DMR report

ruichaohou

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Genomic regions that are called DMR bumpers, and we only select top 20 Differential Bumper of our bumper object, extract through default null distribution of $area = \sum_{i \in R_j} \beta_i$

1 Top 20 DMRs

```r
if(input$topk <= 40){
  kable(res)
}else{
  r = 1
  while(r < input$topk){
    t <- if(r+40-1 < input$topk){
      r+40-1
    }else{
      input$topk
    }
    kable(res[r:t,])
    r = r + 40
  }
}
```

seqnames	start	width	beta0	pvalue
chr10	134597884	4647	2.335	0
chr12	4380025	4866	1.794	0
chr6	29520965	839	2.376	0
chr6	29973669	1759	1.694	0
chr13	78492306	1762	1.837	0
chr16	51183988	4775	1.995	0
chr10	135049208	2797	1.699	0
chr11	2160055	2491	1.453	0
chr18	74960629	2166	2.297	0
chr6	29893273	1903	1.720	0
chr17	35289677	5375	1.916	0
chr6	28602543	1237	1.873	0
chr6	33160067	2440	1.586	0
chr2	63280625	6664	1.862	0
chr6	30094947	856	2.126	0
chr6	30038712	1189	1.469	0
chr14	29234671	2810	2.127	0
chr7	79081455	2742	2.023	0
chr3	147125114	3044	1.708	0
chr14	36985711	5391	2.094	0

These are 20 Differential Region with lowest p value, ans these implies that CpG sites clustered in these regions has highest correlation.