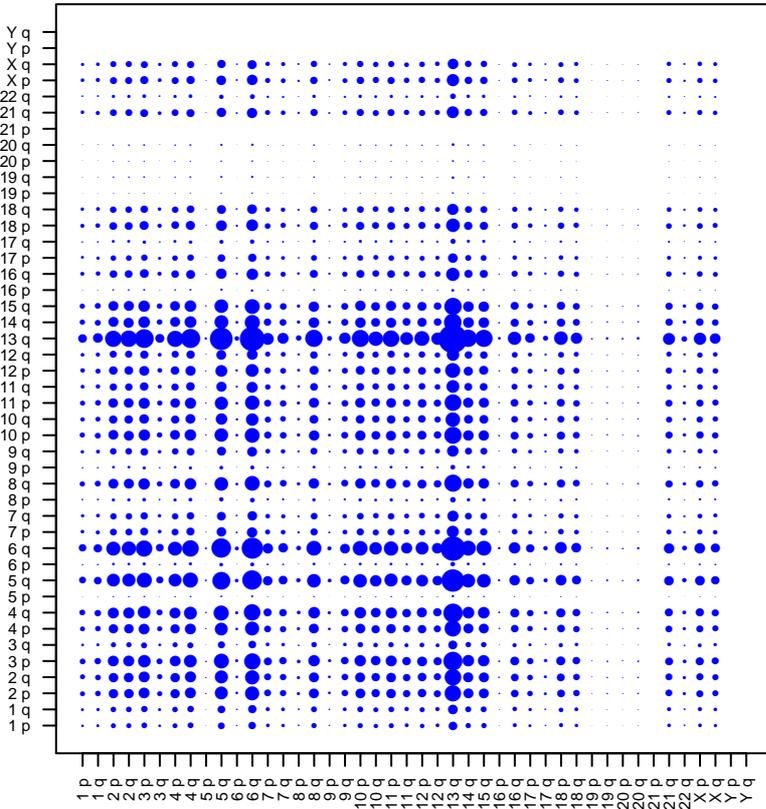
Absolute numbers



Rank	locus	# genes	%	p-value
1	5 q	48	8.2	2e-05
2	2 q	38	6.0	0.03
3	6 q	33	8.9	9e-05
4	14 q	33	6.3	0.02
5	15 q	32	6.3	0.03
6	4 q	30	6.9	0.009
7	11 q	30	4.6	0.4
8	1 p	29	1.1	0.9
9	3 p	29	5.5	0.1
10	13 q	29	6.2	2e-05
11	12 q	28	10.3	2e-05
12	10 q	28	4.5	0.5
13	2 p	25	5.2	0.2
14	8 q	24	5.9	0.08
15	7 q	21	6.2	0.07
16	16 q	20	4.7	0.6
17	9 q	19	4.1	0.6
18	11 p	19	6	0.1
19	3 q	16	3.2	0.9
20	16 q	16	4.8	0.4
21	X q	15	3.8	0.7
22	12 p	13	5.4	0.3
23	17 q	12	1.8	1
24	X p	12	4.4	0.5
25	4 p	11	5.9	0.03
26	7 p	11	3.3	0.6
27	17 p	10	3.5	0.8
28	10 p	8	6.2	0.2
29	21 q	8	4.3	0.6
30	22 q	8	2	1
31	18 q	7	4.1	0.6
32	6 p	6	1.7	1
33	19 q	6	0.9	1
34	8 p	4	2	1
35	16 p	4	1.7	1
36	9 p	3	1.7	1
37	18 p	3	4.9	0.5
38	19 p	3	0.6	1
39	20 q	3	1	1
40	5 p	1	0.9	1
41	20 p	1	0.7	1
42	Y p	0	0	1
43	Y q	0	0	1
44	Y q	0	0	1

H3CHR6-MHC-QBB

Relative numbers



Rank	locus	# genes	%	p-value
1	13 q	29	10.3	2e-05
2	6 q	33	8.9	9e-05
3	5 q	48	8.2	2e-05
4	4 q	30	6.9	0.009
5	3 p	29	6.8	0.01
6	14 q	33	6.3	0.02
7	8 q	21	6.2	0.07
8	15 q	32	6.2	0.03
9	10 p	8	6.2	0.2
10	11 p	19	6	0.1
11	2 q	38	6	0.03
12	2 p	24	5.9	0.08
13	4 p	11	5.9	0.2
14	12 p	13	5.9	0.3
15	10 q	25	5.2	0.5
16	18 q	3	4.9	0.5
17	16 q	16	4.8	0.4
18	11 q	30	4.6	0.4
19	12 q	28	4.5	0.5
20	X p	12	4.4	0.5
21	7 p	11	4.3	0.6
22	21 q	8	4.3	0.6
23	9 q	19	4.1	0.6
24	18 q	7	4.1	0.6
25	7 q	20	4	0.7
26	X q	15	3.8	0.7
27	1 q	29	3.5	0.9
28	17 p	10	3.5	0.8
29	3 q	16	3.2	0.9
30	1 p	29	1	1
31	22 q	8	3	1
32	8 p	8	2	1
33	17 q	4	1.8	1
34	9 p	3	1.7	1
35	16 p	6	1.7	1
36	6 p	4	1	1
37	20 p	3	1	1
38	19 q	6	0.9	1
39	5 p	1	0.9	1
40	20 p	1	0.7	1
41	19 p	3	0.6	1
42	Y p	0	0	1
43	Y q	0	0	1
44	Y q	0	0	1

Spot R

genes in spot = 596 (583 with loci information)

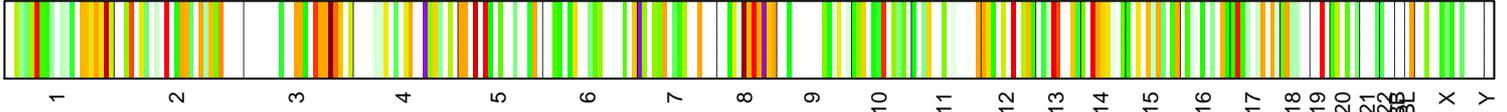
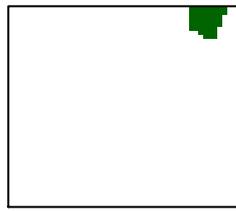
samples with spot = 25 (9.1 %)

Atypical : 5 (6.8 %)

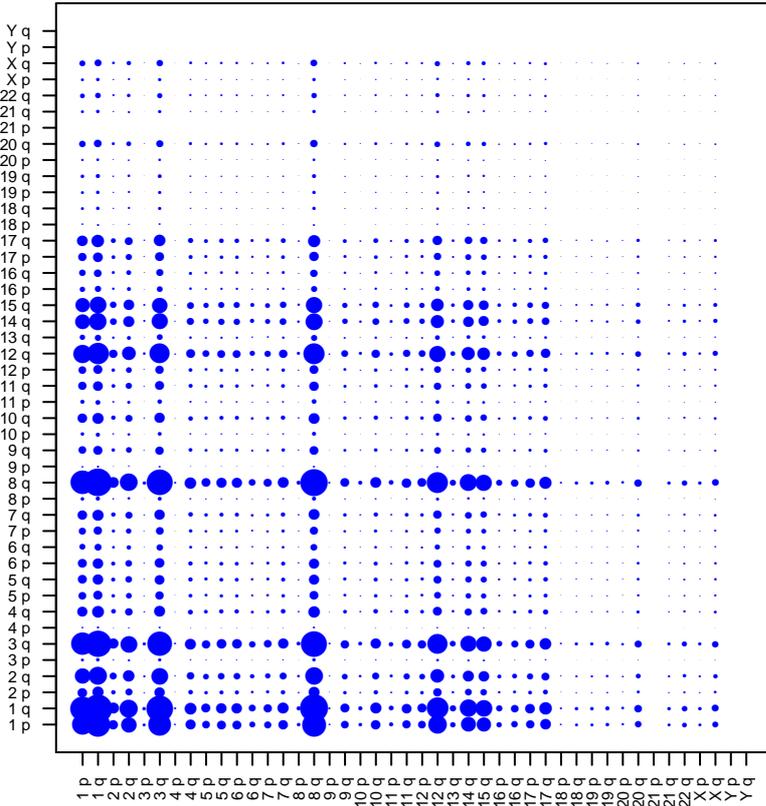
Classical : 6 (18.8 %)

Mesenchymal : 13 (15.3 %)

Basal : 1 (1.2 %)



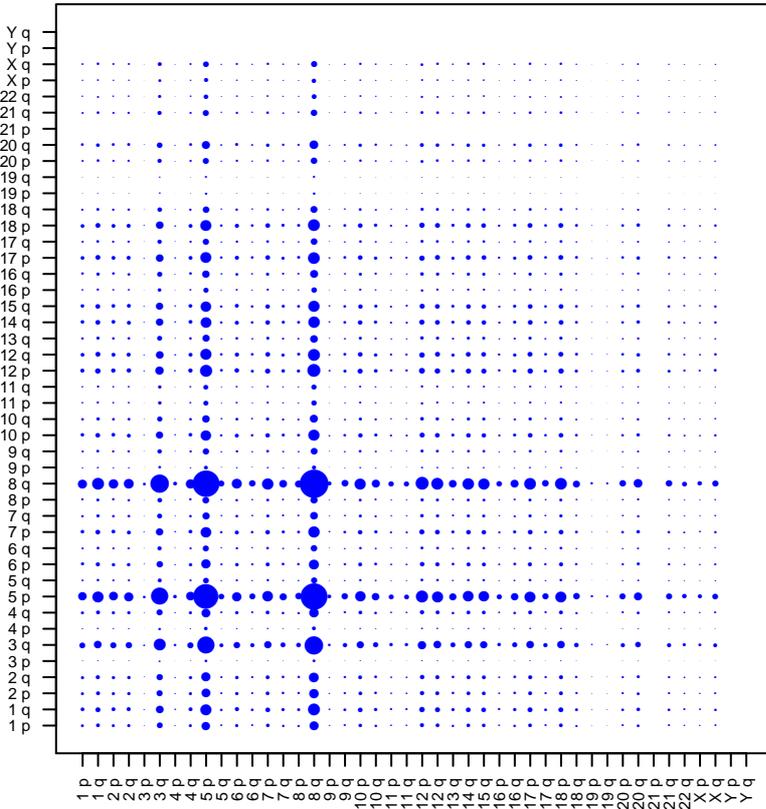
Absolute numbers



Rank	locus	# genes	%	p-value
1	1 q	41	5	0.03
2	8 q	40	11.9	5e-11
3	3 q	38	7.7	2e-05
4	1 p	35	3.8	0.5
5	12 q	31	5	0.06
6	2 q	26	4.1	0.3
7	14 q	25	4.8	0.1
8	15 q	24	4.7	0.1
9	17 q	24	4.7	0.9
10	4 q	18	2.8	0.4
11	2 p	16	3.3	0.4
12	7 q	16	3.2	0.7
13	10 q	16	3.4	0.7
14	5 q	15	2.6	1
15	6 p	15	4.2	0.3
16	11 p	14	2.2	1
17	17 p	14	4.9	0.2
18	5 p	13	11.1	4e-04
19	9 q	13	2.8	0.9
20	12 p	13	5.4	0.1
21	7 p	12	4.7	0.2
22	16 q	11	3.3	0.7
23	20 q	11	3.6	0.6
24	6 q	10	3.7	0.9
25	X q	10	2.6	0.9
26	13 q	9	2.2	0.7
27	16 p	9	2.3	1
28	22 q	8	2.2	1
29	11 p	7	2.2	0.9
30	8 p	6	3	0.8
31	10 p	6	4.7	0.3
32	19 q	6	0.9	1
33	3 p	5	1.2	1
34	18 p	5	2.9	0.8
35	19 p	5	1	1
36	21 q	5	2.7	0.8
37	X p	5	1.9	1
38	20 p	4	2.7	0.8
39	4 p	3	1.6	1
40	9 p	3	1.7	1
41	18 p	3	4.9	0.4
42	21 p	0	0	1
43	Y q	0	0	1
44	Y q	0	0	1

H3CHR6-MHC-QBB

Relative numbers



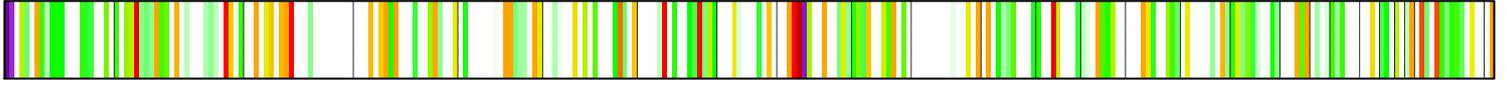
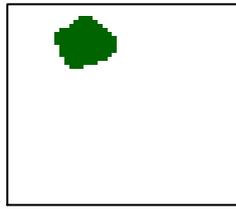
Rank	locus	# genes	%	p-value
1	8 q	40	11.9	5e-11
2	5 p	38	11.1	4e-04
3	3 q	38	7.7	2e-05
4	12 p	31	5.4	0.1
5	1 q	41	5	0.03
6	12 q	31	5	0.06
7	18 p	3	4.9	0.4
8	17 p	14	4.9	0.2
9	14 q	25	4.8	0.1
10	7 p	12	4.7	0.2
11	15 q	24	4.7	0.1
12	10 p	6	4.7	0.3
13	6 p	15	4.2	0.3
14	22 q	9	4.1	0.3
15	2 p	26	4.1	0.3
16	4 q	17	3.9	0.4
17	1 p	35	3.8	0.5
18	20 q	11	3.4	0.6
19	10 q	16	3.4	0.7
20	16 q	11	3.3	0.7
21	7 q	16	3.2	0.7
22	13 q	9	3.2	0.7
23	8 p	6	3	0.8
24	18 q	5	2.9	0.8
25	9 q	13	2.8	0.9
26	17 q	18	2.8	0.9
27	20 p	4	2.7	0.8
28	21 q	5	2.7	0.8
29	6 q	10	2.7	0.9
30	5 q	10	2.6	0.9
31	X q	15	2.6	0.9
32	16 p	9	2.3	1
33	11 p	9	2.3	1
34	11 q	7	2.2	0.9
35	22 q	14	2.2	1
36	11 q	7	2.2	1
37	9 p	5	1.9	1
38	3 p	3	1.7	1
39	3 p	3	1.2	1
40	19 p	5	1	1
41	19 q	6	0.9	1
42	21 p	0	0	1
43	Y p	0	0	1
44	Y q	0	0	1

Spot S

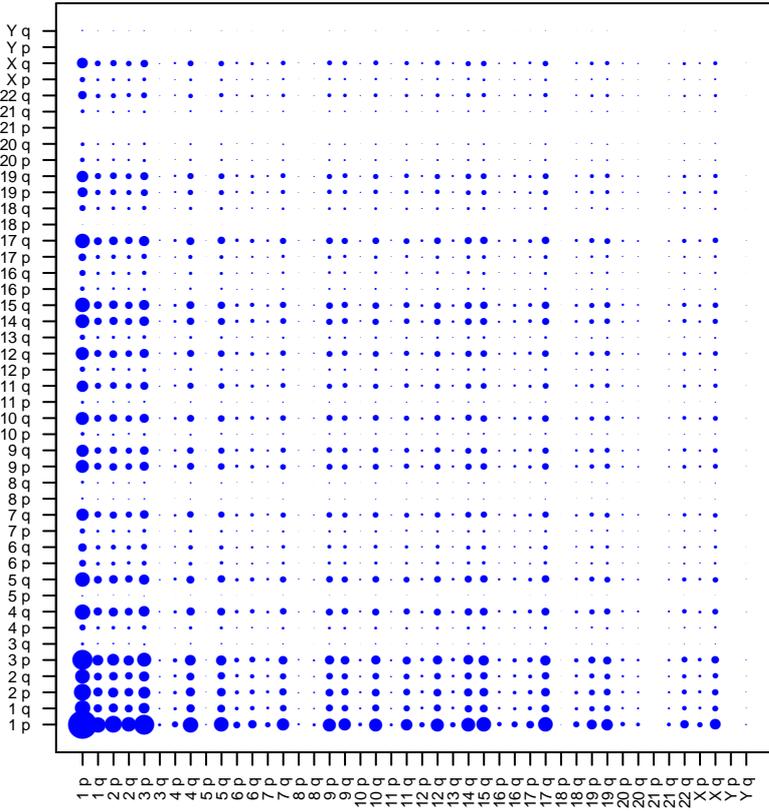
genes in spot = 517 (499 with loci information)

samples with spot = 2 (0.7 %)

Basal : 2 (2.4 %)



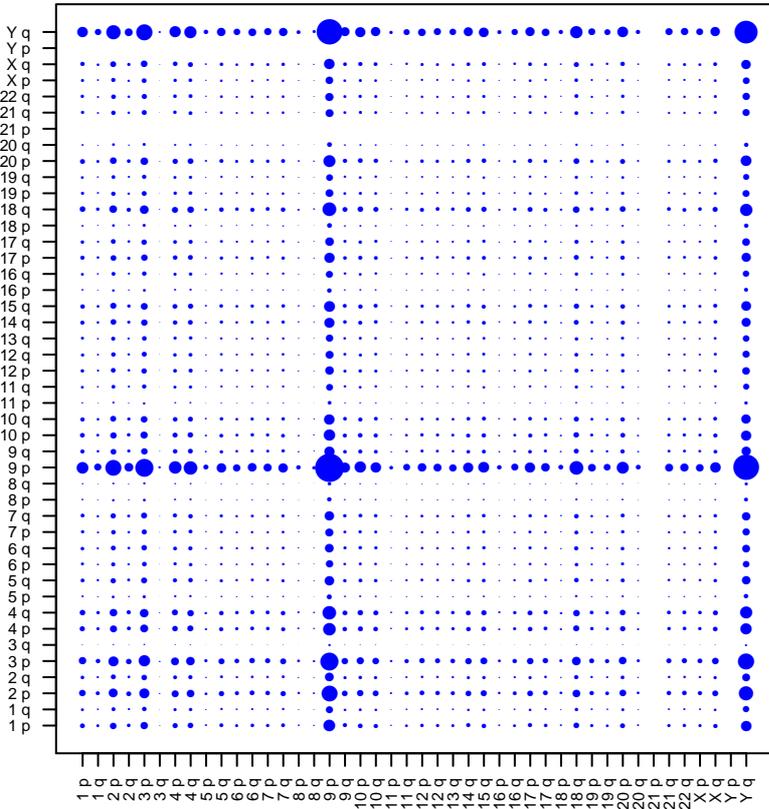
Absolute numbers



Rank	locus	# genes	%	p-value
1	1 p	37	4	0.09
2	3 p	26	6.1	0.001
3	2 p	22	5.4	0.01
4	1 q	20	2.4	0.9
5	4 q	20	4.6	0.06
6	2 q	19	3.3	0.66
7	5 q	19	3.2	0.66
8	15 q	19	3.7	0.003
9	17 q	19	3.9	0.003
10	14 q	18	4.9	0.4
11	9 p	17	3.9	5e-05
12	10 q	17	3.6	0.8
13	12 q	17	3.7	0.8
14	7 q	16	2.2	0.5
15	9 q	16	3.5	0.4
16	11 q	15	2.3	0.9
17	19 q	15	3.6	0.4
18	X q	14	3.6	0.8
19	19 p	13	3.6	0.6
20	6 q	11	2.6	0.7
21	22 q	11	2.8	0.4
22	17 p	10	2.5	0.8
23	6 p	9	2.2	0.8
24	4 p	8	2.5	0.3
25	16 q	8	2.4	0.8
26	18 q	8	4.7	0.002
27	7 p	8	4.7	0.2
28	12 p	7	2.5	0.7
29	13 q	7	2.9	0.8
30	X p	7	2.6	0.8
31	16 p	6	1.5	1
32	20 p	6	4.1	0.3
33	10 p	5	3.9	0.4
34	20 q	5	1.6	1
35	21 q	5	2.7	0.7
36	3 q	4	0.8	1
37	8 q	4	1.2	1
38	11 p	4	1.3	1
39	8 p	3	1.5	1
40	5 p	3	1.7	0.9
41	Y q	2	7.6	0.3
42	18 p	2	8.6	0.9
43	21 p	1	6	0.9
44	Y p	0	0	1

H3CHR6-MHC-QBB

Relative numbers



Rank	locus	# genes	%	p-value
1	9 p	17	9.7	5e-05
2	Y q	17	8.7	0.2
3	3 p	26	6.1	0.001
4	2 p	22	5.4	0.01
5	18 q	8	4.7	0.2
6	4 q	20	4.6	0.06
7	4 p	8	4.3	0.2
8	20 p	6	4.1	0.3
9	1 p	37	4	0.09
10	10 p	5	3.9	0.4
11	15 q	19	3.7	0.3
12	X q	14	3.6	0.4
13	10 q	17	3.6	0.4
14	17 p	10	3.6	0.4
15	9 q	16	3.5	0.4
16	14 q	16	3.4	0.4
17	5 q	16	3.4	0.4
18	7 q	16	3.2	0.5
19	2 q	16	3.3	0.6
20	6 q	11	3	0.6
21	17 q	19	2.9	0.7
22	12 p	7	2.9	0.7
23	22 q	11	2.8	0.7
24	7 p	7	2.8	0.7
25	12 q	17	2.7	0.8
26	21 q	5	2.7	0.7
27	19 p	13	2.7	0.8
28	X p	7	2.6	0.8
29	6 p	9	2.6	0.8
30	13 q	7	2.5	0.8
31	1 q	20	2.4	0.9
32	16 q	8	2.4	0.8
33	11 q	15	2.3	0.9
34	19 q	5	2.3	0.9
35	5 p	2	1.7	0.9
36	20 p	5	1.6	1
37	18 p	1	1.6	0.9
38	16 p	6	1.5	1
39	8 p	3	1.5	1
40	11 p	4	1.3	1
41	8 q	4	1.2	1
42	3 q	4	0.8	1
43	21 p	0	0	1
44	Y p	0	0	1

Spot T

genes in spot = 260 (249 with loci information)

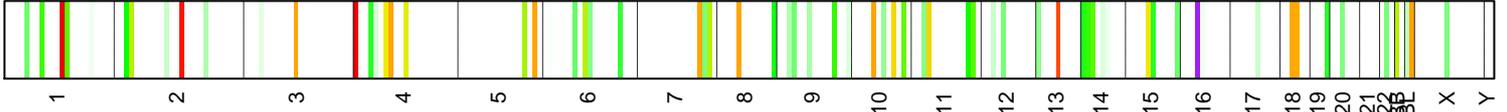
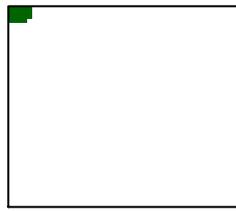
samples with spot = 101 (36.7 %)

Atypical : 11 (14.9 %)

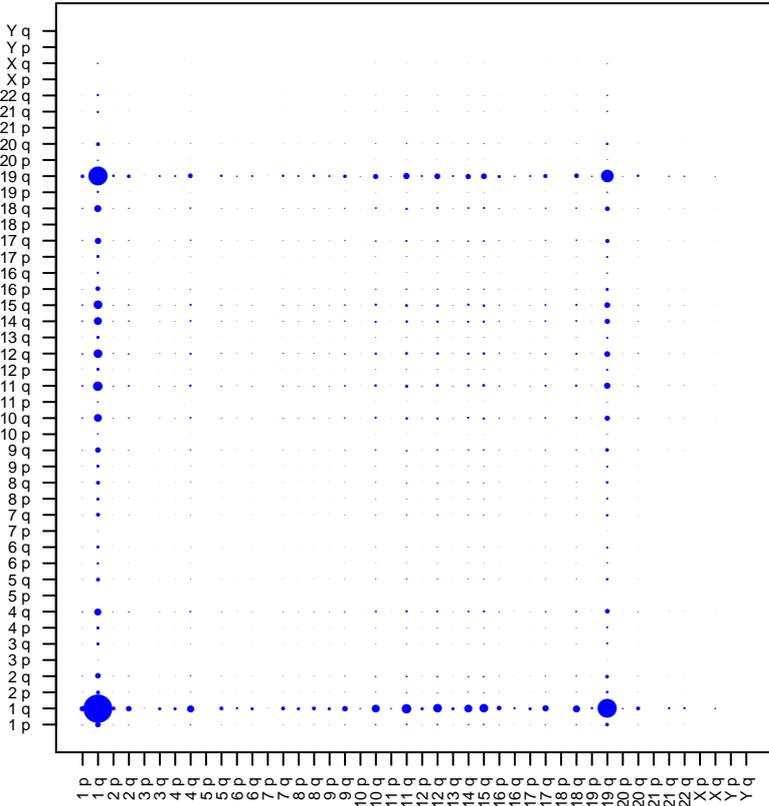
Classical : 7 (21.9 %)

Mesenchymal : 10 (11.8 %)

Basal : 73 (86.9 %)



Absolute numbers

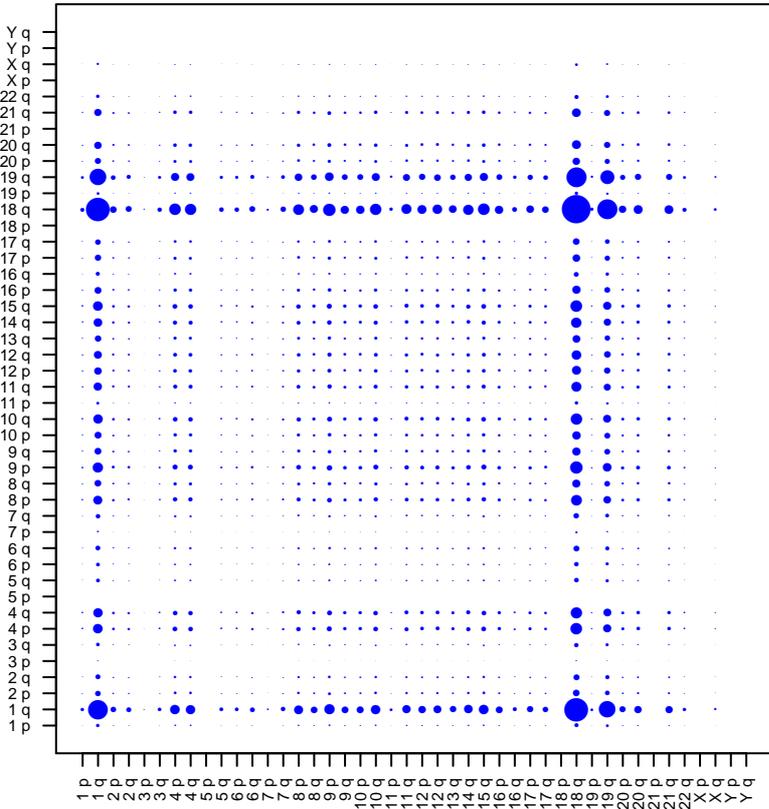


Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	1 q	36	4.4	5e-08
2	19 q	24	3.7	1e-04
3	11 q	12	1.9	0.3
4	12 q	11	1.8	0.4
5	15 q	11	2.1	0.2
6	10 q	10	2.1	0.2
7	4 q	10	2.1	0.2
8	18 q	9	1.9	0.3
9	8 p	9	1.9	0.3
10	14 q	8	1.9	0.3
11	11 p	7	0.8	1
12	2 q	7	1.1	0.6
13	9 q	7	1.5	0.6
14	16 p	6	1.2	0.8
15	2 p	5	0.9	1
16	5 q	5	1.5	0.6
17	7 q	5	1.6	0.5
18	8 q	4	0.8	1
19	20 q	4	2.1	0.4
20	3 q	4	0.8	0.8
21	4 p	4	2.1	0.4
22	6 q	4	1.1	0.8
23	8 p	4	2.2	0.4
24	9 p	4	2.3	0.3
25	10 p	4	2.2	0.3
26	12 p	4	1.7	0.5
27	13 p	4	1.4	0.7
28	17 p	4	1.4	0.7
29	6 p	3	0.8	0.9
30	16 p	3	0.9	0.9
31	19 p	3	0.6	1
32	21 p	3	1.6	0.6
33	22 q	3	0.8	1
34	10 p	2	1.6	0.6
35	11 p	2	0.6	1
36	20 p	2	1.4	0.7
37	X q	2	0.5	1
38	3 p	1	0.2	1
39	7 p	1	0.4	1
40	5 p	0	0	1
41	18 p	0	0	1
42	21 p	0	0	1
43	X p	0	0	1
44	Y q	0	0	1

H3CHR6-MHC-QBB

Relative numbers



Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	18 q	9	5.3	0.002
2	1 q	36	4.4	5e-08
3	19 q	24	3.7	1e-04
4	9 p	4	2.3	0.3
5	15 q	11	2.1	0.2
6	4 p	4	2.1	0.4
7	10 q	10	2.1	0.2
8	4 q	10	2.1	0.2
9	8 p	4	2.1	0.3
10	14 q	4	2	0.4
11	11 q	10	1.9	0.3
12	11 q	12	1.8	0.3
13	12 p	11	1.9	0.3
14	20 p	4	1.7	0.5
15	21 p	5	1.1	0.6
16	10 p	5	1.1	0.6
17	16 p	5	1.1	0.6
18	8 q	5	1.1	0.6
19	9 q	5	1.5	0.6
20	7 q	4	1.4	0.7
21	13 p	4	1.4	0.7
22	20 p	4	1.4	0.7
23	2 p	5	1.2	0.8
24	17 q	8	1.2	0.8
25	2 q	7	1.1	0.9
26	6 q	4	1.1	0.8
27	7 q	5	1.1	0.9
28	16 q	3	0.9	0.9
29	5 q	3	0.9	0.9
30	3 p	1	0.9	0.9
31	6 p	1	0.9	0.9
32	22 q	1	0.8	1
33	11 p	1	0.8	1
34	19 p	1	0.6	1
35	X q	2	0.5	1
36	3 p	1	0.4	1
37	7 p	1	0.4	1
38	5 p	0	0	1
39	18 p	0	0	1
40	21 p	0	0	1
41	X p	0	0	1
42	Y p	0	0	1
43	Y p	0	0	1
44	Y q	0	0	1

Spot U

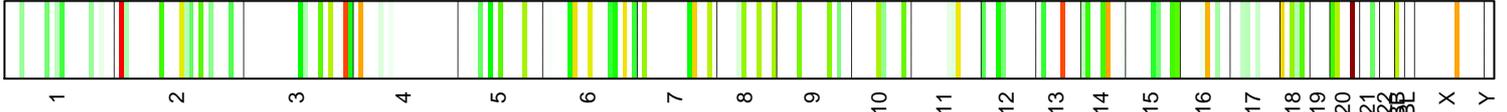
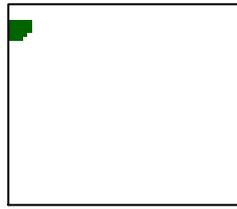
genes in spot = 241 (236 with loci information)

samples with spot = 89 (32.4 %)

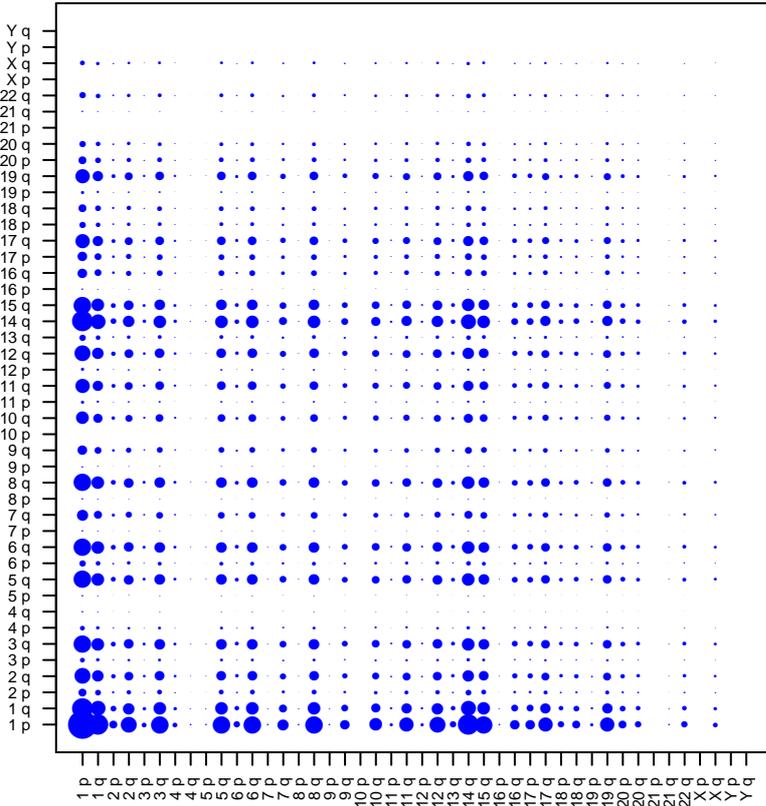
Classical : 2 (6.2 %)

Mesenchymal : 36 (42.4 %)

Basal : 51 (60.7 %)



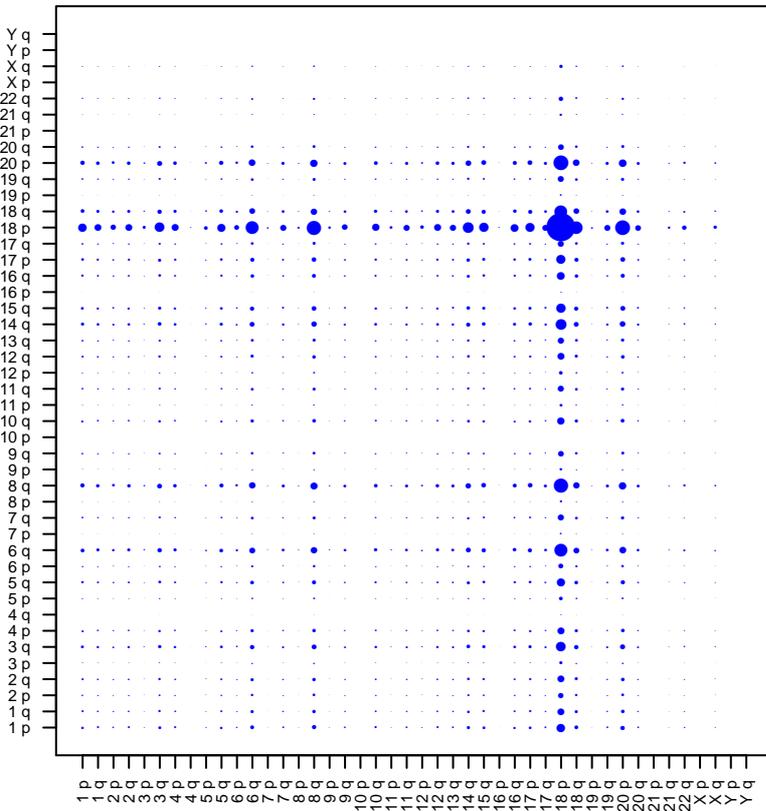
Absolute numbers



Rank	locus	# genes	%	p-value
1	1 p	18	1.9	0.1
2	1 q	13	1.6	0.5
3	14 q	13	2.5	0.05
4	3 q	11	2.2	0.1
5	5 q	11	1.9	0.3
6	6 q	11	3.3	0.02
7	8 q	11	3.3	0.01
8	15 q	11	2.1	0.1
9	17 p	10	1.6	0.5
10	12 q	10	1.6	0.5
11	11 q	9	1.4	0.6
12	17 q	9	1.4	0.6
13	19 q	9	1.4	0.6
14	10 q	8	1.7	0.4
15	7 q	7	1.4	0.6
16	9 q	6	1.3	0.7
17	16 q	6	1.8	0.4
18	17 p	6	2.1	0.3
19	2 p	5	1.2	0.7
20	18 q	5	2.9	0.1
21	20 p	5	3.4	0.07
22	6 p	4	1.1	0.8
23	13 q	4	1.4	0.6
24	18 p	4	1.6	0.5
25	20 q	4	3.3	0.01
26	22 q	4	1.1	0.8
27	3 p	3	0.7	1
28	4 p	3	1.6	0.5
29	X q	3	0.8	0.9
30	11 p	2	0.6	1
31	12 p	2	0.8	0.9
32	19 p	2	0.4	1
33	4 q	1	0.2	1
34	5 p	1	0.9	0.8
35	7 p	1	0.4	1
36	8 p	1	0.5	1
37	9 p	1	0.6	0.9
38	16 p	1	0.3	1
39	21 q	1	5	0.9
40	10 p	0	0	1
41	21 p	0	0	1
42	X p	0	0	1
43	Y p	0	0	1
44	Y q	0	0	1

H3CHR6-MHC-QBB

Relative numbers



Rank	locus	# genes	%	p-value
1	18 p	4	6.6	0.01
2	20 p	5	3.4	0.07
3	8 q	11	3.3	0.01
4	6 q	11	3.3	0.02
5	18 q	5	2.9	0.1
6	14 q	13	2.5	0.05
7	3 q	11	2.2	0.1
8	15 q	11	2.1	0.1
9	17 p	6	2.1	0.3
10	1 p	18	1.9	0.1
11	5 q	11	1.9	0.3
12	16 q	6	1.8	0.4
13	10 q	8	1.7	0.4
14	4 p	8	1.6	0.5
15	12 q	10	6.6	0.01
16	2 q	10	5.5	0.01
17	11 q	13	6.6	0.01
18	13 q	4	1.4	0.6
19	7 q	7	1.4	0.6
20	11 q	9	1.4	0.6
21	17 q	9	1.4	0.6
22	19 q	4	1.4	0.6
23	20 q	4	1.3	0.7
24	9 q	6	1.3	0.7
25	2 p	5	1.2	0.7
26	6 p	4	1.1	0.8
27	22 q	4	1	0.8
28	5 p	1	0.9	0.8
29	12 p	2	0.9	0.9
30	X q	3	0.8	0.9
31	3 p	3	0.7	1
32	11 p	2	0.6	1
33	9 p	1	0.6	0.9
34	21 q	1	5	0.9
35	8 p	1	0.5	1
36	19 p	2	0.4	1
37	7 p	1	0.4	1
38	16 p	1	0.3	1
39	4 q	1	0.2	1
40	10 p	0	0	1
41	21 p	0	0	1
42	X p	0	0	1
43	Y p	0	0	1
44	Y q	0	0	1

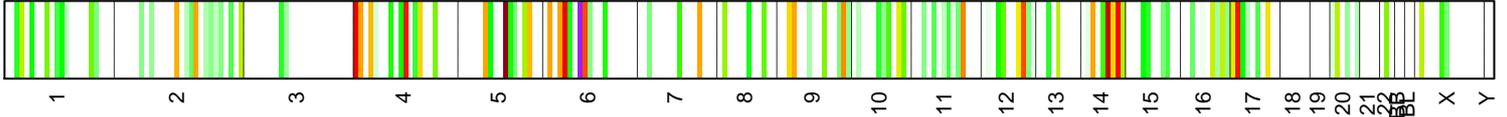
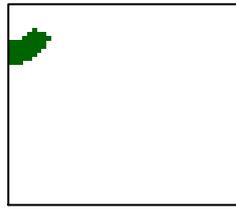
Spot V

genes in spot = 395 (387 with loci information)

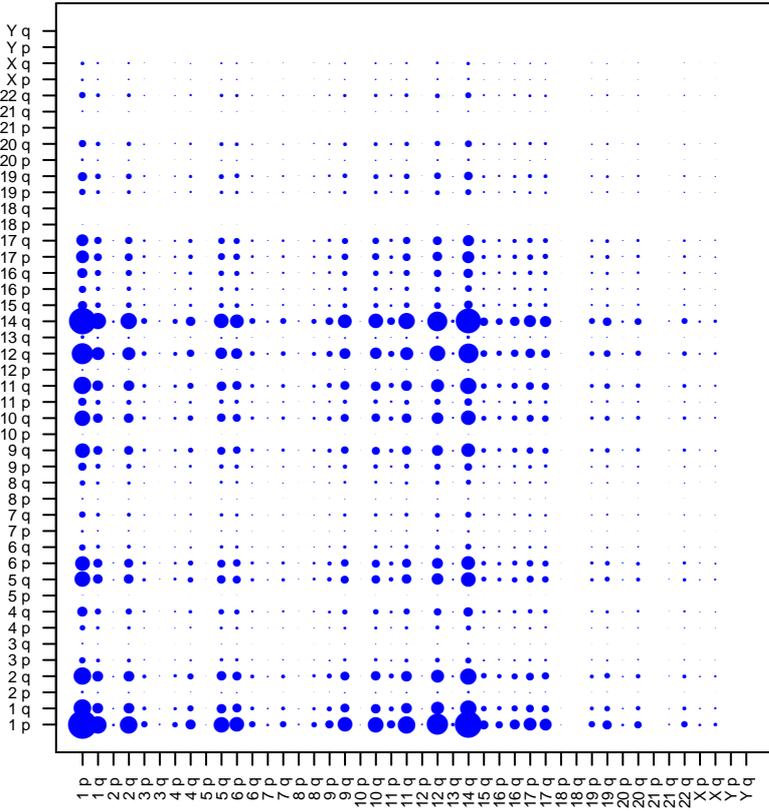
samples with spot = 25 (9.1 %)

Mesenchymal : 12 (14.1 %)

Basal : 13 (15.5 %)



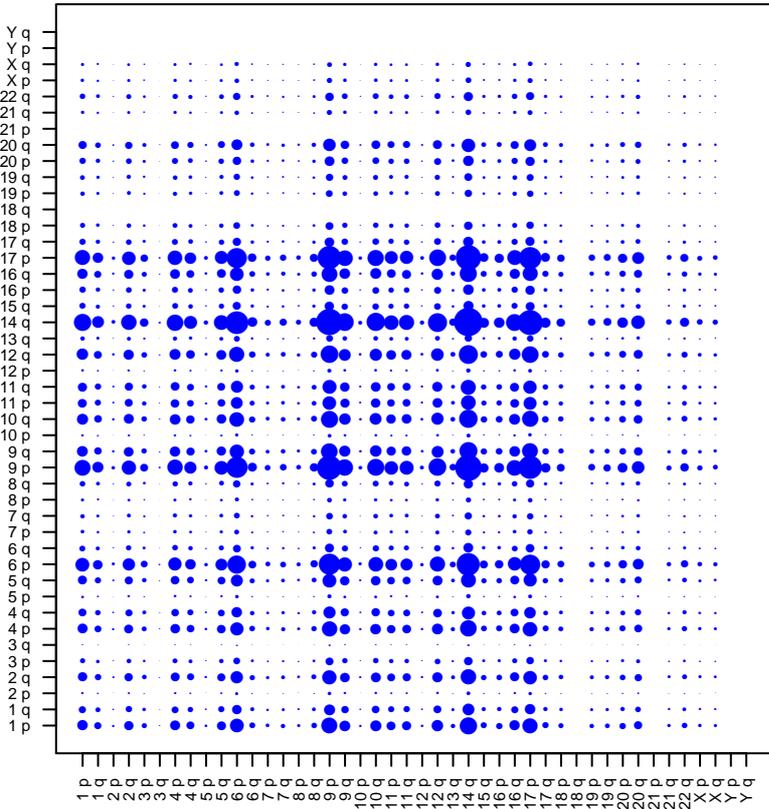
Absolute numbers



Rank	locus	# genes	%	p-value
1	1 p	31	3.3	0.05
2	14 q	29	5.5	3e-05
3	12 q	23	3.7	0.03
4	1 q	19	2.3	0.6
5	2 q	19	3.3	0.02
6	11 q	19	3.6	0.03
7	5 q	17	2.9	0.02
8	10 q	17	2.6	0.08
9	9 p	16	4.4	0.01
10	16 q	16	3.5	0.02
11	17 p	14	4.9	0.001
12	17 q	13	2.9	0.08
13	4 q	11	2.5	0.5
14	16 q	11	3.3	0.2
15	15 q	10	2.5	0.8
16	19 q	10	1.5	1
17	9 p	9	5.1	0.03
18	11 p	9	2.8	0.4
19	16 p	8	2	0.7
20	20 q	8	2.6	0.5
21	3 p	7	1.7	0.9
22	6 q	7	1.9	0.8
23	7 q	7	1.4	1
24	19 p	7	1.4	1
25	22 q	7	1.8	0.8
26	8 q	6	3.2	0.03
27	8 p	6	1.8	0.8
28	13 q	4	1.4	0.9
29	X q	4	1	1
30	2 p	3	0.7	1
31	7 p	3	1.2	0.9
32	20 p	3	2	0.7
33	X p	3	1.1	1
34	3 q	2	0.4	1
35	8 p	2	1	1
36	12 p	2	0.8	1
37	21 q	2	1.1	0.9
38	5 p	1	0.9	0.9
39	10 p	1	0.8	1
40	18 p	1	1.6	0.8
41	18 q	0	0	1
42	21 p	0	0	1
43	Y p	0	0	1
44	Y q	0	0	1

HSCHR6-MHC-DBP

Relative numbers

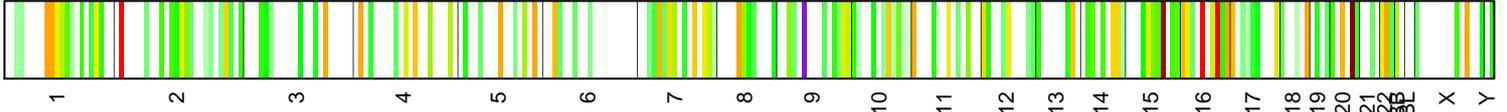
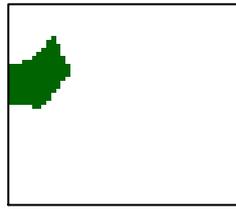


Rank	locus	# genes	%	p-value
1	14 q	29	5.5	3e-05
2	9 p	16	5.1	0.03
3	17 p	14	4.9	0.01
4	6 p	16	4.4	0.01
5	12 q	23	3.7	0.03
6	10 q	17	3.6	0.08
7	9 q	16	3.5	0.1
8	1 p	31	3.3	0.05
9	16 q	11	3.3	0.2
10	4 p	6	3.2	0.03
11	2 q	19	3.3	0.02
12	11 q	19	3.6	0.03
13	5 q	17	2.9	0.02
14	11 p	17	2.9	0.03
15	20 q	8	4.4	0.01
16	4 q	11	5.5	0.001
17	16 p	19	3.5	0.02
18	11 p	9	2.8	0.4
19	16 p	8	2.6	0.5
20	20 p	8	2	0.7
21	17 q	3	1.3	0.8
22	15 q	2	2	0.8
23	6 q	7	1.9	0.8
24	22 q	7	1.8	0.8
25	3 p	7	1.7	0.9
26	18 p	1	1.6	0.8
27	19 q	10	1.5	1
28	19 p	7	1.4	1
29	13 q	4	1.4	0.9
30	7 q	7	1.4	1
31	7 p	3	1.2	0.9
32	X p	3	1.1	1
33	21 q	3	1.1	0.9
34	X q	4	1	1
35	8 p	2	1	1
36	5 p	1	0.9	0.9
37	12 p	2	0.8	1
38	10 p	1	0.8	1
39	2 p	3	0.7	1
40	3 q	2	0.4	1
41	18 p	0	0	1
42	21 p	0	0	1
43	Y p	0	0	1
44	Y q	0	0	1

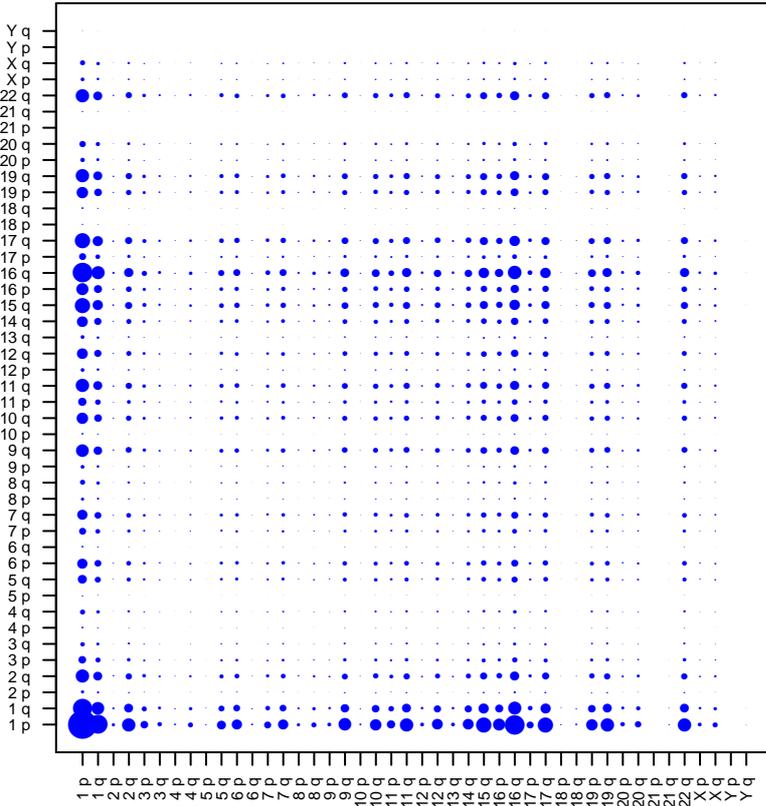
Spot W

genes in spot = 556 (541 with loci information)

samples with spot = 0 (0 %)



Absolute numbers

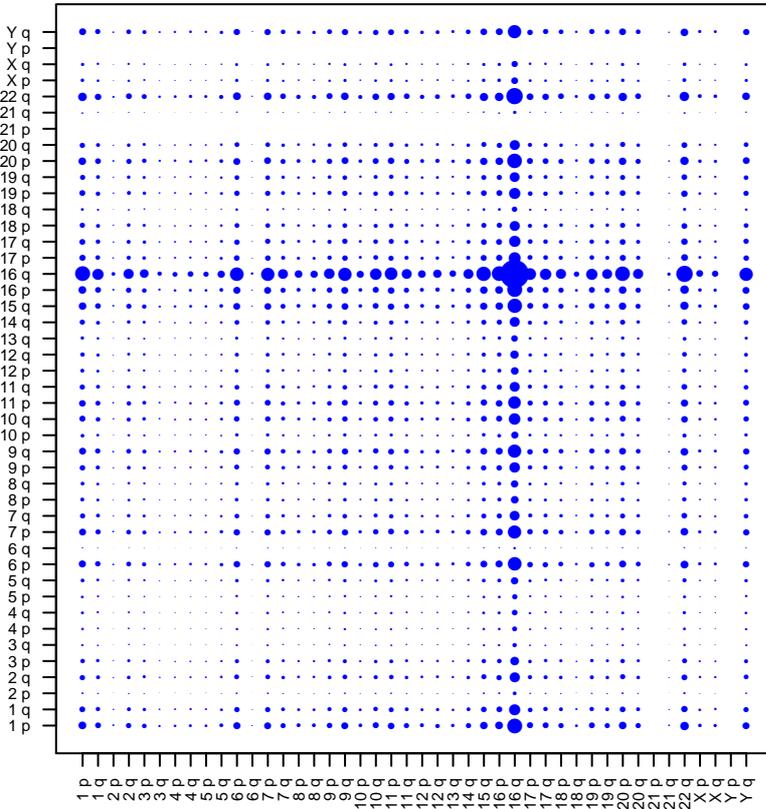


Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	1 p	45	4.9	0.01
2	16 q	31	9.3	5e-07
3	1 q	30	3.6	0.4
4	15 q	24	4.7	0.08
5	17 q	24	3.7	0.4
6	2 q	21	3.3	0.6
7	11 q	21	3.3	0.6
8	19 q	21	3.3	0.6
9	9 q	21	3.3	0.6
10	9 q	20	4.3	0.2
11	16 p	19	4.8	0.08
12	10 q	18	3.8	0.4
13	19 p	18	3.7	0.4
14	12 q	17	2.7	0.9
15	14 q	17	3.3	0.6
16	16 p	16	4.4	0.2
17	7 q	16	3.2	0.6
18	5 q	14	2.4	0.9
19	11 p	13	4.1	0.3
20	3 p	12	2.8	0.8
21	7 p	11	4.3	0.3
22	17 p	11	3.8	0.4
23	20 q	10	3.3	0.6
24	4 q	10	1.8	1
25	8 q	8	2.4	0.9
26	3 q	8	2	1
27	3 q	7	1.4	1
28	20 p	7	4.8	0.2
29	9 p	6	3.4	0.6
30	12 p	6	2.5	0.8
31	13 q	6	2.1	0.9
32	X p	6	2.2	0.9
33	2 p	5	1.2	1
34	8 p	5	2.5	0.8
35	4 p	5	1.6	1
36	6 q	3	0.8	1
37	10 p	3	2.3	0.8
38	18 q	3	1.8	0.9
39	5 p	3	1.7	0.9
40	18 p	2	3.3	0.6
41	21 q	2	1.1	1
42	Y q	1	4.3	0.6
43	21 p	0	0	1
44	Y p	0	0	1

HSCHR6-MHC-DQB1

Relative numbers



Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	16 q	31	9.3	5e-07
2	22 q	21	5.3	0.03
3	1 p	45	4.9	0.01
4	16 p	19	4.8	0.08
5	20 p	7	4.8	0.2
6	15 q	24	4.7	0.08
7	6 p	16	4.4	0.2
8	Y q	1	4.3	0.6
9	9 q	20	4.3	0.2
10	7 p	11	4.3	0.3
11	11 p	13	4.1	0.3
12	17 p	11	3.8	0.4
13	10 q	18	3.8	0.4
14	17 q	24	3.7	0.4
15	19 p	18	3.7	0.4
16	1 q	30	3.6	0.4
17	9 p	21	3.4	0.6
18	2 q	21	3.3	0.6
19	20 q	10	3.3	0.6
20	18 p	2	3.3	0.6
21	14 q	17	3.3	0.6
22	11 q	21	3.2	0.6
23	19 q	21	3.2	0.6
24	7 q	16	3.2	0.6
25	3 p	12	2.8	0.8
26	12 q	17	2.7	0.9
27	12 p	6	2.5	0.8
28	8 p	5	2.5	0.8
29	5 q	14	2.4	0.9
30	8 q	8	2.4	0.9
31	10 p	8	2.4	0.9
32	X p	6	2.2	0.9
33	13 q	6	2.1	0.9
34	4 q	2	1.6	1
35	4 q	5	1.8	0.9
36	18 q	3	1.8	0.9
37	5 p	3	1.7	0.9
38	4 p	3	1.6	0.9
39	3 q	2	1.4	1
40	2 p	5	1.2	1
41	21 q	2	1.1	1
42	6 q	3	0.8	1
43	21 p	0	0	1
44	Y p	0	0	1

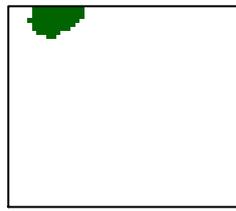
Spot X

genes in spot = 585 (572 with loci information)

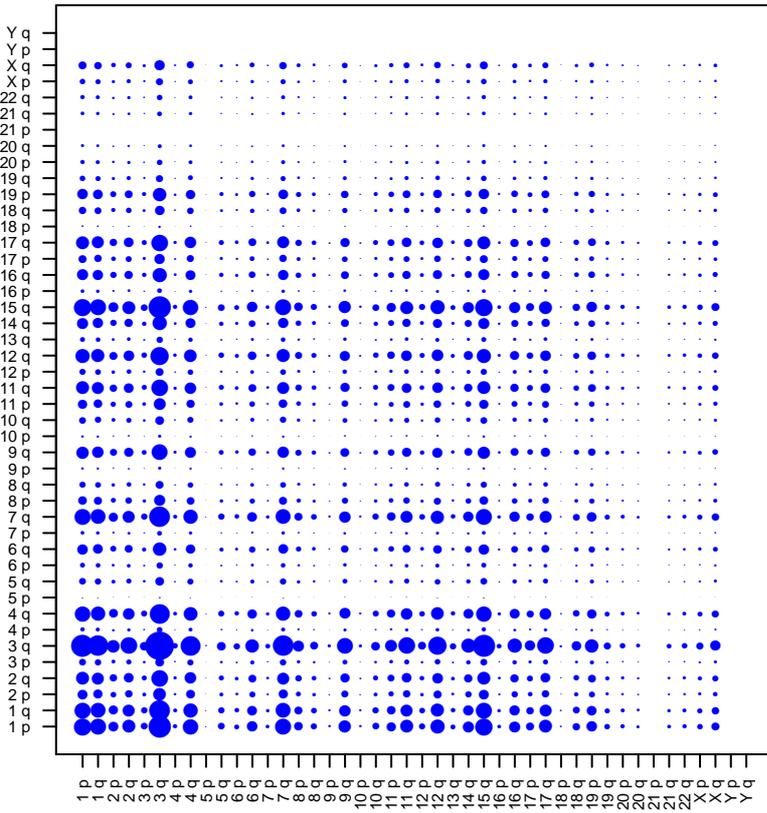
samples with spot = 25 (9.1 %)

Classical : 5 (15.6 %)

Basal : 20 (23.8 %)



Absolute numbers

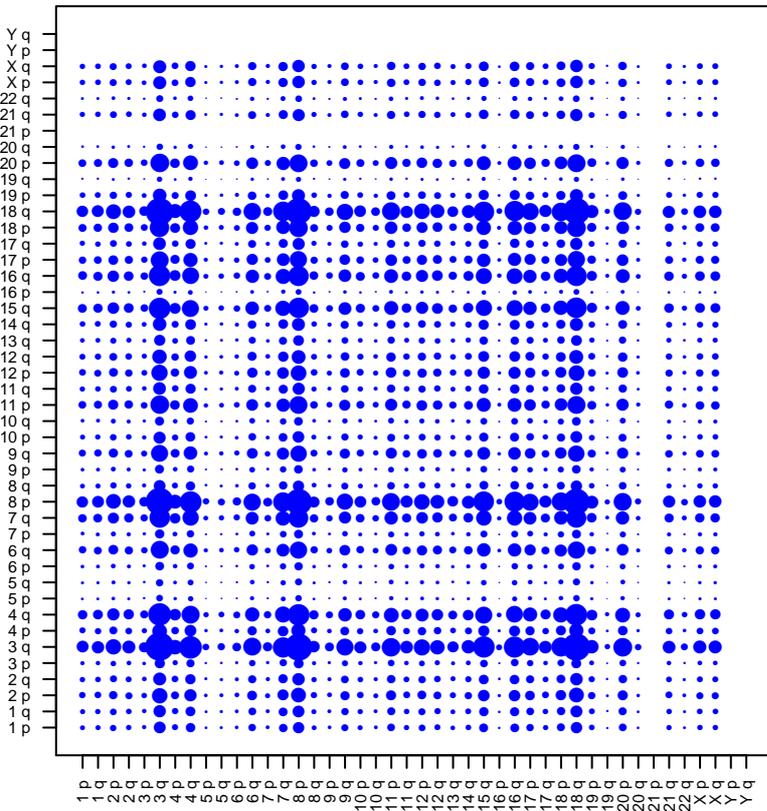


Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	3 q	36	7.3	5e-05
2	1 p	28	3	0.9
3	15 q	28	5.5	0.02
4	1 q	26	3.1	0.8
5	7 q	26	5.2	0.04
6	4 q	25	5.8	0.01
7	12 q	25	5.8	0.01
8	2 q	21	3.3	0.7
9	11 q	21	3.3	0.7
10	17 q	21	3.3	0.7
11	9 q	20	4.3	0.2
12	14 q	18	3.4	0.6
13	16 q	18	5.4	0.06
14	6 q	17	4.6	0.2
15	19 p	17	3.5	0.6
16	2 p	16	3.9	0.4
17	11 p	15	4.7	0.2
18	8 p	14	7	0.01
19	17 p	13	4.5	0.2
20	X q	13	3.3	0.7
21	18 q	12	7	0.02
22	3 p	11	2.6	0.9
23	5 q	11	1.9	1
24	10 q	11	3.3	0.7
25	8 q	10	3	0.8
26	12 p	10	4.1	0.4
27	19 q	9	1.4	1
28	X p	9	3.3	0.6
29	6 p	8	2.2	1
30	13 q	8	2.8	0.8
31	4 p	7	3.7	0.5
32	20 p	7	4.8	0.3
33	22 q	7	1.8	1
34	7 p	6	2.4	0.9
35	16 p	6	1.5	1
36	21 q	6	3.2	0.7
37	20 q	5	1.6	1
38	9 p	4	2.3	0.9
39	10 p	4	3.1	0.7
40	18 p	3	4.9	0.4
41	5 p	3	1.7	0.9
42	21 p	0	0	1
43	Y p	0	0	1
44	Y q	0	0	1

H3CHR6-MHC-DAB

Relative numbers



Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	3 q	36	7.3	5e-05
2	18 q	7	7	0.02
3	8 p	14	5	0.01
4	4 q	25	5.8	0.01
5	15 q	28	5.5	0.02
6	16 q	18	5.4	0.06
7	7 q	26	5.2	0.04
8	18 p	3	4.9	0.4
9	20 p	7	4.8	0.3
10	11 p	15	4.7	0.2
11	6 q	17	4.6	0.2
12	17 p	13	4.5	0.2
13	9 q	20	4.3	0.2
14	12 p	10	4.1	0.4
15	2 p	16	3.9	0.4
16	4 p	7	3.7	0.5
17	12 q	23	3.7	0.5
18	19 q	17	3.5	0.6
19	14 q	18	3.4	0.6
20	X p	9	3.3	0.6
21	X q	13	3.3	0.7
22	2 q	21	3.3	0.7
23	21 q	6	3.2	0.7
24	11 q	21	3.2	0.7
25	17 q	21	3.2	0.7
26	1 q	26	3.1	0.8
27	10 p	4	3.1	0.7
28	1 p	28	3	0.9
29	8 q	10	3	0.8
30	13 q	8	3	0.8
31	3 p	11	3	0.9
32	7 p	6	2.4	0.9
33	10 q	11	2.3	1
34	9 p	4	2.3	0.9
35	6 p	8	2.2	1
36	5 q	11	1.9	1
37	22 q	7	1.8	1
38	5 p	2	1.7	0.9
39	20 q	5	1.6	1
40	16 p	6	1.5	1
41	19 q	9	1.4	1
42	21 p	0	0	1
43	Y p	0	0	1
44	Y q	0	0	1

Spot Y

genes in spot = 734 (710 with loci information)

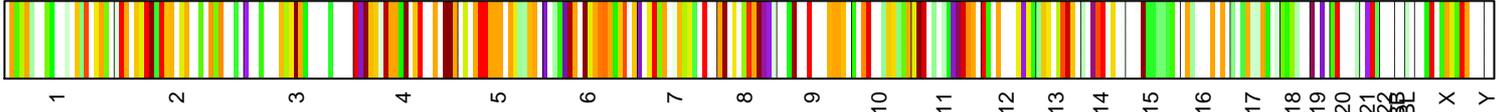
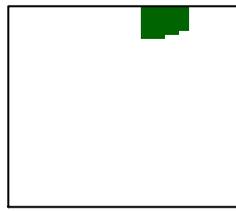
samples with spot = 10 (3.6 %)

Atypical : 1 (1.4 %)

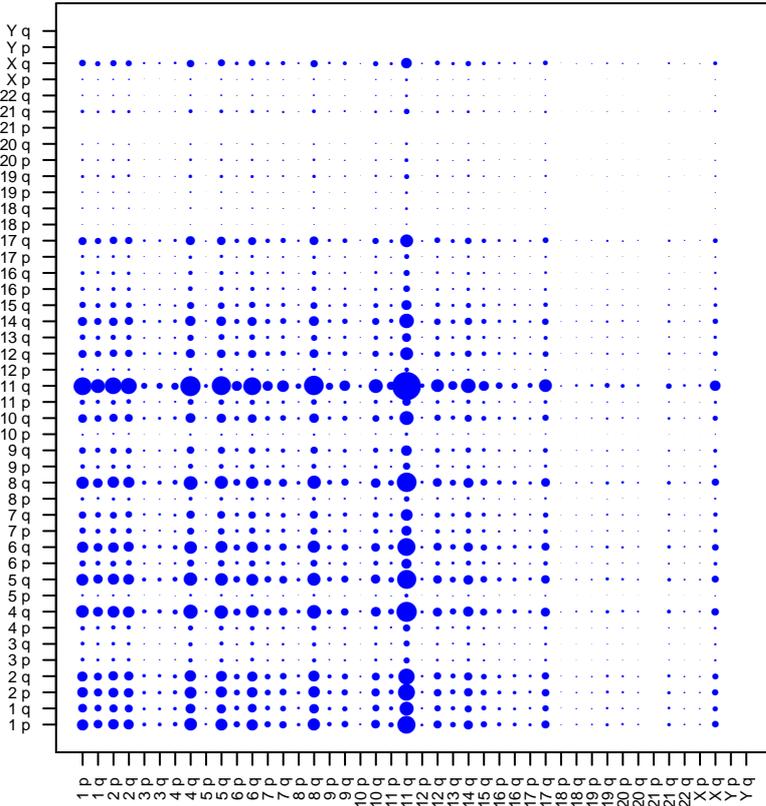
Classical : 1 (3.1 %)

Mesenchymal : 2 (2.4 %)

Basal : 6 (7.1 %)



Absolute numbers

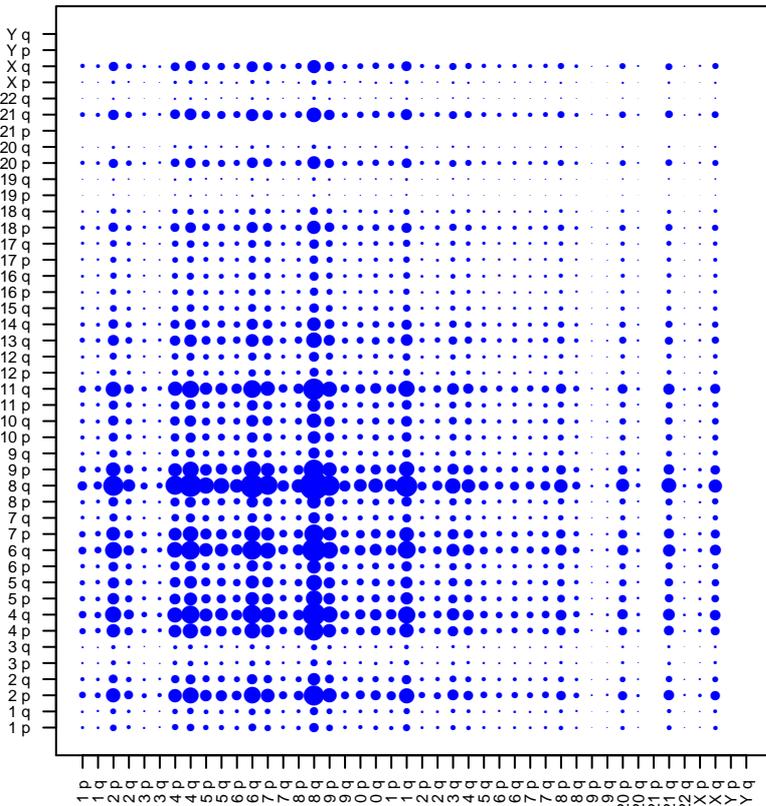


Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	11 q	51	7.9	9e-05
2	4 q	36	8.3	3e-04
3	8 q	35	10.4	4e-06
4	5 q	34	5.8	0.09
5	1 p	33	7.4	1
6	6 q	33	8.6	4e-04
7	2 p	30	7.4	0.006
8	7 p	29	4.6	0.005
9	11 q	29	5.5	0.3
10	1 p	29	5.5	0.3
11	10 q	29	5.5	0.3
12	12 q	29	5.5	0.3
13	17 q	23	3.5	0.9
14	7 q	21	4.2	0.7
15	9 q	19	4.1	0.7
16	X q	19	4.9	0.4
17	6 p	18	5	0.4
18	7 p	18	7.1	0.04
19	15 q	18	3.5	0.9
20	13 q	16	5.7	0.2
21	11 p	15	4.7	0.5
22	4 p	13	7.7	0.08
23	9 p	13	7.4	0.05
24	16 p	12	3.1	0.9
25	3 p	11	3.3	0.9
26	16 q	11	1	1
27	16 q	11	1	1
28	8 p	10	5.4	0.4
29	21 q	10	5.4	0.3
30	17 p	9	3.1	0.9
31	19 q	9	1.4	1
32	12 p	8	3.3	0.9
33	5 p	7	6	0.3
34	20 p	7	4.8	0.5
35	10 p	6	4.7	0.5
36	18 q	5	2.9	0.9
37	19 p	5	1	1
38	20 q	5	1.6	1
39	22 q	5	1.3	1
40	X p	5	1.9	1
41	18 p	5	4.9	0.5
42	21 p	0	0	1
43	Y q	0	0	1
44	Y q	0	0	1

H3CHR6-MHC-QBB

Relative numbers

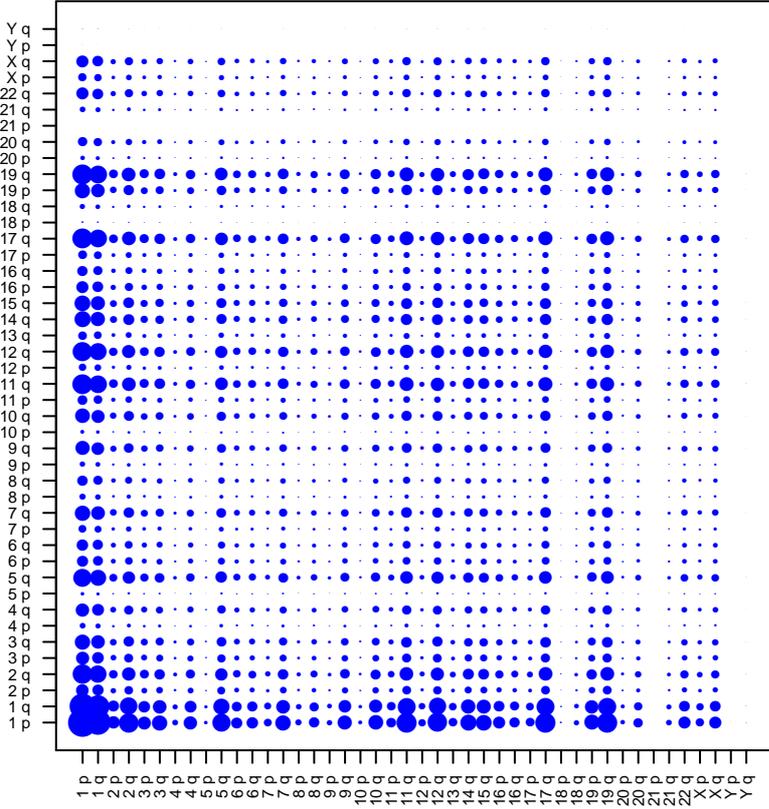


Rank locus # genes % p-value

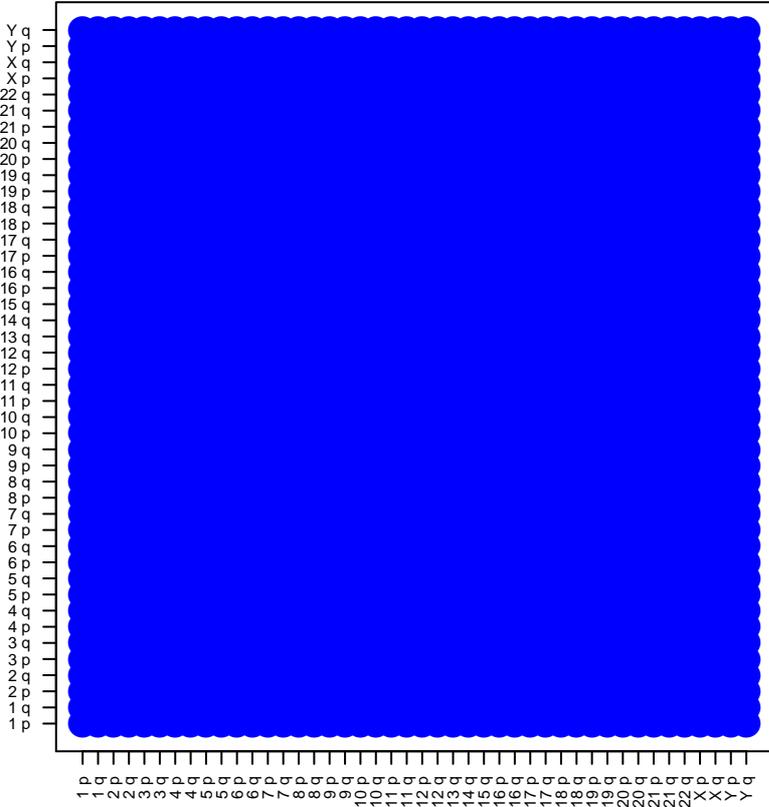
Rank	locus	# genes	%	p-value
1	8 q	35	10.4	4e-06
2	6 q	32	8.6	4e-04
3	4 q	36	8.3	3e-04
4	11 q	51	7.9	9e-05
5	9 p	13	7.4	0.05
6	2 p	30	7.4	0.006
7	7 p	18	7.1	0.04
8	4 p	13	7.7	0.08
9	5 p	7	6	0.3
10	5 q	34	5.8	0.09
11	13 q	16	5.7	0.2
12	21 q	10	5.4	0.3
13	10 q	25	5.2	0.3
14	6 p	18	5.5	0.4
15	8 p	10	5	0.4
16	14 q	20	5	0.5
17	18 p	6	4.9	0.5
18	X q	19	4.9	0.4
19	20 p	7	4.8	0.5
20	11 p	15	4.7	0.5
21	10 p	6	4.7	0.5
22	2 q	29	4.6	0.5
23	7 q	21	4.2	0.7
24	9 q	19	4.1	0.7
25	12 q	23	3.7	0.9
26	17 q	23	3.5	0.9
27	15 q	18	3.5	0.9
28	1 p	32	3.5	1
29	12 p	8	3.3	0.9
30	16 q	11	3.3	0.9
31	17 q	9	3.3	0.9
32	16 p	15	1	1
33	1 q	5	1	1
34	18 q	5	2.9	0.9
35	3 p	11	1	1
36	2 q	11	2.2	1
37	X p	5	1.9	1
38	20 q	5	1.6	1
39	19 q	9	1.4	1
40	22 q	5	1.3	1
41	19 p	5	1	1
42	21 p	0	0	1
43	Y p	0	0	1
44	Y q	0	0	1

Spot summary

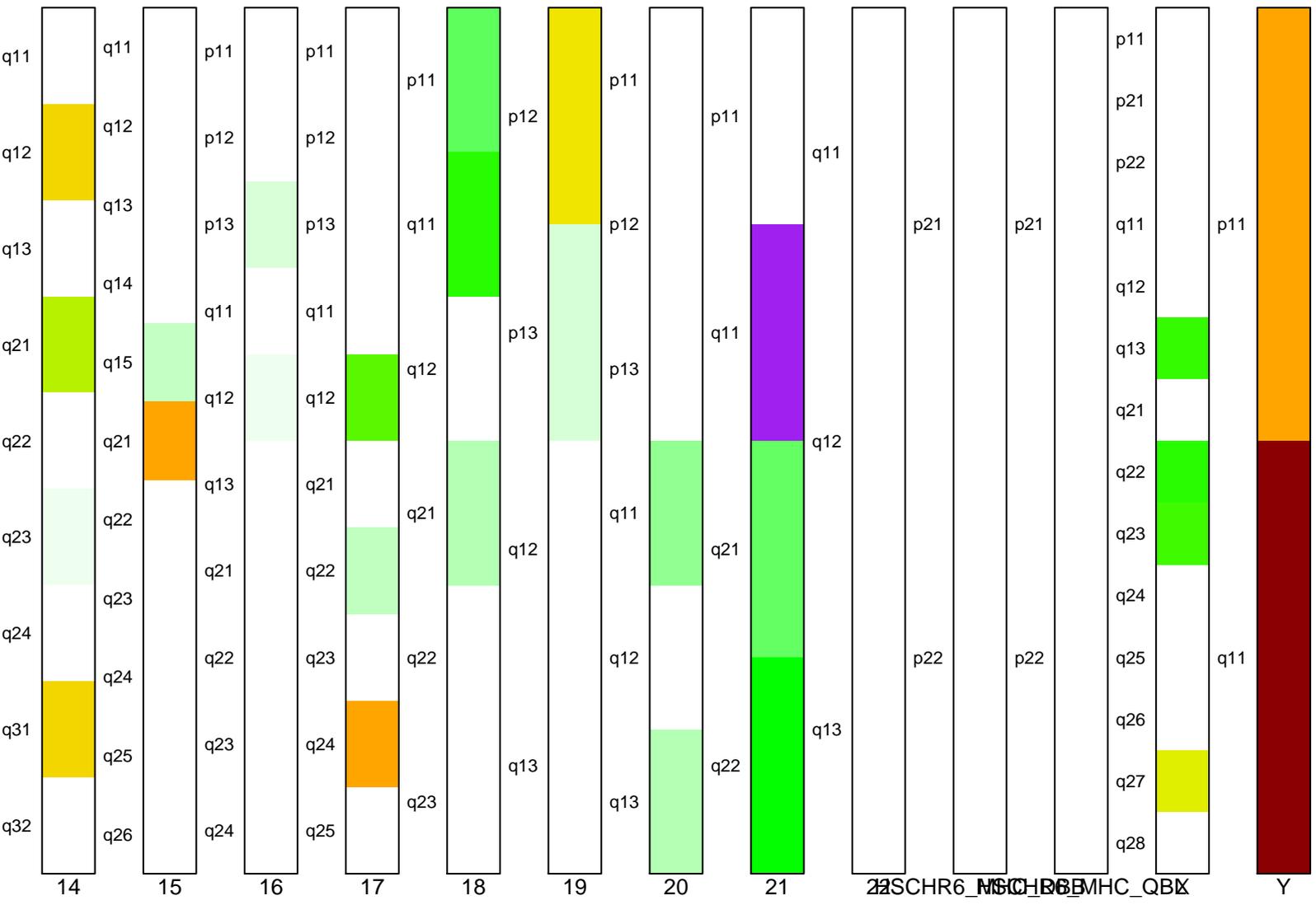
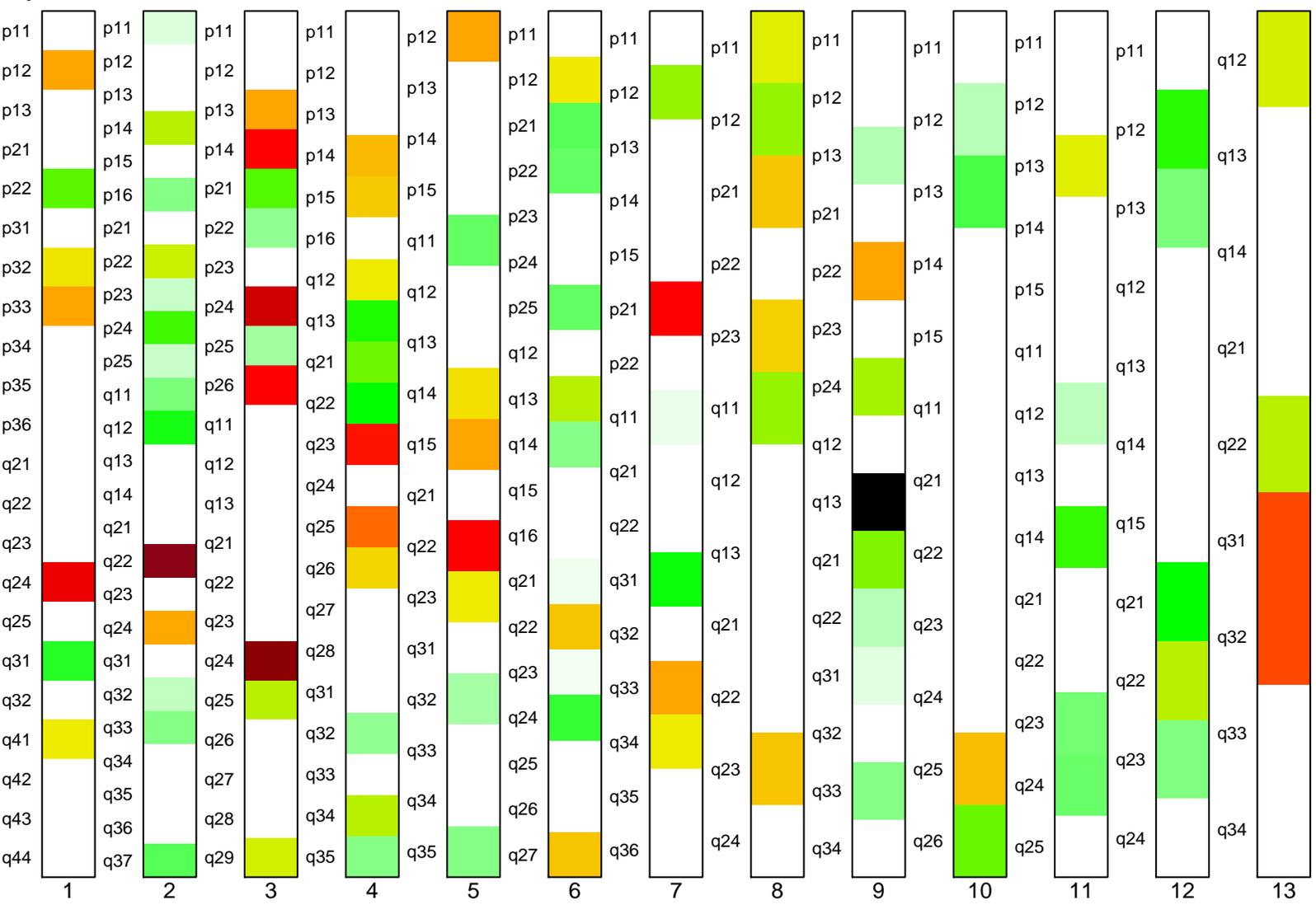
Absolute numbers



Relative numbers

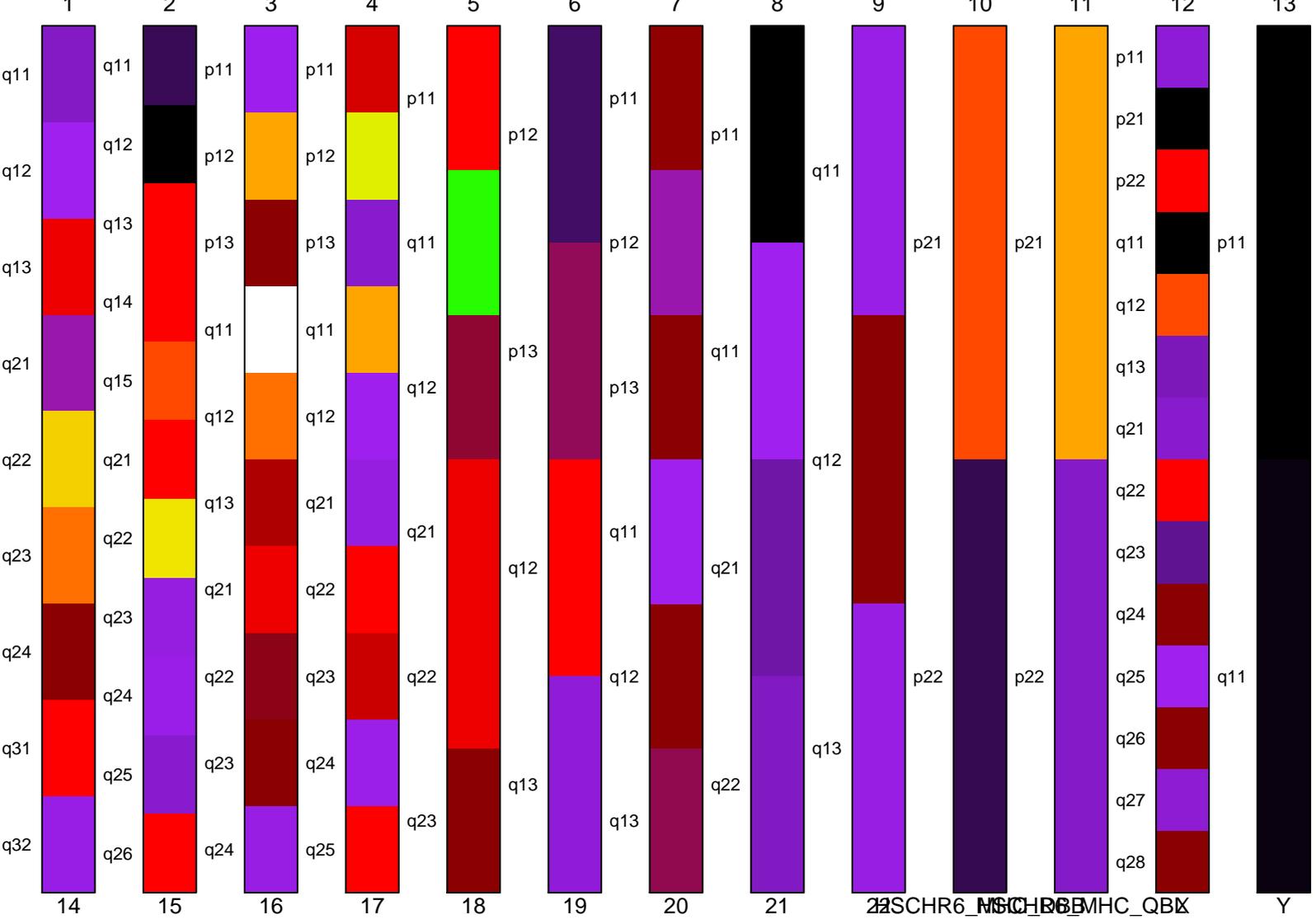
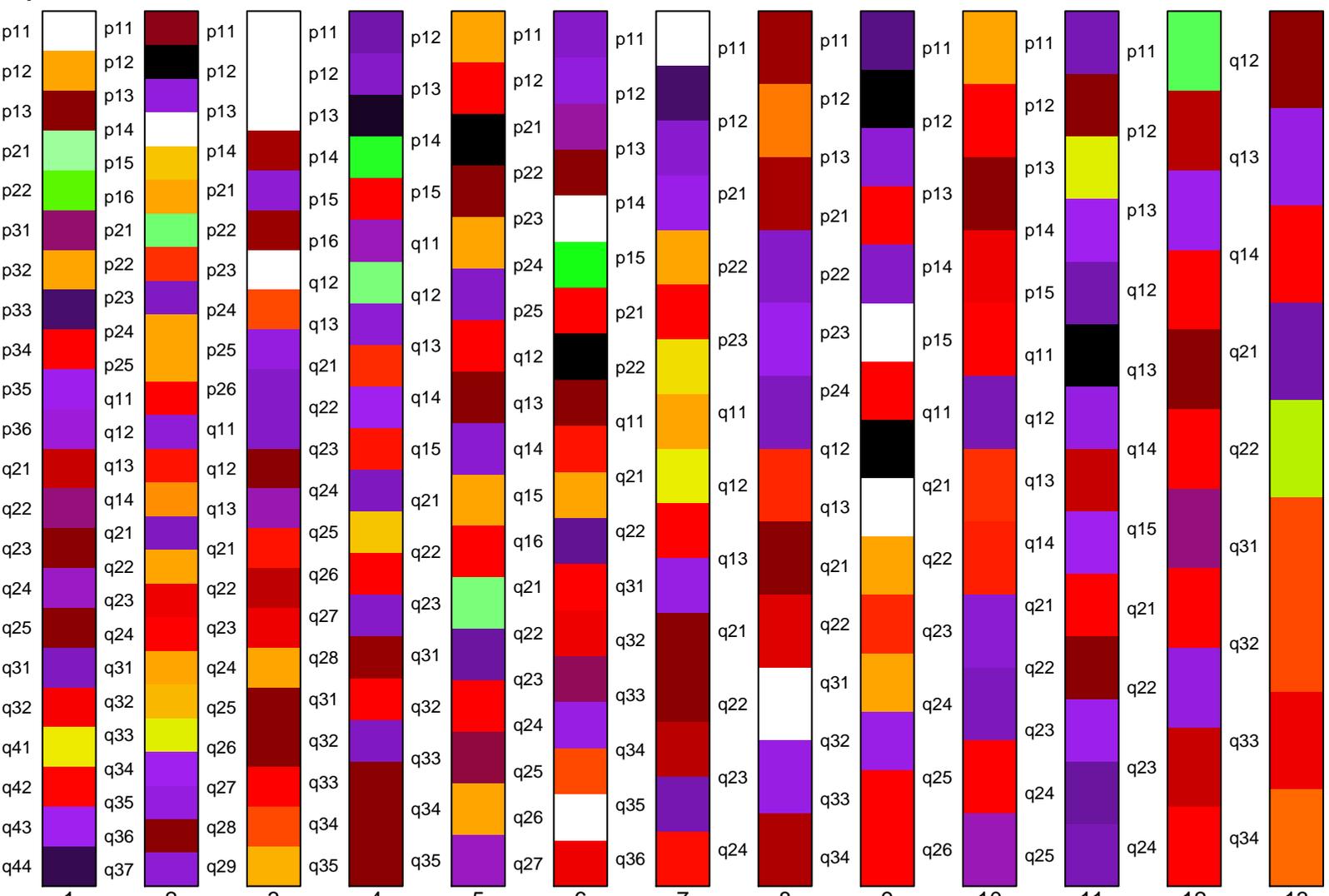


Spot A

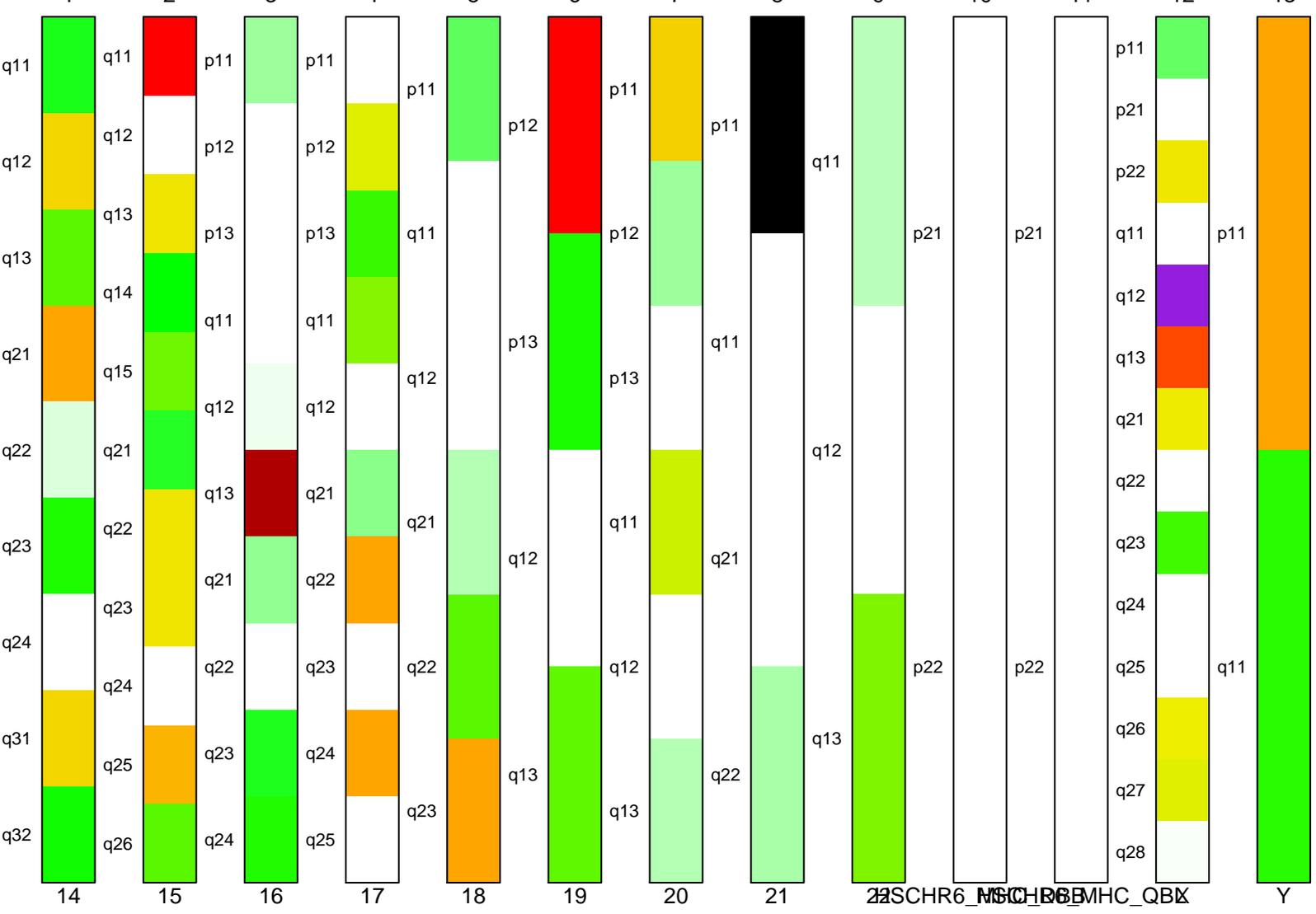
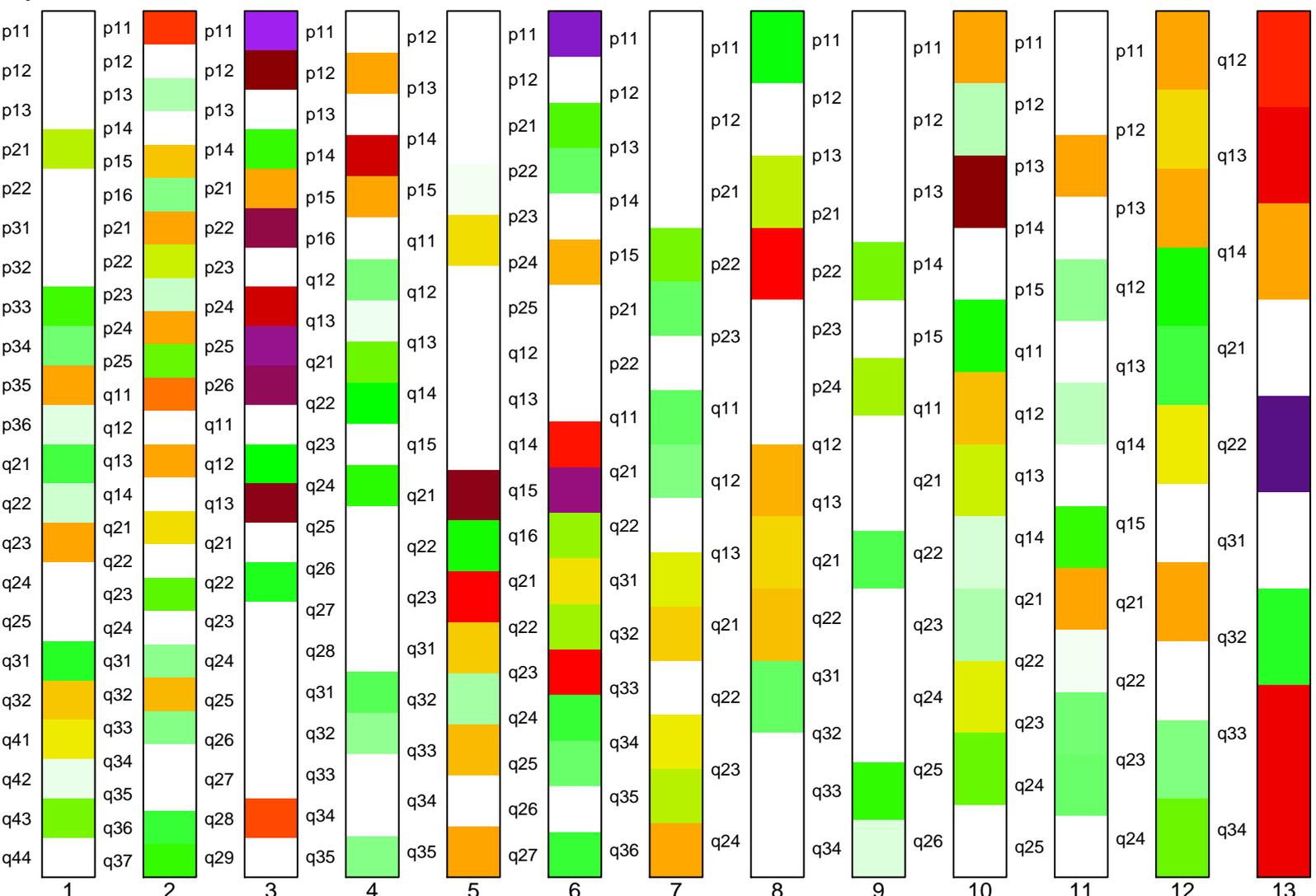


22:23:24:25:26:27:28:29:30:31:32:33:34:35:36:37:38:39:40:41:42:43:44:45:46:47:48:49:50:51:52:53:54:55:56:57:58:59:60:61:62:63:64:65:66:67:68:69:70:71:72:73:74:75:76:77:78:79:80:81:82:83:84:85:86:87:88:89:90:91:92:93:94:95:96:97:98:99:100:101:102:103:104:105:106:107:108:109:110:111:112:113:114:115:116:117:118:119:120:121:122:123:124:125:126:127:128:129:130:131:132:133:134:135:136:137:138:139:140:141:142:143:144:145:146:147:148:149:150:151:152:153:154:155:156:157:158:159:160:161:162:163:164:165:166:167:168:169:170:171:172:173:174:175:176:177:178:179:180:181:182:183:184:185:186:187:188:189:190:191:192:193:194:195:196:197:198:199:200:201:202:203:204:205:206:207:208:209:210:211:212:213:214:215:216:217:218:219:220:221:222:223:224:225:226:227:228:229:230:231:232:233:234:235:236:237:238:239:240:241:242:243:244:245:246:247:248:249:250:251:252:253:254:255:256:257:258:259:260:261:262:263:264:265:266:267:268:269:270:271:272:273:274:275:276:277:278:279:280:281:282:283:284:285:286:287:288:289:290:291:292:293:294:295:296:297:298:299:300:301:302:303:304:305:306:307:308:309:310:311:312:313:314:315:316:317:318:319:320:321:322:323:324:325:326:327:328:329:330:331:332:333:334:335:336:337:338:339:340:341:342:343:344:345:346:347:348:349:350:351:352:353:354:355:356:357:358:359:360:361:362:363:364:365:366:367:368:369:370:371:372:373:374:375:376:377:378:379:380:381:382:383:384:385:386:387:388:389:390:391:392:393:394:395:396:397:398:399:400:401:402:403:404:405:406:407:408:409:410:411:412:413:414:415:416:417:418:419:420:421:422:423:424:425:426:427:428:429:430:431:432:433:434:435:436:437:438:439:440:441:442:443:444:445:446:447:448:449:450:451:452:453:454:455:456:457:458:459:460:461:462:463:464:465:466:467:468:469:470:471:472:473:474:475:476:477:478:479:480:481:482:483:484:485:486:487:488:489:490:491:492:493:494:495:496:497:498:499:500:501:502:503:504:505:506:507:508:509:510:511:512:513:514:515:516:517:518:519:520:521:522:523:524:525:526:527:528:529:530:531:532:533:534:535:536:537:538:539:540:541:542:543:544:545:546:547:548:549:550:551:552:553:554:555:556:557:558:559:560:561:562:563:564:565:566:567:568:569:570:571:572:573:574:575:576:577:578:579:580:581:582:583:584:585:586:587:588:589:590:591:592:593:594:595:596:597:598:599:600:601:602:603:604:605:606:607:608:609:610:611:612:613:614:615:616:617:618:619:620:621:622:623:624:625:626:627:628:629:630:631:632:633:634:635:636:637:638:639:640:641:642:643:644:645:646:647:648:649:650:651:652:653:654:655:656:657:658:659:660:661:662:663:664:665:666:667:668:669:670:671:672:673:674:675:676:677:678:679:680:681:682:683:684:685:686:687:688:689:690:691:692:693:694:695:696:697:698:699:700:701:702:703:704:705:706:707:708:709:710:711:712:713:714:715:716:717:718:719:720:721:722:723:724:725:726:727:728:729:730:731:732:733:734:735:736:737:738:739:740:741:742:743:744:745:746:747:748:749:750:751:752:753:754:755:756:757:758:759:760:761:762:763:764:765:766:767:768:769:770:771:772:773:774:775:776:777:778:779:780:781:782:783:784:785:786:787:788:789:790:791:792:793:794:795:796:797:798:799:800:801:802:803:804:805:806:807:808:809:810:811:812:813:814:815:816:817:818:819:820:821:822:823:824:825:826:827:828:829:830:831:832:833:834:835:836:837:838:839:840:841:842:843:844:845:846:847:848:849:850:851:852:853:854:855:856:857:858:859:860:861:862:863:864:865:866:867:868:869:870:871:872:873:874:875:876:877:878:879:880:881:882:883:884:885:886:887:888:889:890:891:892:893:894:895:896:897:898:899:900:901:902:903:904:905:906:907:908:909:910:911:912:913:914:915:916:917:918:919:920:921:922:923:924:925:926:927:928:929:930:931:932:933:934:935:936:937:938:939:940:941:942:943:944:945:946:947:948:949:950:951:952:953:954:955:956:957:958:959:960:961:962:963:964:965:966:967:968:969:970:971:972:973:974:975:976:977:978:979:980:981:982:983:984:985:986:987:988:989:990:991:992:993:994:995:996:997:998:999:1000

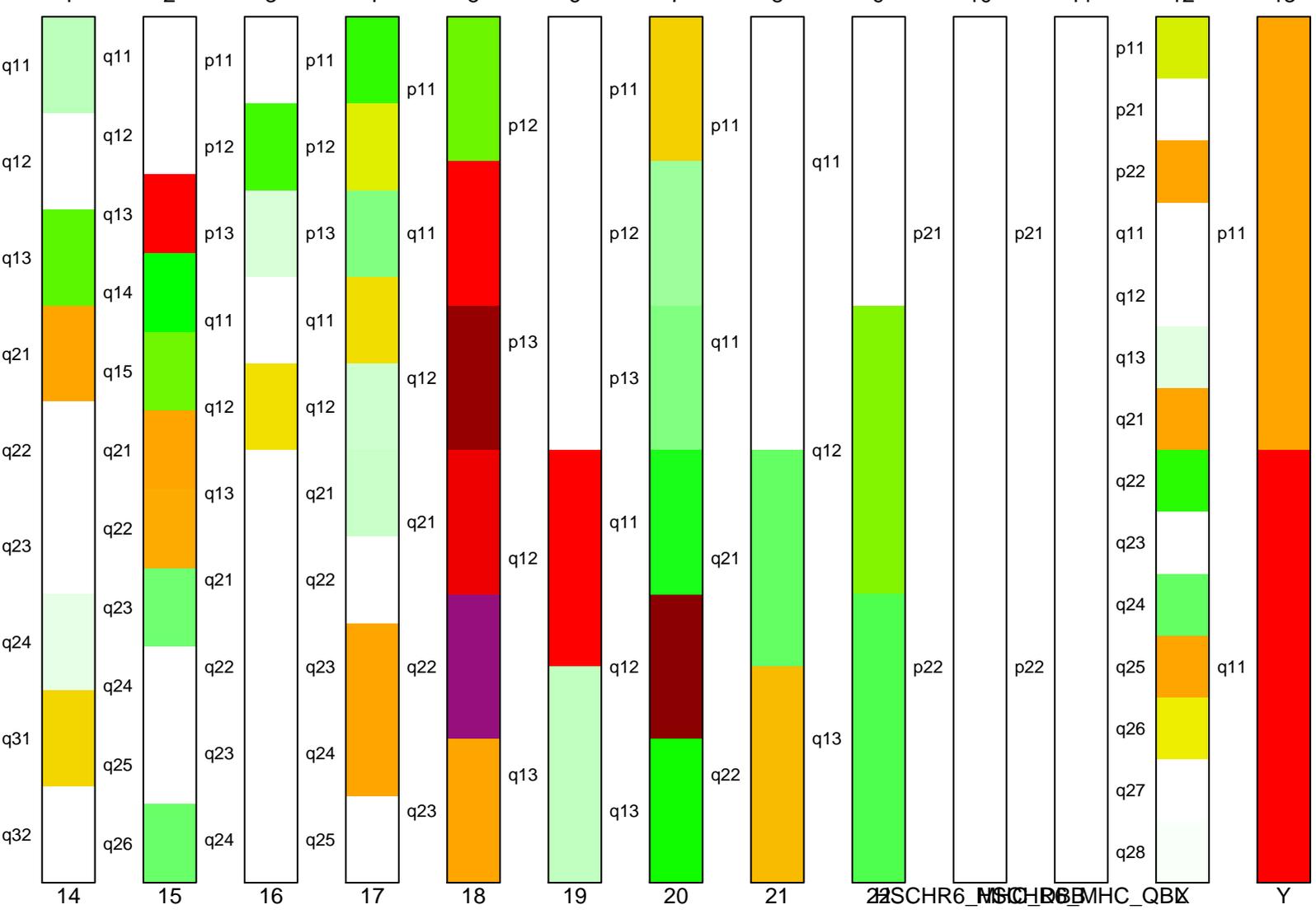
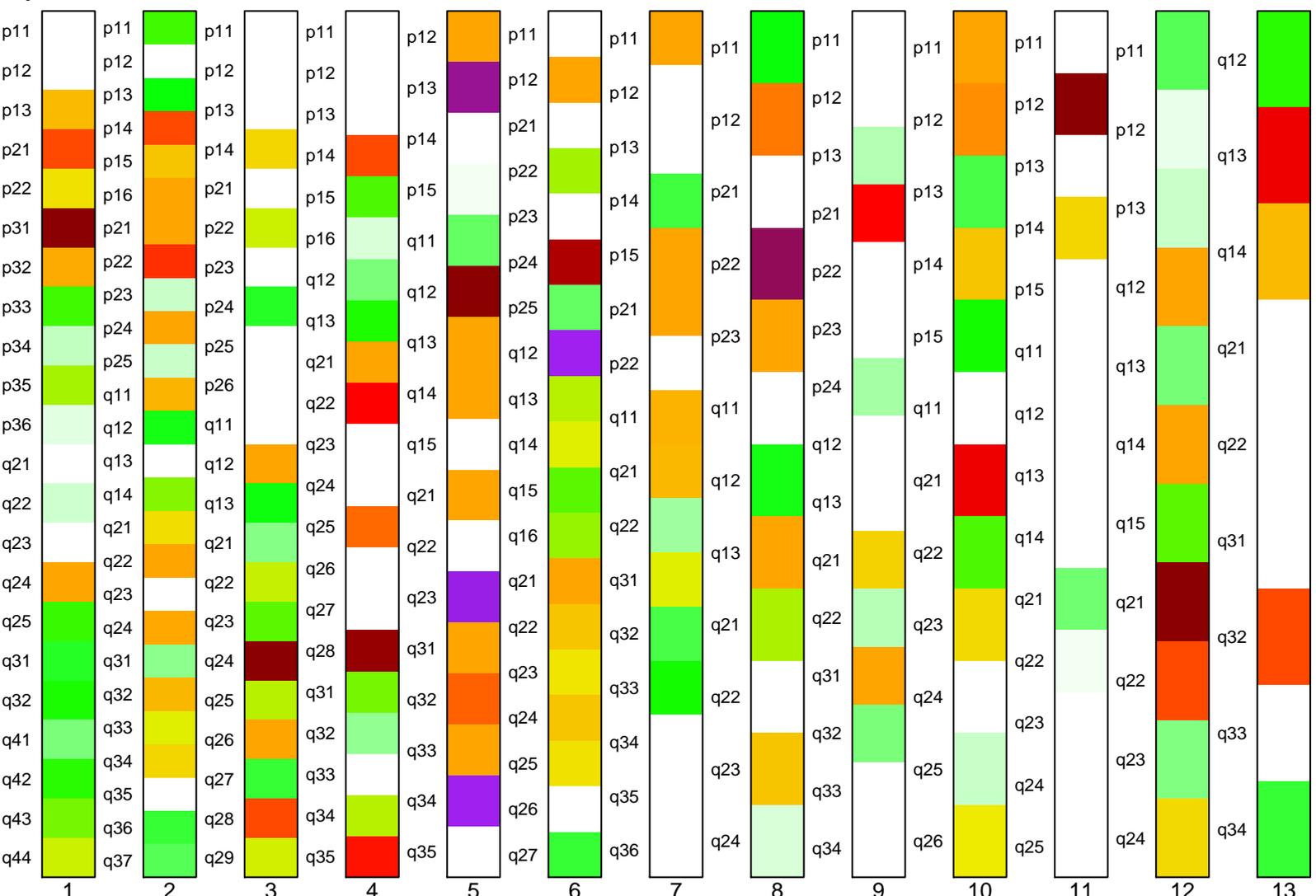
Spot B



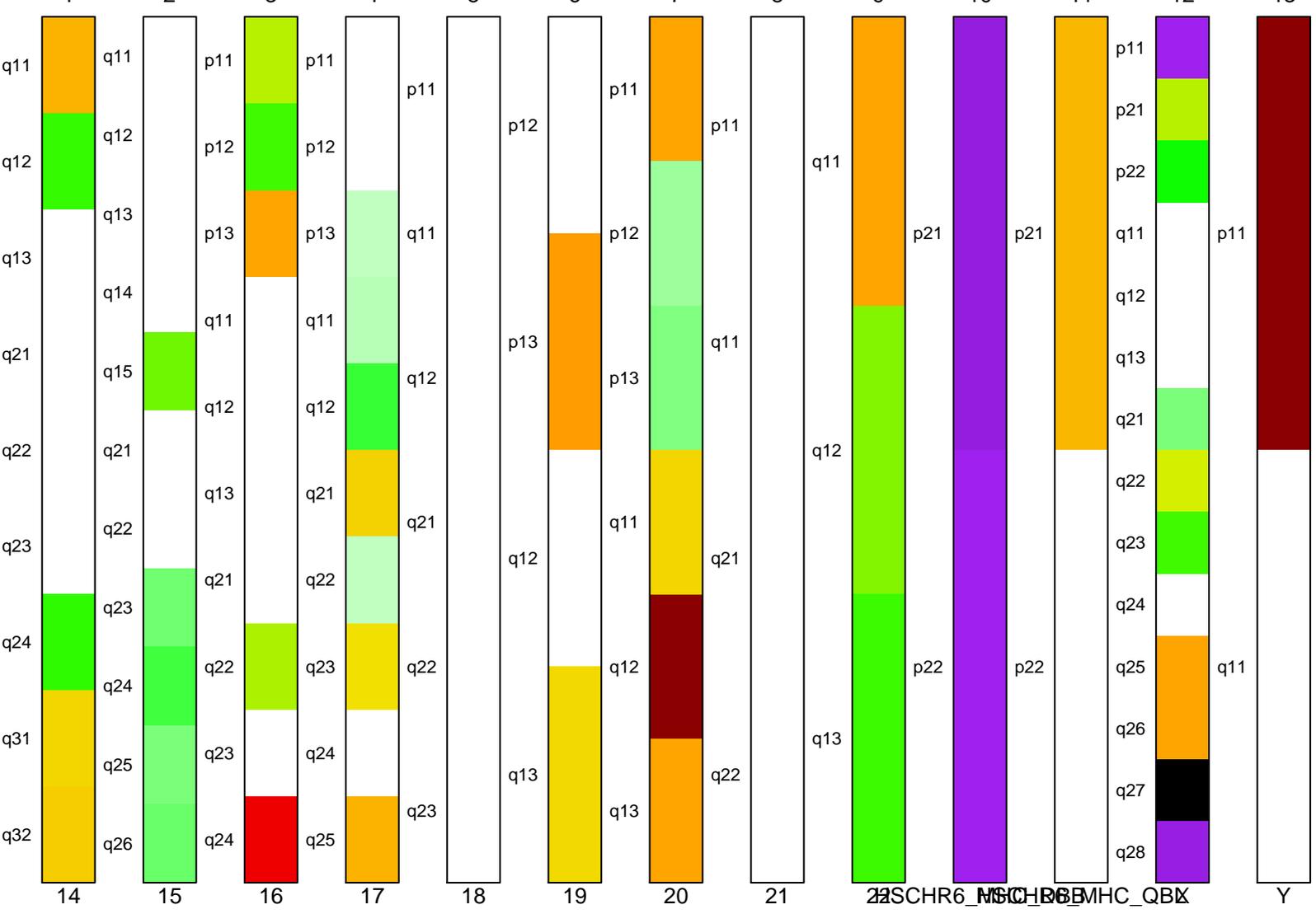
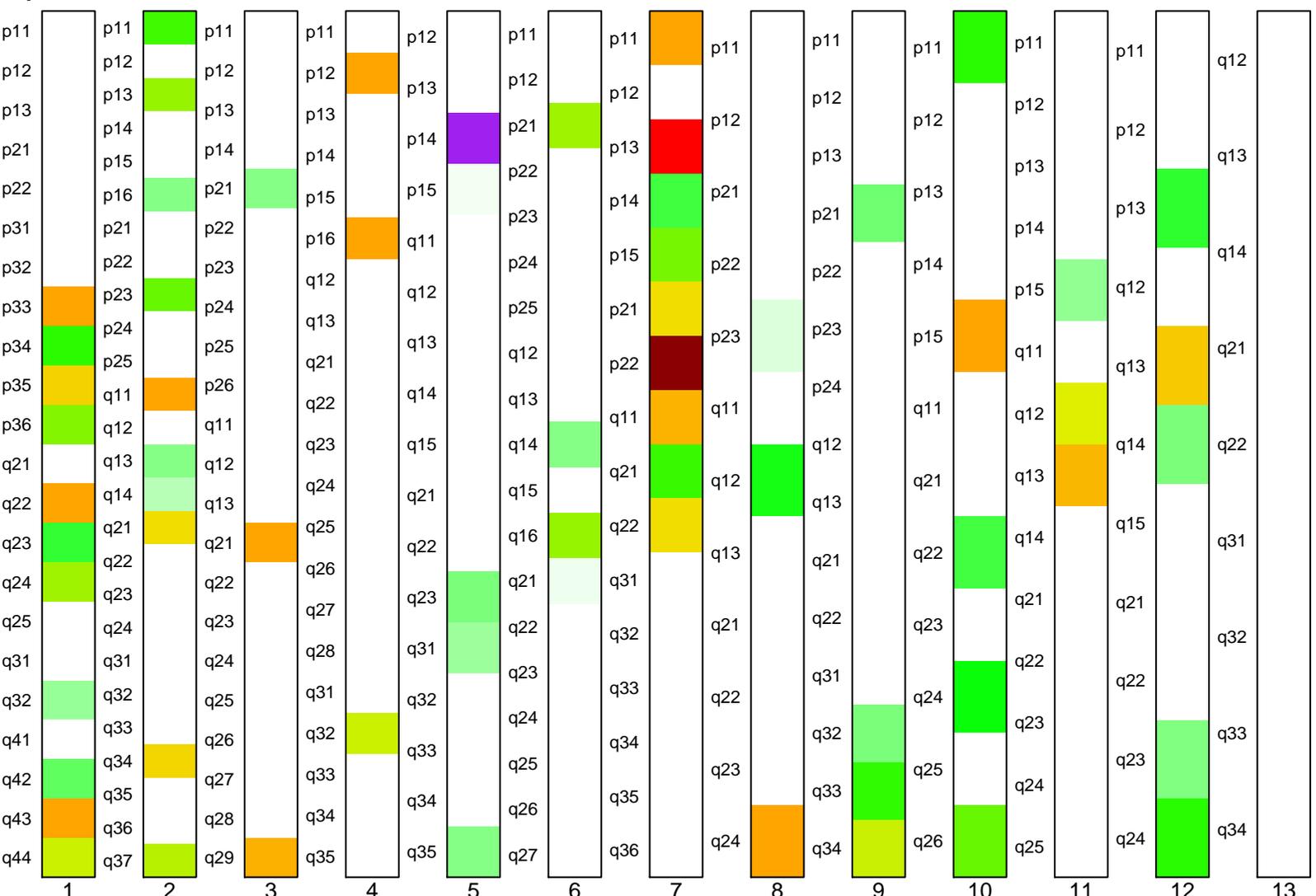
Spot C



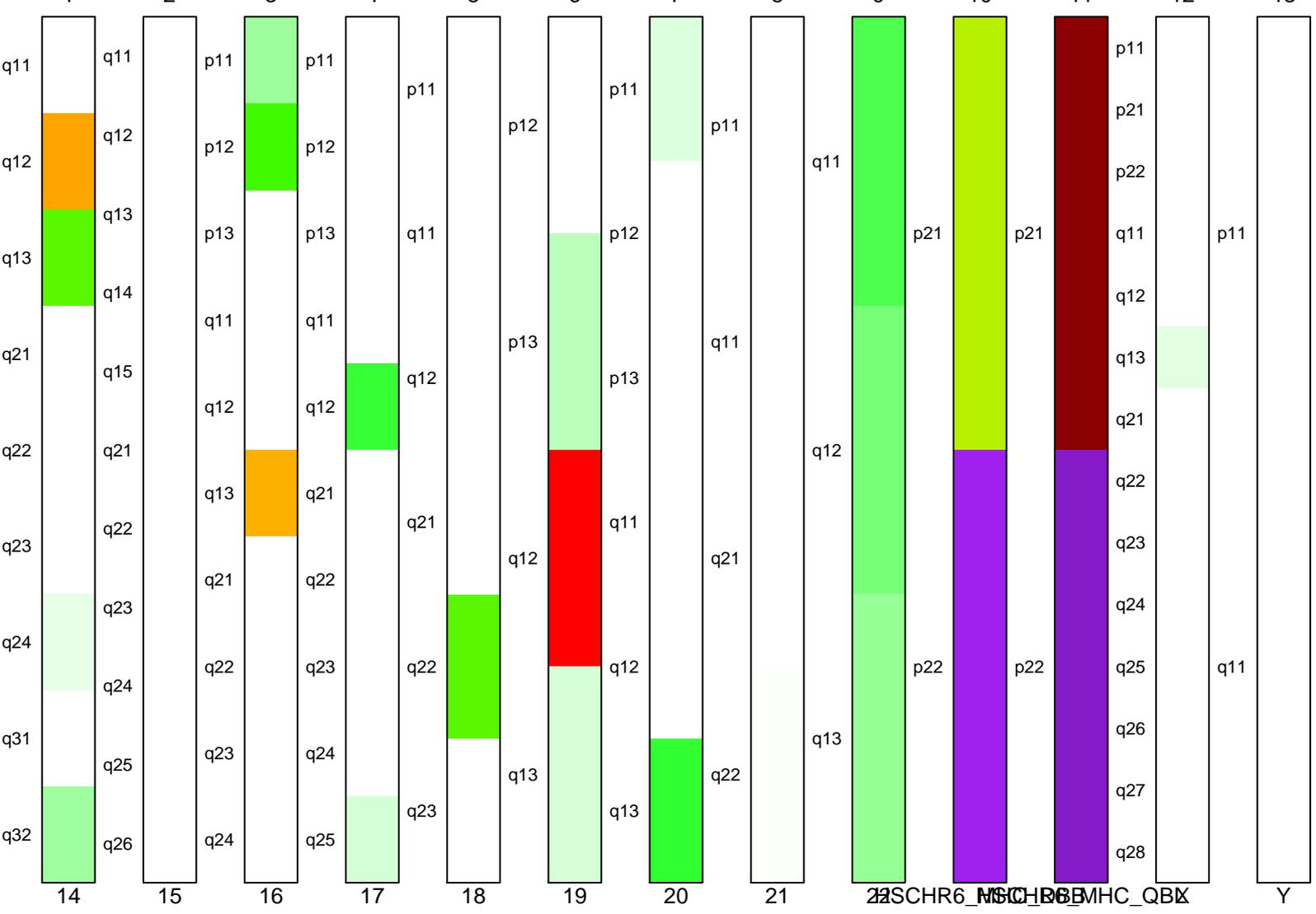
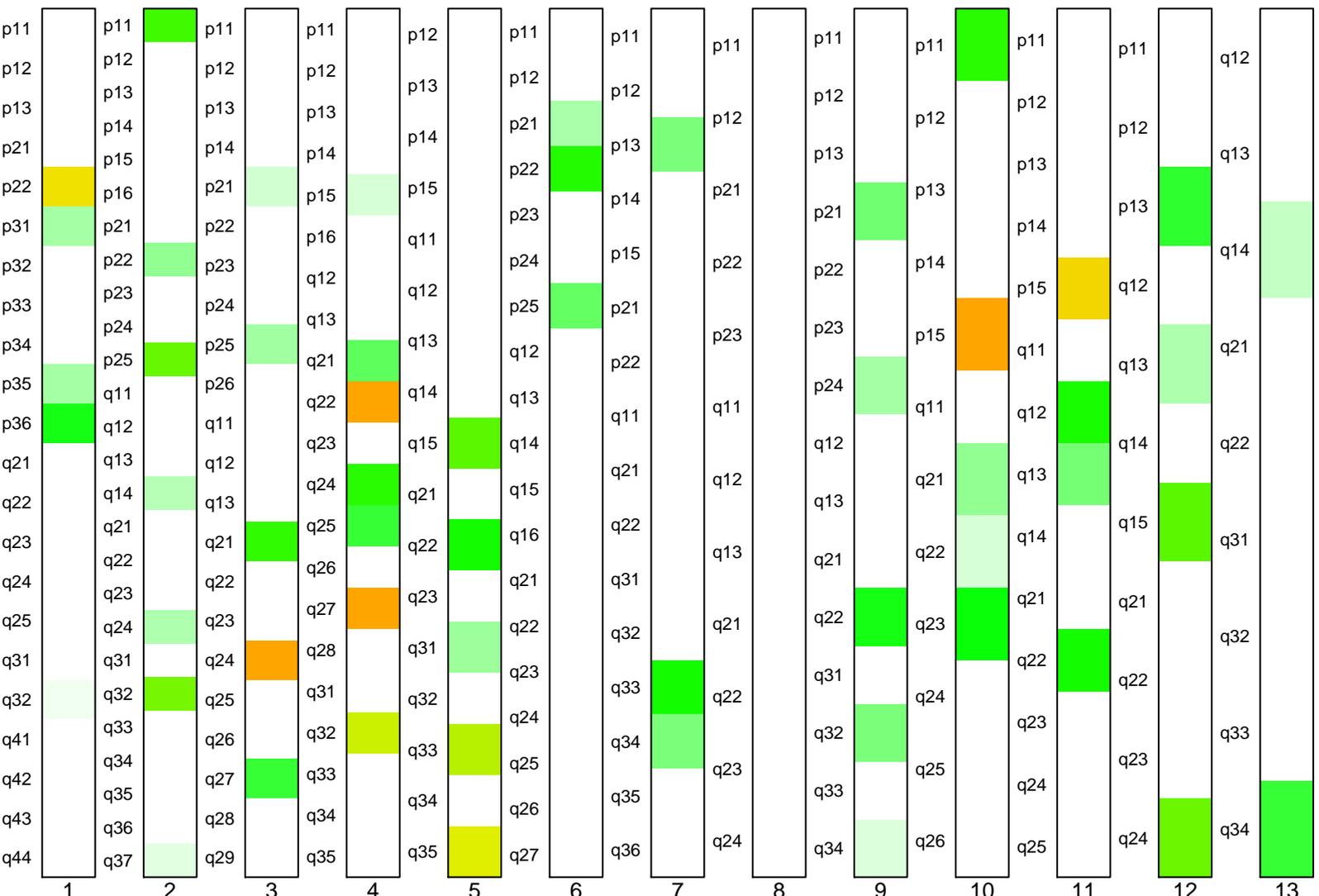
Spot D



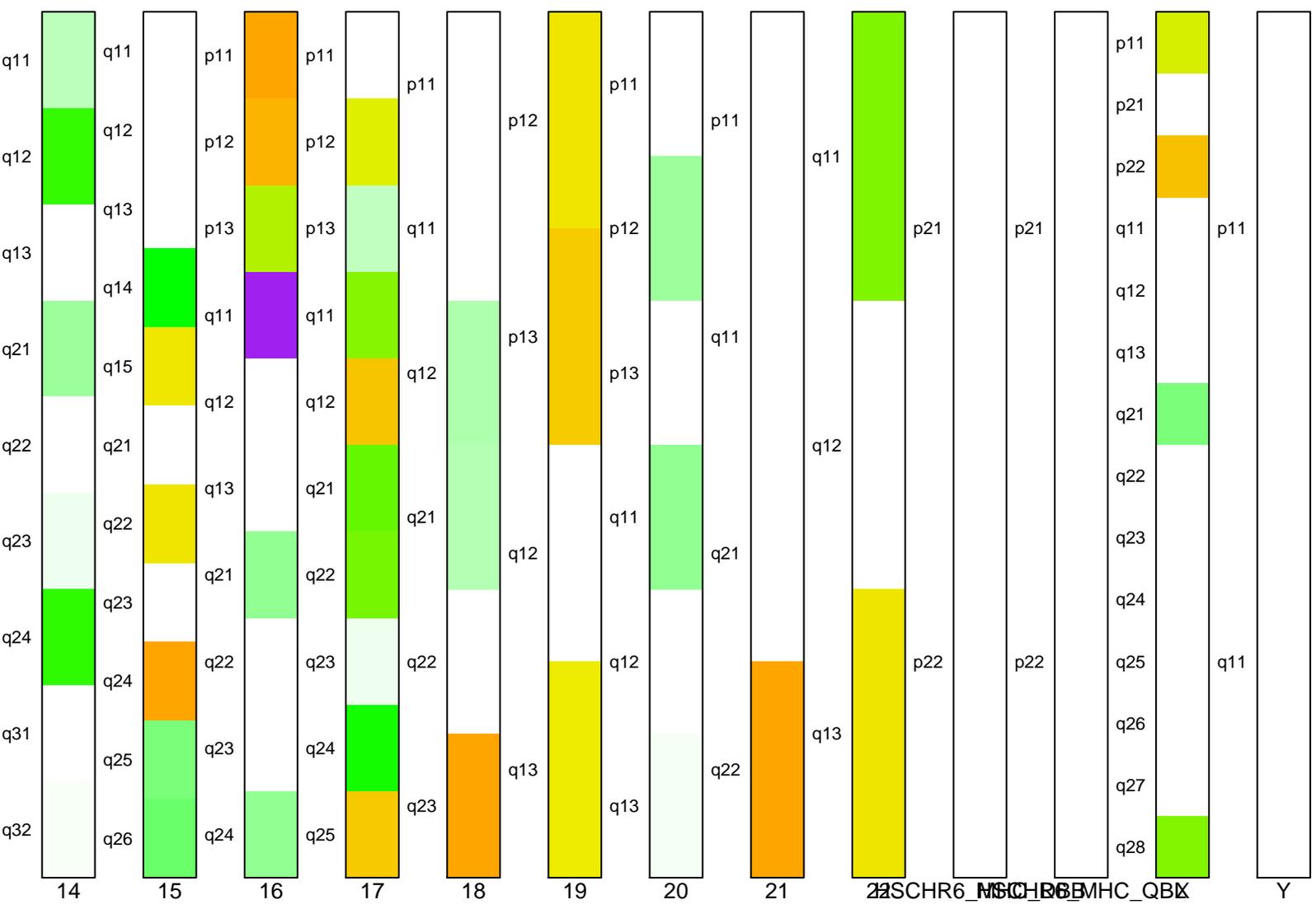
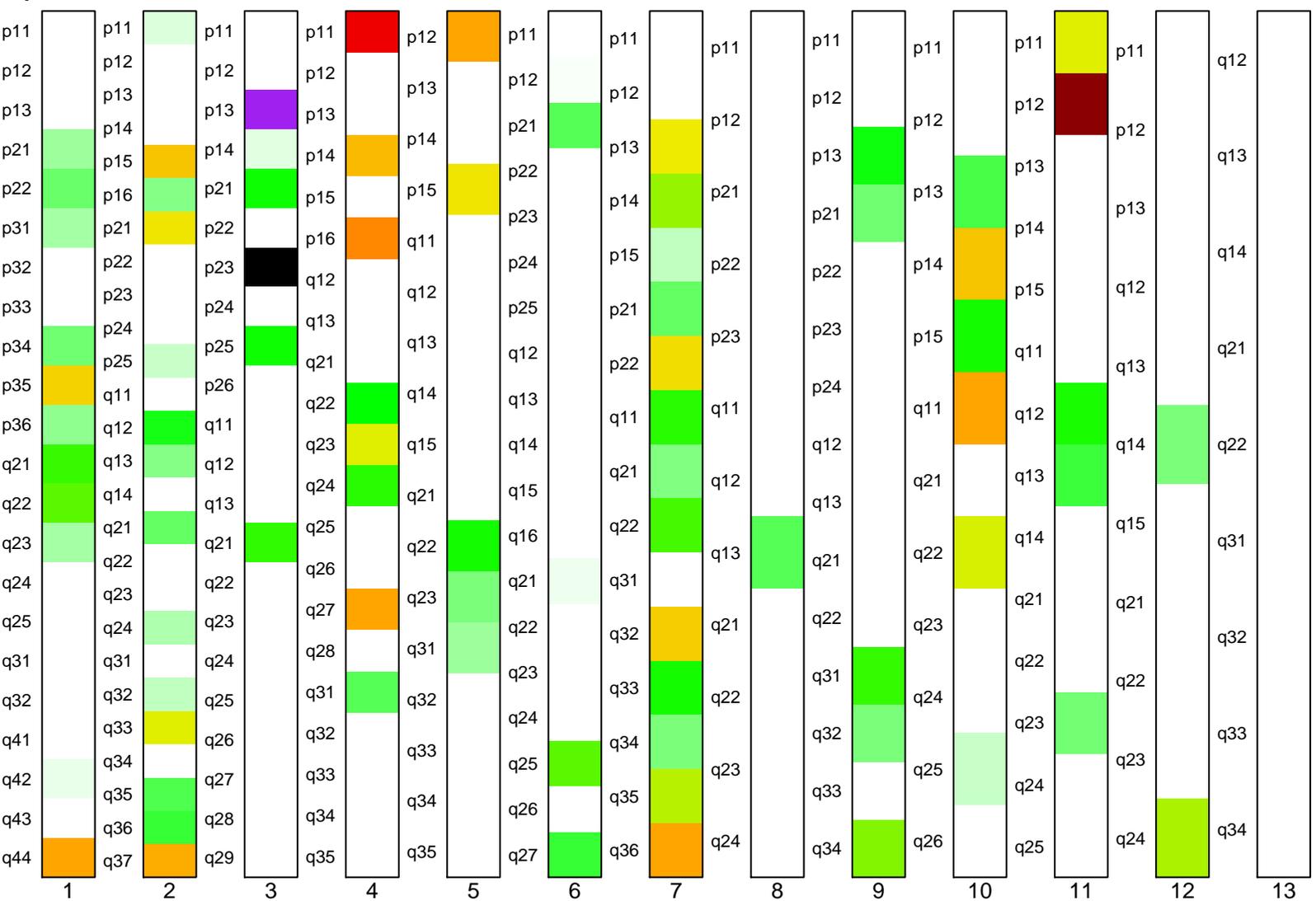
Spot E



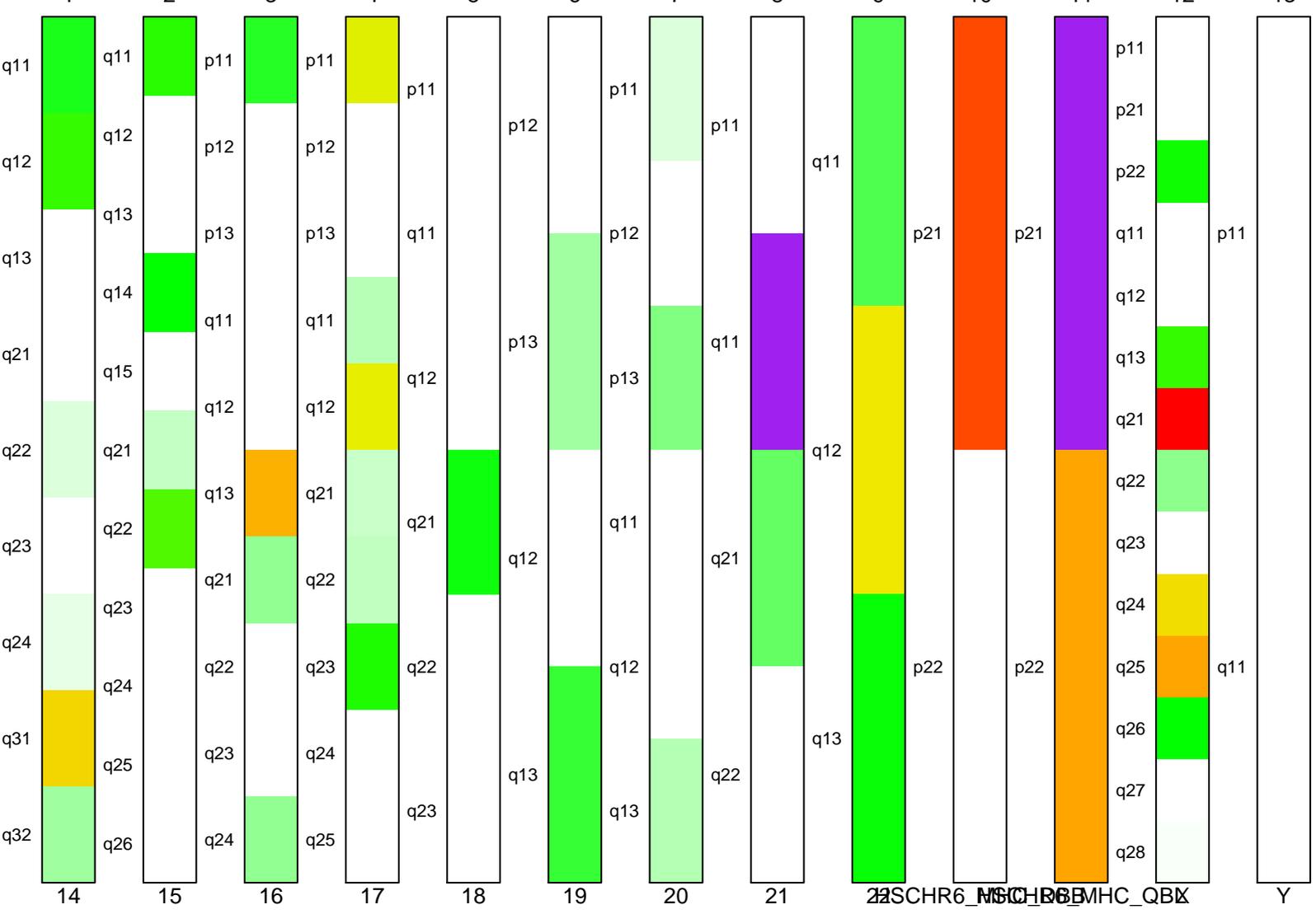
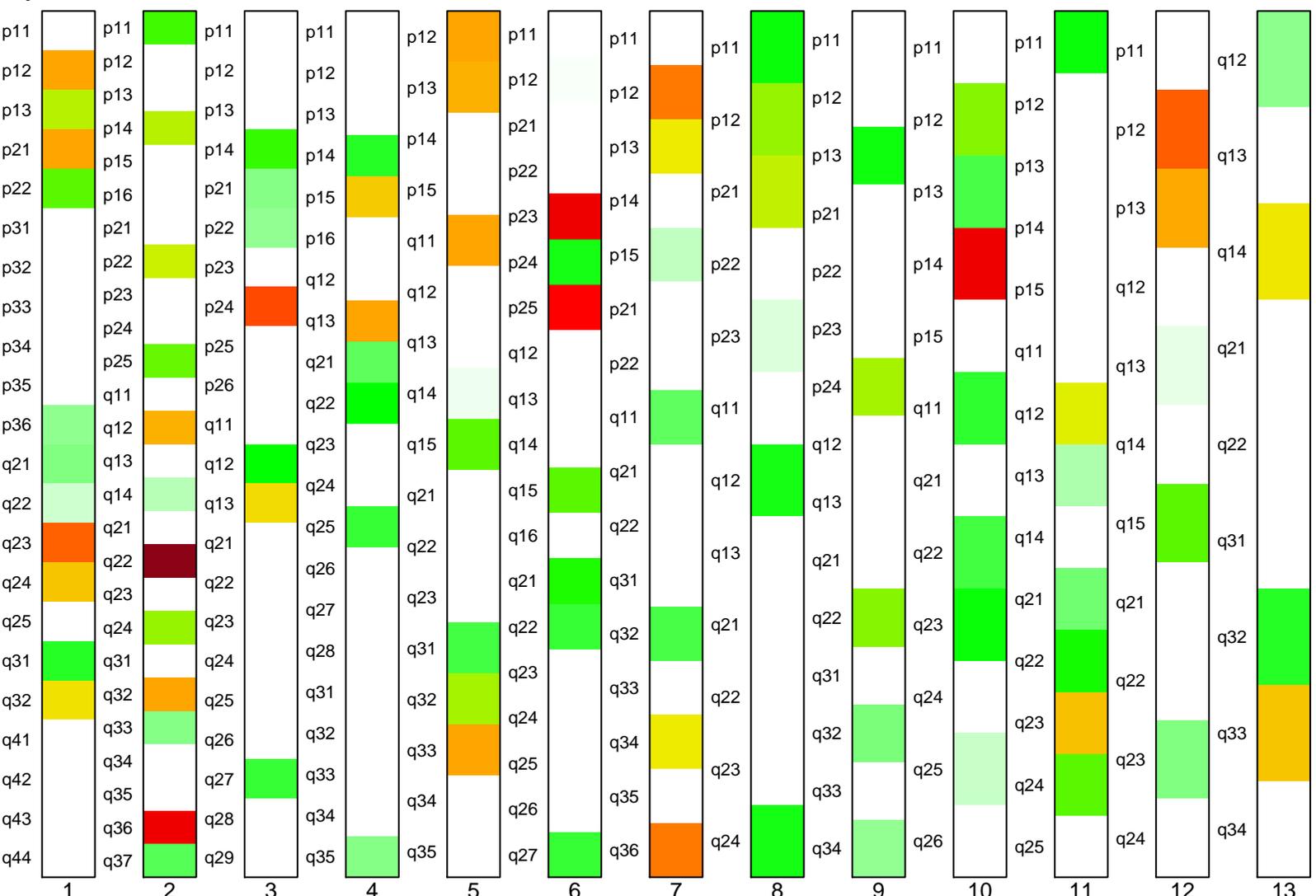
Spot F



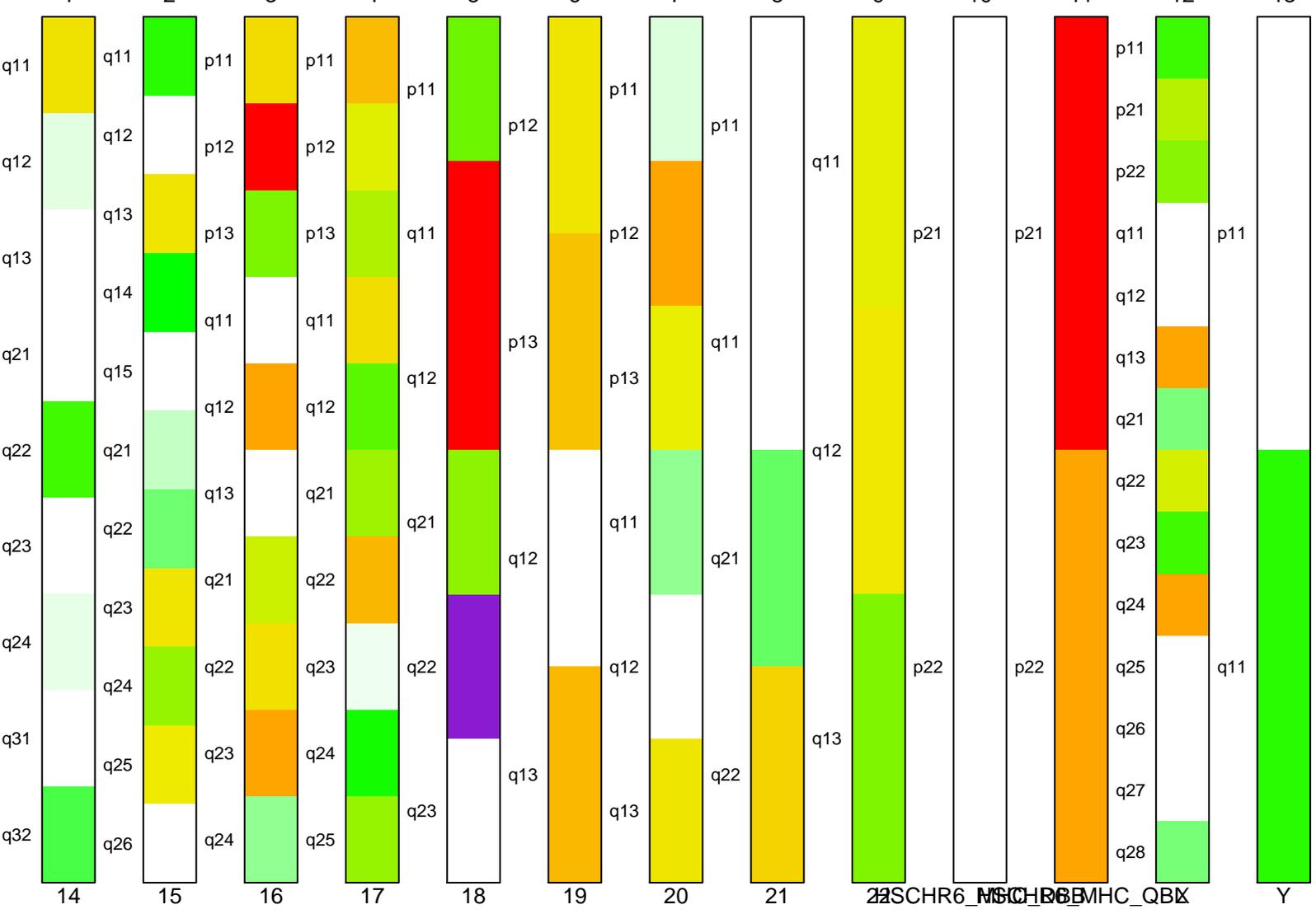
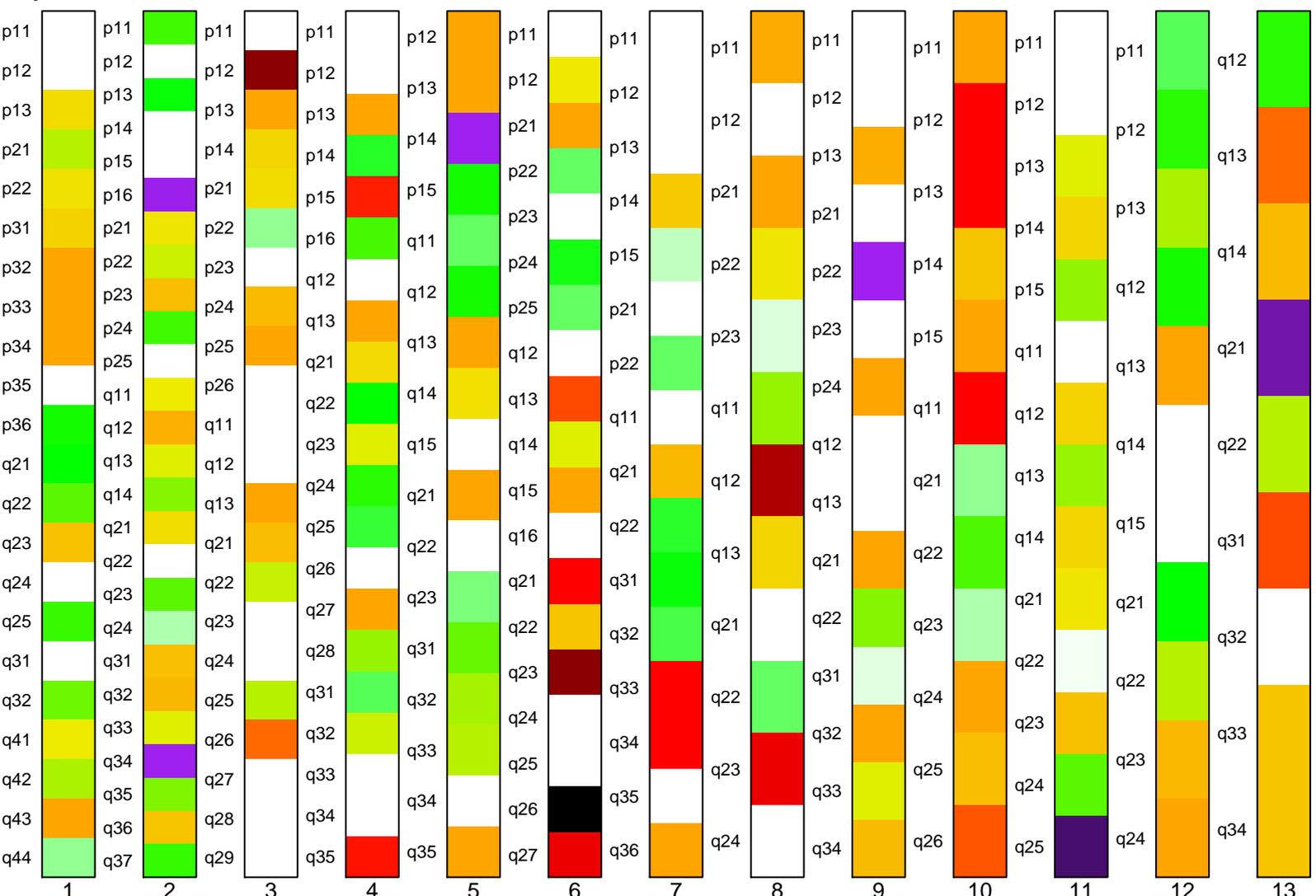
Spot G



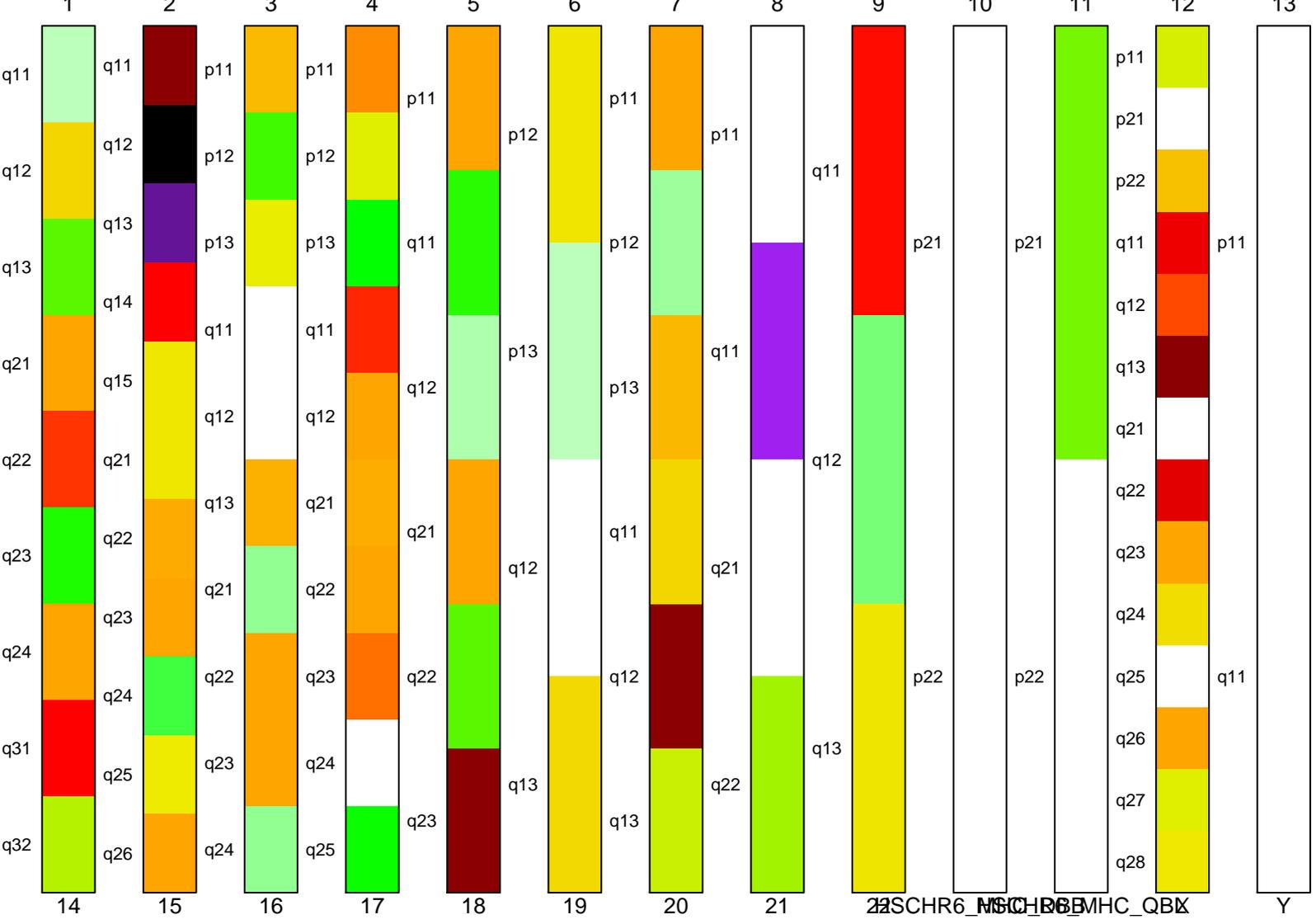
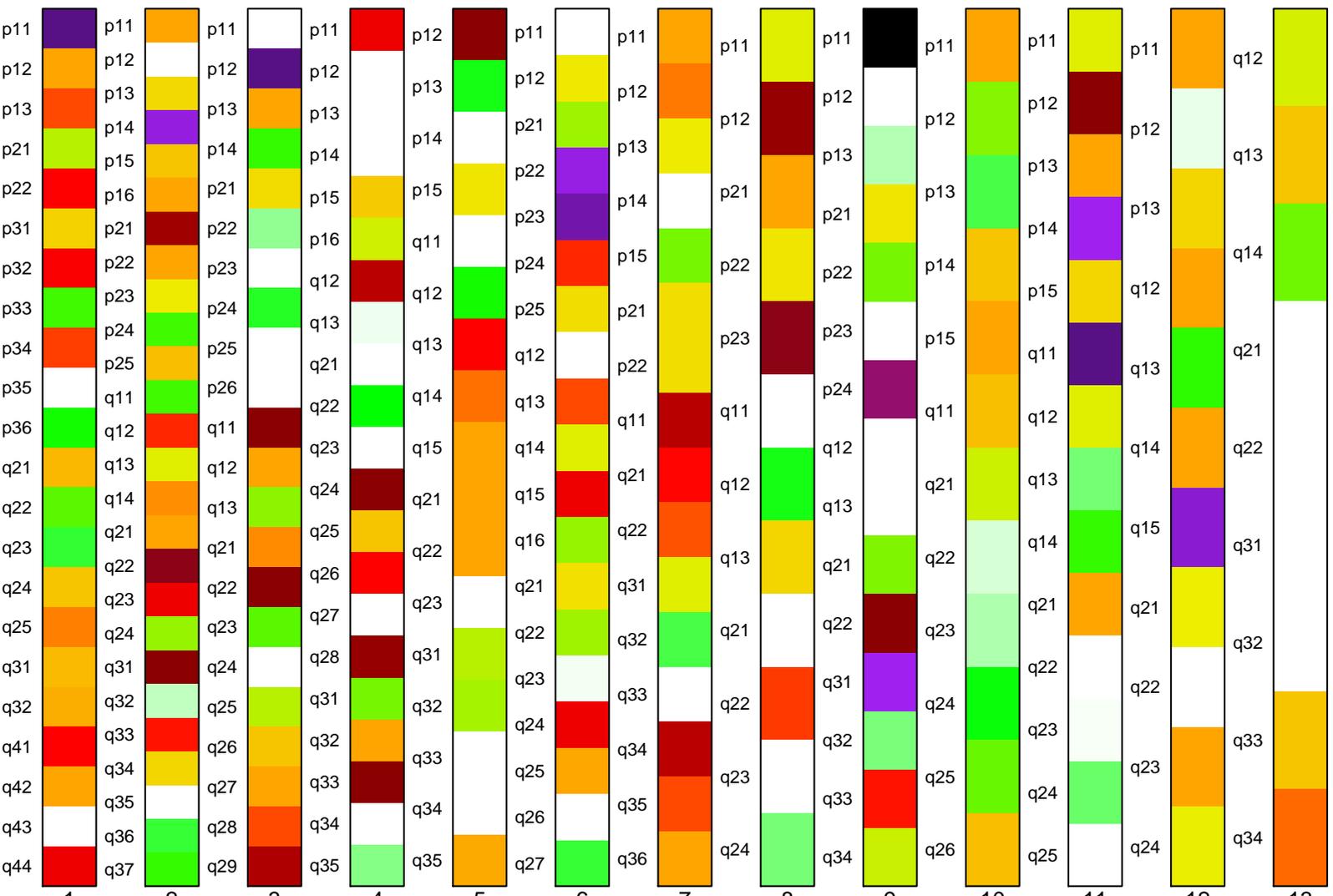
Spot H



Spot I

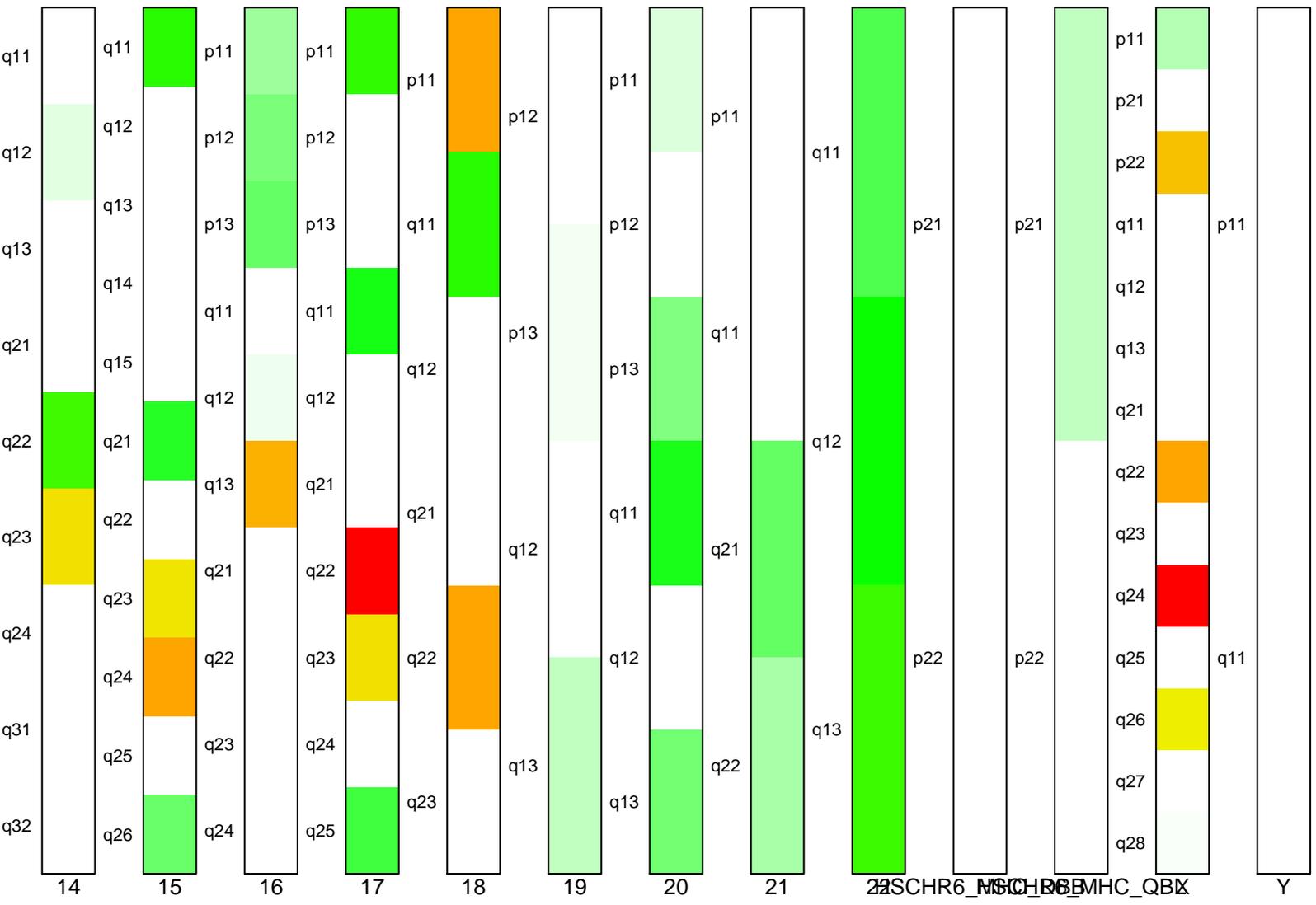
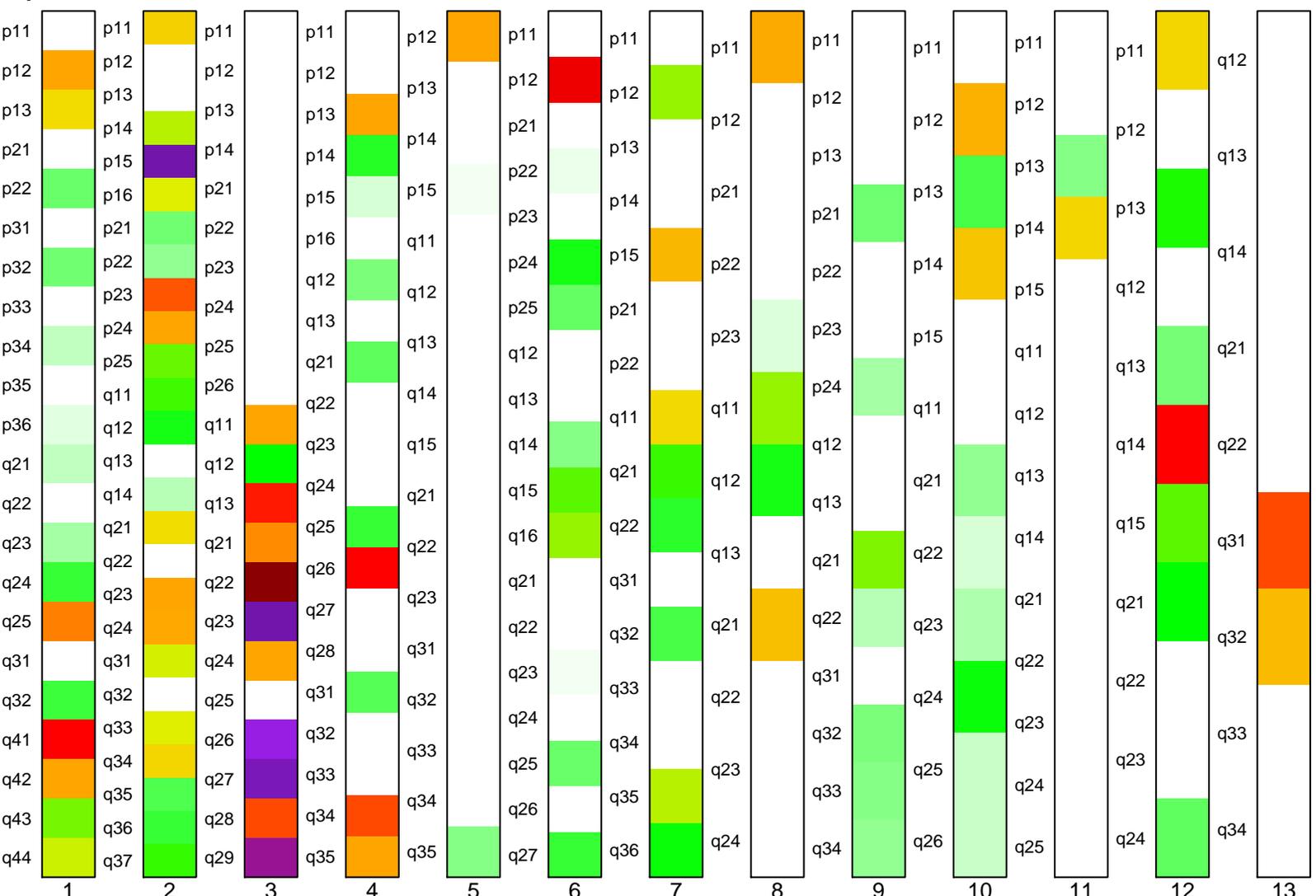


Spot J

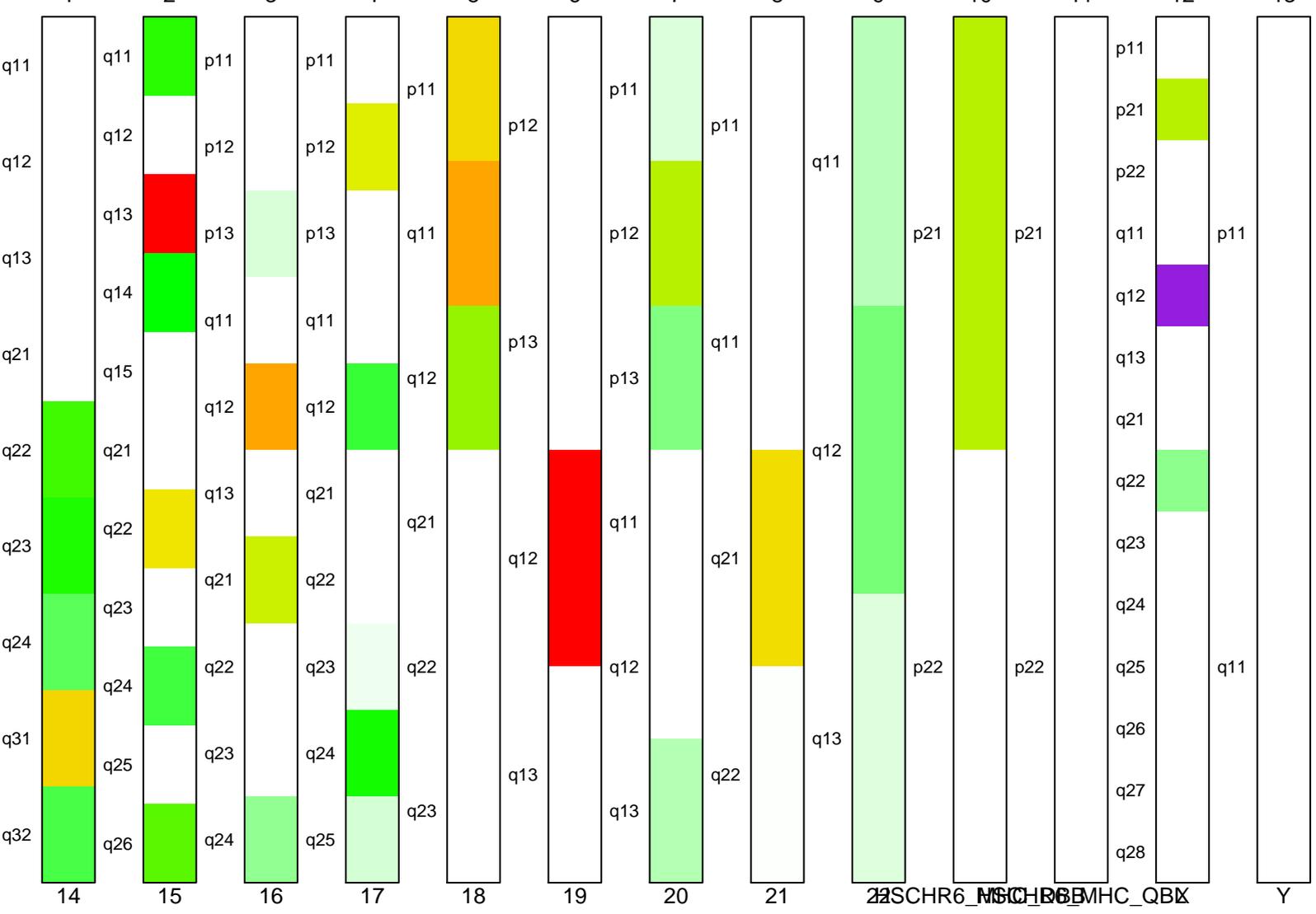
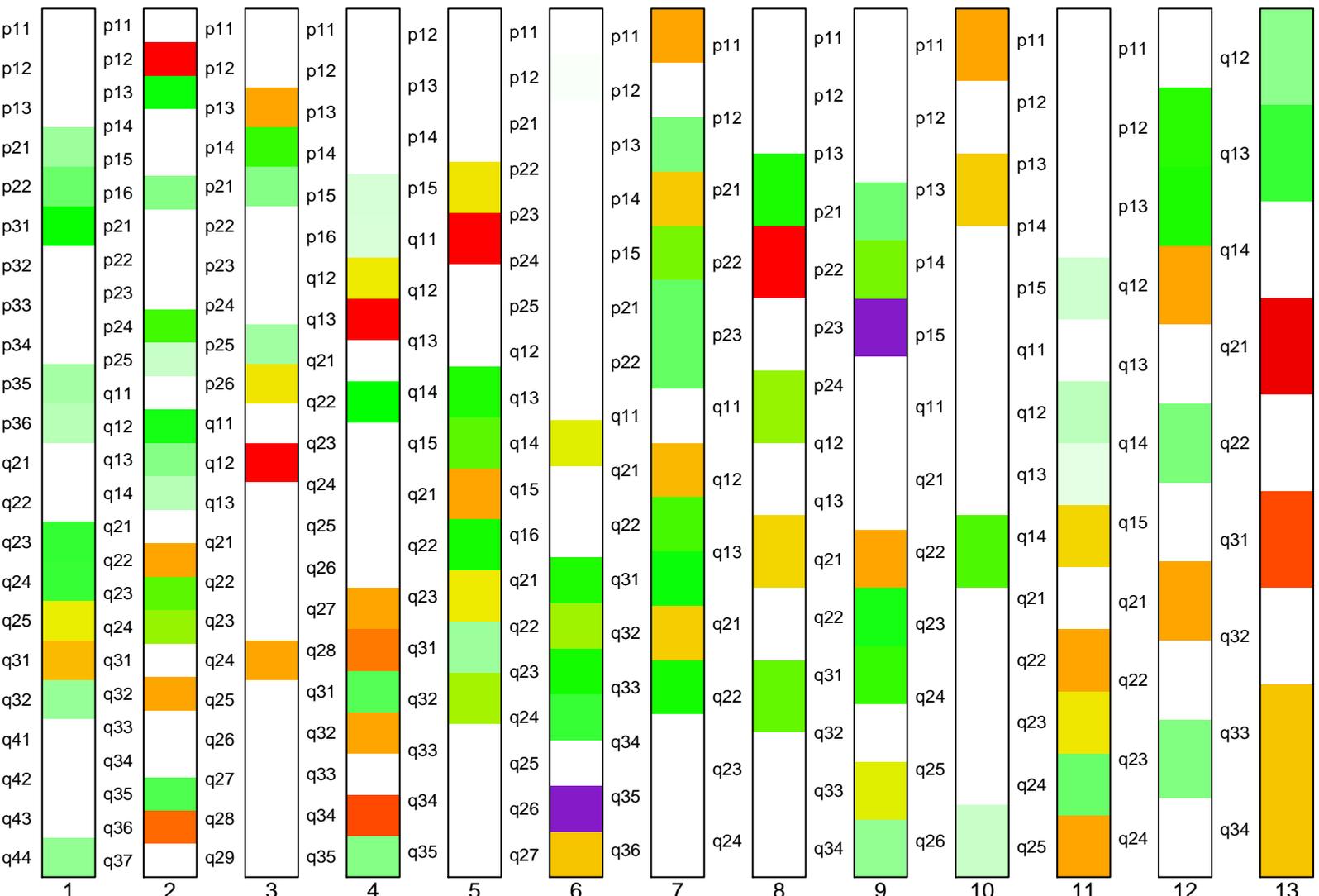


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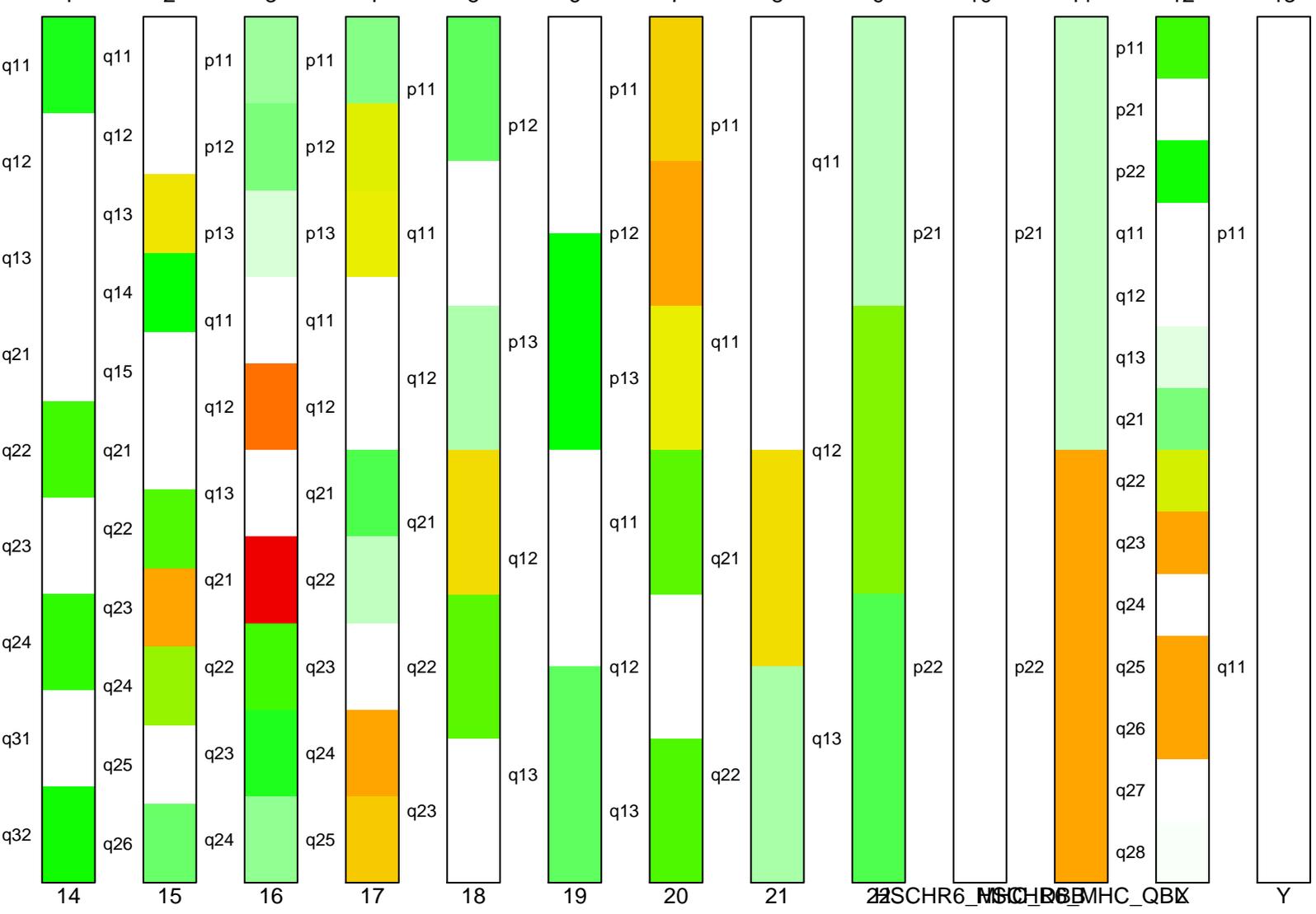
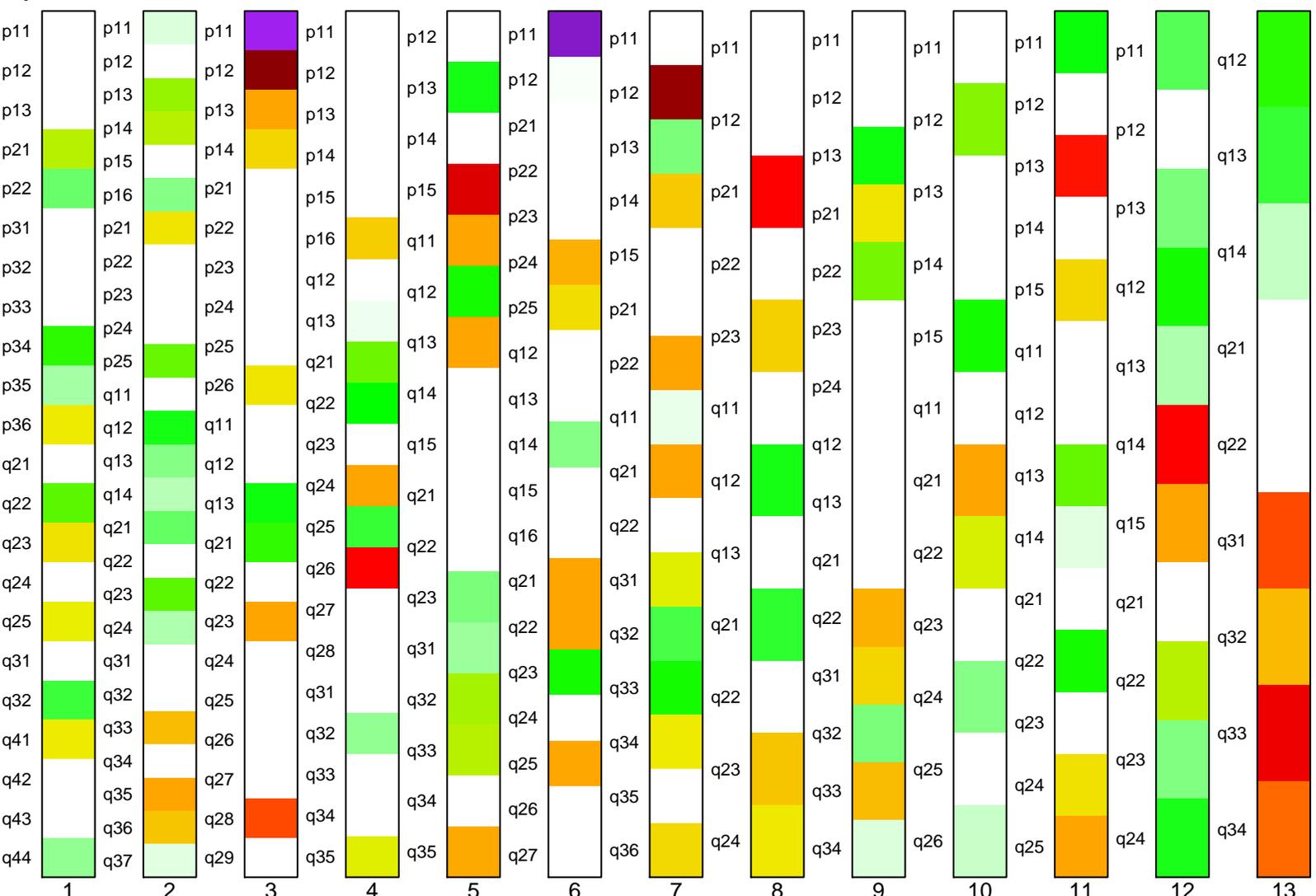
Spot K



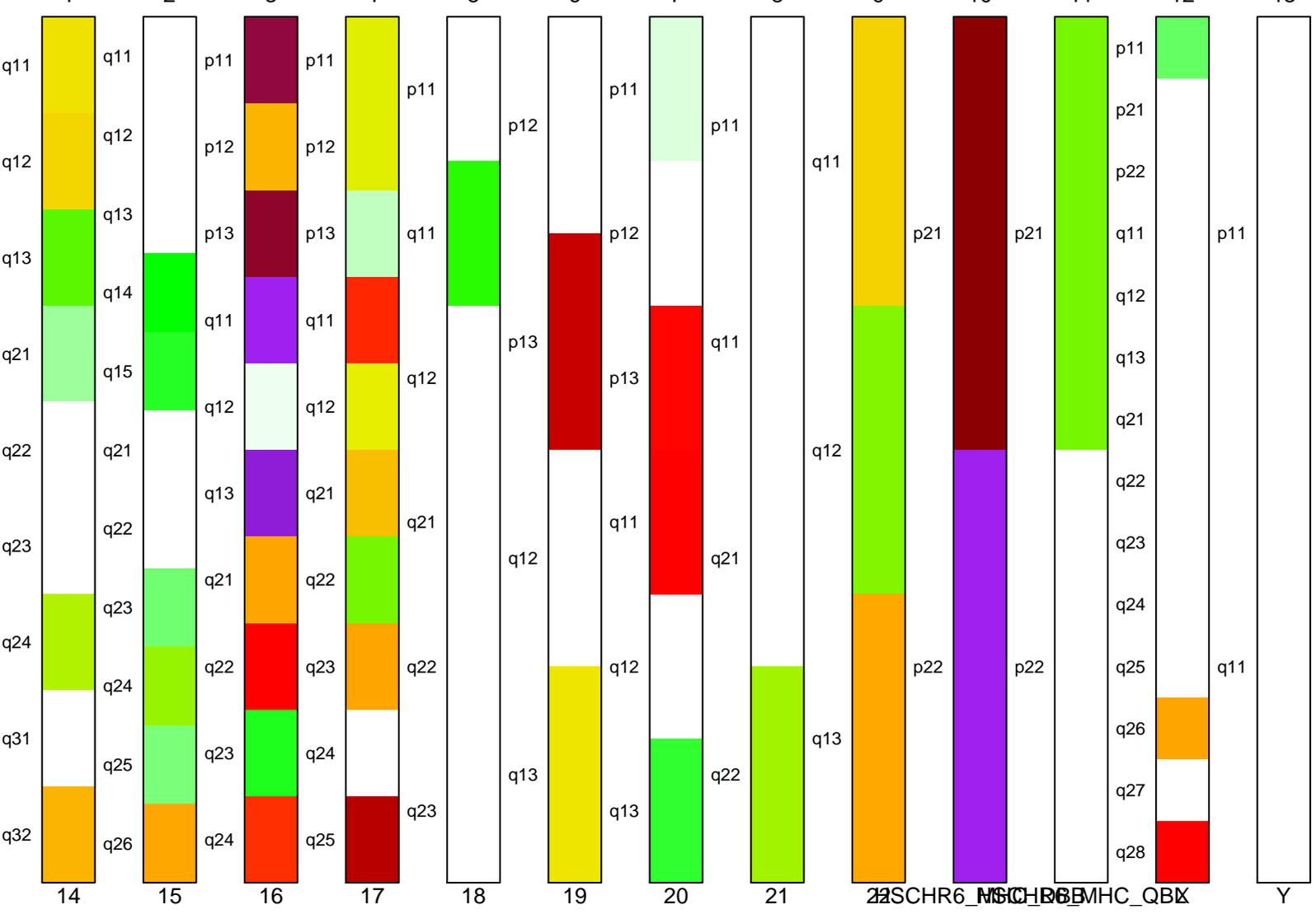
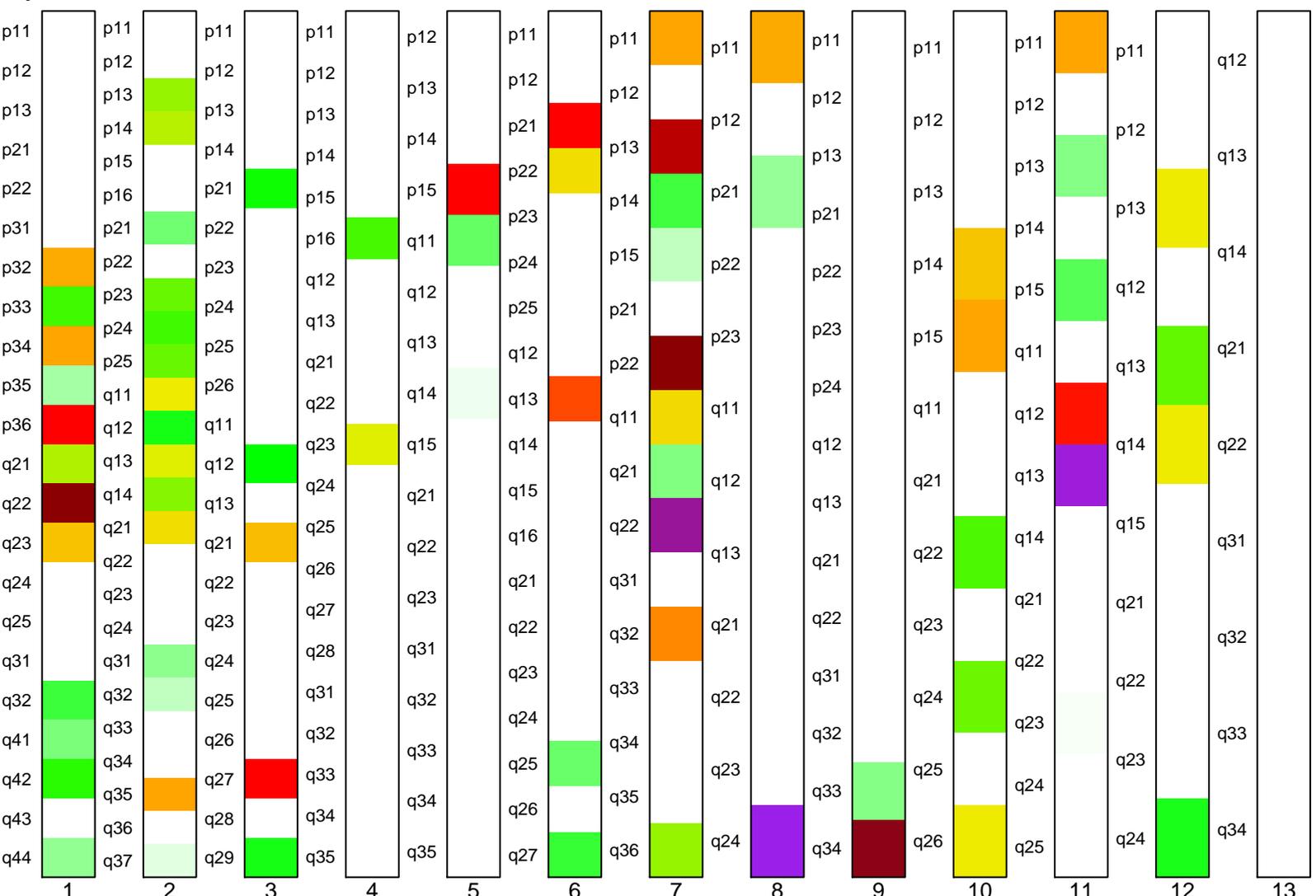
Spot L



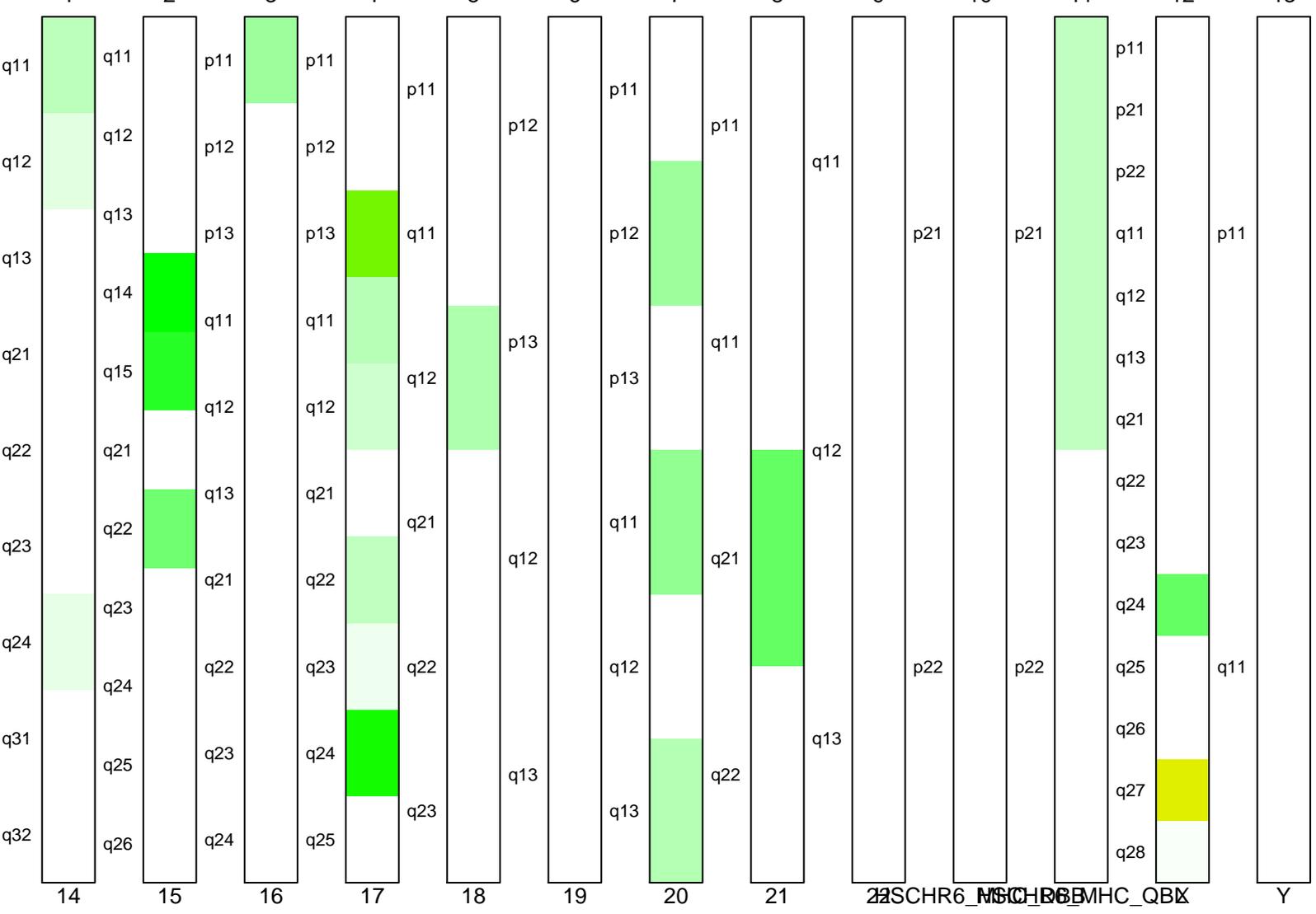
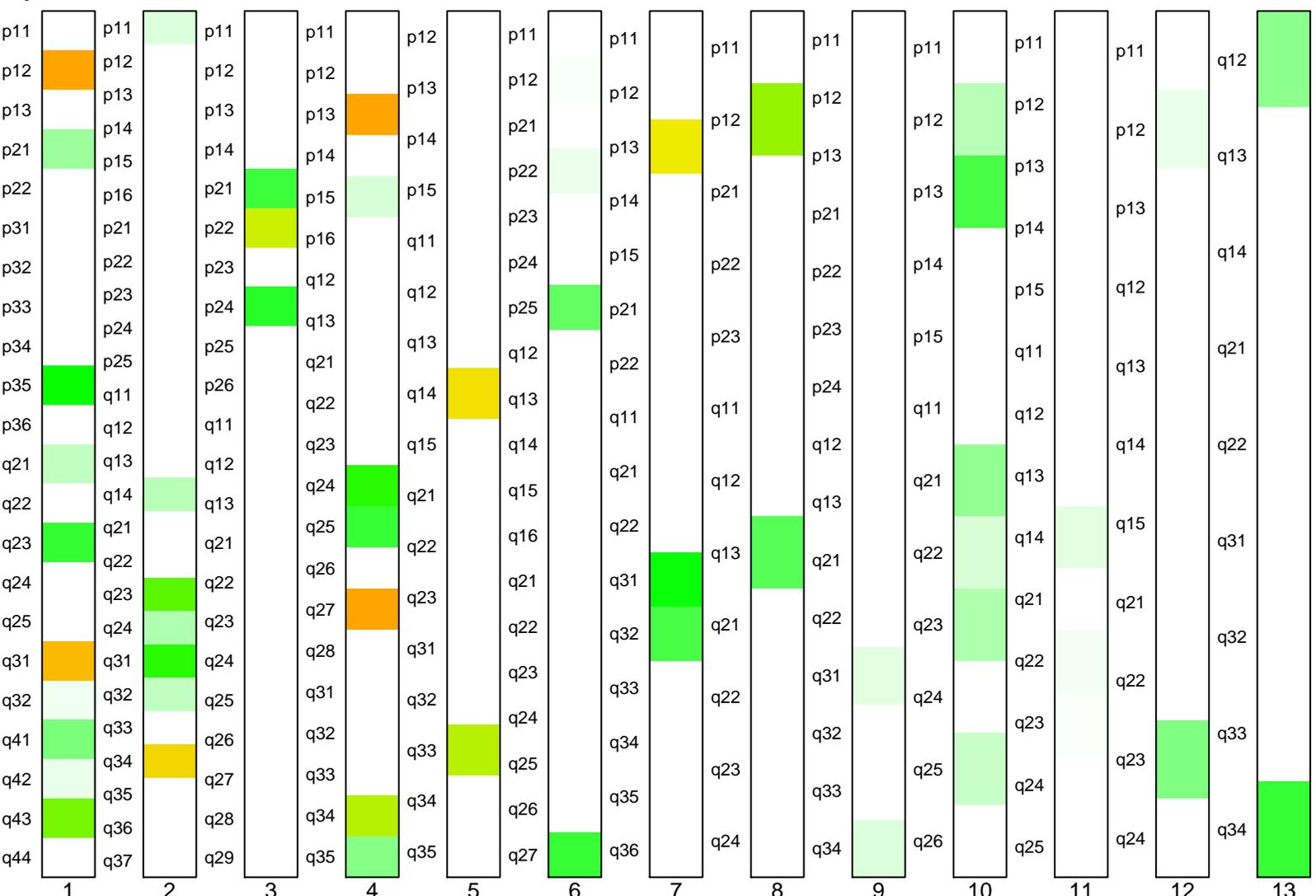
Spot M



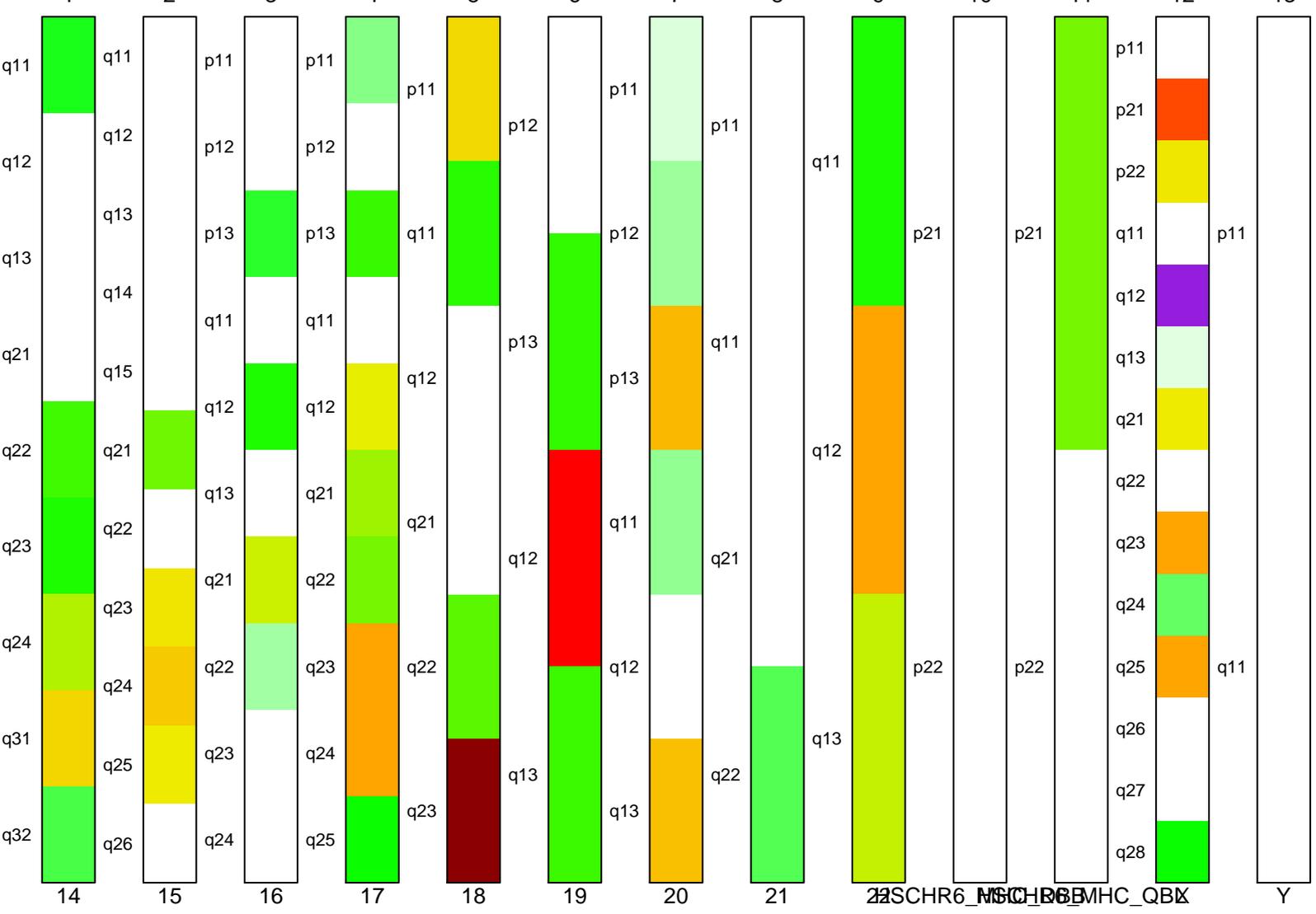
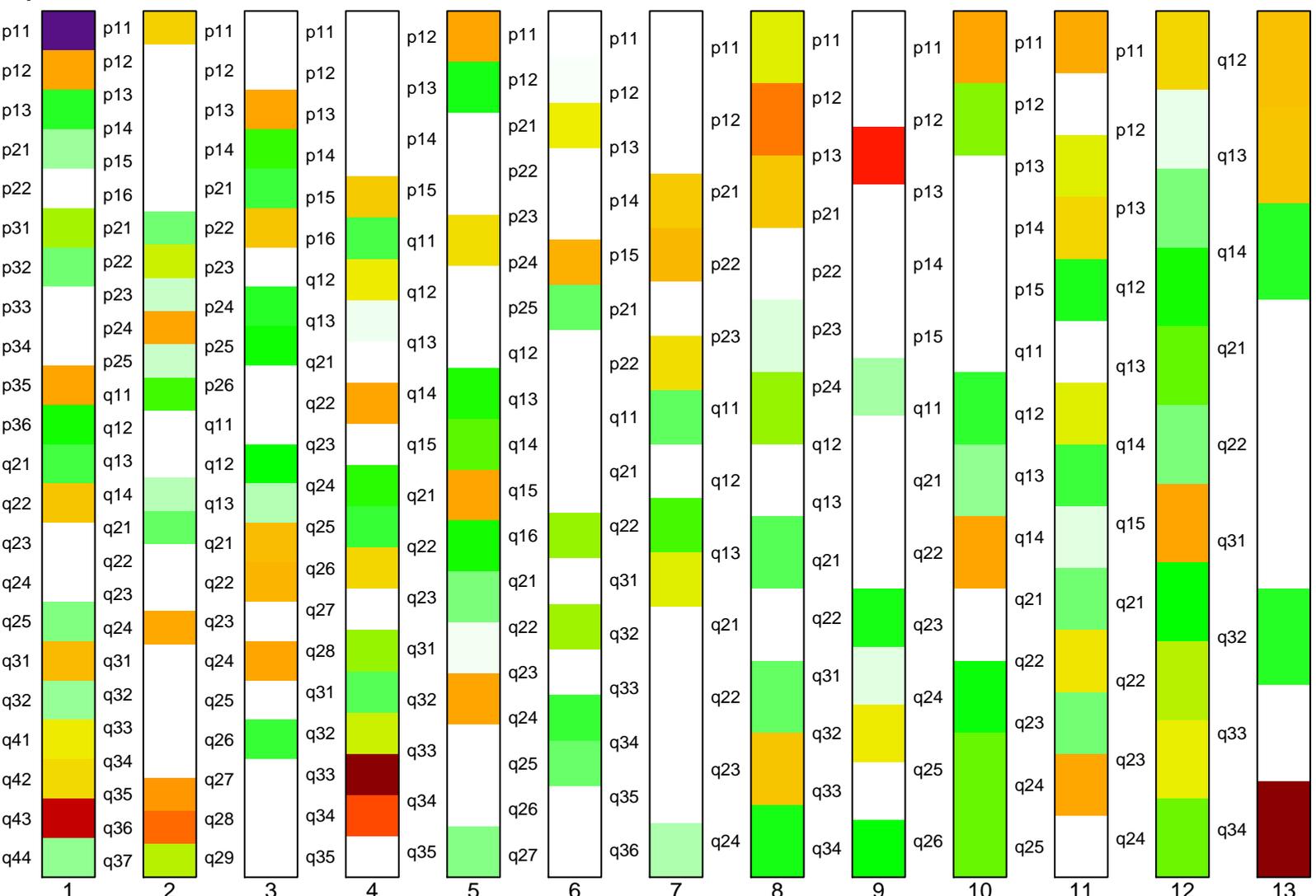
Spot N



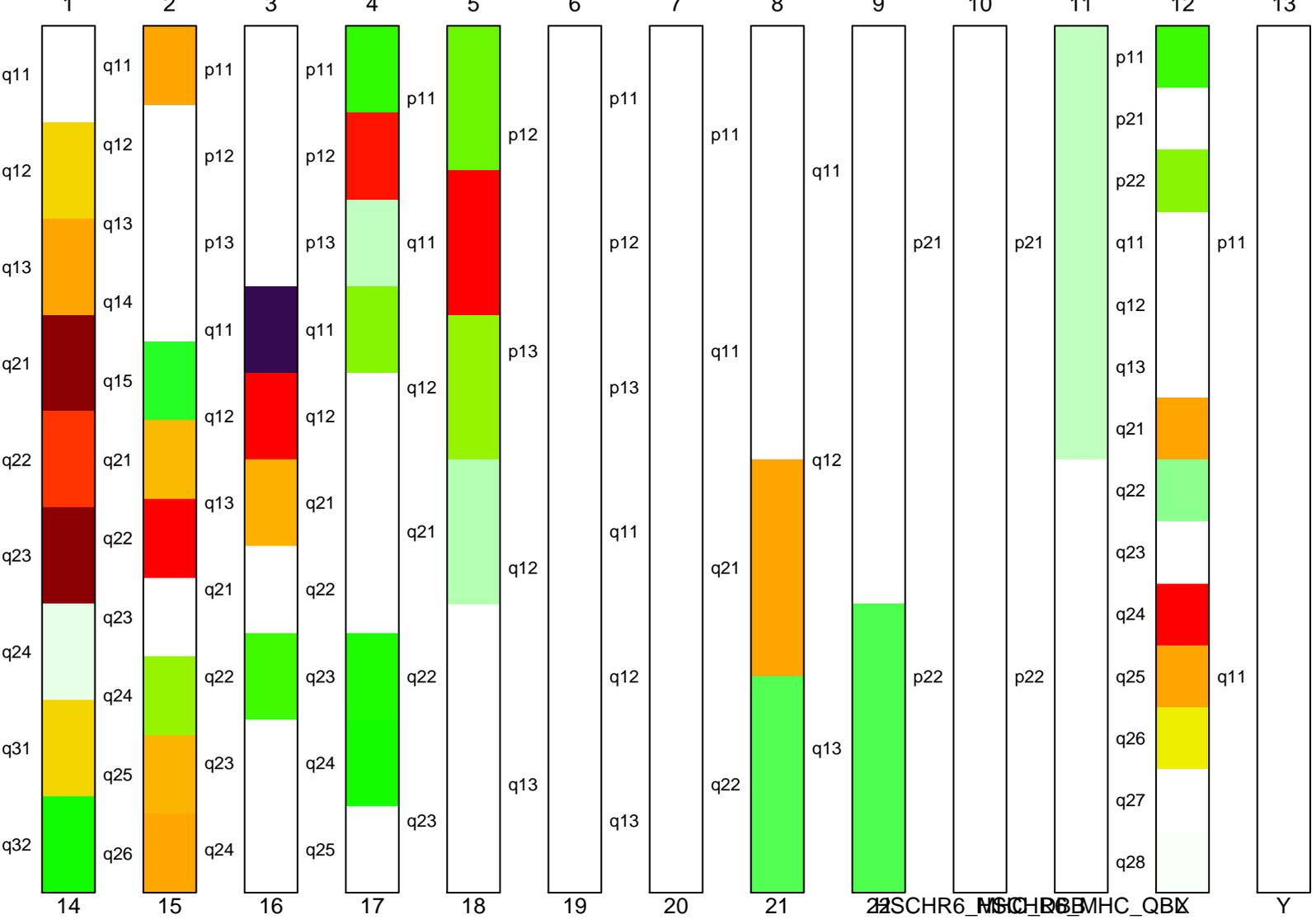
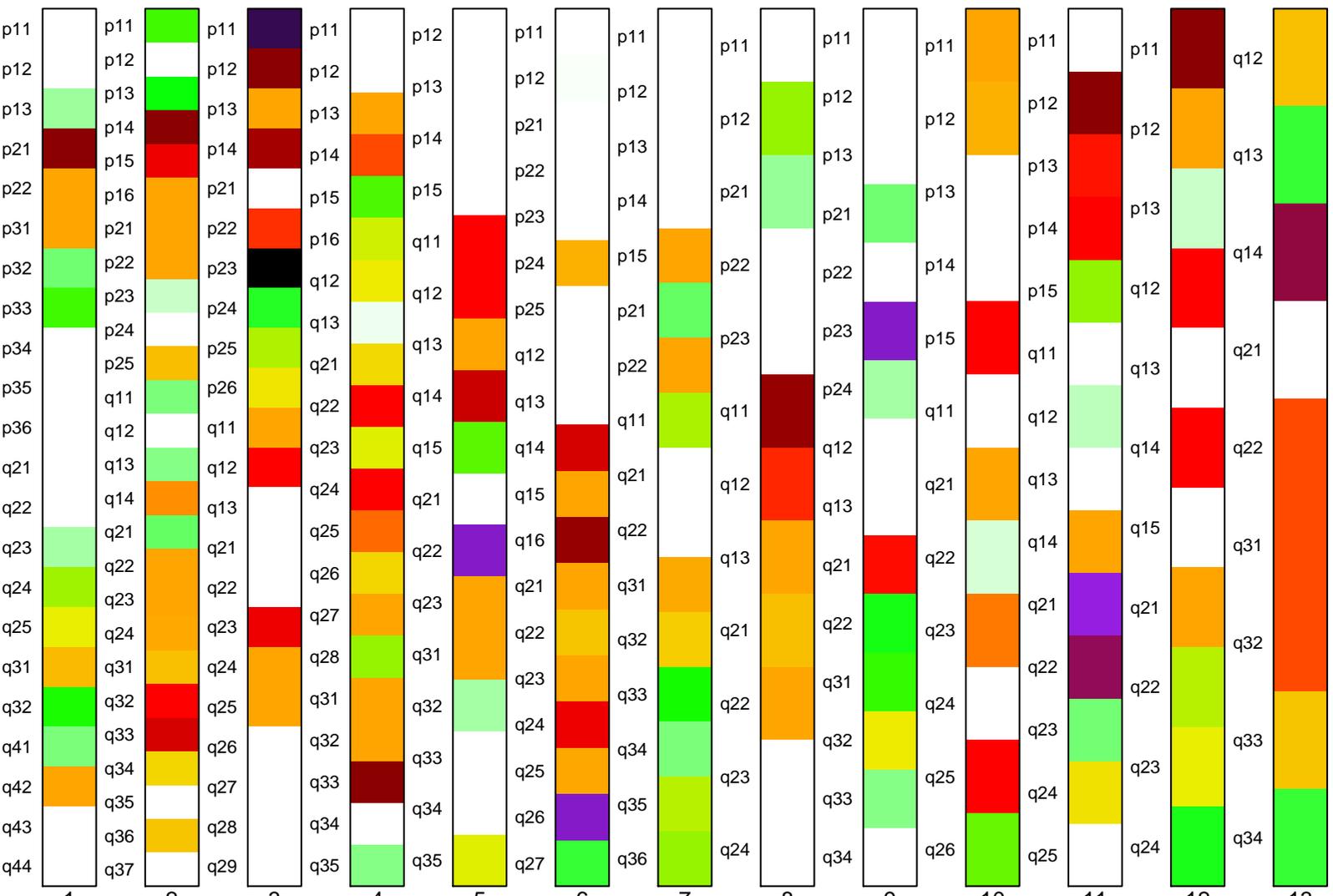
Spot O



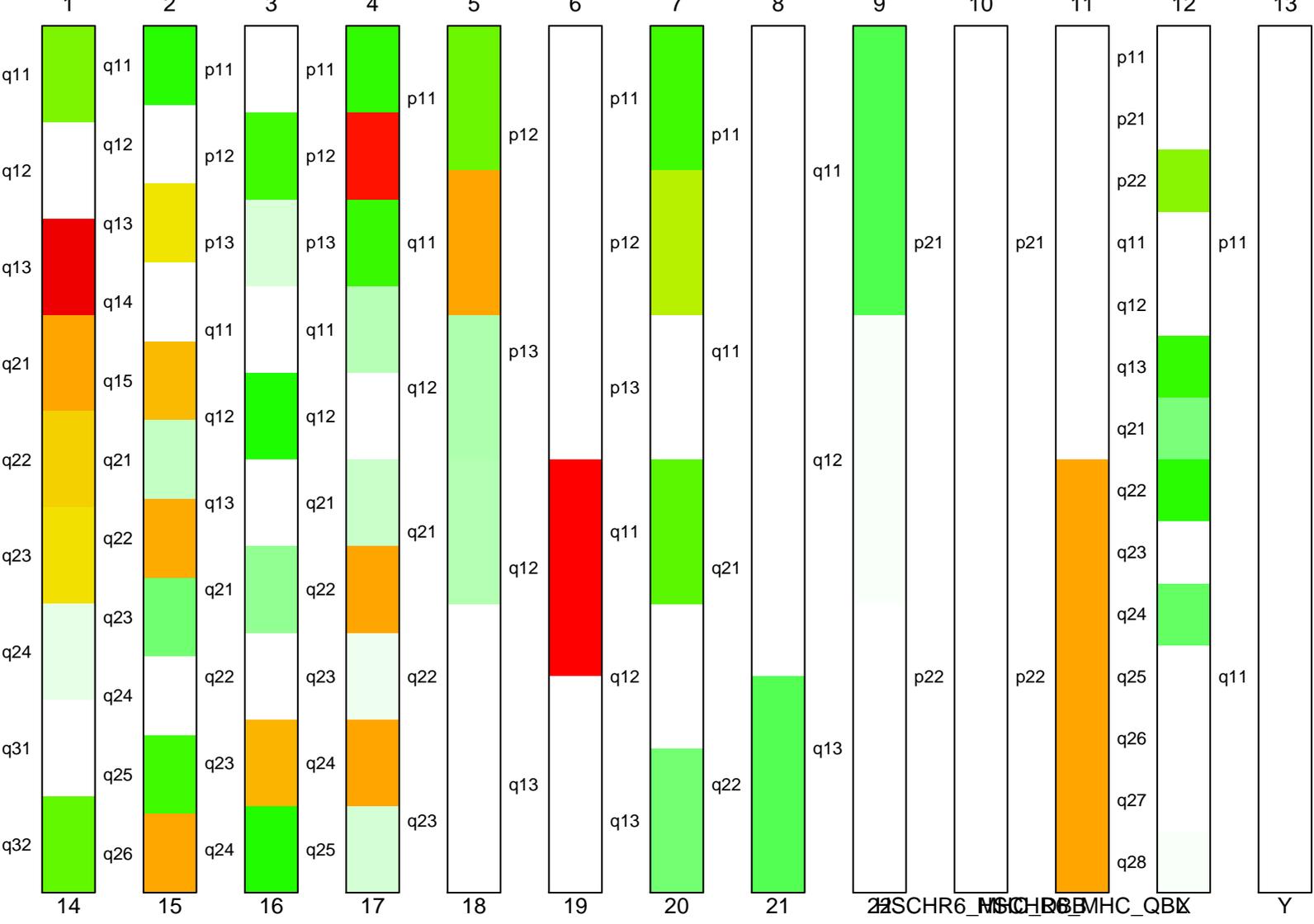
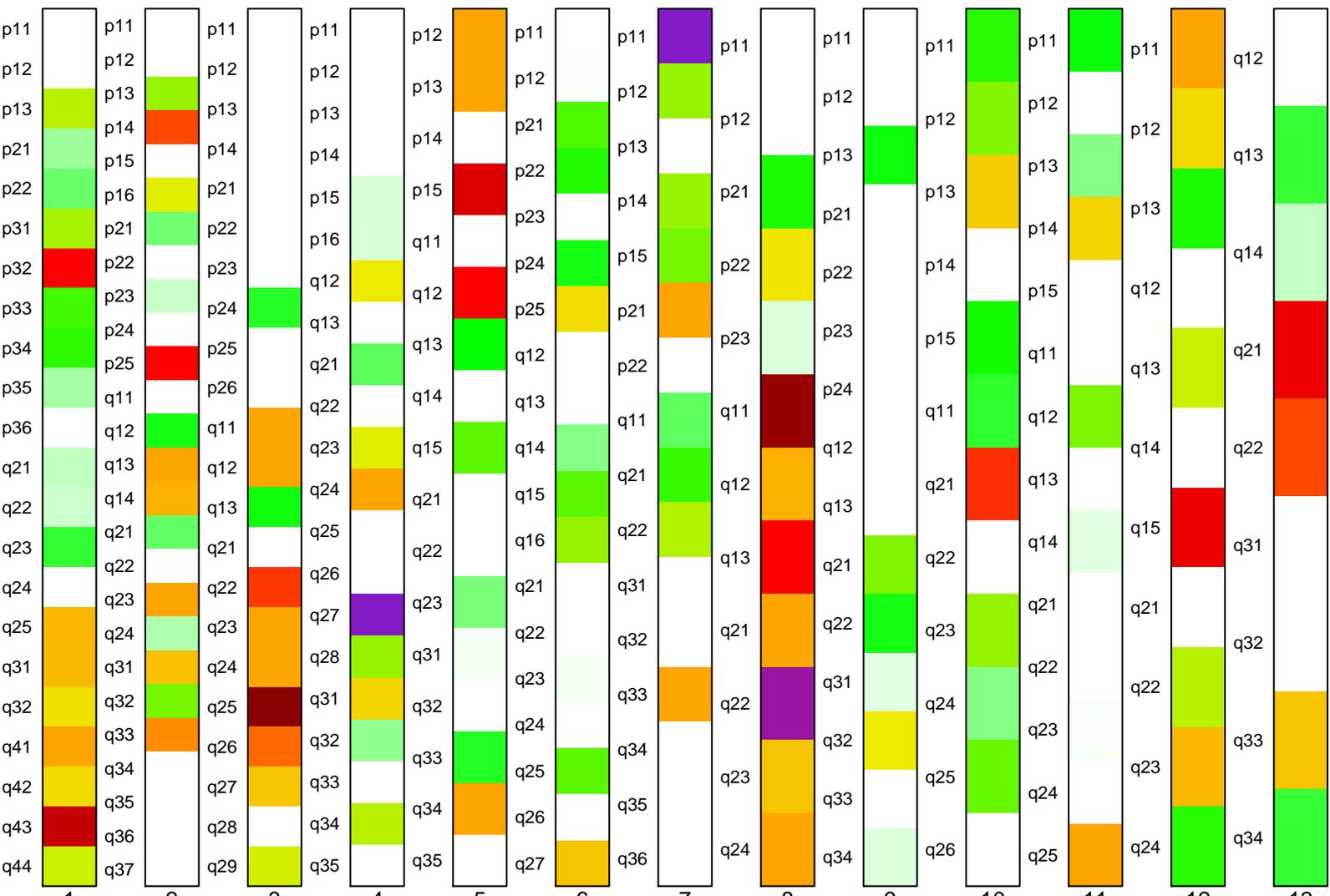
Spot P



Spot Q

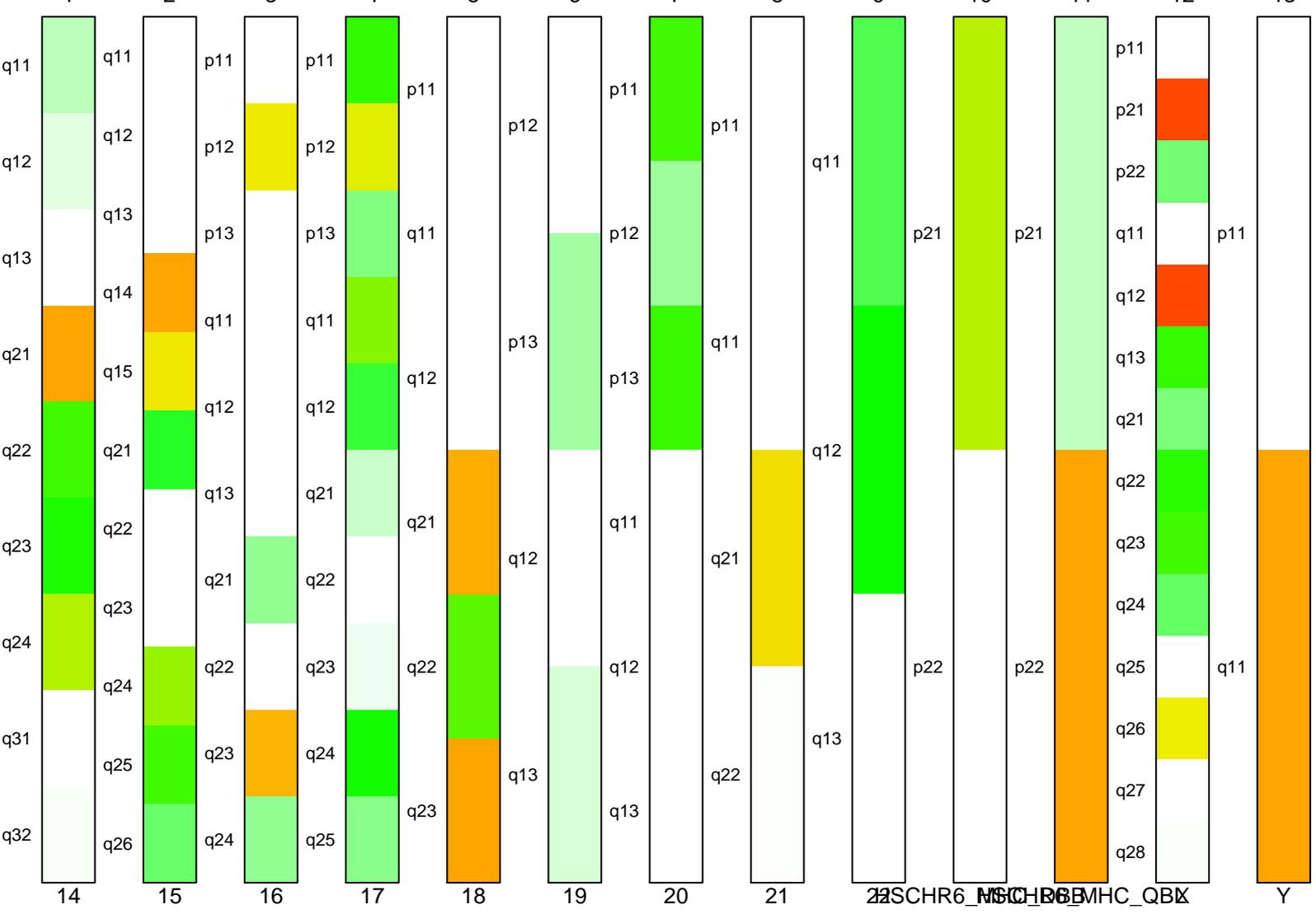
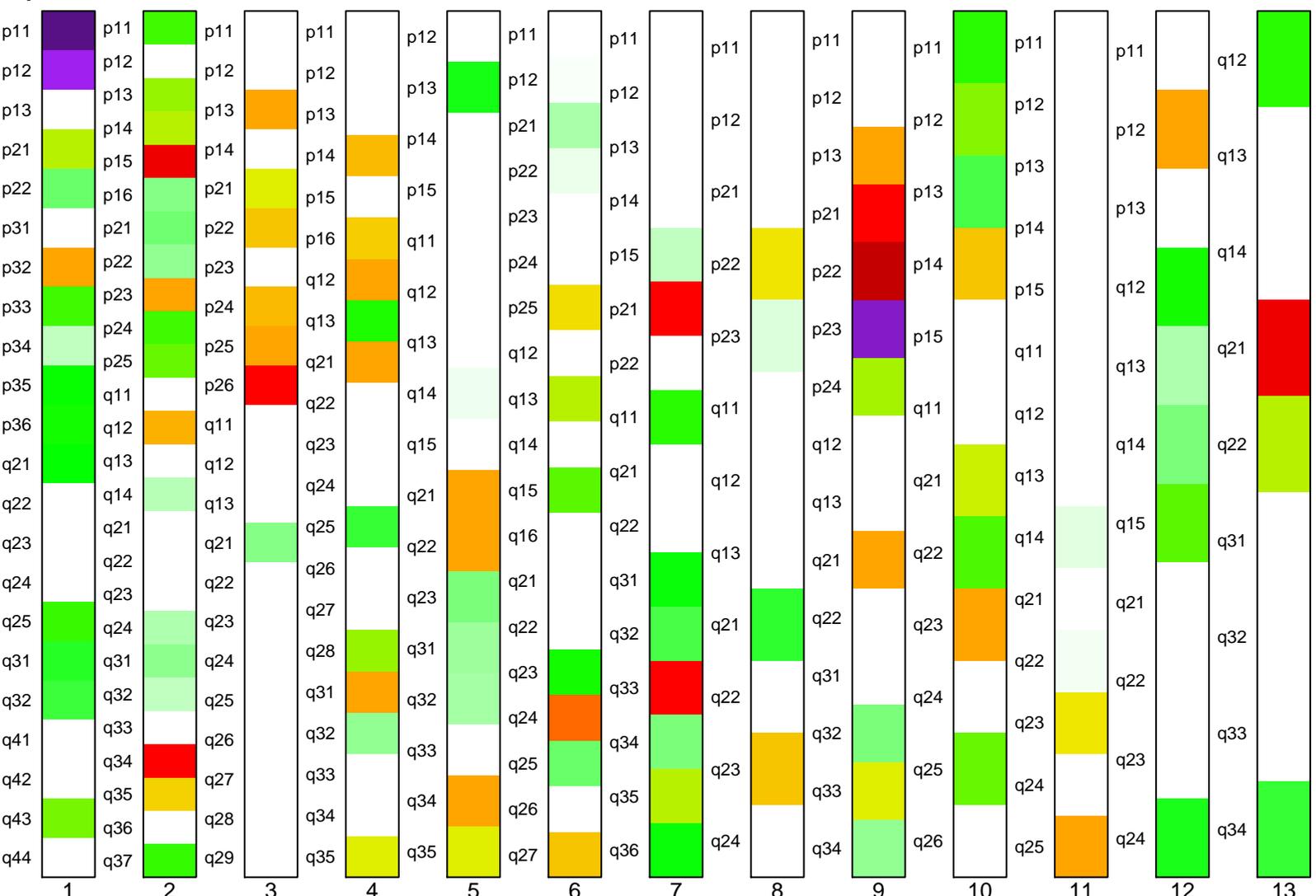


Spot R

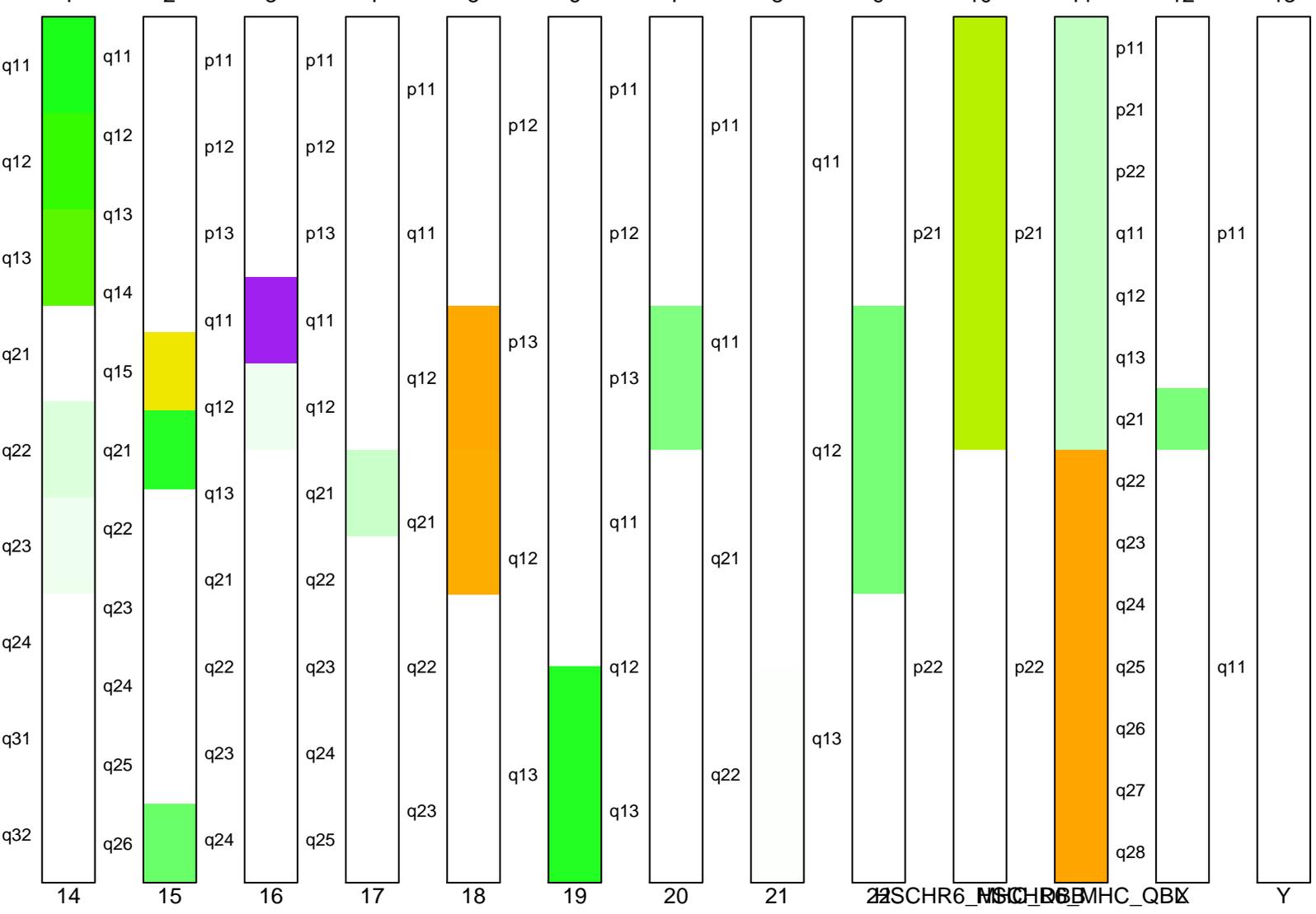
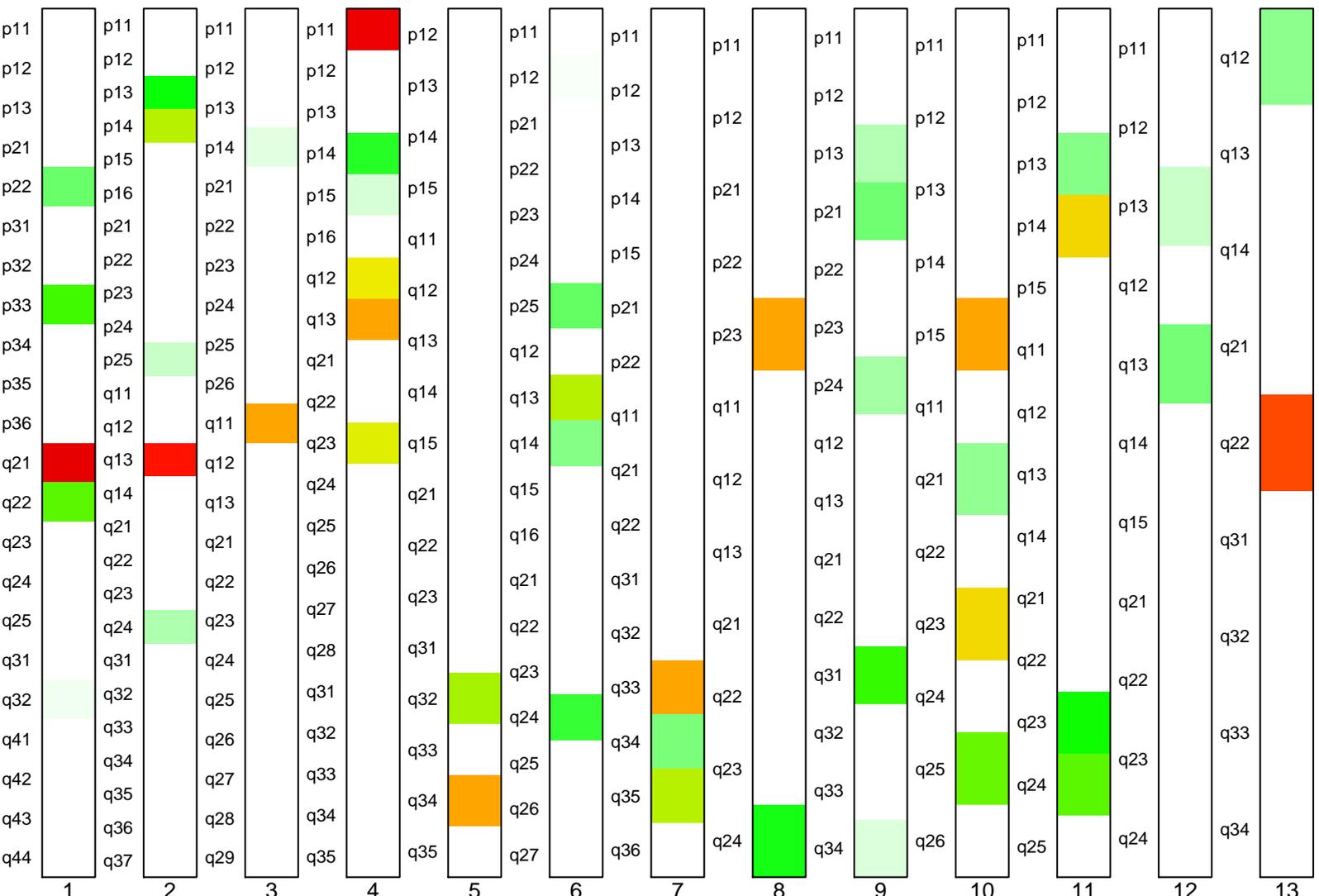


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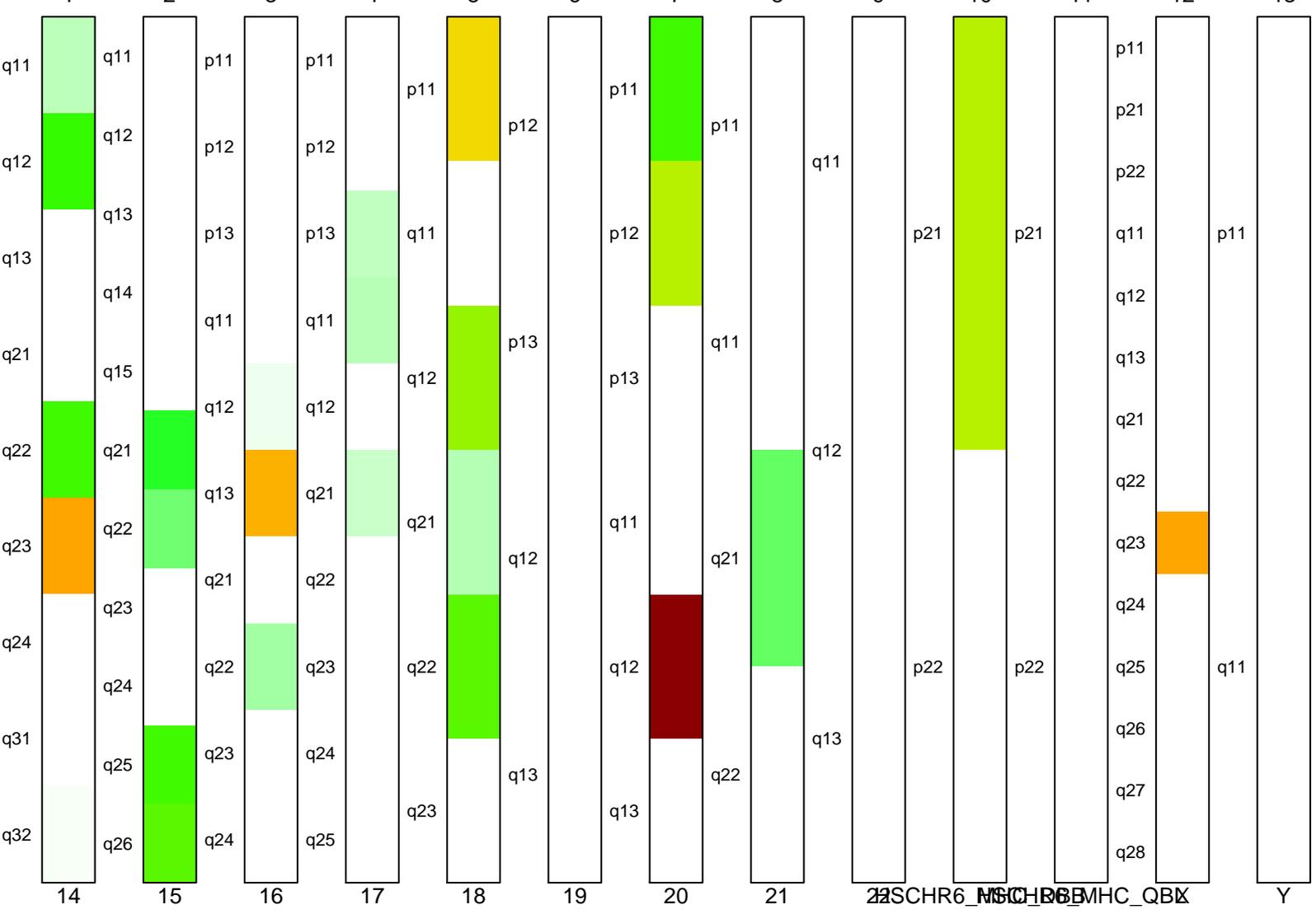
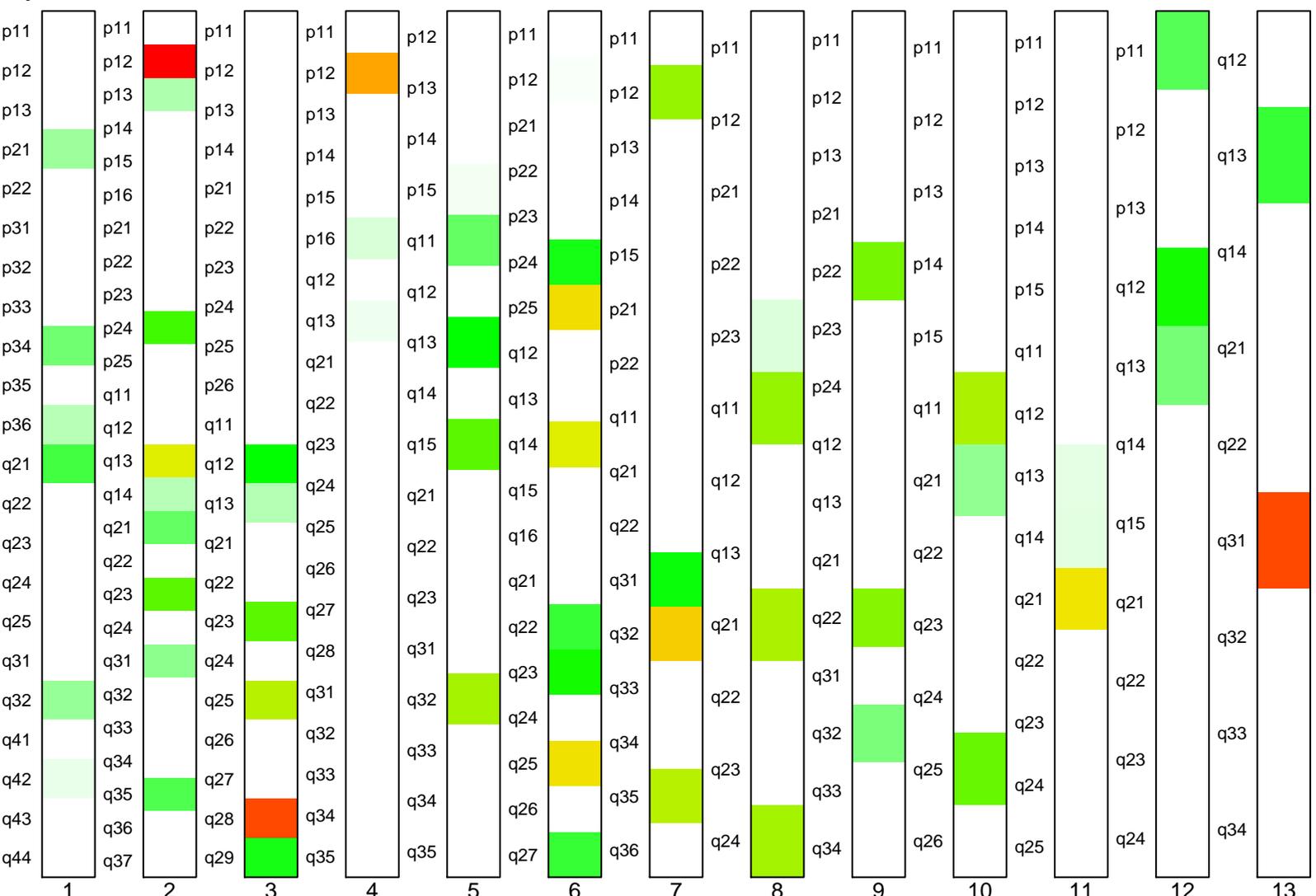
Spot S



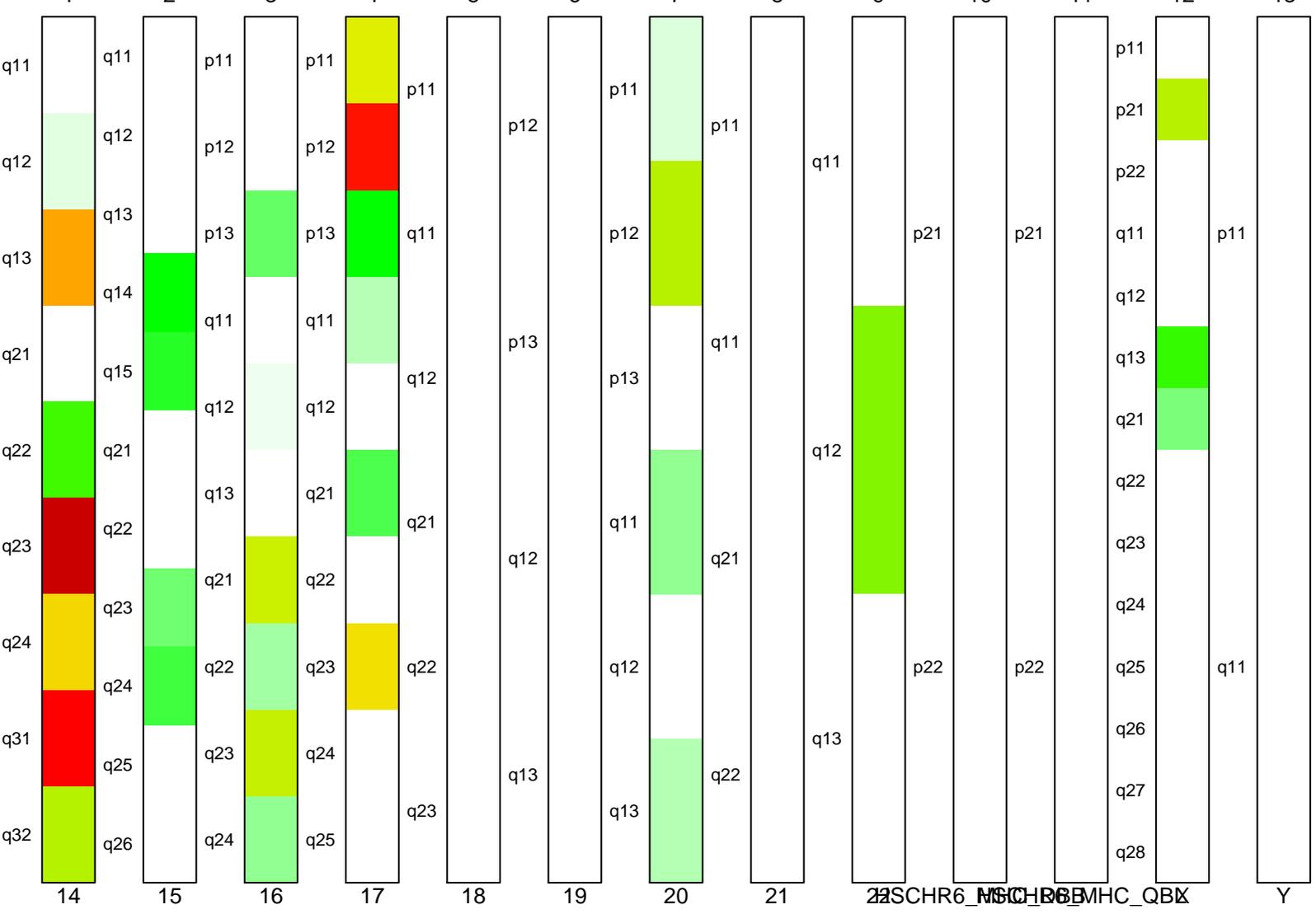
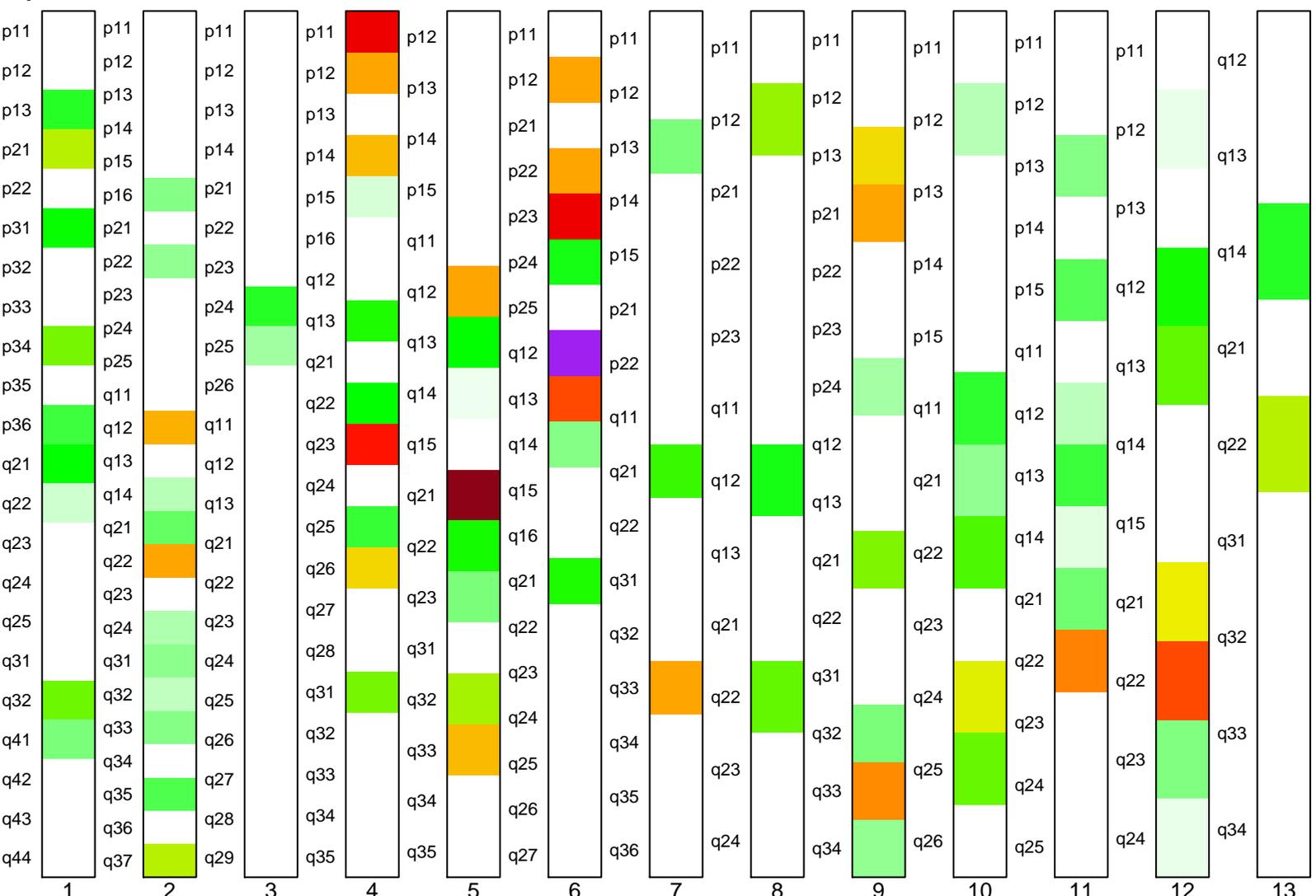
Spot T



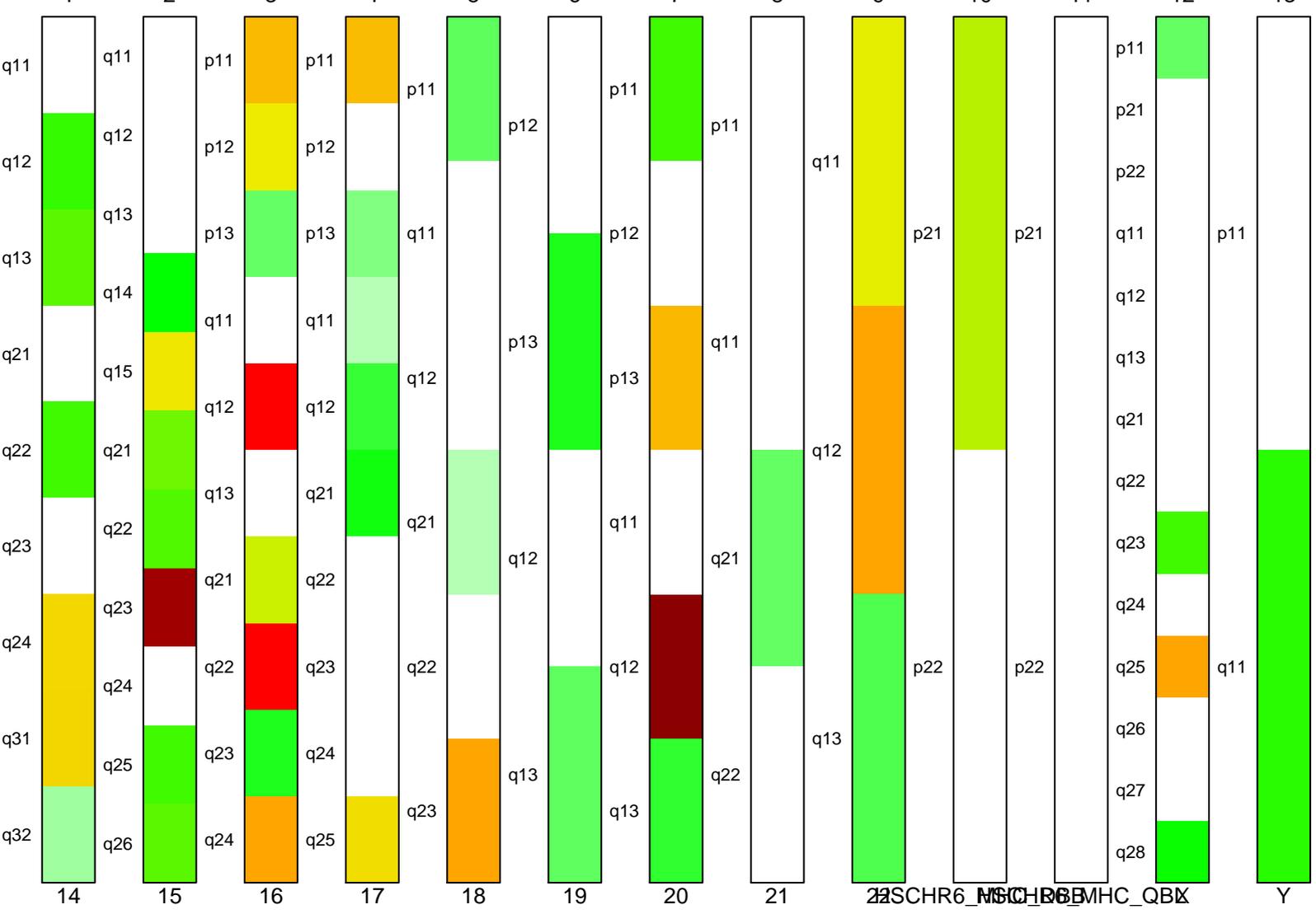
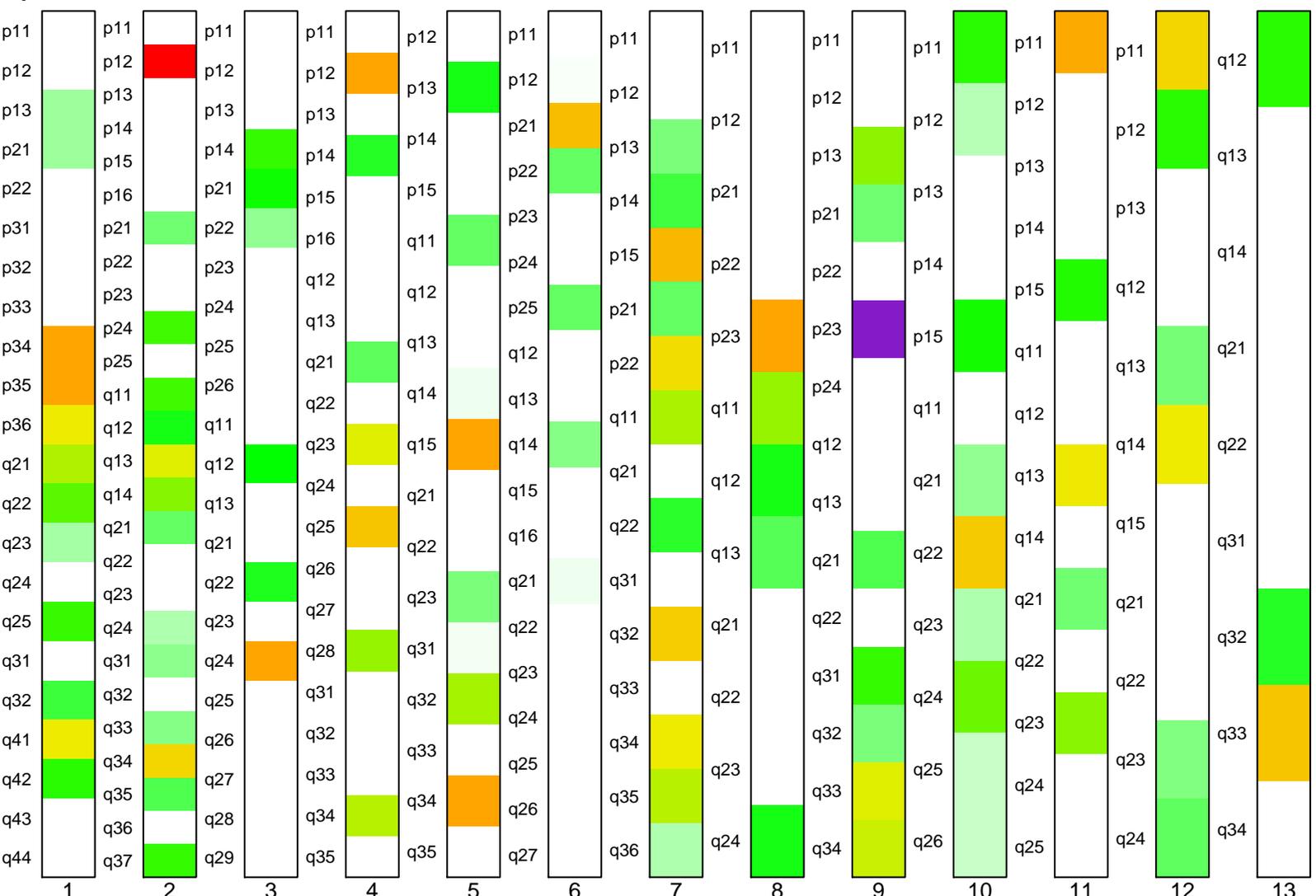
Spot U



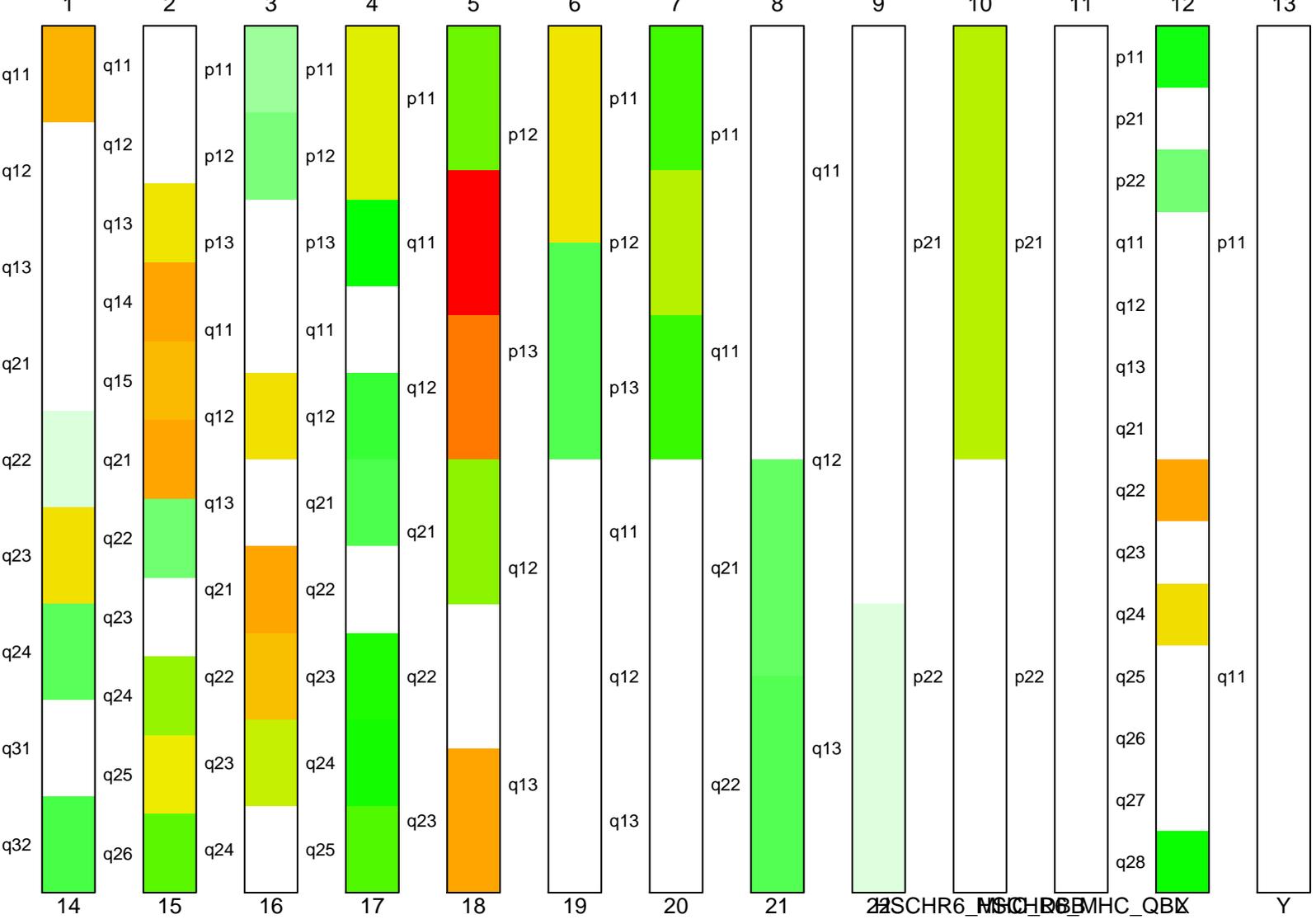
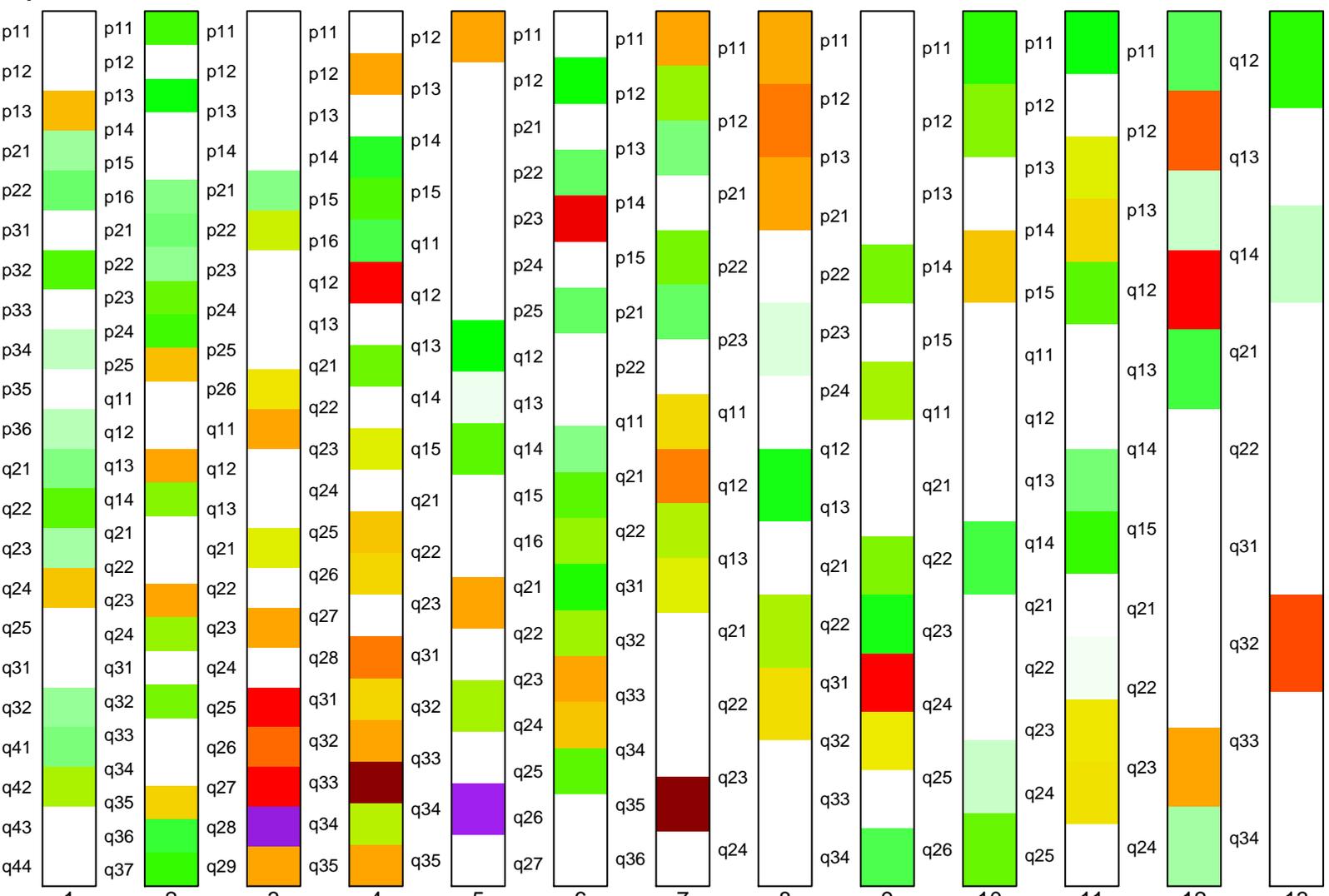
Spot V



Spot W



Spot X



Spot Y

