For entire genome analysis, We analysed the frequency of GATA AAAG sequence while increasing the spacer length from 0-30

Entire genomes of Oryza Sativa were obtained.
Entire genomes are available in the fastq format so there were several stages of complex codes needed for conversion and output of usable data.

**The data obtained for Oryza Sativa:**

| Spacer | Freq | Spacer | Freq | Spacer | Freq | Spacer | Freq |
|--------|------|--------|------|--------|------|--------|------|
| 0 | 5808 | 8 | 4895 | 16 | 4429 | 24 | 3908 |
| 1 | 5259 | 9 | 5021 | 17 | 4458 | 25 | 3837 |
| 2 | 5614 | 10 | 4719 | 18 | 4169 | 26 | 4105 |
| 3 | 5507 | 11 | 4886 | 19 | 4281 | 27 | 3925 |
| 4 | 5476 | 12 | 4541 | 20 | 4432 | 28 | 3958 |
| 5 | 5276 | 13 | 4661 | 21 | 4201 | 29 | 3962 |
| 6 | 5044 | 14 | 4809 | 22 | 3941 | 30 | 3882 |
| 7 | 5117 | 15 | 4436 | 23 | 4073 | | |

Highest frequency found at spacer length of **0 of 5808**
Lowest frequence found at spacer length of **25 of 3837**
Top 3 frequencies are found at spacer length **0,2,3**
Least 3 frequencies at **24,25,30**
Frequencies of around 5000 found from spacer lengths 0-9

Oryza Sativa Genome analysis