Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 17:21:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080690.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_SRR3080690 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080690.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 17:21:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080690.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,443,228
Mapped reads	2,121,811 / 86.84%
Unmapped reads	321,417 / 13.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,862 / 0.89%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	153,322 / 6.28%
Duplication rate	5.91%
Clipped reads	764,607 / 31.29%

2.2. ACGT Content

Number/percentage of A's	43,088,027 / 29.45%
Number/percentage of C's	26,518,684 / 18.12%
Number/percentage of T's	46,856,292 / 32.02%
Number/percentage of G's	29,852,087 / 20.4%
Number/percentage of N's	2,191 / 0%
GC Percentage	38.53%

2.3. Coverage

Mean	0.0473

Standard Deviation	0.4551

2.4. Mapping Quality

Mean Mapping Quality	47.6

2.5. Mismatches and indels

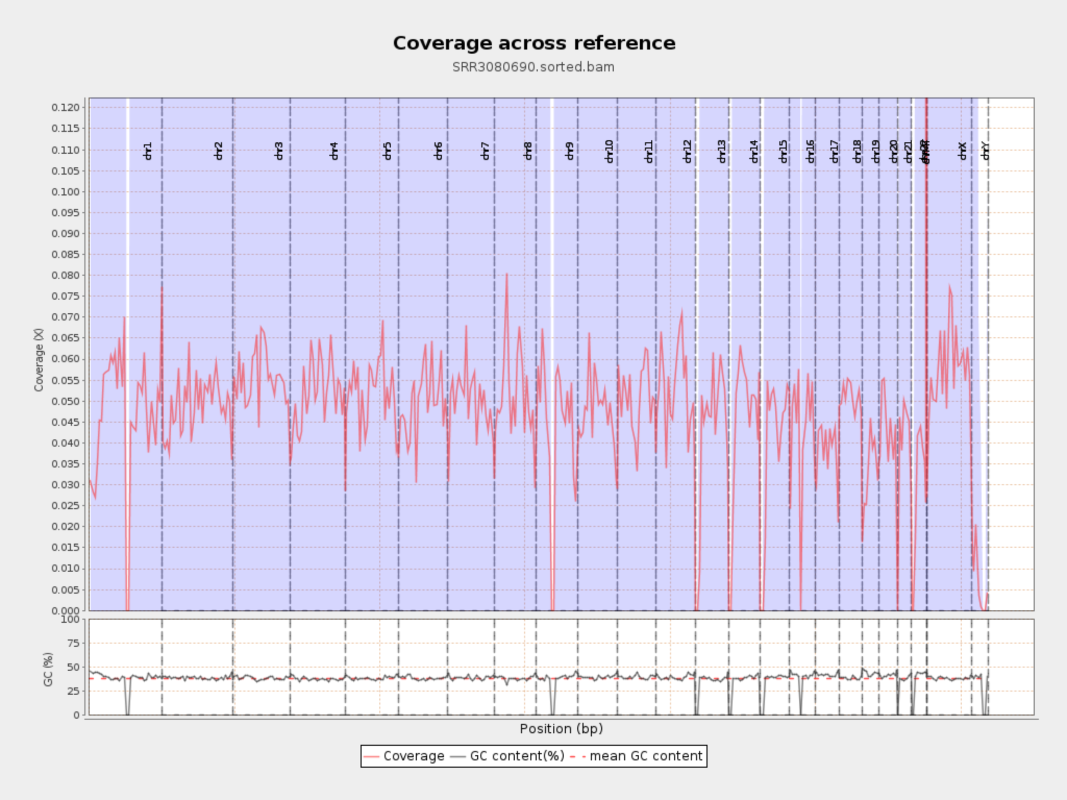
General error rate	0.82%
Mismatches	1,173,924
Insertions	11,510
Mapped reads with at least one insertion	0.54%
Deletions	30,354
Mapped reads with at least one deletion	1.41%
Homopolymer indels	48.05%

2.6. Chromosome stats

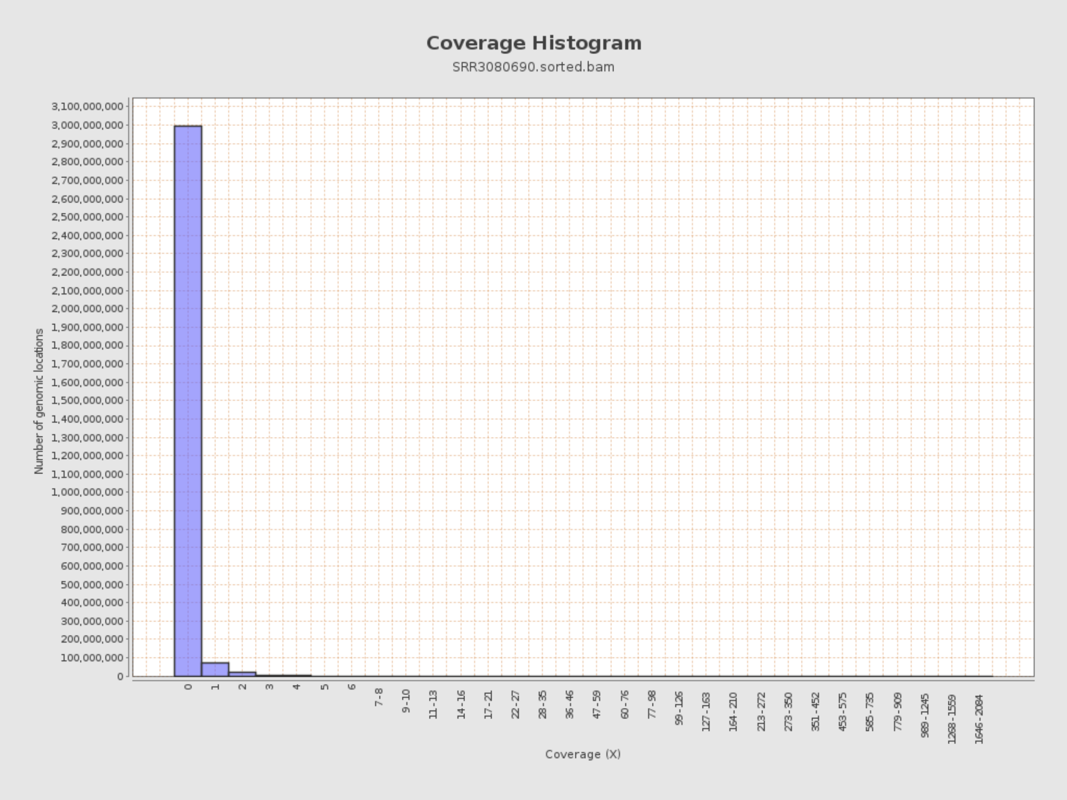
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11594462	0.0465	0.5196
chr2	243199373	11905211	0.049	0.4059
chr3	198022430	10991018	0.0555	0.3224
chr4	191154276	9928440	0.0519	0.3276
chr5	180915260	9448858	0.0522	0.3127
chr6	171115067	8501619	0.0497	0.3146
chr7	159138663	8021884	0.0504	0.4794

chr8	146364022	7500592	0.0512	1.3077
chr9	141213431	6177571	0.0437	0.3653
chr10	135534747	6497465	0.0479	0.3702
chr11	135006516	6828664	0.0506	0.3318
chr12	133851895	7112041	0.0531	0.3181
chr13	115169878	4811069	0.0418	0.2822
chr14	107349540	4729879	0.0441	0.2997
chr15	102531392	4016687	0.0392	0.2679
chr16	90354753	3869055	0.0428	0.2943
chr17	81195210	3070152	0.0378	0.2742
chr18	78077248	3984437	0.051	0.5708
chr19	59128983	1996476	0.0338	0.3826
chr20	63025520	2730990	0.0433	0.2873
chr21	48129895	1892671	0.0393	0.2885
chr22	51304566	1423732	0.0278	0.2203
chrMT	16571	40848	2.465	2.3656
chrX	155270560	8930859	0.0575	0.3359
chrY	59373566	366324	0.0062	0.1663

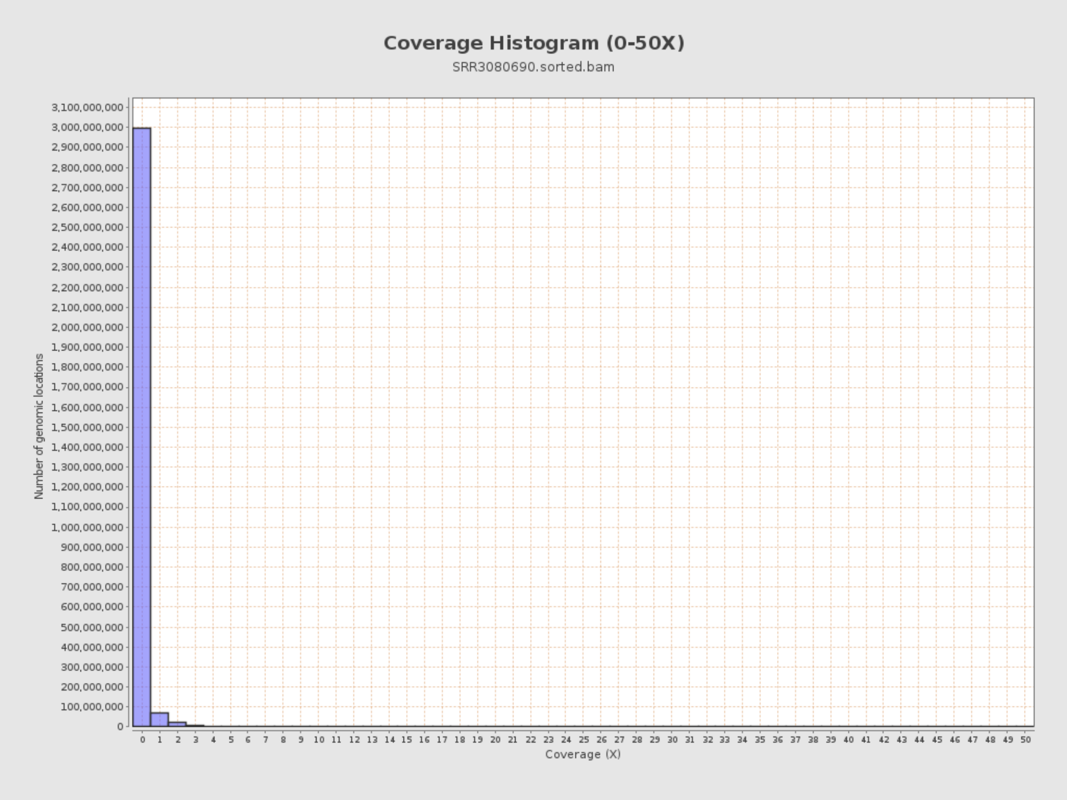
3. Results : Coverage across reference



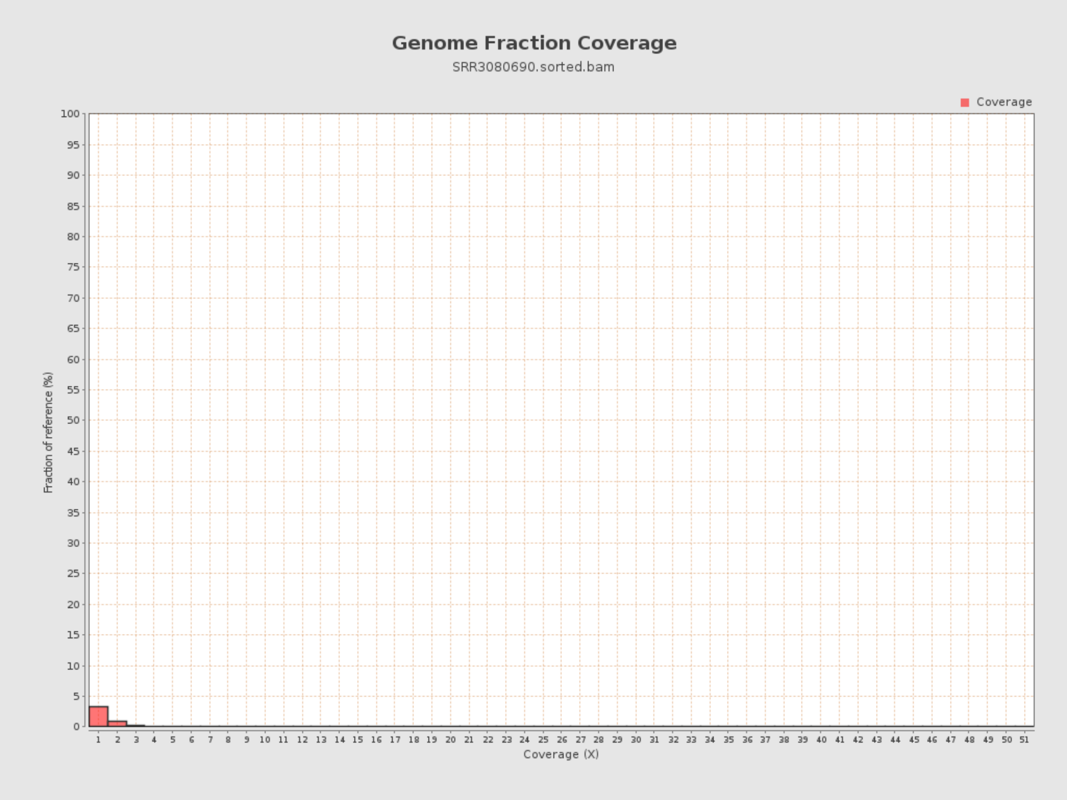
4. Results : Coverage Histogram



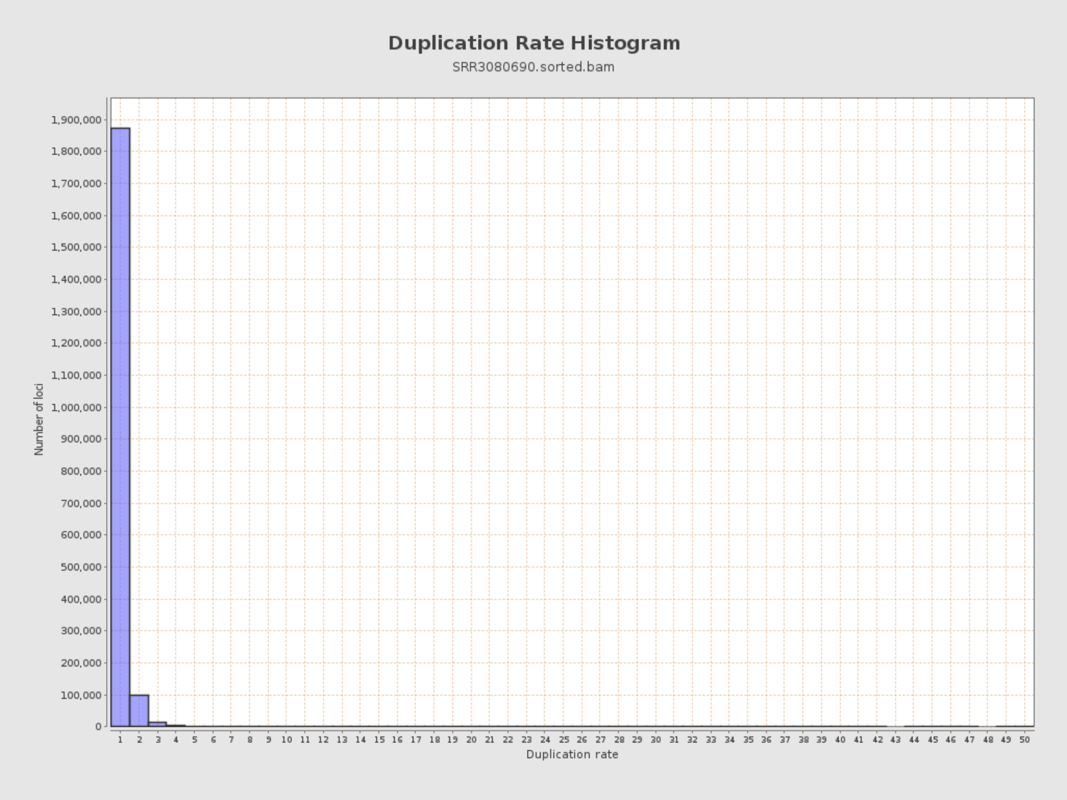
5. Results : Coverage Histogram (0-50X)



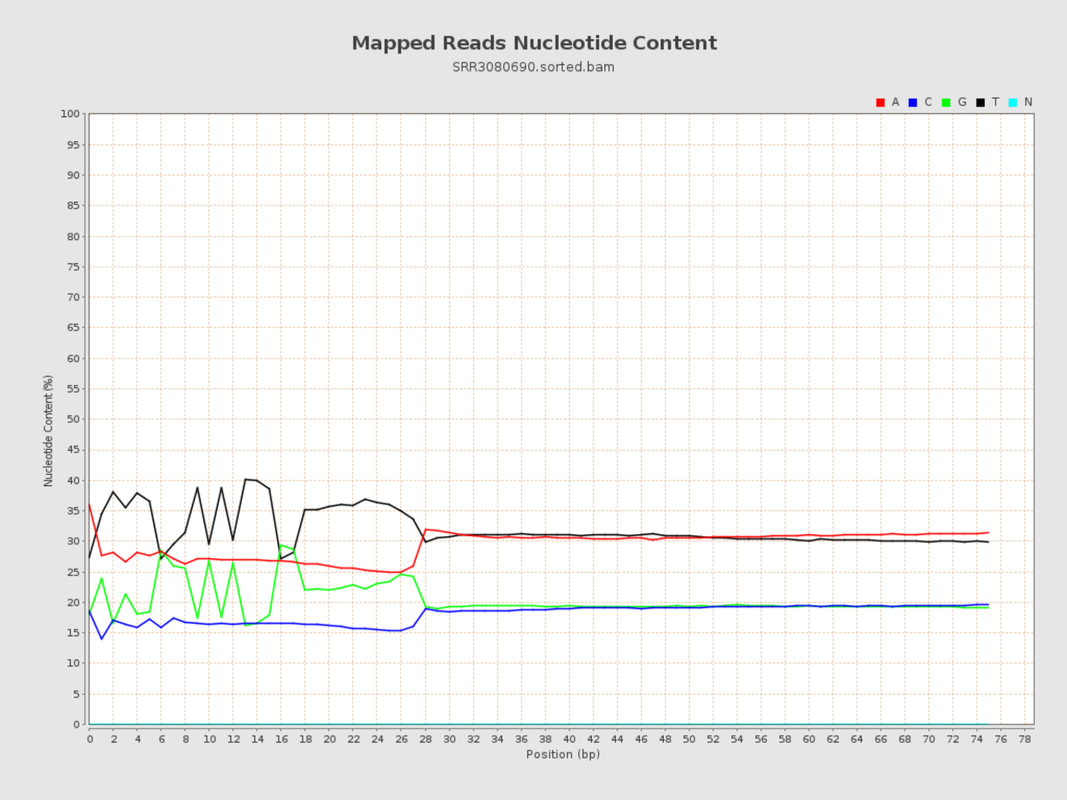
6. Results : Genome Fraction Coverage



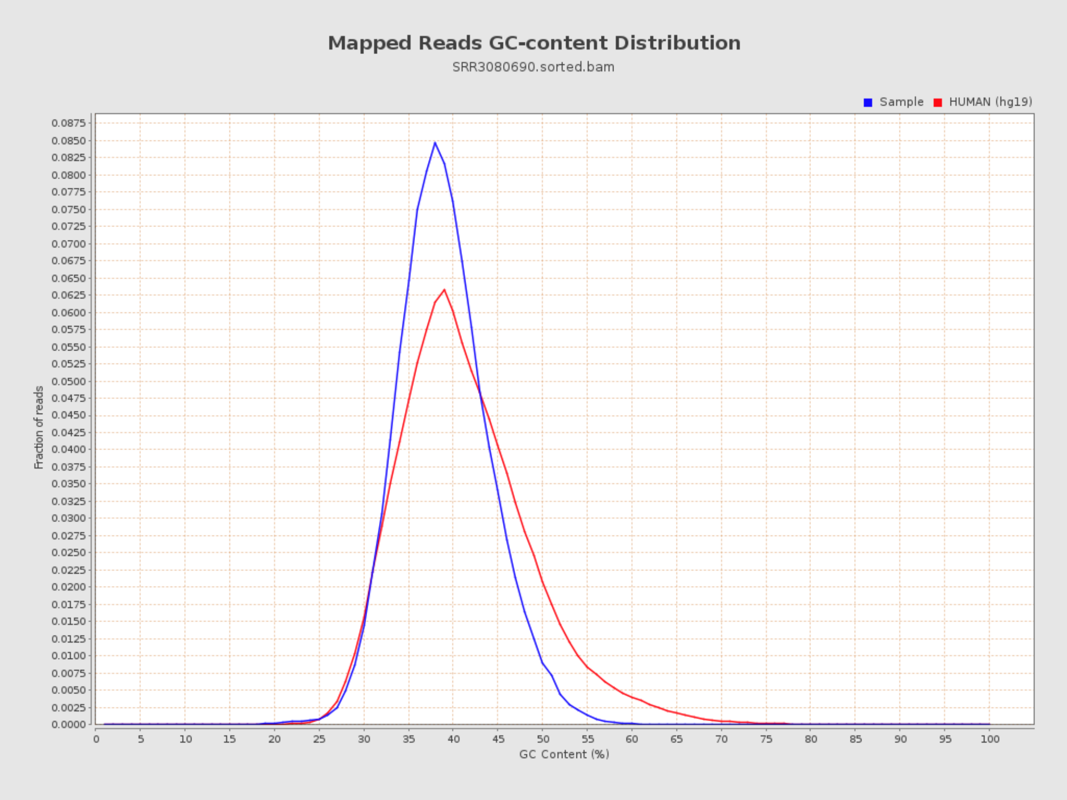
7. Results : Duplication Rate Histogram



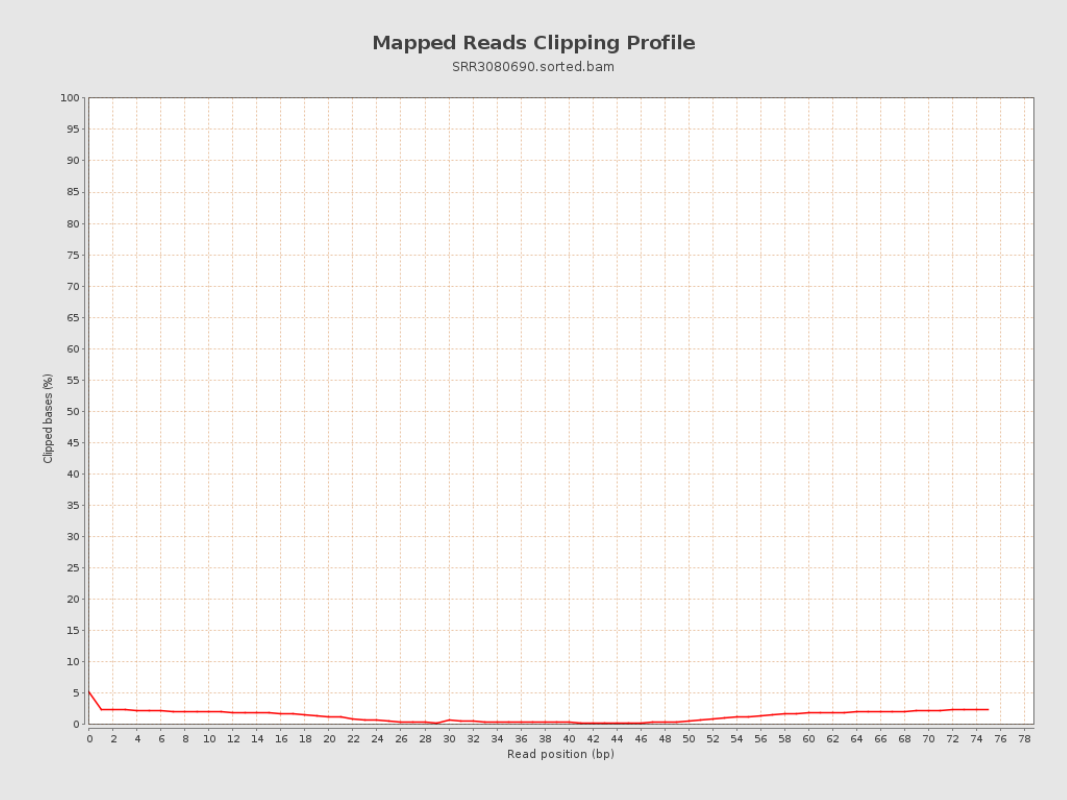
8. Results : Mapped Reads Nucleotide Content



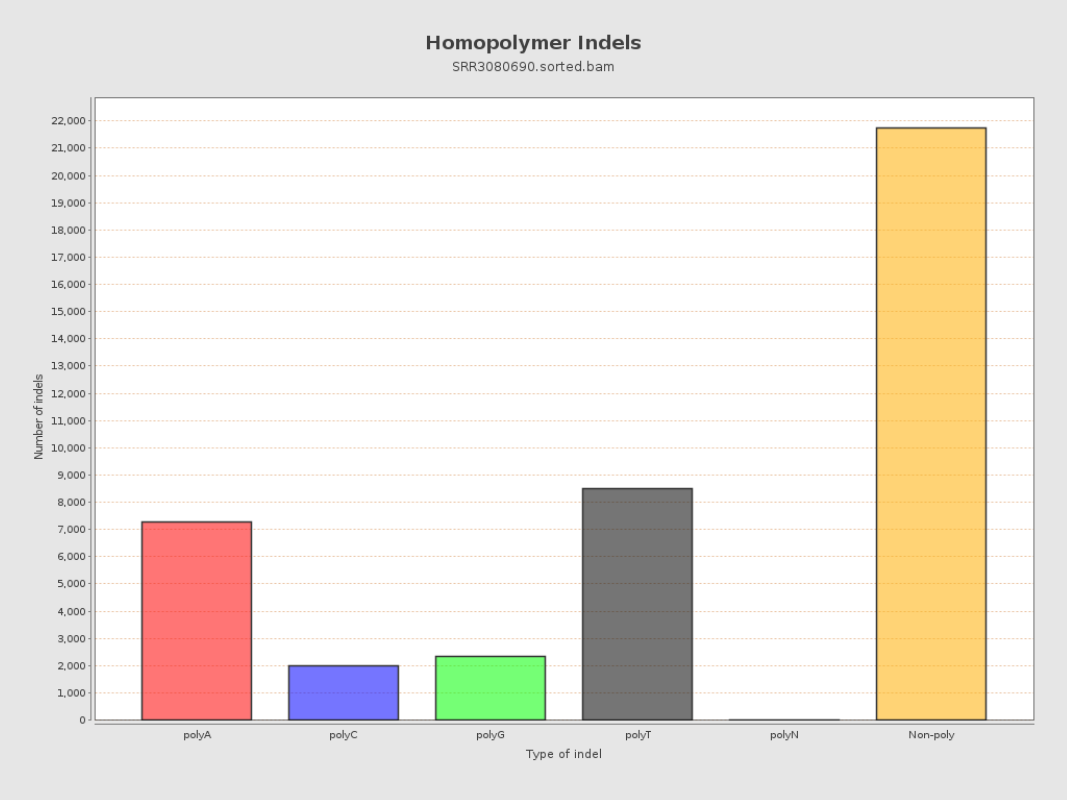
9. Results : Mapped Reads GC-content Distribution



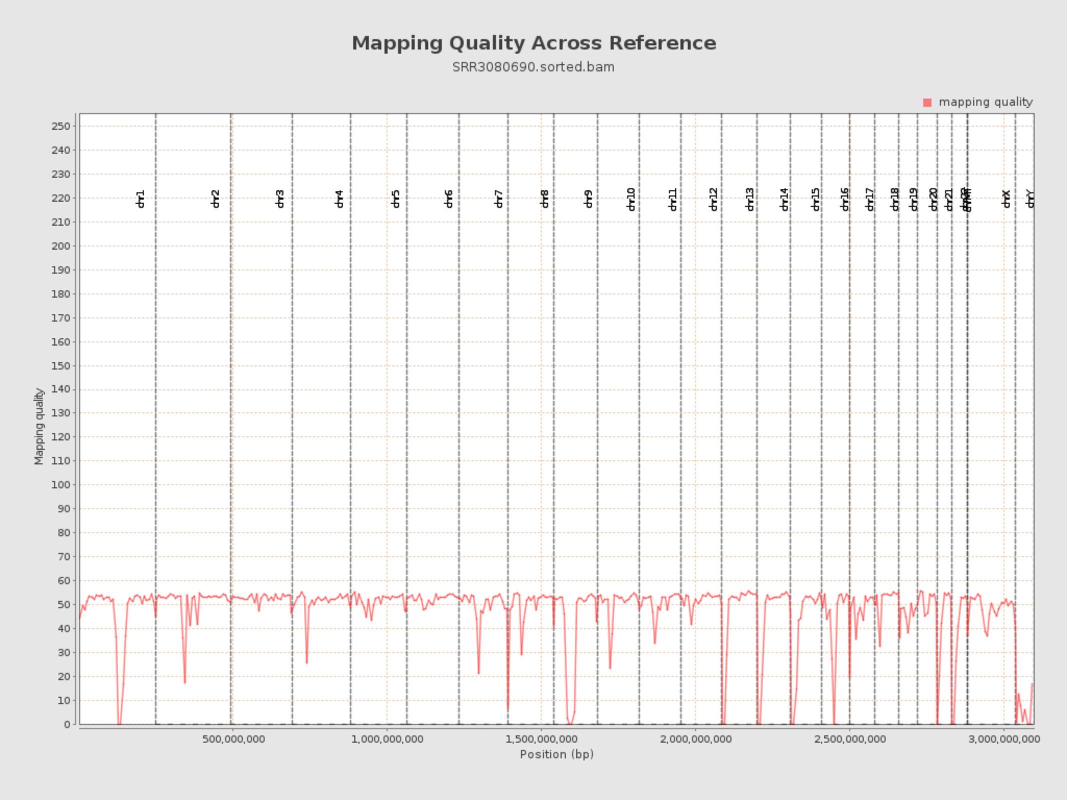
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram