Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:03:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080811.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_SRR3080811 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080811.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:03:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080811.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,044,821
Mapped reads	2,786,869 / 91.53%
Unmapped reads	257,952 / 8.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,999 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	205,820 / 6.76%
Duplication rate	6.15%
Clipped reads	1,108,730 / 36.41%

2.2. ACGT Content

Number/percentage of A's	54,108,711 / 28.55%
Number/percentage of C's	35,245,476 / 18.59%
Number/percentage of T's	59,978,455 / 31.64%
Number/percentage of G's	40,185,082 / 21.2%
Number/percentage of N's	26,322 / 0.01%
GC Percentage	39.8%

2.3. Coverage

Mean	0.0613

Standard Deviation	0.4537

2.4. Mapping Quality

Mean Mapping Quality	46.82

2.5. Mismatches and indels

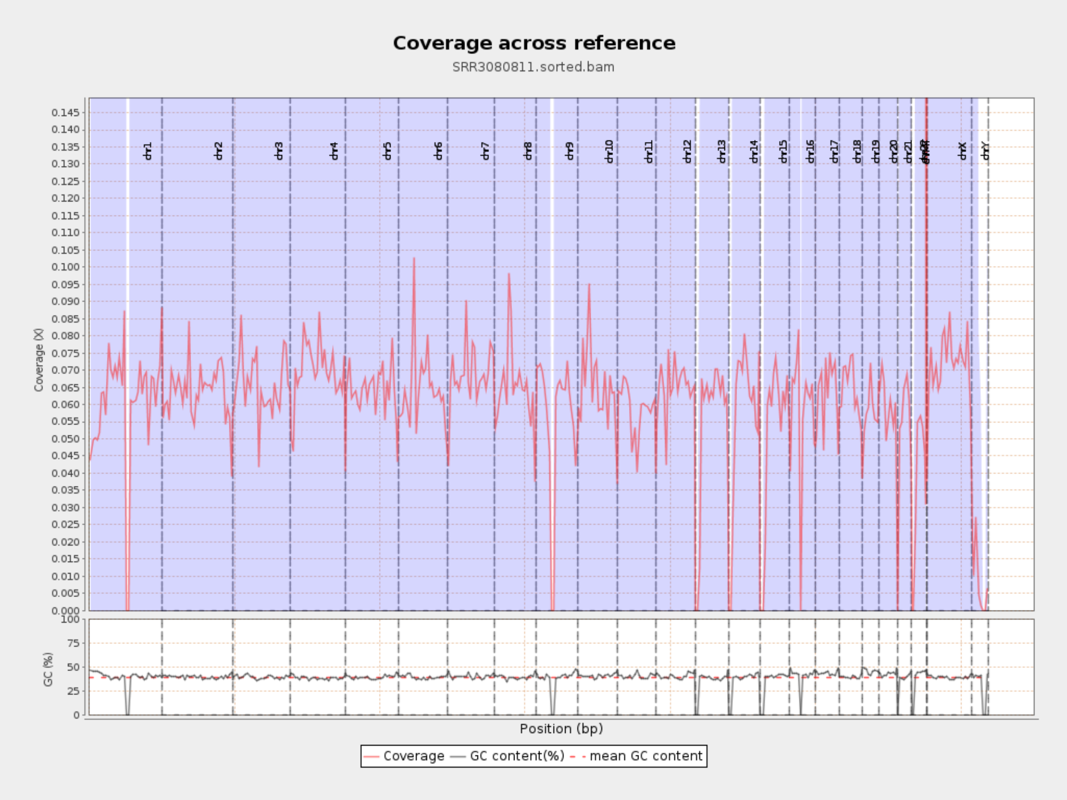
General error rate	0.83%
Mismatches	1,549,430
Insertions	14,074
Mapped reads with at least one insertion	0.5%
Deletions	39,259
Mapped reads with at least one deletion	1.4%
Homopolymer indels	48.82%

2.6. Chromosome stats

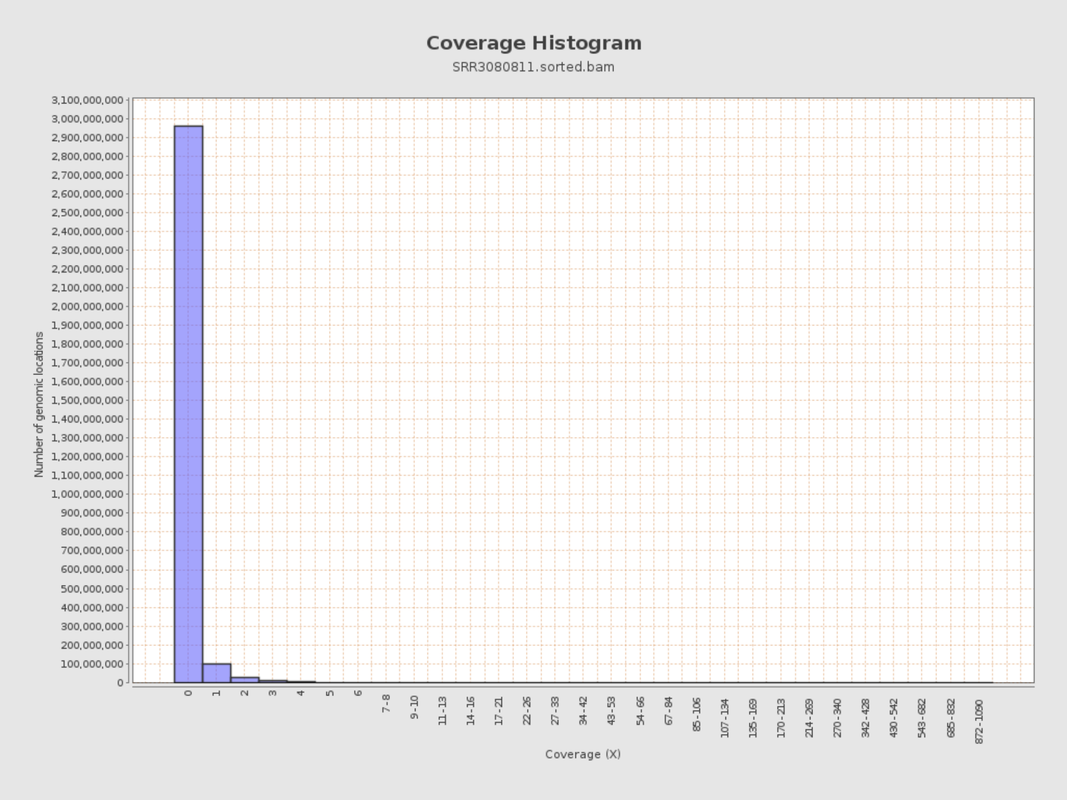
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14945482	0.06	0.6989
chr2	243199373	15544994	0.0639	0.4888
chr3	198022430	13043016	0.0659	0.3355
chr4	191154276	13336673	0.0698	0.3652
chr5	180915260	11645265	0.0644	0.3318
chr6	171115067	11049131	0.0646	0.4368
chr7	159138663	11002251	0.0691	0.5341

chr8	146364022	9478738	0.0648	0.7243
chr9	141213431	7844409	0.0556	0.4035
chr10	135534747	8907718	0.0657	0.4434
chr11	135006516	7864723	0.0583	0.3558
chr12	133851895	8725806	0.0652	0.3392
chr13	115169878	6194039	0.0538	0.3038
chr14	107349540	5944097	0.0554	0.3226
chr15	102531392	5211215	0.0508	0.2946
chr16	90354753	5246795	0.0581	0.3497
chr17	81195210	5133109	0.0632	0.3365
chr18	78077248	5073765	0.065	0.748
chr19	59128983	3438598	0.0582	0.5059
chr20	63025520	3724554	0.0591	0.3266
chr21	48129895	2552547	0.053	0.32
chr22	51304566	1862905	0.0363	0.2472
chrMT	16571	239472	14.4513	7.8842
chrX	155270560	11118144	0.0716	0.3663
chrY	59373566	486042	0.0082	0.2045

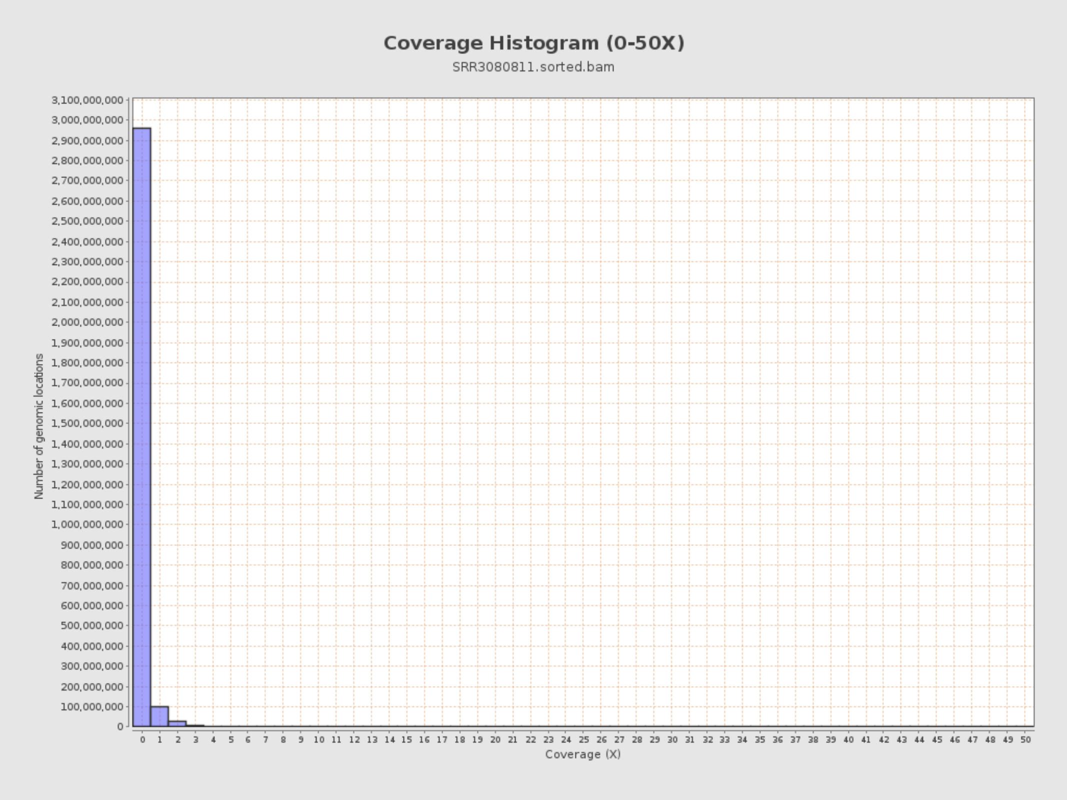
3. Results : Coverage across reference



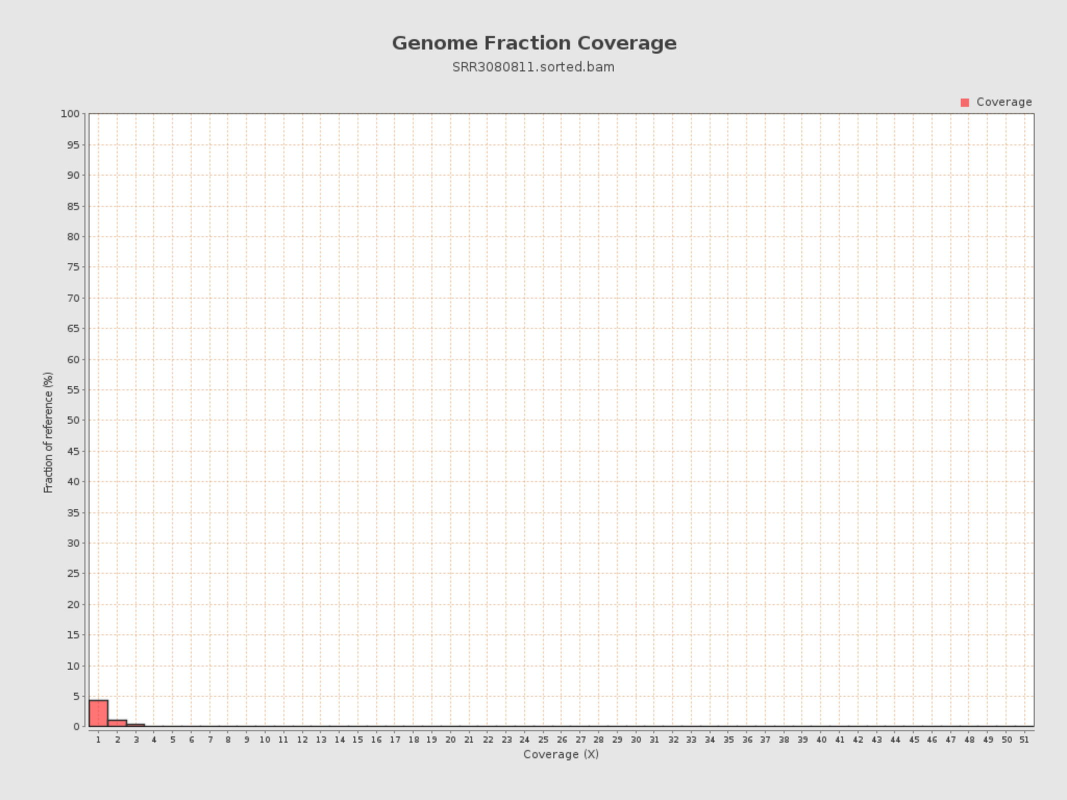
4. Results : Coverage Histogram



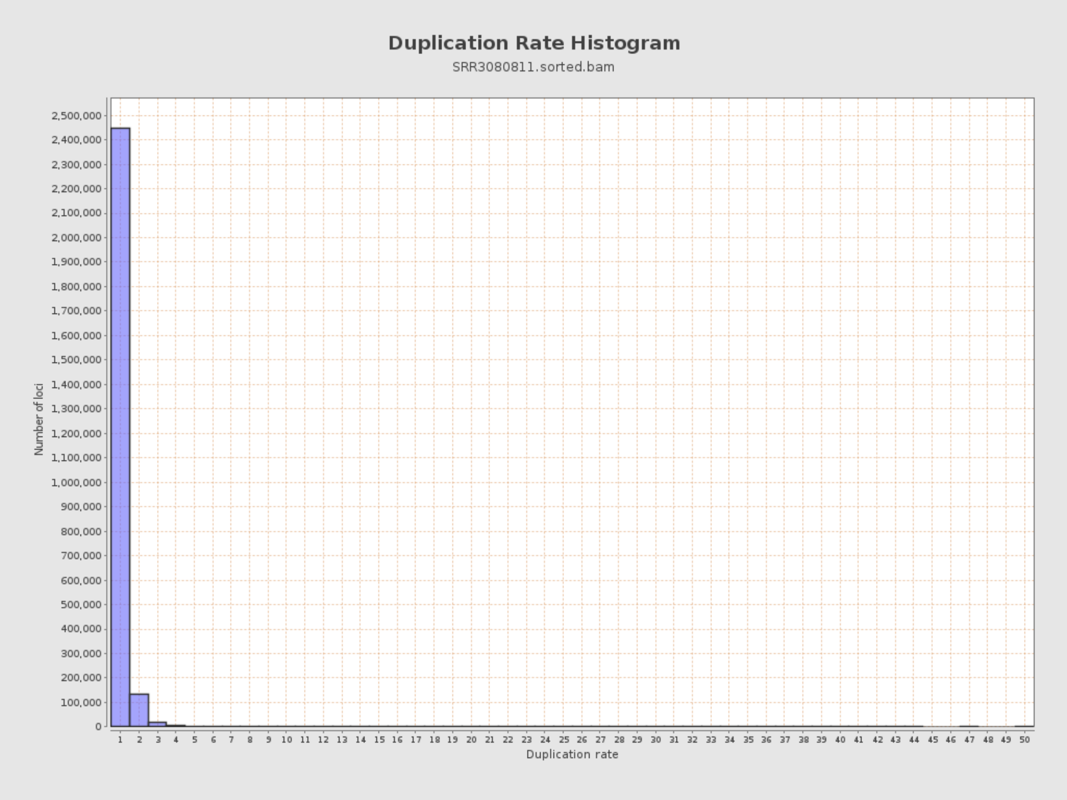
5. Results : Coverage Histogram (0-50X)



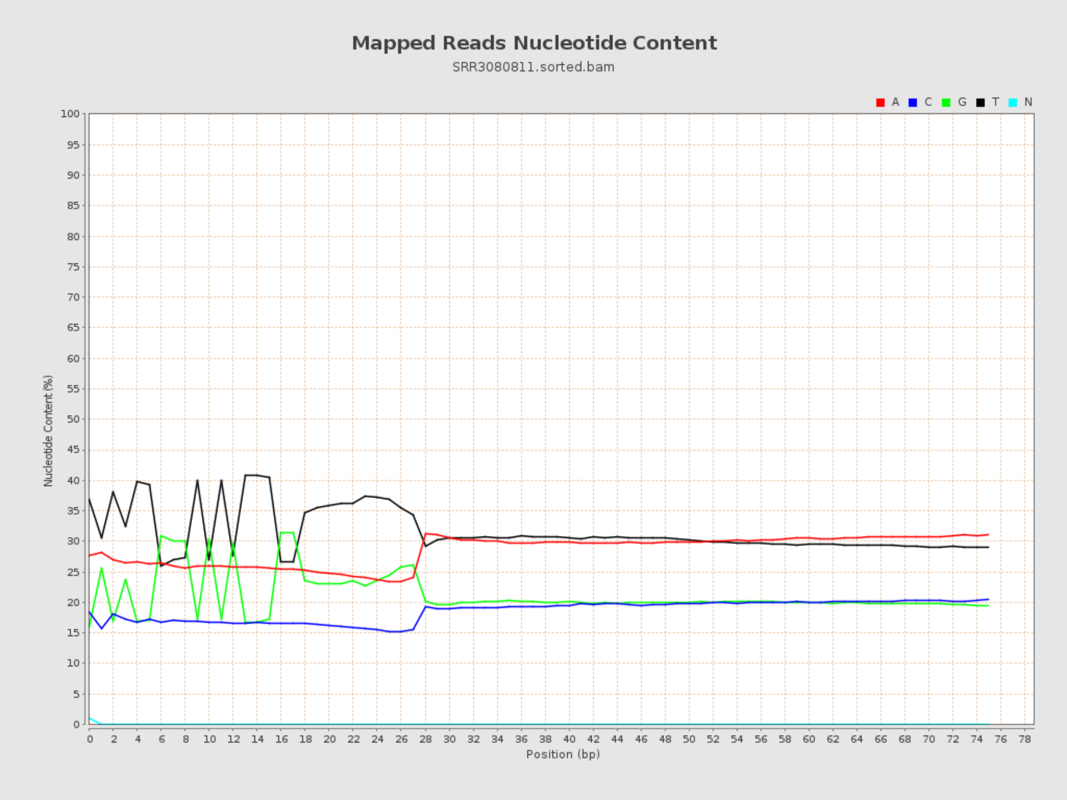
6. Results : Genome Fraction Coverage



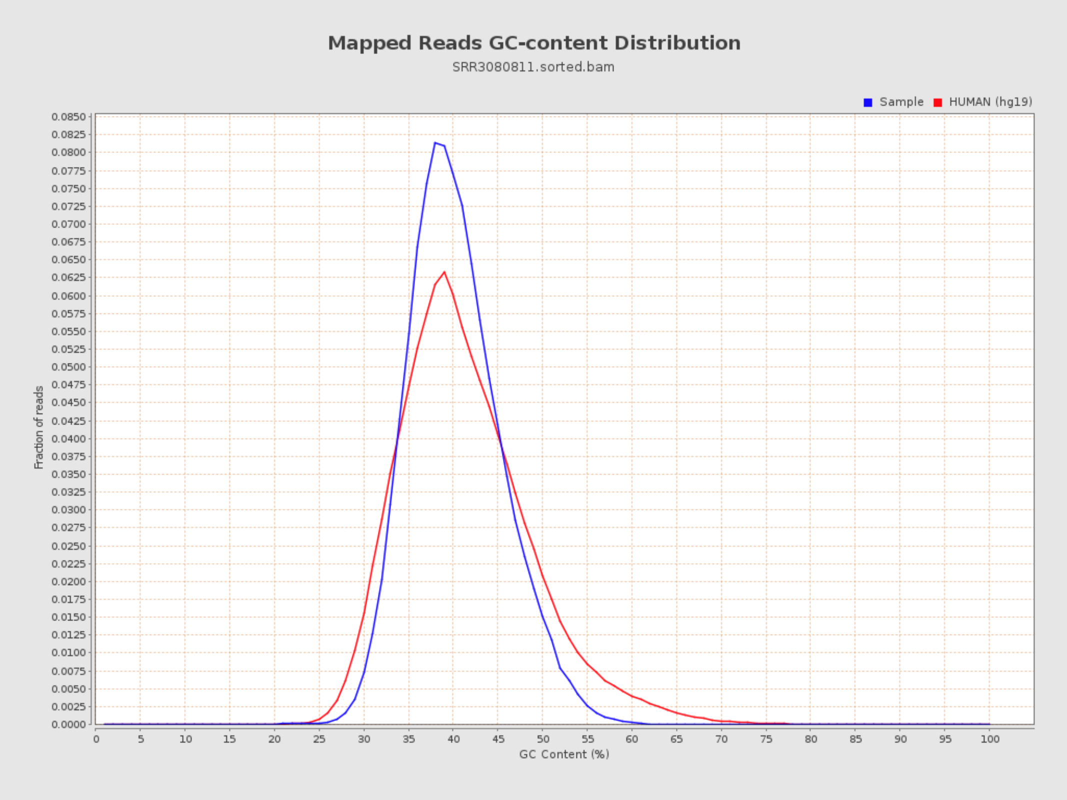
7. Results : Duplication Rate Histogram



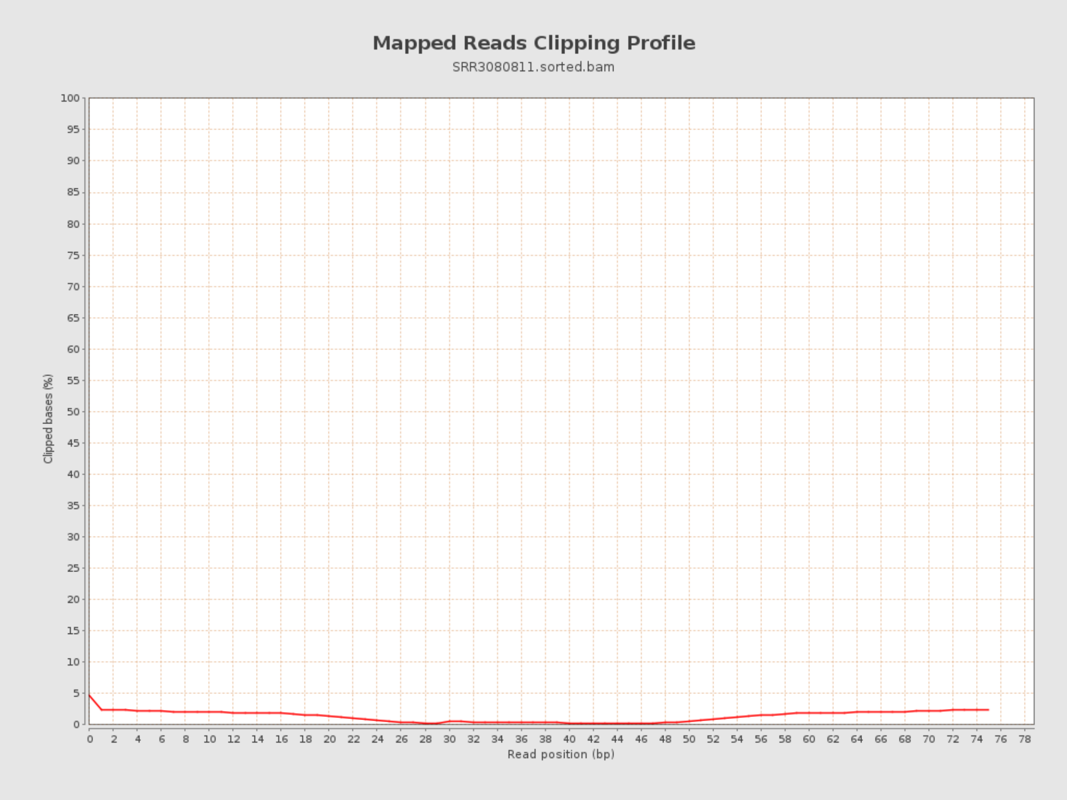
8. Results : Mapped Reads Nucleotide Content



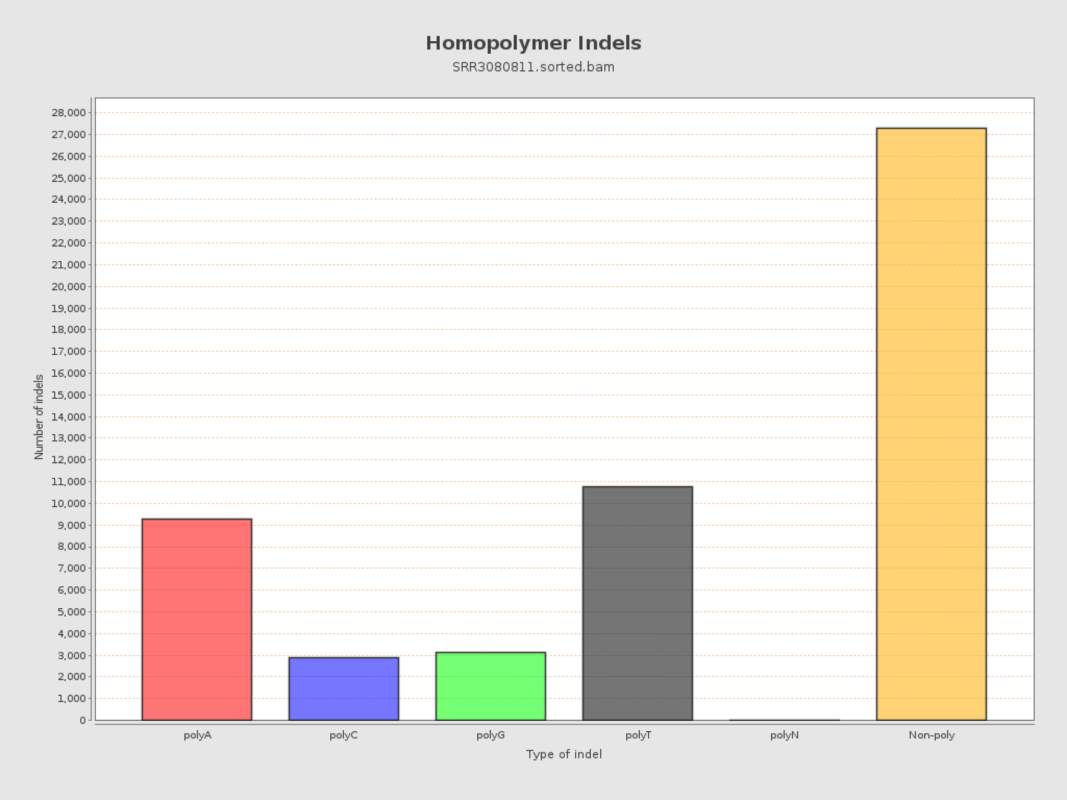
9. Results : Mapped Reads GC-content Distribution



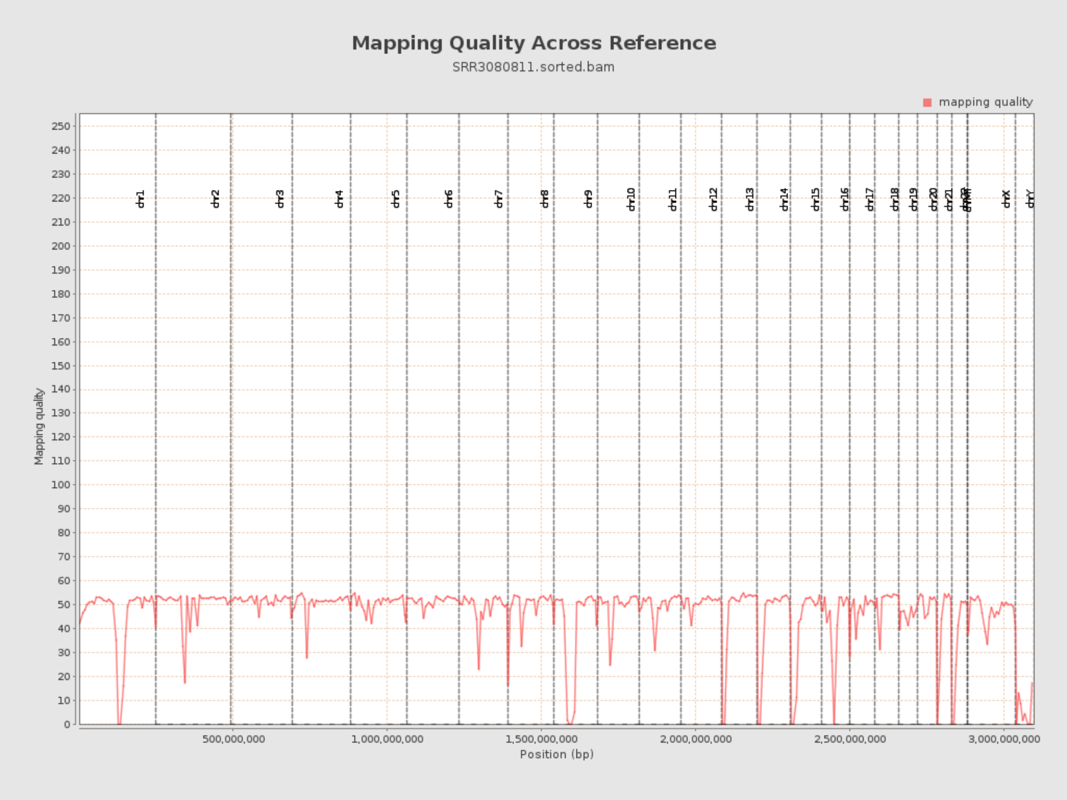
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram