Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 19:41:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080701.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_SRR3080701 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080701.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 19:41:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080701.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,661,024
Mapped reads	2,340,760 / 87.96%
Unmapped reads	320,264 / 12.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,577 / 1.04%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	119,173 / 4.48%
Duplication rate	4.02%
Clipped reads	683,760 / 25.7%

2.2. ACGT Content

Number/percentage of A's	50,750,563 / 30.65%
Number/percentage of C's	30,899,027 / 18.66%
Number/percentage of T's	50,738,681 / 30.64%
Number/percentage of G's	33,183,433 / 20.04%
Number/percentage of N's	2,572 / 0%
GC Percentage	38.7%

2.3. Coverage

Mean	0.0535

Standard Deviation	0.6184

2.4. Mapping Quality

Mean Mapping Quality	47.96

2.5. Mismatches and indels

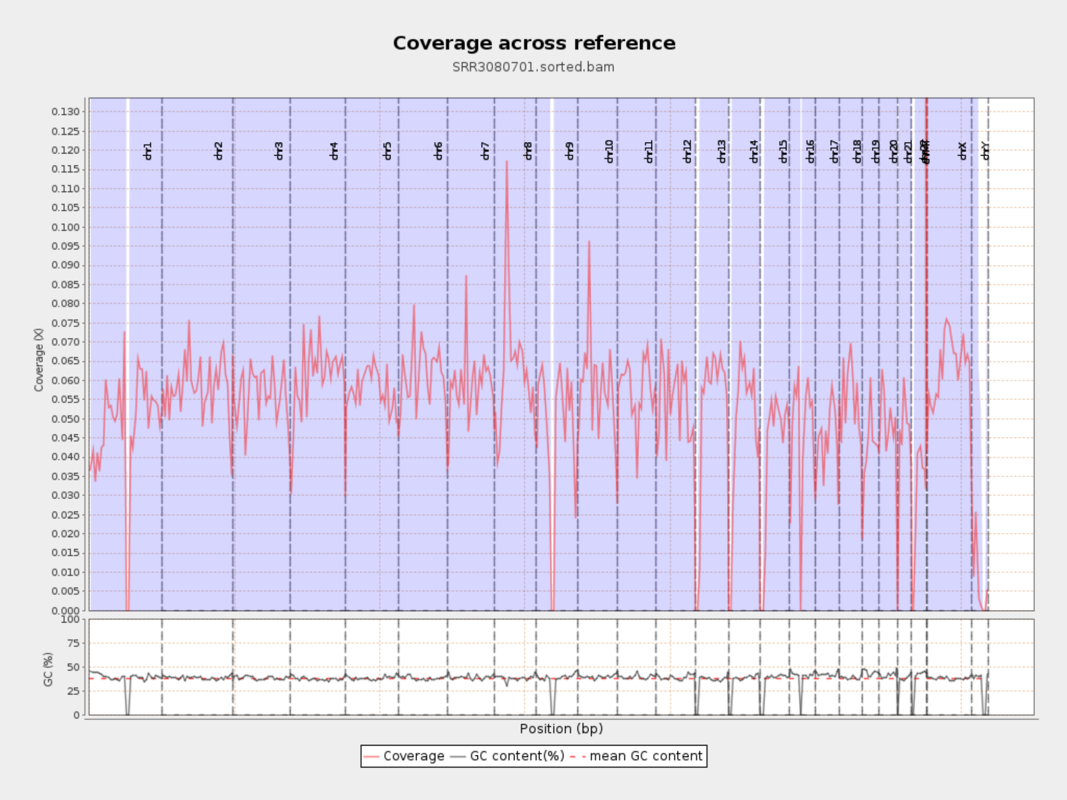
General error rate	0.86%
Mismatches	1,403,846
Insertions	13,223
Mapped reads with at least one insertion	0.56%
Deletions	35,709
Mapped reads with at least one deletion	1.51%
Homopolymer indels	46.2%

2.6. Chromosome stats

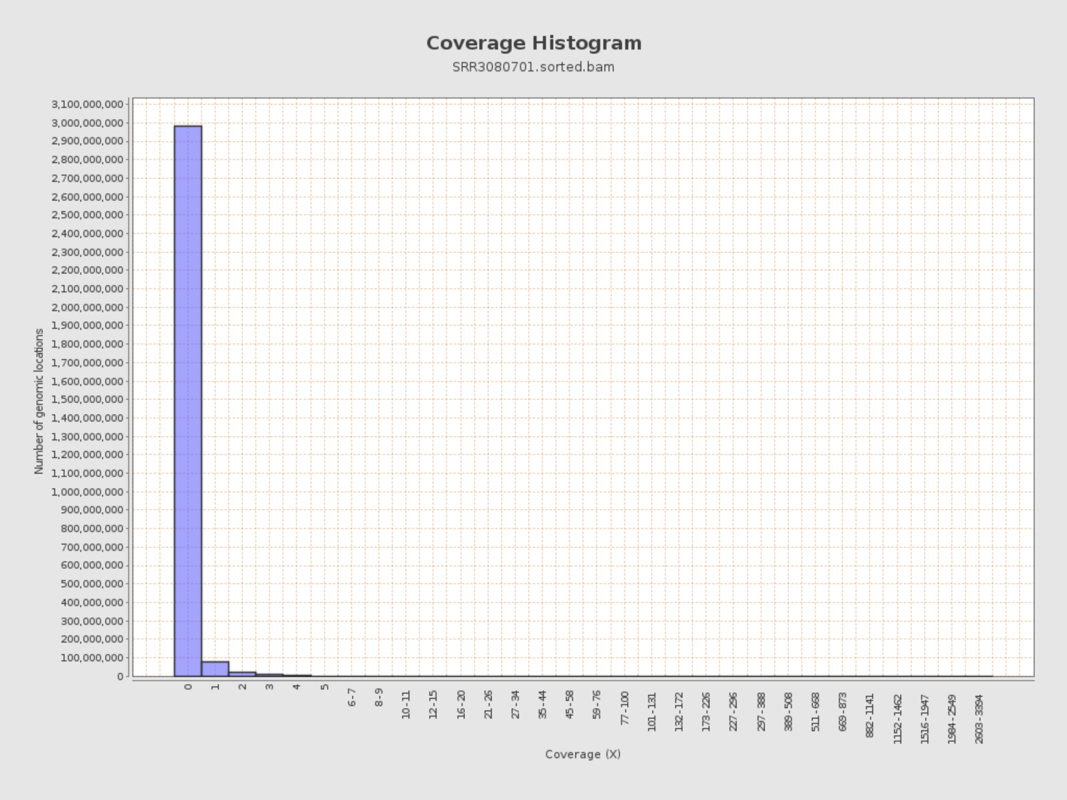
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11941348	0.0479	0.5969
chr2	243199373	14191626	0.0584	0.4232
chr3	198022430	11222299	0.0567	0.3272
chr4	191154276	11703300	0.0612	0.3696
chr5	180915260	10463544	0.0578	0.3322
chr6	171115067	10501299	0.0614	0.3697
chr7	159138663	9455305	0.0594	0.6586

chr8	146364022	9158177	0.0626	2.1017
chr9	141213431	6680790	0.0473	0.389
chr10	135534747	8026997	0.0592	0.4865
chr11	135006516	7744596	0.0574	0.3898
chr12	133851895	7227438	0.054	0.3222
chr13	115169878	5899324	0.0512	0.3114
chr14	107349540	5115017	0.0476	0.3267
chr15	102531392	4172543	0.0407	0.2721
chr16	90354753	4192787	0.0464	0.3211
chr17	81195210	3611623	0.0445	0.3098
chr18	78077248	4326431	0.0554	0.6997
chr19	59128983	2554220	0.0432	0.4636
chr20	63025520	3105834	0.0493	0.3087
chr21	48129895	2111047	0.0439	0.3111
chr22	51304566	1432220	0.0279	0.2199
chrMT	16571	545920	32.9443	18.045
chrX	155270560	9813935	0.0632	0.3568
chrY	59373566	441613	0.0074	0.2118

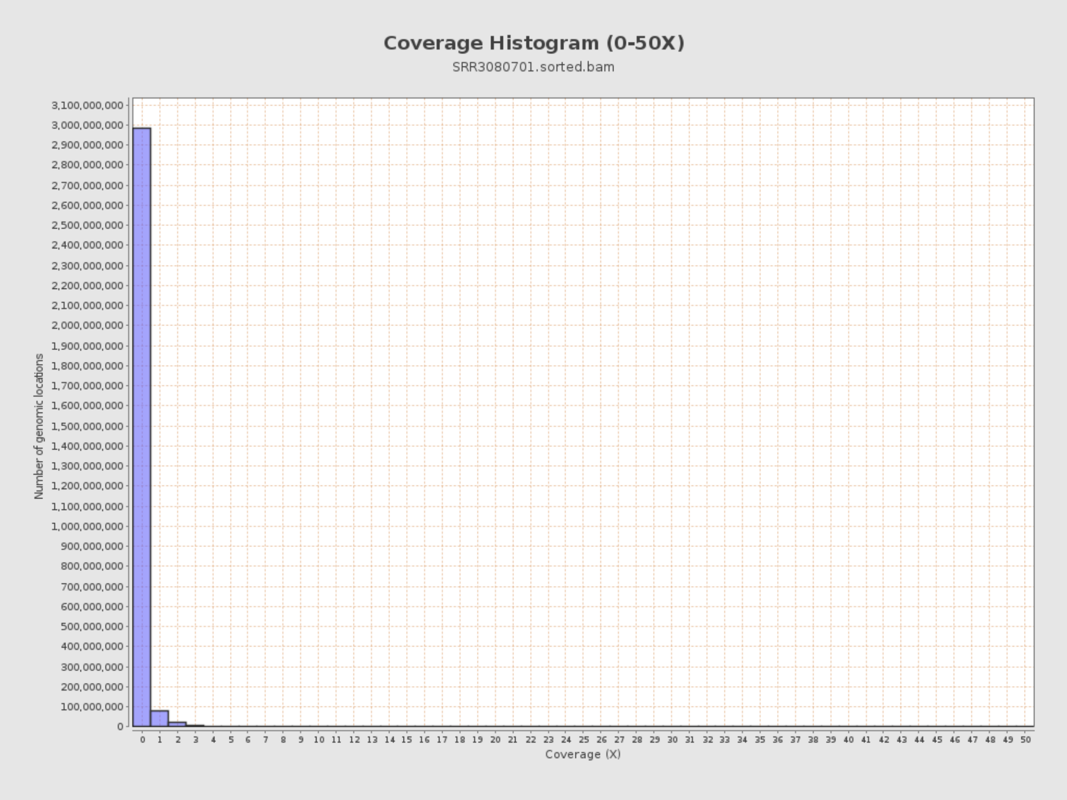
3. Results : Coverage across reference



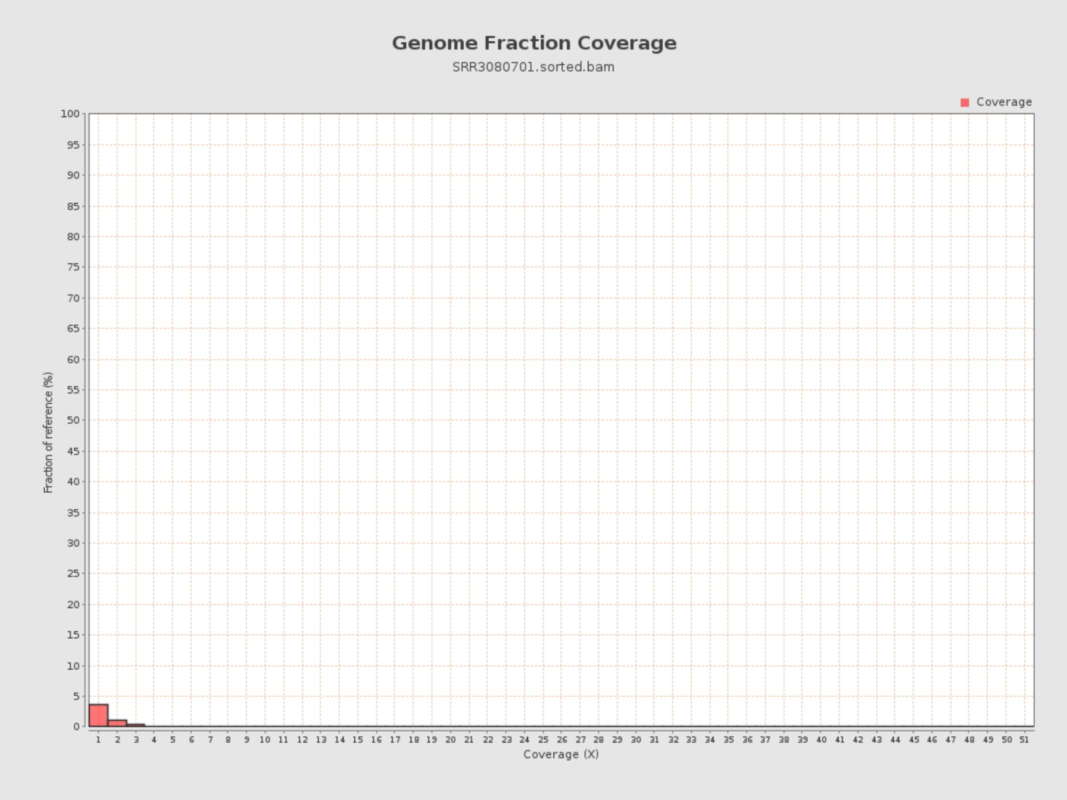
4. Results : Coverage Histogram



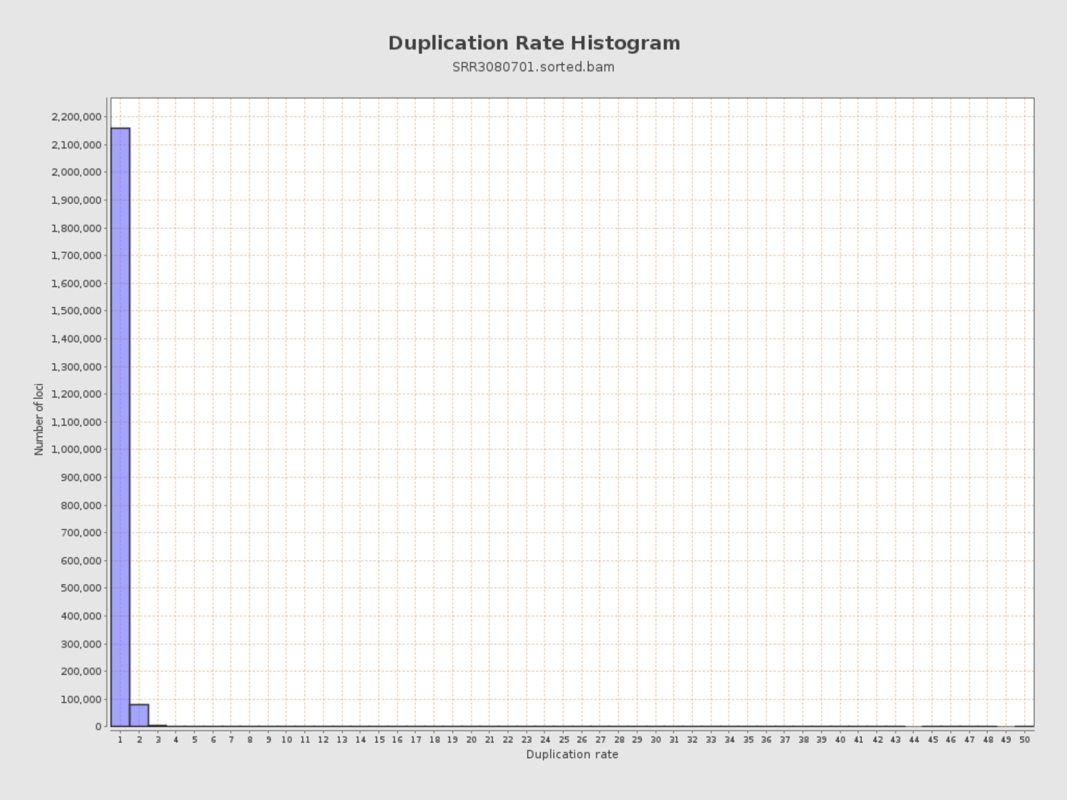
5. Results : Coverage Histogram (0-50X)



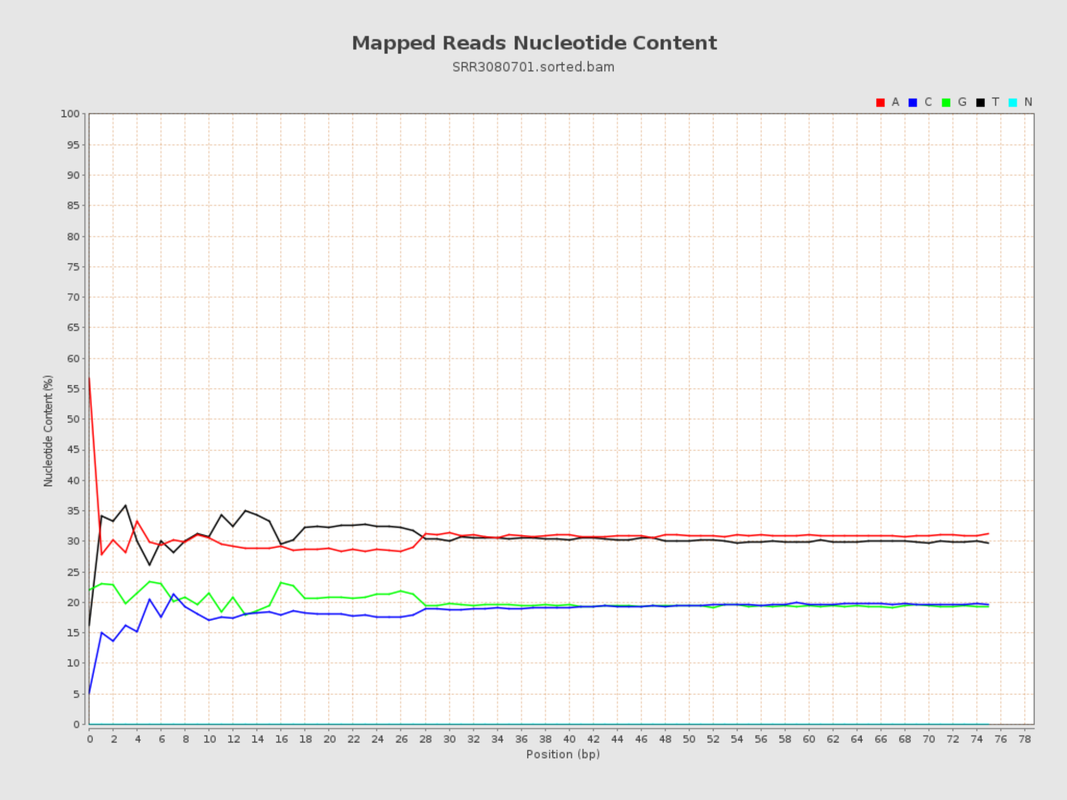
6. Results : Genome Fraction Coverage



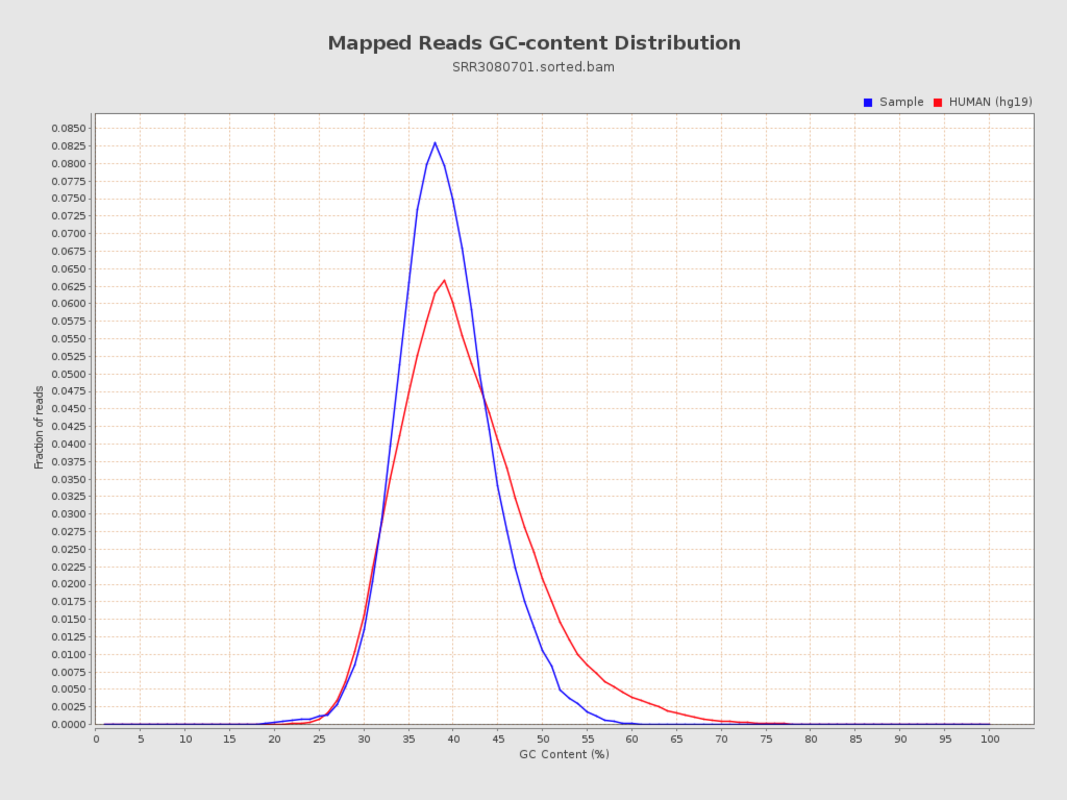
7. Results : Duplication Rate Histogram



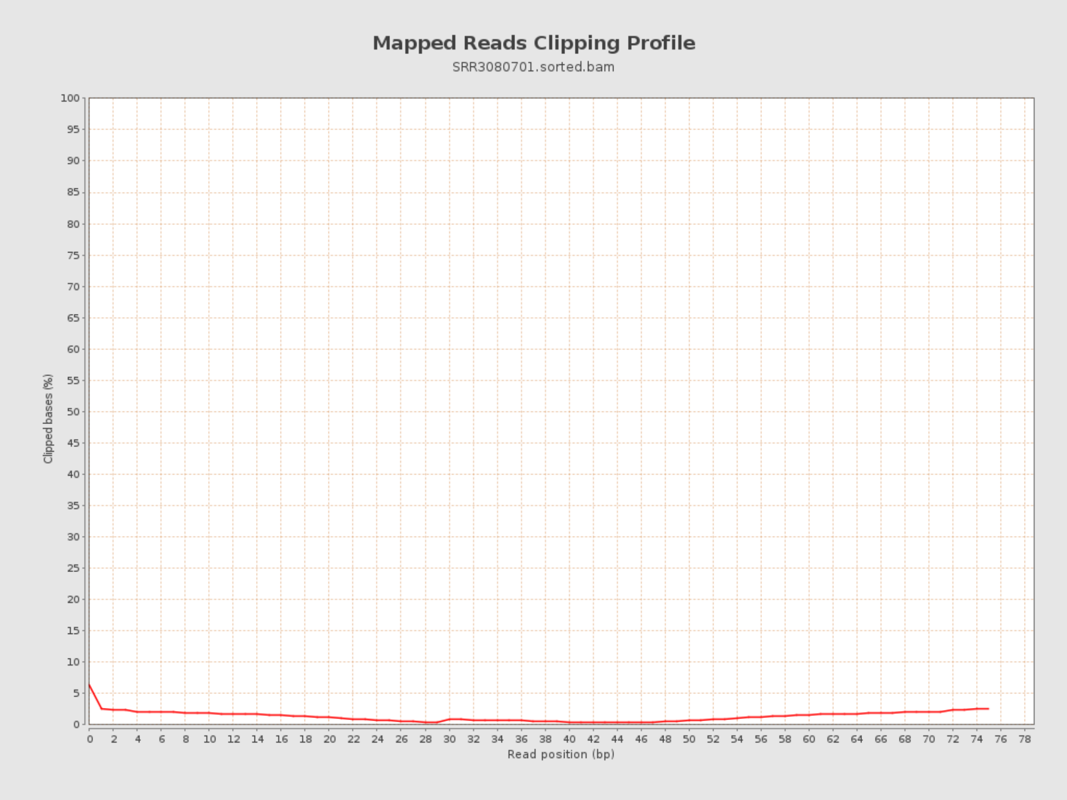
8. Results : Mapped Reads Nucleotide Content



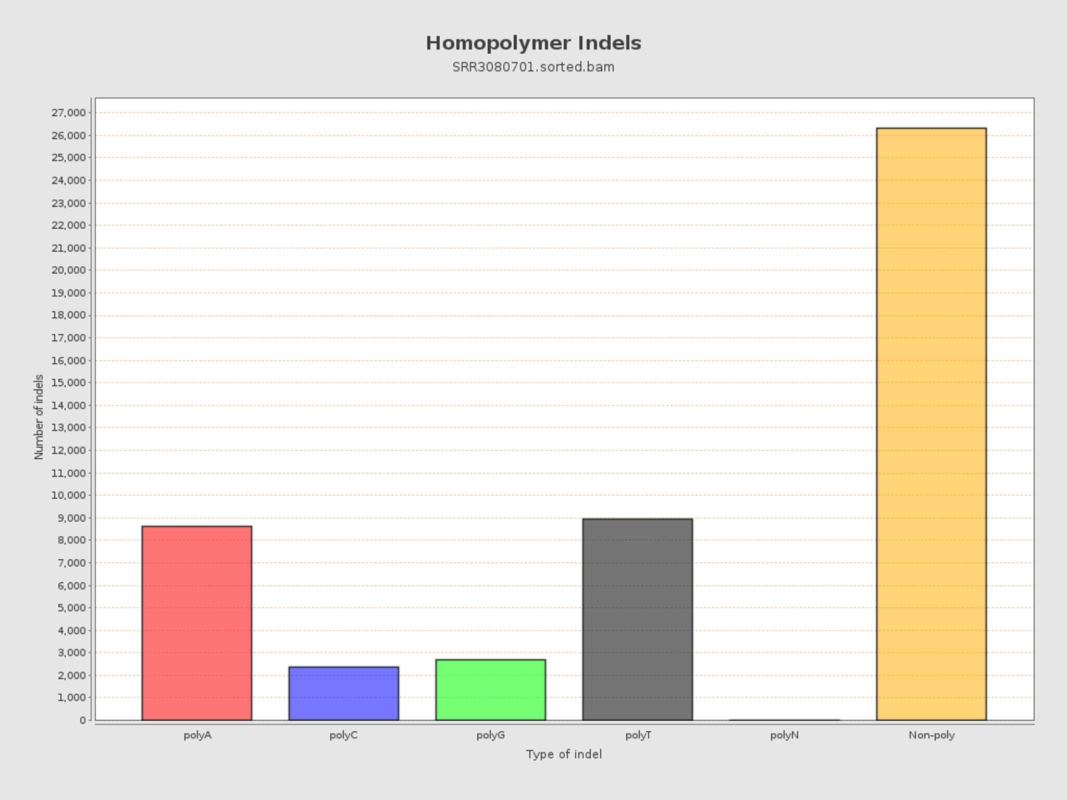
9. Results : Mapped Reads GC-content Distribution



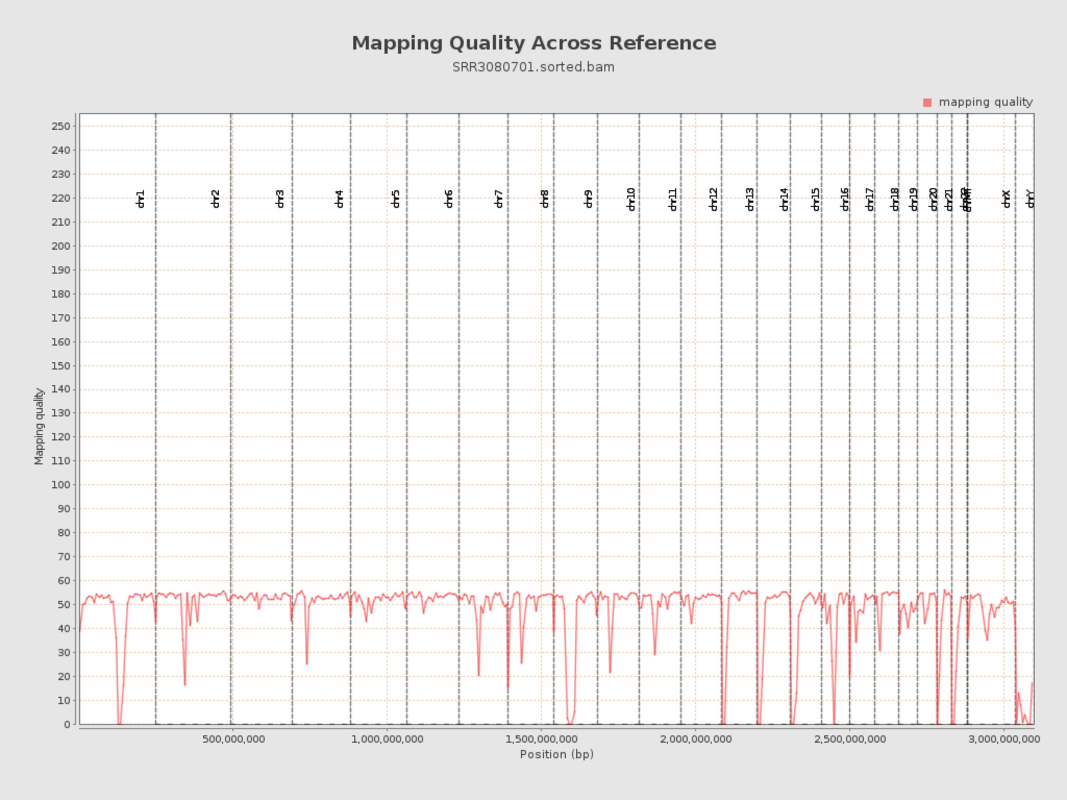
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram