Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 17:31:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013239.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6013239 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013239.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 17:31:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013239.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,220,771
Mapped reads	591,267 / 48.43%
Unmapped reads	629,504 / 51.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,304 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	34,971 / 2.86%
Duplication rate	5.16%
Clipped reads	333,575 / 27.32%

2.2. ACGT Content

Number/percentage of A's	10,429,854 / 27.61%
Number/percentage of C's	6,802,198 / 18.01%
Number/percentage of T's	12,186,093 / 32.26%
Number/percentage of G's	8,350,969 / 22.11%
Number/percentage of N's	8,787 / 0.02%
GC Percentage	40.11%

2.3. Coverage

Mean	0.0122

Standard Deviation	0.1547

2.4. Mapping Quality

Mean Mapping Quality	44.62

2.5. Mismatches and indels

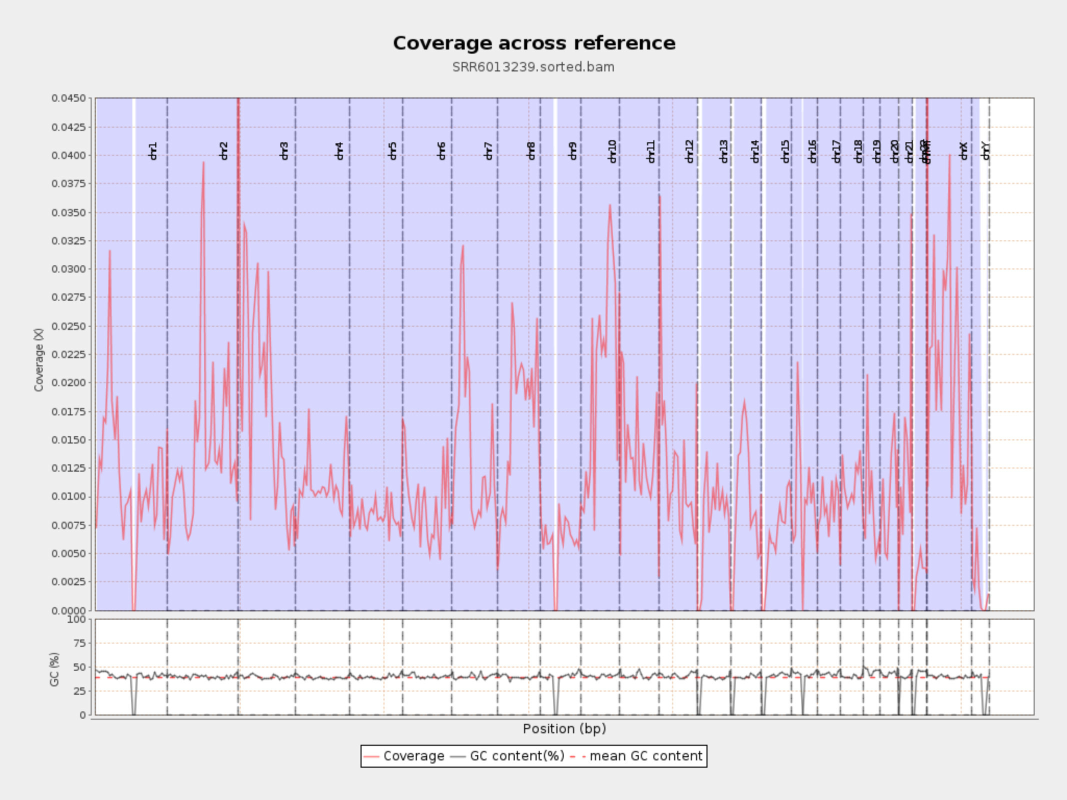
General error rate	0.91%
Mismatches	340,177
Insertions	2,682
Mapped reads with at least one insertion	0.45%
Deletions	15,570
Mapped reads with at least one deletion	2.58%
Homopolymer indels	43.39%

2.6. Chromosome stats

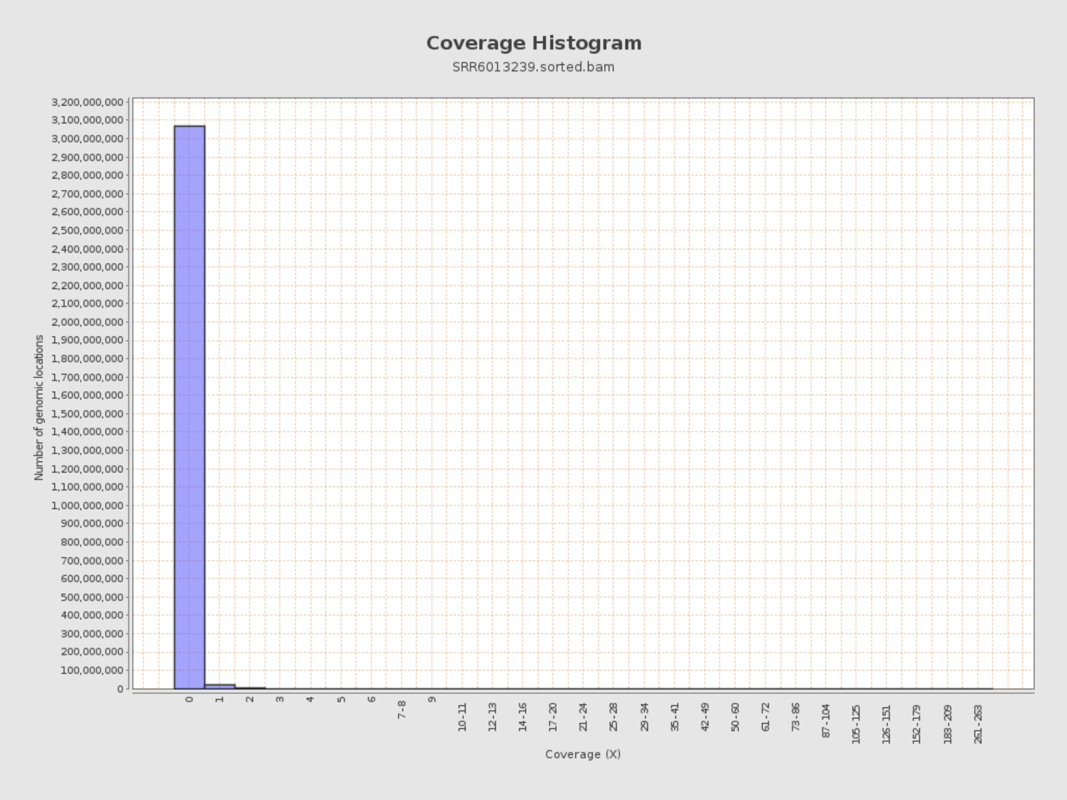
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2871614	0.0115	0.1815
chr2	243199373	3493694	0.0144	0.1921
chr3	198022430	3738474	0.0189	0.1734
chr4	191154276	2113186	0.0111	0.1311
chr5	180915260	1515938	0.0084	0.111
chr6	171115067	1598974	0.0093	0.1286
chr7	159138663	2285386	0.0144	0.1913

chr8	146364022	2486630	0.017	0.1993
chr9	141213431	850981	0.006	0.103
chr10	135534747	2803142	0.0207	0.1988
chr11	135006516	1908843	0.0141	0.1553
chr12	133851895	1668978	0.0125	0.1422
chr13	115169878	922949	0.008	0.1113
chr14	107349540	1046485	0.0097	0.1214
chr15	102531392	655289	0.0064	0.0979
chr16	90354753	865320	0.0096	0.1221
chr17	81195210	732313	0.009	0.1189
chr18	78077248	869862	0.0111	0.1625
chr19	59128983	548527	0.0093	0.1504
chr20	63025520	634983	0.0101	0.1264
chr21	48129895	622476	0.0129	0.1447
chr22	51304566	158988	0.0031	0.0672
chrMT	16571	14463	0.8728	1.2418
chrX	155270560	3281743	0.0211	0.1908
chrY	59373566	115722	0.0019	0.0619

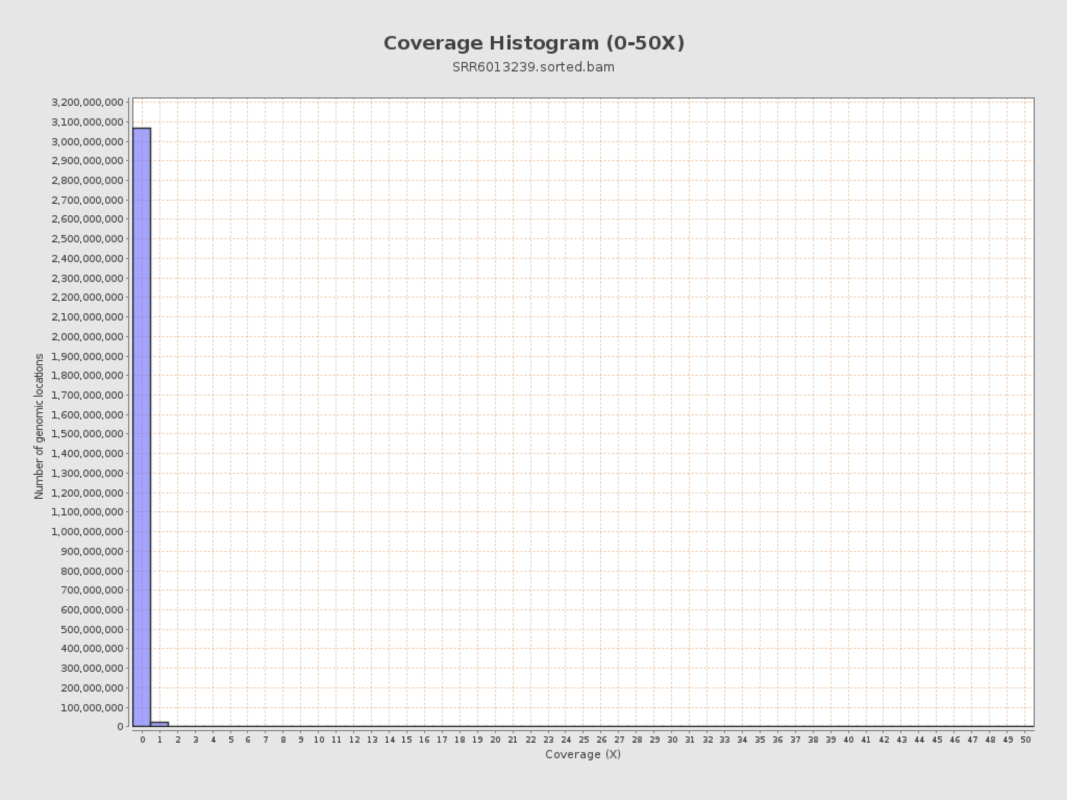
3. Results : Coverage across reference



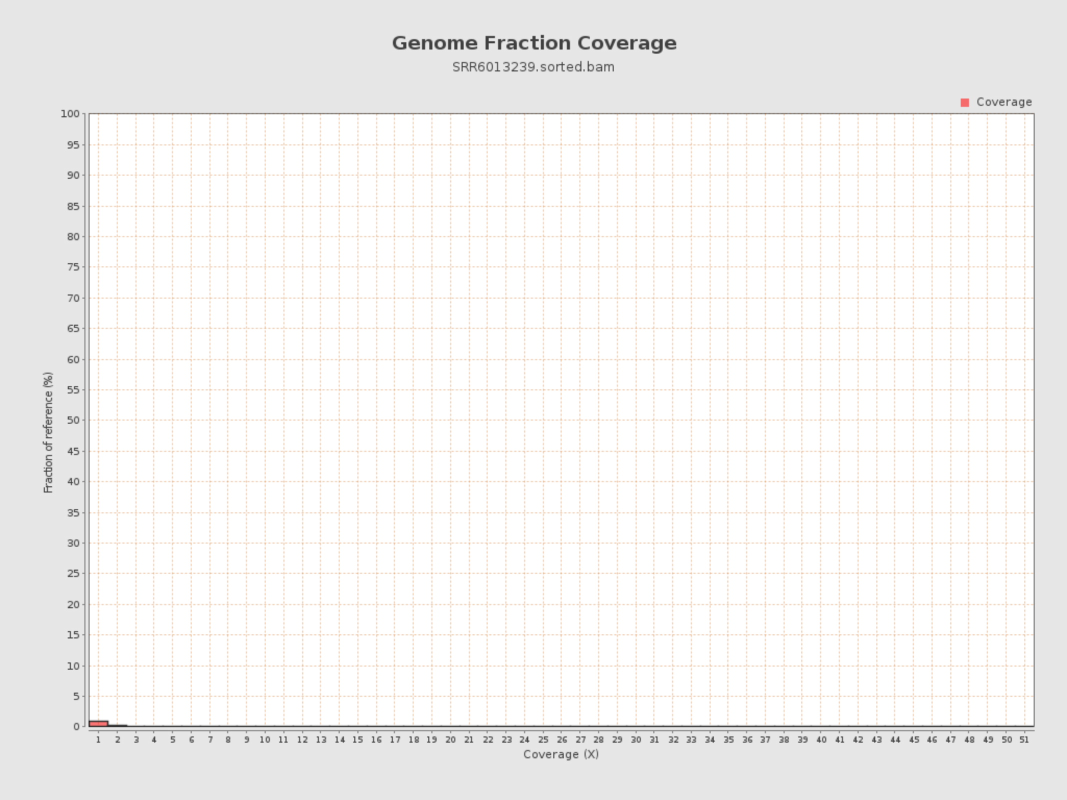
4. Results : Coverage Histogram



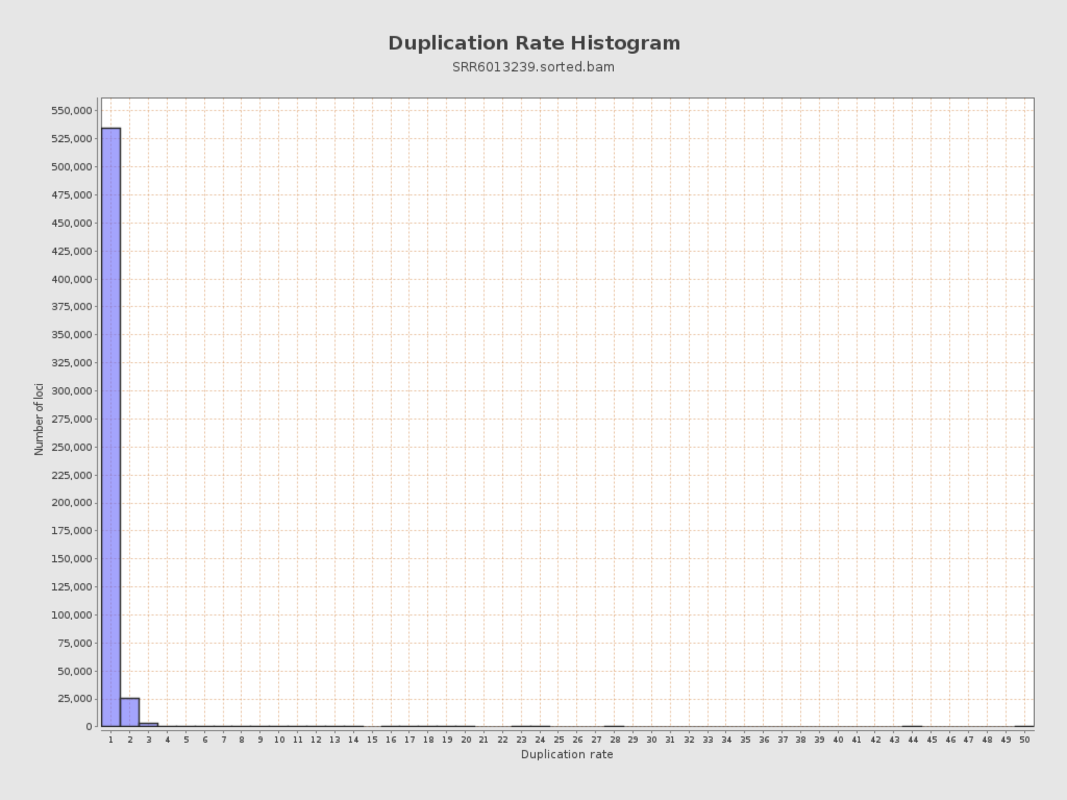
5. Results : Coverage Histogram (0-50X)



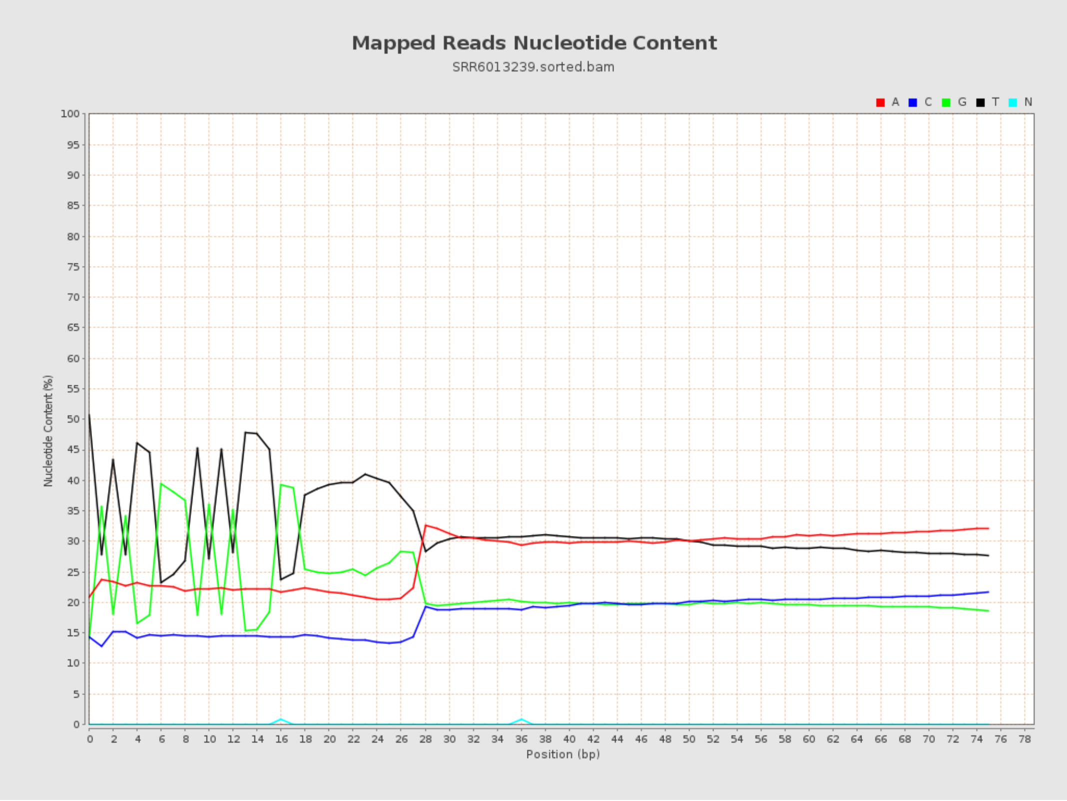
6. Results : Genome Fraction Coverage



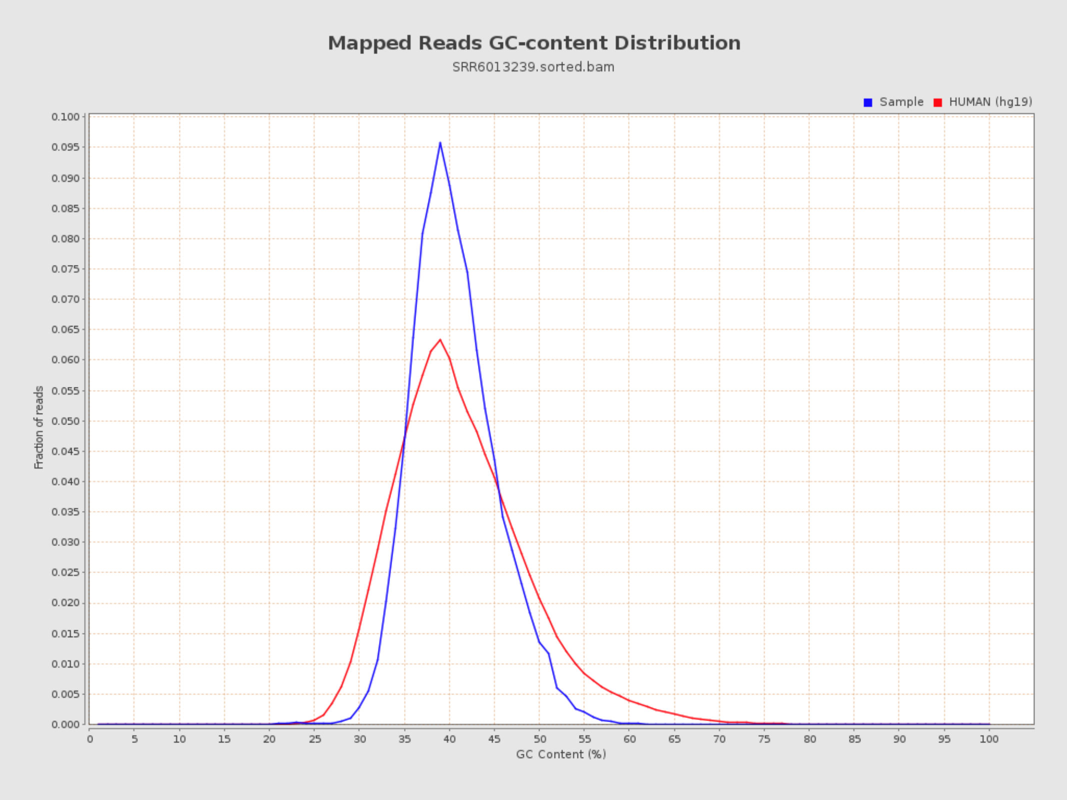
7. Results : Duplication Rate Histogram



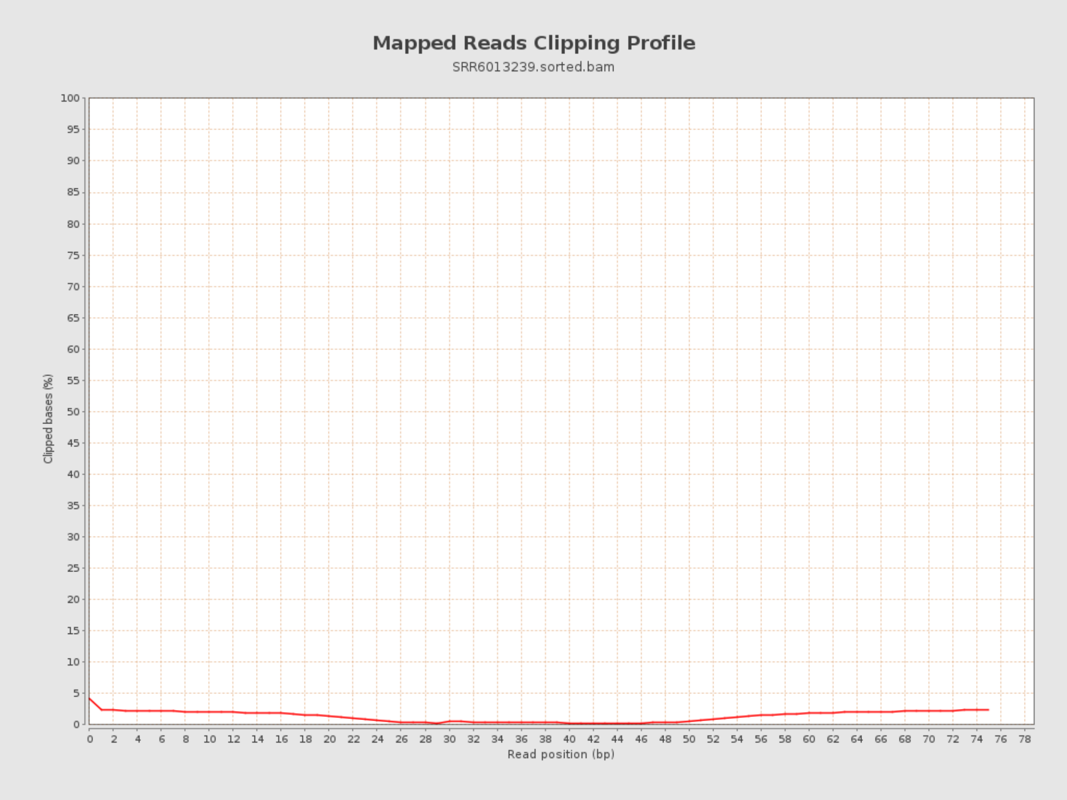
8. Results : Mapped Reads Nucleotide Content



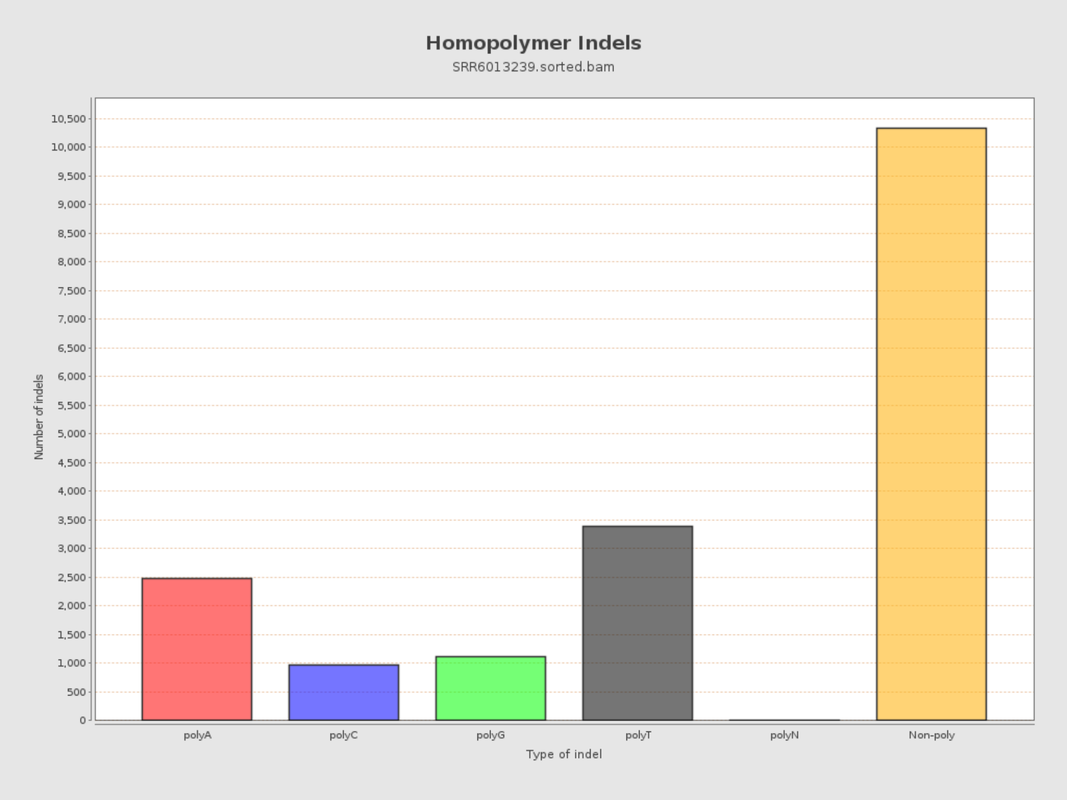
9. Results : Mapped Reads GC-content Distribution



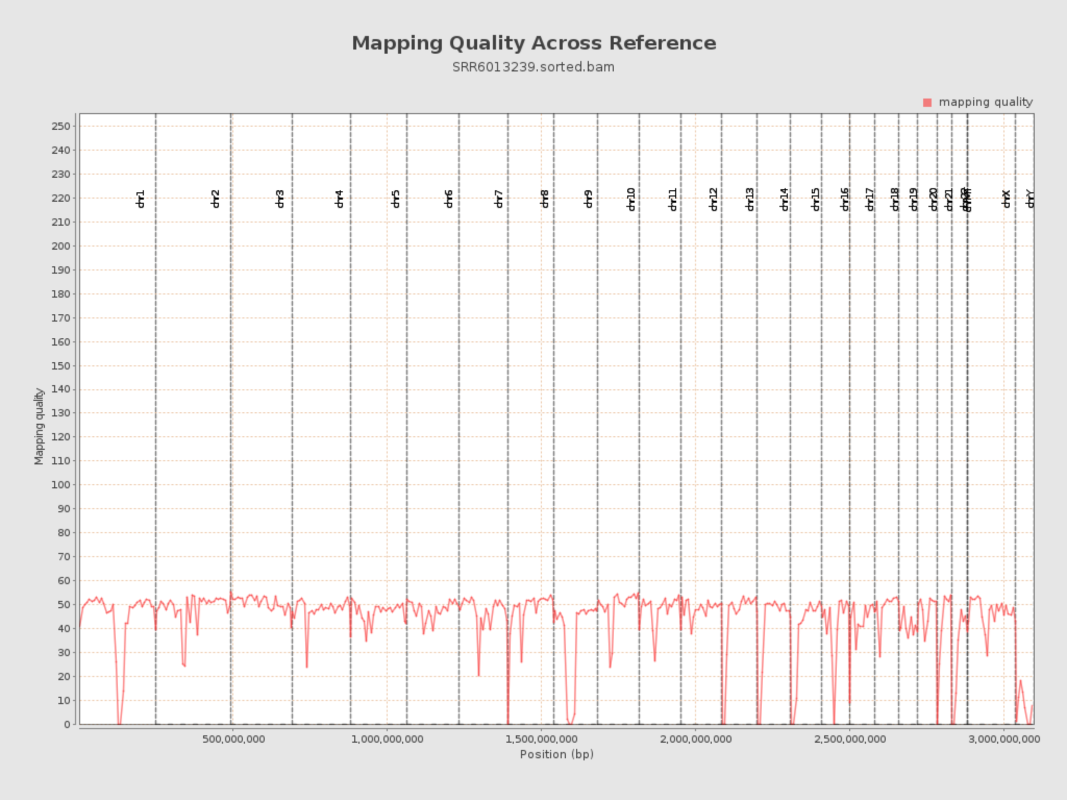
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram