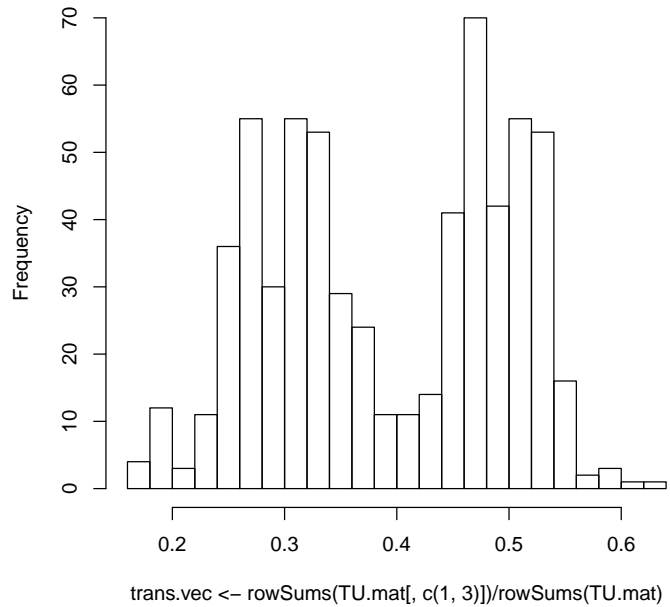


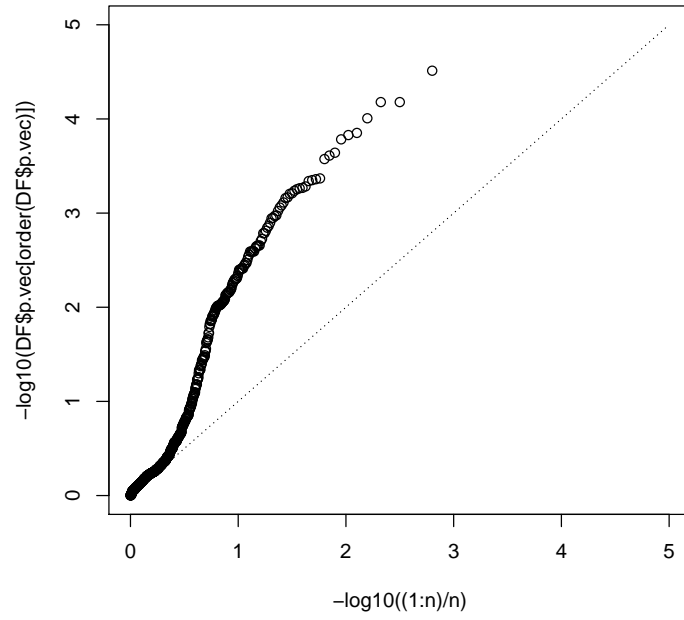
listogram of `trans.vec <- rowSums(TU.mat[, c(1, 3)])/rowSums(TU`



```
> c(length(DF$grange), length(reduce(DF$grange)))
```

```
[1] 632 45
```

	seqnames	start	end	width	strand	p.min	p.median
1	chr15	19768826	19982036	213211	*	3.072890e-05	0.0013693170
2	chr7	141419097	141441259	22163	*	9.833931e-05	0.0006589259
3	chr15	19341464	19545168	203705	*	1.406718e-04	0.0012756571
4	chr8	39356825	39497557	140733	*	2.204028e-03	0.0123763747
5	chr6	32611466	32643872	32407	*	2.219750e-03	0.0150874888
6	chr6	32059186	32065343	6158	*	2.559934e-03	0.0068369823
7	chr15	19095051	19205581	110531	*	4.306767e-03	0.0150366480
8	chr17	41785962	41914286	128325	*	6.285804e-03	0.0109696610
9	chr6	32094298	32107594	13297	*	3.234971e-02	0.0462509861
10	chr6	32066939	32093133	26195	*	3.593753e-02	0.3073202023
11	chr6	32650822	32664356	13535	*	3.960053e-02	0.0660979881
12	chr16	33778130	33820307	42178	*	4.223034e-02	0.3164738758
13	chr11	55124465	55209499	85035	*	5.743147e-02	0.5299039325
14	chr3	75502426	75719139	216714	*	5.824234e-02	0.3020937569
15	chr14	18347035	18372086	25052	*	5.876744e-02	0.4131212565
16	chr5	97074222	97125076	50855	*	7.162678e-02	0.0854169058



17	chr1	103941535	104099390	157856	*	1.051024e-01	0.2673147358
18	chr5	69359352	69433008	73657	*	1.057531e-01	0.1806520425
19	chr6	31388080	31397263	9184	*	1.339235e-01	0.3760967641
20	chr19	20404485	20507068	102584	*	1.456802e-01	0.3730938842
21	chr11	48890168	48918267	28100	*	1.614379e-01	0.4851229715
22	chr16	32404517	32530051	125535	*	1.906860e-01	0.6826270270
23	chr12	36404411	36532019	127609	*	2.296317e-01	0.3155882184
24	chr1	195087039	195087039	1	*	2.583597e-01	0.2583597159
25	chr9	43594114	43674189	80076	*	2.810095e-01	0.4630093877

	trans.median	n.cmp
1	0.3303571	21
2	0.5410959	8
3	0.3333333	30
4	0.5363128	17
5	0.3614458	43
6	0.4492754	5
7	0.3563218	13
8	0.4536878	22
9	0.2575758	11
10	0.2727273	15
11	0.2238806	9
12	0.5162338	12
13	0.5345796	26
14	0.4319249	15
15	0.4548281	12
16	0.4782609	5
17	0.4800000	25
18	0.2622951	9
19	0.4776119	14
20	0.5013089	6
21	0.4652926	20
22	0.2768730	123
23	0.1846154	7
24	0.4035088	1
25	0.3715278	14

GRanges with 1 range and 4 metadata columns:

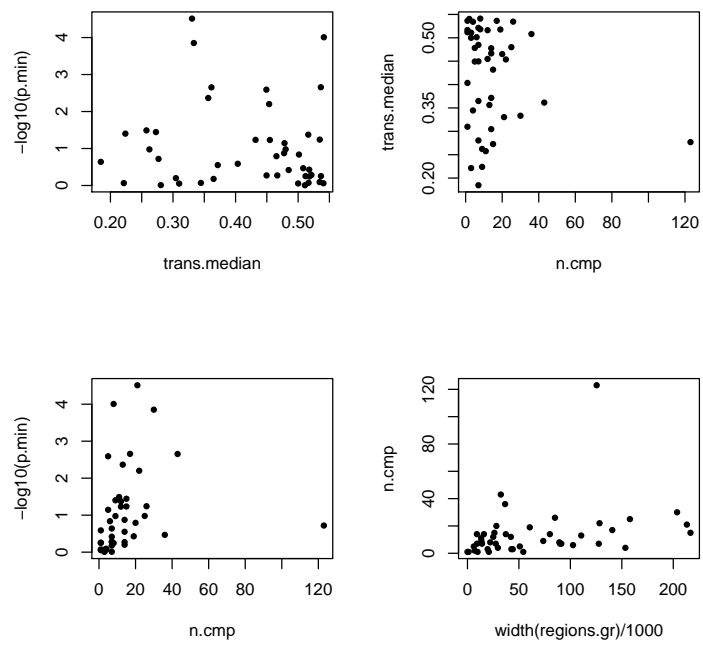
	seqnames	ranges	strand	p.min
	<Rle>	<IRanges>	<Rle>	<numeric>
[1]	chr16	[32404517, 32530051]	*	0.190686032146876

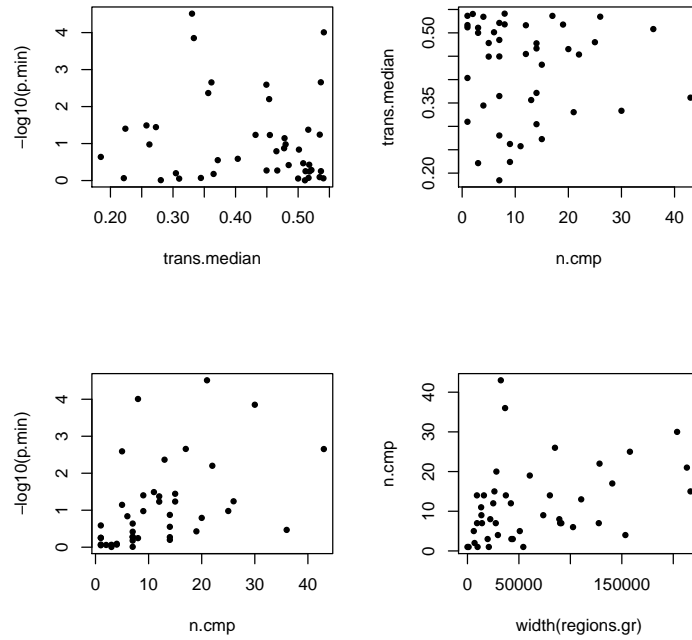
  

	p.median	trans.median	n.cmp
	<numeric>	<numeric>	<integer>
[1]	0.682627027049546	0.276872964169381	123

---

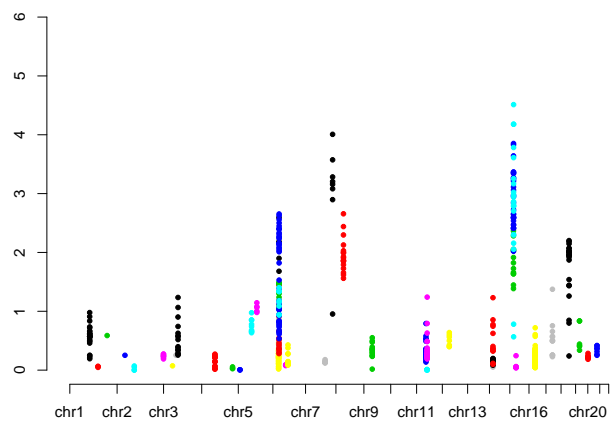
seqlengths:



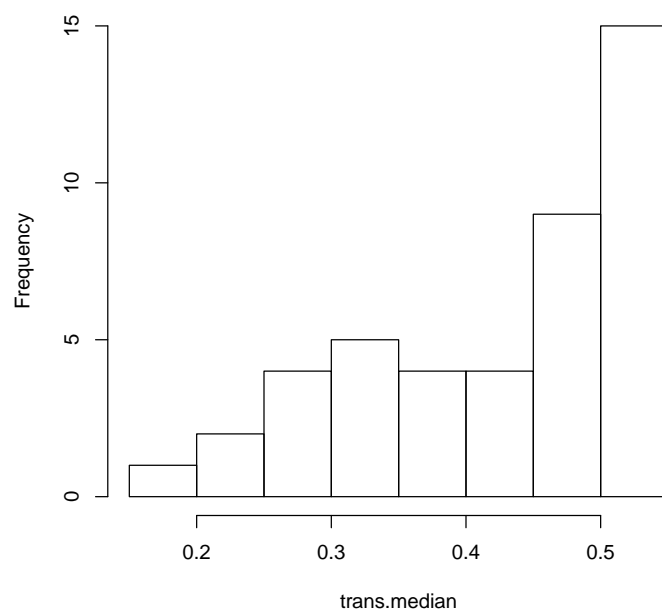


chr1	chr1_random	chr2 ...	chrY	chrM
247249719	1663265	242951149 ...	57772954	16571

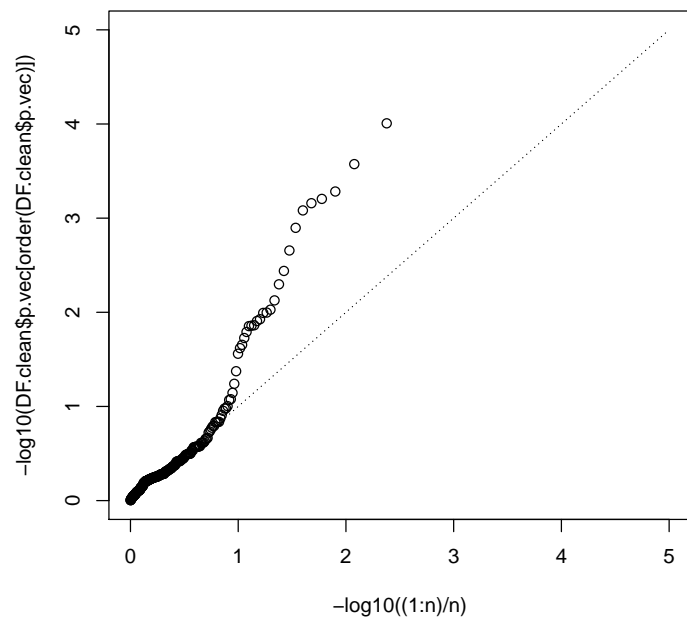
The outlier is on chromosome 16. It is a region with 123 components, and has width 125.535 kB. chr16:32404517-32530051. If we remove the outlying region on chromosome 16 we see the following.



**Histogram of trans.median**



```
> thresh <- with(as(values(regions.gr), "data.frame"), median(trans.median))
> regions.gr.clean <- regions.gr[which(values(regions.gr)$trans.median >=
  thresh)]
```



```
> DF.clean <- DF[queryHits(findOverlaps(DF$grange, regions.gr.clean)),
  ]
```

