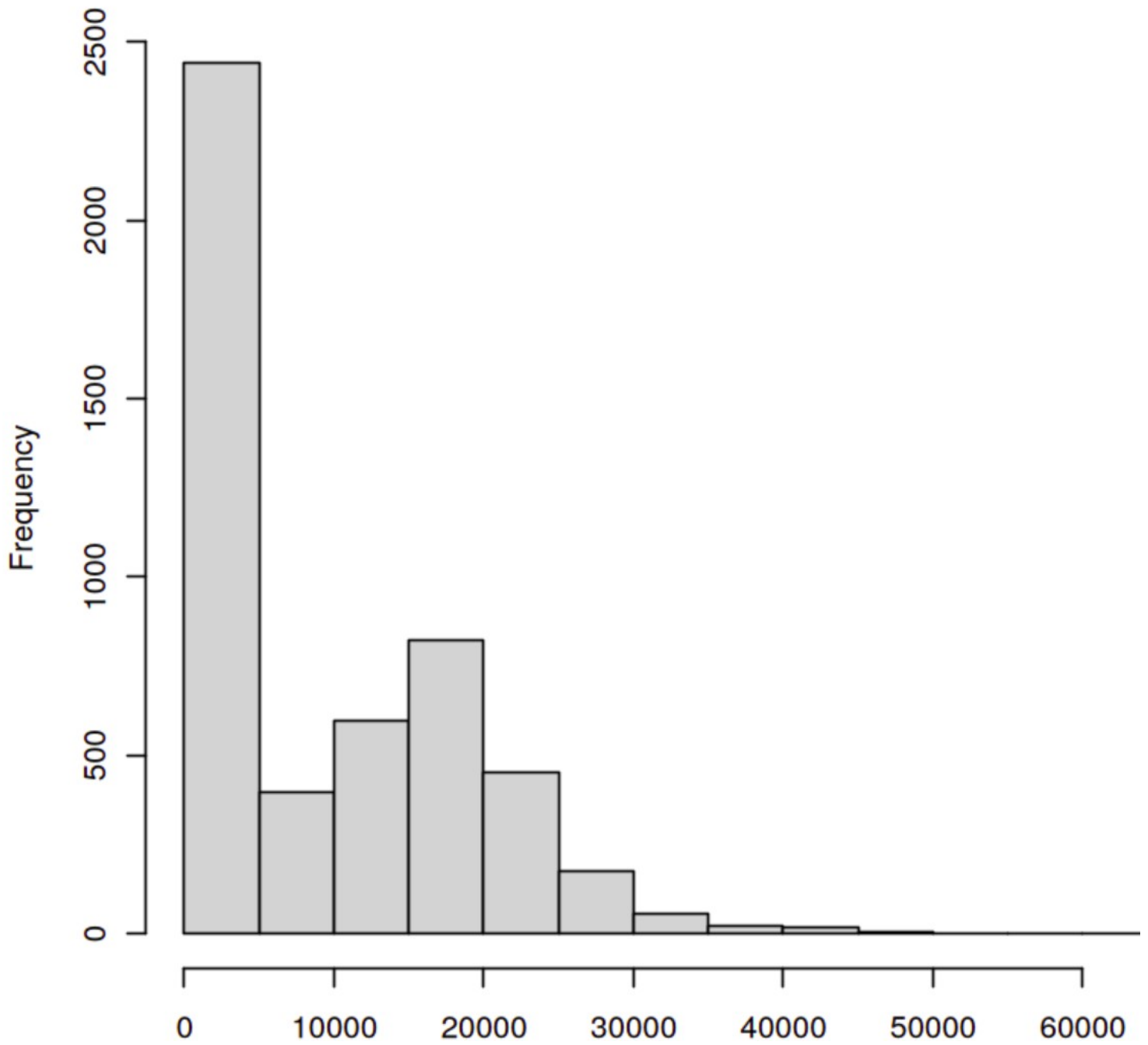


Histogram of libsize



A data.frame: 6 × 1

AAACAACGAATAGTTC.1

<chr>

1 AAACAAGTATCTCCCA-1

2 AAACAATCTACTAGCA-1

3 AAACACCAATAACTGC-1

4 AAACAGAGCGACTCCT-1

5 AAACAGCTTTCAGAAG-1

6 AAACAGGGTCTATATT-1

A data.frame: 6 × 1

V1

<chr>

1	ENSMUSG00000051951 Xkr4 Gene Expression
2	ENSMUSG00000089699 Gm1992 Gene Expression
3	ENSMUSG00000102331 Gm19938 Gene Expression
4	ENSMUSG00000102343 Gm37381 Gene Expression
5	ENSMUSG00000025900 Rp1 Gene Expression
6	ENSMUSG00000025902 Sox17 Gene Expression

A data.frame: 6 × 3

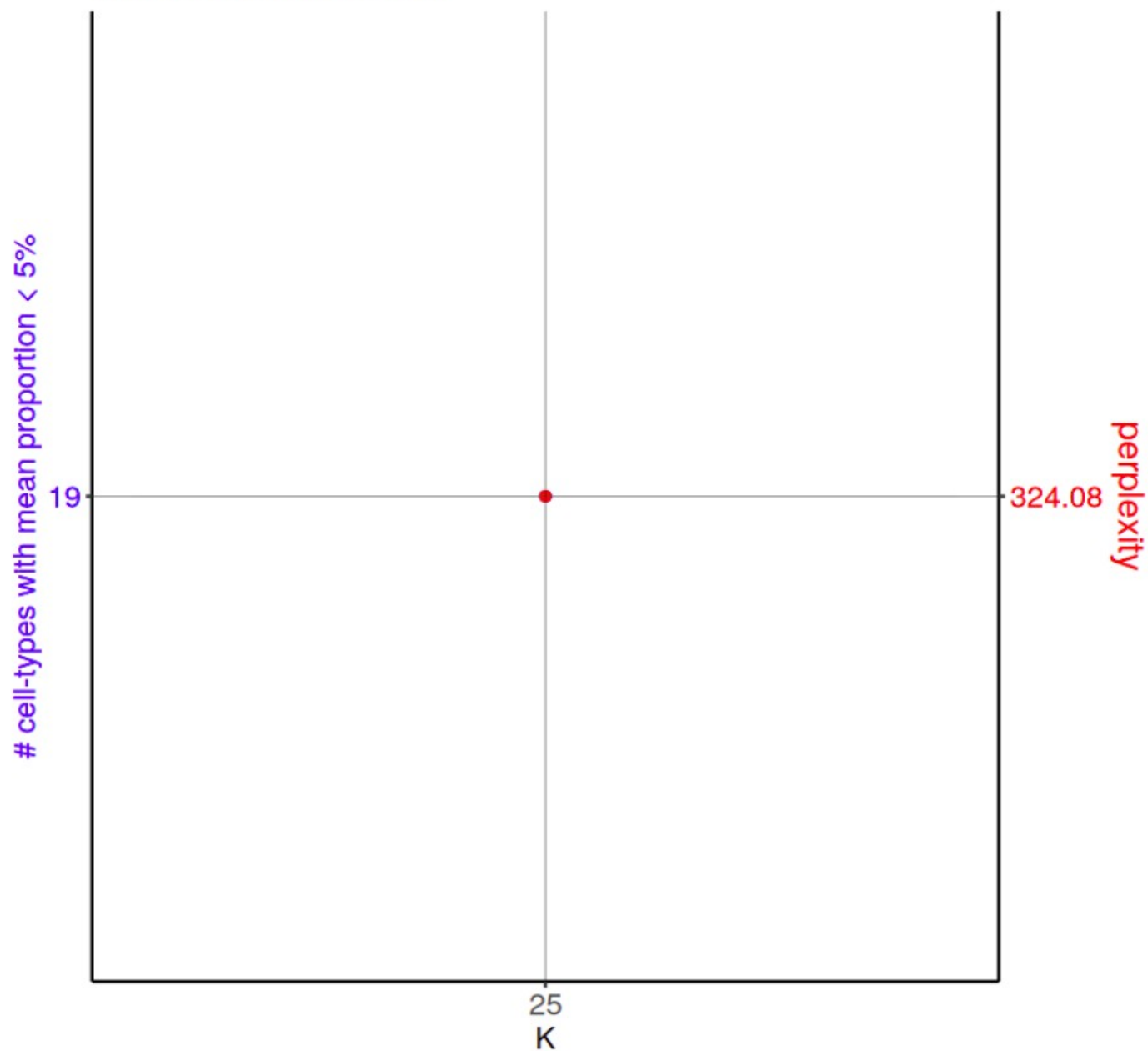
	V1	V2	V3
	<chr>	<chr>	<chr>
1	ENSMUSG00000051951	Xkr4	Gene Expression
2	ENSMUSG00000089699	Gm1992	Gene Expression
3	ENSMUSG00000102331	Gm19938	Gene Expression
4	ENSMUSG00000102343	Gm37381	Gene Expression
5	ENSMUSG00000025900	Rp1	Gene Expression
6	ENSMUSG00000025902	Sox17	Gene Expression

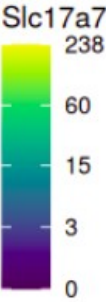
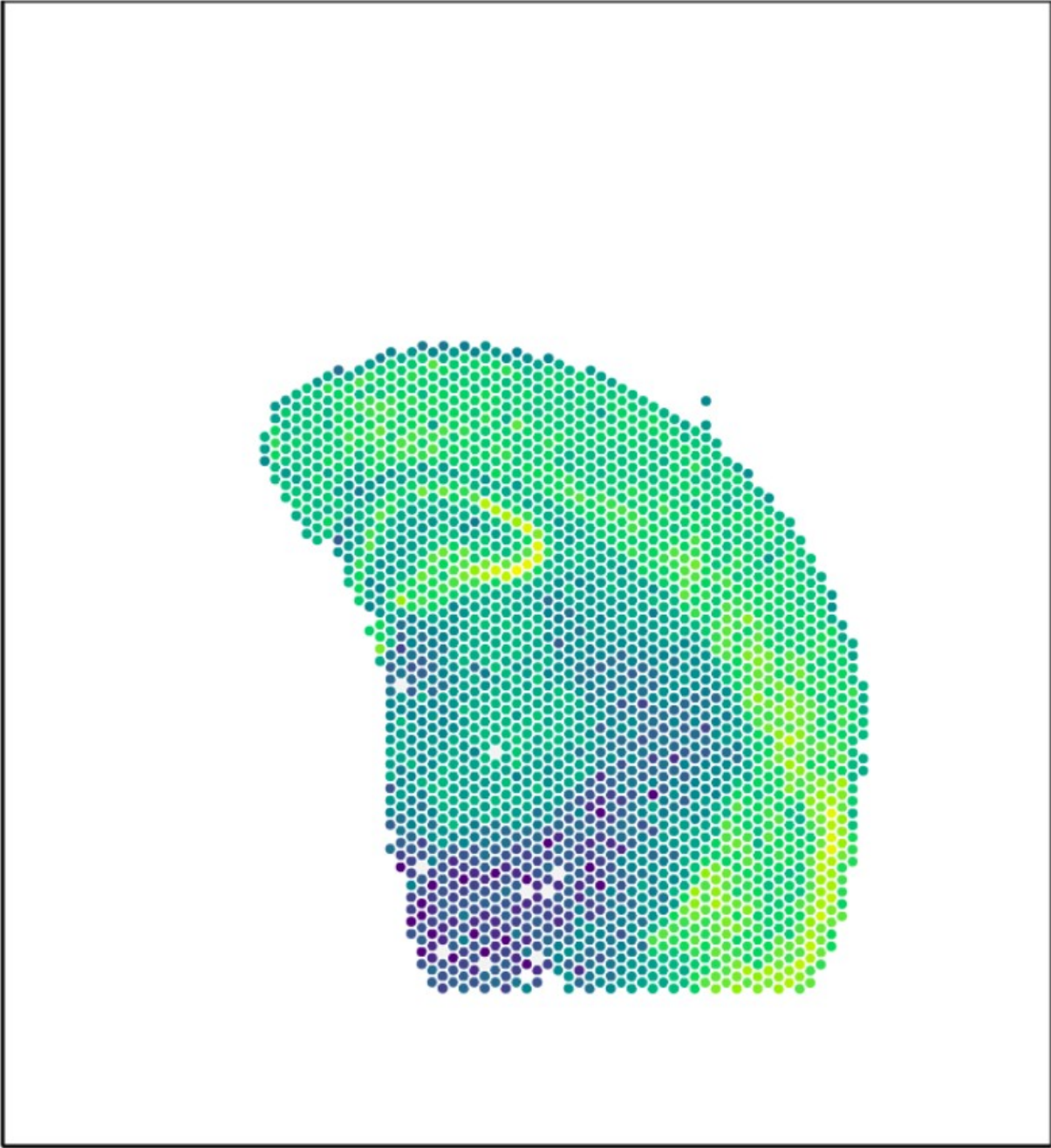


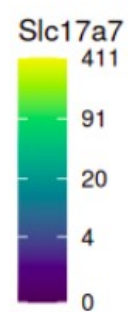
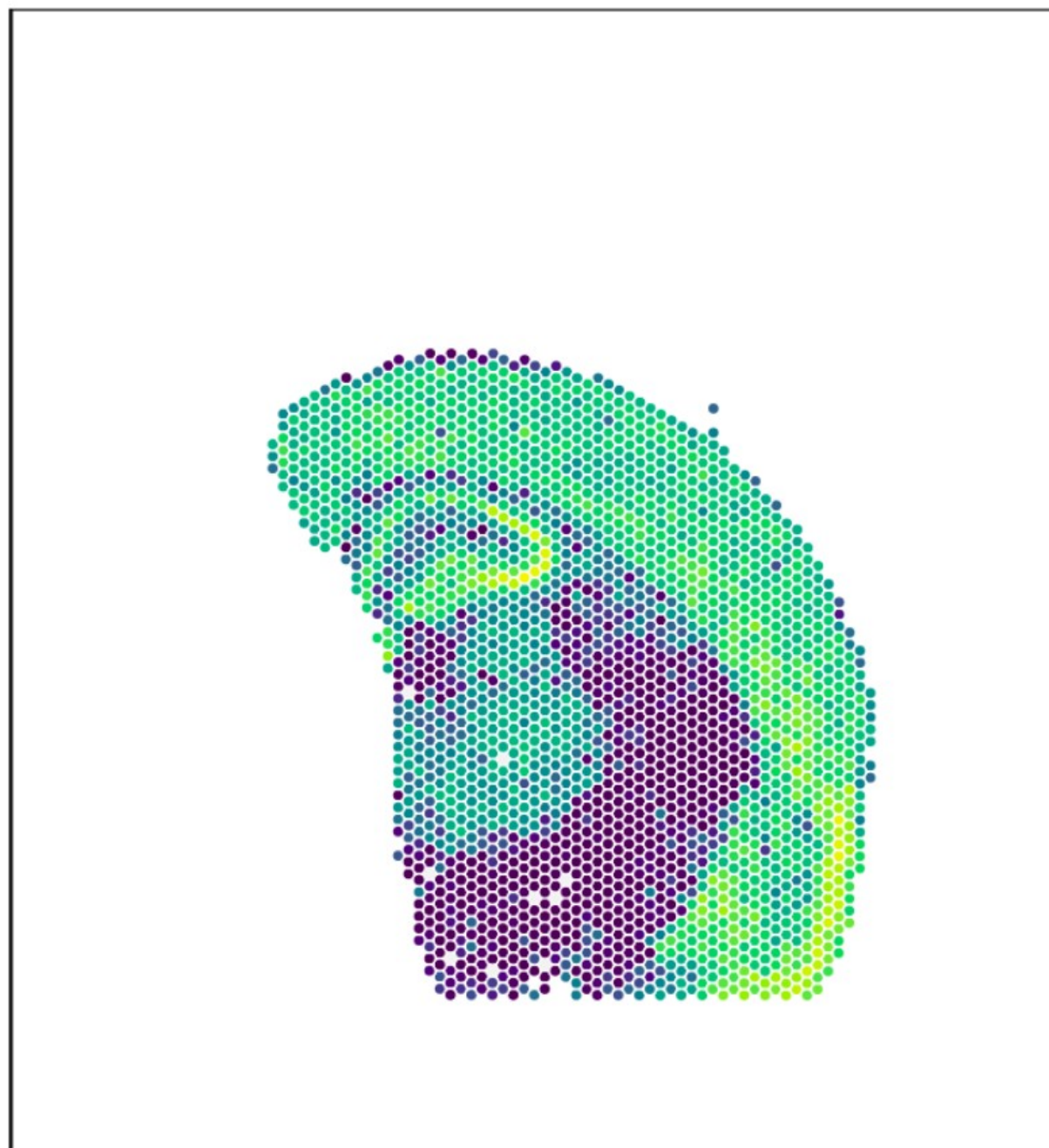


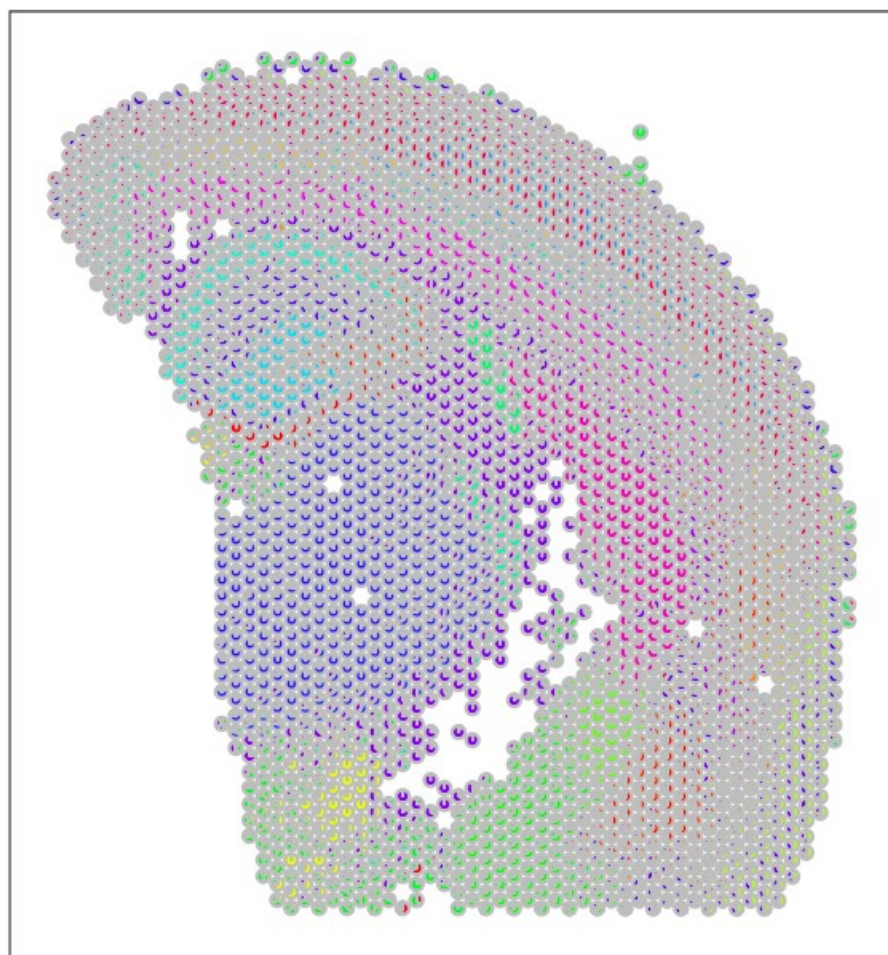
Fitted model K's vs deconvolved cell-types and perplexity

LDA models with $\alpha > 1$ shaded

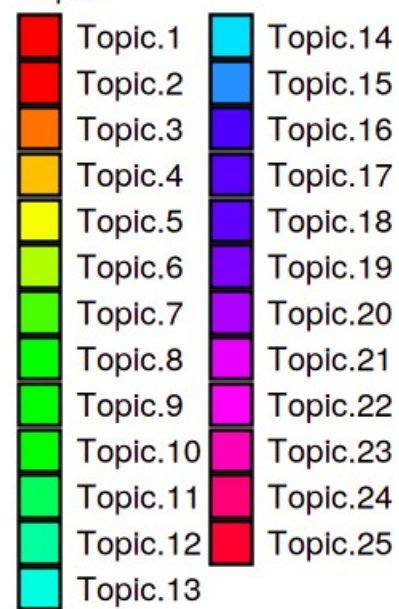






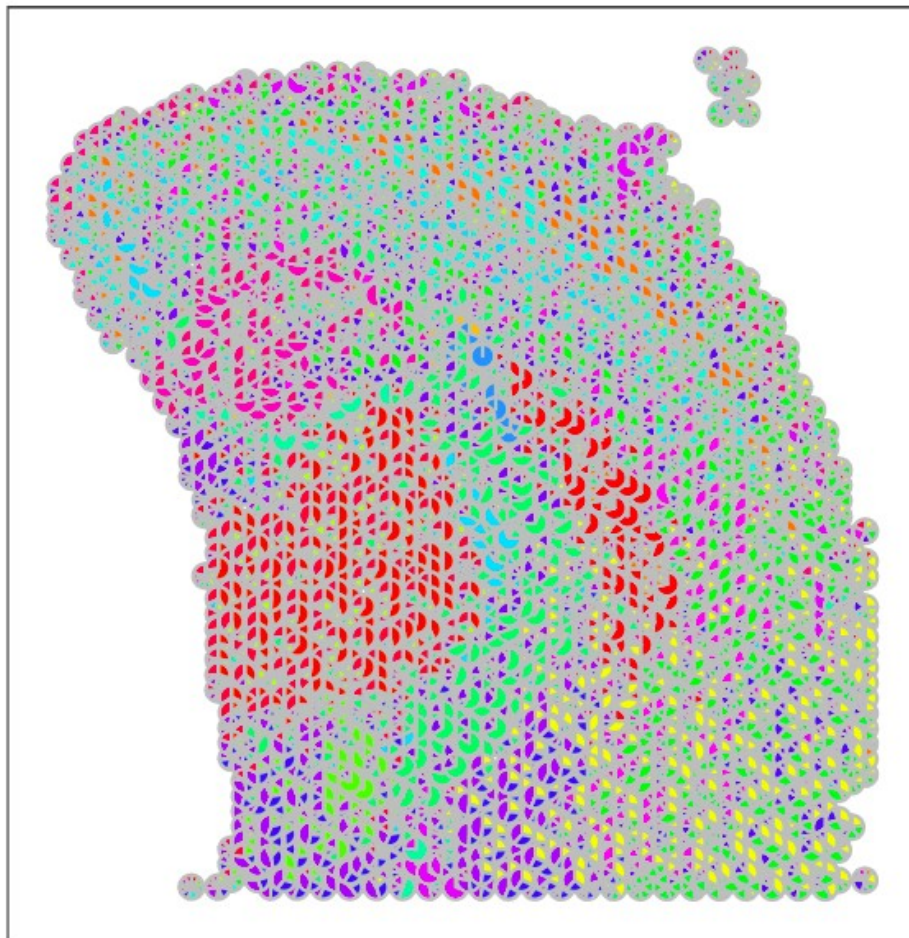


Topics

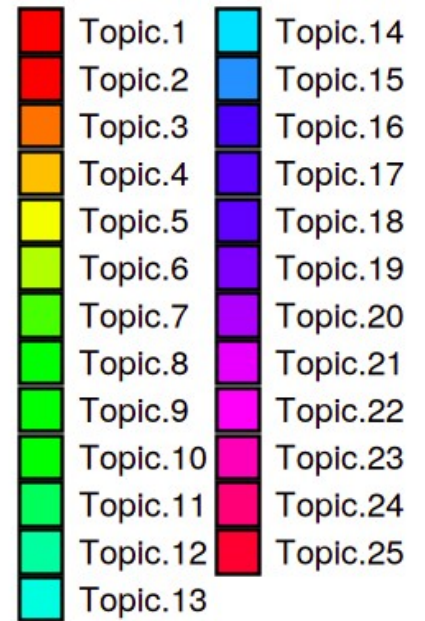


Pixel.Groups



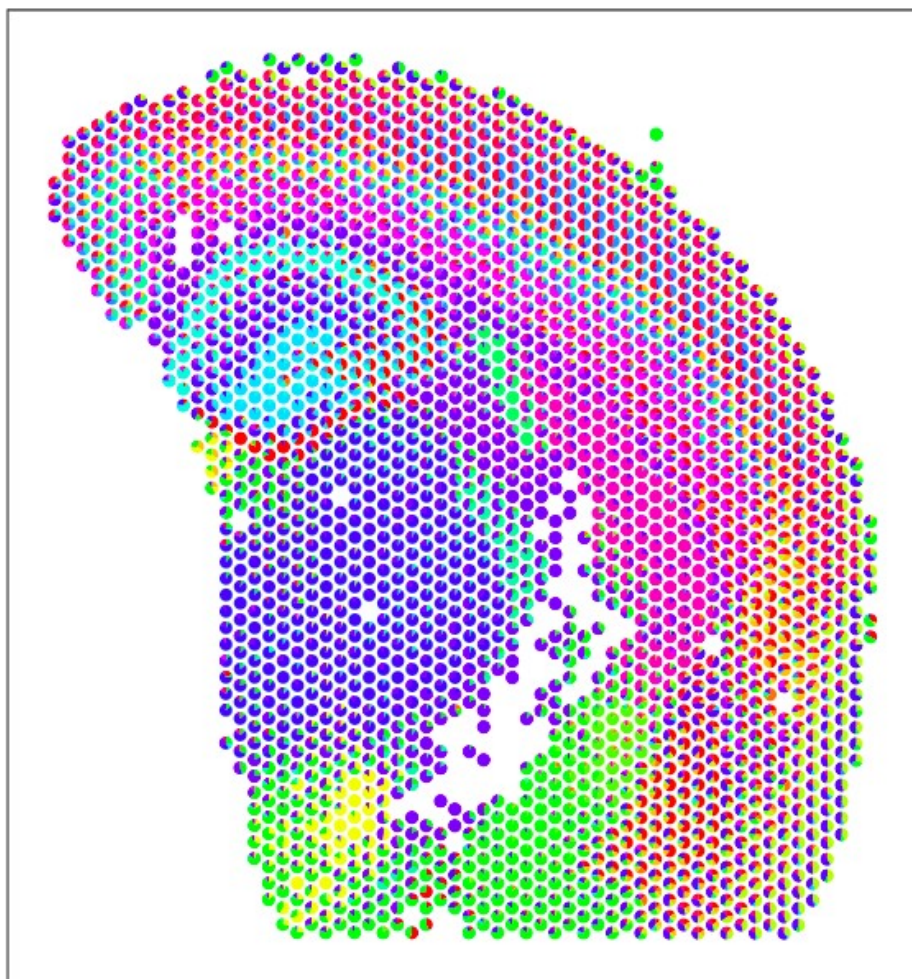


Topics

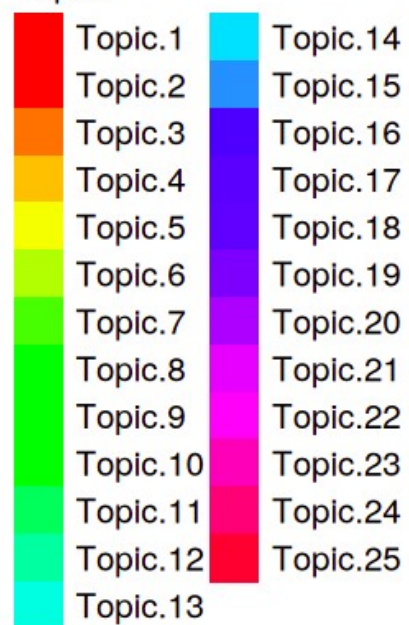


Pixel.Groups





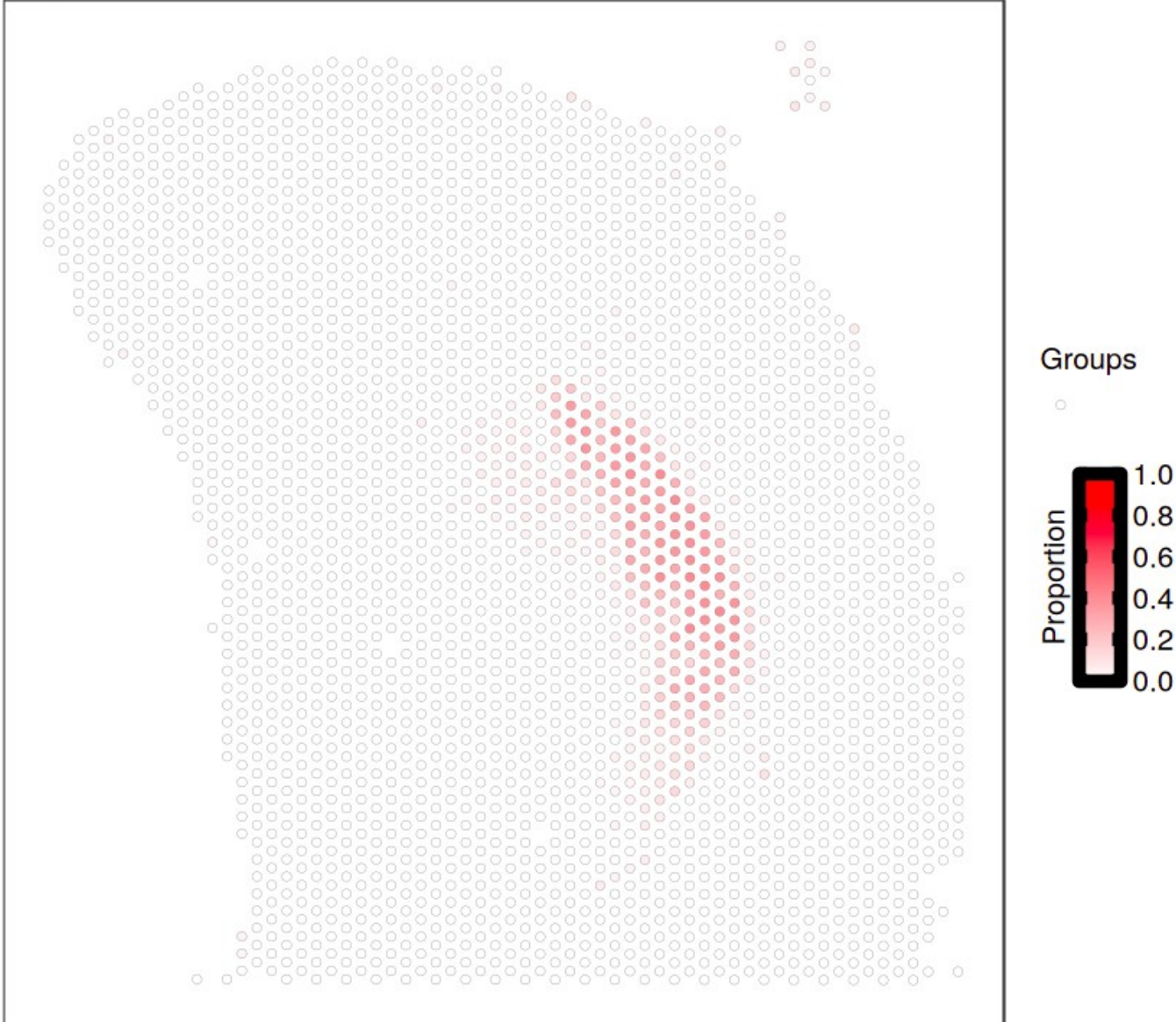
Topics



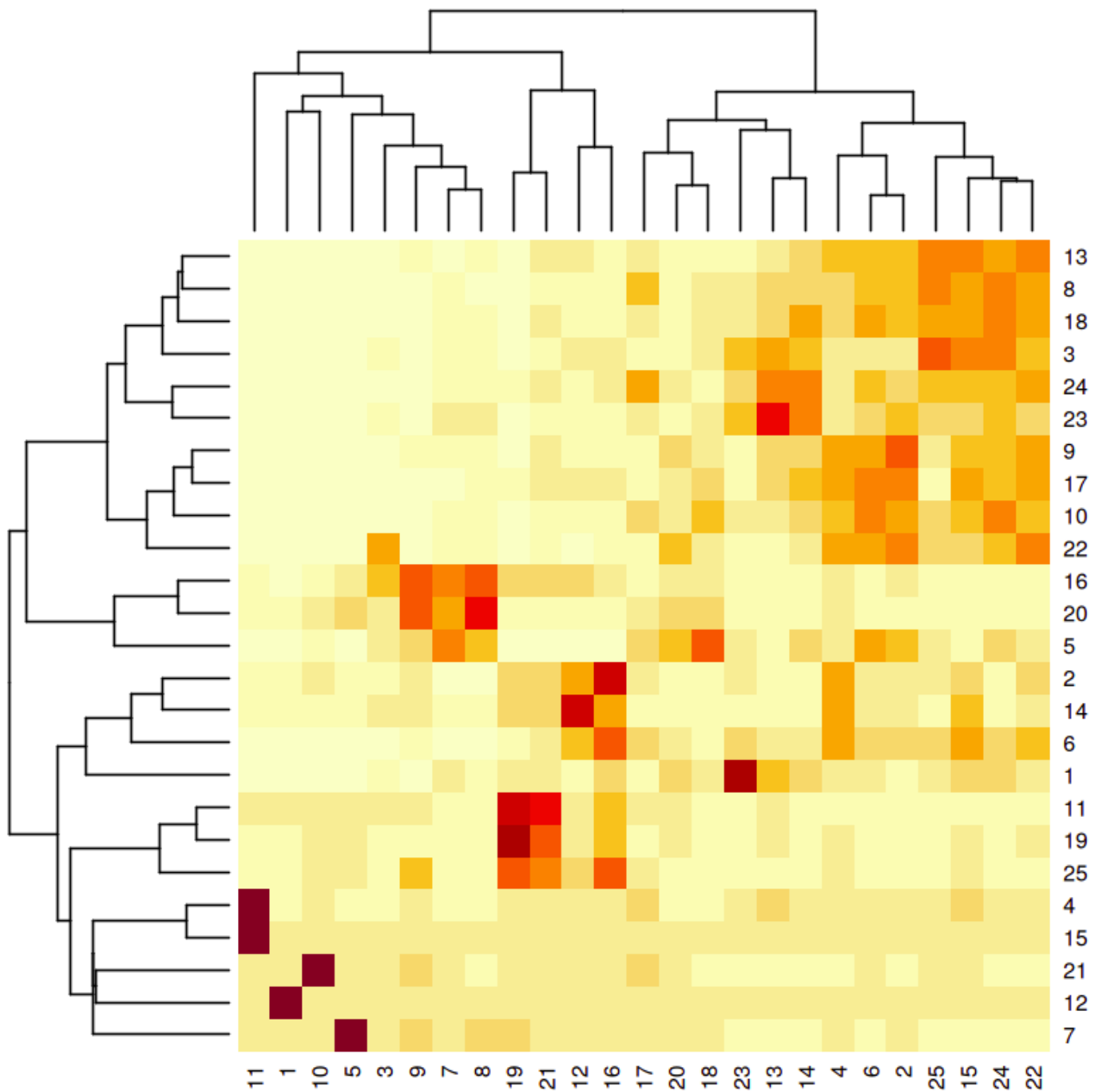
Pixel.Groups

0

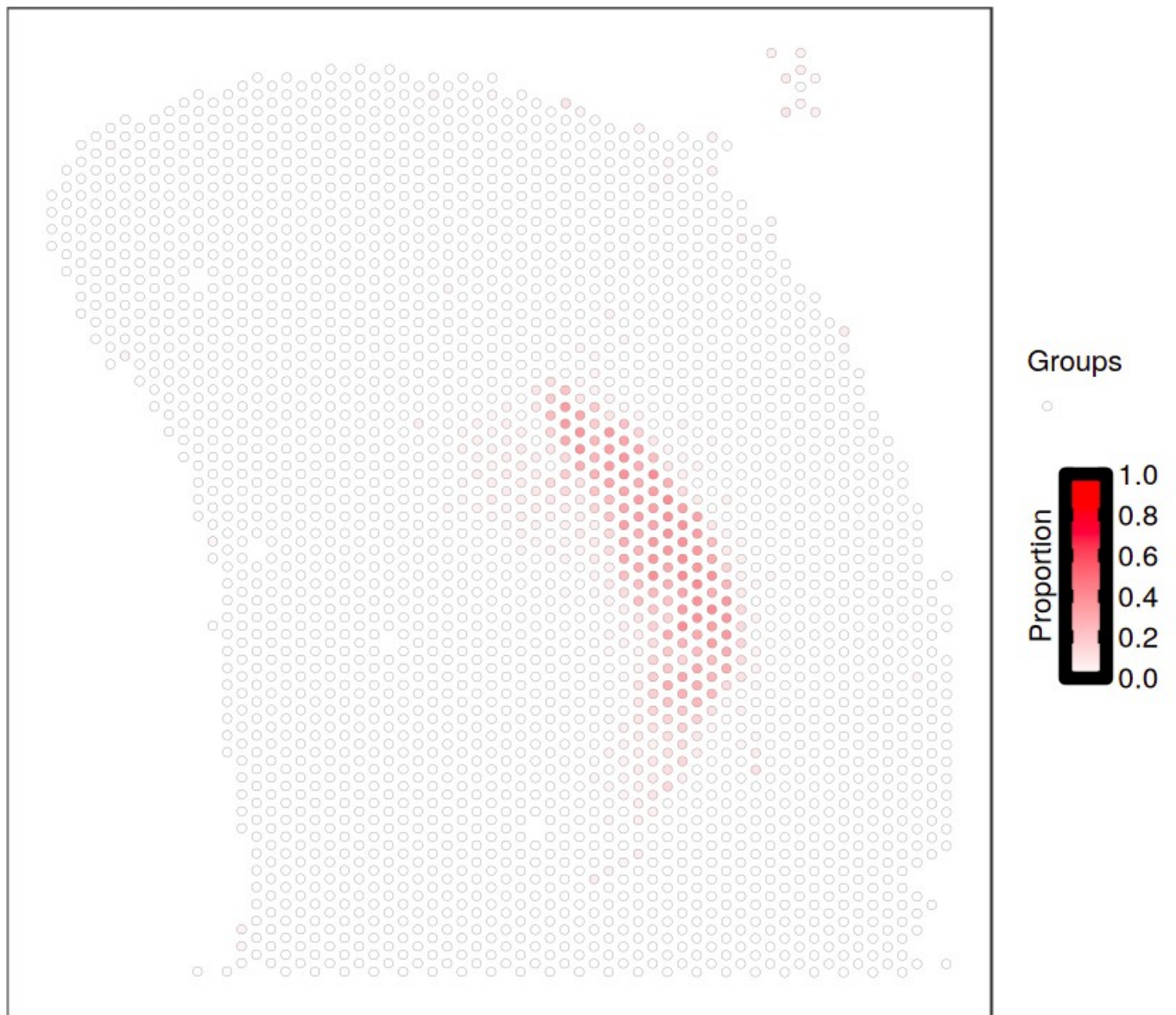
X12



```
] : heatmap(cmat)
```



STdeconvolve vanilla: topic 1



STdeconvolve Spotclean: topic 21

