Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 23:04:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013355.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_SRR6013355 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013355.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 23:04:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013355.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,320,943
Mapped reads	2,050,985 / 88.37%
Unmapped reads	269,958 / 11.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,027 / 0.73%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	121,694 / 5.24%
Duplication rate	4.4%
Clipped reads	841,228 / 36.25%

2.2. ACGT Content

Number/percentage of A's	38,969,553 / 28.1%
Number/percentage of C's	25,539,949 / 18.41%
Number/percentage of T's	44,280,765 / 31.93%
Number/percentage of G's	29,874,702 / 21.54%
Number/percentage of N's	29,229 / 0.02%
GC Percentage	39.95%

2.3. Coverage

Mean	0.0448

Standard Deviation	0.5354

2.4. Mapping Quality

Mean Mapping Quality	45.14

2.5. Mismatches and indels

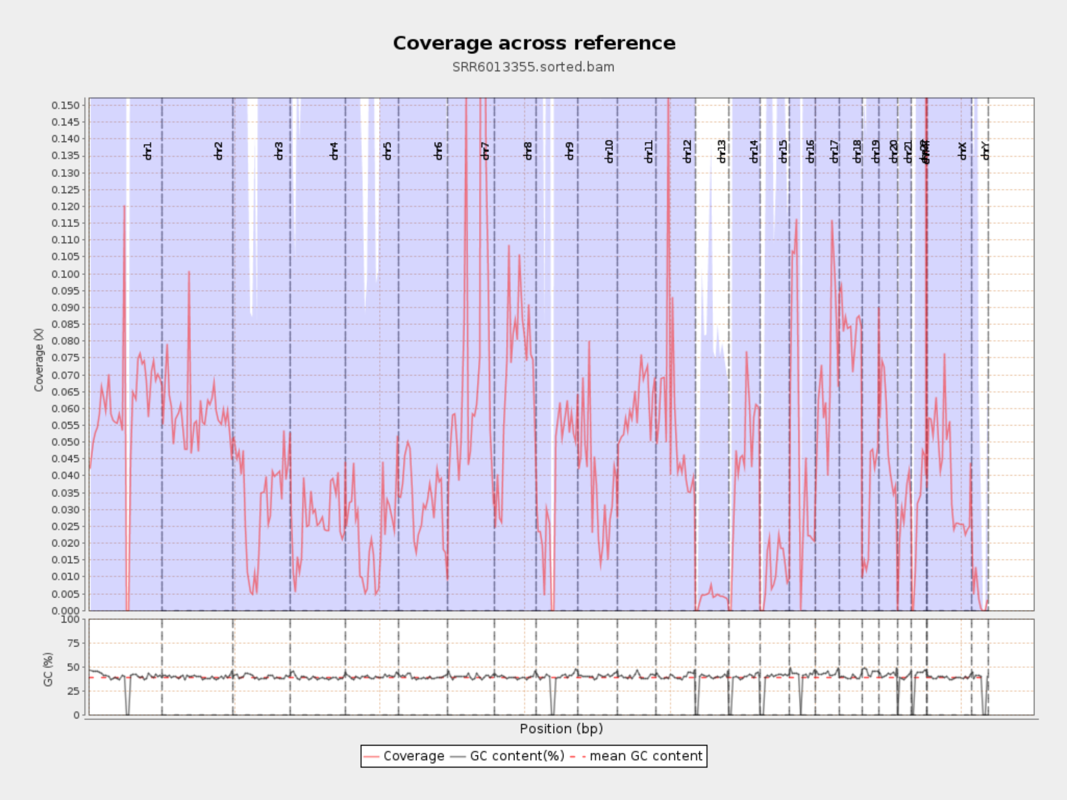
General error rate	0.81%
Mismatches	1,110,331
Insertions	10,064
Mapped reads with at least one insertion	0.49%
Deletions	33,173
Mapped reads with at least one deletion	1.6%
Homopolymer indels	47.61%

2.6. Chromosome stats

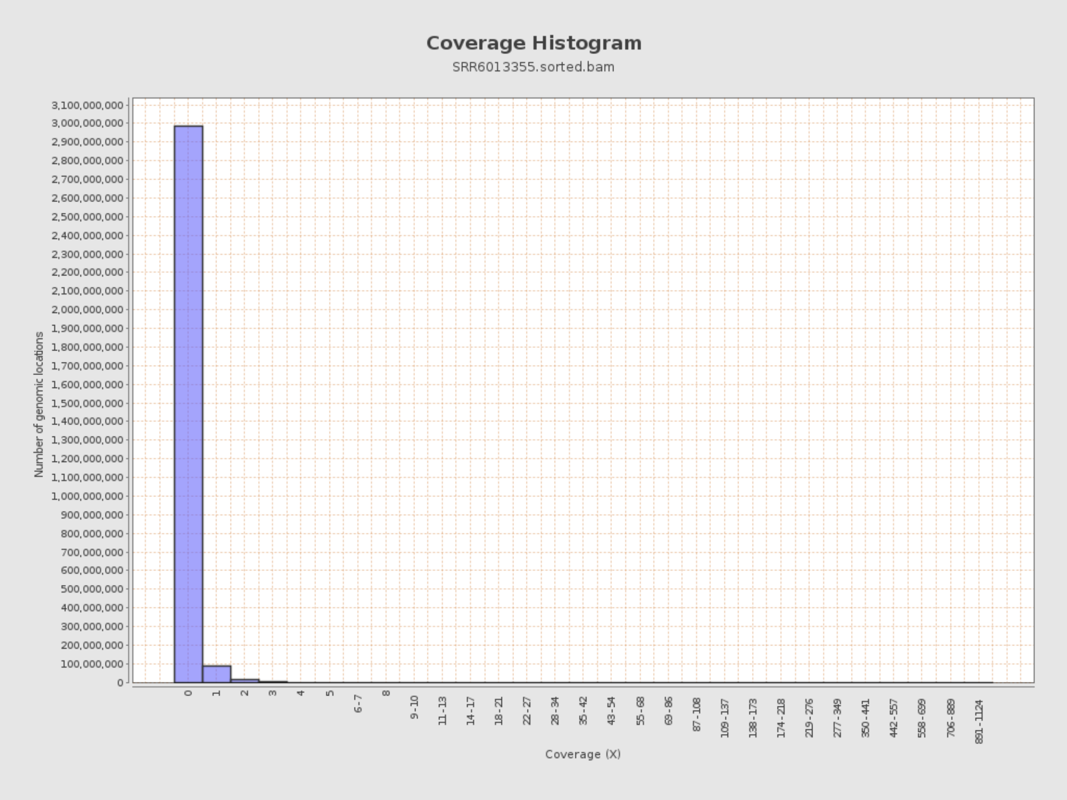
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15013225	0.0602	1.0006
chr2	243199373	14347928	0.059	0.6086
chr3	198022430	6478593	0.0327	0.2167
chr4	191154276	4921813	0.0257	0.2184
chr5	180915260	4238680	0.0234	0.1822
chr6	171115067	5520385	0.0323	0.2235
chr7	159138663	14120503	0.0887	1.3301

chr8	146364022	10175795	0.0695	0.524
chr9	141213431	5376059	0.0381	0.3874
chr10	135534747	5084821	0.0375	0.466
chr11	135006516	8164723	0.0605	0.3632
chr12	133851895	7554755	0.0564	0.2936
chr13	115169878	455335	0.004	0.0778
chr14	107349540	4716903	0.0439	0.2548
chr15	102531392	1187149	0.0116	0.1315
chr16	90354753	4519543	0.05	0.2781
chr17	81195210	5617624	0.0692	0.3946
chr18	78077248	6610815	0.0847	0.579
chr19	59128983	1981746	0.0335	0.7591
chr20	63025520	3237022	0.0514	0.2738
chr21	48129895	1368980	0.0284	0.2147
chr22	51304566	1404773	0.0274	0.1937
chrMT	16571	30797	1.8585	1.7357
chrX	155270560	6361136	0.041	0.2846
chrY	59373566	262755	0.0044	0.1215

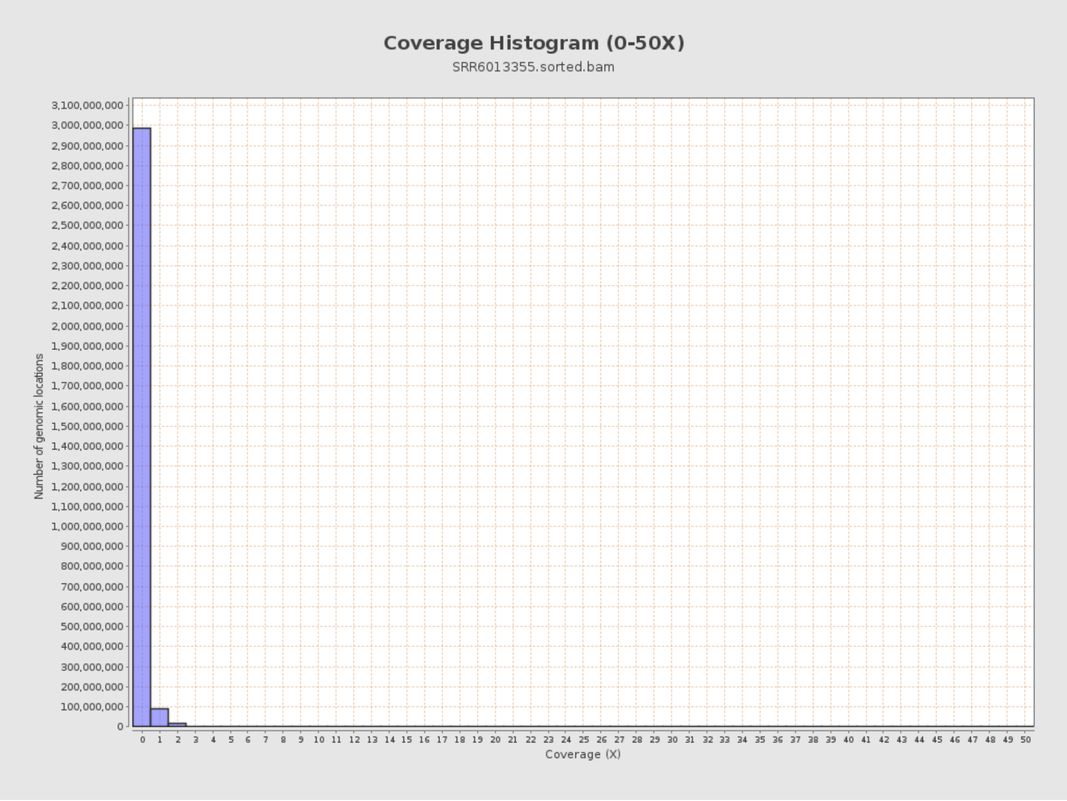
3. Results : Coverage across reference



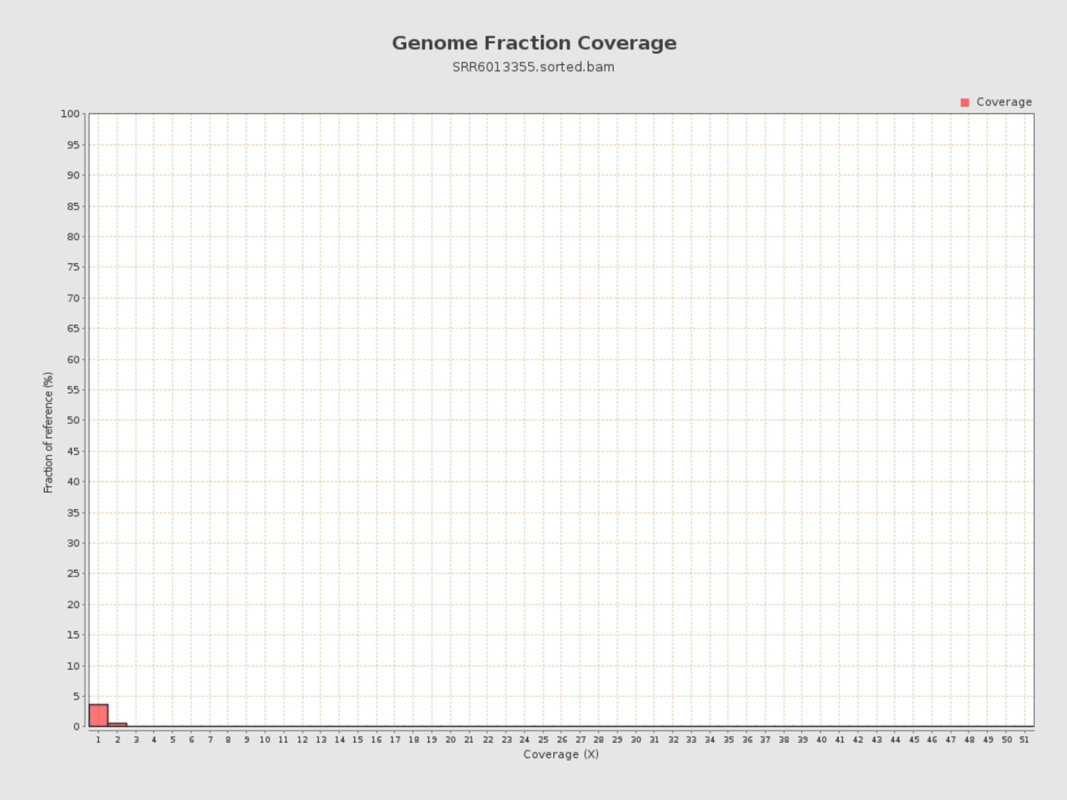
4. Results : Coverage Histogram



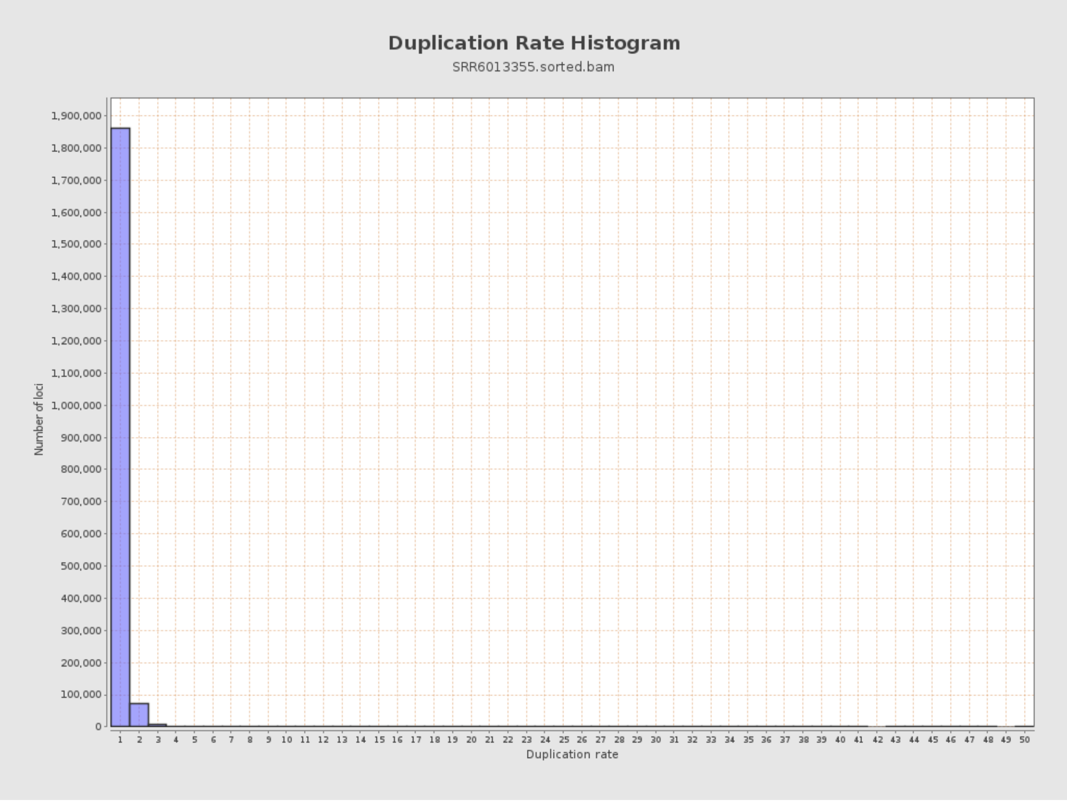
5. Results : Coverage Histogram (0-50X)



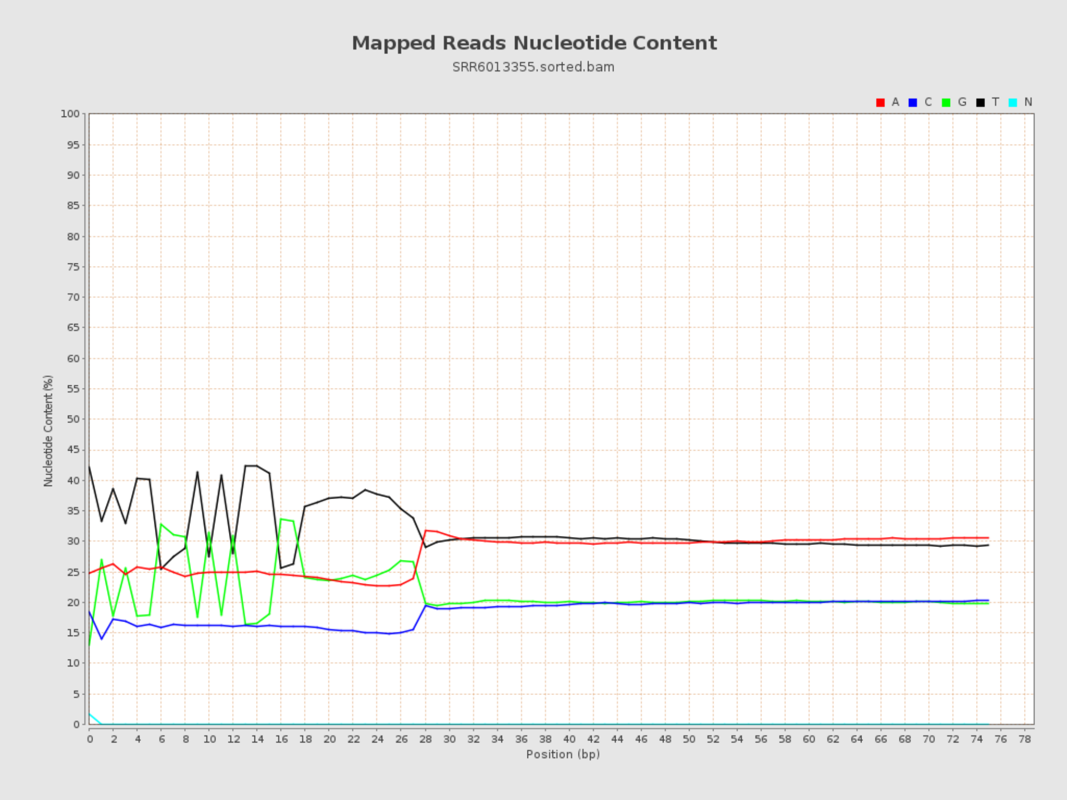
6. Results : Genome Fraction Coverage



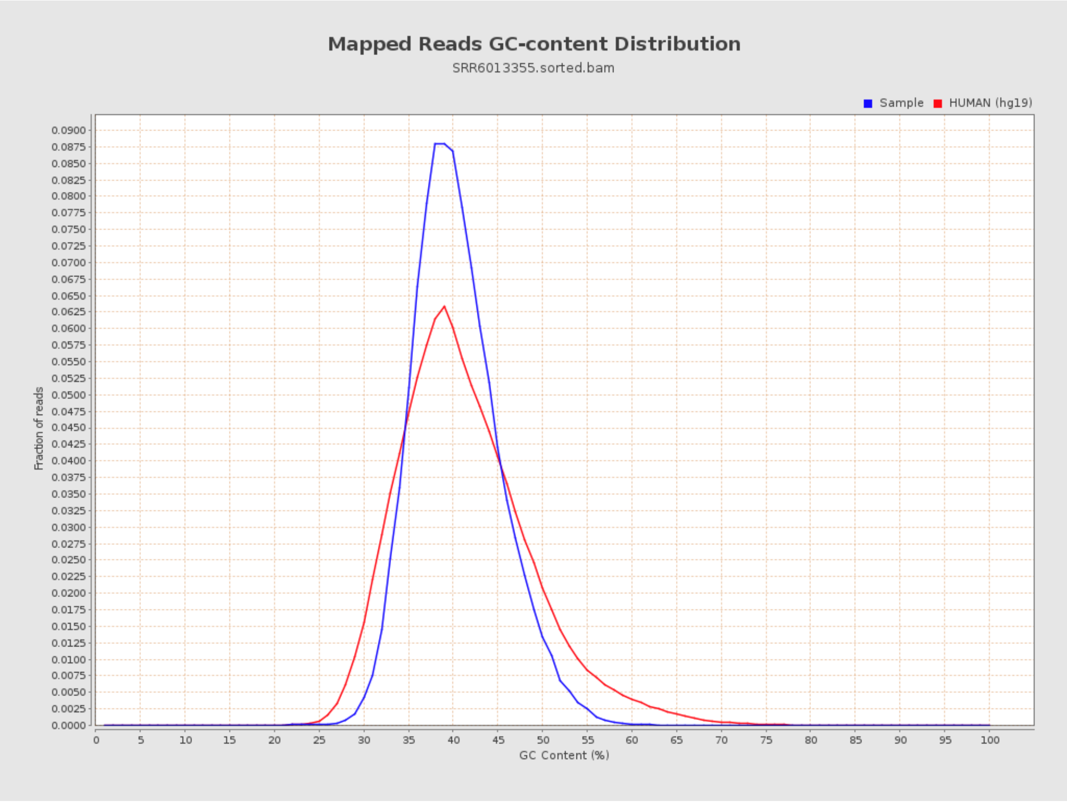
7. Results : Duplication Rate Histogram



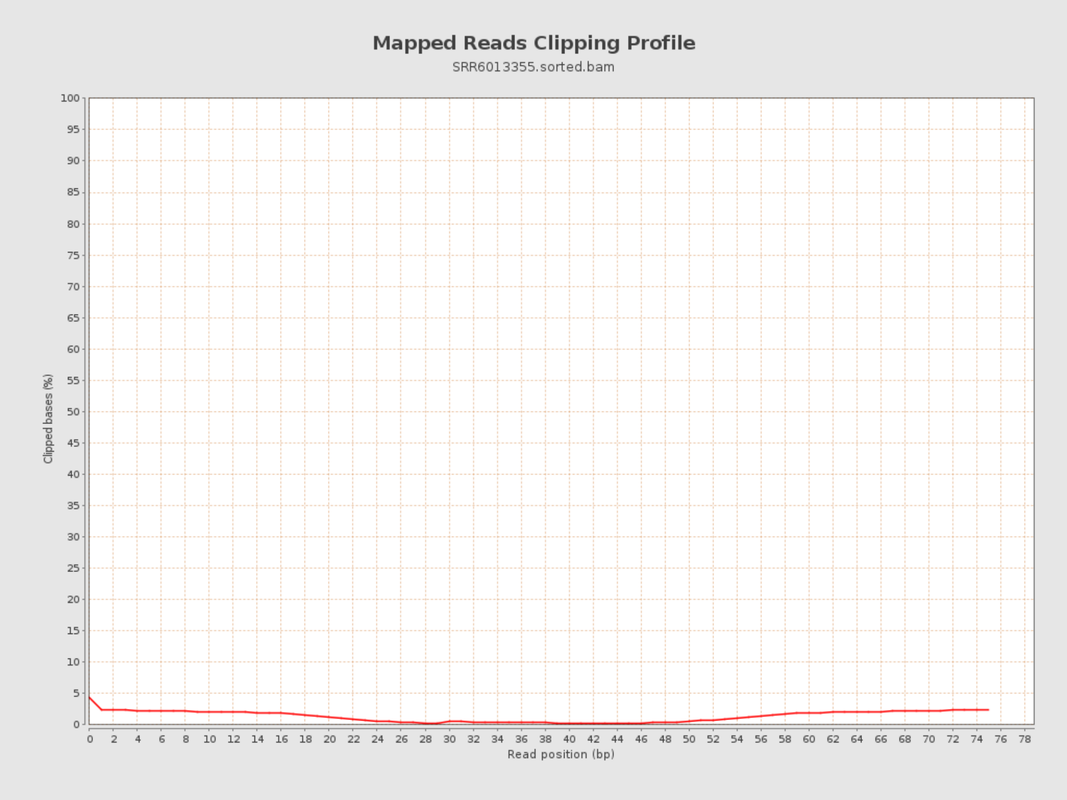
8. Results : Mapped Reads Nucleotide Content



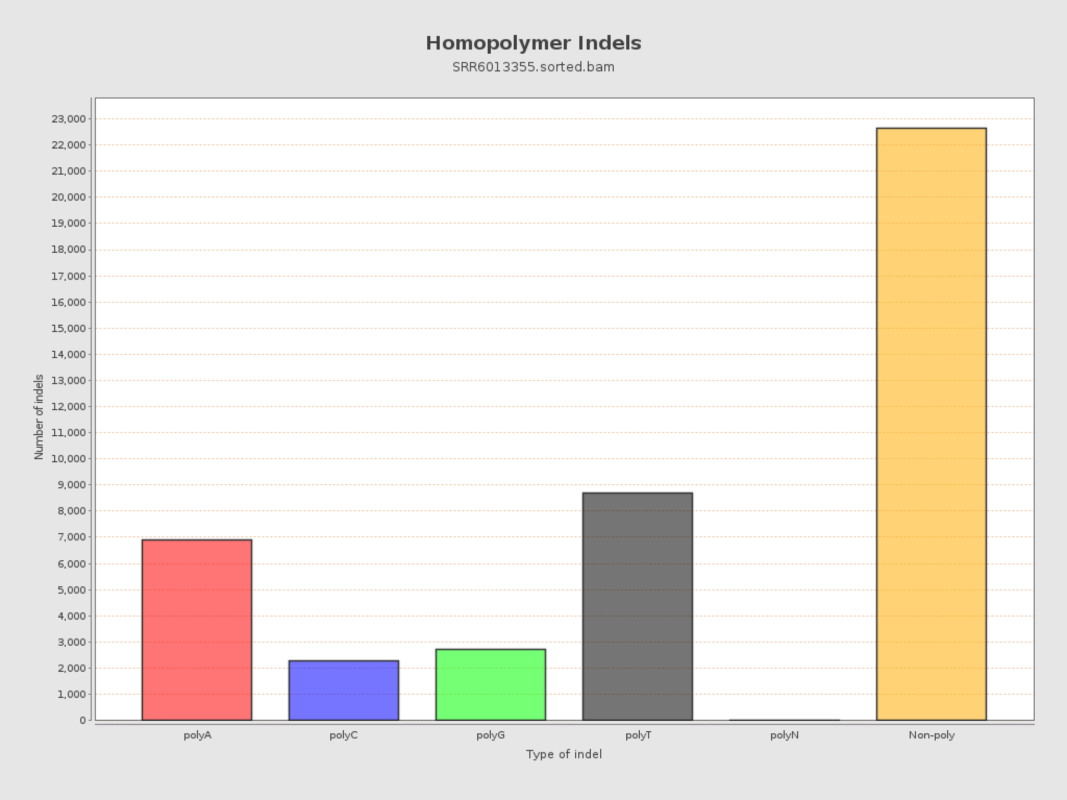
9. Results : Mapped Reads GC-content Distribution



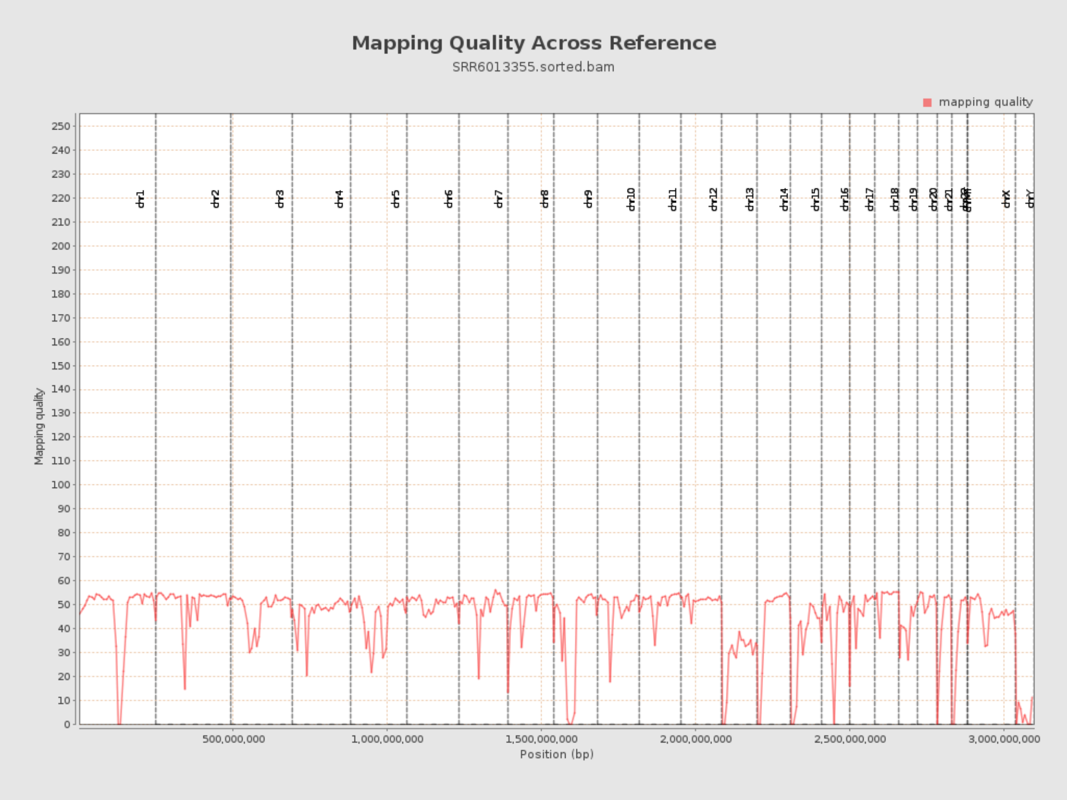
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram