Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 08:05:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068070.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_SRR6068070 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068070.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 08:05:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068070.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,569,825
Mapped reads	4,310,390 / 94.32%
Unmapped reads	259,435 / 5.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,584 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	821,182 / 17.97%
Duplication rate	14.99%
Clipped reads	2,307,912 / 50.5%

2.2. ACGT Content

Number/percentage of A's	70,944,504 / 25.64%
Number/percentage of C's	50,123,050 / 18.11%
Number/percentage of T's	89,896,296 / 32.49%
Number/percentage of G's	65,722,093 / 23.75%
Number/percentage of N's	31,803 / 0.01%
GC Percentage	41.86%

2.3. Coverage

Mean	0.0894

Standard Deviation	1.0493

2.4. Mapping Quality

Mean Mapping Quality	45.4

2.5. Mismatches and indels

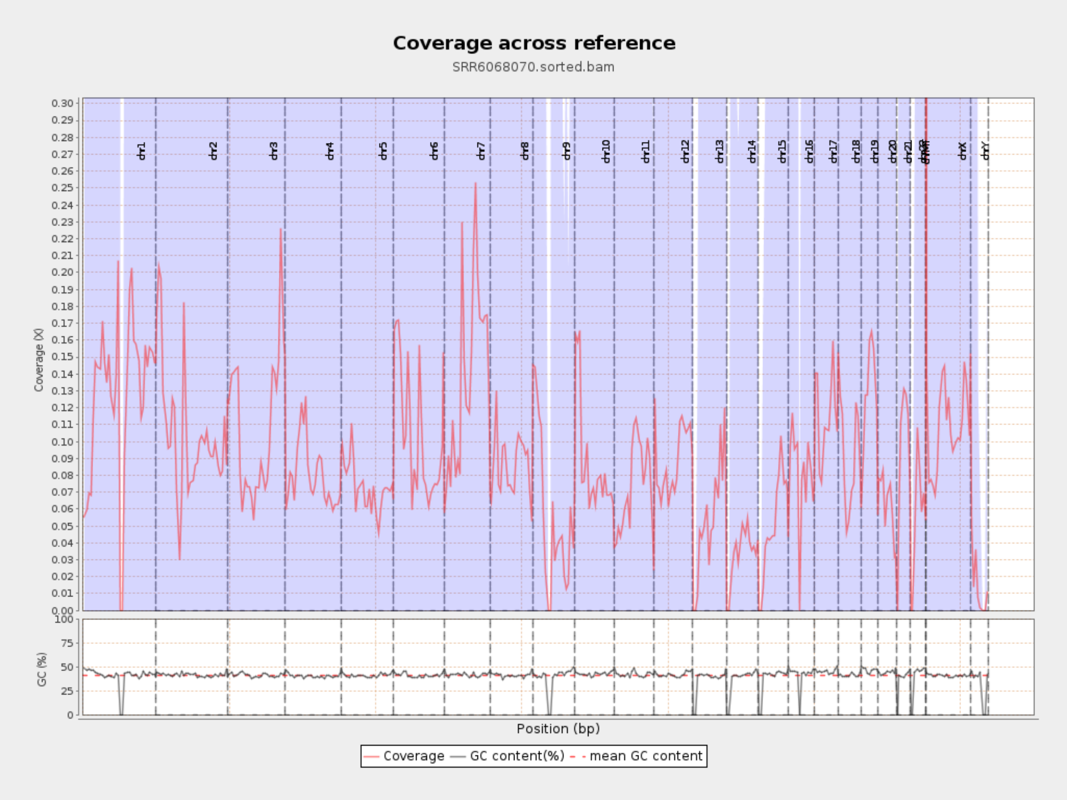
General error rate	0.54%
Mismatches	1,477,382
Insertions	16,827
Mapped reads with at least one insertion	0.39%
Deletions	60,020
Mapped reads with at least one deletion	1.38%
Homopolymer indels	43.82%

2.6. Chromosome stats

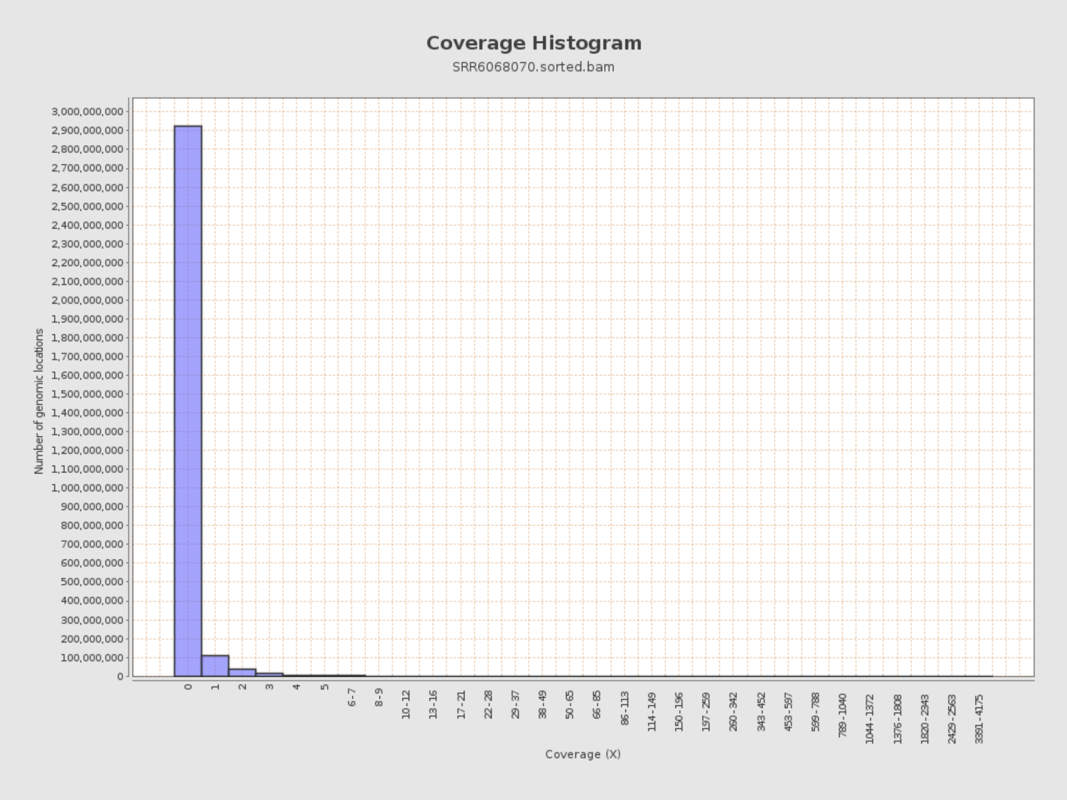
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	31813084	0.1276	2.121
chr2	243199373	25460917	0.1047	1.9287
chr3	198022430	21356847	0.1079	0.4971
chr4	191154276	15378938	0.0805	0.4532
chr5	180915260	13229968	0.0731	0.4099
chr6	171115067	17883151	0.1045	0.6837
chr7	159138663	22266076	0.1399	1.6113

chr8	146364022	12562196	0.0858	1.2386
chr9	141213431	7491598	0.0531	0.6036
chr10	135534747	11887467	0.0877	0.5577
chr11	135006516	9991889	0.074	0.4922
chr12	133851895	11869862	0.0887	0.4767
chr13	115169878	6252367	0.0543	0.4163
chr14	107349540	3646572	0.034	0.3355
chr15	102531392	5102111	0.0498	0.3862
chr16	90354753	7092041	0.0785	0.4449
chr17	81195210	9439557	0.1163	0.5305
chr18	78077248	7154633	0.0916	1.17
chr19	59128983	7601431	0.1286	1.2658
chr20	63025520	3962769	0.0629	0.407
chr21	48129895	4501828	0.0935	0.47
chr22	51304566	2867993	0.0559	0.346
chrMT	16571	350737	21.1657	13.329
chrX	155270560	16846841	0.1085	0.5834
chrY	59373566	811150	0.0137	0.3381

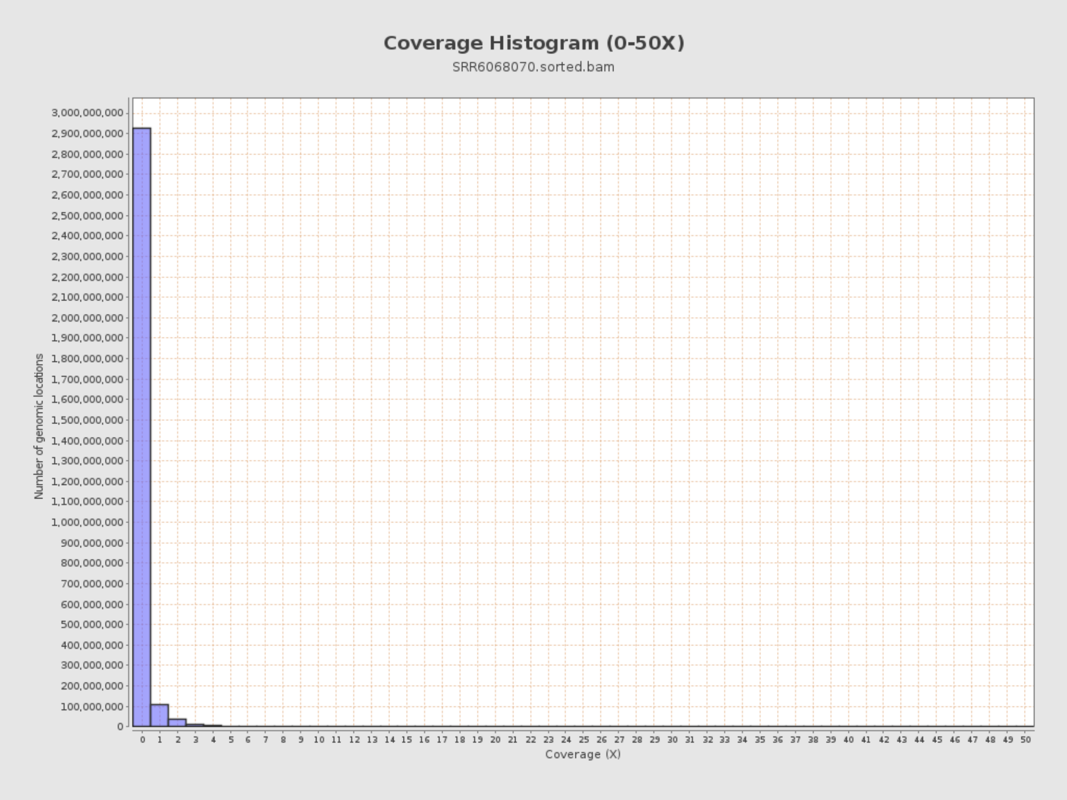
3. Results : Coverage across reference



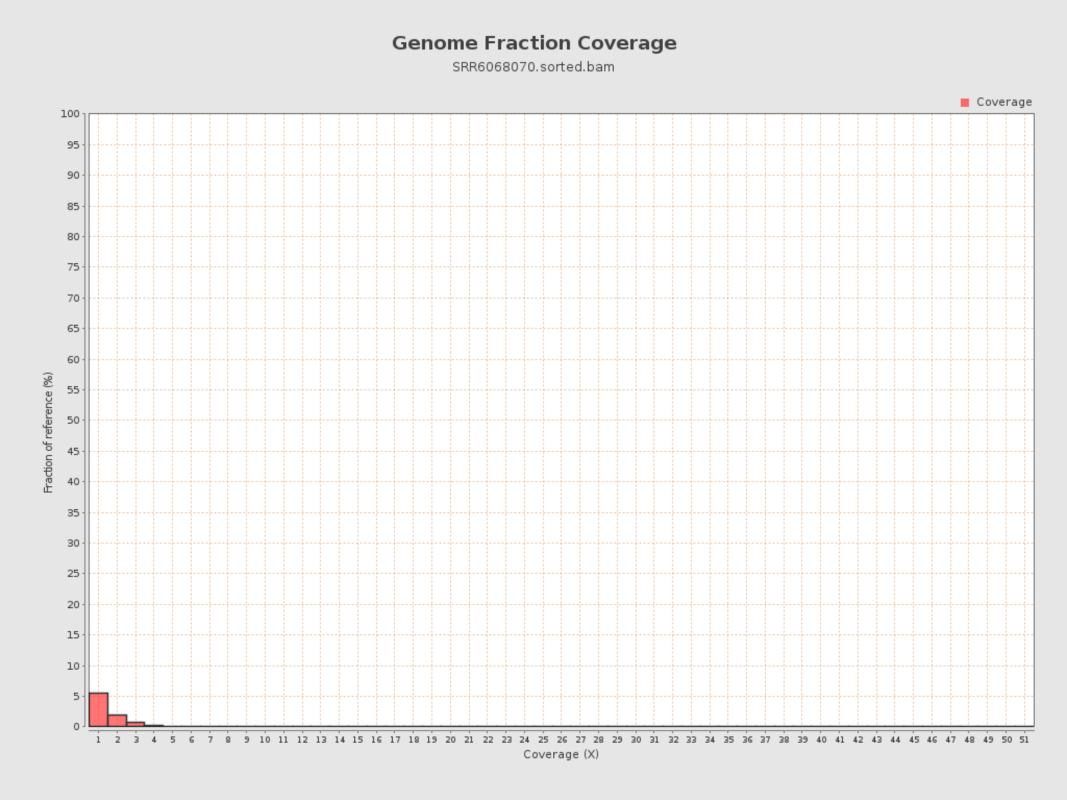
4. Results : Coverage Histogram



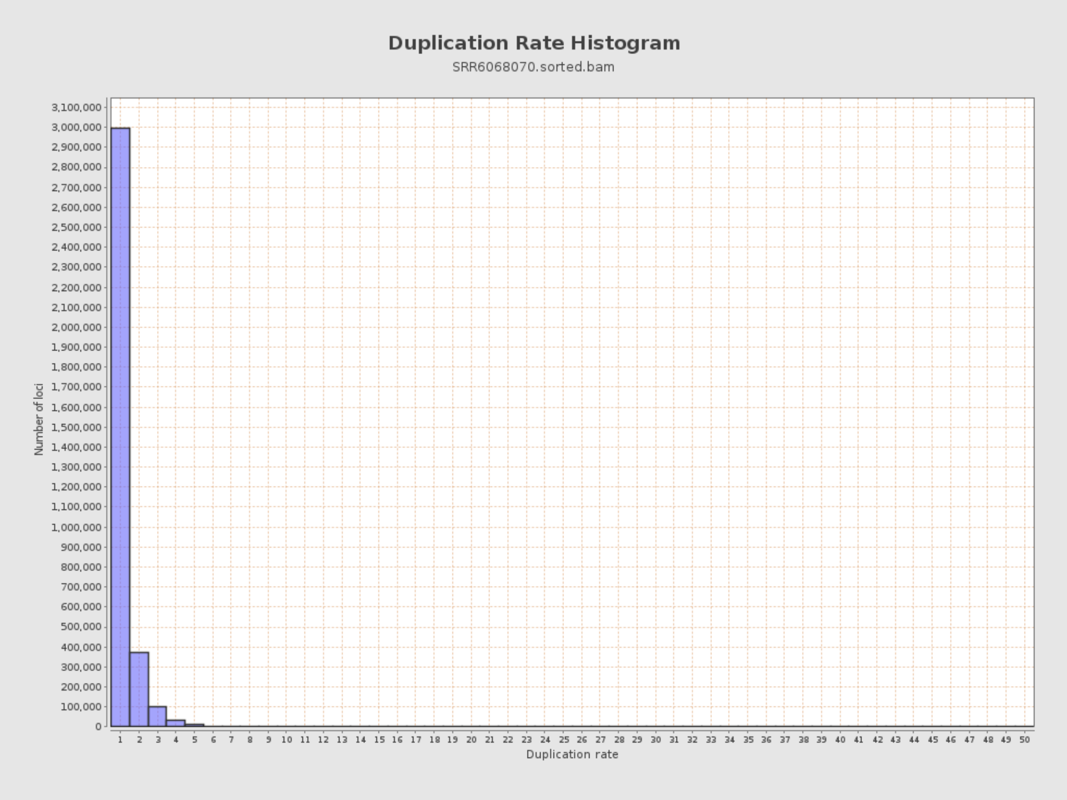
5. Results : Coverage Histogram (0-50X)



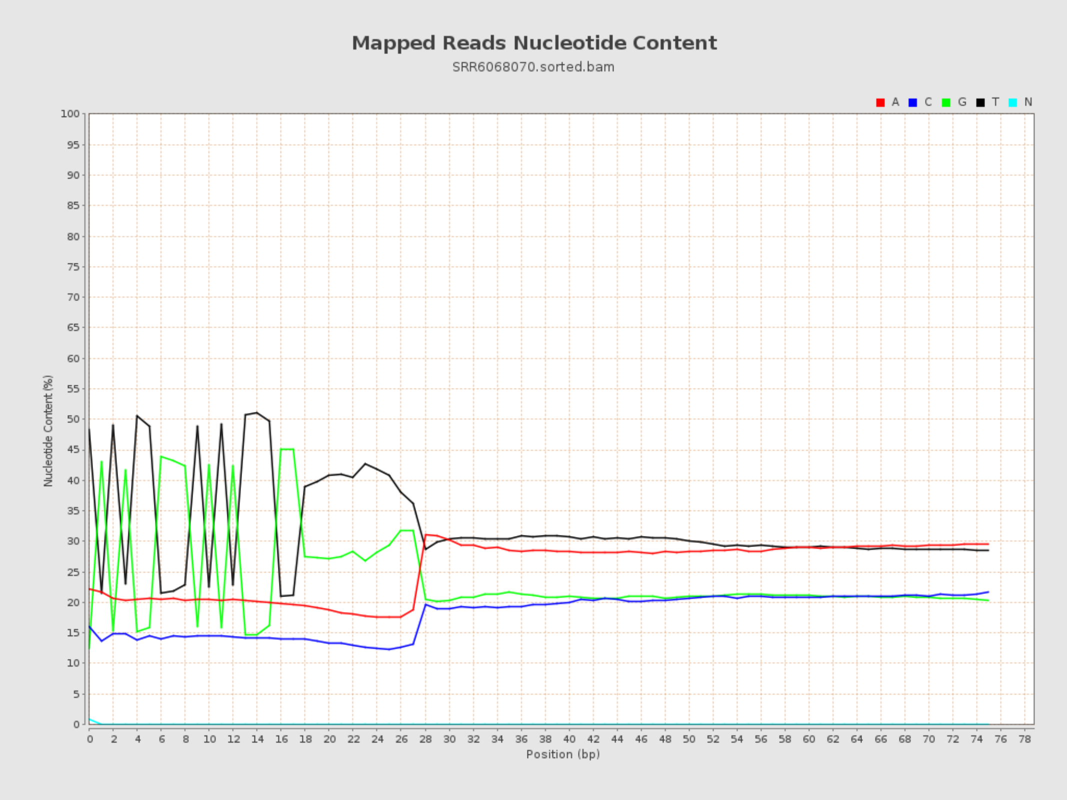
6. Results : Genome Fraction Coverage



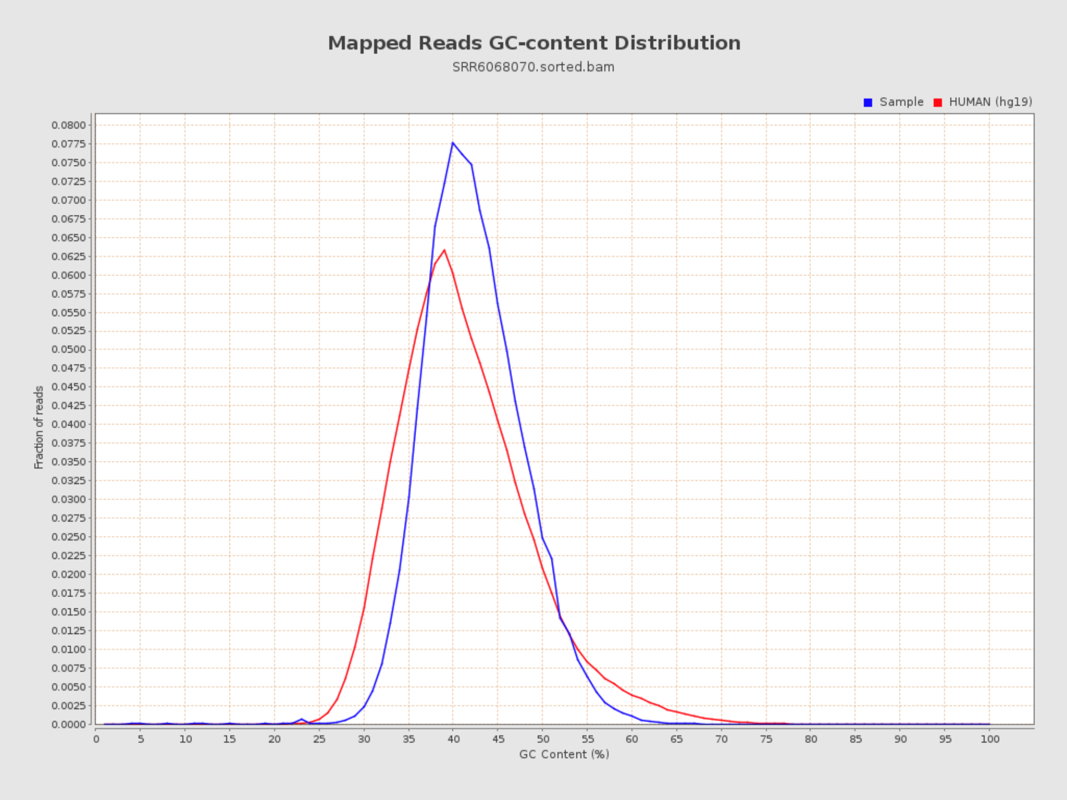
7. Results : Duplication Rate Histogram



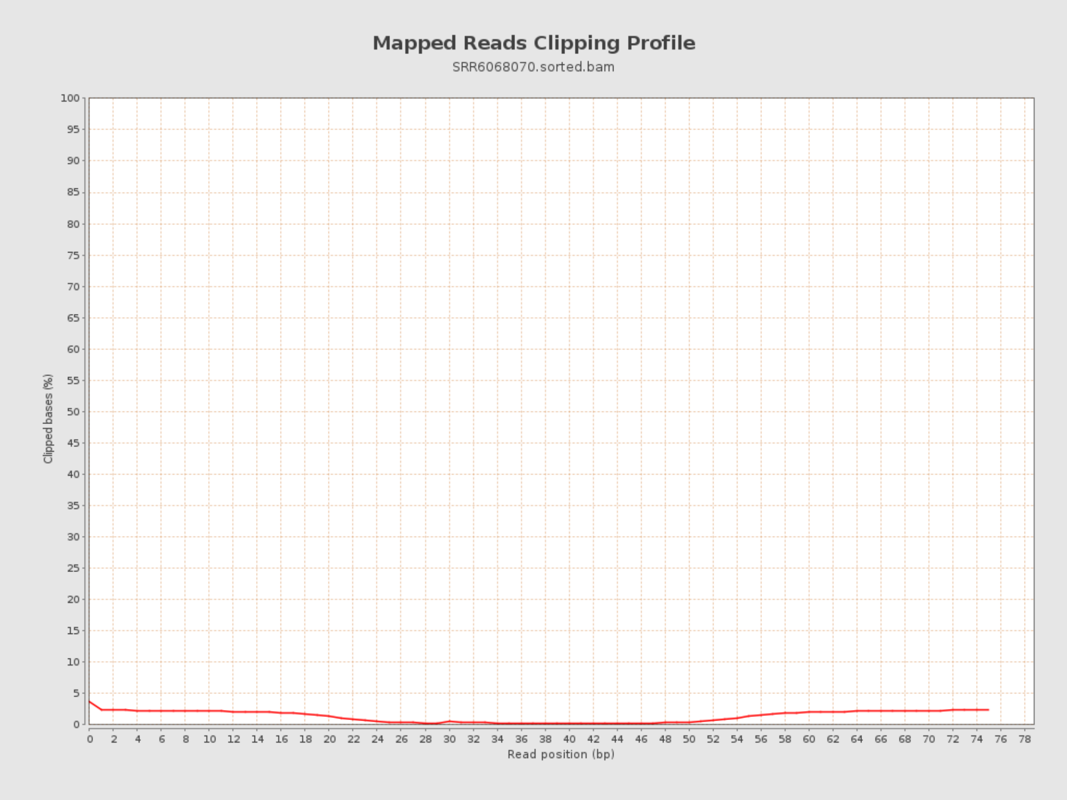
8. Results : Mapped Reads Nucleotide Content



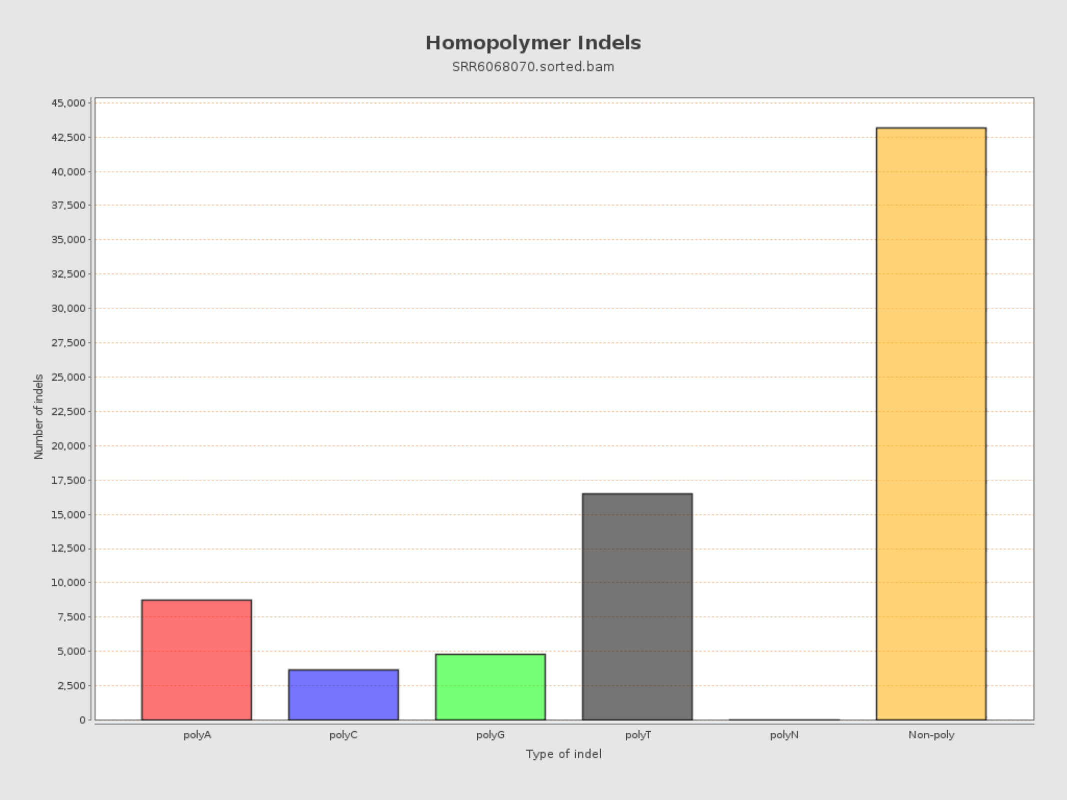
9. Results : Mapped Reads GC-content Distribution



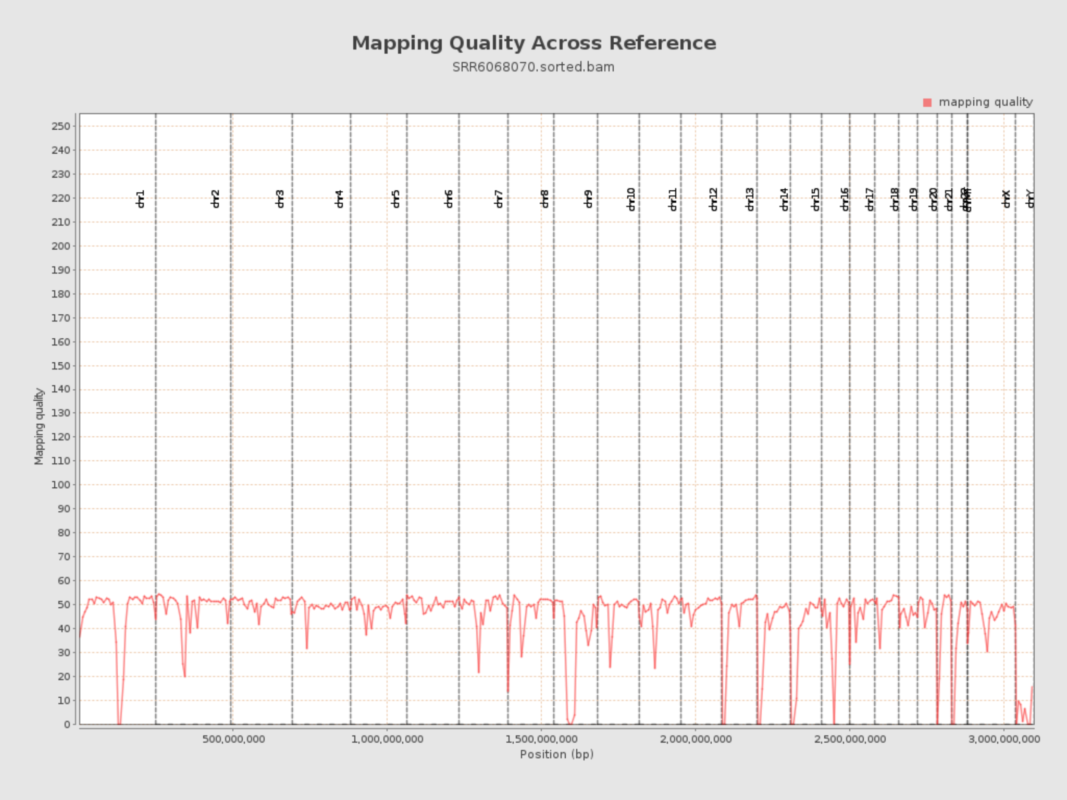
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram