Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 18:21:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080694.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_SRR3080694 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080694.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 18:21:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080694.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,125,207
Mapped reads	1,869,414 / 87.96%
Unmapped reads	255,793 / 12.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,206 / 1.04%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	89,840 / 4.23%
Duplication rate	4.15%
Clipped reads	599,956 / 28.23%

2.2. ACGT Content

Number/percentage of A's	39,864,989 / 30.46%
Number/percentage of C's	24,171,875 / 18.47%
Number/percentage of T's	40,715,820 / 31.11%
Number/percentage of G's	26,108,589 / 19.95%
Number/percentage of N's	2,076 / 0%
GC Percentage	38.42%

2.3. Coverage

Mean	0.0423

Standard Deviation	0.368

2.4. Mapping Quality

Mean Mapping Quality	48

2.5. Mismatches and indels

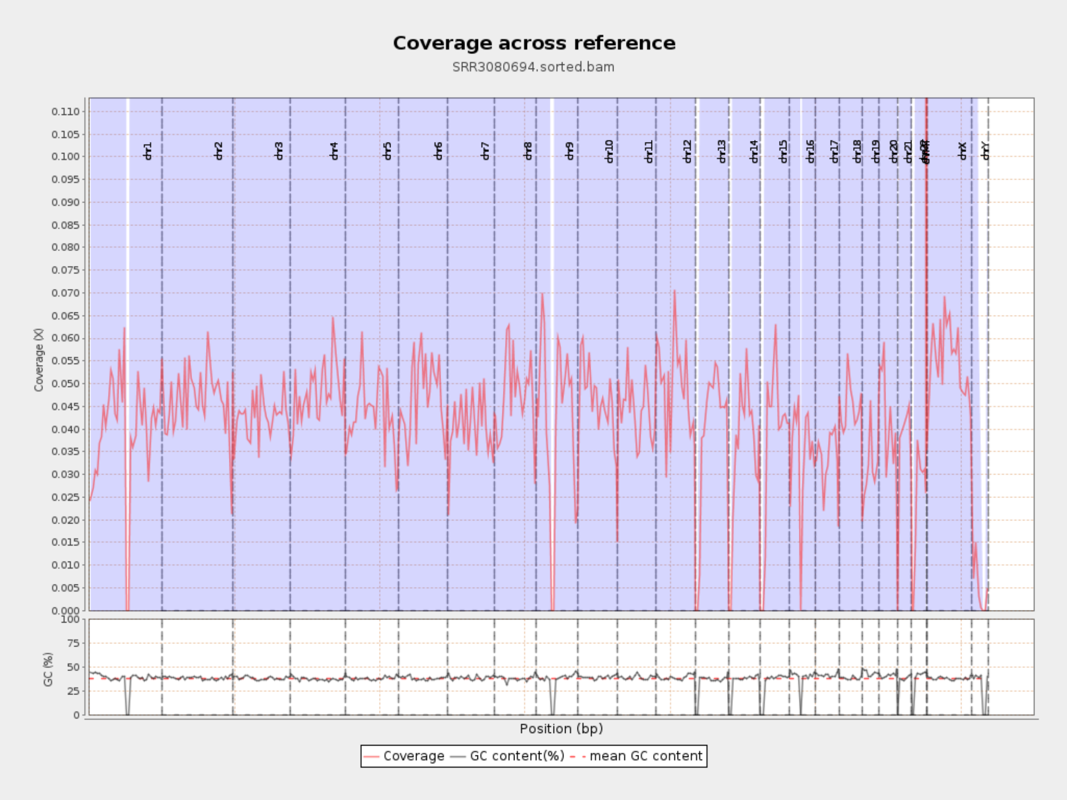
General error rate	0.79%
Mismatches	1,009,544
Insertions	9,783
Mapped reads with at least one insertion	0.52%
Deletions	27,503
Mapped reads with at least one deletion	1.45%
Homopolymer indels	47.89%

2.6. Chromosome stats

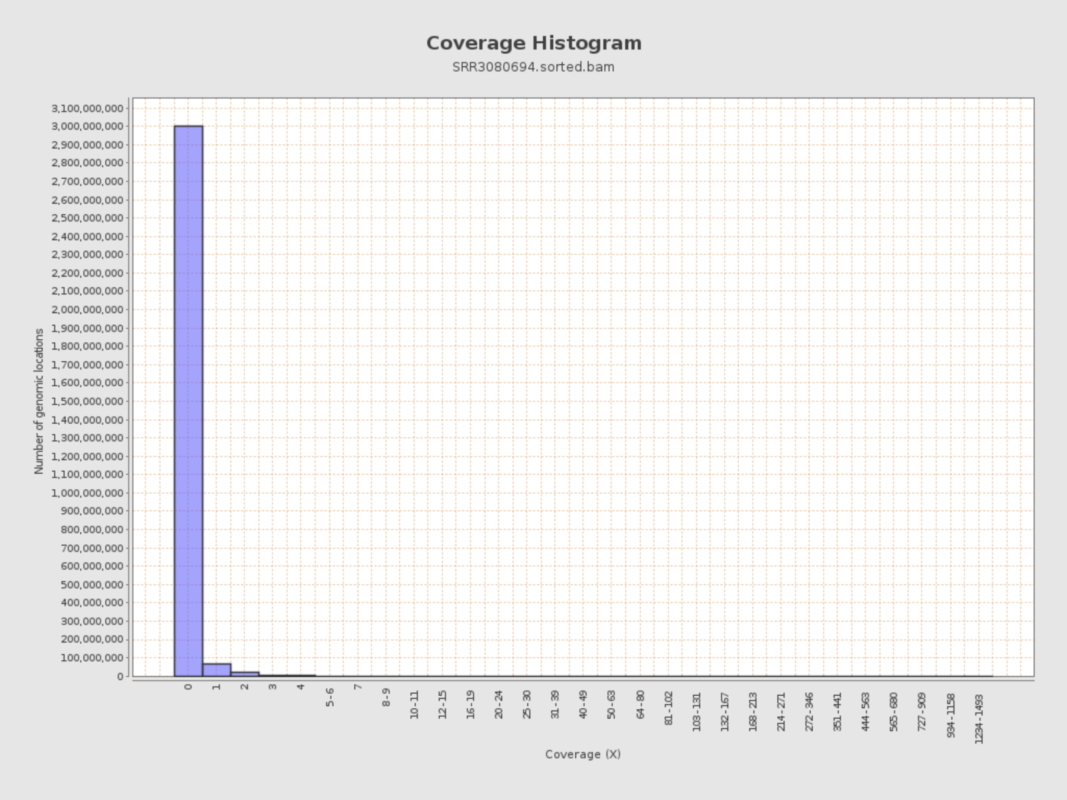
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9852100	0.0395	0.3812
chr2	243199373	11280398	0.0464	0.3445
chr3	198022430	8528954	0.0431	0.2765
chr4	191154276	9191414	0.0481	0.2953
chr5	180915260	7880999	0.0436	0.2771
chr6	171115067	8048390	0.047	0.3003
chr7	159138663	6479760	0.0407	0.3556

chr8	146364022	6941483	0.0474	0.9789
chr9	141213431	6003023	0.0425	0.3041
chr10	135534747	6342672	0.0468	0.323
chr11	135006516	5911458	0.0438	0.3115
chr12	133851895	6651193	0.0497	0.2946
chr13	115169878	4448073	0.0386	0.2615
chr14	107349540	3737216	0.0348	0.2536
chr15	102531392	3820463	0.0373	0.2535
chr16	90354753	3124891	0.0346	0.2514
chr17	81195210	2696851	0.0332	0.2475
chr18	78077248	3491500	0.0447	0.4113
chr19	59128983	1882888	0.0318	0.313
chr20	63025520	2660644	0.0422	0.2749
chr21	48129895	1748567	0.0363	0.2573
chr22	51304566	1167571	0.0228	0.195
chrMT	16571	196713	11.8709	6.9922
chrX	155270560	8502188	0.0548	0.3186
chrY	59373566	322903	0.0054	0.1131

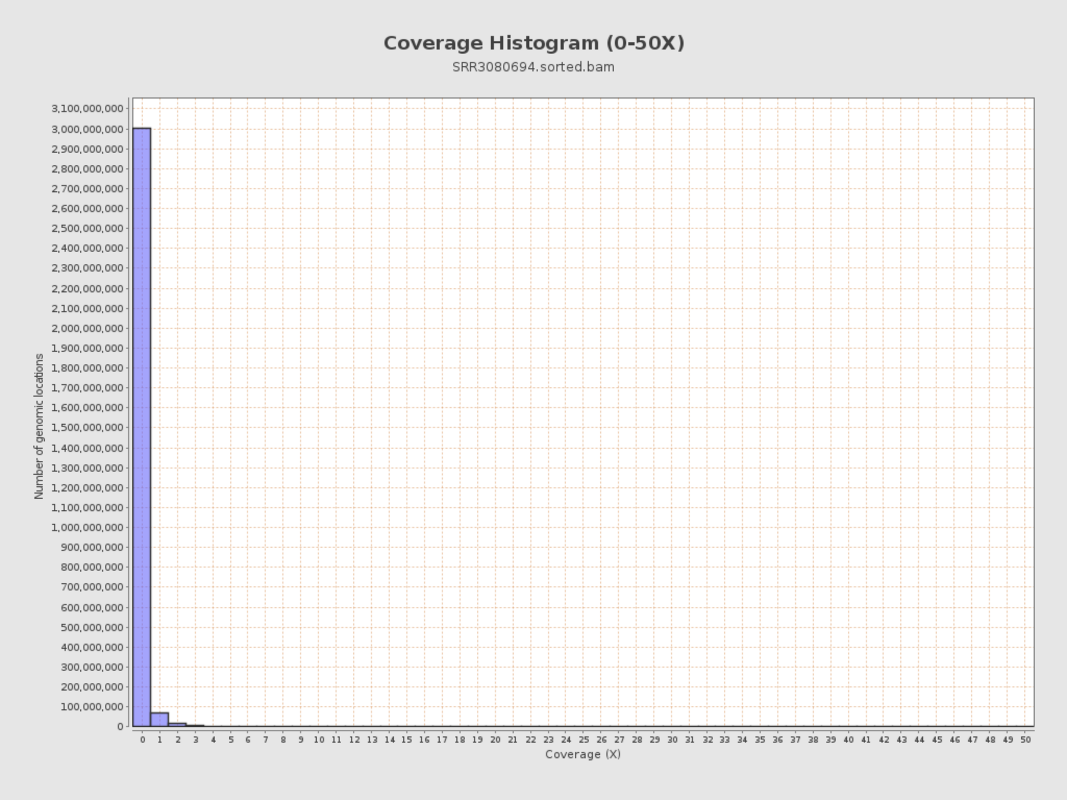
3. Results : Coverage across reference



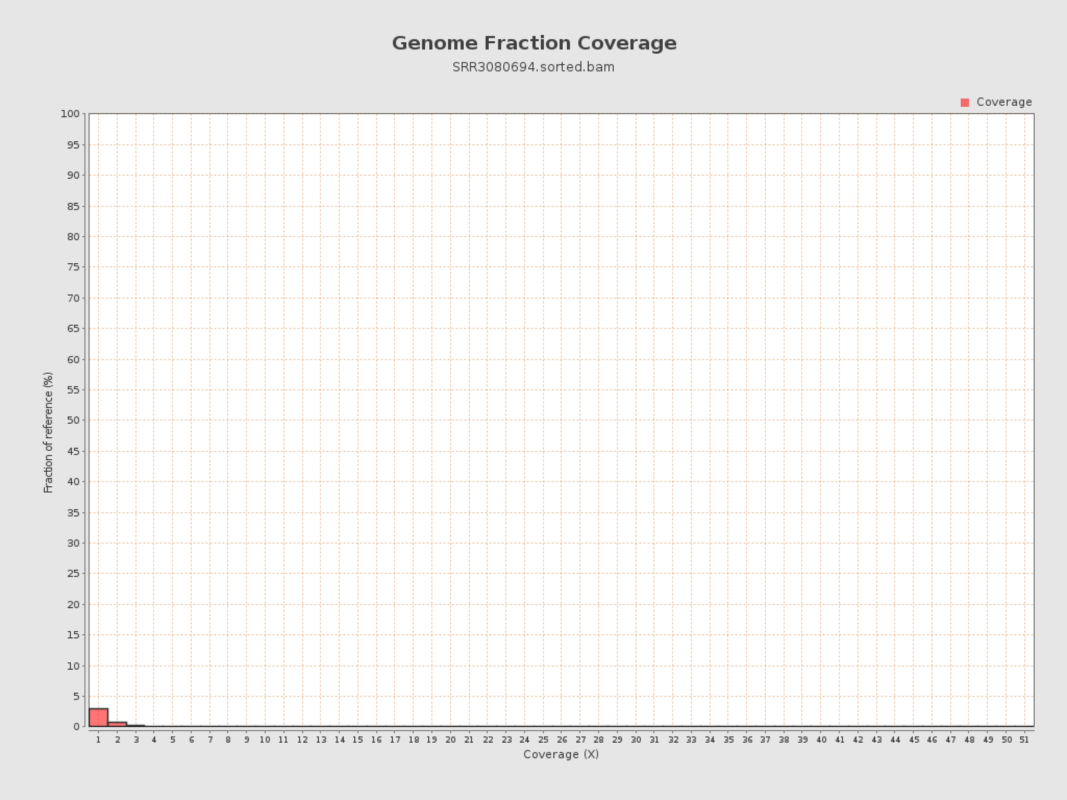
4. Results : Coverage Histogram



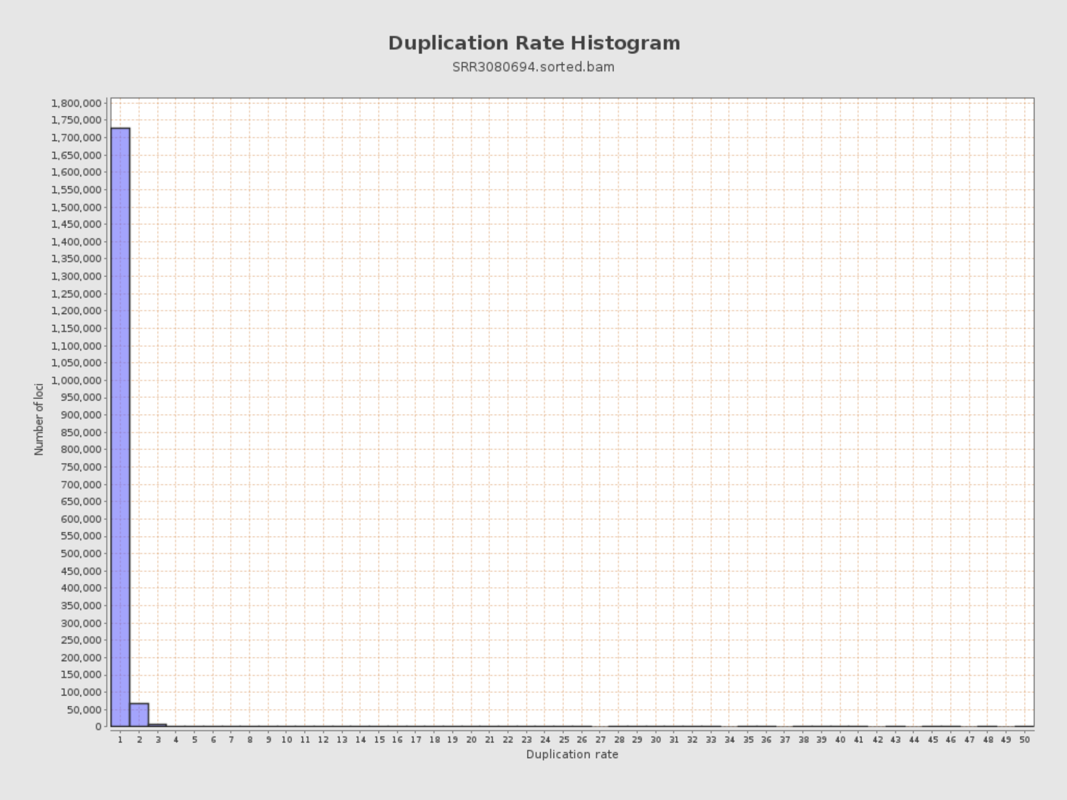
5. Results : Coverage Histogram (0-50X)



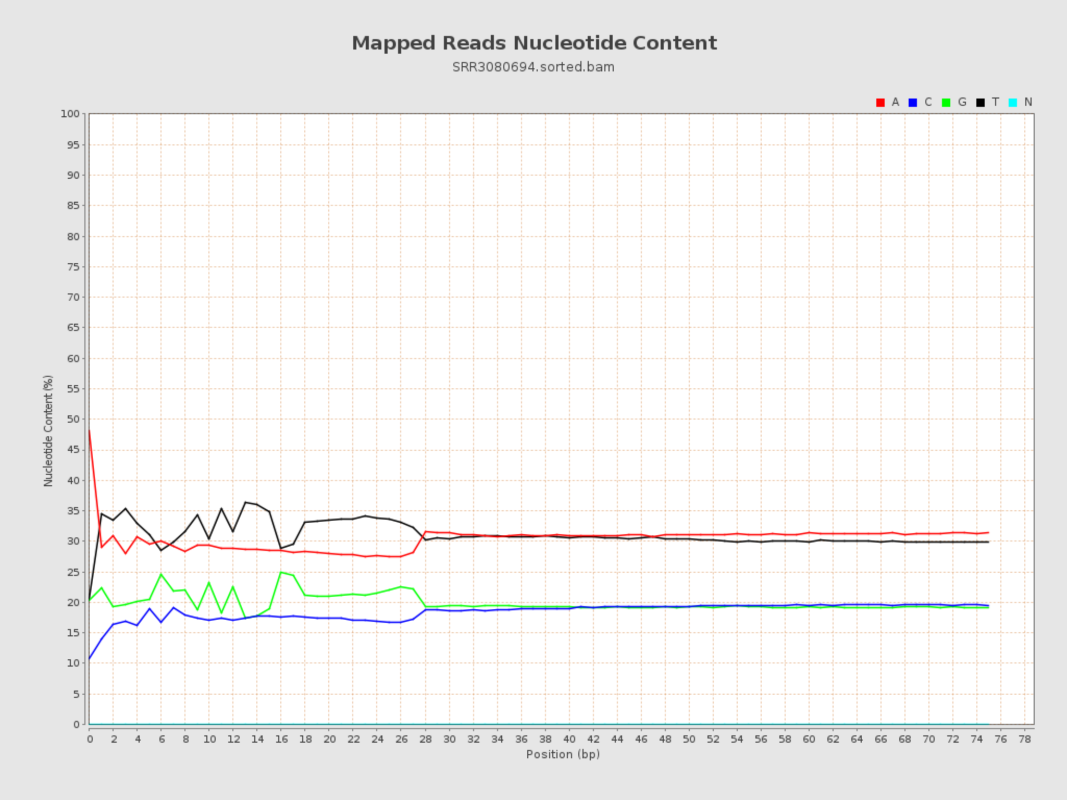
6. Results : Genome Fraction Coverage



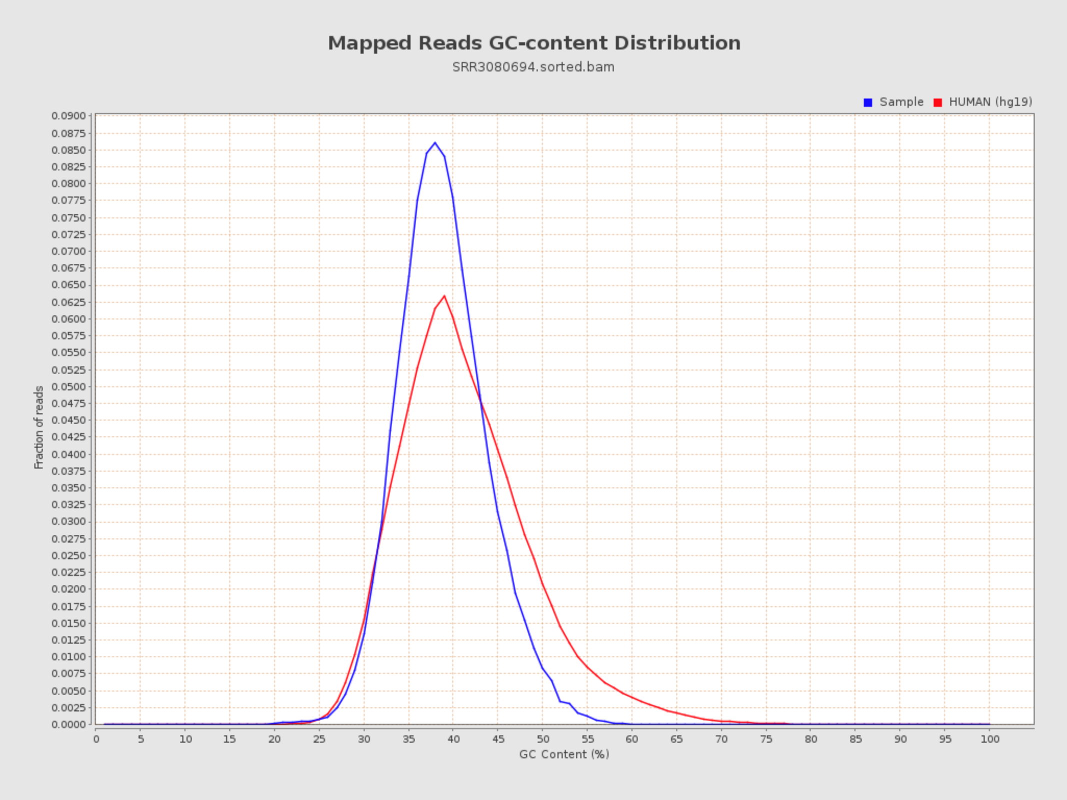
7. Results : Duplication Rate Histogram



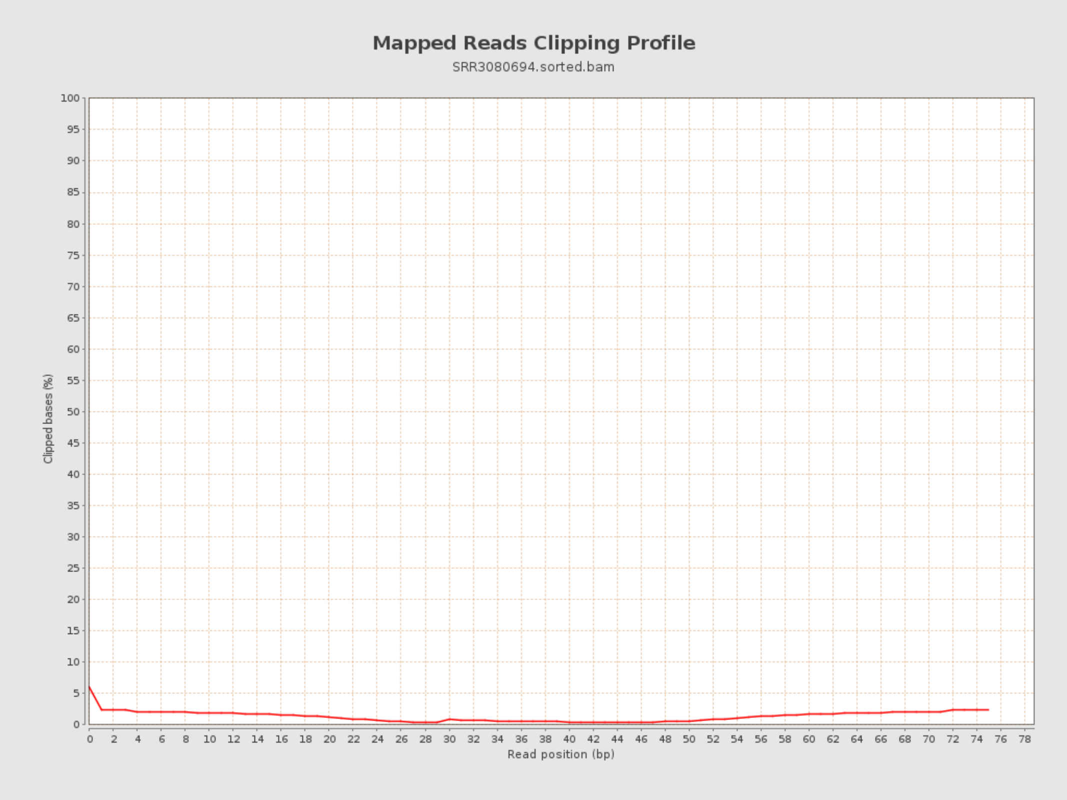
8. Results : Mapped Reads Nucleotide Content



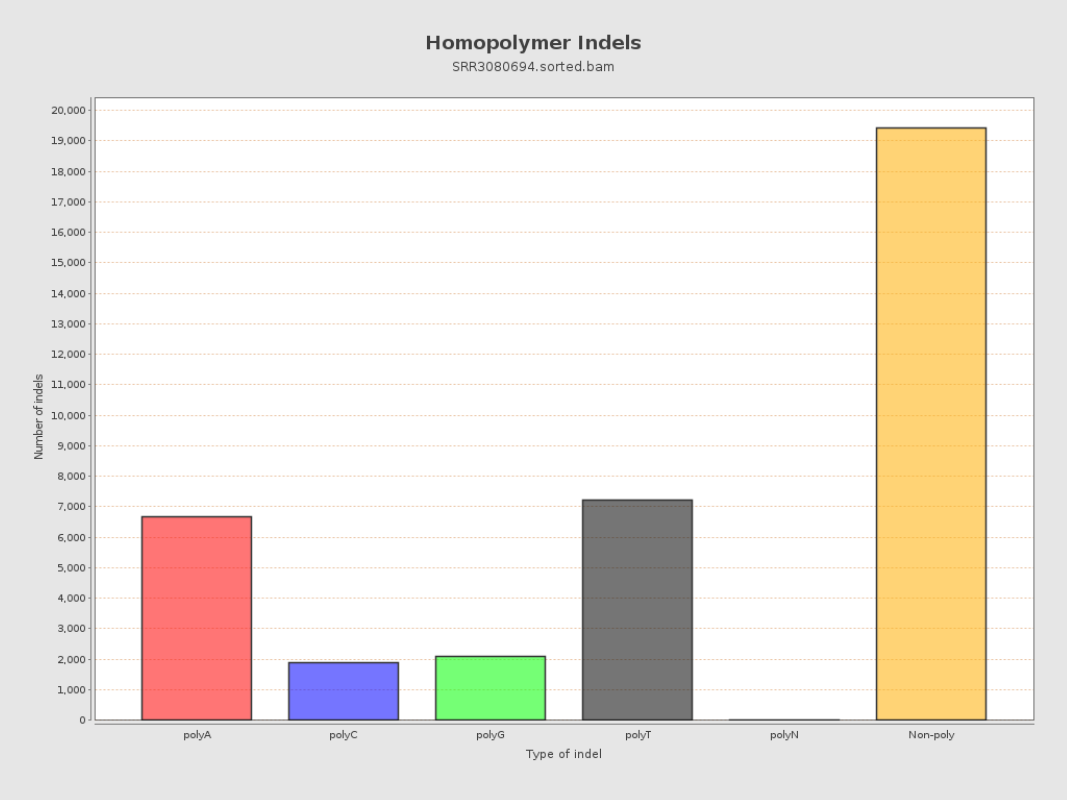
9. Results : Mapped Reads GC-content Distribution



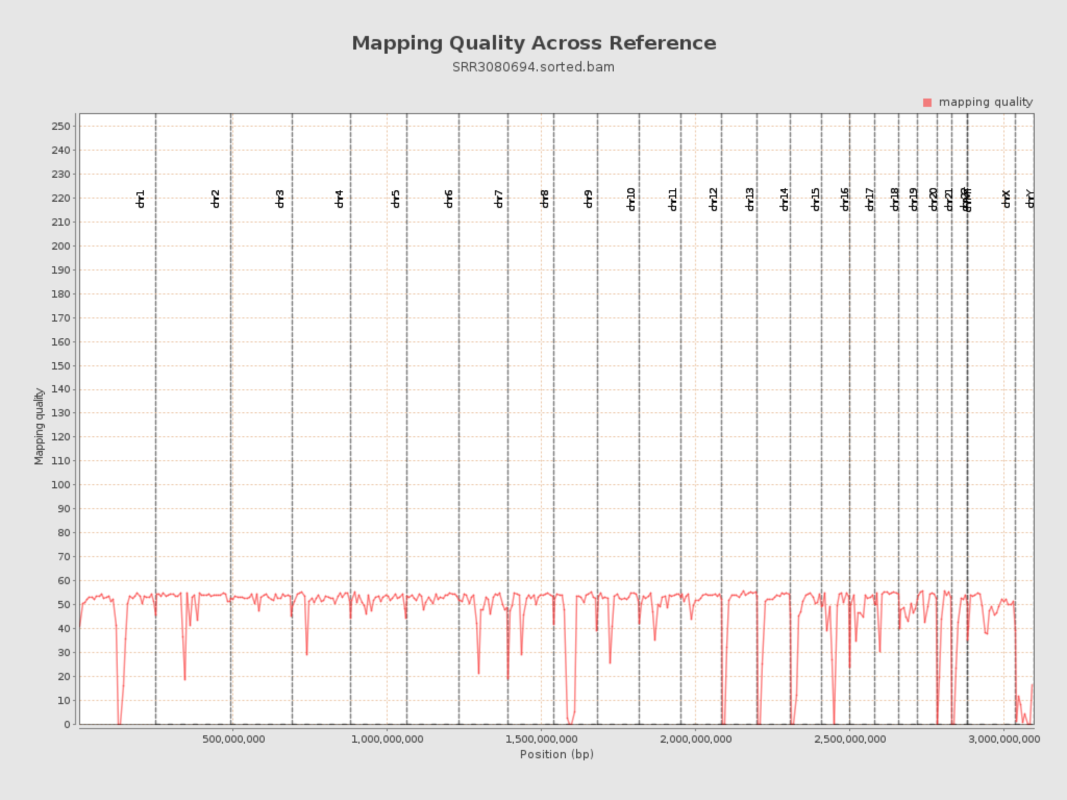
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram