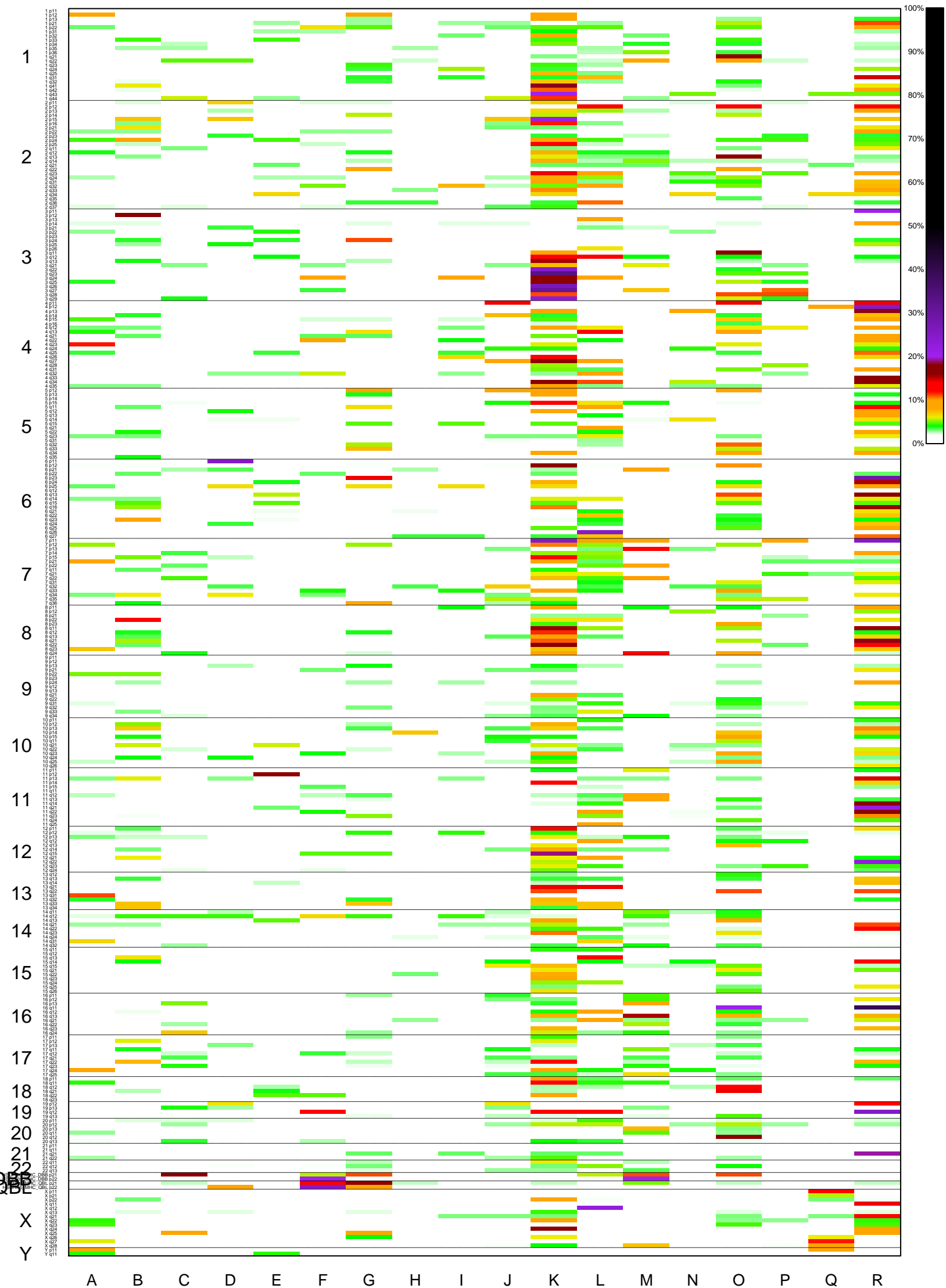


# Overexpression Spot Chromosome Map



# Spot A

# genes in spot = 126 ( 123 with loci information)

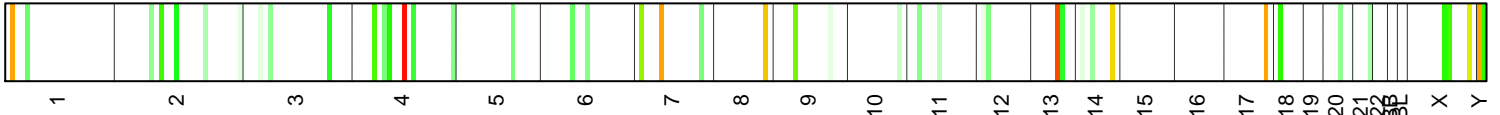
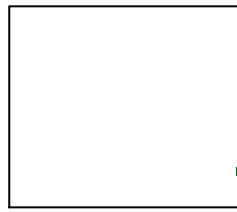
# samples with spot = 35 ( 12.7 % )

Atypical : 10 ( 13.5 % )

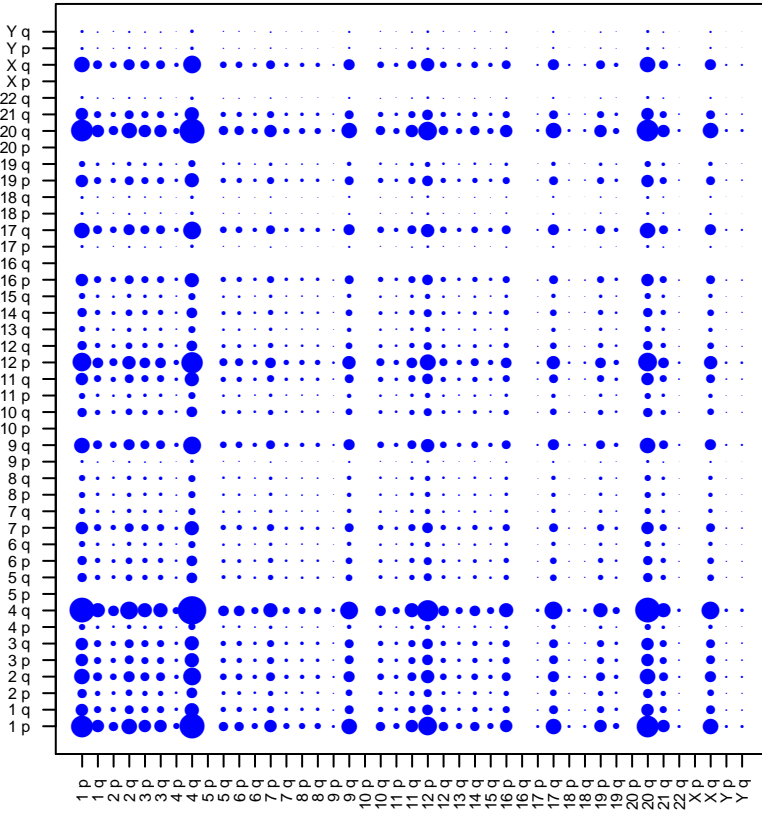
Classical : 6 ( 18.8 % )

Mesenchymal : 8 ( 9.4 % )

Basal : 11 ( 13.1 % )



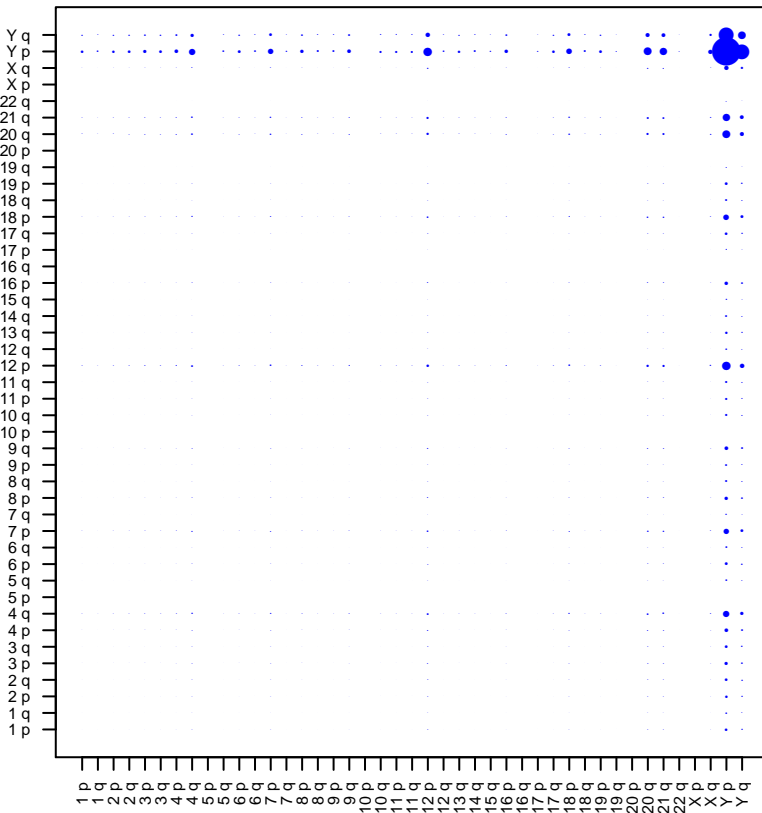
Absolute numbers



Rank	locus	# genes	%	p-value
1	4 q	8	1.8	0.02
2	1 p	7	0.8	0.6
3	20 q	7	2.3	0.01
4	12 p	6	2.5	0.01
5	2 q	6	0.8	0.06
6	9 q	5	1.3	0.3
7	17 q	5	1.1	0.6
8	X q	5	0.8	0.2
9	1 q	4	0.5	0.9
10	3 p	4	0.9	0.4
11	3 q	4	0.8	0.5
12	7 p	4	1.6	0.1
13	11 q	4	0.6	0.7
14	16 p	4	1	0.4
15	19 p	4	0.8	0.5
16	21 q	4	2.2	0.06
17	2 p	3	0.7	0.6
18	5 q	3	0.5	0.8
19	6 q	3	0.8	0.5
20	10 q	3	0.6	0.7
21	12 q	3	0.5	0.9
22	14 q	3	0.6	0.8
23	4 p	2	1.1	0.4
24	6 q	2	0.5	0.8
25	7 q	2	0.4	0.9
26	8 p	2	1	0.5
27	8 q	2	0.6	0.7
28	11 p	2	0.6	0.7
29	13 q	2	0.7	0.6
30	15 q	2	0.4	0.9
31	19 q	2	0.3	1
32	9 p	1	0.6	0.7
33	17 p	1	0.3	0.9
34	18 p	1	1.6	0.4
35	18 q	1	0.6	0.7
36	22 q	1	0.3	1
37	Y p	1	8.3	0.09
38	Y q	1	4.3	0.2
39	5 p	0	0	1
40	10 p	0	0	1
41	16 q	0	0	1
42	20 q	0	0	1
43	X p	0	0	1

H3CHR6-MHC-QBB

Relative numbers



Rank	locus	# genes	%	p-value
1	Y p	1	8.3	0.09
2	Y q	1	4.3	0.2
3	12 p	6	2.5	0.01
4	20 q	7	2.3	0.01
5	21 q	4	2.2	0.06
6	4 q	8	1.8	0.02
7	18 p	1	1.6	0.4
8	7 p	4	1.6	0.1
9	X q	5	1.3	0.2
10	9 q	5	1.1	0.3
11	4 p	2	1.1	0.4
12	16 p	4	1	0.4
13	8 p	2	1	0.5
14	3 p	4	0.9	0.4
15	6 p	3	0.8	0.5
16	19 p	4	0.8	0.5
17	3 q	4	0.8	0.5
18	2 q	5	0.8	0.6
19	17 q	5	0.8	0.6
20	1 p	7	0.8	0.6
21	2 p	3	0.7	0.6
22	13 q	3	0.7	0.6
23	11 q	3	0.6	0.7
24	10 q	3	0.6	0.7
25	11 q	4	0.6	0.7
26	8 q	2	0.6	0.7
27	18 q	1	0.6	0.7
28	14 q	3	0.6	0.8
29	9 p	1	0.6	0.7
30	6 q	2	0.5	0.8
31	5 q	3	0.5	0.8
32	1 q	4	0.5	0.9
33	12 q	3	0.5	0.9
34	7 q	3	0.5	0.9
35	15 q	2	0.4	0.9
36	17 p	1	0.3	0.9
37	19 q	2	0.3	0.9
38	22 q	1	0.3	1
39	5 p	0	0	1
40	10 p	0	0	1
41	16 q	0	0	1
42	20 q	0	0	1
43	X p	0	0	1

# Spot B

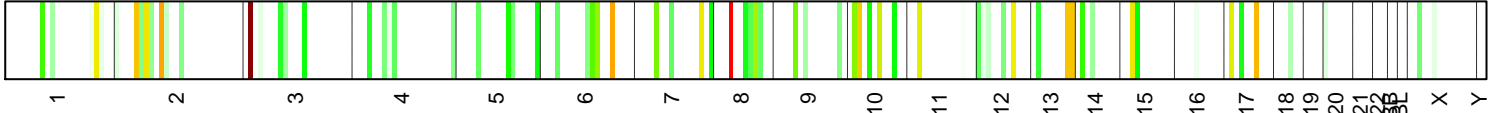
# genes in spot = 198 ( 193 with loci information)

# samples with spot = 38 ( 13.8 % )

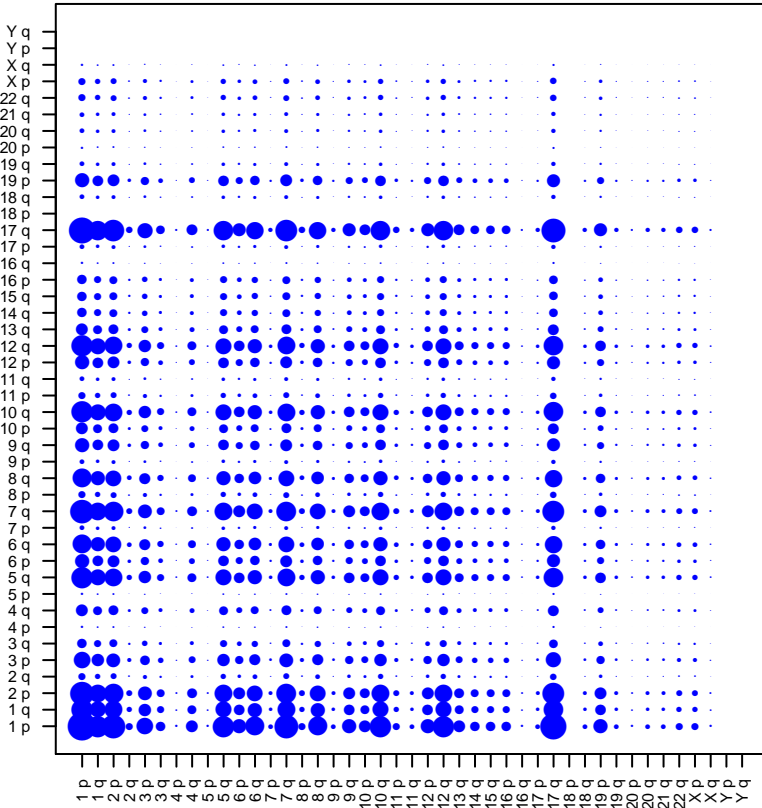
Atypical : 36 ( 48.6 % )

Mesenchymal : 1 ( 1.2 % )

Basal : 1 ( 1.2 % )



Absolute numbers

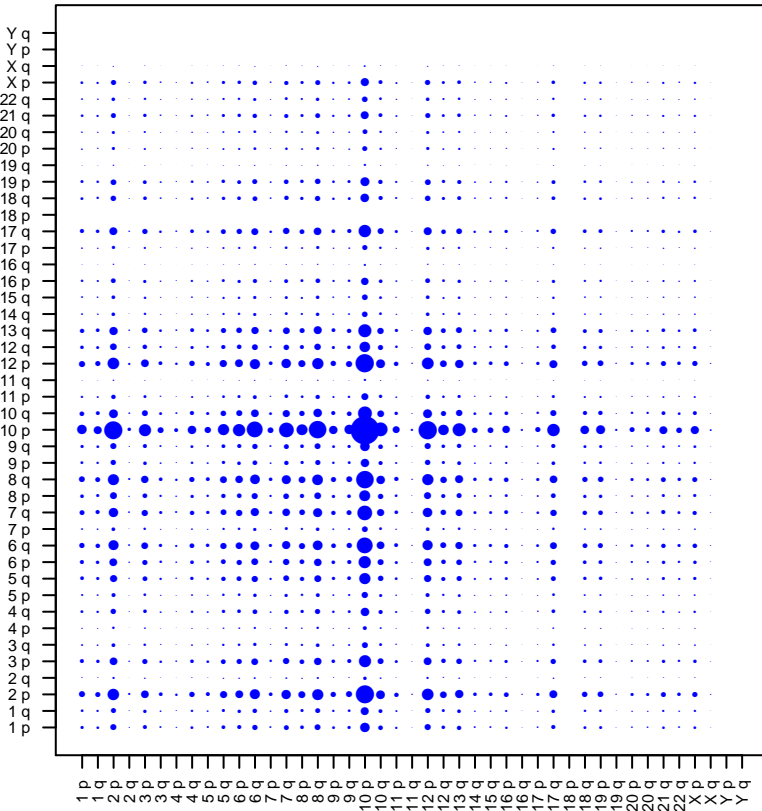


Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	1 p	12	1.3	0.5
2	17 q	11	1.7	0.2
3	2 p	10	2.5	0.03
4	7 q	10	2.1	0.09
5	1 q	9	1.1	0.7
6	5 q	9	1.5	0.3
7	10 q	9	1.9	0.1
8	12 q	8	1.4	0.4
9	6 q	8	2.2	0.09
10	8 q	8	2.4	0.05
11	3 p	7	1.7	0.3
12	6 p	6	1.7	0.3
13	9 q	6	1.3	0.5
14	12 p	6	2.5	0.08
15	19 p	6	1.2	0.6
16	4 q	6	1.2	0.6
17	10 p	5	3.9	0.02
18	13 q	5	0.8	0.9
19	3 q	4	0.8	0.9
20	14 q	4	0.8	0.9
21	15 q	4	0.8	0.9
22	16 p	4	1	0.7
23	2 q	3	0.5	1
24	8 p	3	1.5	0.4
25	11 p	3	0.9	0.7
26	22 q	3	0.8	0.9
27	X p	3	1.1	0.6
28	7 p	3	0.8	0.8
29	9 p	3	1.1	0.6
30	11 q	3	0.3	1
31	17 p	3	0.7	0.9
32	18 q	3	1.2	0.6
33	19 q	2	0.3	1
34	20 q	2	0.7	0.9
35	21 q	2	1.1	0.7
36	4 p	1	0.5	0.9
37	5 p	1	0.9	0.8
38	16 q	1	0.3	1
39	20 p	1	0.7	0.8
40	X q	1	0.3	1
41	18 p	0	0	1
42	Y p	0	0	1
43	Y q	0	0	1

H3CHR6-MHC-QBB

Relative numbers



Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	10 p	5	3.9	0.02
2	12 p	6	2.5	0.08
3	2 p	10	2.5	0.03
4	8 q	8	2.4	0.05
5	6 q	8	2	0.09
6	7 q	10	2	0.09
7	10 q	9	1.9	0.1
8	13 q	5	1.8	0.3
9	17 q	11	1.7	0.2
10	3 p	7	1.7	0.3
11	5 p	6	1.7	0.3
12	6 p	6	1.5	0.3
13	8 p	6	1.5	0.3
14	12 q	6	1.4	0.4
15	9 q	6	1.3	0.5
16	1 p	12	1.3	0.5
17	19 p	6	1.2	0.6
18	18 q	5	1.2	0.6
19	4 q	5	1.2	0.6
20	9 p	3	1.1	0.6
21	X p	3	1.1	0.6
22	1 q	3	1.1	0.7
23	21 q	3	1.1	0.7
24	16 p	4	1	0.7
25	11 p	3	0.9	0.7
26	5 p	1	0.9	0.8
27	3 q	4	0.8	0.8
28	7 p	2	0.8	0.8
29	15 q	4	0.8	0.9
30	14 q	4	0.8	0.9
31	22 q	3	0.8	0.9
32	17 p	2	0.7	0.9
33	20 p	1	0.7	0.9
34	20 q	1	0.7	0.9
35	4 p	1	0.5	0.9
36	2 q	2	0.5	0.9
37	11 q	3	0.3	1
38	19 q	2	0.3	1
39	16 q	1	0.3	1
40	X q	1	0.3	1
41	18 p	0	0	1
42	Y p	0	0	1
43	Y q	0	0	1

# Spot C

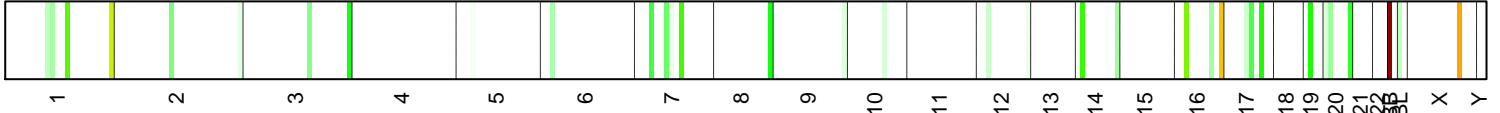
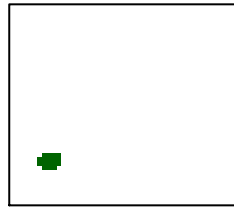
# genes in spot = 185 ( 172 with loci information)

# samples with spot = 14 ( 5.1 %)

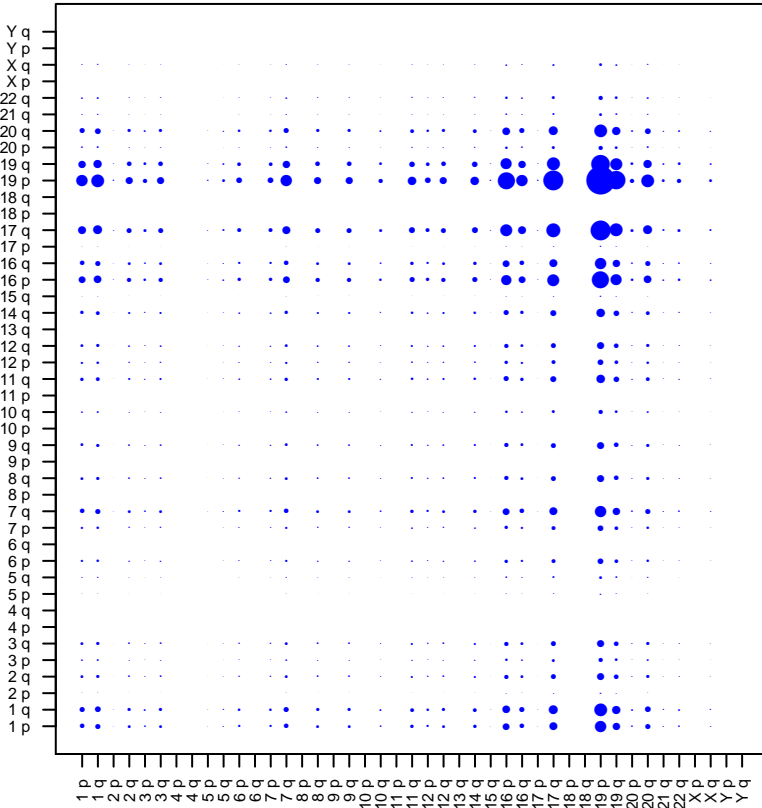
Atypical : 8 ( 10.8 %)

Mesenchymal : 5 ( 5.9 %)

Basal : 1 ( 1.2 %)



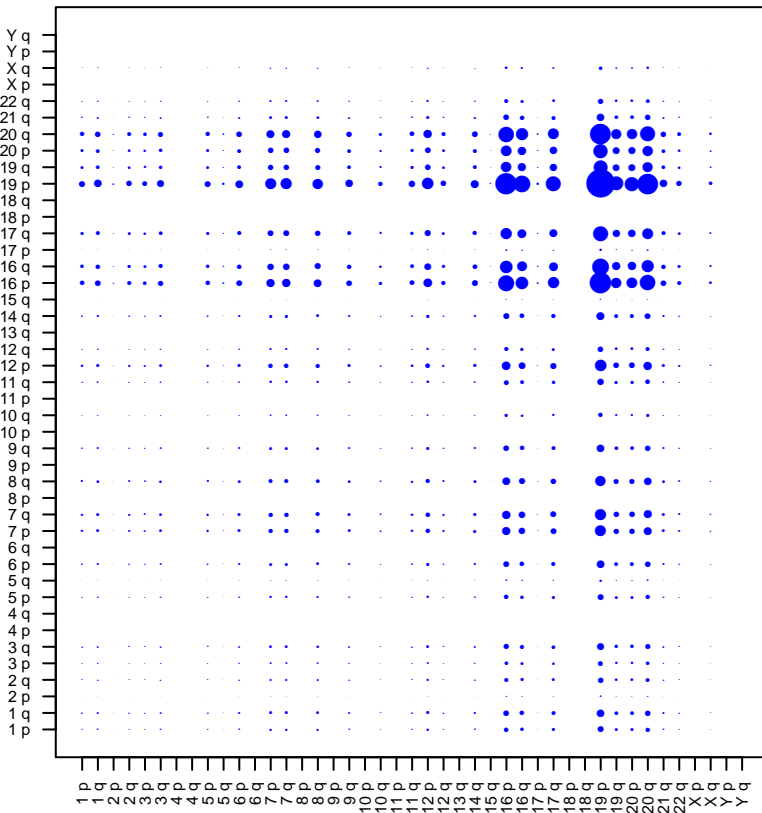
Absolute numbers



Rank	locus	# genes	%	p-value
1	19 p	20	4.1	9e-07
2	17 q	14	2.2	0.02
3	19 q	13	2.2	0.04
4	16 p	12	3.1	0.002
5	1 q	9	1.1	0.6
6	20 q	9	3.3	0.008
7	1 p	8	0.9	0.8
8	7 q	8	1.6	0.2
9	16 q	8	2.4	0.04
10	11 q	6	0.9	0.8
11	14 q	5	1.1	0.6
12	2 q	5	0.8	0.9
13	3 q	5	1	0.7
14	8 q	5	1.5	0.3
15	9 q	5	1.1	0.6
16	12 q	5	0.8	0.9
17	6 p	4	1.1	0.6
18	7 p	4	1.6	0.3
19	12 p	4	1.7	0.3
20	3 p	3	0.7	0.9
21	10 p	3	0.6	0.9
22	20 p	3	2	0.2
23	22 q	3	0.8	0.8
24	5 q	2	0.3	1
25	21 q	2	1.1	0.6
26	X q	2	0.5	0.9
27	2 p	1	0.2	1
28	5 p	1	0.9	0.7
29	15 q	1	0.2	1
30	17 p	1	0.3	1
31	4 p	0	0	1
32	4 q	0	0	1
33	6 q	0	0	1
34	8 p	0	0	1
35	9 p	0	0	1
36	10 p	0	0	1
37	11 p	0	0	1
38	13 q	0	0	1
39	18 p	0	0	1
40	18 q	0	0	1
41	X p	0	0	1
42	Y p	0	0	1
43	Y q	0	0	1

H3CHR6-MHC-QBB

Relative numbers



Rank	locus	# genes	%	p-value
1	19 p	20	4.1	9e-07
2	16 p	12	3.1	0.002
3	20 q	9	3	0.008
4	16 q	8	2.4	0.04
5	17 q	14	2.2	0.02
6	20 p	3	2	0.2
7	19 q	13	2	0.04
8	12 p	4	1.7	0.3
9	7 q	8	1.6	0.2
10	7 p	4	1.6	0.2
11	8 q	4	1.5	0.3
12	14 q	5	1.1	0.6
13	6 p	4	1.1	0.6
14	1 q	9	1.1	0.6
15	9 q	5	1.1	0.6
16	21 q	5	1.1	0.6
17	3 q	1	1	0.7
18	11 q	6	0.9	0.8
19	1 p	8	0.9	0.8
20	5 p	1	0.9	0.7
21	12 q	5	0.9	0.8
22	2 q	5	0.8	0.9
23	2 q	5	0.8	0.9
24	3 p	3	0.7	0.9
25	10 q	3	0.6	0.9
26	X q	2	0.5	0.9
27	17 p	2	0.3	1
28	5 q	2	0.3	1
29	2 p	1	0.2	1
30	15 q	2	0.2	1
31	4 p	0	0	1
32	4 q	0	0	1
33	6 q	0	0	1
34	8 p	0	0	1
35	9 p	0	0	1
36	10 p	0	0	1
37	11 p	0	0	1
38	13 q	0	0	1
39	18 p	0	0	1
40	18 q	0	0	1
41	X p	0	0	1
42	Y p	0	0	1
43	Y q	0	0	1

# Spot D

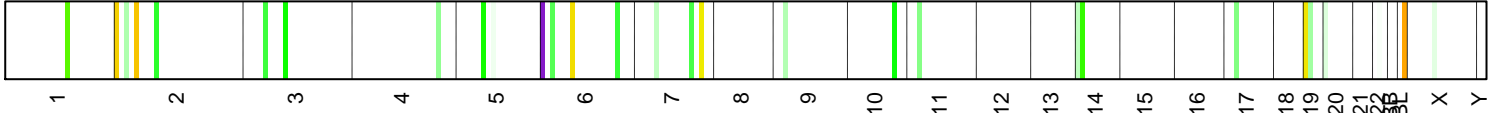
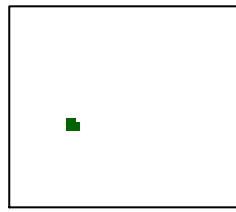
# genes in spot = 139 ( 132 with loci information)

# samples with spot = 11 ( 4 % )

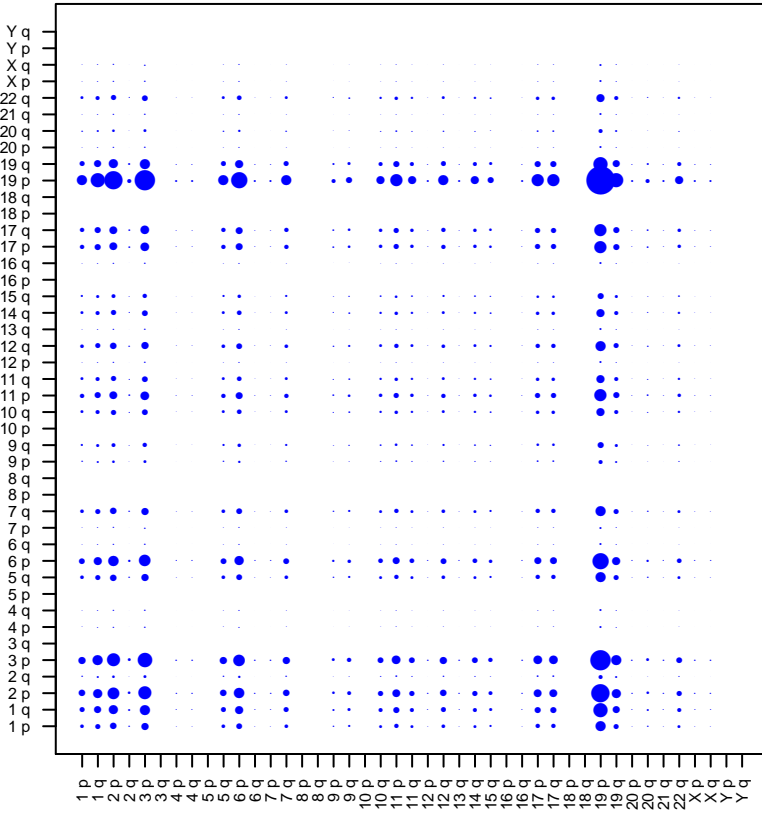
Atypical : 5 ( 6.8 % )

Mesenchymal : 1 ( 1.2 % )

Basal : 5 ( 6 % )



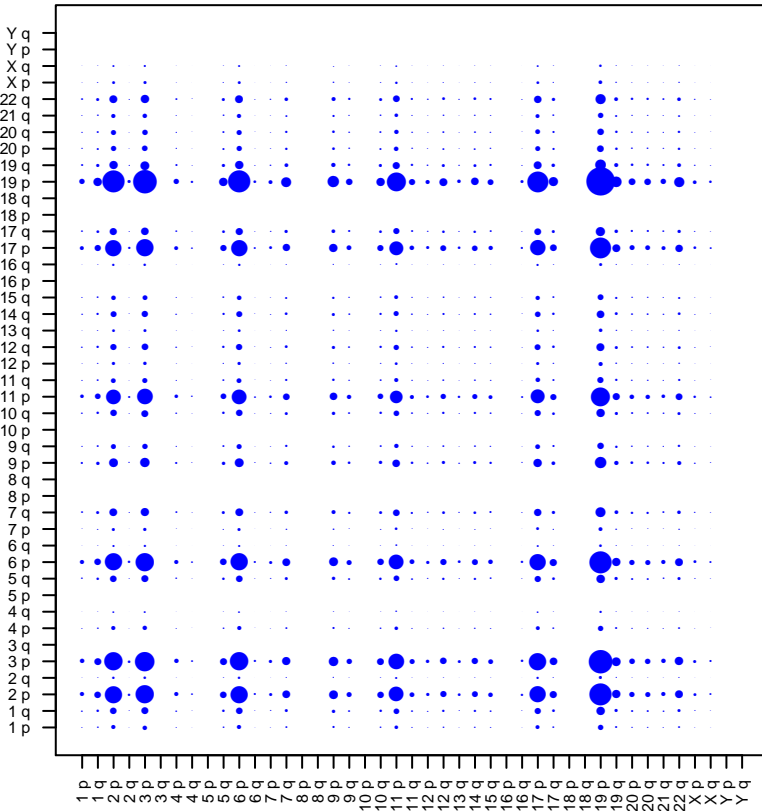
Absolute numbers



Rank	locus	# genes	%	p-value
1	19 p	14	2.9	8e-05
2	3 p	10	2.4	0.004
3	2 p	9	2.2	0.008
4	6 p	8	2.2	0.01
5	1 q	7	2.8	0.001
6	11 p	7	1.1	0.06
7	19 q	7	1.1	0.03
8	17 p	6	1.9	0.05
9	17 q	6	2.1	0.04
10	17 q	6	0.9	0.5
11	1 p	5	0.9	0.6
12	5 q	5	0.8	0.4
13	7 q	5	0.8	0.6
14	10 q	4	0.8	0.6
15	11 q	4	0.6	0.8
16	14 q	4	0.8	0.7
17	22 q	4	1	0.4
18	9 q	4	0.7	0.8
19	15 q	3	0.6	0.8
20	2 q	3	0.3	1
21	9 p	2	1.1	0.4
22	20 q	2	0.7	0.7
23	4 p	2	0.5	0.8
24	4 q	1	0.2	1
25	6 q	1	0.3	1
26	7 p	1	0.4	0.9
27	12 p	1	0.4	0.9
28	13 q	1	0.4	0.9
29	16 q	1	0.3	0.9
30	20 p	1	0.7	0.7
31	21 q	1	0.5	0.8
32	X p	1	0.4	0.9
33	X q	0	0.3	1
34	3 q	0	0	1
35	5 p	0	0	1
36	8 p	0	0	1
37	8 q	0	0	1
38	10 p	0	0	1
39	16 p	0	0	1
40	18 p	0	0	1
41	18 q	0	0	1
42	Y p	0	0	1
43	Y q	0	0	1

H3CHR6-MHC-DBB

Relative numbers



Rank	locus	# genes	%	p-value
1	19 p	14	2.9	8e-05
2	3 p	10	2.4	0.004
3	2 p	9	2.2	0.008
4	6 p	8	2.2	0.01
5	17 p	6	2.1	0.04
6	11 p	6	1.9	0.05
7	9 p	2	1.1	0.4
8	19 q	2	1.1	0.3
9	22 q	4	1	0.4
10	7 q	4	1	0.4
11	17 q	5	0.9	0.5
12	5 q	5	0.9	0.6
13	1 q	7	0.8	0.6
14	10 q	4	0.8	0.6
15	12 q	5	0.8	0.6
16	14 q	4	0.8	0.7
17	20 p	1	0.7	0.7
18	20 q	2	0.7	0.7
19	9 q	3	0.7	0.8
20	11 q	4	0.6	0.8
21	15 q	3	0.6	0.8
22	21 q	1	0.5	0.8
23	1 p	5	0.5	0.9
24	4 p	5	0.5	0.8
25	12 p	1	0.4	0.9
26	7 p	1	0.4	0.9
27	X p	1	0.4	0.9
28	13 q	1	0.4	0.9
29	2 q	2	0.3	1
30	16 q	1	0.3	0.9
31	6 q	1	0.3	0.9
32	X q	1	0.3	1
33	4 q	1	0.2	1
34	3 q	0	0	1
35	5 p	0	0	1
36	8 p	0	0	1
37	8 q	0	0	1
38	10 p	0	0	1
39	16 p	0	0	1
40	18 p	0	0	1
41	18 q	0	0	1
42	Y p	0	0	1
43	Y q	0	0	1

# Spot E

# genes in spot = 66 ( 65 with loci information)

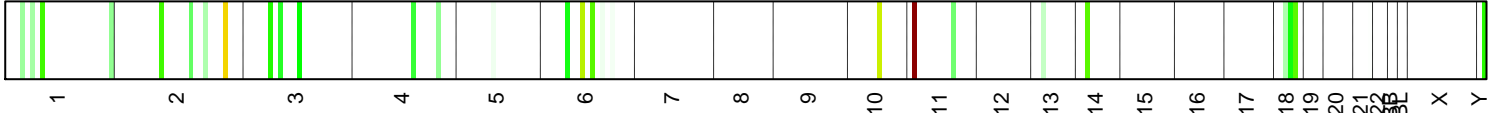
# samples with spot = 14 ( 5.1 % )

Atypical : 10 ( 13.5 % )

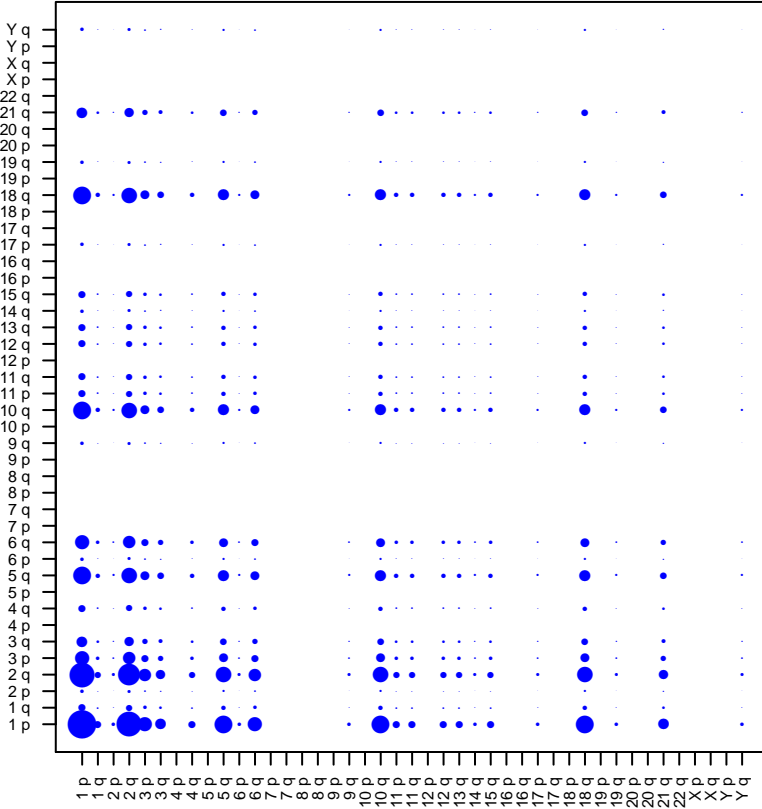
Classical : 1 ( 3.1 % )

Mesenchymal : 1 ( 1.2 % )

Basal : 2 ( 2.4 % )



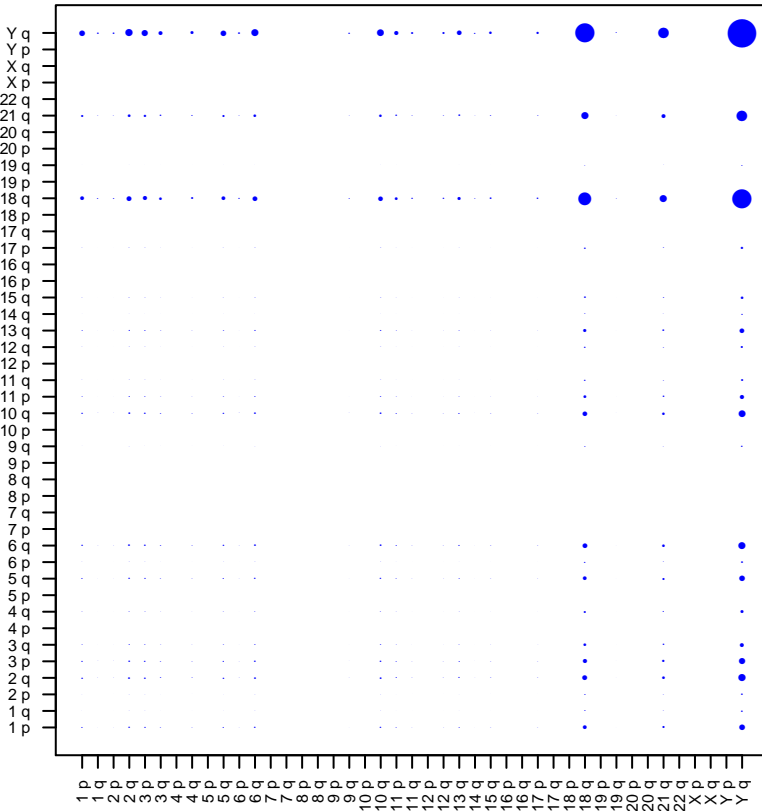
Absolute numbers



Rank	locus	# genes	%	p-value
1	1 p	8	0.9	0.03
2	2 q	7	1.1	0.01
3	5 q	5	0.9	0.09
4	10 q	5	0.9	0.04
5	18 q	5	2.9	7e-04
6	6 q	4	0.9	0.06
7	3 p	4	1.1	0.01
8	3 q	4	1.1	0.01
9	21 q	3	1.6	0.04
10	1 q	3	0.9	0.03
11	4 q	2	1.6	0.04
12	11 p	2	0.5	0.5
13	11 q	2	0.6	0.4
14	12 q	2	0.3	0.7
15	13 q	2	0.3	0.7
16	15 q	2	0.7	0.3
17	17 q	2	0.4	0.6
18	2 p	1	0.3	0.8
19	6 p	1	0.2	0.8
20	9 q	1	0.3	0.9
21	14 q	1	0.2	0.9
22	17 p	1	0.3	0.7
23	19 q	1	0.2	0.9
24	4 p	0	0	0.9
25	5 p	0	4.3	0.09
26	7 p	0	0	1
27	7 q	0	0	1
28	8 p	0	0	1
29	8 q	0	0	1
30	9 p	0	0	1
31	10 p	0	0	1
32	12 p	0	0	1
33	16 p	0	0	1
34	16 q	0	0	1
35	17 q	0	0	1
36	18 p	0	0	1
37	19 p	0	0	1
38	20 p	0	0	1
39	20 q	0	0	1
40	22 q	0	0	1
41	X p	0	0	1
42	X q	0	0	1
43	Y p	0	0	1

H3CHR6-MHC-DBP

Relative numbers



Rank	locus	# genes	%	p-value
1	Y q	1	4.3	0.09
2	18 q	1	2.9	7e-04
3	21 q	3	1.6	0.04
4	2 q	3	1.1	0.01
5	6 q	4	1.1	0.06
6	10 q	5	1.1	0.04
7	3 p	4	0	0.09
8	1 p	4	0.9	0.03
9	5 q	5	0.9	0.03
10	13 q	5	0.6	0.9
11	11 p	2	0.7	0.4
12	3 q	2	0.6	0.3
13	4 q	2	0.5	0.3
14	15 q	2	0.4	0.6
15	17 p	1	0.4	0.6
16	12 q	2	0.3	0.7
17	11 q	2	0.3	0.7
18	6 p	1	0.3	0.8
19	2 p	1	0.3	0.8
20	1 q	2	0	0.9
21	9 q	1	0	0.9
22	14 q	1	0	0.9
23	19 q	1	0	0.9
24	4 p	0	0	0.9
25	5 p	0	0	0.9
26	7 p	0	0	1
27	7 q	0	0	1
28	8 p	0	0	1
29	8 q	0	0	1
30	9 p	0	0	1
31	10 p	0	0	1
32	12 p	0	0	1
33	16 p	0	0	1
34	16 q	0	0	1
35	17 q	0	0	1
36	18 p	0	0	1
37	19 p	0	0	1
38	20 p	0	0	1
39	20 q	0	0	1
40	22 q	0	0	1
41	X p	0	0	1
42	X q	0	0	1
43	Y p	0	0	1

# Spot F

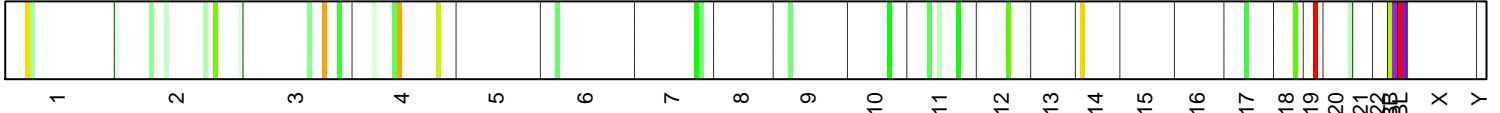
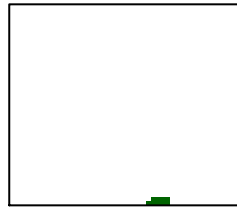
# genes in spot = 130 ( 113 with loci information)

# samples with spot = 58 ( 21.1 % )

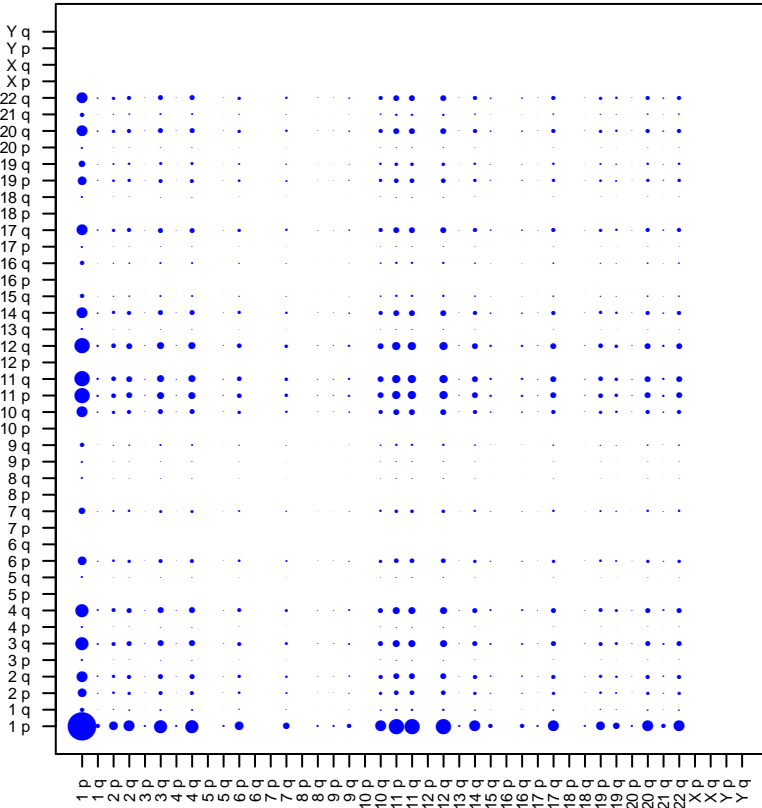
Atypical : 16 ( 21.6 % )

Mesenchymal : 27 ( 31.8 % )

Basal : 15 ( 17.9 % )



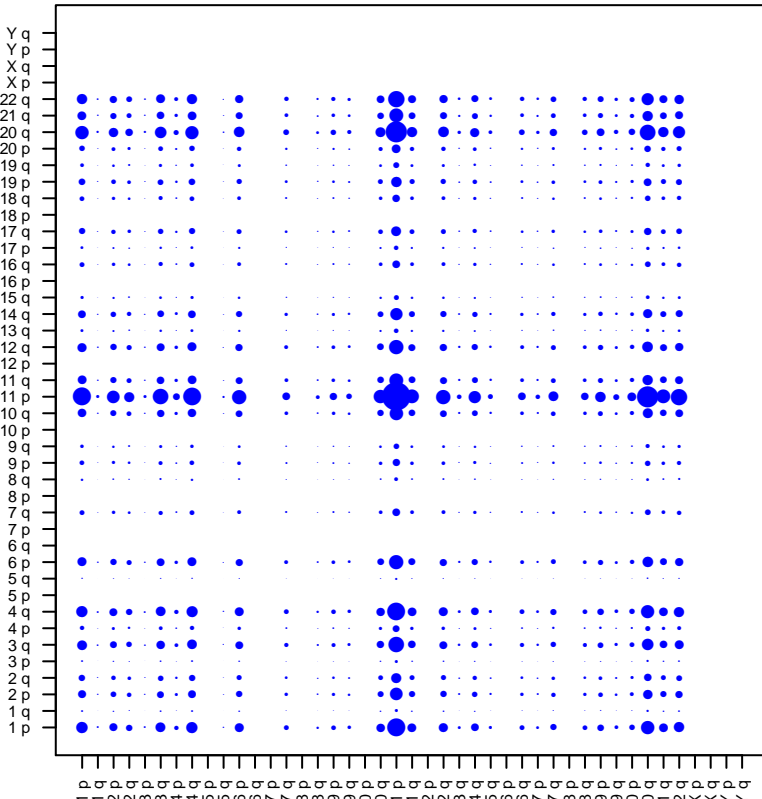
Absolute numbers



Rank	locus	# genes	%	p-value
1	1 p	13	1.4	0.04
2	11 p	7	2.2	0.01
3	11 q	7	1.1	0.3
4	12 q	7	1.1	0.2
5	4 q	6	1.2	0.3
6	22 q	6	1.2	0.4
7	3 q	5	0.8	0.6
8	12 q	5	1.0	0.6
9	6 p	4	1.0	0.4
10	21 q	4	1.3	0.2
11	10 q	4	1.1	0.4
12	20 q	4	1.1	0.3
13	22 q	4	0.8	0.6
14	6 p	4	0.6	0.8
15	19 p	4	0.5	0.9
16	7 q	3	0.4	0.9
17	1 q	3	0.2	1.0
18	9 q	3	0.2	0.9
19	16 q	3	0.4	0.8
20	15 q	2	0.6	0.9
21	16 q	2	1.1	0.4
22	21 q	2	0.2	0.8
23	3 q	2	0.2	0.9
24	4 p	1	0.5	0.8
25	5 q	1	0.2	1.0
26	8 q	1	0.3	0.9
27	9 p	1	0.6	0.8
28	13 q	1	0.4	0.9
29	17 p	1	0.3	0.9
30	18 q	1	0.6	0.7
31	20 p	0	0.0	0.7
32	5 q	0	0.0	1.0
33	6 q	0	0.0	1.0
34	7 p	0	0.0	1.0
35	8 p	0	0.0	1.0
36	10 p	0	0.0	1.0
37	12 p	0	0.0	1.0
38	16 p	0	0.0	1.0
39	18 p	0	0.0	1.0
40	X p	0	0.0	1.0
41	X q	0	0.0	1.0
42	Y p	0	0.0	1.0
43	Y q	0	0.0	1.0

H3CHR6-MHC-QBB

Relative numbers



Rank	locus	# genes	%	p-value
1	11 p	7	2.2	0.01
2	20 q	5	1.6	0.1
3	1 p	13	1.4	0.04
4	4 q	6	1.4	0.1
5	22 q	5	1.3	0.2
6	3 q	5	1.2	0.2
7	12 q	4	1.1	0.2
8	6 p	4	1.1	0.3
9	21 q	2	1.1	0.4
10	11 q	2	1.1	0.4
11	10 q	5	1.1	0.3
12	2 p	5	1.1	0.4
13	14 q	4	1.1	0.4
14	19 p	4	0.8	0.6
15	2 q	5	0.8	0.6
16	17 q	5	0.7	0.6
17	20 p	1	0.7	0.7
18	7 q	3	0.6	0.8
19	16 q	2	0.6	0.8
20	18 q	1	0.6	0.7
21	9 p	1	0.6	0.8
22	4 p	1	0.5	0.8
23	19 q	5	0.5	0.8
24	9 q	3	0.4	0.9
25	15 q	2	0.4	0.9
26	13 q	1	0.4	0.9
27	17 p	1	0.3	0.9
28	8 q	1	0.3	0.9
29	1 q	2	0.2	1.0
30	3 p	1	0.2	1.0
31	5 q	1	0.2	1.0
32	5 q	0	0.0	1.0
33	6 q	0	0.0	1.0
34	7 p	0	0.0	1.0
35	8 p	0	0.0	1.0
36	10 p	0	0.0	1.0
37	12 p	0	0.0	1.0
38	16 p	0	0.0	1.0
39	18 p	0	0.0	1.0
40	X p	0	0.0	1.0
41	X q	0	0.0	1.0
42	Y p	0	0.0	1.0
43	Y q	0	0.0	1.0

# Spot G

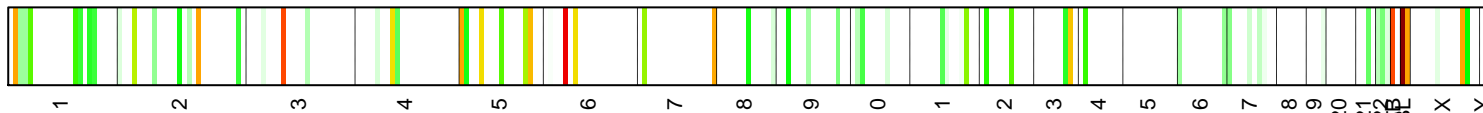
# genes in spot = 229 ( 211 with loci information)

# samples with spot = 63 ( 22.9 % )

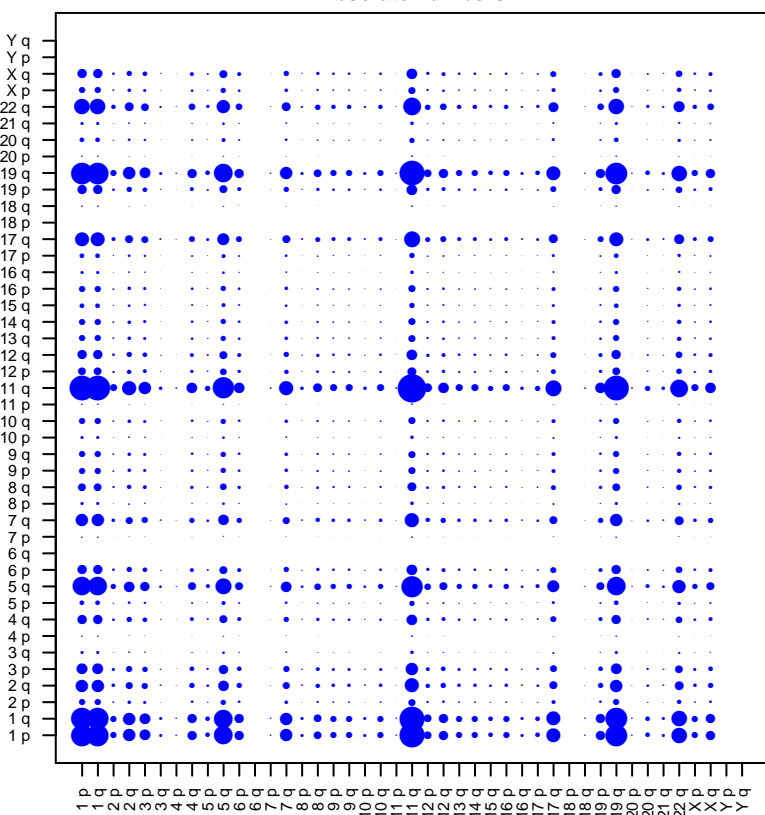
Atypical : 48 ( 64.9 % )

Mesenchymal : 9 ( 10.6 % )

Basal : 6 ( 7.1 % )



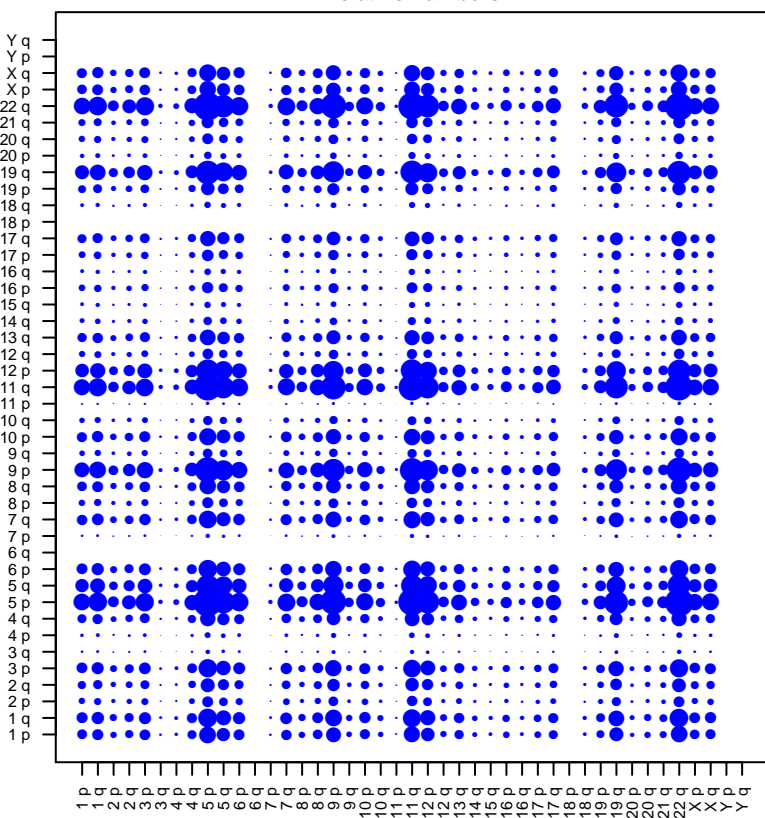
Absolute numbers



Rank	locus	# genes	%	p-value
1	11 q	16	2.5	0.02
2	1 p	14	1.5	0.4
3	1 q	14	1.7	0.3
4	19 q	14	2.1	0.08
5	5 q	12	2.5	0.1
6	22 q	10	2.5	0.05
7	17 q	9	1.4	0.6
8	2 q	8	1.3	0.7
9	7 q	8	1.6	0.4
10	3 p	7	1.7	0.4
11	4 q	6	1.4	0.6
12	6 p	6	1.7	0.4
13	12 q	6	1	0.9
14	19 p	6	1.2	0.7
15	X q	6	1.5	0.5
16	8 q	5	1.5	0.5
17	12 p	5	2.1	0.3
18	2 p	4	2.3	0.2
19	9 p	4	0.9	0.9
20	9 q	4	0.8	0.9
21	10 q	4	1.4	0.6
22	13 q	4	0.8	0.9
23	14 q	4	1.4	0.6
24	16 p	4	1	0.8
25	X p	4	1.5	0.5
26	5 p	3	2.6	0.2
27	15 q	3	0.6	1
28	17 p	3	1	0.8
29	20 q	3	1	0.8
30	3 q	3	0.4	1
31	8 p	2	1	0.8
32	10 p	2	1.6	0.5
33	16 p	2	0.6	1
34	21 q	2	1.1	0.7
35	4 p	1	0.5	0.9
36	7 p	1	0.4	1
37	11 p	1	0.3	1
38	18 q	1	0.6	0.9
39	20 p	1	0.7	0.9
40	6 q	0	0	1
41	18 p	0	0	1
42	Y p	0	0	1
43	Y q	0	0	1

HSCHR6-MHC-DDB

Relative numbers



Rank	locus	# genes	%	p-value
1	5 p	3	2.6	0.2
2	22 q	10	2.5	0.05
3	11 q	16	2.5	0.02
4	9 p	4	2.3	0.2
5	19 q	14	2.1	0.08
6	12 p	5	2.1	0.3
7	5 q	12	2	0.1
8	1 q	14	1.7	0.3
9	6 p	6	1.7	0.4
10	3 p	7	1.7	0.4
11	7 q	8	1.6	0.4
12	10 q	8	1.6	0.5
13	X q	6	1.5	0.5
14	1 p	14	1.5	0.4
15	8 q	5	1.5	0.5
16	X p	4	1.5	0.5
17	13 q	4	1.4	0.6
18	4 q	6	1.4	0.6
19	17 q	9	1.4	0.6
20	2 q	8	1.3	0.7
21	19 p	6	1.2	0.7
22	21 q	3	1.1	0.7
23	17 p	3	1	0.8
24	16 p	4	1	0.8
25	8 p	2	1	0.8
26	20 q	3	1	0.8
27	2 p	4	1	0.8
28	12 q	6	1	0.9
29	9 q	4	0.9	0.9
30	10 q	4	0.8	0.9
31	14 q	4	0.8	0.9
32	20 p	1	0.7	0.9
33	16 q	2	0.6	1
34	15 q	3	0.6	1
35	18 q	1	0.6	0.9
36	4 p	1	0.5	0.9
37	3 q	2	0.4	1
38	7 p	1	0.4	1
39	11 p	1	0.3	1
40	6 q	0	0	1
41	18 p	0	0	1
42	Y p	0	0	1
43	Y q	0	0	1



# Spot H

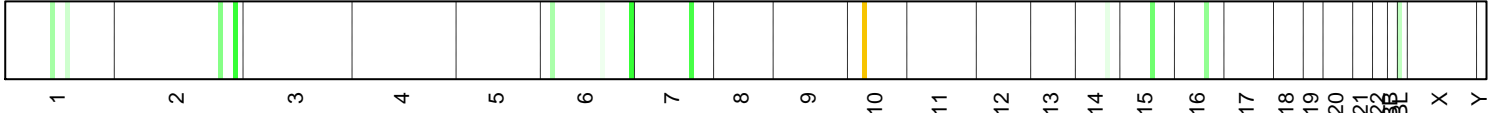
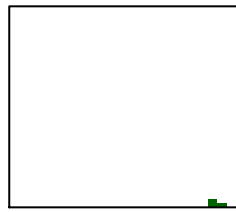
# genes in spot = 68 ( 65 with loci information)

# samples with spot = 50 ( 18.2 % )

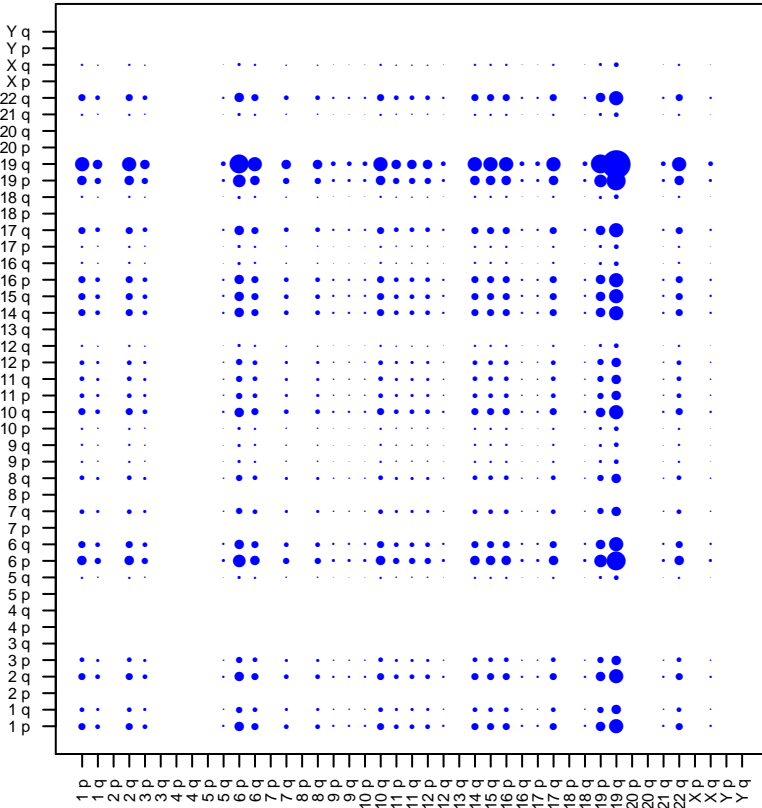
Atypical : 41 ( 55.4 % )

Mesenchymal : 6 ( 7.1 % )

Basal : 3 ( 3.6 % )



Absolute numbers

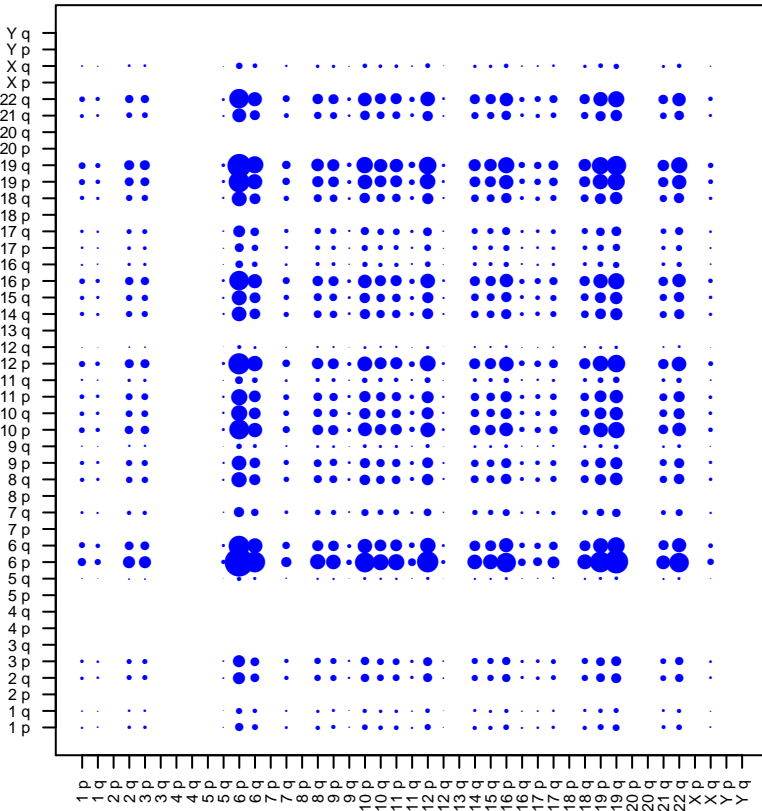


Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	19 q	6	0.9	0.06
2	6 p	4	1.1	0.06
3	19 p	4	0.8	0.2
4	2 p	3	0.8	0.2
5	2 q	3	0.8	0.2
6	10 q	3	0.8	0.2
7	14 q	3	0.8	0.2
8	16 p	3	0.8	0.2
9	16 q	3	0.8	0.2
10	17 q	3	0.8	0.2
11	22 q	3	0.8	0.2
12	11 q	3	0.8	0.2
13	3 p	2	0.5	0.9
14	7 q	2	0.4	0.6
15	8 q	2	0.5	0.4
16	11 p	2	0.6	0.4
17	11 q	2	0.6	0.4
18	12 p	2	0.6	0.4
19	12 q	2	0.6	0.4
20	5 q	2	0.5	0.9
21	9 p	2	0.5	0.9
22	9 q	2	0.5	0.9
23	10 p	2	0.8	0.4
24	12 p	2	0.9	0.9
25	16 q	2	0.8	0.9
26	17 p	2	0.7	0.5
27	18 q	2	0.5	0.8
28	21 q	2	0.5	0.8
29	X q	1	0.5	0.8
30	2 p q	1	0.8	0.6
31	3 p	1	0.0	1.1
32	3 q	1	0.0	1.1
33	4 q	1	0.0	1.1
34	5 p	1	0.0	1.1
35	7 p	1	0.0	1.1
36	8 p	1	0.0	1.1
37	13 q	1	0.0	1.1
38	18 p	1	0.0	1.1
39	20 p	1	0.0	1.1
40	20 q	1	0.0	1.1
41	X p	1	0.0	1.1
42	Y p	1	0.0	1.1
43	Y q	1	0.0	1.1

H3CHR6-MHC-QBB

Relative numbers



Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	6 p	4	1.1	0.06
2	19 q	4	0.9	0.06
3	12 p	2	0.8	0.3
4	19 p	2	0.8	0.2
5	6 q	2	0.8	0.2
6	10 p	2	0.8	0.4
7	16 p	2	0.8	0.2
8	22 q	2	0.8	0.2
9	11 p	2	0.6	0.4
10	10 q	2	0.6	0.3
11	8 q	2	0.6	0.4
12	15 q	2	0.6	0.4
13	18 q	2	0.6	0.4
14	14 q	2	0.6	0.4
15	9 p	2	0.6	0.5
16	21 q	2	0.5	0.5
17	2 q	2	0.5	0.5
18	3 p	2	0.5	0.5
19	17 q	2	0.5	0.5
20	7 q	2	0.4	0.6
21	17 p	1	0.4	0.7
22	1 p	1	0.0	0.8
23	11 p	1	0.0	0.8
24	16 q	1	0.0	0.8
25	X q	1	0.0	0.8
26	1 q	1	0.0	0.9
27	9 q	1	0.0	0.9
28	5 q	1	0.0	0.9
29	12 q	1	0.0	0.9
30	2 p	1	0.0	0.9
31	3 q	1	0.0	1.1
32	4 q	1	0.0	1.1
33	5 p	1	0.0	1.1
34	7 p	1	0.0	1.1
35	8 p	1	0.0	1.1
36	13 q	1	0.0	1.1
37	18 p	1	0.0	1.1
38	20 p	1	0.0	1.1
39	20 q	1	0.0	1.1
40	X p	1	0.0	1.1
41	Y p	1	0.0	1.1
42	Y q	1	0.0	1.1
43	Y q	1	0.0	1.1

# Spot I

# genes in spot = 89 ( 88 with loci information)

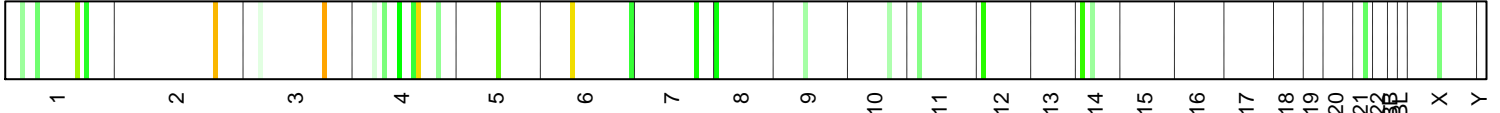
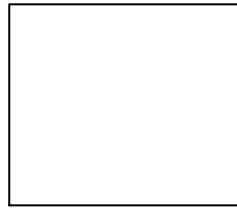
# samples with spot = 46 ( 16.7 % )

Atypical : 21 ( 28.4 % )

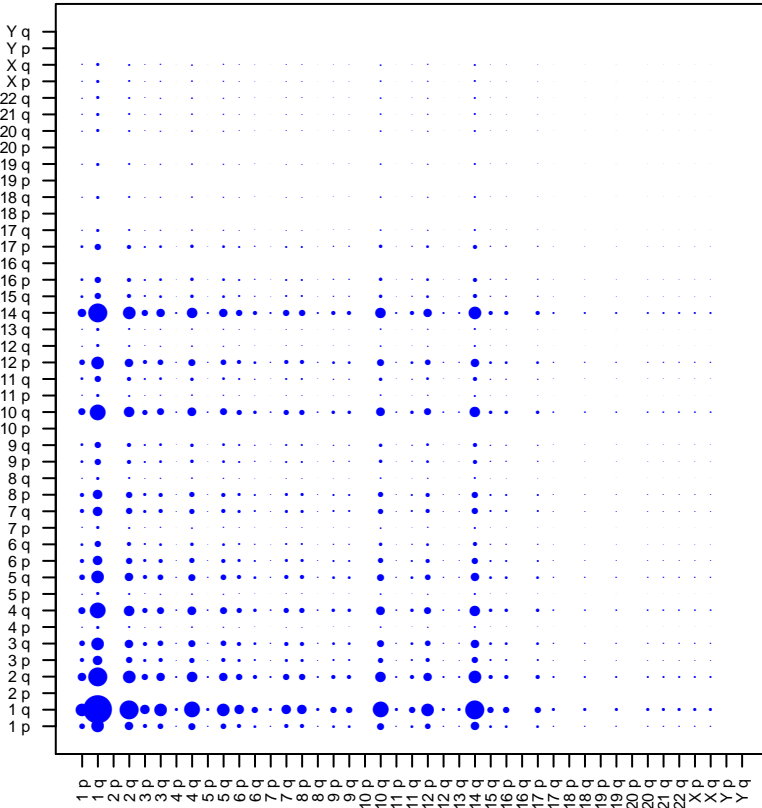
Classical : 2 ( 6.2 % )

Mesenchymal : 18 ( 21.2 % )

Basal : 5 ( 6 % )



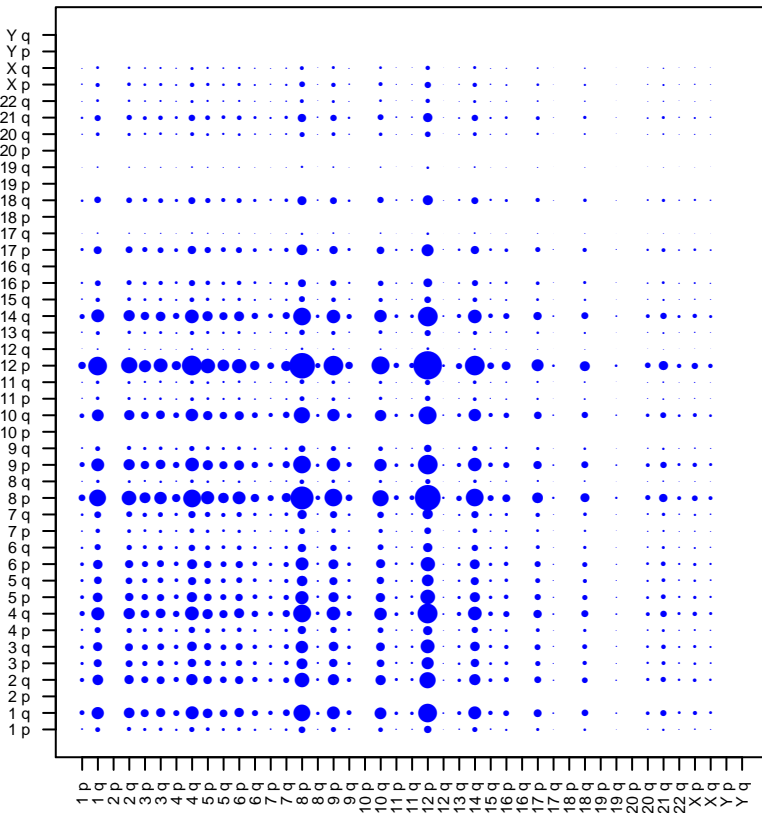
Absolute numbers



Rank	locus	# genes	%	p-value
1	1 q	9	1.1	0.04
2	2 q	6	0.9	0.1
3	14 q	6	1.1	0.07
4	4 q	6	1.2	0.09
5	10 q	5	1	0.1
6	1 p	4	0.4	0.08
7	3 q	4	0.8	0.3
8	5 q	4	0.7	0.4
9	12 p	4	1.7	0.04
10	3 p	4	0.6	0.5
11	6 p	3	0.8	0.3
12	7 q	3	0.6	0.5
13	8 p	3	1.5	0.1
14	6 q	3	0.5	0.6
15	9 p	3	1.1	0.2
16	9 q	2	0.4	0.7
17	11 q	2	0.3	0.9
18	15 q	2	0.4	0.8
19	16 q	2	0.5	0.6
20	17 p	2	0.7	0.5
21	4 p	1	0.5	0.6
22	5 p	1	0.9	0.5
23	7 p	1	0.4	0.8
24	8 q	1	0.3	0.8
25	11 p	1	0.3	0.8
26	12 q	1	0.2	1
27	13 q	1	0.4	0.8
28	17 q	1	0.2	1
29	18 q	1	0.2	0.6
30	19 q	1	0.2	1
31	20 q	1	0.2	1
32	21 q	1	0.5	0.6
33	22 q	1	0.5	0.6
34	X q	1	0.3	0.9
35	X q	1	0.3	0.9
36	2 p	1	0	1
37	10 p	0	0	1
38	16 q	0	0	1
39	18 p	0	0	1
40	19 p	0	0	1
41	20 p	0	0	1
42	Y p	0	0	1
43	Y q	0	0	1

H3CHR6-MHC-QBB

Relative numbers



Rank	locus	# genes	%	p-value
1	12 p	4	1.7	0.04
2	8 p	3	1.5	0.1
3	4 q	3	1.2	0.09
4	14 q	3	1.1	0.07
5	9 p	2	1.1	0.2
6	1 q	2	1.1	0.04
7	10 q	1	1	0.1
8	2 q	1	0.9	0.1
9	5 p	1	0.9	0.5
10	6 p	1	0.8	0.5
11	3 q	1	0.8	0.3
12	3 p	1	0.7	0.4
13	17 p	1	0.7	0.5
14	5 q	1	0.7	0.4
15	7 q	1	0.6	0.5
16	18 q	1	0.6	0.6
17	21 q	1	0.5	0.6
18	6 q	1	0.5	0.6
19	4 p	2	0.5	0.6
20	16 p	2	0.5	0.6
21	9 q	2	0.4	0.7
22	1 p	4	0.4	0.8
23	7 p	1	0.4	0.8
24	15 q	2	0.4	0.8
25	X p	1	0.4	0.8
26	13 q	1	0.4	0.8
27	20 q	1	0.3	0.8
28	11 p	1	0.3	0.8
29	11 q	2	0.3	0.9
30	8 q	1	0.3	0.8
31	X q	1	0.3	0.9
32	22 q	1	0.3	0.9
33	12 q	1	0	1
34	17 q	1	0	1
35	19 q	1	0	1
36	2 p	0	0	1
37	10 p	0	0	1
38	16 q	0	0	1
39	18 p	0	0	1
40	19 p	0	0	1
41	20 p	0	0	1
42	Y p	0	0	1
43	Y q	0	0	1

# Spot J

# genes in spot = 211 ( 185 with loci information)

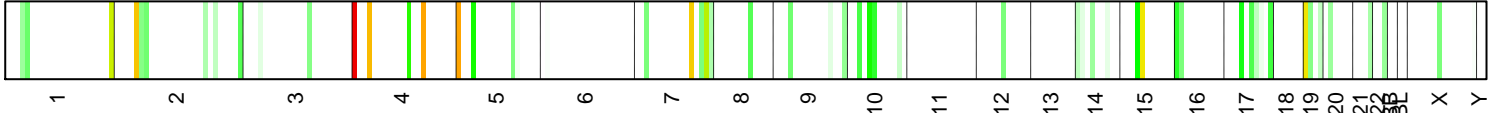
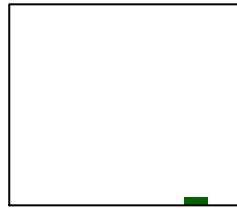
# samples with spot = 30 ( 10.9 % )

Atypical : 22 ( 29.7 % )

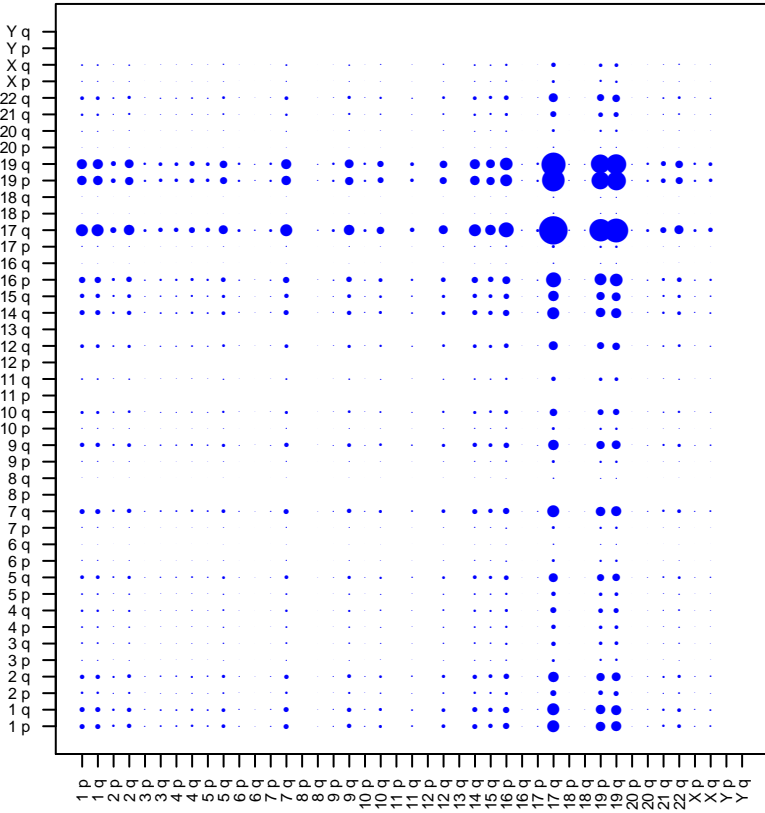
Classical : 1 ( 3.1 % )

Mesenchymal : 4 ( 4.7 % )

Basal : 3 ( 3.6 % )



Absolute numbers

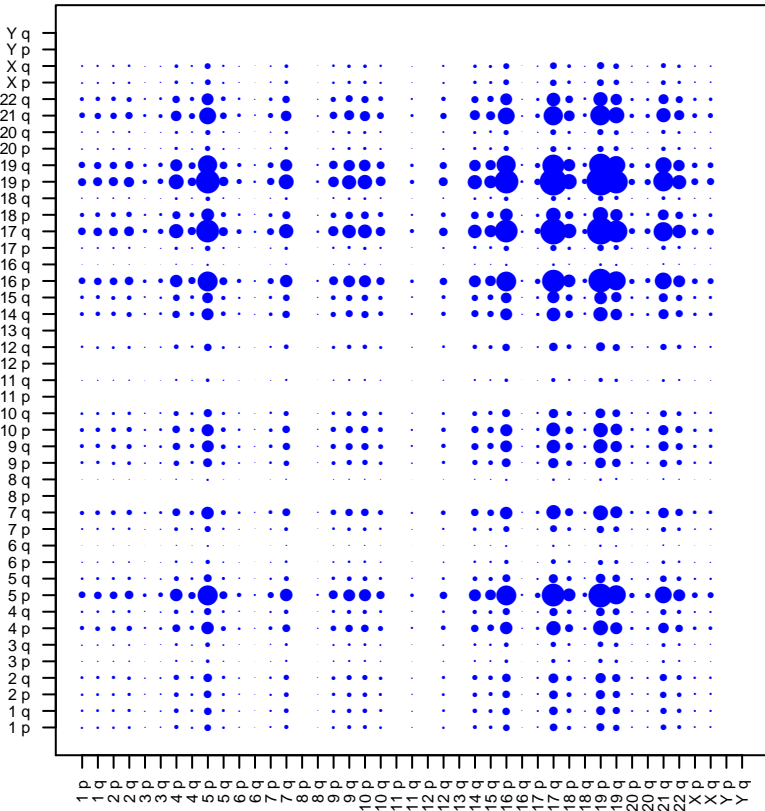


Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	17q	19	2.9	9e-04
2	19q	16	2.5	0.01
3	19p	15	3.1	0.002
4	16p	10	2.6	0.03
5	1p	9	0.9	0.08
6	1q	8	1.1	0.38
7	14q	7	1.6	0.33
8	21q	7	1.5	0.4
9	9q	7	1.5	0.7
10	12q	6	1.4	0.4
11	15q	6	1.4	0.5
12	5q	6	1.1	0.8
13	22q	6	1.1	0.8
14	10q	5	1.5	0.4
15	2p	4	1.1	0.7
16	4q	4	1.1	0.8
17	21q	4	0.9	0.2
18	3q	3	0.6	0.8
19	4p	3	0.6	0.8
20	4p	3	1.6	0.4
21	5p	3	2.6	0.2
22	11q	3	0.5	1
23	Xq	3	0.8	0.9
24	3p	2	0.5	1
25	6p	2	0.6	1
26	7p	2	0.8	0.8
27	9p	2	1.1	0.7
28	10p	2	1.6	0.5
29	17p	2	0.7	0.9
30	20q	2	0.7	0.9
31	Xp	2	0.7	0.9
32	6q	1	0.3	1
33	8q	1	0.3	1
34	16q	1	0.3	1
35	18p	1	1.6	0.6
36	18q	1	0.6	0.9
37	20p	1	0.7	0.9
38	8p	0	0	1
39	11p	0	0	1
40	12p	0	0	1
41	13q	0	0	1
42	Yp	0	0	1
43	Yq	0	0	1

H3CHR6-MHC-QBB

Relative numbers



Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	19p	15	3.1	0.002
2	17q	19	2.9	9e-04
3	5p	3	0.2	0.2
4	16p	10	2.6	0.03
5	19q	16	2.5	0.01
6	21q	4	2.2	0.2
7	18p	1	1.6	0.6
8	4p	3	1.6	0.4
9	7q	8	1.6	0.3
10	10p	8	1.1	0.5
11	14q	8	1.5	0.4
12	22q	6	1.5	0.4
13	9q	7	1.5	0.4
14	15q	7	1.4	0.5
15	9p	2	1.1	0.7
16	2q	7	1.1	0.7
17	10q	5	1.1	0.7
18	5q	6	1.1	0.8
19	2p	4	1.1	0.8
20	1q	8	1.1	0.8
21	12q	6	1.1	0.8
22	4q	8	0	0.8
23	1q	4	0	0.8
24	7p	8	0	0.8
25	Xq	3	0.8	0.9
26	Xp	2	0.7	0.9
27	17p	2	0.7	0.9
28	20p	1	0.7	0.9
29	20q	2	0.7	0.9
30	3q	3	0.6	1
31	18q	1	0.6	0.9
32	6p	2	0.6	1
33	3p	2	0.5	1
34	11q	3	0.5	1
35	16q	1	0.3	1
36	8q	1	0.3	1
37	6q	1	0.3	1
38	8p	0	0	1
39	11p	0	0	1
40	12p	0	0	1
41	13q	0	0	1
42	Yp	0	0	1
43	Yq	0	0	1

# Spot K

# genes in spot = 766 ( 757 with loci information)

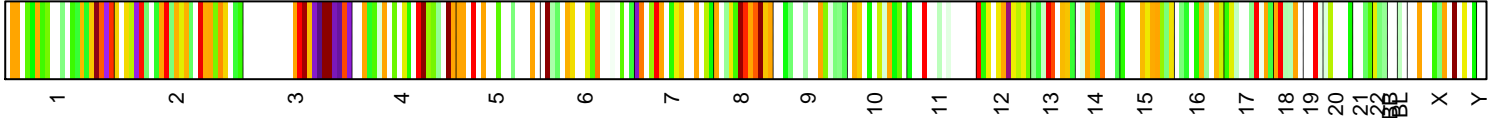
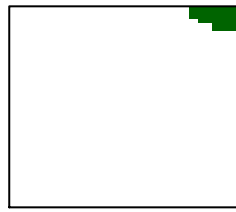
# samples with spot = 14 ( 5.1 % )

Atypical : 3 ( 4.1 % )

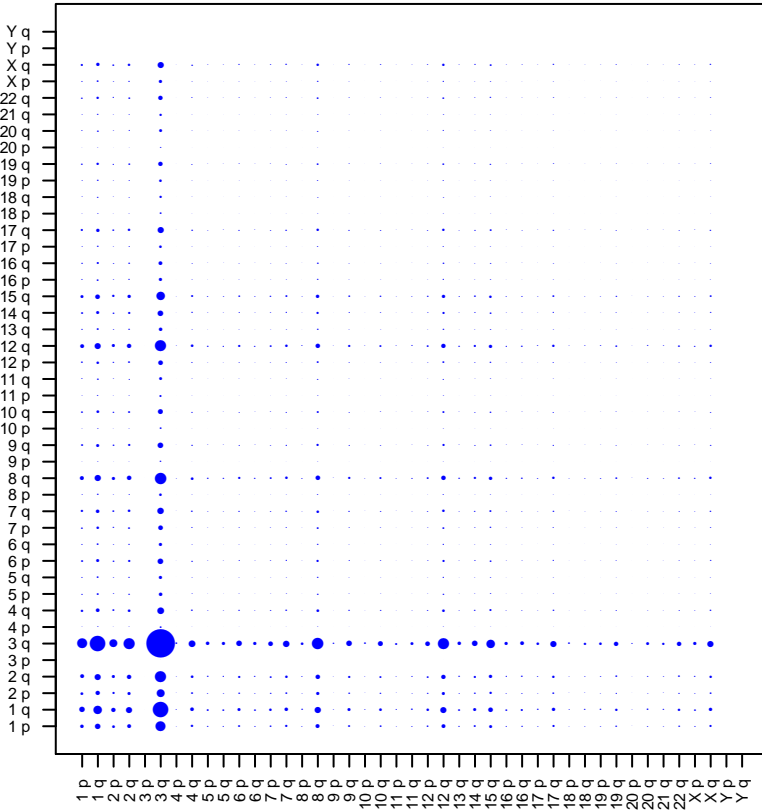
Classical : 8 ( 25 % )

Mesenchymal : 2 ( 2.4 % )

Basal : 1 ( 1.2 % )



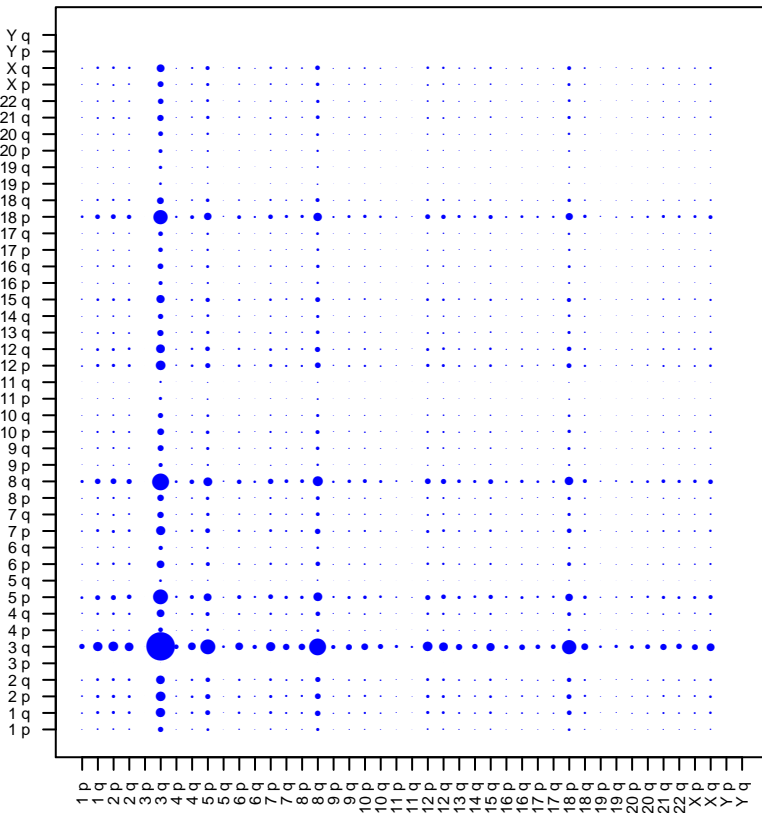
Absolute numbers



Rank	locus	# genes	%	p-value
1	3 q	97	19.6	<2e-16
2	1 q	53	6.4	0.01
3	8 q	39	11.6	2e-07
4	2 q	38	6	0.08
5	12 q	38	6.1	0.07
6	1 p	34	9.7	1
7	15 q	29	5.7	0.2
8	2 p	27	6.7	0.05
9	4 q	23	5.3	0.3
10	7 q	22	4.4	0.7
11	17 q	21	3.2	1
12	X q	21	5.4	0.3
13	6 p	19	5.3	0.3
14	9 q	19	4.1	0.8
15	14 q	19	3.6	0.9
16	10 q	17	3.6	0.9
17	7 p	16	6.3	0.1
18	12 p	16	6.6	0.1
19	19 q	16	6.6	0.1
20	22 q	15	3.8	0.8
21	16 q	13	3.9	0.8
22	5 p	12	10.3	0.009
23	13 q	12	4.3	0.7
24	5 q	11	1.9	1
25	6 q	11	3	1
26	16 p	11	2.8	1
27	X p	11	4.1	0.7
28	11 q	10	1.5	1
29	20 q	10	3.3	0.9
30	8 p	9	4.5	0.6
31	17 p	9	3.1	0.9
32	19 p	9	1.8	1
33	18 q	8	4.7	0.6
34	21 q	8	4.3	0.7
35	11 p	7	2.2	1
36	4 p	6	3.2	0.9
37	10 p	6	4.7	0.6
38	18 p	6	9.8	0.07
39	9 p	5	2.9	0.9
40	20 p	4	2.7	0.9
41	3 p	1	0.2	1
42	Y p	0	0	1
43	Y q	0	0	1

H3CHR6-MHC-QBB

Relative numbers



Rank	locus	# genes	%	p-value
1	3 q	97	19.6	<2e-16
2	8 q	39	11.6	2e-07
3	5 p	12	10.3	0.009
4	18 p	6	9.8	0.07
5	2 p	27	6.7	0.05
6	12 p	16	6.6	0.1
7	1 q	53	6.4	0.01
8	7 p	16	6.3	0.1
9	12 q	38	6.1	0.07
10	2 q	38	6.1	0.07
11	15 q	29	5.7	0.2
12	X q	21	5.4	0.3
13	4 q	23	5.3	0.3
14	6 p	19	5.3	0.3
15	18 q	8	4.7	0.6
16	10 p	6	4.7	0.6
17	8 p	9	4.5	0.6
18	7 q	22	4.4	0.7
19	21 q	8	4.3	0.7
20	13 q	12	4.3	0.7
21	9 q	19	4.1	0.8
22	X p	11	4.1	0.7
23	16 q	13	3.9	0.8
24	22 q	15	3.8	0.8
25	1 p	34	3.7	1
26	14 q	19	3.6	0.9
27	10 q	17	3.6	0.9
28	20 q	10	3.3	0.9
29	17 q	21	3.2	1
30	4 p	6	3.2	0.9
31	17 p	9	3.1	0.9
32	6 q	11	3	1
33	9 p	5	2.9	0.9
34	16 p	11	2.8	1
35	20 p	4	2.7	0.9
36	19 q	15	2.3	1
37	11 p	7	2.2	1
38	5 q	11	1.9	1
39	19 p	9	1.8	1
40	11 q	10	1.5	1
41	3 p	1	0.2	1
42	Y p	0	0	1
43	Y q	0	0	1

# Spot L

# genes in spot = 348 ( 342 with loci information)

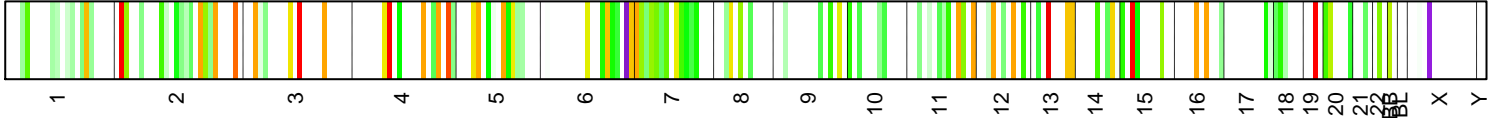
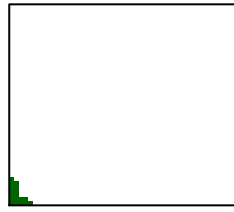
# samples with spot = 48 ( 17.5 % )

Atypical : 3 ( 4.1 % )

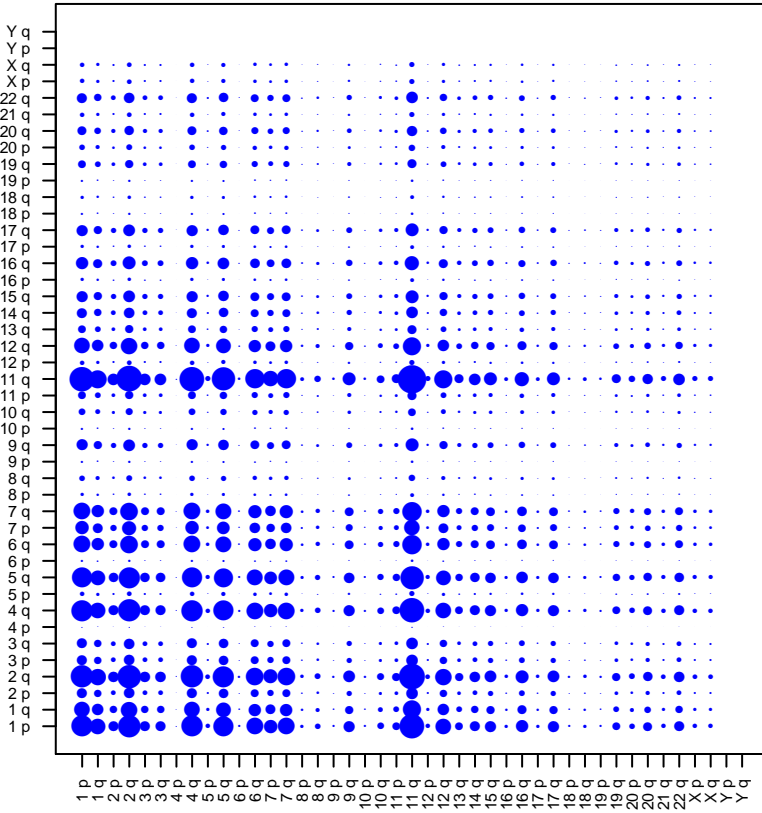
Classical : 1 ( 3.1 % )

Mesenchymal : 43 ( 50.6 % )

Basal : 1 ( 1.2 % )



Absolute numbers

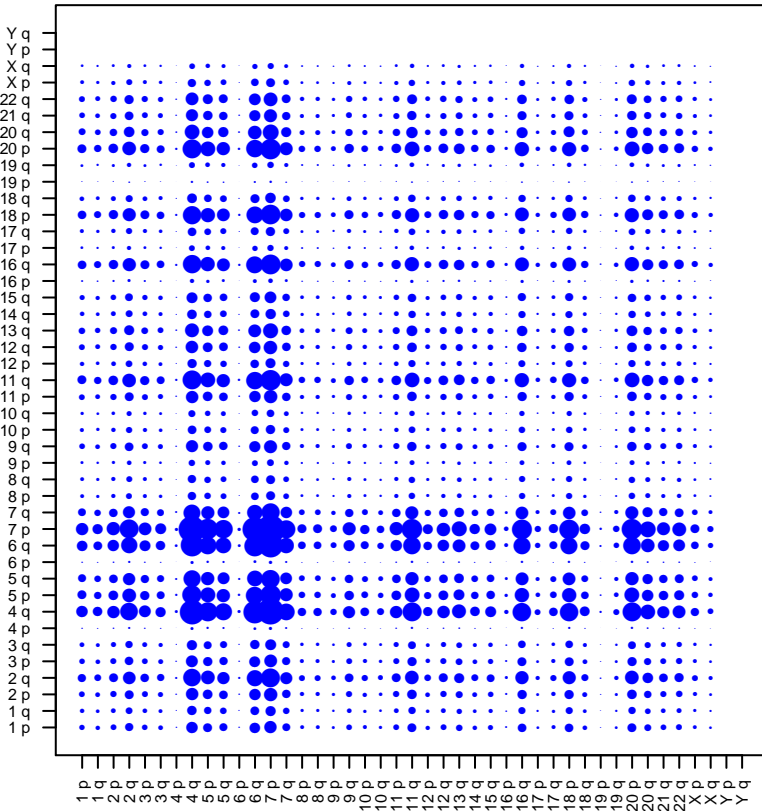


Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	11 q	22	3.4	0.02
2	2 q	20	3.1	0.06
3	1 p	19	2.6	0.6
4	4 q	19	4.4	0.003
5	5 q	18	3.1	0.08
6	6 q	15	4.4	0.01
7	7 q	14	3	0.1
8	1 q	14	1.7	0.9
9	12 q	14	2.2	0.5
10	7 p	12	4.7	0.009
11	16 q	11	3.3	0.1
12	9 q	10	2.2	0.5
13	15 q	10	2	0.7
14	17 q	10	1.5	0.9
15	2 p	9	2.2	0.5
16	3 p	9	2.1	0.6
17	3 q	9	1.8	0.7
18	14 q	9	1.7	0.8
19	22 q	9	2.3	0.5
20	20 q	8	2.6	0.3
21	11 p	7	2.2	0.5
22	13 q	7	2.5	0.4
23	19 q	7	1.1	1
24	10 q	6	1.3	0.9
25	8 q	5	1.5	0.9
26	20 p	5	3.4	0.2
27	5 p	4	3.4	0.2
28	12 p	4	1.7	0.8
29	21 q	4	2.2	0.6
30	X p	4	1.5	0.8
31	X q	4	1	1
32	8 p	4	1.5	0.8
33	16 p	3	0.8	1
34	17 p	3	1	0.9
35	18 q	3	1.8	0.7
36	6 p	2	0.6	1
37	9 p	2	1.1	0.9
38	10 p	2	1.6	0.8
39	18 p	2	3.3	0.4
40	19 p	2	0.4	1
41	4 p	1	0.5	1
42	Y p	0	0	1
43	Y q	0	0	1

H3CHR6-MHC-QBB

Relative numbers



Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	7 p	12	4.7	0.009
2	4 q	19	4.4	0.003
3	6 q	15	4	0.01
4	5 p	4	3.4	0.2
5	20 p	5	3.4	0.2
6	11 q	22	3.4	0.02
7	16 q	11	3.3	0.1
8	18 p	2	3.3	0.4
9	2 q	20	3.1	0.06
10	5 q	18	3.1	0.08
11	7 q	15	3.3	0.1
12	20 q	8	2.6	0.3
13	13 q	7	2.5	0.4
14	22 q	9	2.3	0.5
15	12 q	14	2.2	0.5
16	2 p	9	2.2	0.5
17	11 p	7	2.2	0.5
18	9 q	10	2.2	0.5
19	21 q	4	2.2	0.6
20	3 p	9	2.1	0.6
21	1 p	19	2	0.6
22	15 q	10	2	0.7
23	3 q	9	1.8	0.7
24	18 q	3	1.8	0.7
25	14 q	9	1.7	0.8
26	1 q	14	1.7	0.9
27	12 p	4	1.7	0.8
28	10 p	2	1.6	0.8
29	17 q	10	1.5	0.9
30	8 p	3	1.5	0.8
31	8 q	5	1.5	0.9
32	X p	4	1.5	0.8
33	10 q	6	1.3	0.9
34	9 p	2	1.1	0.9
35	19 q	2	1.1	0.9
36	17 p	3	1	0.9
37	X q	4	1	1
38	16 p	3	0.8	1
39	6 p	2	0.6	1
40	4 p	1	0.5	1
41	19 p	2	0.4	1
42	Y p	0	0	1
43	Y q	0	0	1

# Spot M

# genes in spot = 354 ( 332 with loci information)

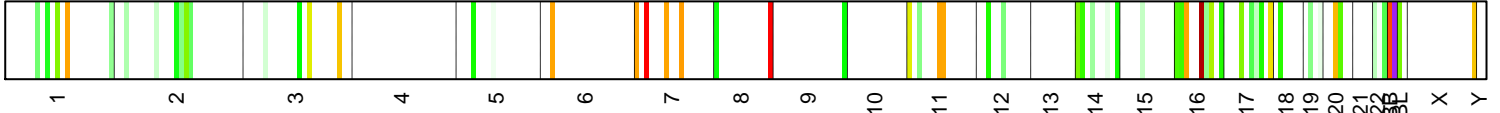
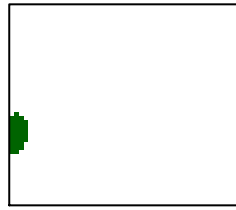
# samples with spot = 13 ( 4.7 % )

Atypical : 3 ( 4.1 % )

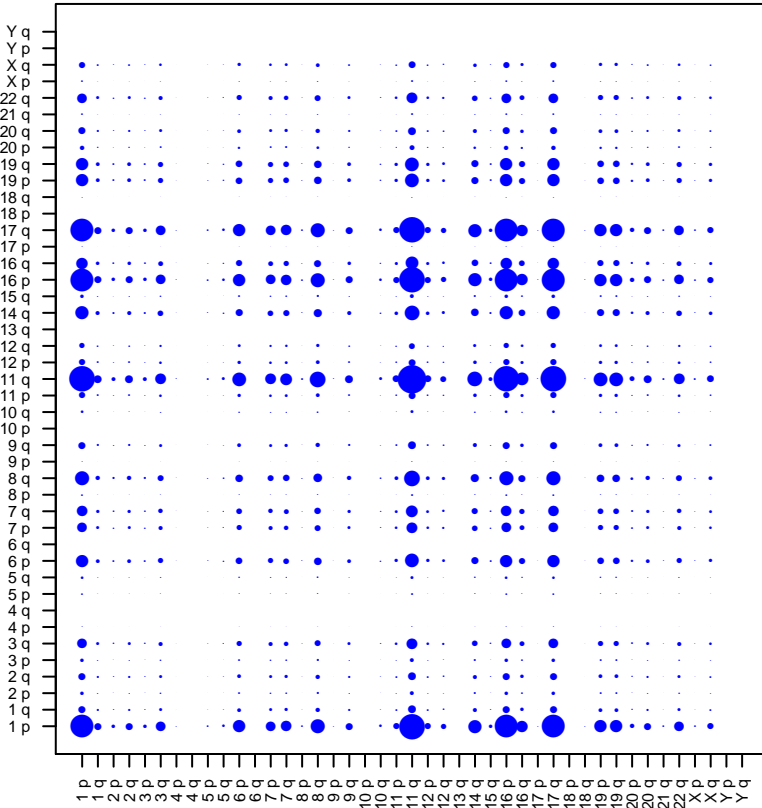
Classical : 1 ( 3.1 % )

Mesenchymal : 6 ( 7.1 % )

Basal : 3 ( 3.6 % )



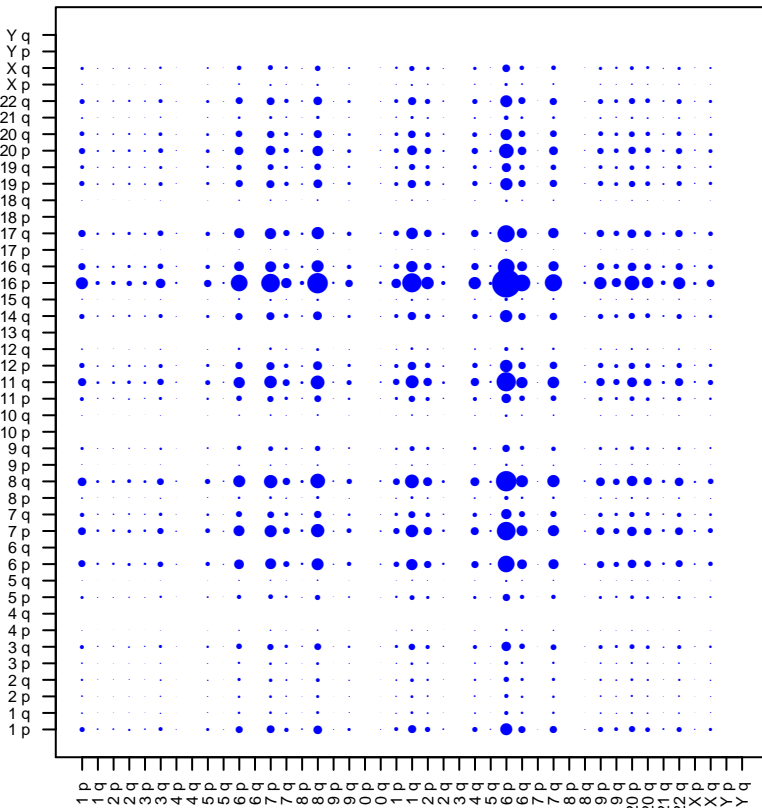
Absolute numbers



Rank	locus	# genes	%	p-value
1	11 q	29	4.5	2e-04
2	1 p	26	2.8	0.1
3	16 p	26	6.6	5e-07
4	17 q	26	4	0.002
5	8 q	16	4.8	0.003
6	14 q	15	2.9	0.2
7	6 p	14	3.9	0.03
8	19 p	14	3.9	0.2
9	19 q	14	2.1	0.6
10	16 q	13	3.9	0.03
11	7 q	12	2.4	0.4
12	3 q	11	2.2	0.5
13	7 p	11	4.3	0.02
14	22 q	11	2.8	0.2
15	1 q	8	1	1
16	2 q	8	1.3	1
17	9 q	8	1.7	0.8
18	20 q	8	2.6	0.3
19	11 p	7	2.9	0.5
20	12 p	7	2.9	0.3
21	X q	7	1.8	0.8
22	12 q	6	1	1
23	20 p	5	3.4	0.2
24	2 p	4	1	1
25	3 p	4	0.9	1
26	15 q	4	0.8	1
27	5 q	3	0.5	1
28	10 q	3	0.6	1
29	5 p	3	1.7	0.7
30	8 p	2	1	1
31	21 q	2	1.1	0.9
32	X p	2	0.7	1
33	4 p	1	0.5	1
34	9 p	1	0.6	1
35	17 p	1	0.3	1
36	18 q	1	0.6	1
37	4 q	0	0	1
38	6 q	0	0	1
39	10 p	0	0	1
40	13 q	0	0	1
41	18 p	0	0	1
42	Y p	0	0	1
43	Y q	0	0	1

H3CHR6-MHC-GBB

Relative numbers



Rank	locus	# genes	%	p-value
1	16 p	26	6.6	5e-07
2	8 q	16	4.8	0.003
3	11 q	29	4.5	2e-04
4	7 p	11	4.3	0.02
5	17 q	26	4	0.002
6	16 q	13	3.9	0.03
7	6 p	14	3.9	0.03
8	20 p	5	3.4	0.2
9	12 p	7	2.9	0.3
10	14 q	15	2.9	0.2
11	19 p	14	2.9	0.2
12	1 p	26	2.8	0.1
13	22 q	11	2.8	0.2
14	20 q	8	2.6	0.3
15	7 q	12	2.4	0.4
16	3 q	11	2.2	0.5
17	11 p	7	2.2	0.5
18	19 q	14	2.1	0.6
19	X q	7	1.8	0.8
20	9 q	8	1.7	0.8
21	5 p	3	1.7	0.7
22	2 q	3	1.3	1
23	21 q	2	1.1	0.9
24	8 p	2	1	1
25	2 p	4	1	1
26	1 q	8	1	1
27	12 q	6	1	1
28	3 p	4	0.9	1
29	15 q	4	0.8	1
30	X p	2	0.7	1
31	10 q	3	0.6	1
32	18 q	1	0.6	1
33	9 p	1	0.6	1
34	4 p	1	0.5	1
35	5 q	3	0.5	1
36	17 p	1	0.3	1
37	4 q	0	0	1
38	6 q	0	0	1
39	10 p	0	0	1
40	13 q	0	0	1
41	18 p	0	0	1
42	Y p	0	0	1
43	Y q	0	0	1

# Spot N

# genes in spot = 101 ( 100 with loci information)

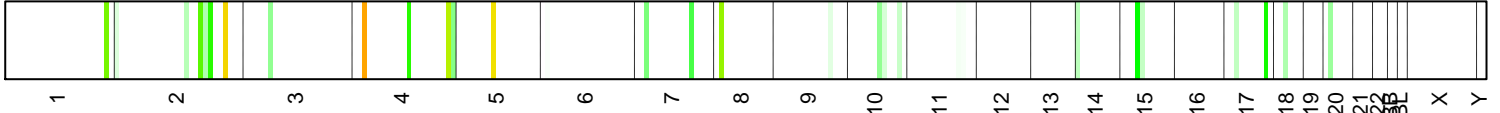
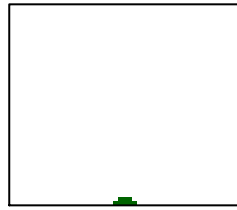
# samples with spot = 39 ( 14.2 % )

Atypical : 9 ( 12.2 % )

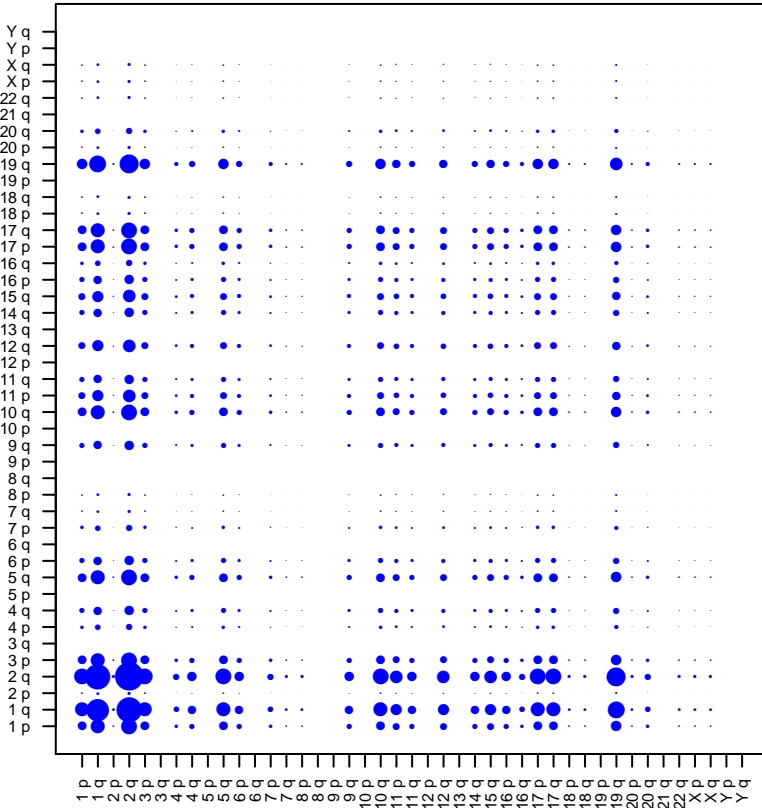
Classical : 4 ( 12.5 % )

Mesenchymal : 18 ( 21.2 % )

Basal : 8 ( 9.5 % )



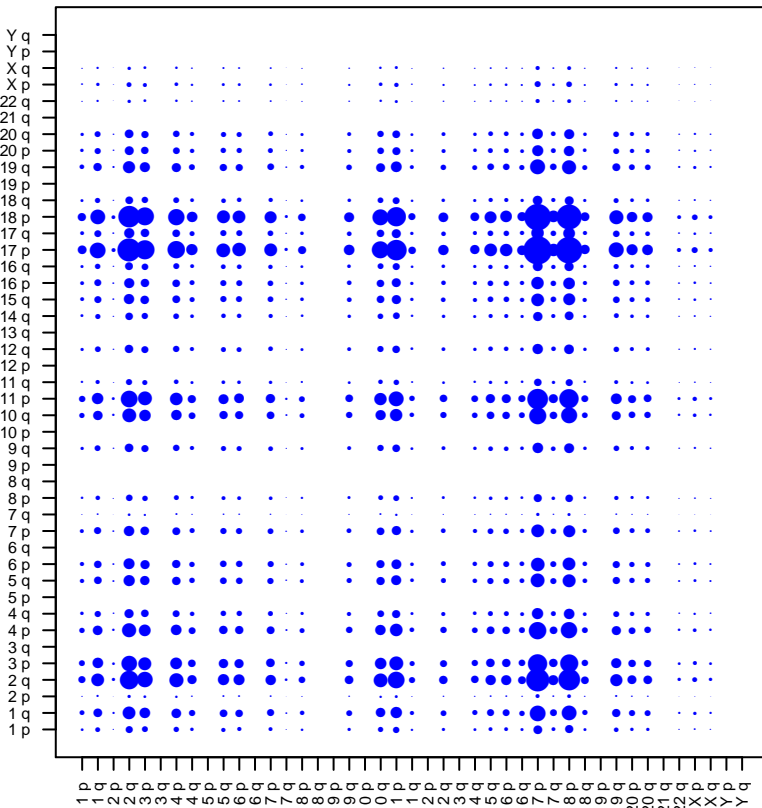
Absolute numbers



Rank	locus	# genes	%	p-value
1	2 q	9	1.4	0.02
2	1 q	1	1	0.1
3	19 q	1	0.9	0.2
4	1 p	1	0.5	0.7
5	3 p	5	0.5	0.1
6	5 q	1	0.9	0.3
7	10 q	1	0.9	0.3
8	17 p	1	1.7	0.03
9	17 q	1	0.8	0.4
10	11 q	4	1.3	0.1
11	12 q	4	0.6	0.5
12	15 q	4	0.8	0.4
13	4 q	3	0.7	0.5
14	6 p	3	0.8	0.4
15	9 q	3	0.7	0.5
16	11 q	3	0.5	0.6
17	14 q	3	0.8	0.4
18	16 p	3	0.8	0.4
19	4 p	1	1.1	0.3
20	7 p	1	0.8	0.5
21	16 q	2	0.6	0.6
22	20 q	2	0.7	0.6
23	2 p	1	0.2	0.9
24	7 q	1	0.2	1
25	8 p	1	0.5	0.7
26	18 p	1	1.6	0.3
27	18 q	1	0.6	0.7
28	20 p	1	0.7	0.6
29	22 q	1	0.3	0.9
30	X p	1	0.4	0.8
31	X q	1	0.4	0.8
32	X q	1	0.3	0.9
33	5 q	0	0	1
34	6 q	0	0	1
35	8 q	0	0	1
36	9 p	0	0	1
37	10 p	0	0	1
38	12 p	0	0	1
39	13 q	0	0	1
40	19 p	0	0	1
41	21 q	0	0	1
42	Y p	0	0	1
43	Y q	0	0	1

H3CHR6-MHC-DDB

Relative numbers



Rank	locus	# genes	%	p-value
1	17 p	5	1.7	0.03
2	18 p	1	1.6	0.3
3	2 q	9	1.4	0.02
4	11 p	4	1.3	0.1
5	3 p	5	1.2	0.1
6	4 p	2	1.1	0.3
7	10 q	5	1.2	0.2
8	1 q	1	1.1	0.1
9	19 q	1	0.9	0.2
10	5 q	1	0.9	0.3
11	6 p	1	0.8	0.4
12	7 p	1	0.8	0.5
13	15 q	4	0.8	0.4
14	17 q	5	0.8	0.4
15	16 p	3	0.8	0.4
16	4 q	3	0.7	0.5
17	20 p	1	0.7	0.6
18	20 q	3	0.7	0.6
19	9 q	3	0.7	0.6
20	12 q	4	0.6	0.5
21	16 q	2	0.6	0.6
22	14 q	1	0.6	0.7
23	1 p	5	0.5	0.6
24	1 p	5	0.5	0.7
25	8 p	1	0.5	0.7
26	11 q	3	0.5	0.8
27	X p	1	0.4	0.8
28	X q	1	0.3	0.9
29	22 q	1	0.3	0.9
30	2 p	1	0.2	0.9
31	7 q	1	0.2	1
32	3 q	0	0	1
33	5 p	0	0	1
34	6 q	0	0	1
35	8 q	0	0	1
36	9 p	0	0	1
37	10 p	0	0	1
38	12 p	0	0	1
39	13 q	0	0	1
40	19 p	0	0	1
41	21 q	0	0	1
42	Y p	0	0	1
43	Y q	0	0	1

# Spot O

# genes in spot = 488 ( 475 with loci information)

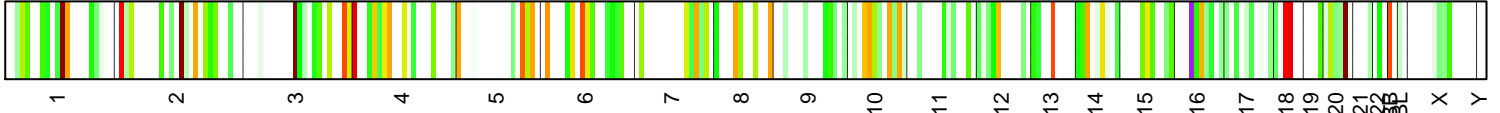
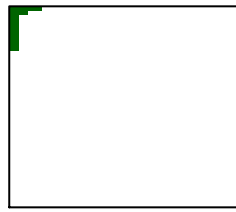
# samples with spot = 70 ( 25.5 % )

Atypical : 1 ( 1.4 % )

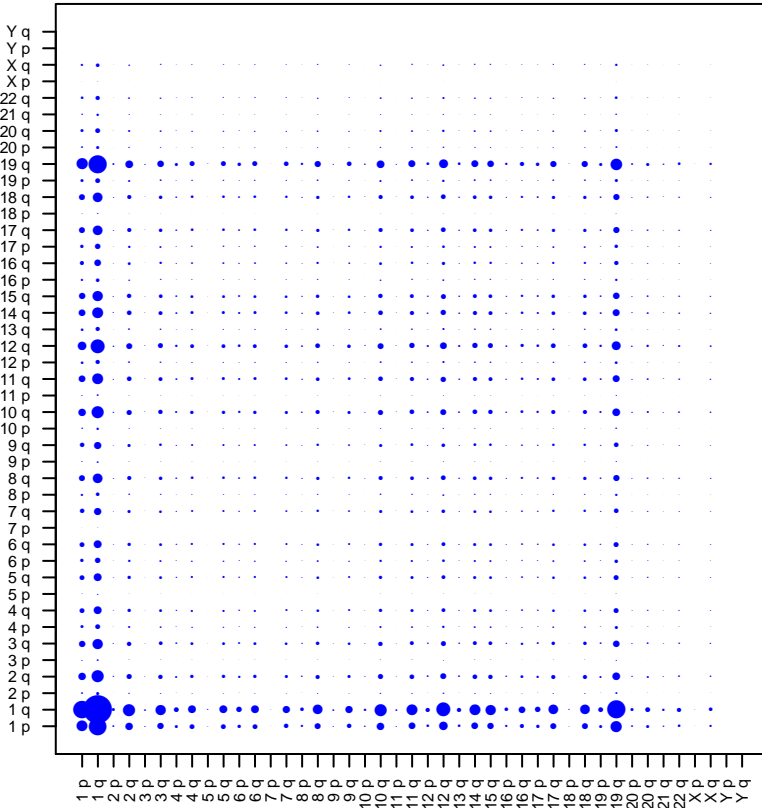
Classical : 1 ( 3.1 % )

Mesenchymal : 5 ( 5.9 % )

Basal : 63 ( 75 % )



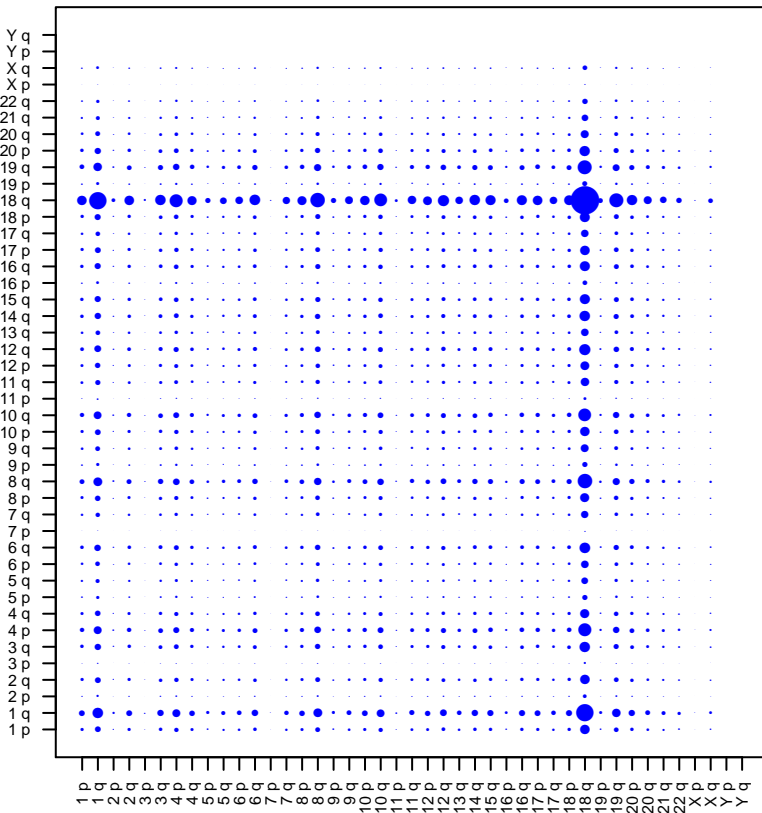
Absolute numbers



Rank	locus	# genes	%	p-value
1	1 q	47	5.7	2e-05
2	19 q	30	4.6	0.01
3	1 p	29	3.1	0.4
4	12 q	23	3.7	0.2
5	2 q	20	3.1	0.5
6	10 q	20	4.2	0.09
7	11 q	18	3.4	0.7
8	14 q	18	3.4	0.3
9	3 q	17	3.4	0.3
10	15 q	17	3.3	0.4
11	8 q	16	4.8	0.05
12	17 q	16	2.5	0.8
13	18 q	16	9.4	6e-05
14	4 q	13	3	0.5
15	5 q	13	2.2	0.9
16	6 q	13	3.5	0.3
17	7 q	12	2.4	0.8
18	9 q	12	2.4	0.7
19	16 q	12	3.3	0.4
20	6 p	11	2.5	0.8
21	17 p	9	3.1	0.5
22	4 p	8	4.3	0.2
23	19 p	8	1.6	1
24	20 q	8	2.6	0.7
25	12 p	7	2.9	0.6
26	13 q	7	2.5	0.7
27	22 q	7	1.8	1
28	8 p	6	3	0.6
29	16 p	6	1.5	1
30	X q	6	1.5	1
31	2 p	5	3.2	0.5
32	20 p	5	3.4	0.5
33	10 p	4	3.1	0.5
34	21 q	4	2.2	0.8
35	3 p	3	0.7	1
36	9 p	3	1.7	0.9
37	11 p	3	0.9	1
38	5 p	2	1.7	0.9
39	18 p	2	3.3	0.6
40	7 p	1	0.4	1
41	X p	1	0.4	1
42	Y p	0	0	1
43	Y q	0	0	1

H3CHR6-MHC-QBB

Relative numbers



Rank	locus	# genes	%	p-value
1	18 q	16	9.4	6e-05
2	1 q	47	5.7	2e-05
3	8 q	16	4.8	0.01
4	19 q	30	4.6	0.05
5	4 p	8	4.3	0.2
6	10 q	20	4.2	0.09
7	12 q	23	3.7	0.2
8	6 q	13	3.5	0.3
9	14 q	18	3.4	0.3
10	3 q	17	3.4	0.3
11	20 p	5	3.4	0.5
12	15 q	17	3.3	0.4
13	16 q	11	3.3	0.4
14	18 p	2	3.3	0.6
15	2 q	20	3.1	0.5
16	17 p	9	3.1	0.5
17	1 p	29	3.1	0.4
18	10 p	4	3.1	0.5
19	4 q	13	3.3	0.5
20	8 p	6	3	0.6
21	12 p	7	2.9	0.6
22	11 q	18	2.9	0.7
23	20 q	8	2.6	0.7
24	9 q	12	2.6	0.7
25	6 p	9	2.5	0.8
26	13 q	7	2.5	0.7
27	17 q	16	2.5	0.8
28	7 q	12	2.4	0.8
29	5 q	13	2.2	0.9
30	21 q	4	2.2	0.8
31	22 q	7	1.8	1
32	9 p	3	1.7	0.9
33	5 p	2	1.7	0.9
34	19 p	6	1.6	1
35	X q	6	1.5	1
36	16 p	6	1.5	1
37	2 p	5	1.2	1
38	11 p	3	0.9	1
39	3 p	3	0.7	1
40	7 p	1	0.4	1
41	X p	1	0.4	1
42	Y p	0	0	1
43	Y q	0	0	1



# Spot P

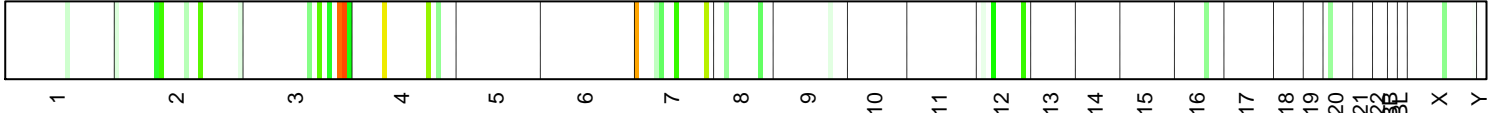
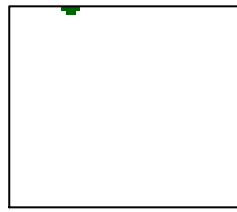
# genes in spot = 110 ( 106 with loci information)

# samples with spot = 31 ( 11.3 % )

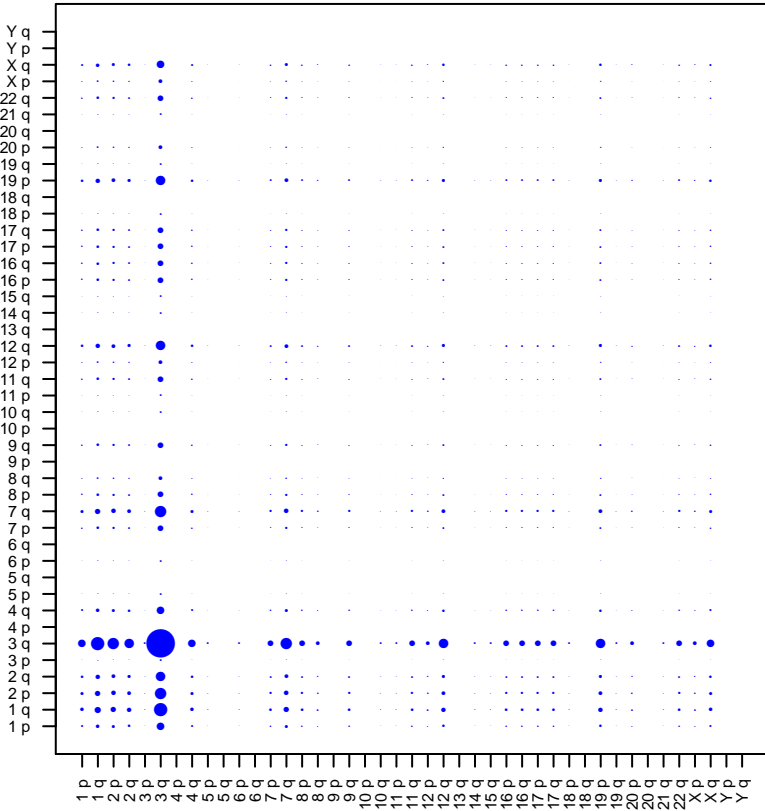
Classical : 13 ( 40.6 % )

Mesenchymal : 4 ( 4.7 % )

Basal : 14 ( 16.7 % )



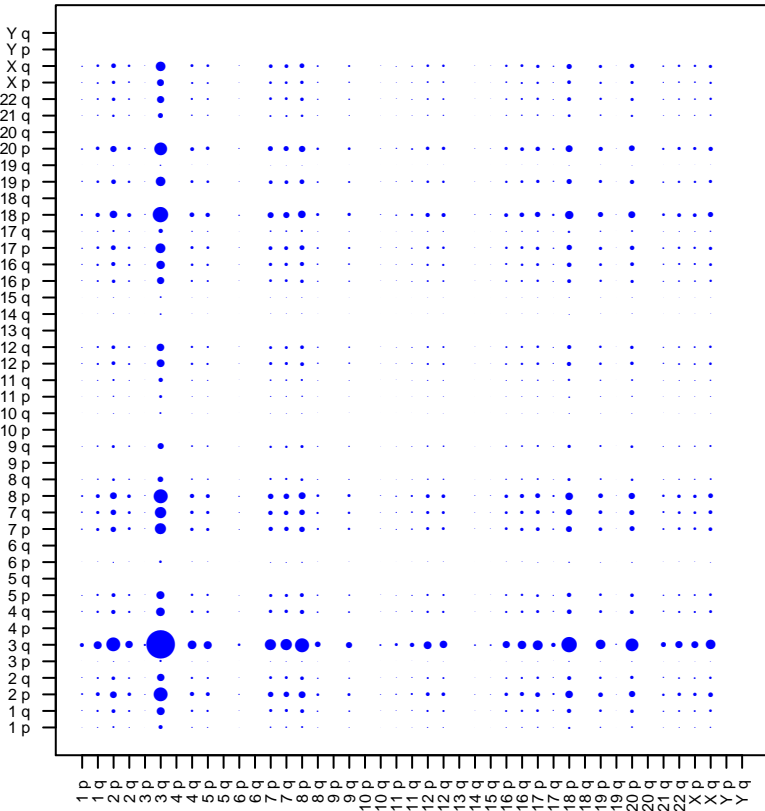
Absolute numbers



Rank	locus	# genes	%	p-value
1	3 q	15	3	1e-06
2	1 q	6	0.8	0.3
3	7 q	2	0.2	0.06
4	2 q	1	0.1	0.1
5	12 q	1	0.1	0.4
6	19 p	1	0.1	0.2
7	1 p	4	0.4	0.02
8	4 q	4	0.4	0.02
9	X q	4	0.4	0.02
10	X q	4	0.4	0.02
11	7 p	3	0.3	0.2
12	8 p	3	0.3	0.2
13	9 q	3	0.3	0.6
14	11 q	3	0.3	0.8
15	16 p	3	0.3	0.5
16	16 q	3	0.3	0.4
17	17 p	3	0.3	0.3
18	17 q	3	0.3	0.8
19	22 q	3	0.3	0.5
20	22 q	3	0.3	0.7
21	8 q	2	0.2	0.5
22	12 p	2	0.2	0.5
23	X p	2	0.2	0.3
24	3 p	1	0.1	0.9
25	5 p	1	0.1	0.6
26	6 p	1	0.1	0.9
27	10 q	1	0.1	0.9
28	11 p	1	0.1	0.9
29	14 q	1	0.1	0.9
30	15 q	1	0.1	1
31	18 q	1	0.1	0.3
32	19 q	1	0.1	1
33	21 q	1	0.1	0.7
34	4 p	1	0.1	1
35	5 q	0	0	1
36	6 q	0	0	1
37	9 p	0	0	1
38	10 p	0	0	1
39	13 q	0	0	1
40	18 q	0	0	1
41	20 q	0	0	1
42	Y p	0	0	1
43	Y q	0	0	1

H3CHR6-MHC-QBB

Relative numbers



Rank	locus	# genes	%	p-value
1	3 q	15	3	1e-06
2	18 p	1	1.1	0.3
3	8 p	1	1.1	0.2
4	2 p	6	1.5	0.06
5	20 p	2	1.4	0.3
6	7 q	6	1.2	0.1
7	7 p	2	1.2	0.2
8	17 p	3	1.1	0.2
9	X q	4	1.1	0.3
10	19 p	5	1.1	0.3
11	4 q	4	1.1	0.3
12	16 q	3	0.9	0.4
13	5 p	1	0.9	0.6
14	1 q	7	0.8	0.3
15	12 p	7	0.8	0.5
16	12 q	5	0.8	0.4
17	2 q	5	0.8	0.4
18	16 p	3	0.8	0.5
19	22 q	3	0.8	0.5
20	X p	2	0.7	0.5
21	9 q	2	0.7	0.6
22	8 q	2	0.7	0.7
23	11 q	1	0.5	0.7
24	11 p	3	0.5	0.8
25	17 q	3	0.5	0.8
26	1 p	4	0.4	0.9
27	11 p	1	0.3	0.9
28	6 p	1	0.3	0.9
29	3 p	1	0.2	0.9
30	10 q	2	0.2	0.9
31	15 q	1	0.2	1
32	14 q	1	0.2	1
33	19 q	1	0.2	1
34	4 p	0	0	1
35	5 q	0	0	1
36	6 q	0	0	1
37	9 p	0	0	1
38	10 p	0	0	1
39	13 q	0	0	1
40	18 q	0	0	1
41	20 q	0	0	1
42	Y p	0	0	1
43	Y q	0	0	1

# Spot Q

# genes in spot = 61 ( 60 with loci information)

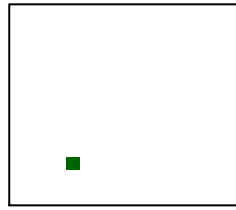
# samples with spot = 34 ( 12.4 % )

Atypical : 5 ( 6.8 % )

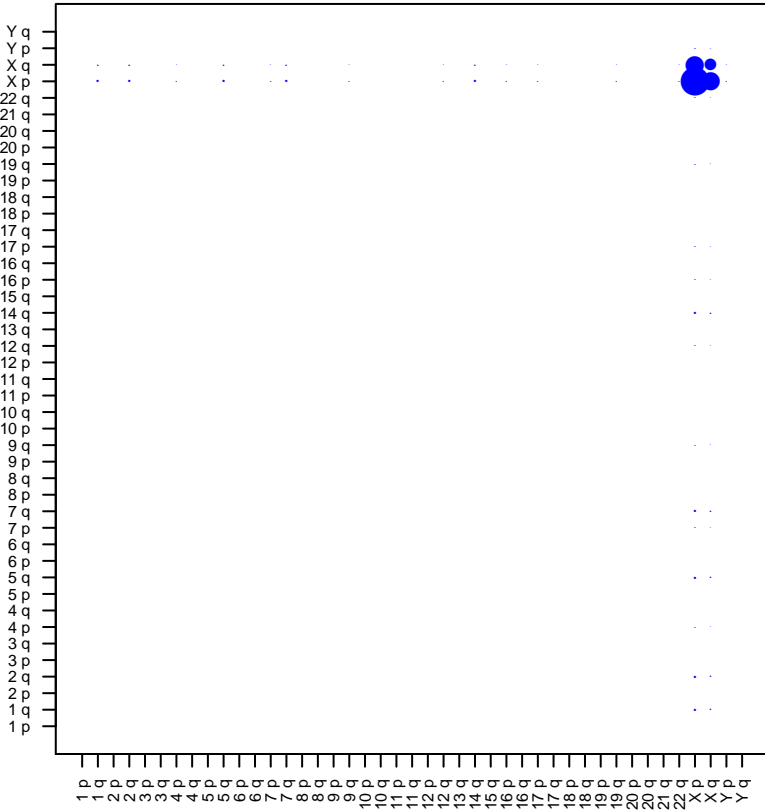
Classical : 5 ( 15.6 % )

Mesenchymal : 12 ( 14.1 % )

Basal : 12 ( 14.3 % )



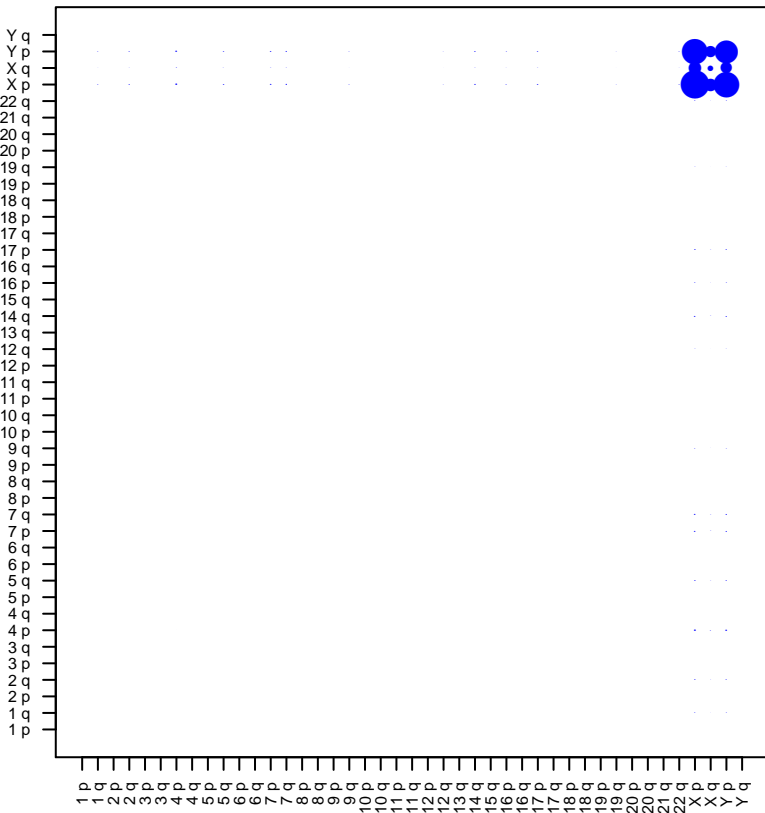
Absolute numbers



Rank	locus	# genes	%	p-value
1	X p	25	9.3	<2e-16
2	X q	16	4.1	7e-13
3	1 q	2	0.2	0.8
4	2 q	2	0.3	0.7
5	7 q	2	0.4	0.6
6	14 q	2	0.4	0.6
7	7 q	2	0.4	0.6
8	4 p	2	0.5	0.6
9	7 p	2	0.4	0.6
10	9 q	2	0.4	0.6
11	12 p	2	0.3	0.8
12	16 p	2	0.3	0.8
13	17 p	2	0.3	0.7
14	19 q	2	0.3	0.8
15	22 q	2	0.3	0.8
16	16 p	2	0.3	0.8
17	17 p	2	0.3	0.7
18	19 q	2	0.3	0.8
19	17 p	2	0.3	0.8
20	16 p	2	0.3	0.8
21	15 q	2	0.3	0.8
22	14 q	2	0.3	0.8
23	13 q	2	0.3	0.8
24	12 q	2	0.3	0.8
25	11 q	2	0.3	0.8
26	10 p	2	0.3	0.8
27	9 q	2	0.3	0.8
28	8 p	2	0.3	0.8
29	10 p	2	0.3	0.8
30	10 q	2	0.3	0.8
31	11 p	2	0.3	0.8
32	11 q	2	0.3	0.8
33	12 p	2	0.3	0.8
34	13 q	2	0.3	0.8
35	15 q	2	0.3	0.8
36	16 q	2	0.3	0.8
37	17 q	2	0.3	0.8
38	18 p	2	0.3	0.8
39	18 q	2	0.3	0.8
40	19 p	2	0.3	0.8
41	20 p	2	0.3	0.8
42	20 q	2	0.3	0.8
43	Y q	0	0	1

H3CHR6-MHC-QBB

Relative numbers



Rank	locus	# genes	%	p-value
1	X p	25	9.3	<2e-16
2	Y p	1	8.3	0.04
3	X q	16	4.1	7e-13
4	4 p	1	0.5	0.5
5	7 q	2	0.4	0.6
6	7 p	1	0.4	0.6
7	14 q	2	0.4	0.6
8	4 p	1	0.4	0.6
9	5 q	2	0.3	0.7
10	2 q	2	0.3	0.7
11	16 p	2	0.3	0.8
12	22 q	2	0.3	0.8
13	1 q	2	0.3	0.8
14	9 q	2	0.3	0.8
15	12 q	2	0.3	0.8
16	19 q	2	0.3	0.9
17	17 p	2	0.3	0.9
18	1 p	0	0	1
19	2 p	0	0	1
20	3 q	0	0	1
21	4 q	0	0	1
22	5 p	0	0	1
23	6 p	0	0	1
24	6 q	0	0	1
25	8 p	0	0	1
26	8 q	0	0	1
27	9 p	0	0	1
28	10 p	0	0	1
29	10 q	0	0	1
30	11 p	0	0	1
31	11 q	0	0	1
32	12 p	0	0	1
33	13 q	0	0	1
34	15 q	0	0	1
35	16 q	0	0	1
36	17 q	0	0	1
37	18 p	0	0	1
38	18 q	0	0	1
39	19 p	0	0	1
40	20 p	0	0	1
41	20 q	0	0	1
42	21 q	0	0	1
43	Y q	0	0	1

# Spot R

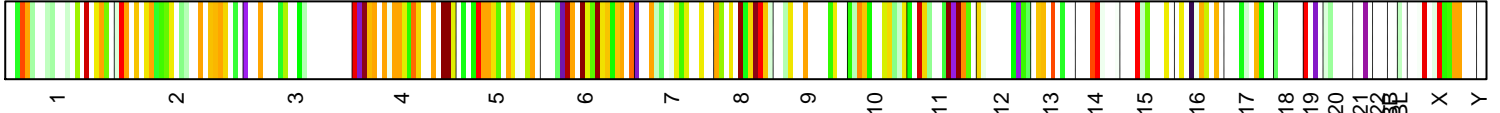
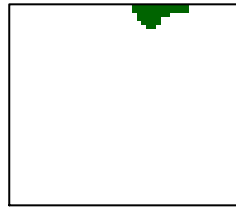
# genes in spot = 547 ( 532 with loci information)

# samples with spot = 5 ( 1.8 % )

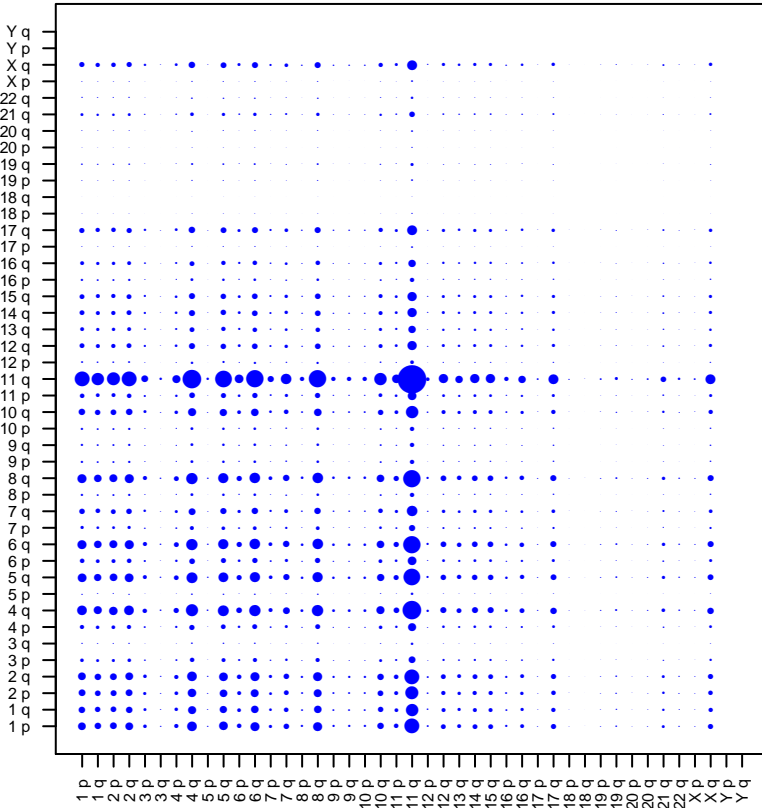
Atypical : 1 ( 1.4 % )

Classical : 1 ( 3.1 % )

Basal : 3 ( 3.6 % )



Absolute numbers

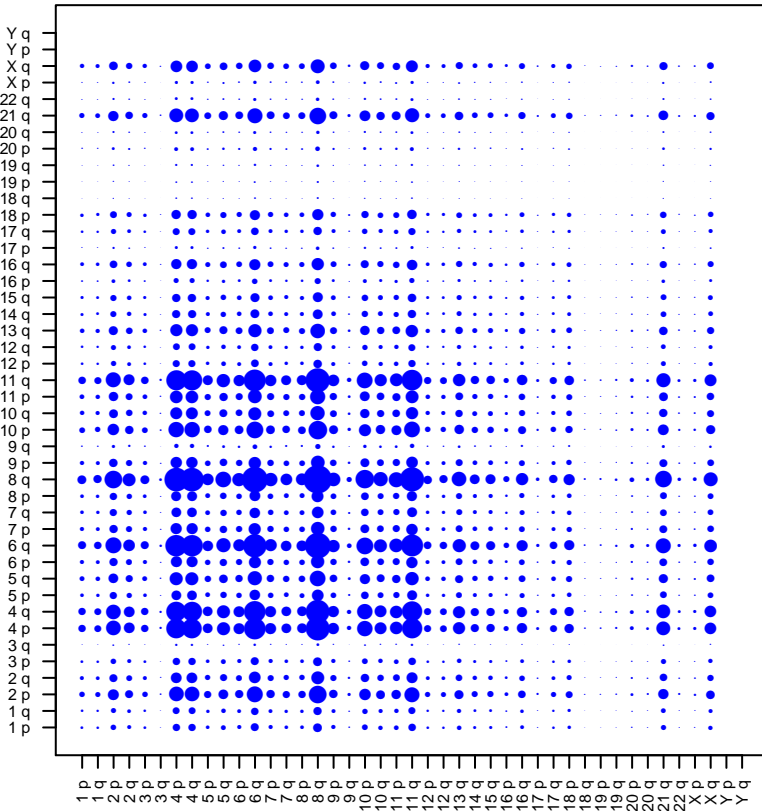


Rank locus # genes % p-value

Rank	locus	# genes	%	p-value
1	11 q	46	7.1	2e-06
2	4 q	30	6.9	2e-04
3	6 q	28	7.5	6e-05
4	8 q	28	8.3	1e-05
5	5 q	27	4.6	0.007
6	1 p	24	2.6	0.009
7	2 q	24	3.3	0.03
8	1 q	21	5.2	0.04
9	1 q	20	2.4	1
10	10 q	20	4.2	0.2
11	7 q	17	3.4	0.5
12	17 q	16	2.5	0.9
13	X q	16	4.1	0.2
14	12 q	15	2.4	0.9
15	14 q	15	2.9	0.8
16	15 q	15	2.9	0.7
17	6 p	14	3.9	0.3
18	11 p	14	4.4	0.2
19	4 p	13	7	0.01
20	15 q	12	4.3	0.2
21	16 q	12	3.6	0.4
22	3 p	11	2.6	0.9
23	7 p	10	3.9	0.4
24	21 q	9	4.9	0.2
25	8 p	7	3.5	0.5
26	9 p	7	4	0.4
27	9 q	7	1.5	1
28	10 p	7	5.4	0.1
29	16 p	7	1.8	1
30	12 p	6	2.5	0.8
31	19 q	5	0.8	1
32	3 q	4	0.8	1
33	5 p	4	3.4	0.6
34	22 q	4	1	1
35	17 p	3	1	1
36	19 p	3	0.6	1
37	20 q	3	1	1
38	X p	3	1.1	1
39	18 p	2	3.3	0.6
40	20 p	2	1.4	1
41	18 q	1	0.6	1
42	Y p	0	0	1
43	Y q	0	0	1

H3CHR6-MHC-DBB

Relative numbers

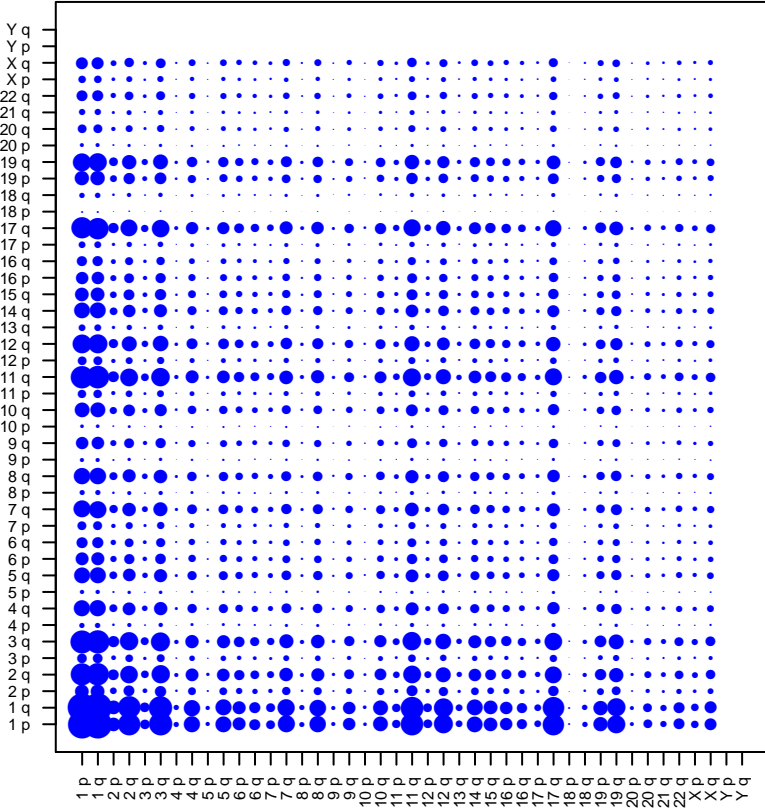


Rank locus # genes % p-value

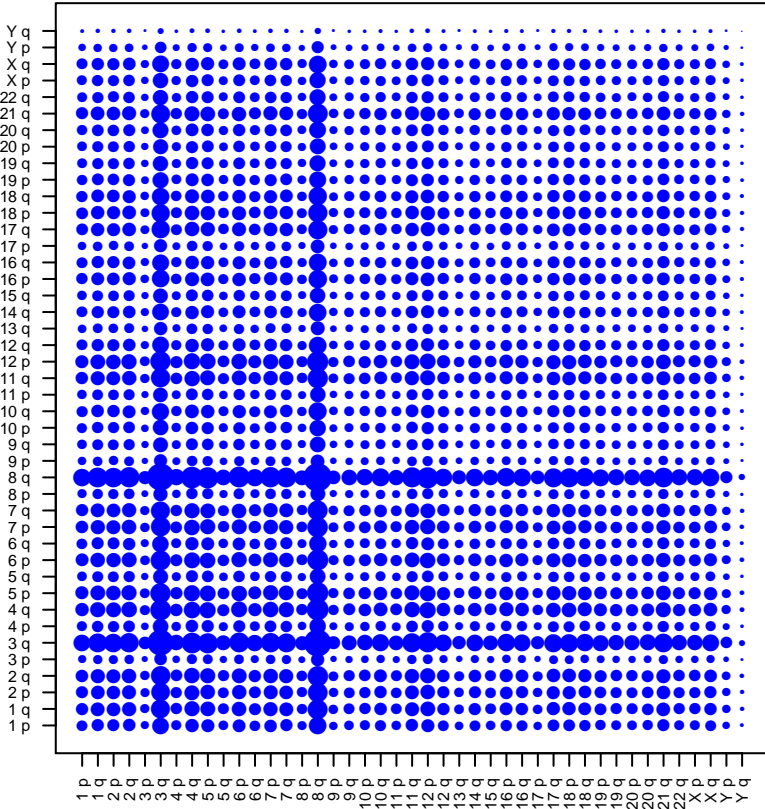
Rank	locus	# genes	%	p-value
1	8 q	28	8.3	1e-05
2	6 q	28	7.5	6e-05
3	11 q	46	7.1	2e-06
4	4 p	13	7	0.01
5	4 q	30	6.9	2e-04
6	10 p	7	5.4	0.1
7	2 p	21	5.2	0.04
8	21 q	9	4.9	0.2
9	5 q	27	4.6	0.007
10	11 p	14	4.4	0.2
11	13 q	12	4.3	0.2
12	10 q	20	4.2	0.2
13	X q	16	4.1	0.2
14	9 p	7	4	0.4
15	7 p	10	3.9	0.4
16	6 p	14	3.9	0.3
17	2 q	24	3.8	0.3
18	16 q	12	3.6	0.4
19	8 p	7	3.5	0.5
20	5 p	4	3.4	0.6
21	7 q	17	3.4	0.5
22	18 p	2	3.3	0.6
23	15 q	15	2.9	0.7
24	14 q	15	2.9	0.8
25	3 p	11	2.6	0.9
26	1 p	24	2.6	0.9
27	12 p	6	2.5	0.8
28	17 q	16	2.5	0.9
29	1 q	20	2.4	1
30	12 q	15	2.4	0.9
31	16 p	7	1.8	1
32	9 q	7	1.5	1
33	20 p	2	1.4	1
34	X p	3	1.1	1
35	17 p	3	1	1
36	22 q	4	1	1
37	20 q	3	1	1
38	3 q	4	0.8	1
39	19 q	5	0.8	1
40	19 p	3	0.6	1
41	18 q	1	0.6	1
42	Y p	0	0	1
43	Y q	0	0	1

# Spot summary

Absolute numbers

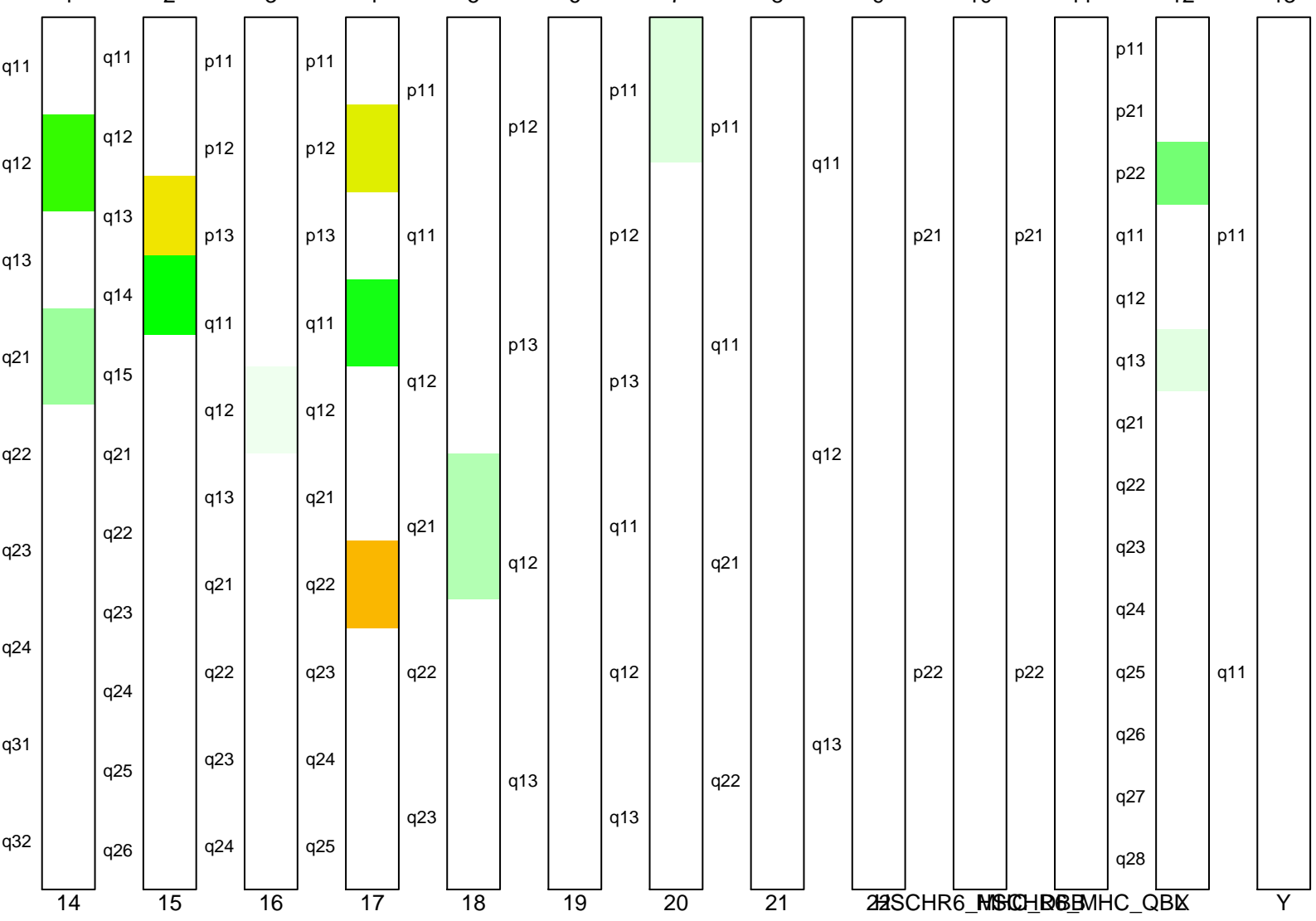
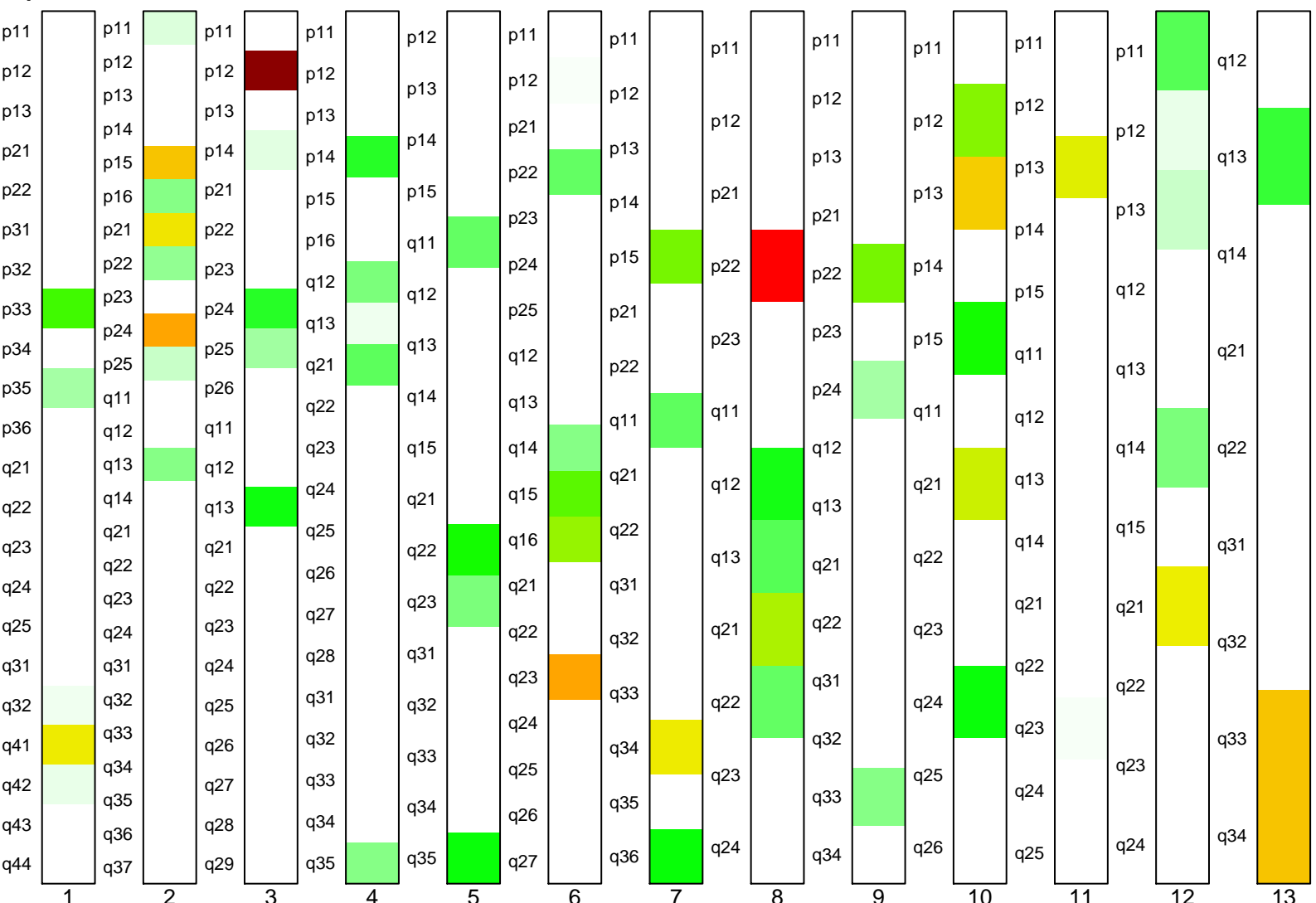


Relative numbers

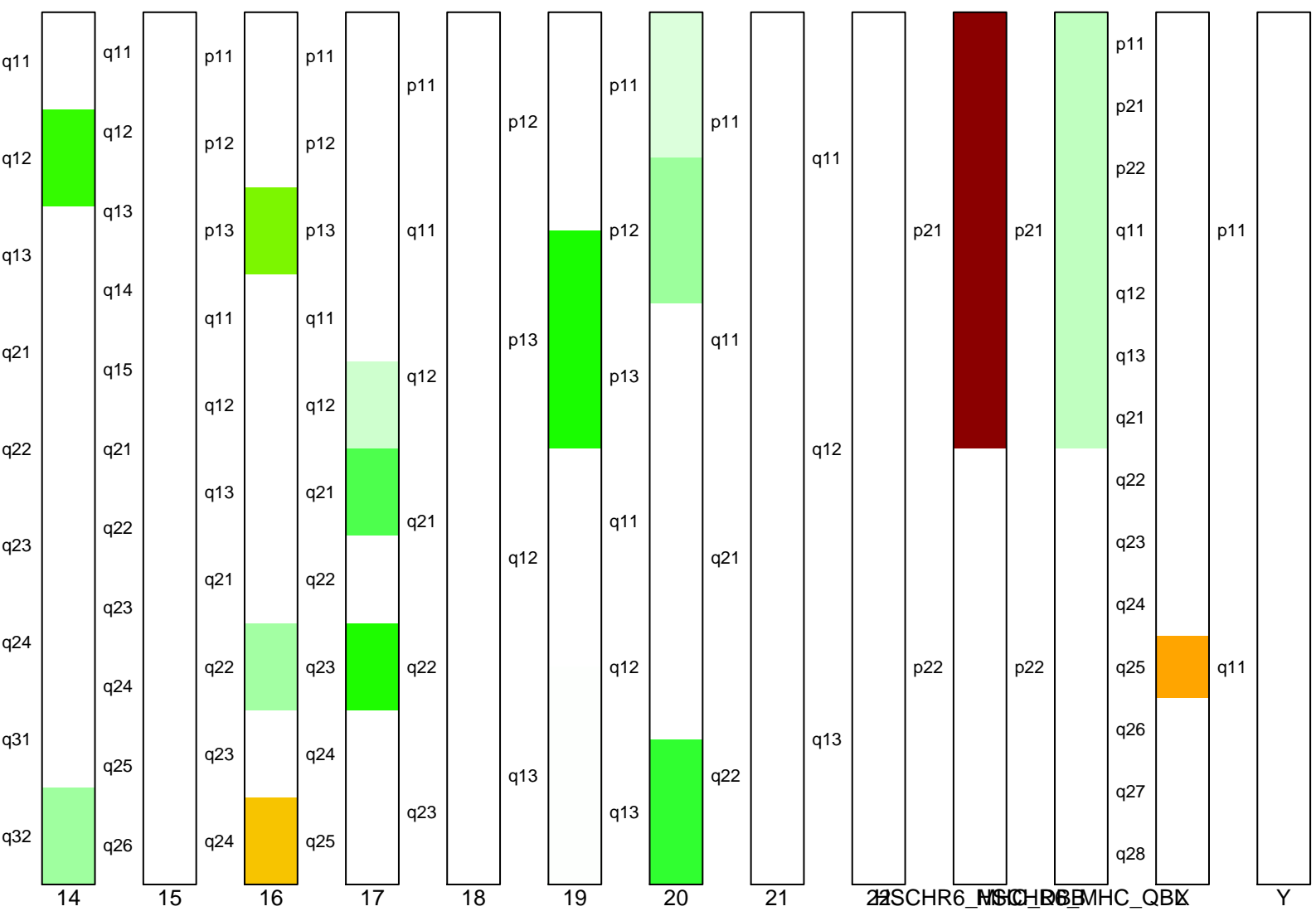
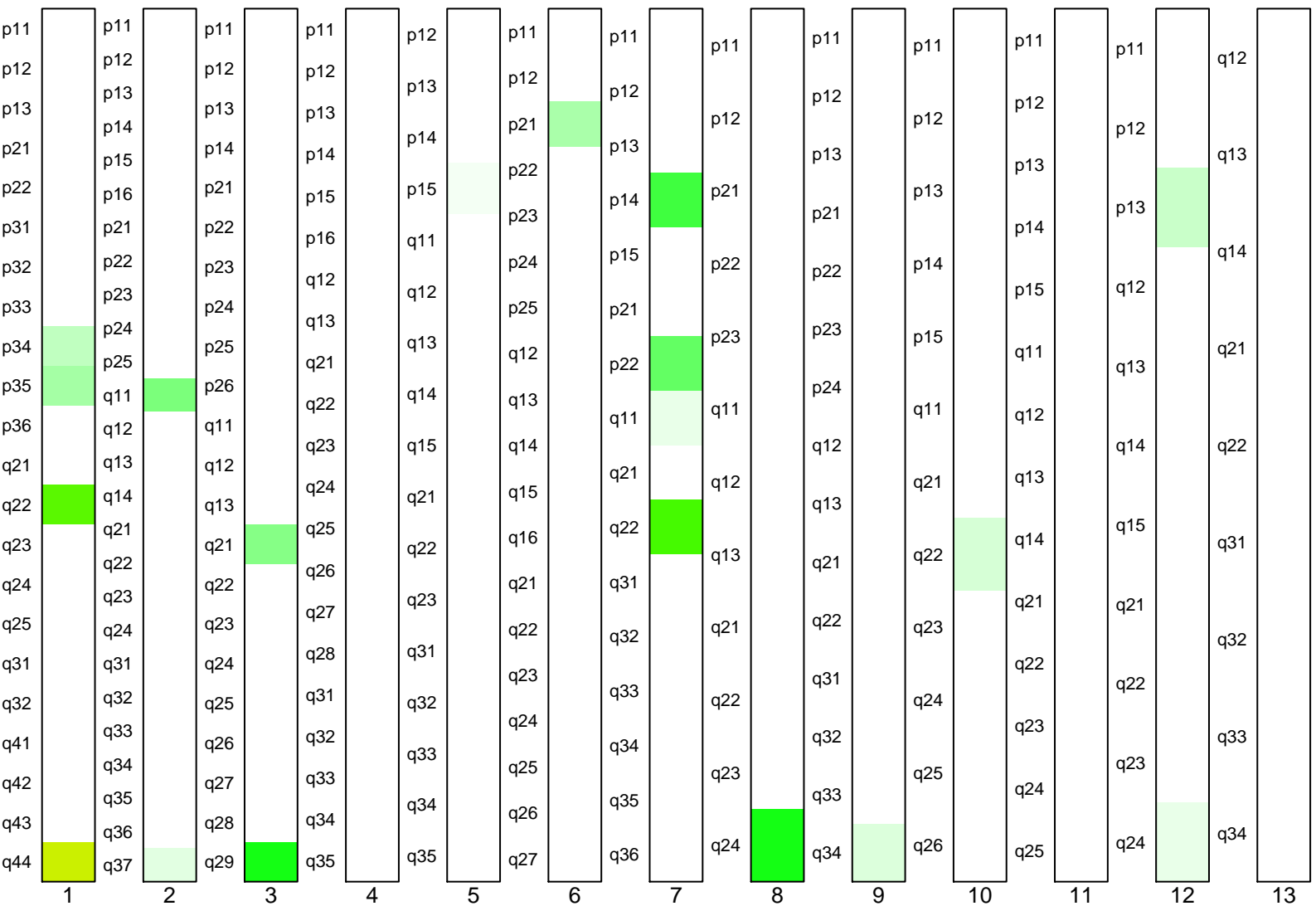




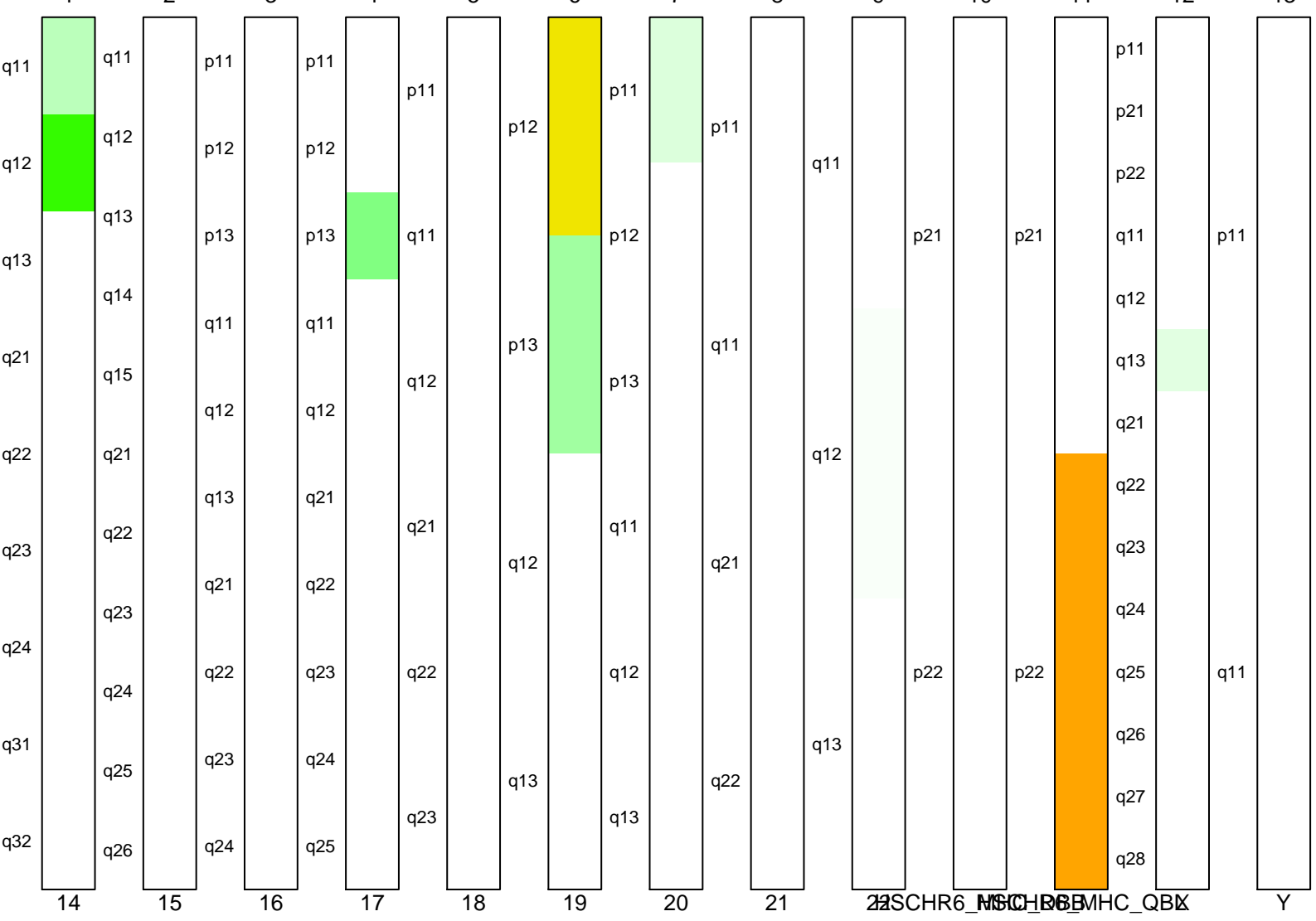
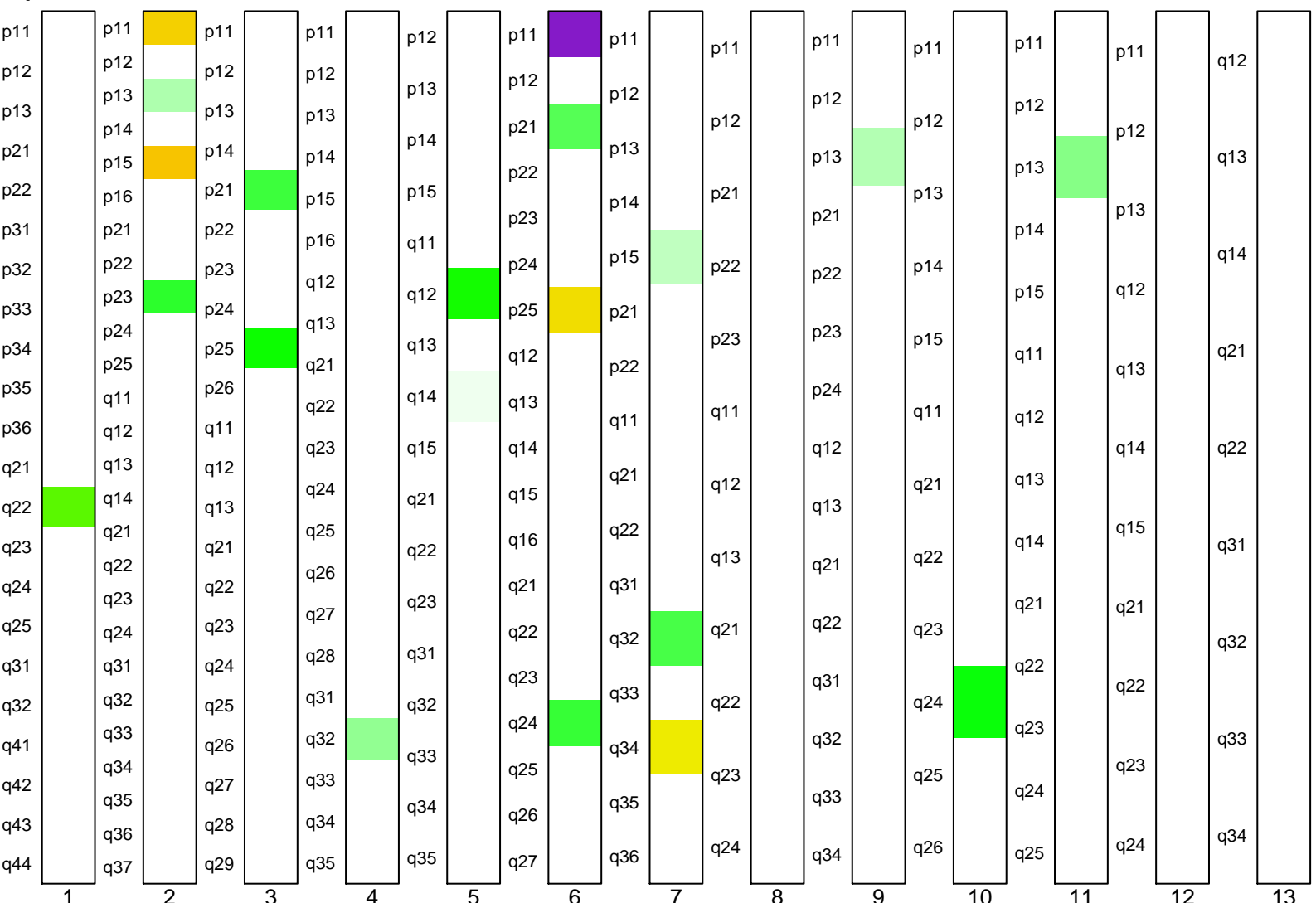
# Spot B



# Spot C

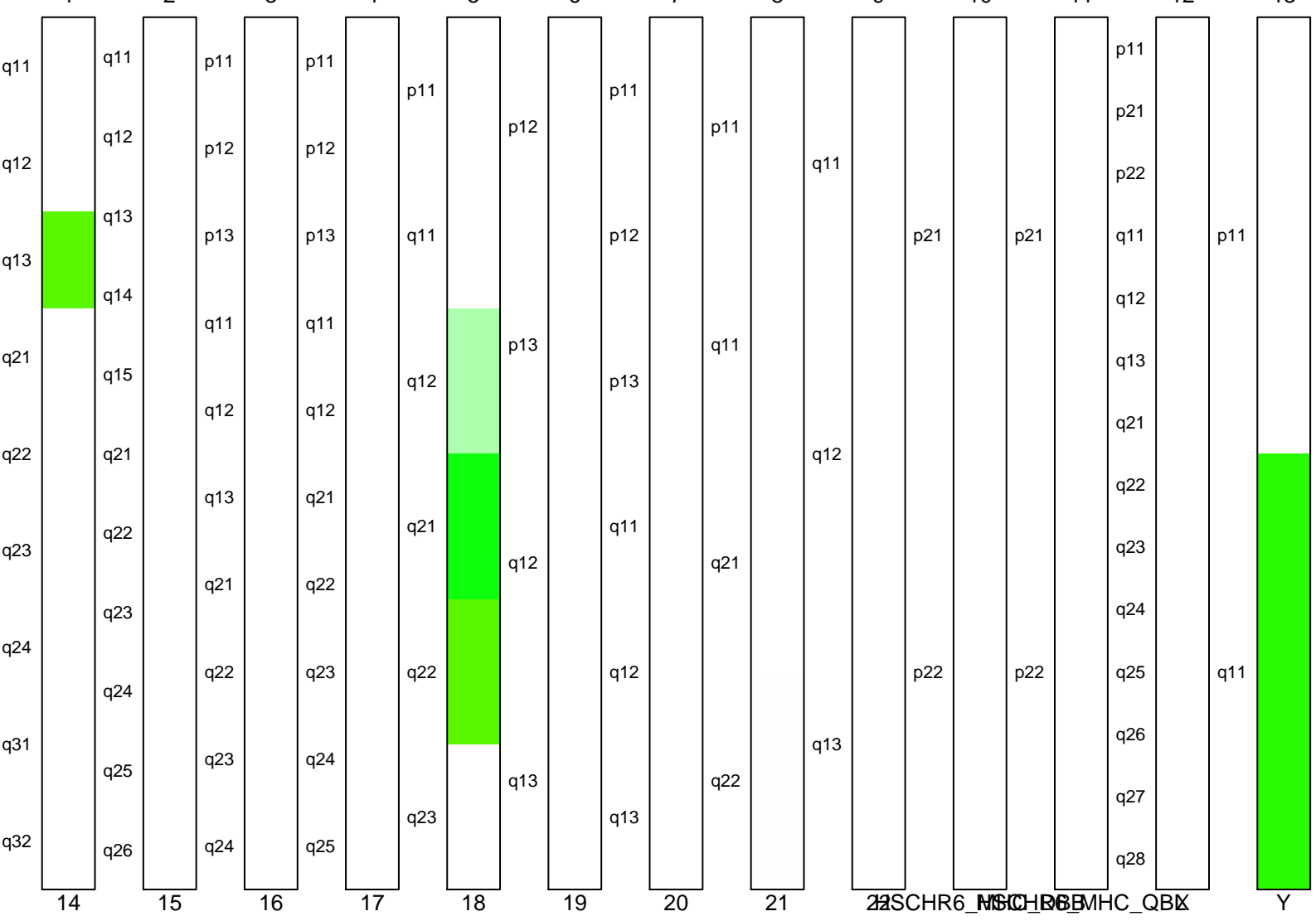
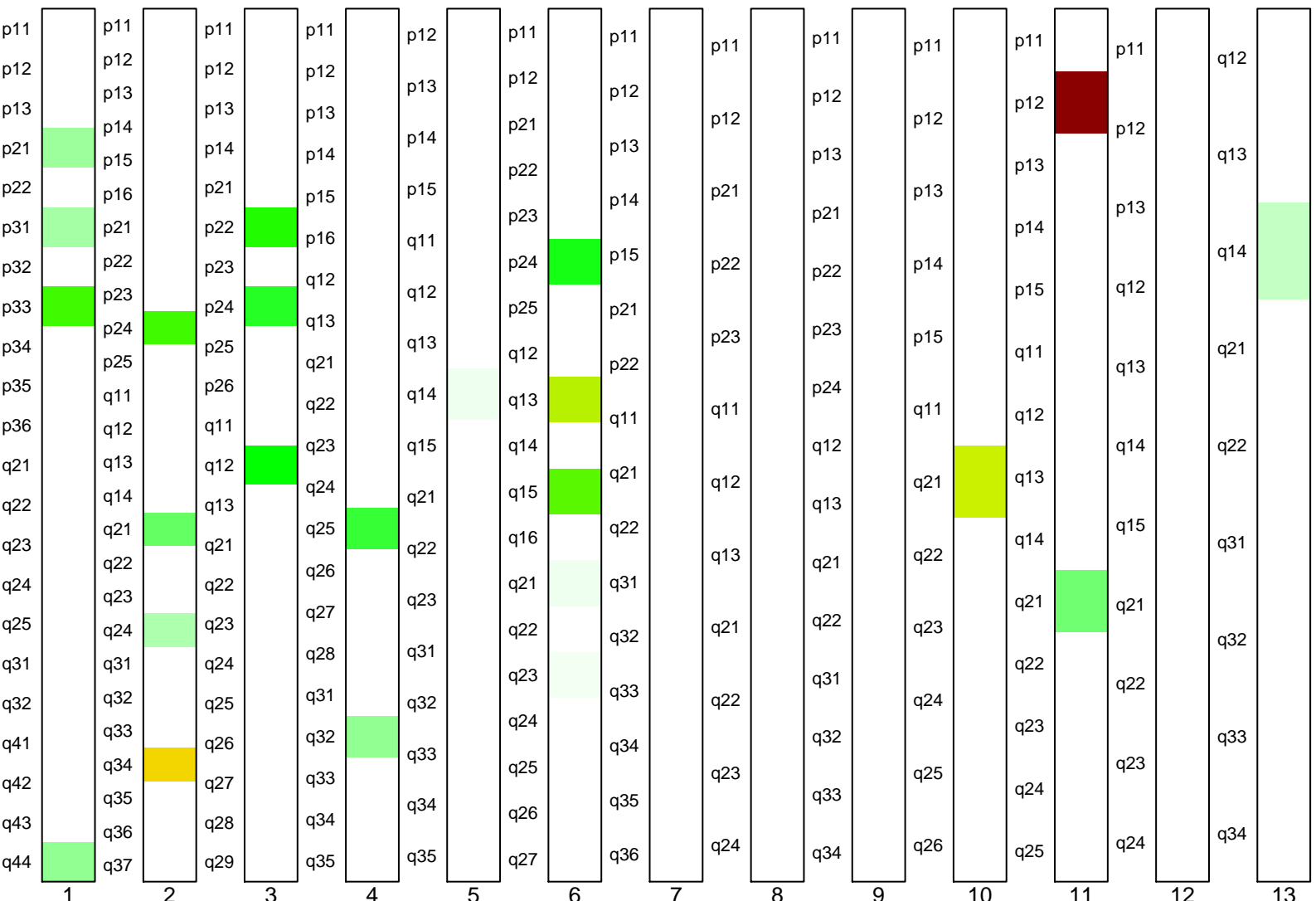


# Spot D



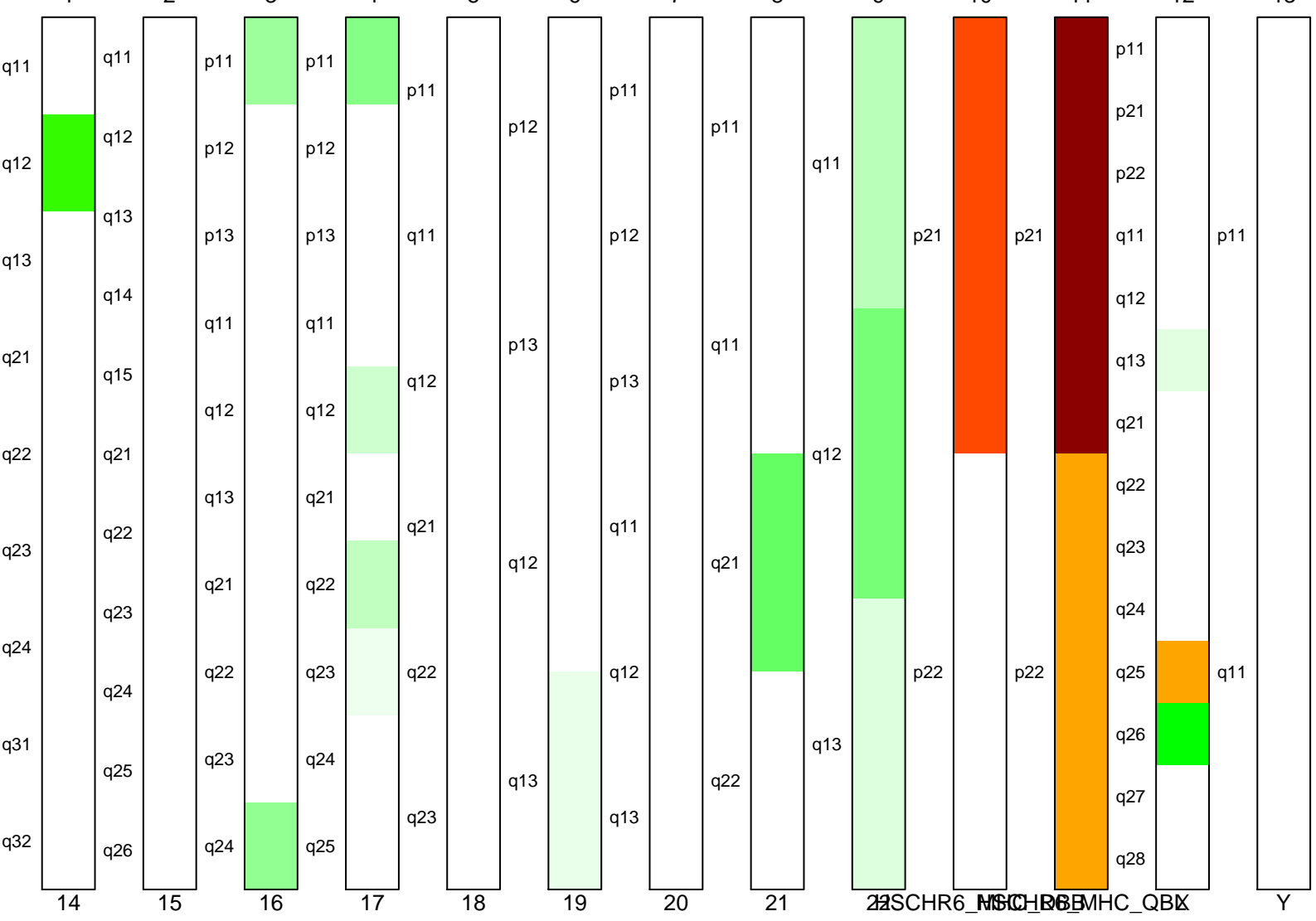
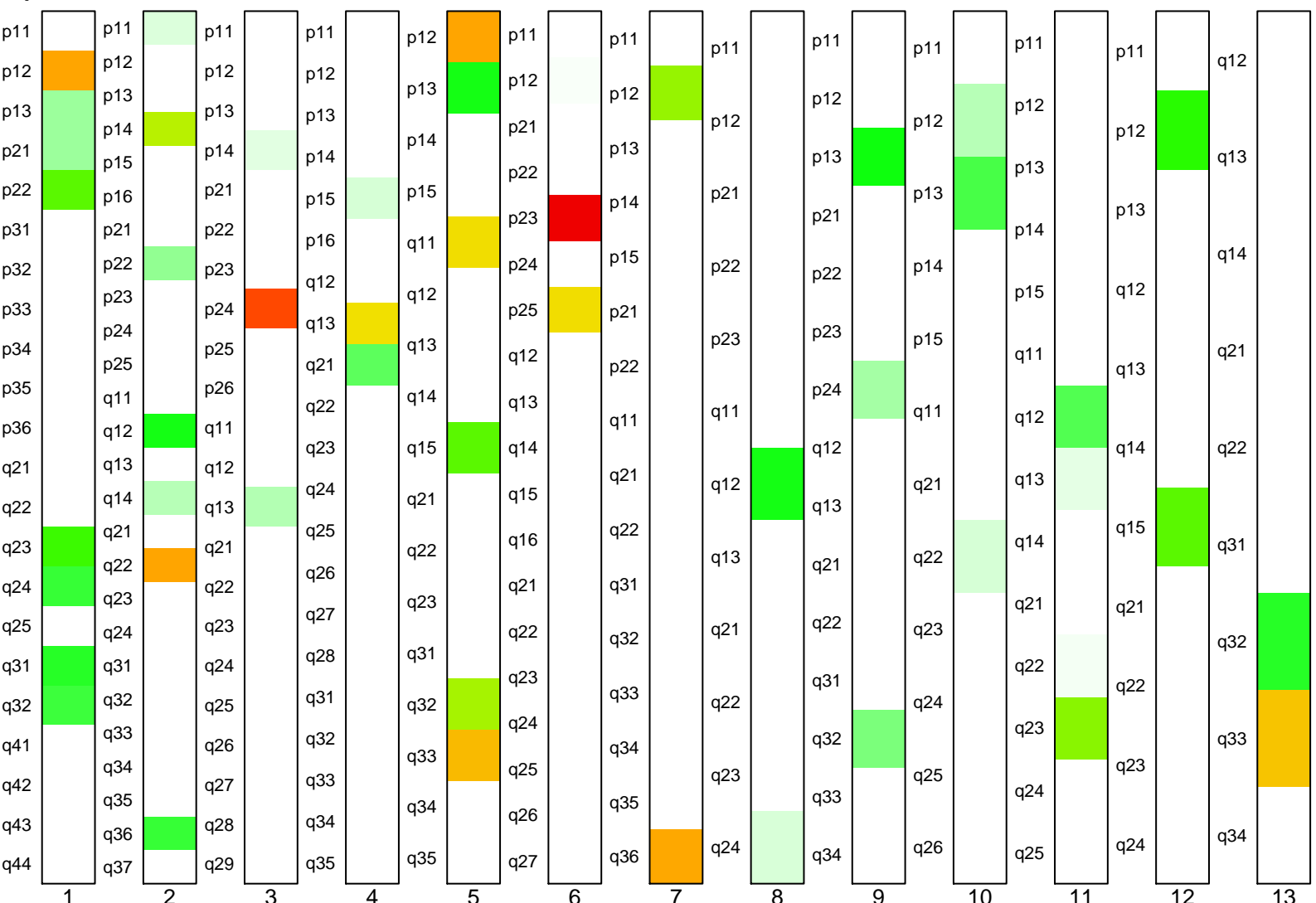


# Spot E

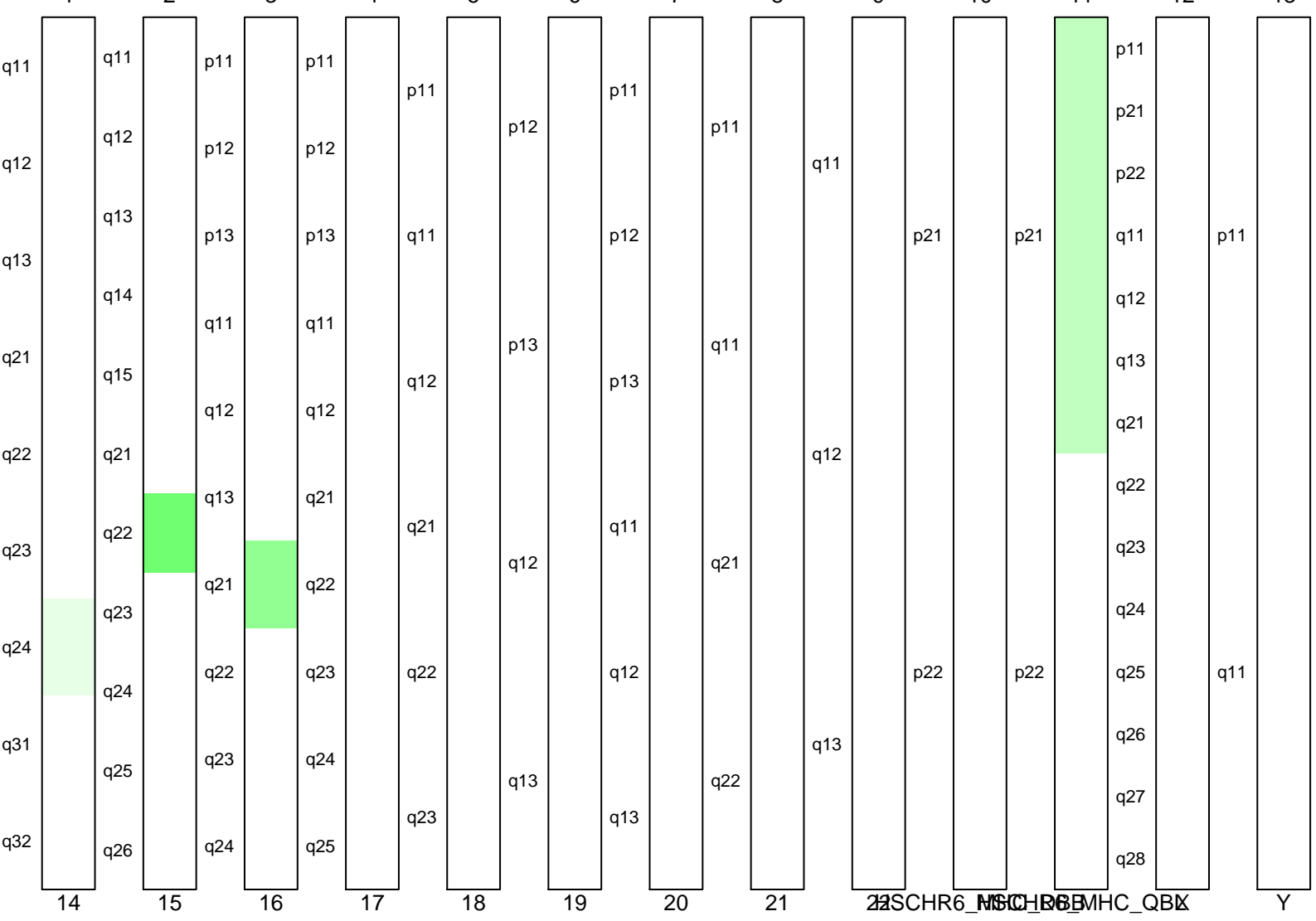
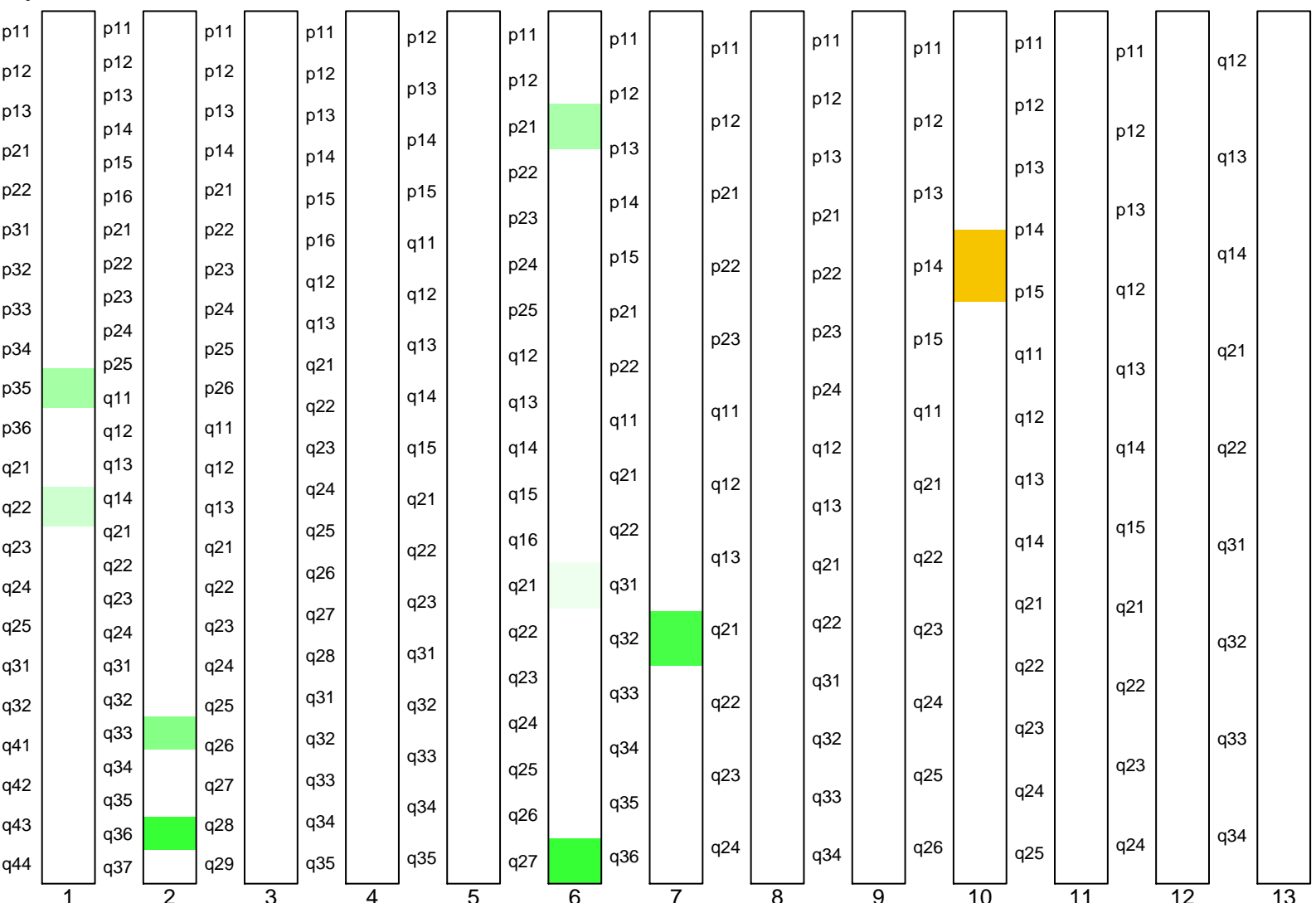




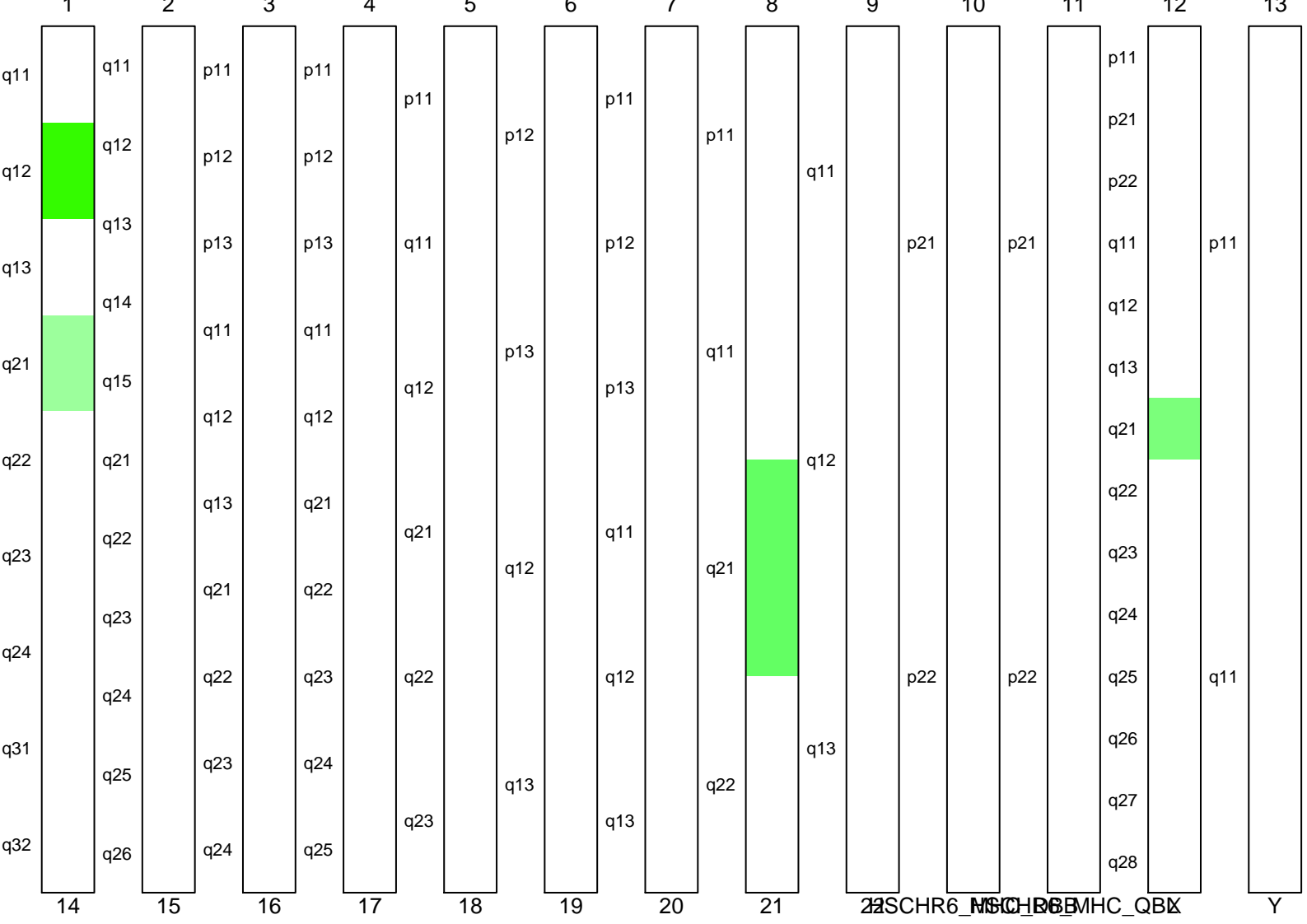
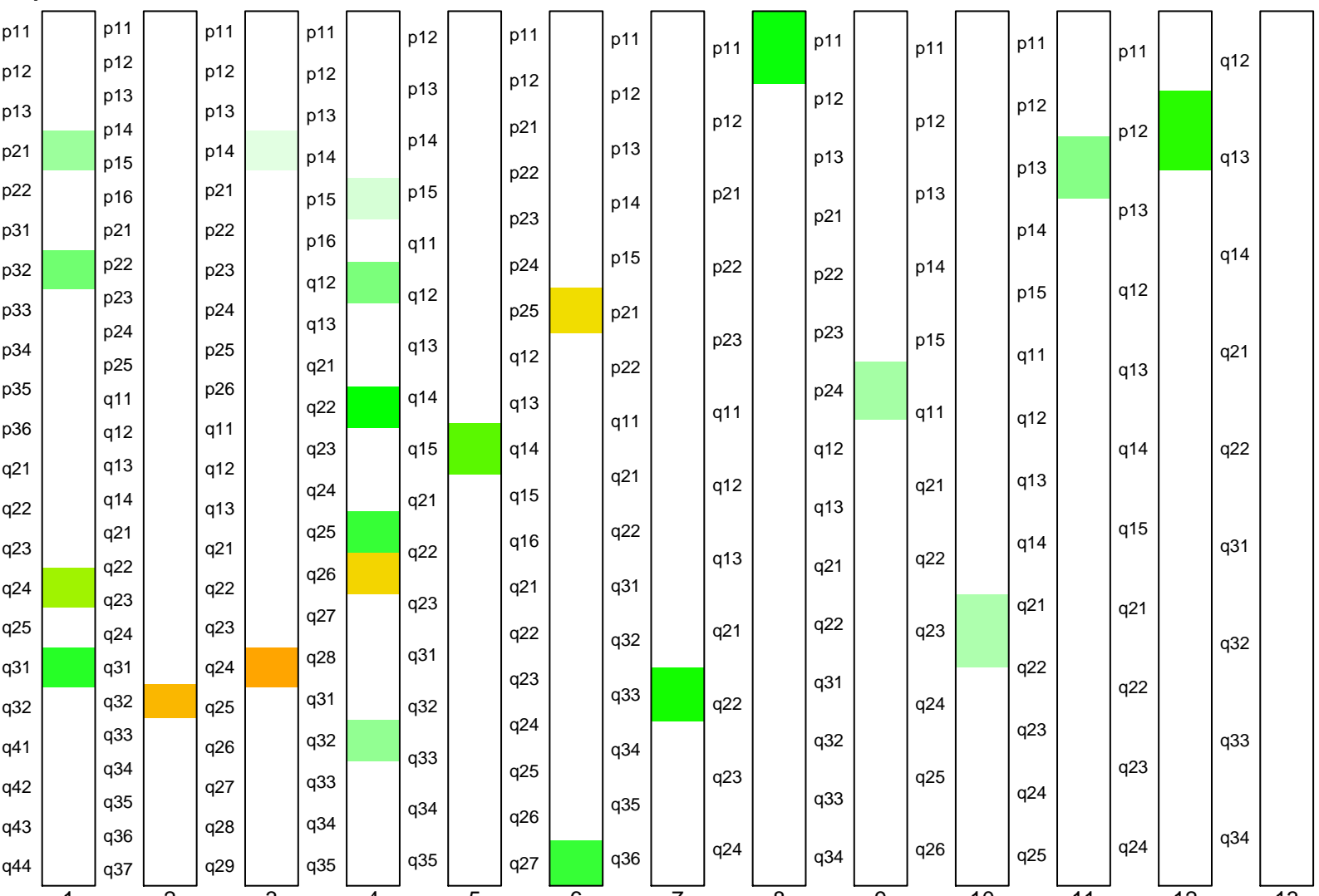
# Spot G



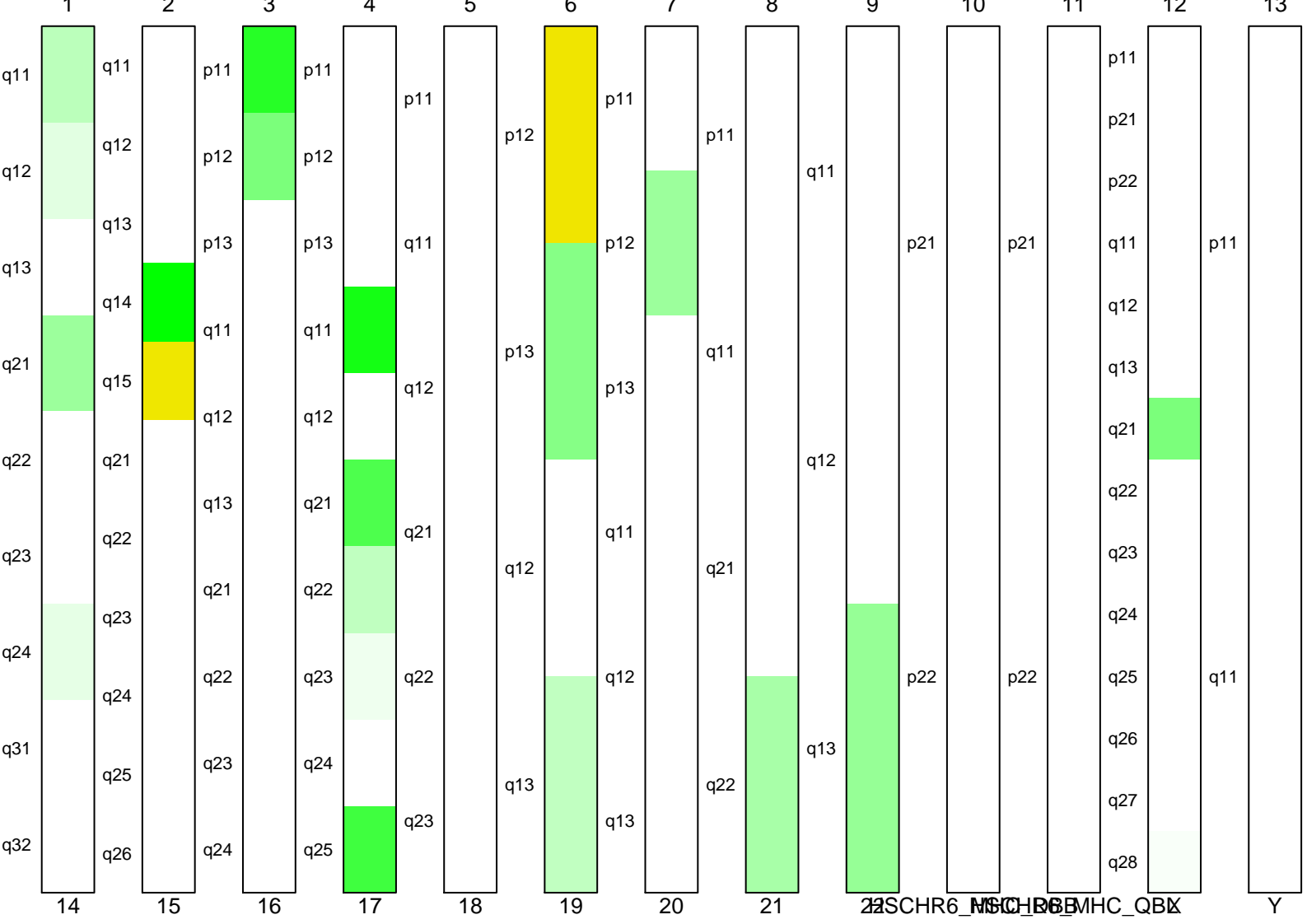
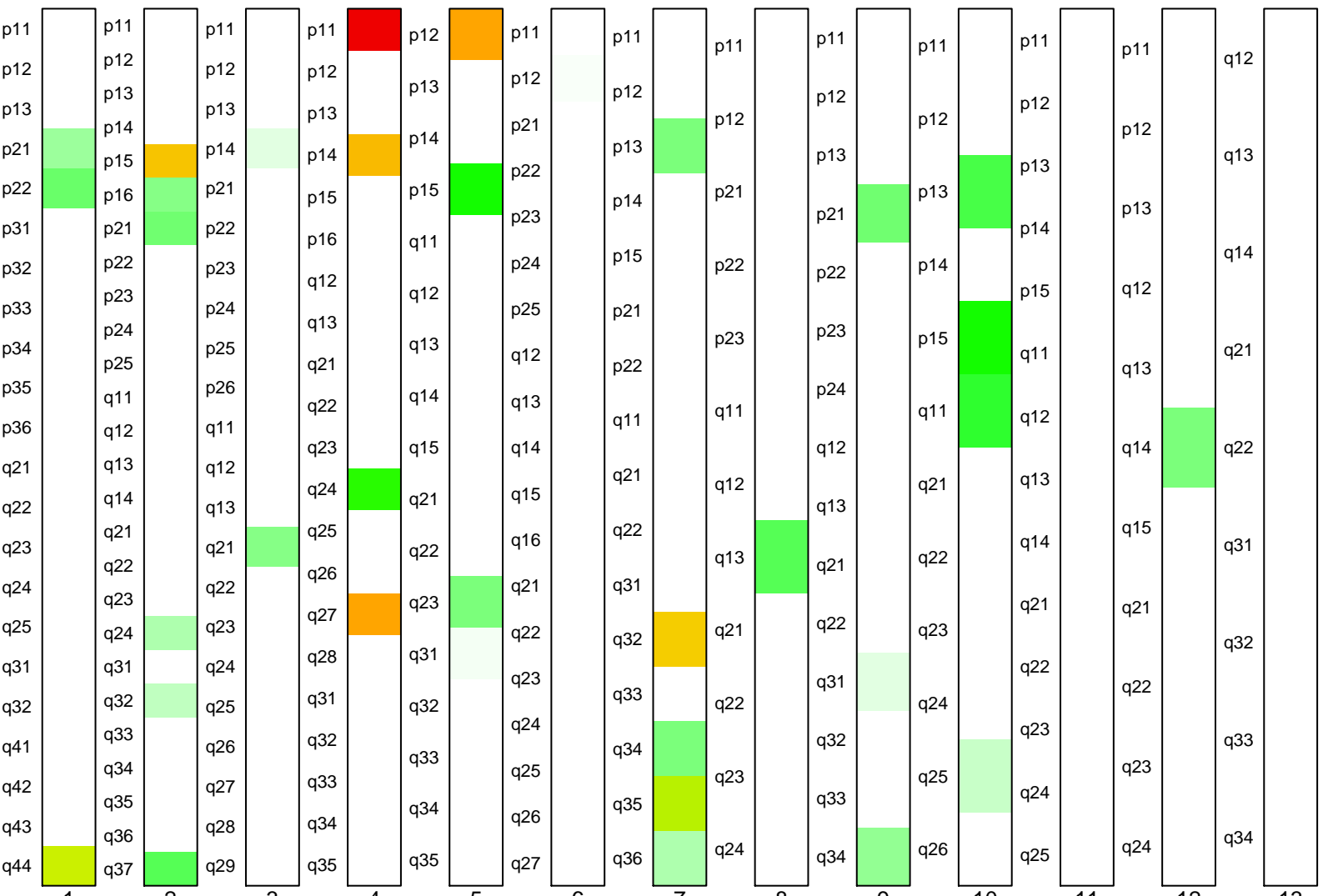
# Spot H



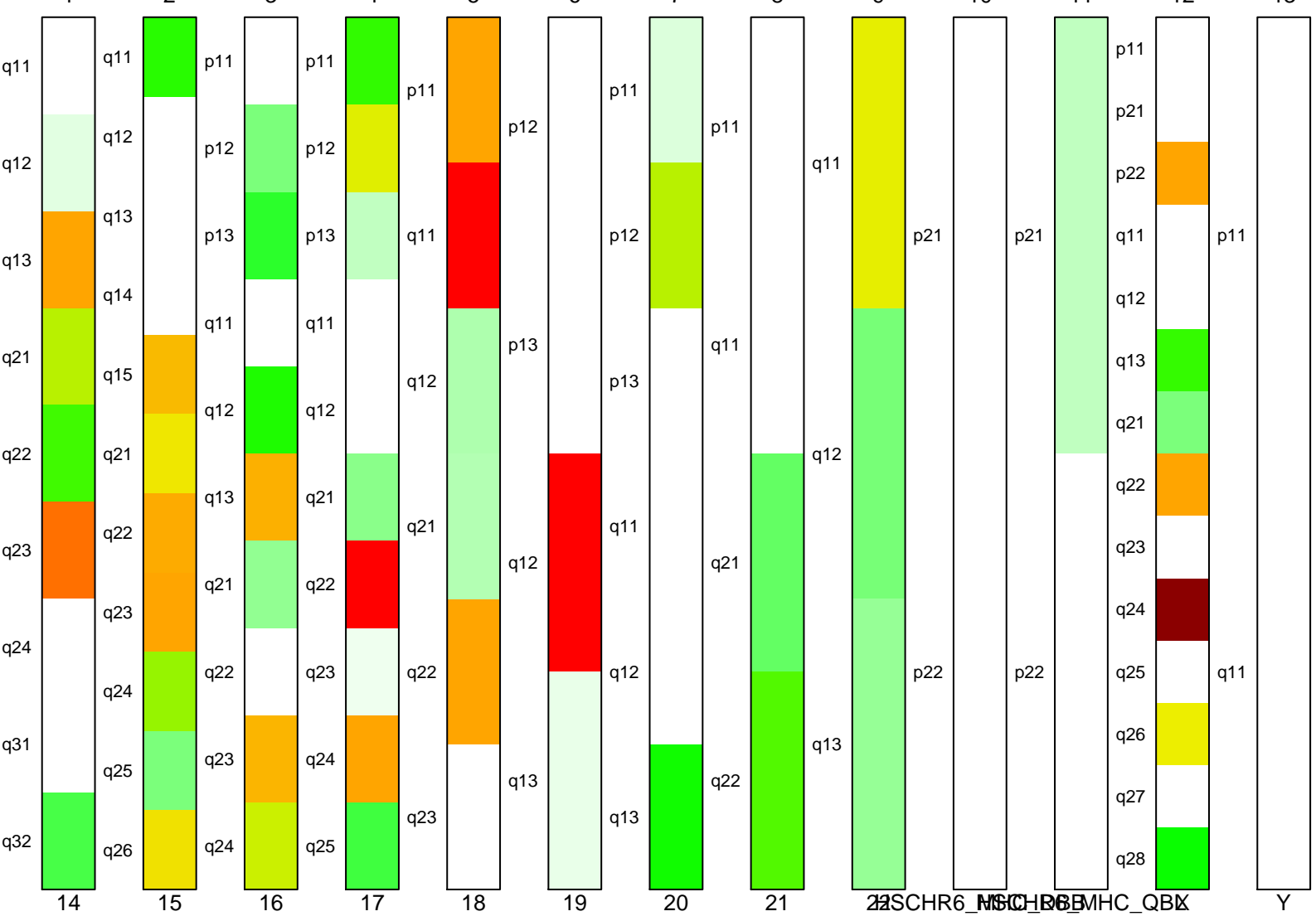
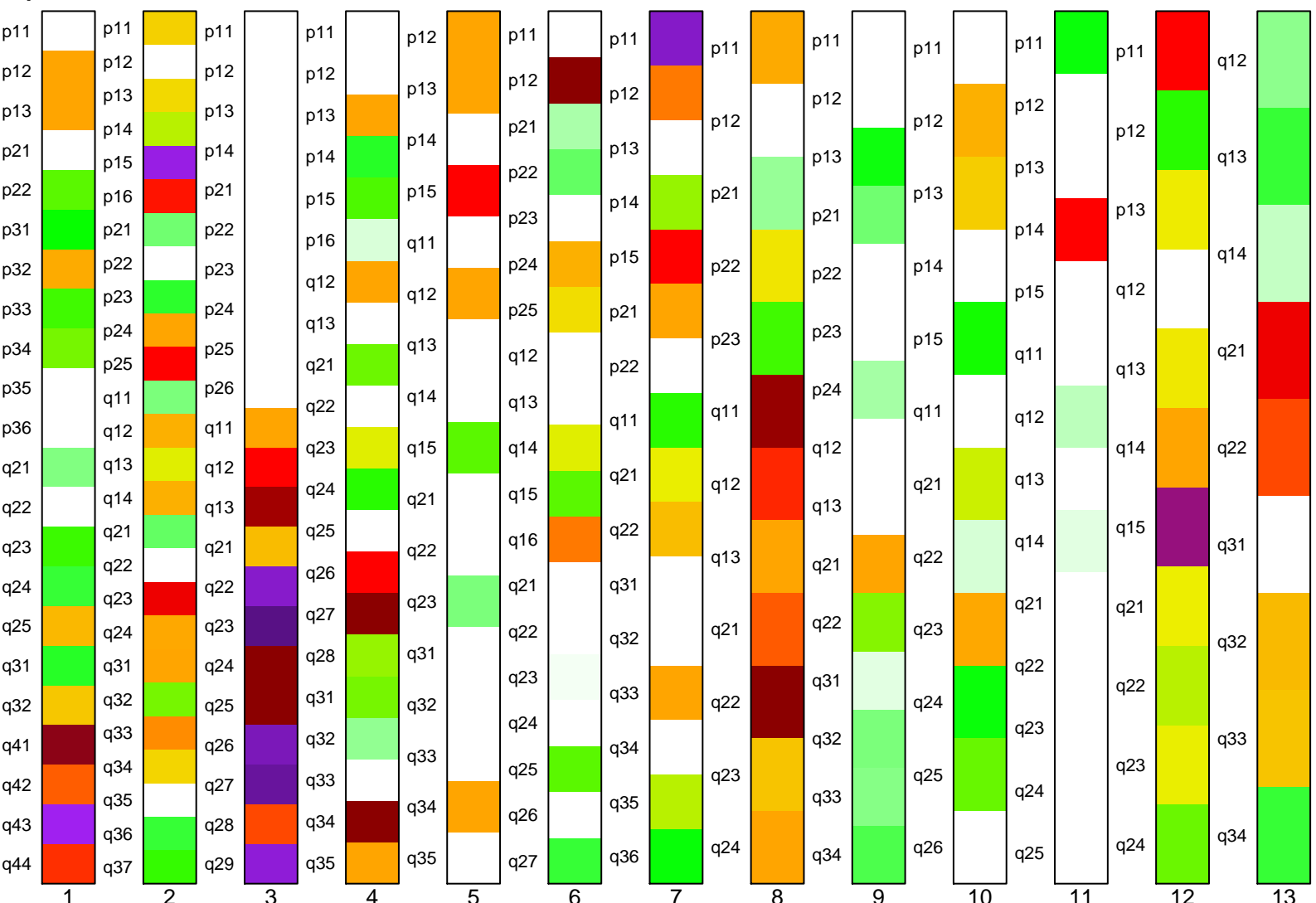
# Spot I



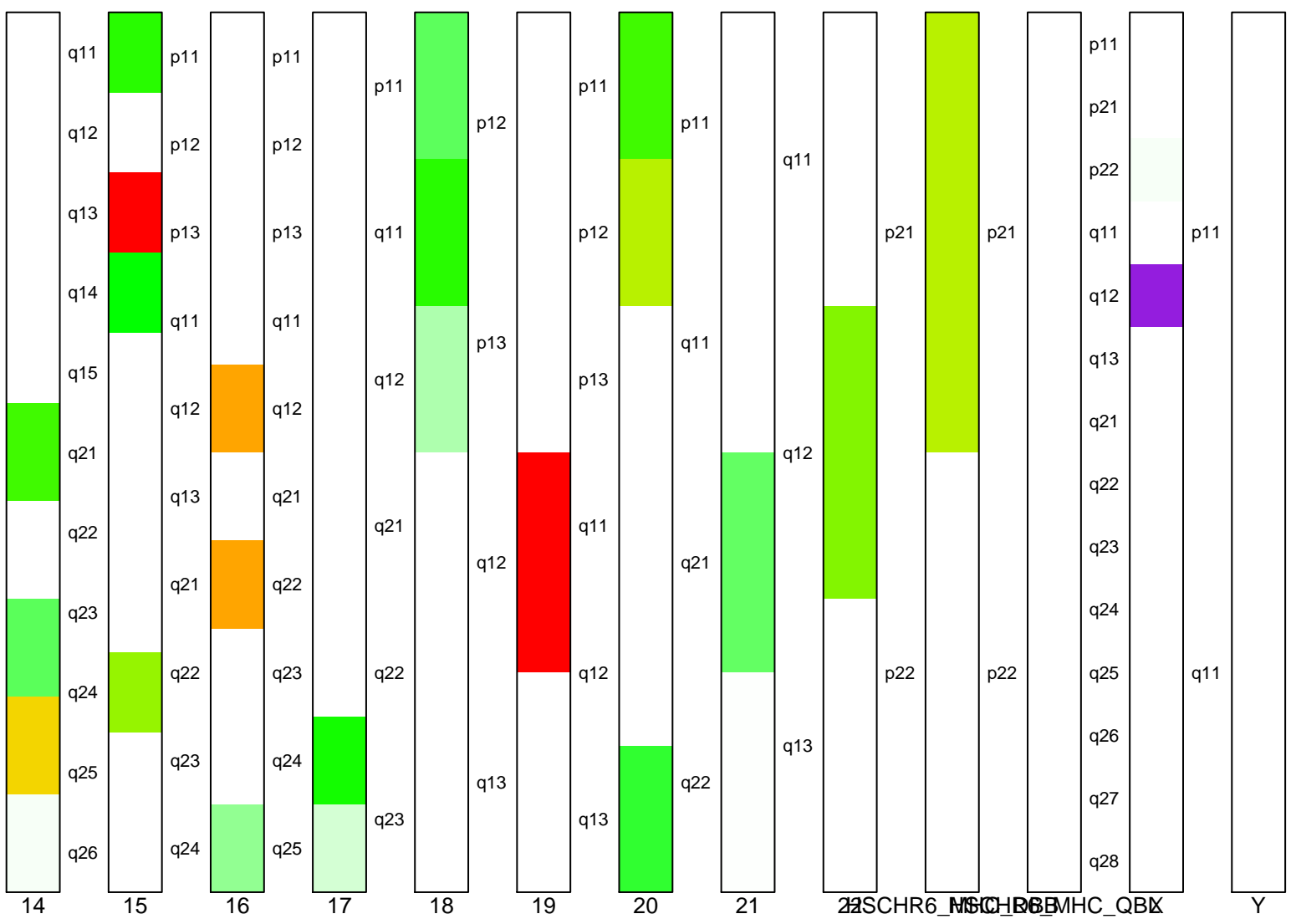
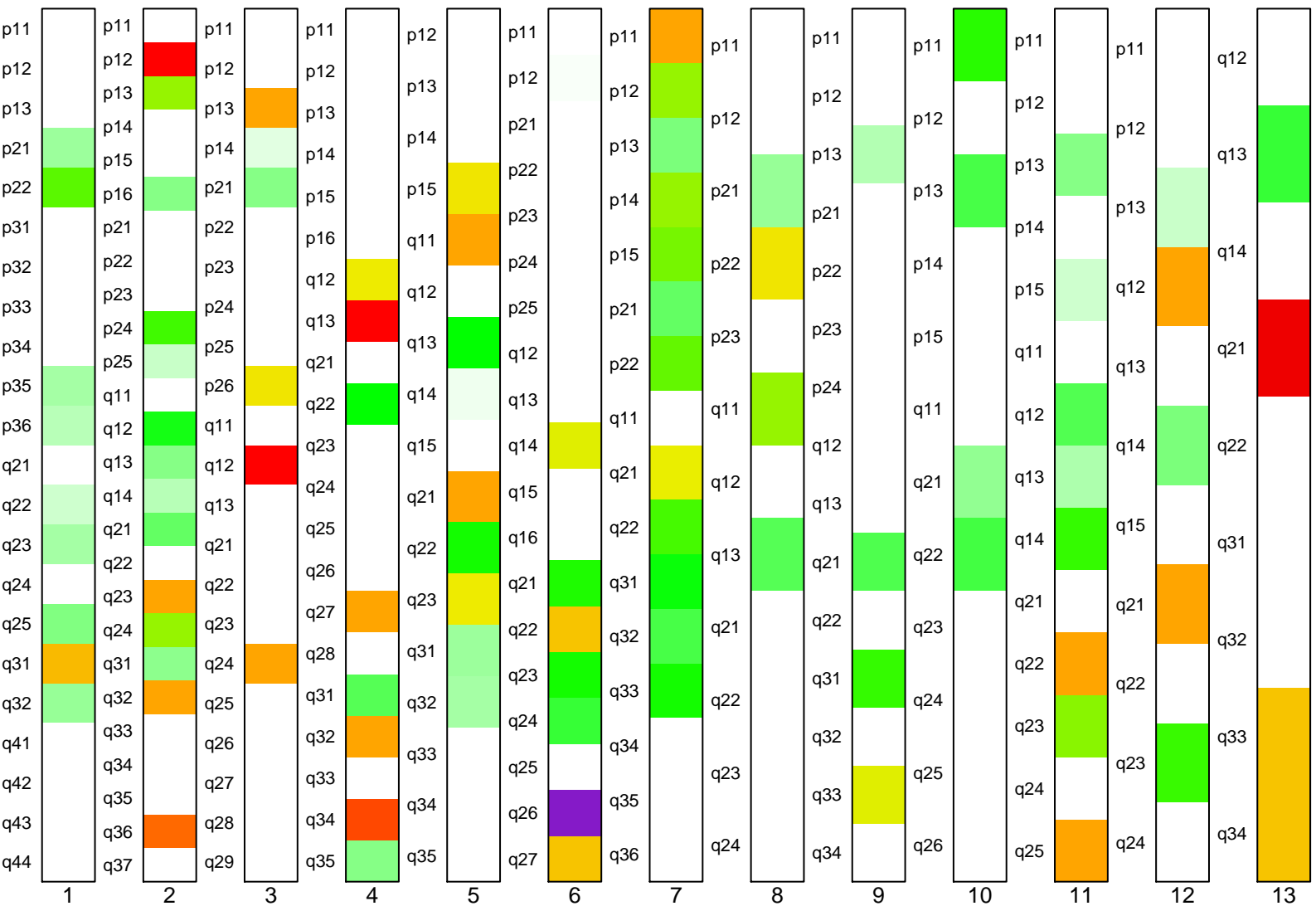
# Spot J



# Spot K

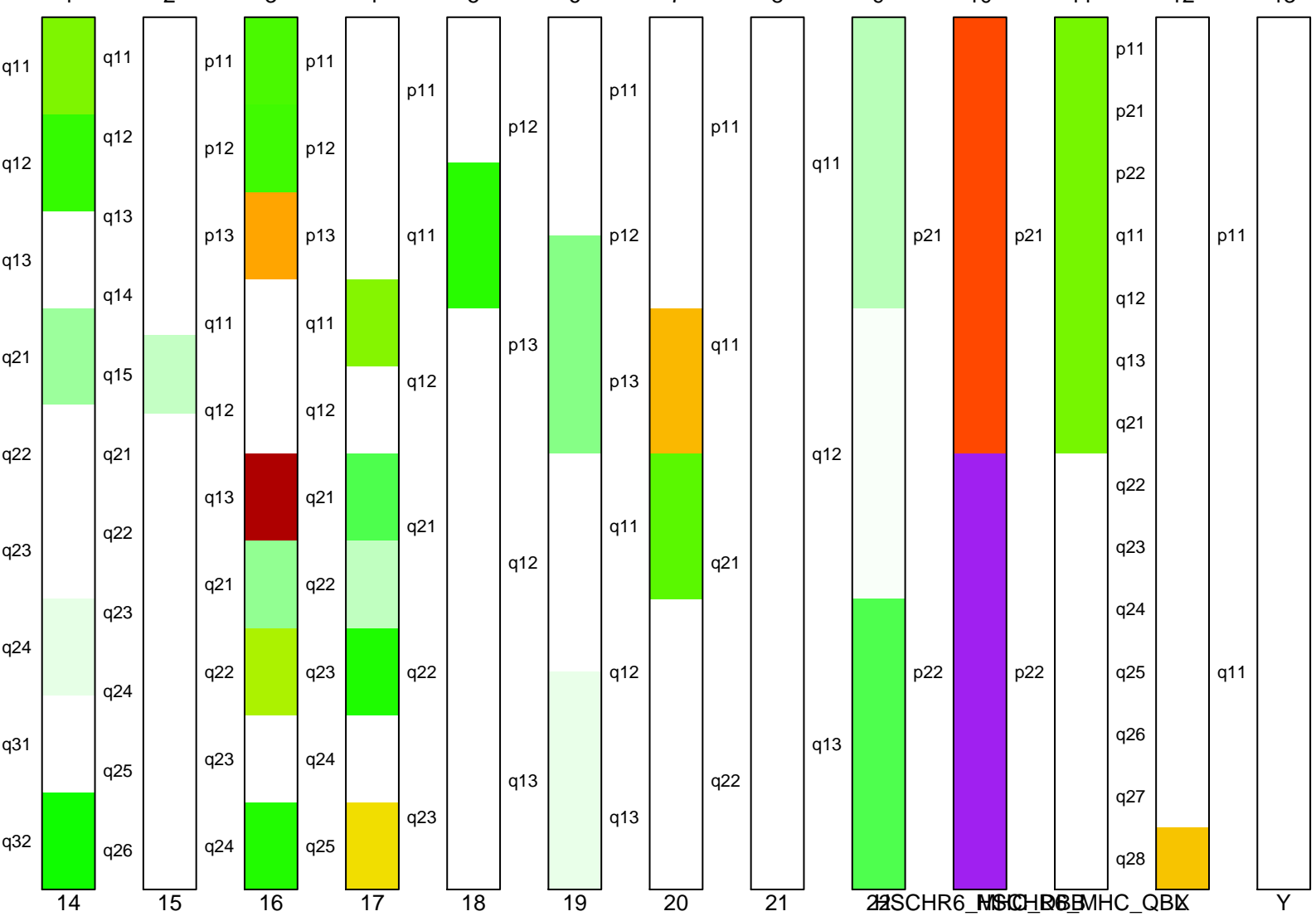
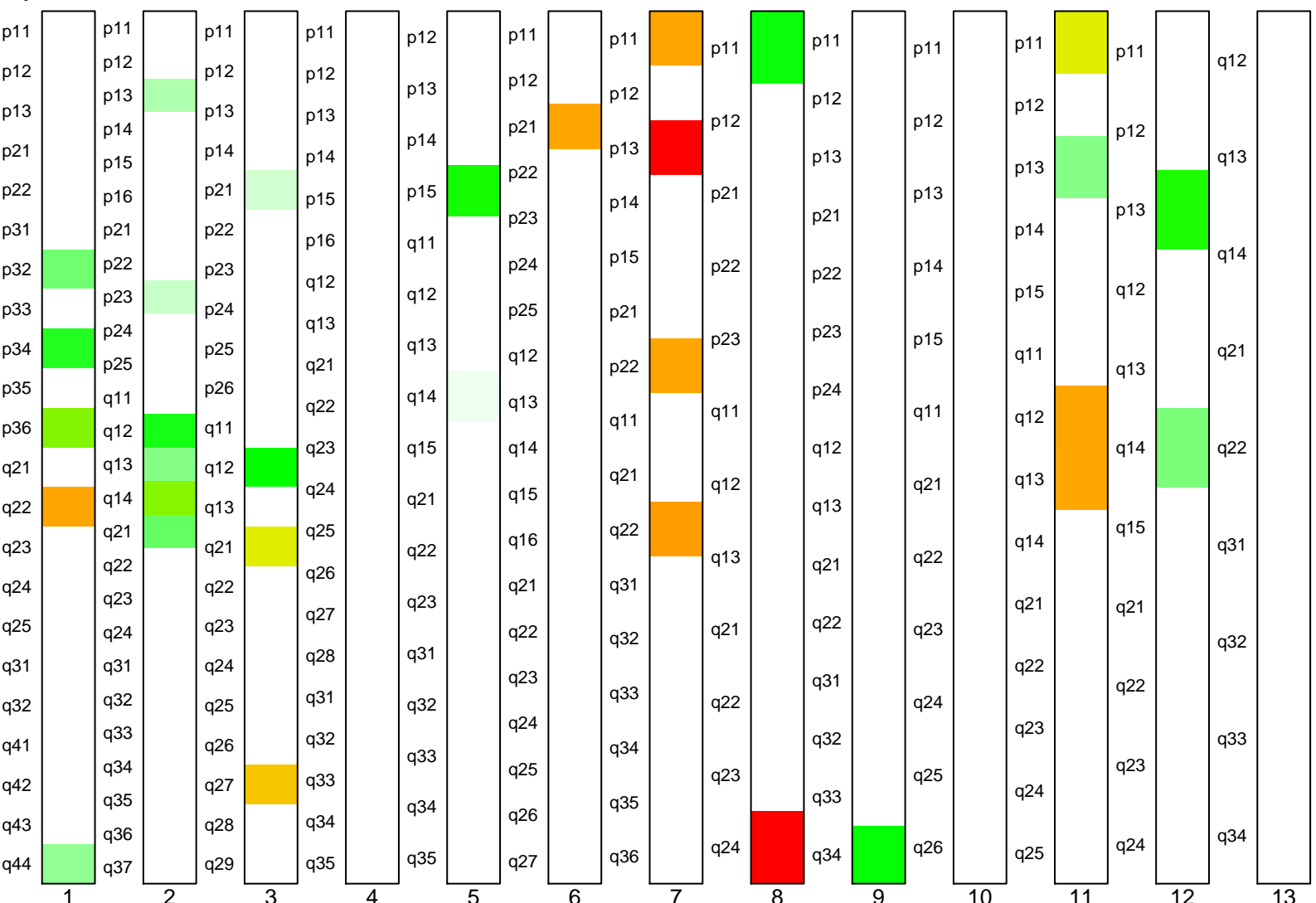


# Spot L

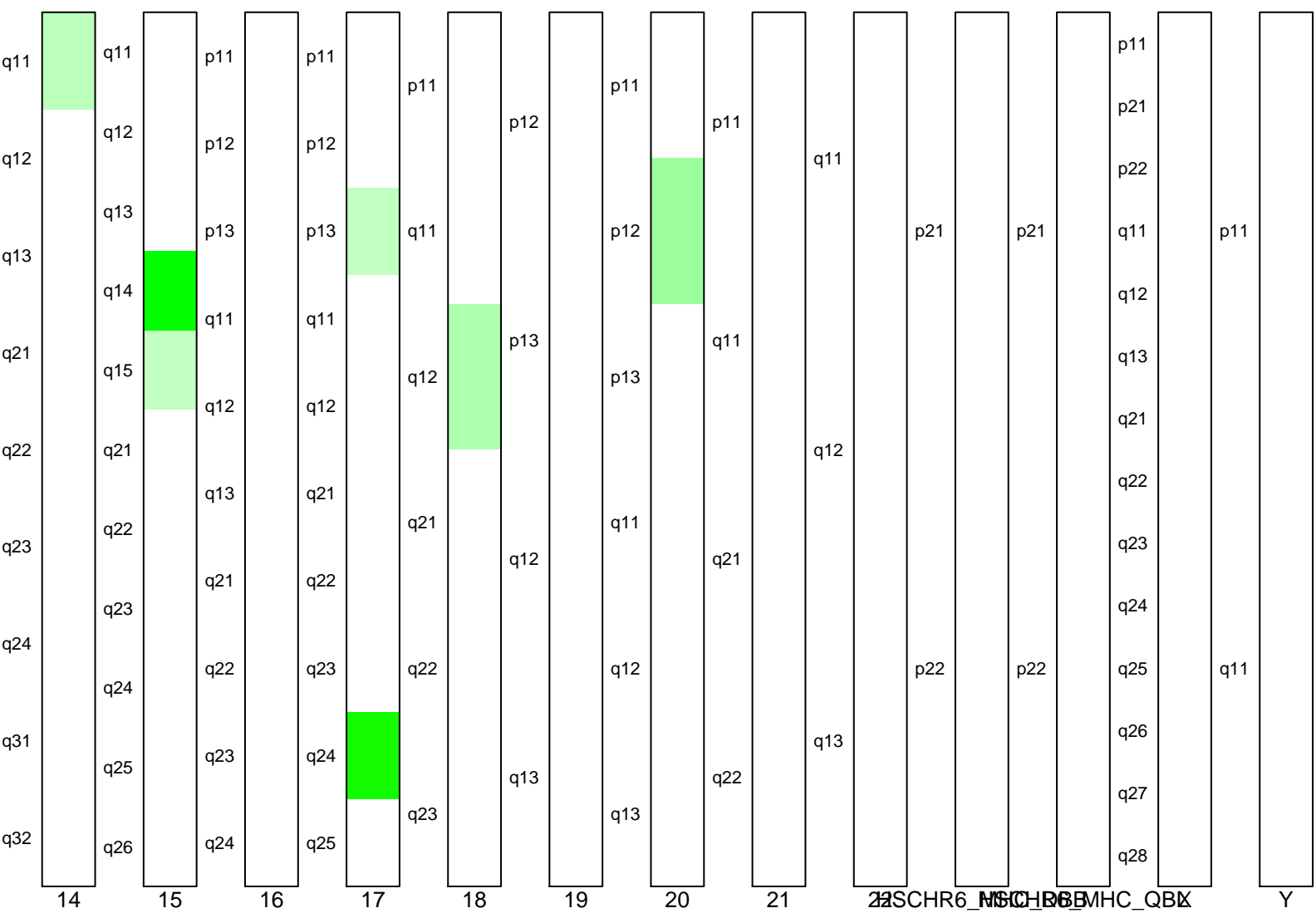
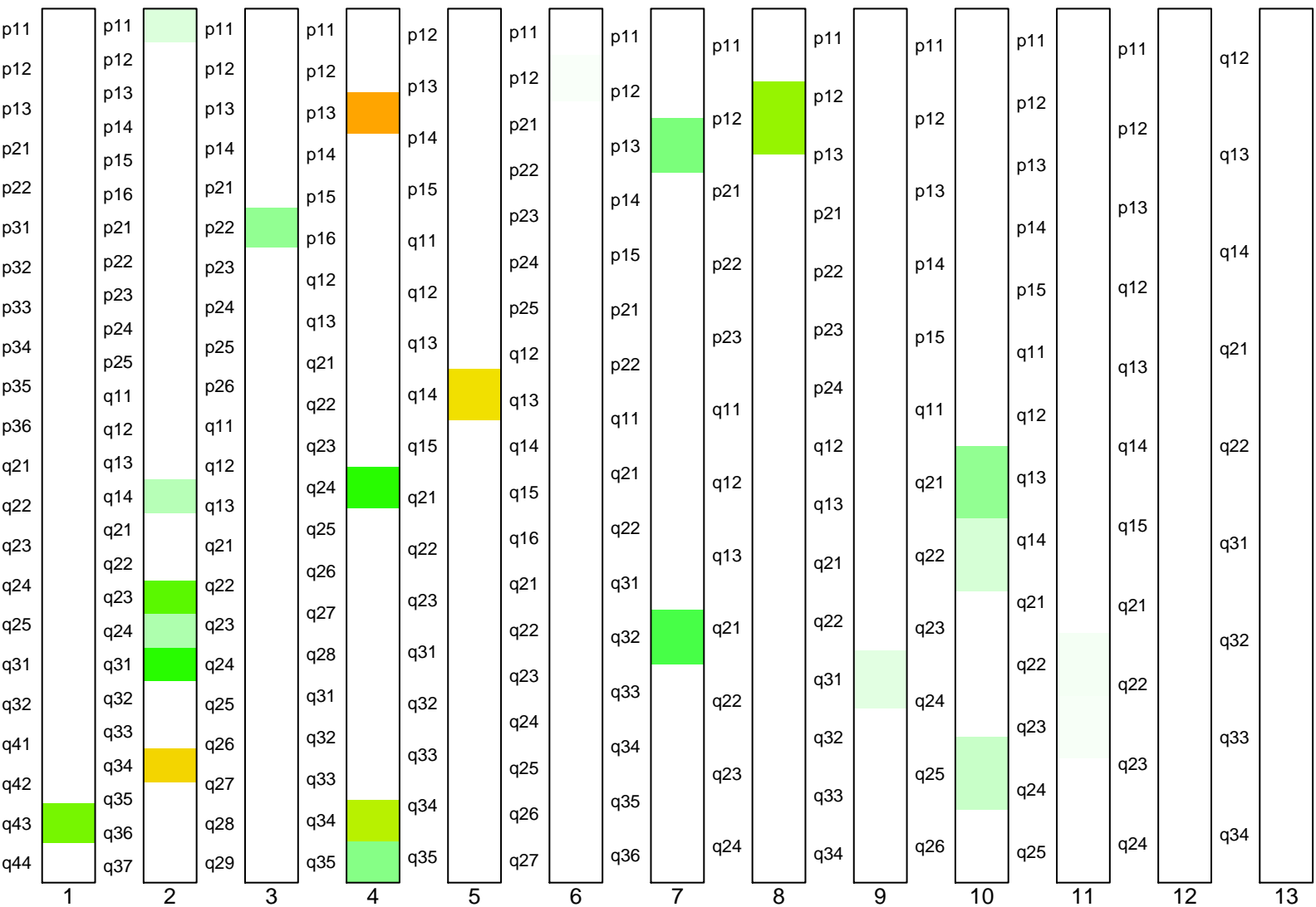




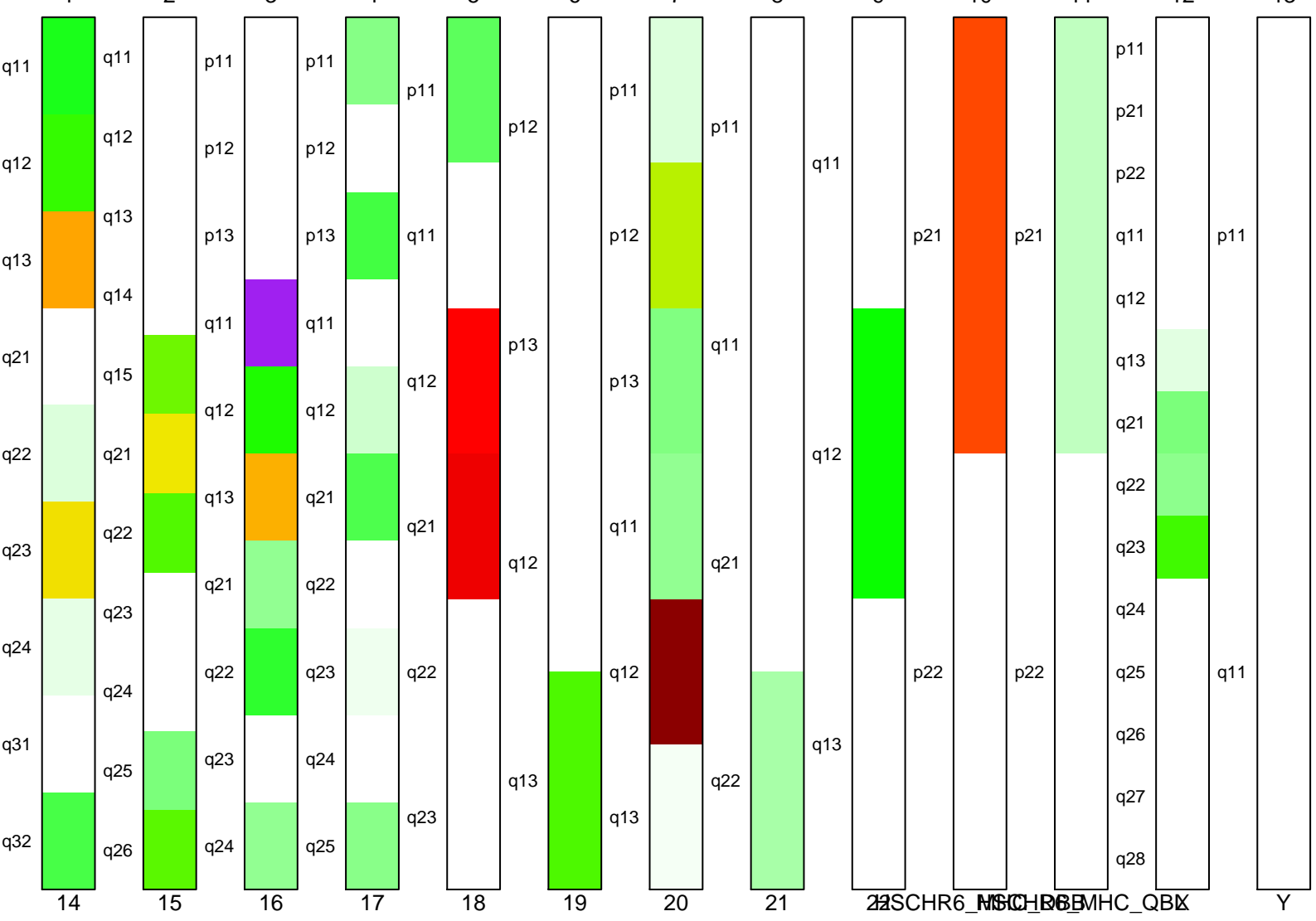
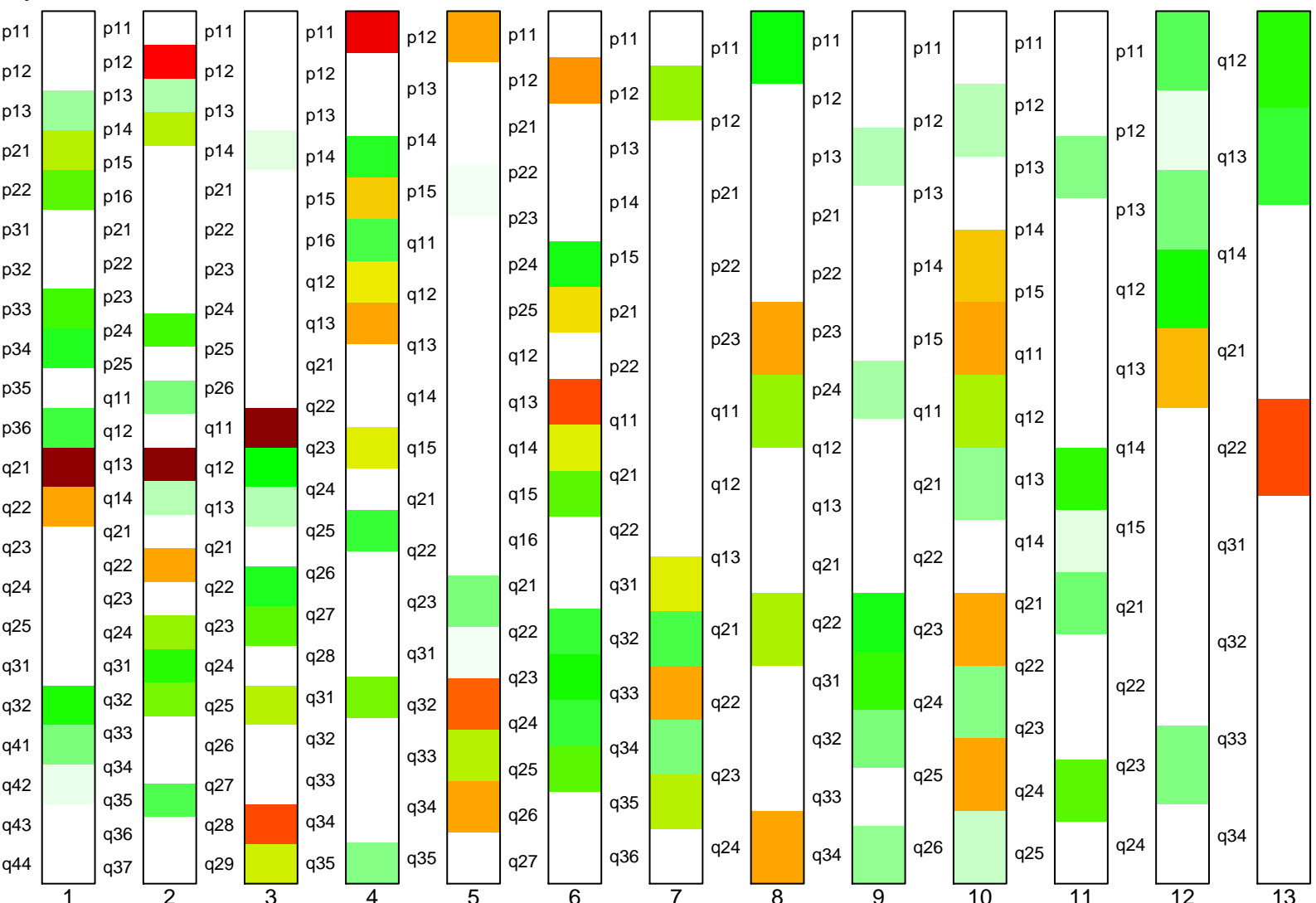
# Spot M



# Spot N

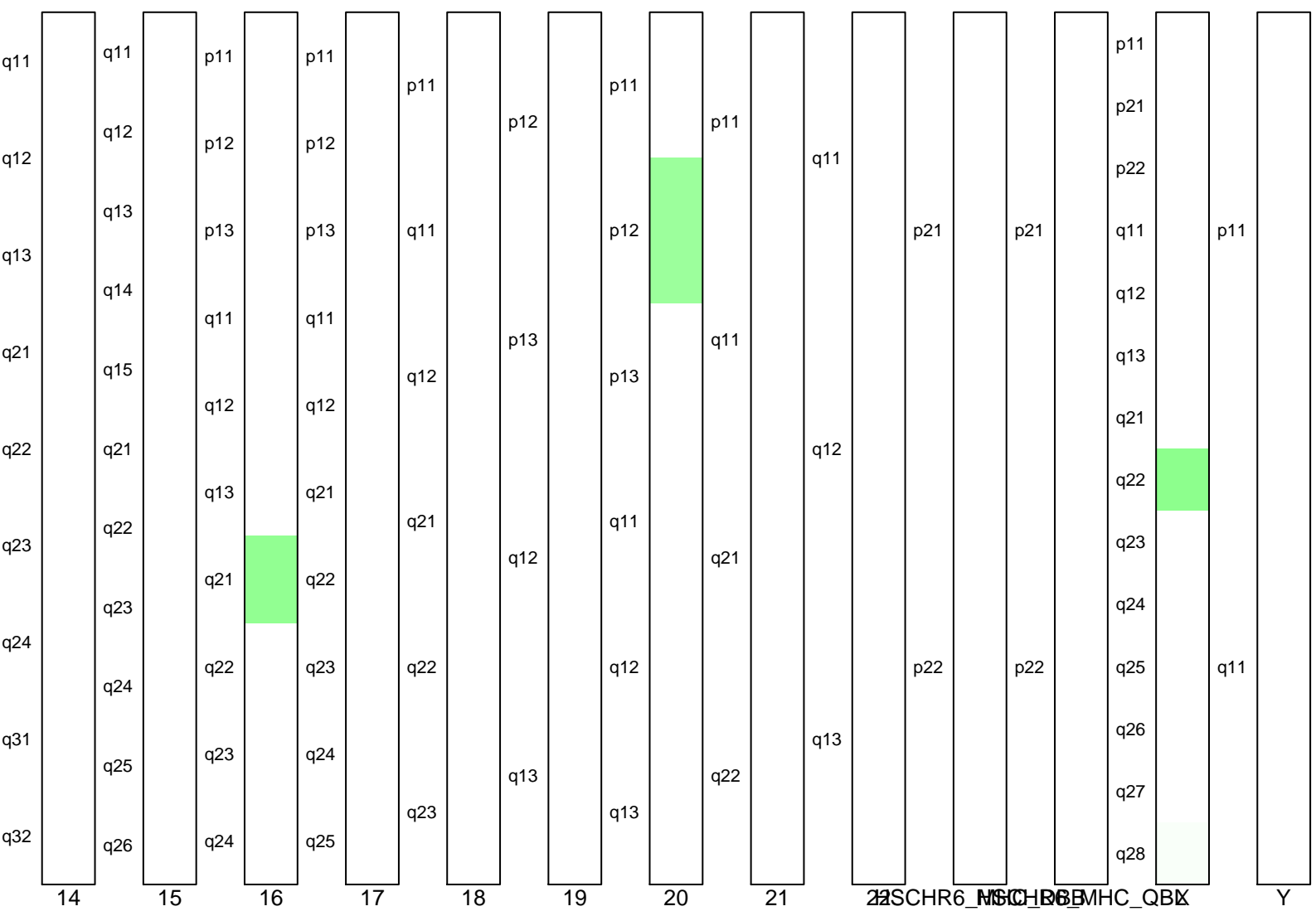
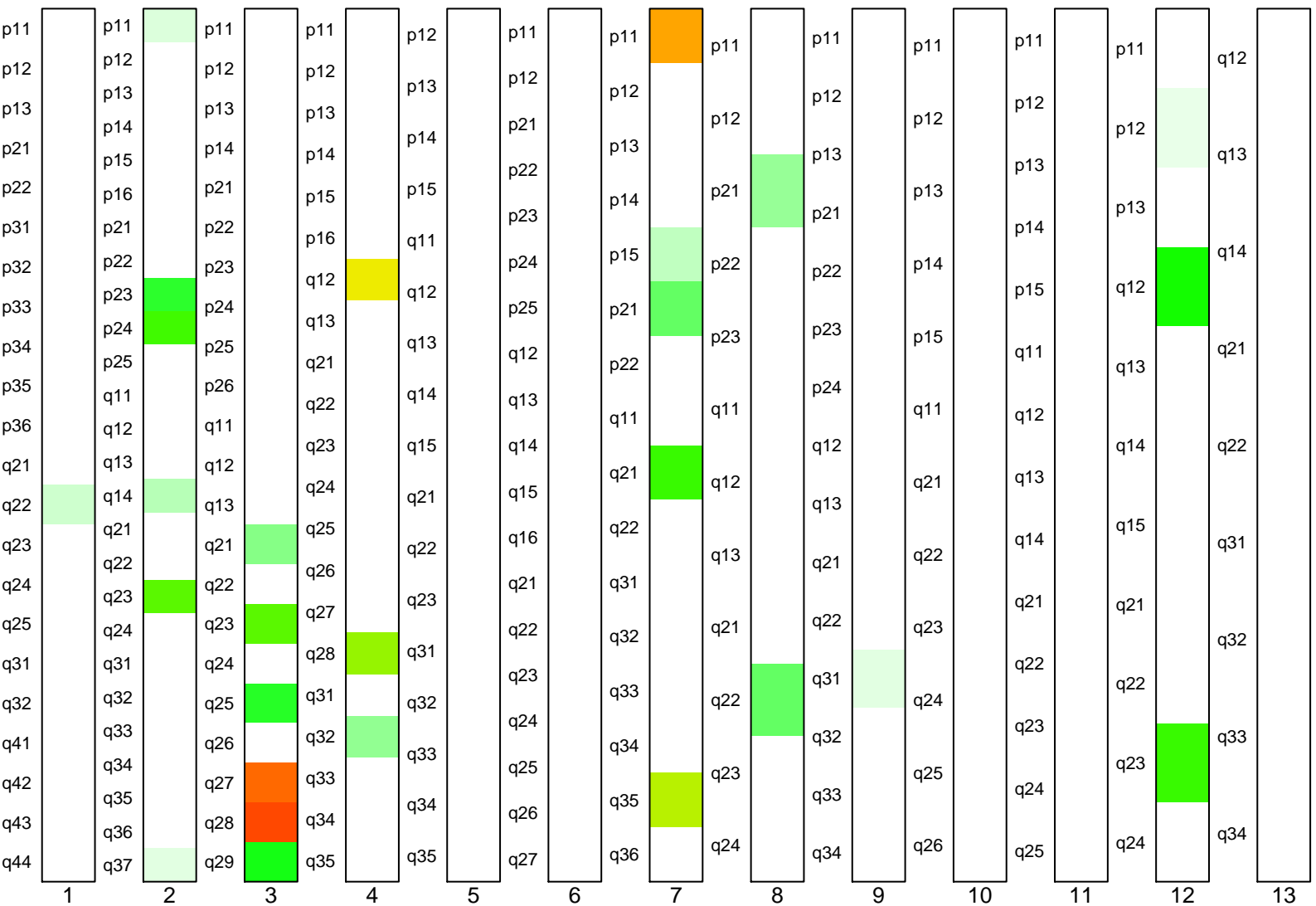


# Spot O

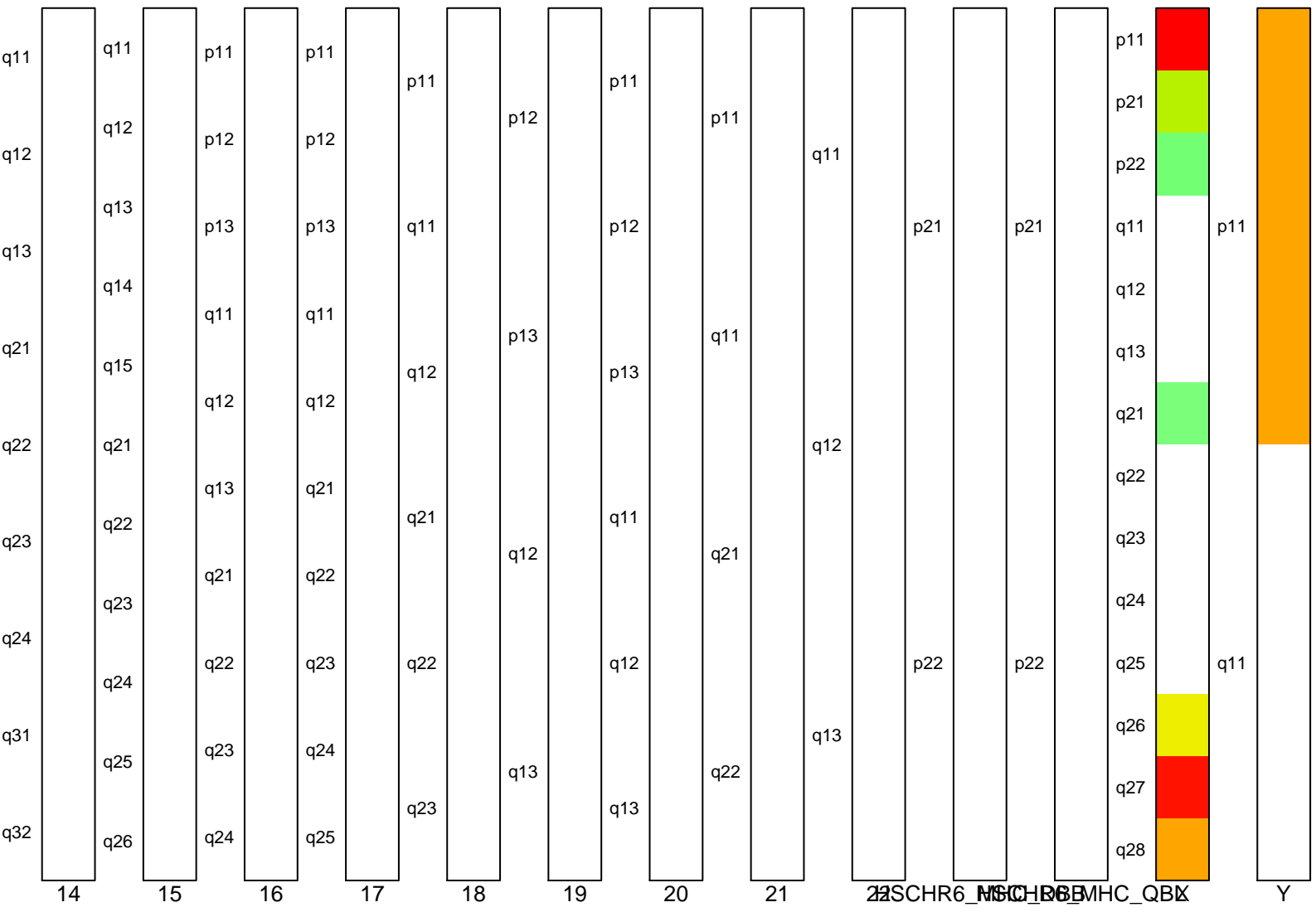
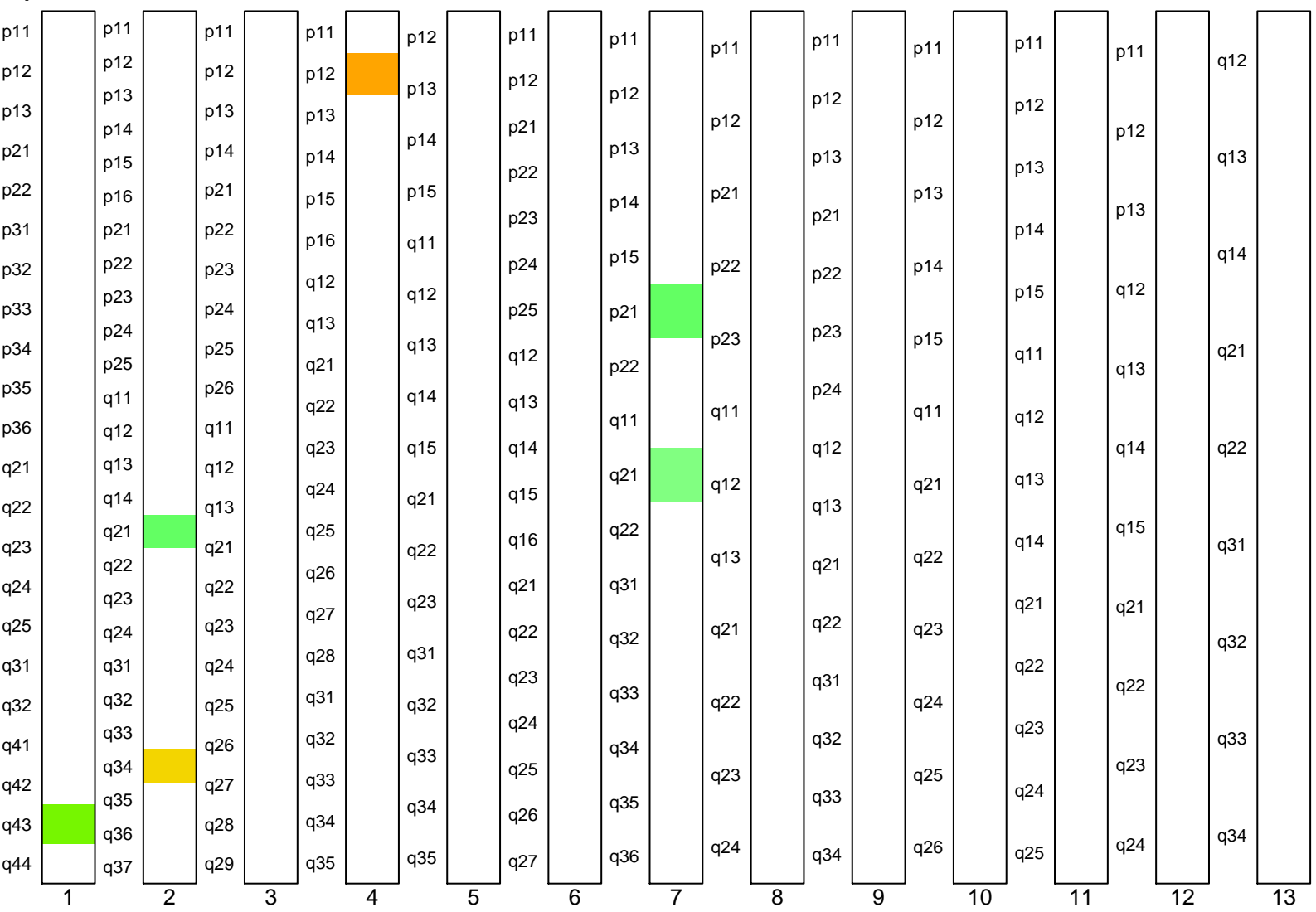


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# Spot P



# Spot Q



# Spot R

