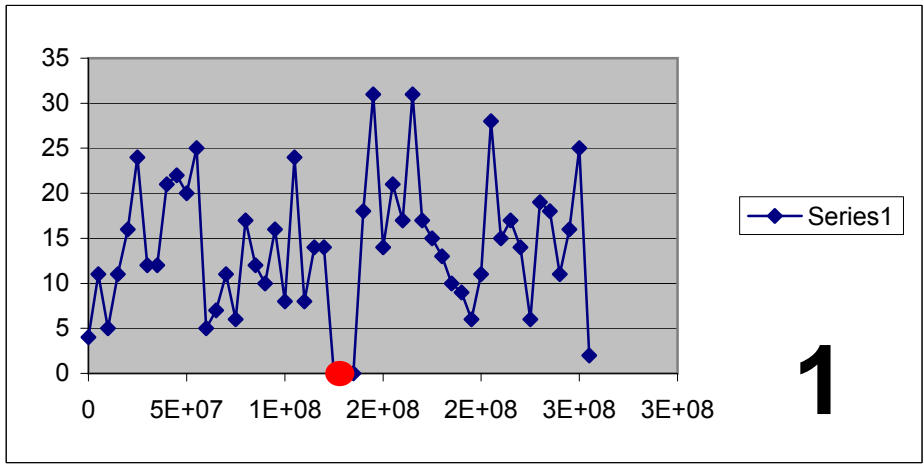


## Distribution of the processed pseudogene along the chromosomes

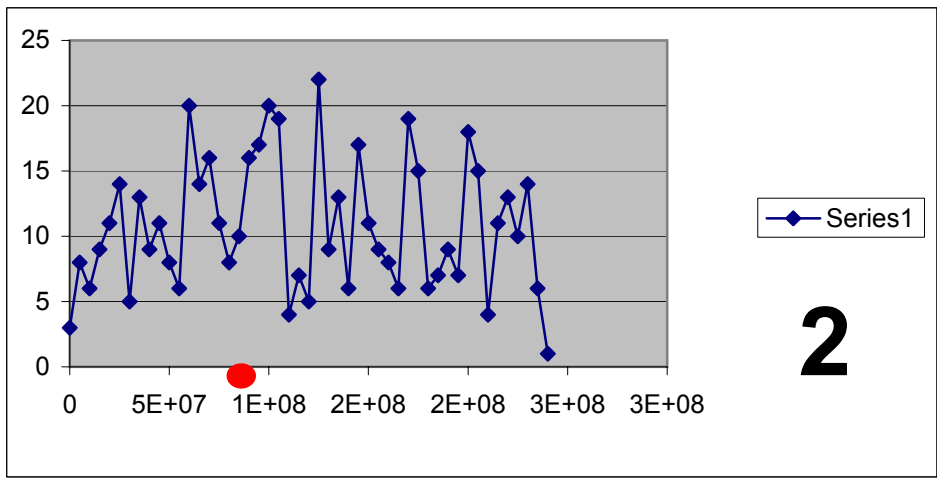
The following graphs show, for each chromosome, the processed pseudogene density (per 5 Mb) along the chromosomes (see RESULTS page 11).

*...We also checked to see whether, in conjunction with the local GC content, there are any “pseudogenic hot spots” on the chromosomes where the processed pseudogenes are more densely populated. For this purpose, we divided chromosomes into non-overlapping windows of 5 Mb and counted number of processed pseudogenes in each window. It appeared that the regions near the telomeres and centromeres often had less processed pseudogenes than the other parts of the chromosome, which could be partially explained by a faster DNA turnover and recombination rate near the telomeres and poor GC composition near the centromeres. However, sequencing in these parts are also the most incomplete, thus could have introduced potential biases in the detection of pseudogenes.*

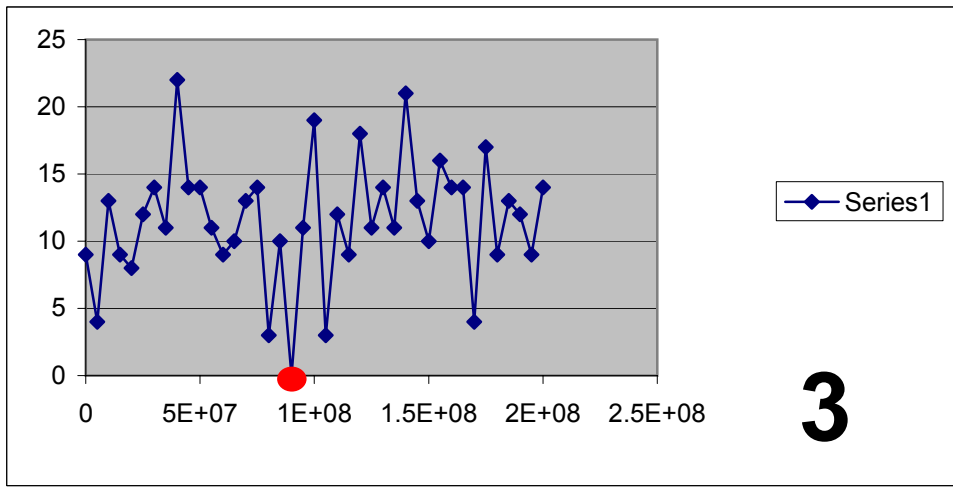
The chromosome names are labeled on each of the 24 graphs. Each chromosome is divided into windows of 5Mb and the numbers of processed pseudogenes in each window are plotted on the Y-axis. The X-axis indicates the interval along the chromosome. The red filled circles ● indicate the location of the centromeres.



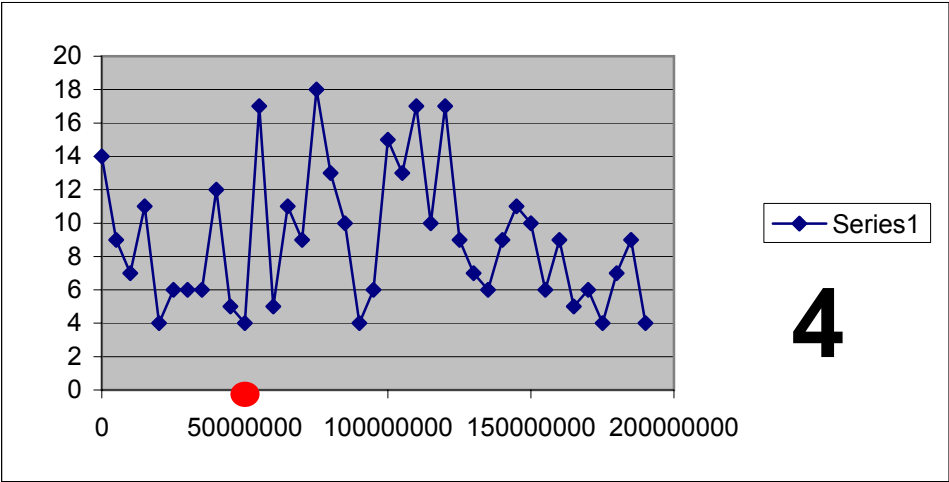
1



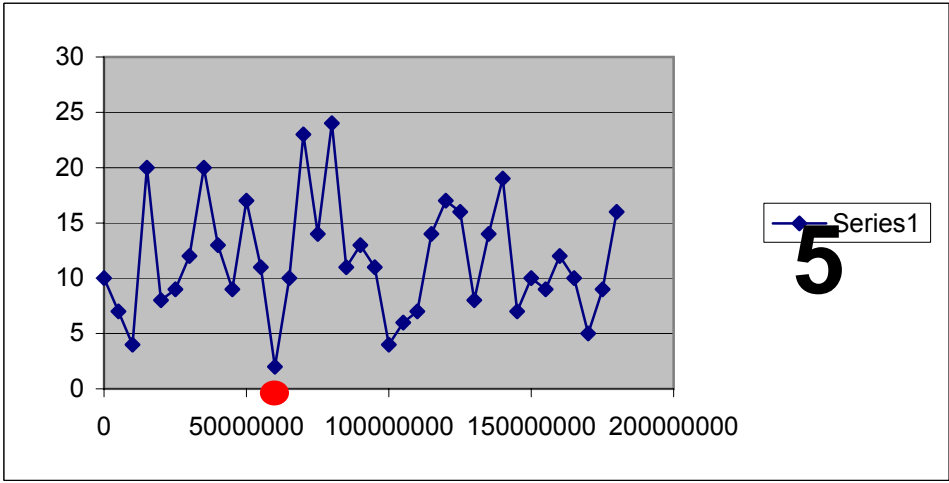
2



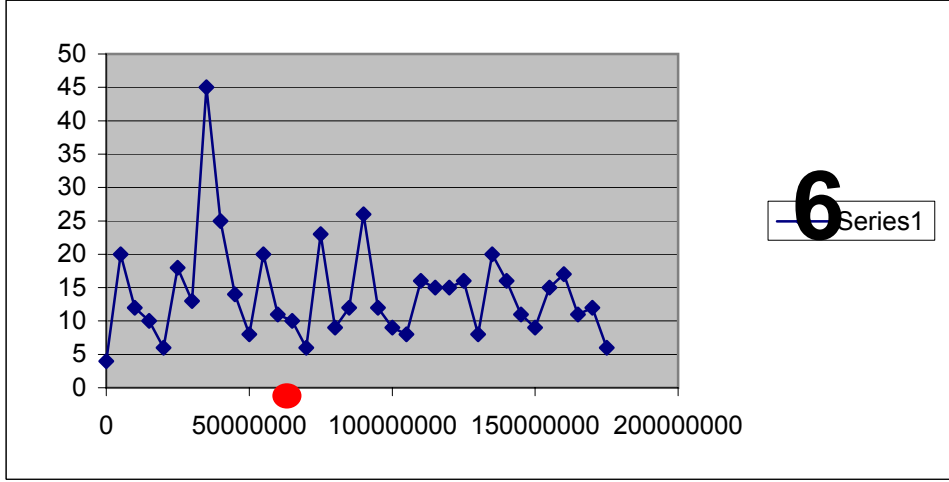
3



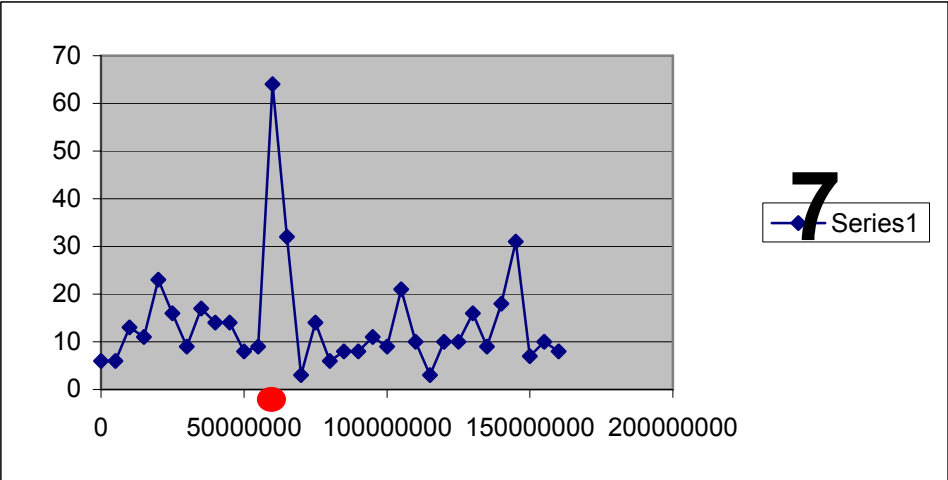
4

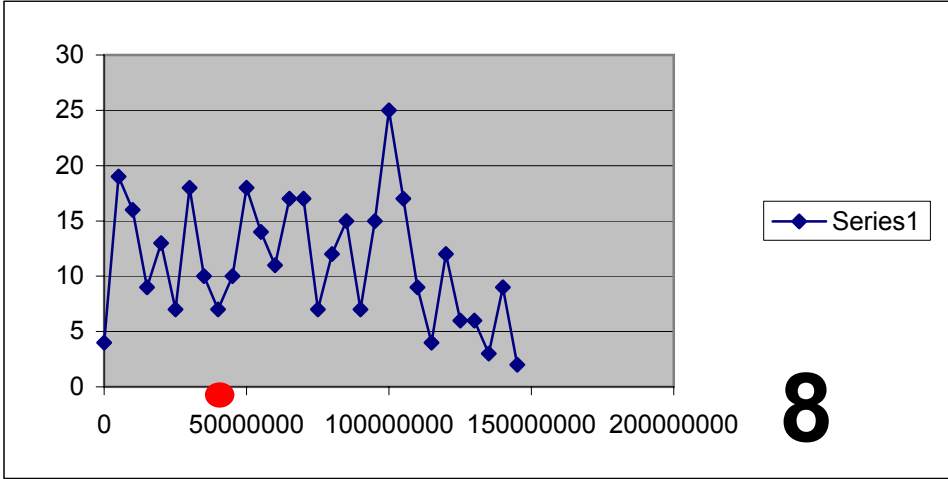


5

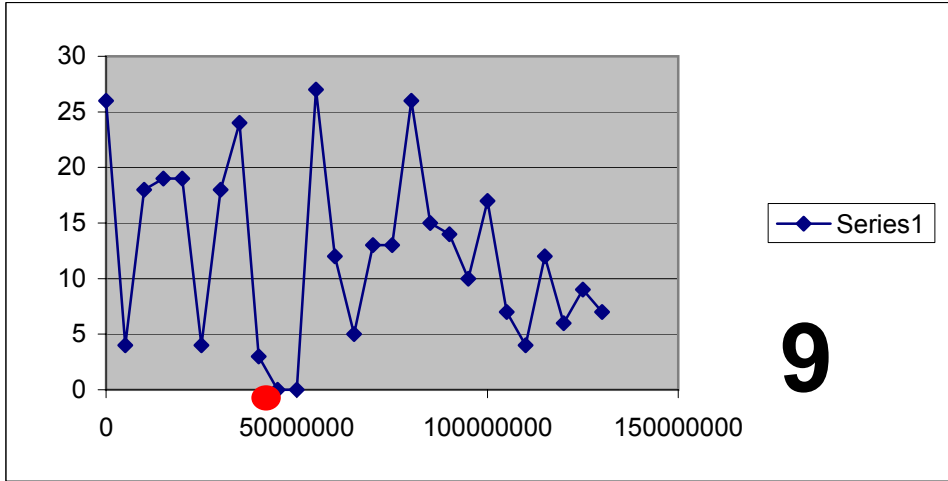


6

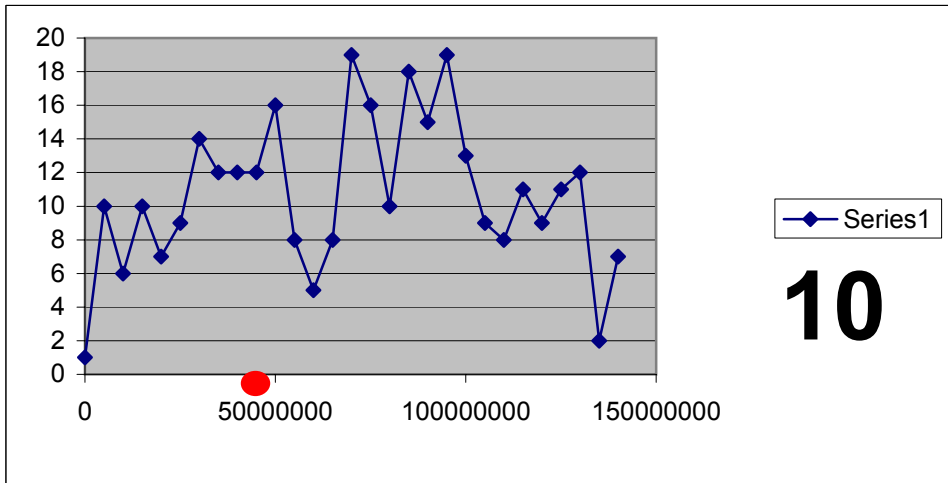




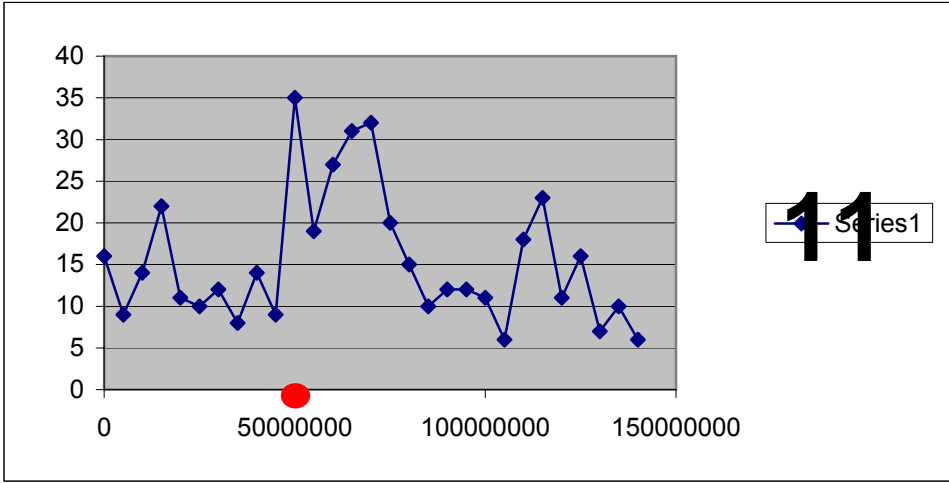
8



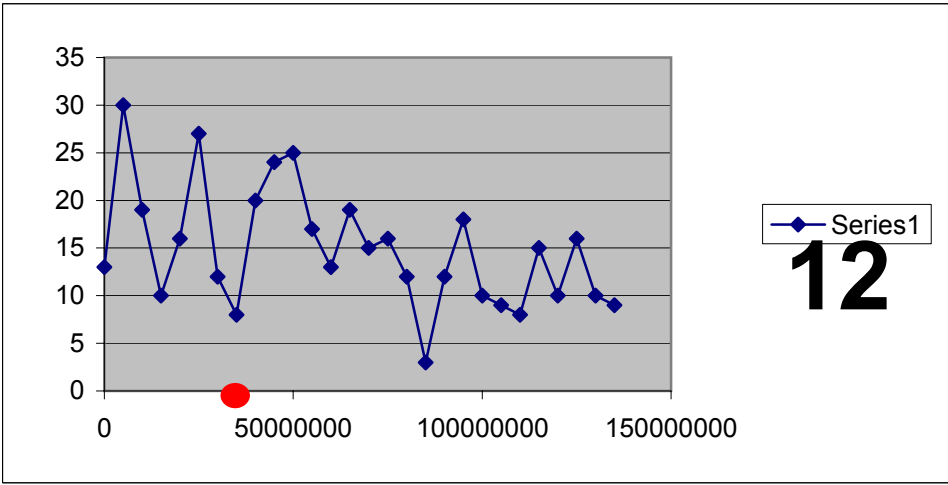
9



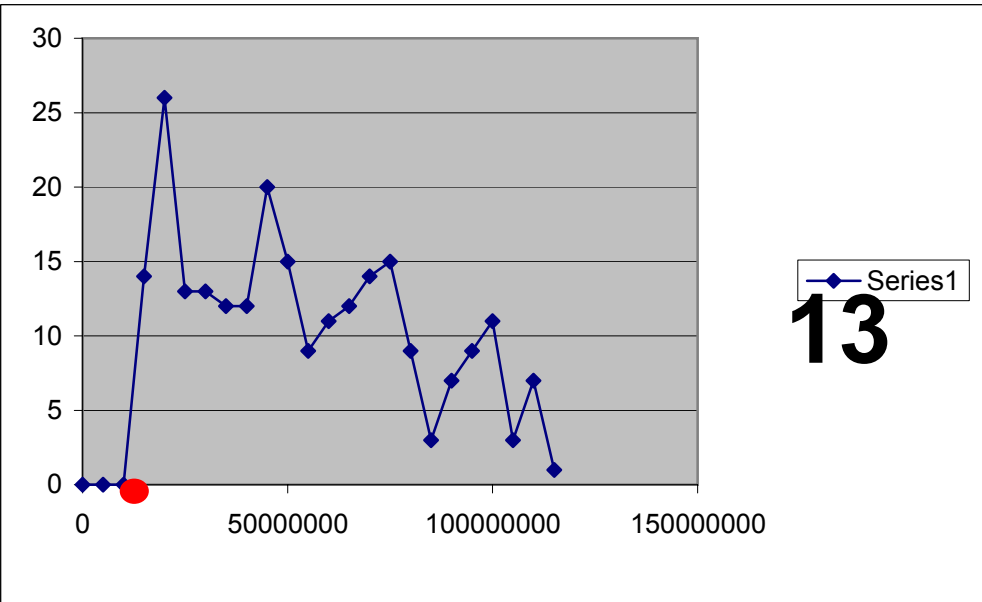
10



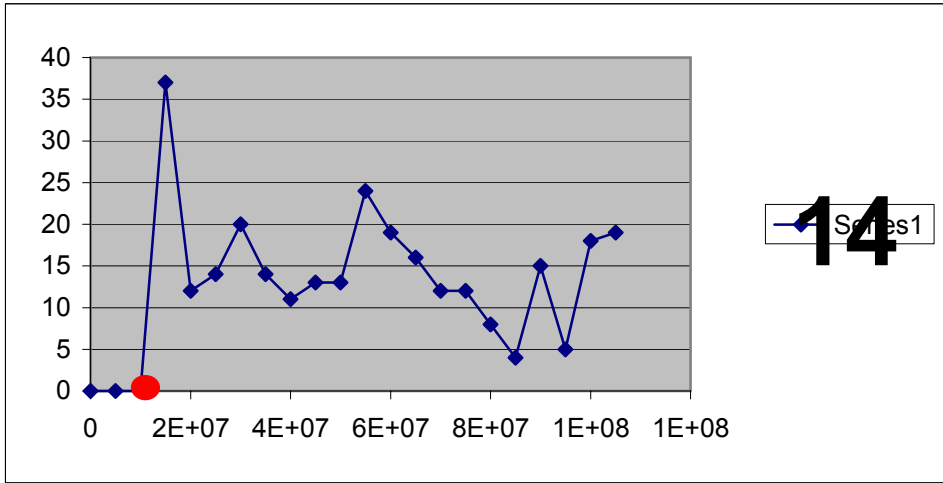
11

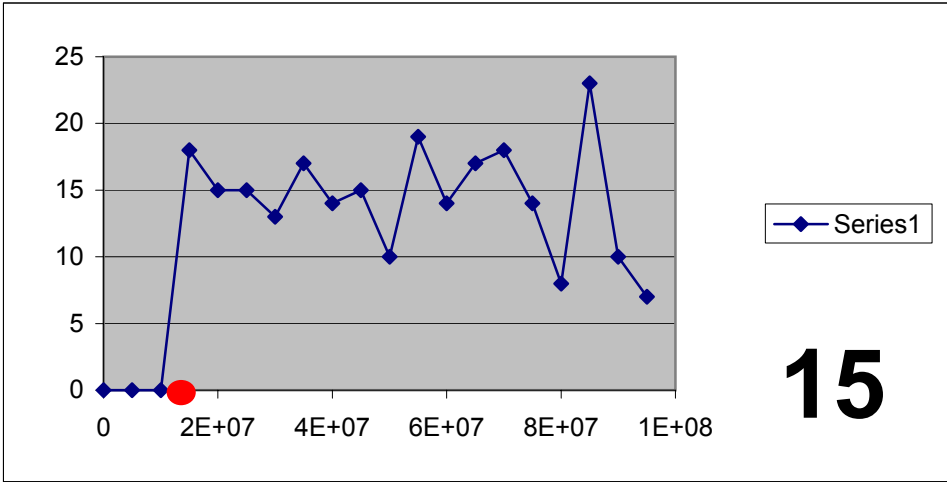


12

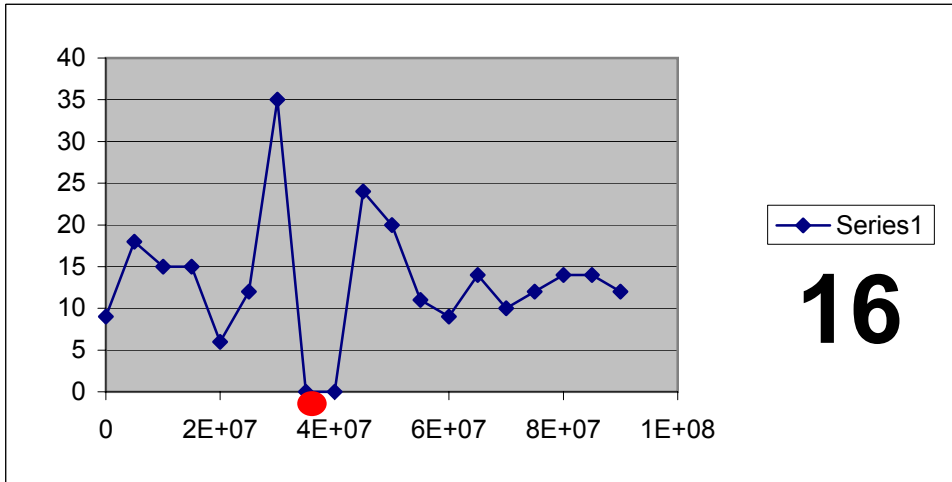


13

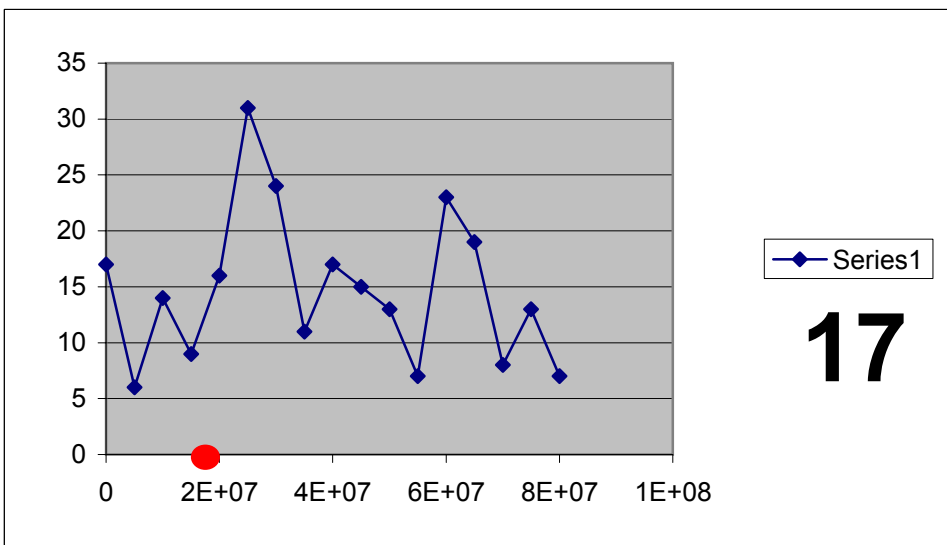




**15**

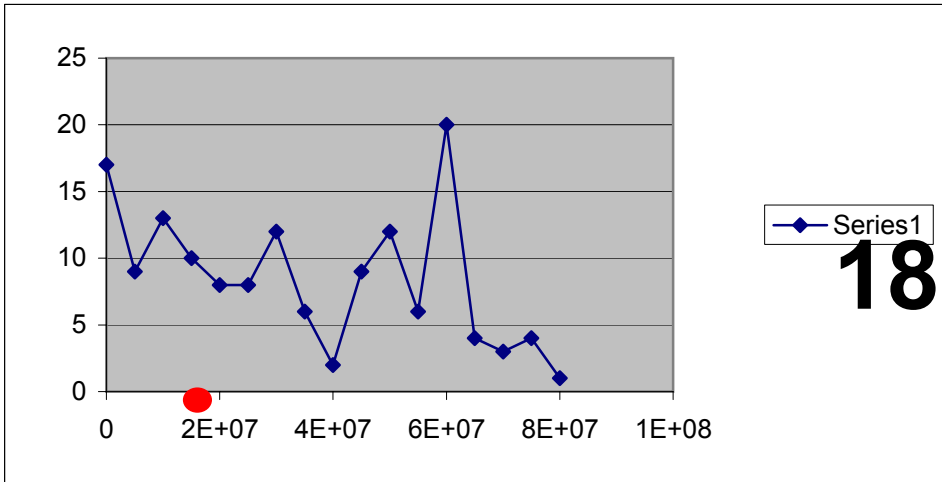


**16**

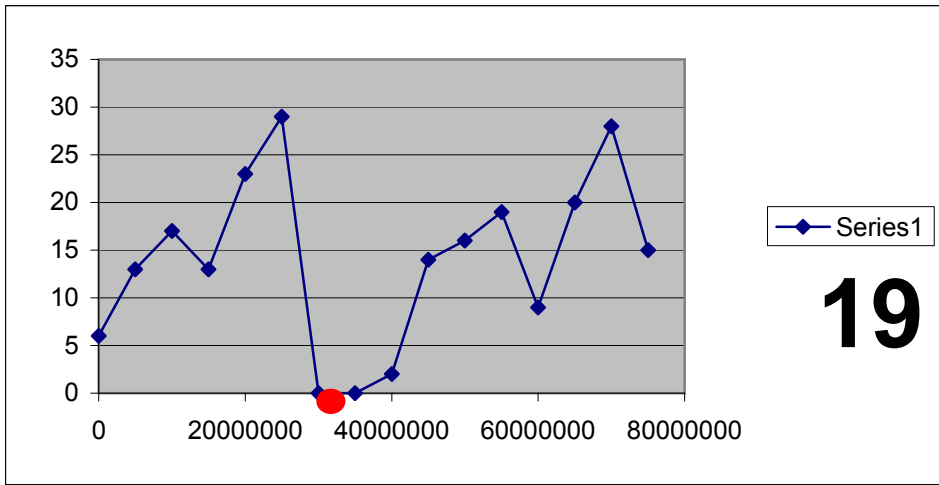


**17**

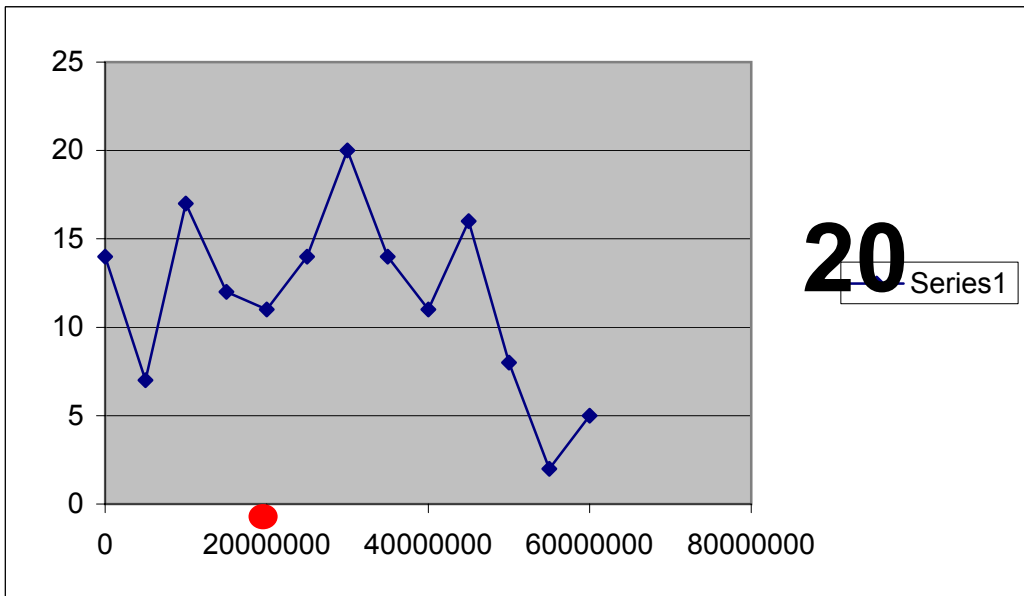




18



19



20

