```
In [13]: %time input_file = 'GSM1055800_HiC.IMR90.rep1.nodup.summary.head.reg'
CPU times: user 4 µs, sys: 0 ns, total: 4 µs
Wall time: 10 µs

In [14]: %time res = int(1024000)
CPU times: user 5 µs, sys: 1 µs, total: 6 µs
Wall time: 12.2 µs

In [15]: %time data = pd.read_csv('hg19.genome.bed', sep='\t', header=None)
CPU times: user 1.92 ms, sys: 715 µs, total: 2.63 ms
Wall time: 2.44 ms

In [16]: %time chrom_names = list(data.ix[:, 0])
CPU times: user 655 µs, sys: 138 µs, total: 793 µs
Wall time: 722 µs

In [17]: %time chrom_sizes = list(data.ix[:, 2])
CPU times: user 363 µs, sys: 39 µs, total: 402 µs
Wall time: 381 µs

In [18]: %time bin_num = [int(ceil(chrom_size/res)) for chrom_size in chrom_sizes]
CPU times: user 74 µs, sys: 20 µs, total: 94 µs
Wall time: 88 µs

In [19]: %time chrom_vector = [list(itertools.repeat(chrom_name,bin_num)) for chrom_name,b
in_num in zip(chrom_names,bin_num)]
CPU times: user 84 µs, sys: 24 µs, total: 108 µs
Wall time: 104 µs

In [20]: %time chrom_vector = [item for sublist in chrom_vector for item in sublist]
CPU times: user 574 µs, sys: 305 µs, total: 879 µs
Wall time: 625 µs
```