Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 09:07:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068085.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_SRR6068085 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068085.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 09:07:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068085.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,351,675
Mapped reads	3,021,362 / 90.14%
Unmapped reads	330,313 / 9.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,133 / 0.93%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	194,386 / 5.8%
Duplication rate	4.95%
Clipped reads	1,375,048 / 41.03%

2.2. ACGT Content

Number/percentage of A's	56,825,158 / 28.21%
Number/percentage of C's	36,930,884 / 18.34%
Number/percentage of T's	64,122,241 / 31.83%
Number/percentage of G's	43,538,853 / 21.62%
Number/percentage of N's	4,262 / 0%
GC Percentage	39.95%

2.3. Coverage

Mean	0.0651

Standard Deviation	0.7442

2.4. Mapping Quality

Mean Mapping Quality	45.98

2.5. Mismatches and indels

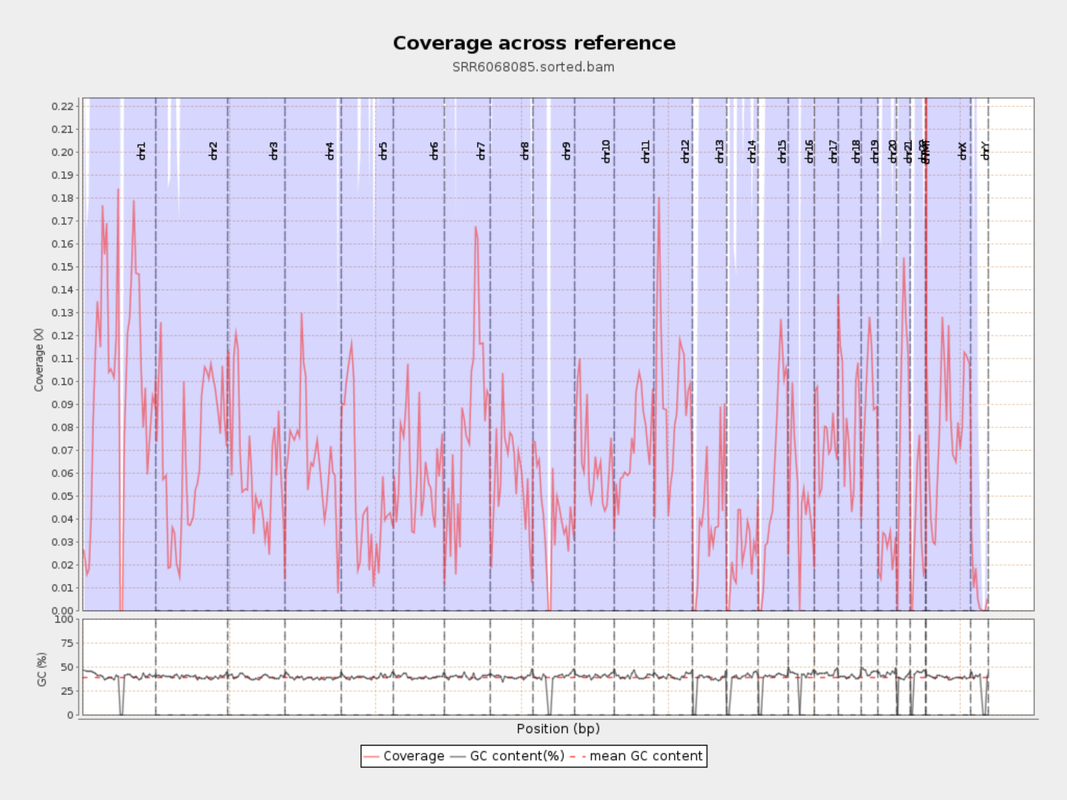
General error rate	0.8%
Mismatches	1,590,507
Insertions	15,390
Mapped reads with at least one insertion	0.51%
Deletions	59,279
Mapped reads with at least one deletion	1.94%
Homopolymer indels	46.63%

2.6. Chromosome stats

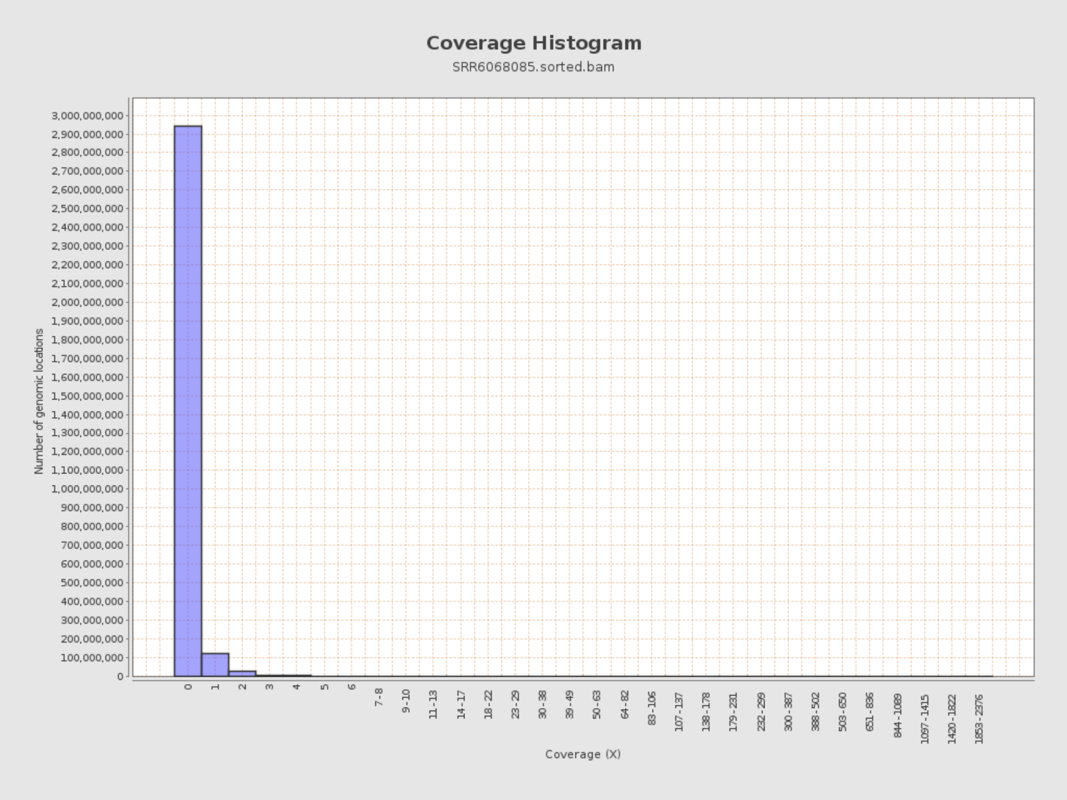
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25006676	0.1003	1.8356
chr2	243199373	16646990	0.0684	0.6263
chr3	198022430	12612282	0.0637	0.3157
chr4	191154276	12863422	0.0673	0.3346
chr5	180915260	9294450	0.0514	0.2883
chr6	171115067	10366068	0.0606	0.3626
chr7	159138663	12718439	0.0799	0.5784

chr8	146364022	8385206	0.0573	1.404
chr9	141213431	5691655	0.0403	0.5197
chr10	135534747	8913042	0.0658	0.4703
chr11	135006516	9725370	0.072	0.4611
chr12	133851895	12531159	0.0936	0.4125
chr13	115169878	4629993	0.0402	0.2521
chr14	107349540	2601874	0.0242	0.279
chr15	102531392	5985497	0.0584	0.3074
chr16	90354753	4400070	0.0487	0.3176
chr17	81195210	6077427	0.0748	0.3742
chr18	78077248	6612953	0.0847	1.0147
chr19	59128983	5559540	0.094	1.058
chr20	63025520	1640114	0.026	0.2778
chr21	48129895	4410296	0.0916	0.3878
chr22	51304566	1697378	0.0331	0.2213
chrMT	16571	110155	6.6475	5.3483
chrX	155270560	12560299	0.0809	0.4266
chrY	59373566	477684	0.008	0.1385

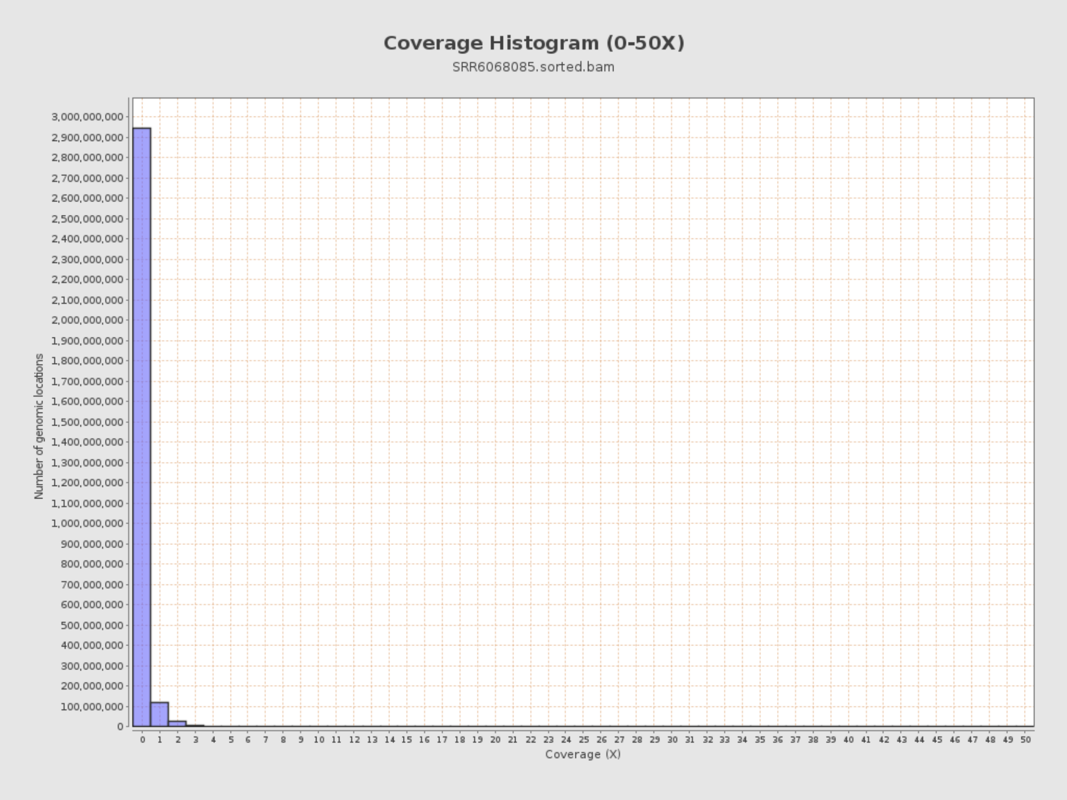
3. Results : Coverage across reference



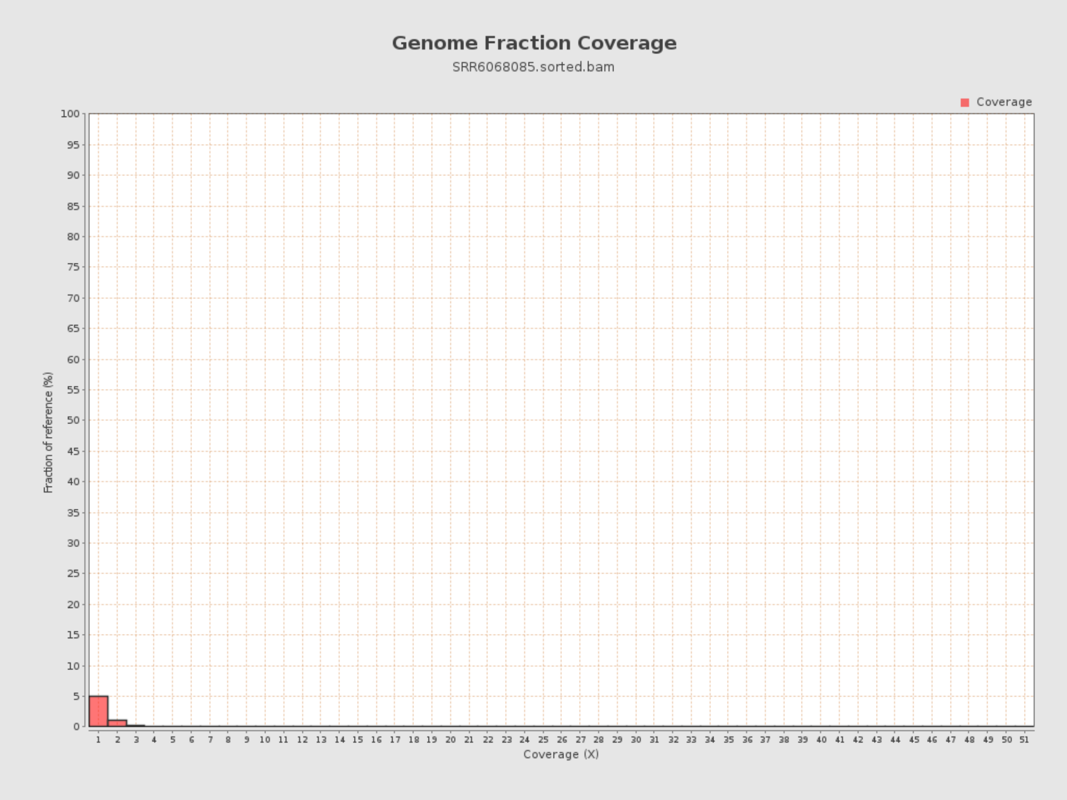
4. Results : Coverage Histogram



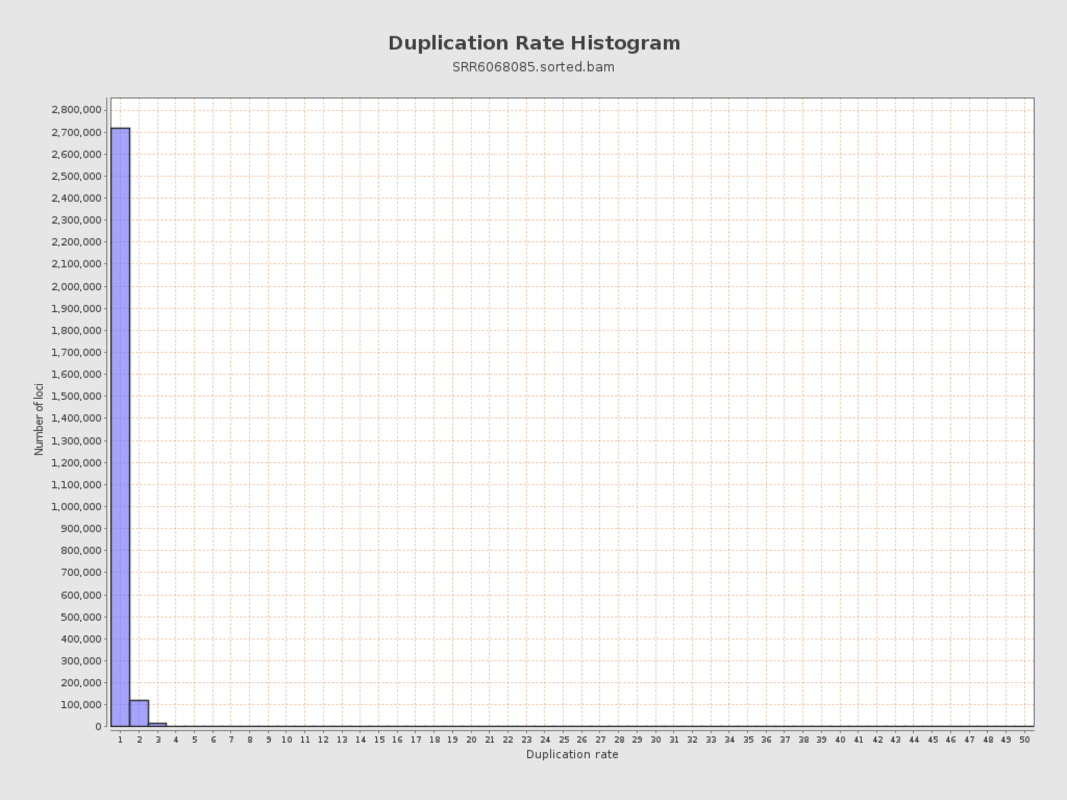
5. Results : Coverage Histogram (0-50X)



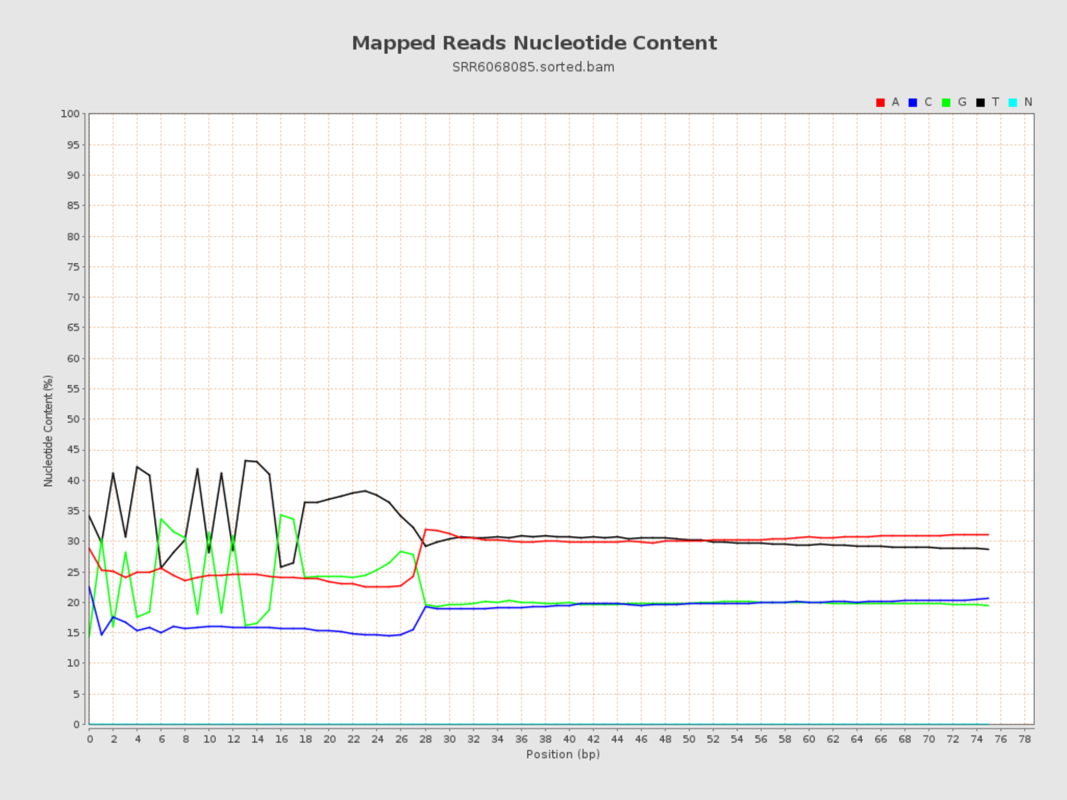
6. Results : Genome Fraction Coverage



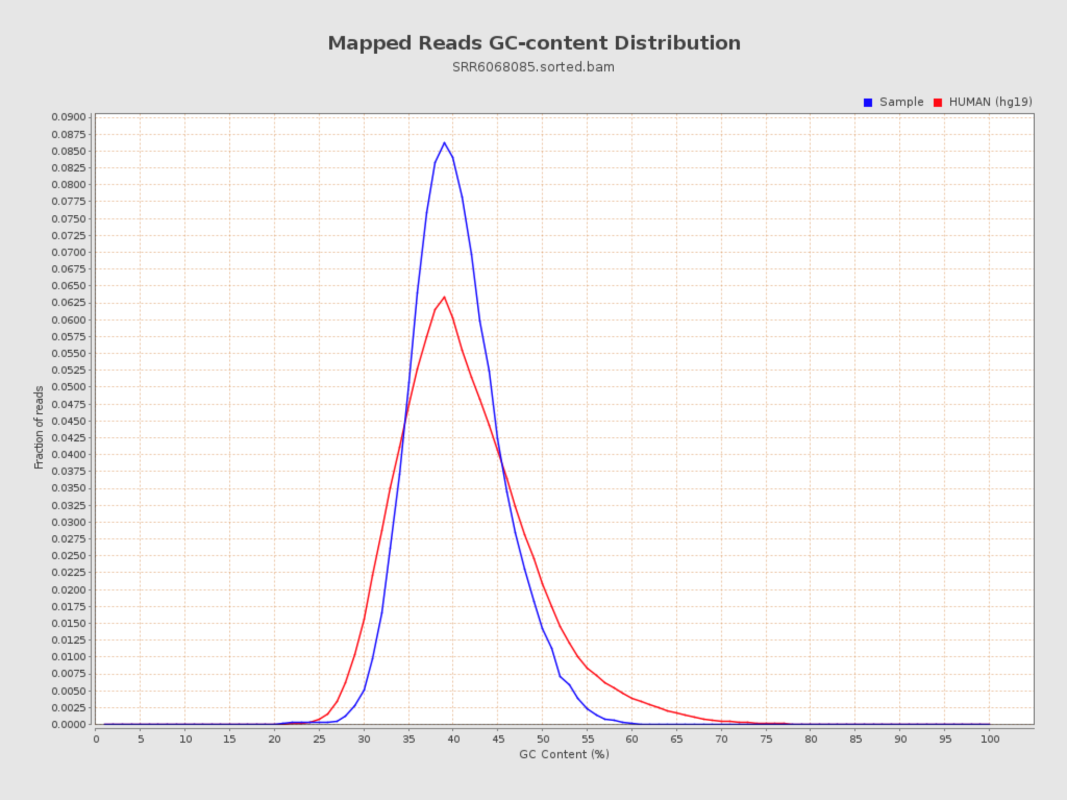
7. Results : Duplication Rate Histogram



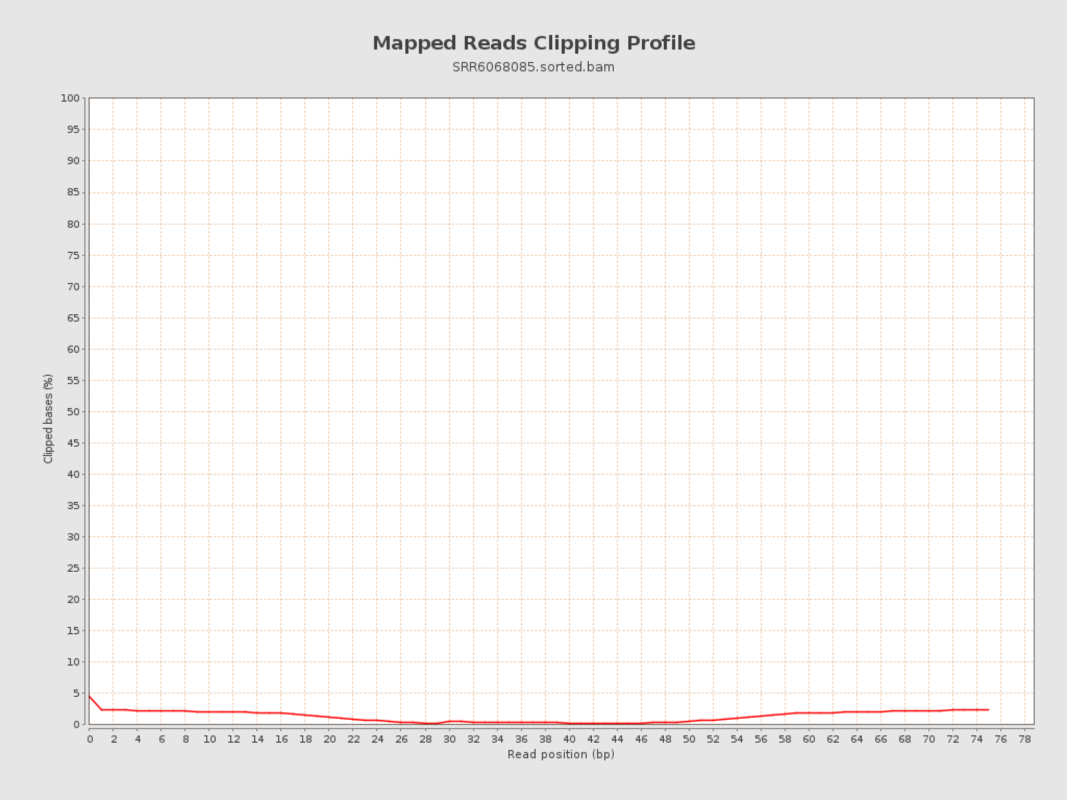
8. Results : Mapped Reads Nucleotide Content



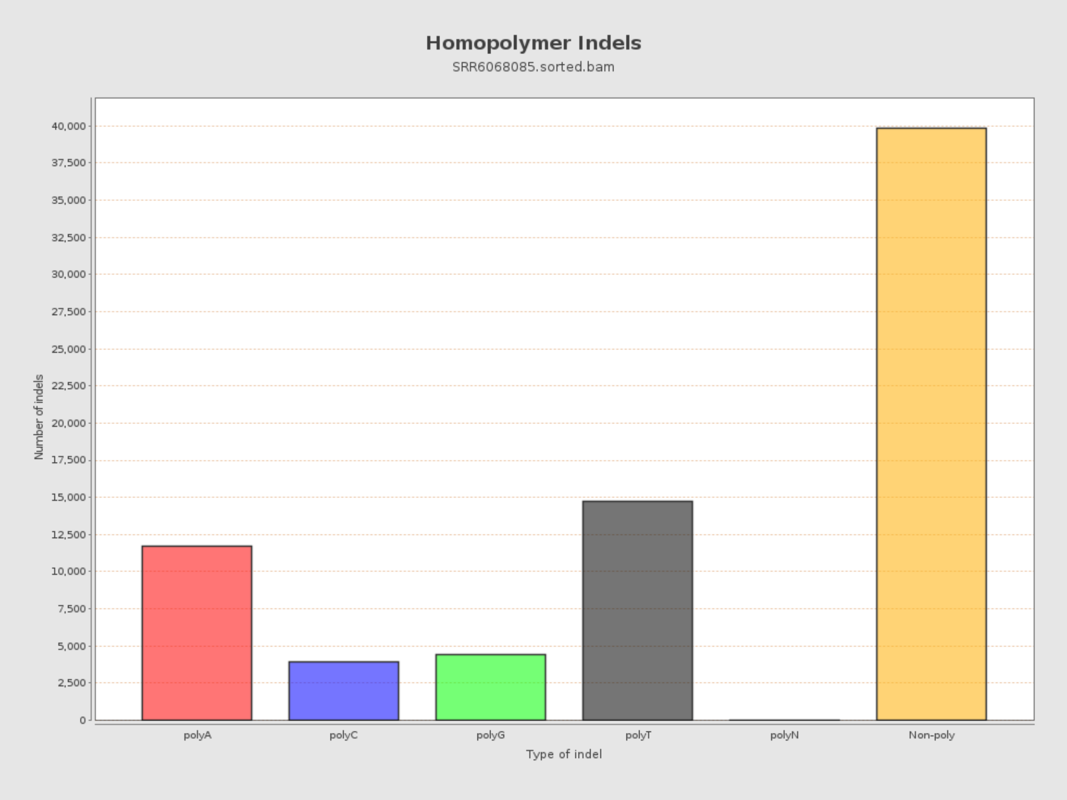
9. Results : Mapped Reads GC-content Distribution



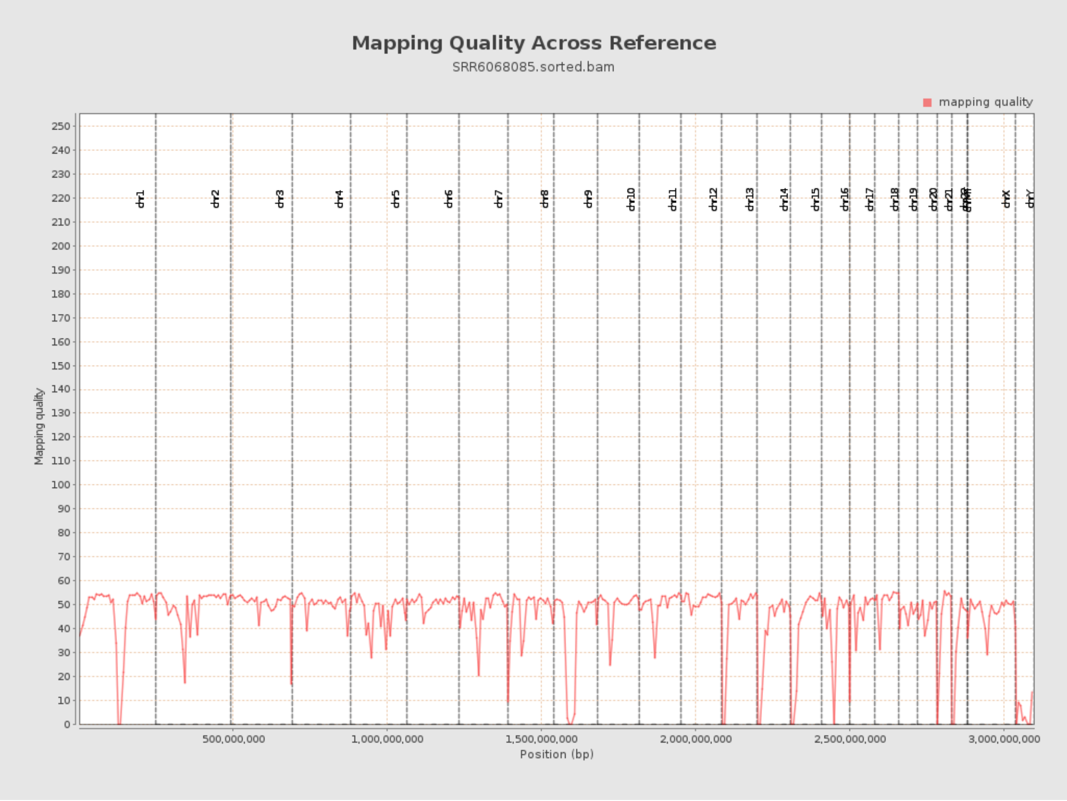
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram