Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 06:19:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080770.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_SRR3080770 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080770.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 06:19:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080770.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,278,308
Mapped reads	3,128,569 / 73.13%
Unmapped reads	1,149,739 / 26.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,793 / 0.58%
Read min/max/mean length	30 / 66 / 66.19
Duplicated reads (estimated)	351,920 / 8.23%
Duplication rate	8.92%
Clipped reads	458,361 / 10.71%

2.2. ACGT Content

Number/percentage of A's	60,843,054 / 30.41%
Number/percentage of C's	40,516,273 / 20.25%
Number/percentage of T's	53,628,503 / 26.81%
Number/percentage of G's	44,996,801 / 22.49%
Number/percentage of N's	64,009 / 0.03%
GC Percentage	42.75%

2.3. Coverage

Mean	0.0646

Standard Deviation	0.4067

2.4. Mapping Quality

Mean Mapping Quality	44.92

2.5. Mismatches and indels

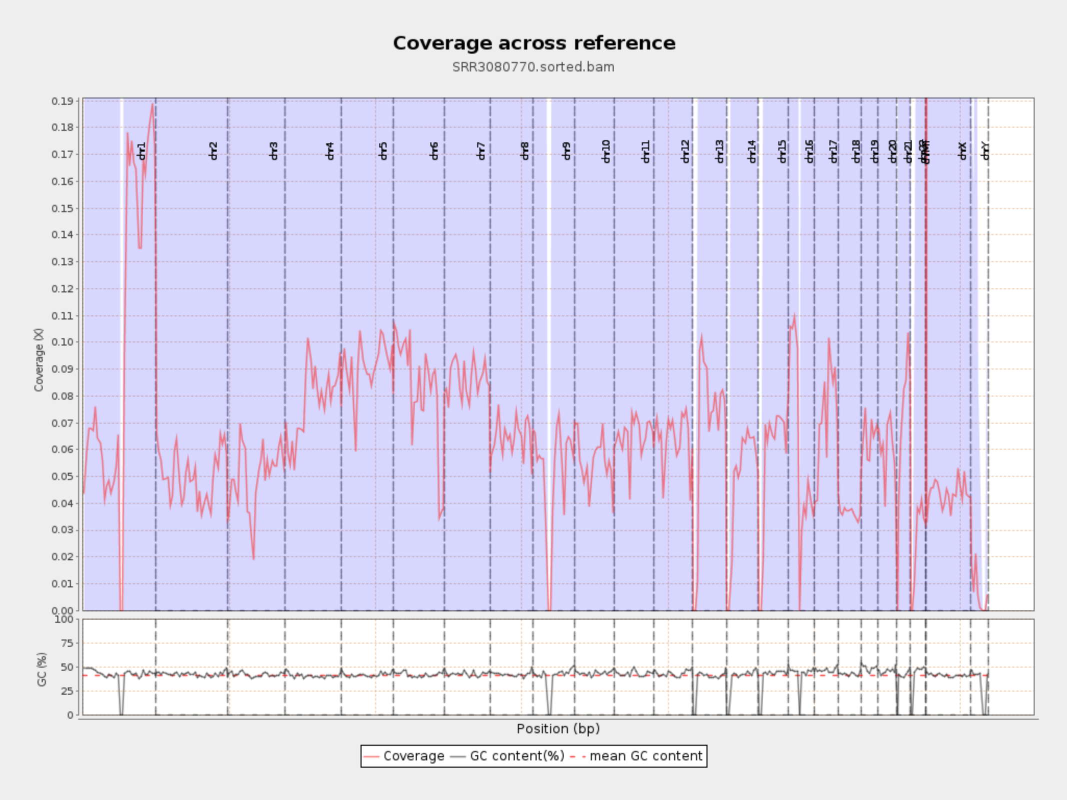
General error rate	0.75%
Mismatches	1,486,234
Insertions	13,147
Mapped reads with at least one insertion	0.42%
Deletions	35,153
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.99%

2.6. Chromosome stats

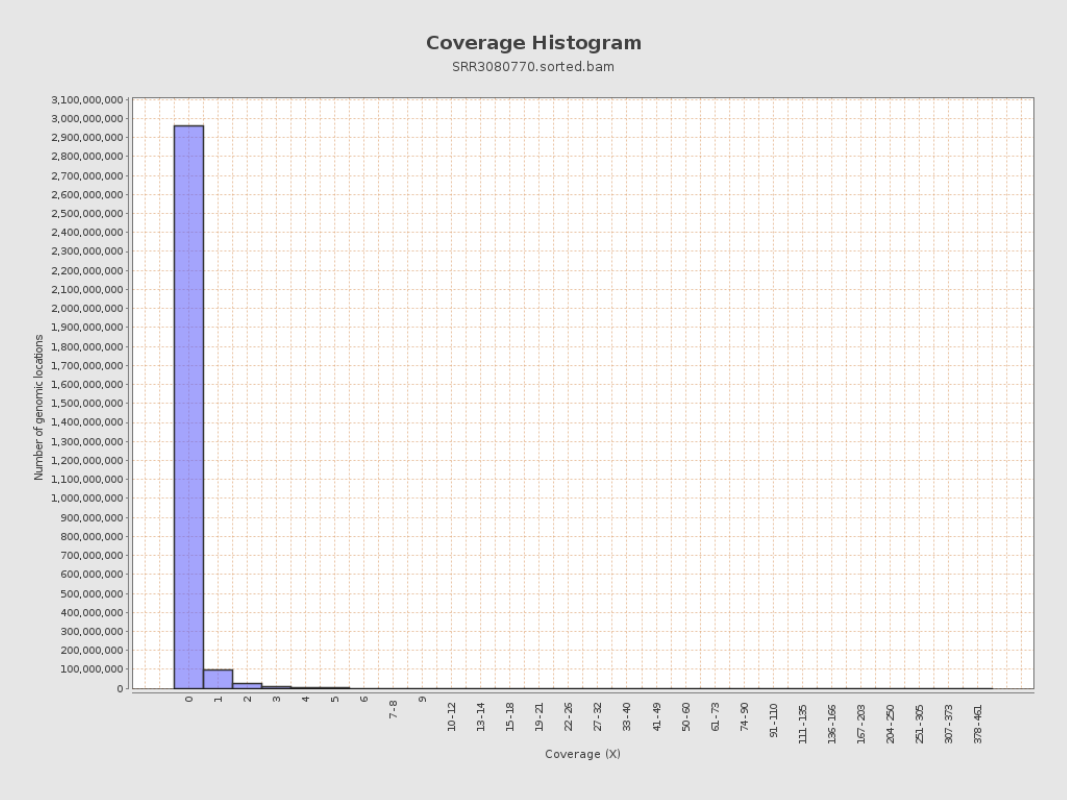
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24827014	0.0996	0.5896
chr2	243199373	12199265	0.0502	0.3393
chr3	198022430	9827726	0.0496	0.3098
chr4	191154276	14851560	0.0777	0.405
chr5	180915260	16461517	0.091	0.4298
chr6	171115067	14237771	0.0832	0.4984
chr7	159138663	13756991	0.0864	0.5086

chr8	146364022	9491126	0.0648	0.4614
chr9	141213431	7131528	0.0505	0.3304
chr10	135534747	7532373	0.0556	0.3648
chr11	135006516	8772719	0.065	0.3883
chr12	133851895	8626533	0.0644	0.3585
chr13	115169878	7855750	0.0682	0.373
chr14	107349540	5256773	0.049	0.3261
chr15	102531392	5601721	0.0546	0.3317
chr16	90354753	5398354	0.0597	0.3561
chr17	81195210	5947684	0.0733	0.3995
chr18	78077248	2854075	0.0366	0.349
chr19	59128983	3829093	0.0648	0.5905
chr20	63025520	3773947	0.0599	0.3539
chr21	48129895	3327924	0.0691	0.3981
chr22	51304566	1306433	0.0255	0.2225
chrMT	16571	47280	2.8532	3.0992
chrX	155270560	6797271	0.0438	0.2971
chrY	59373566	400224	0.0067	0.1504

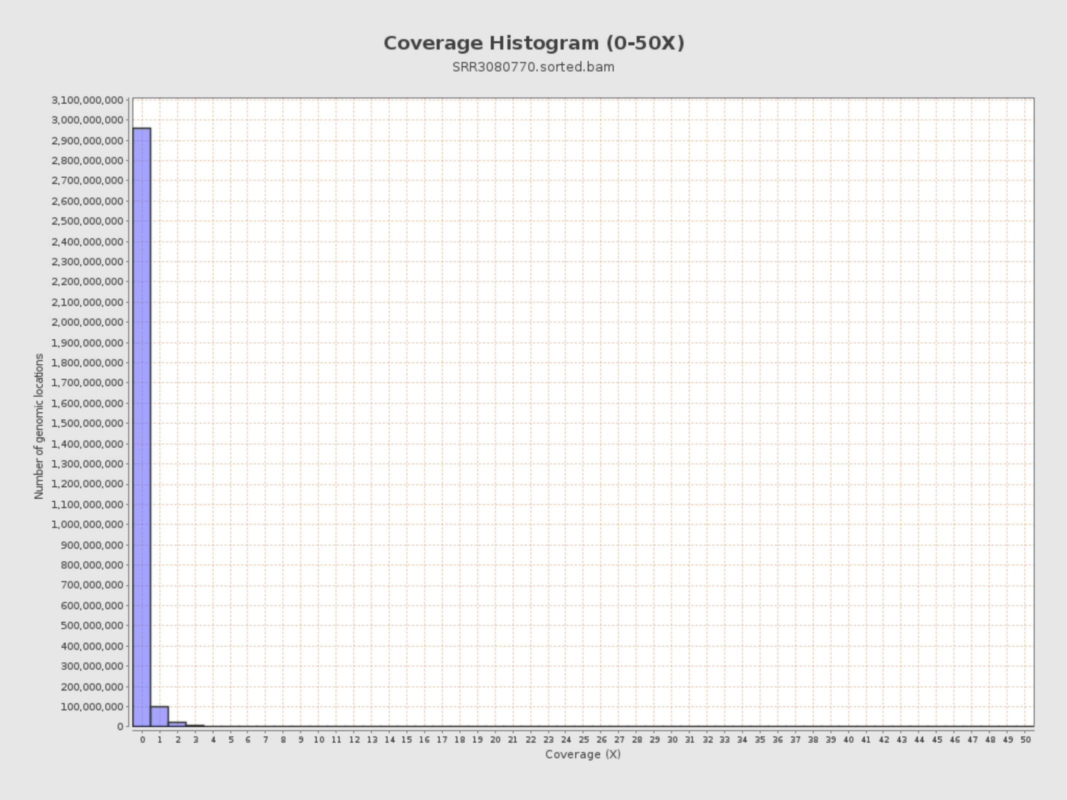
3. Results : Coverage across reference



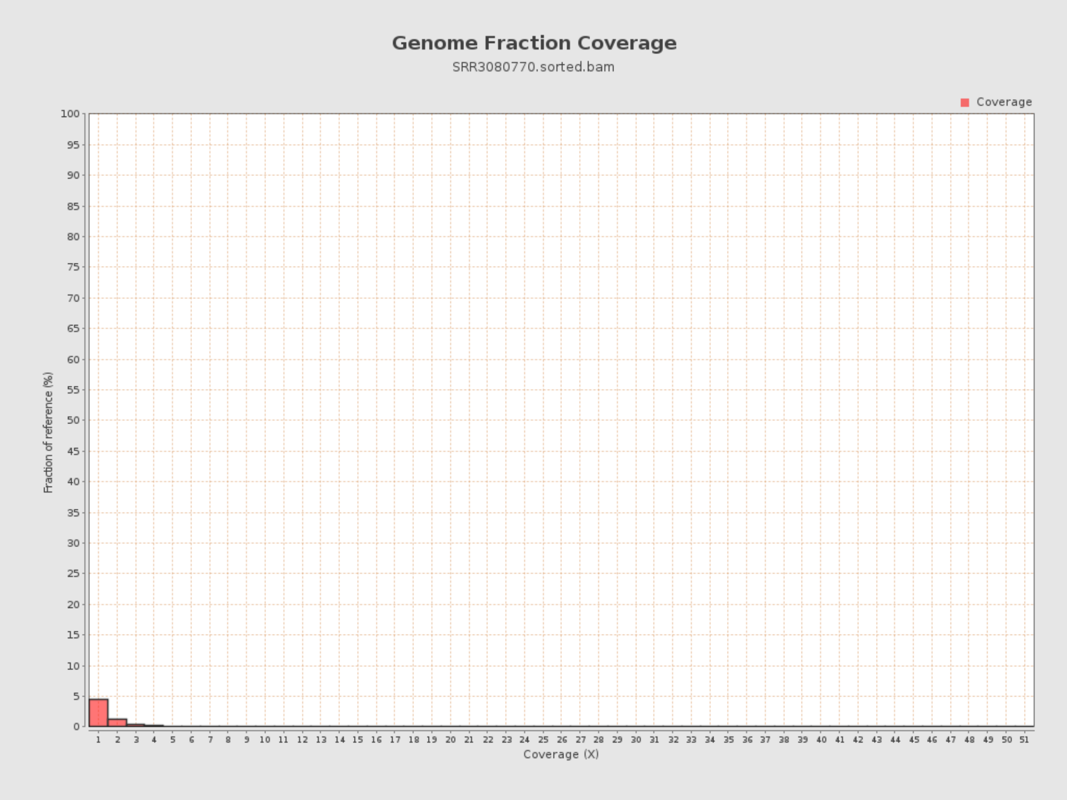
4. Results : Coverage Histogram



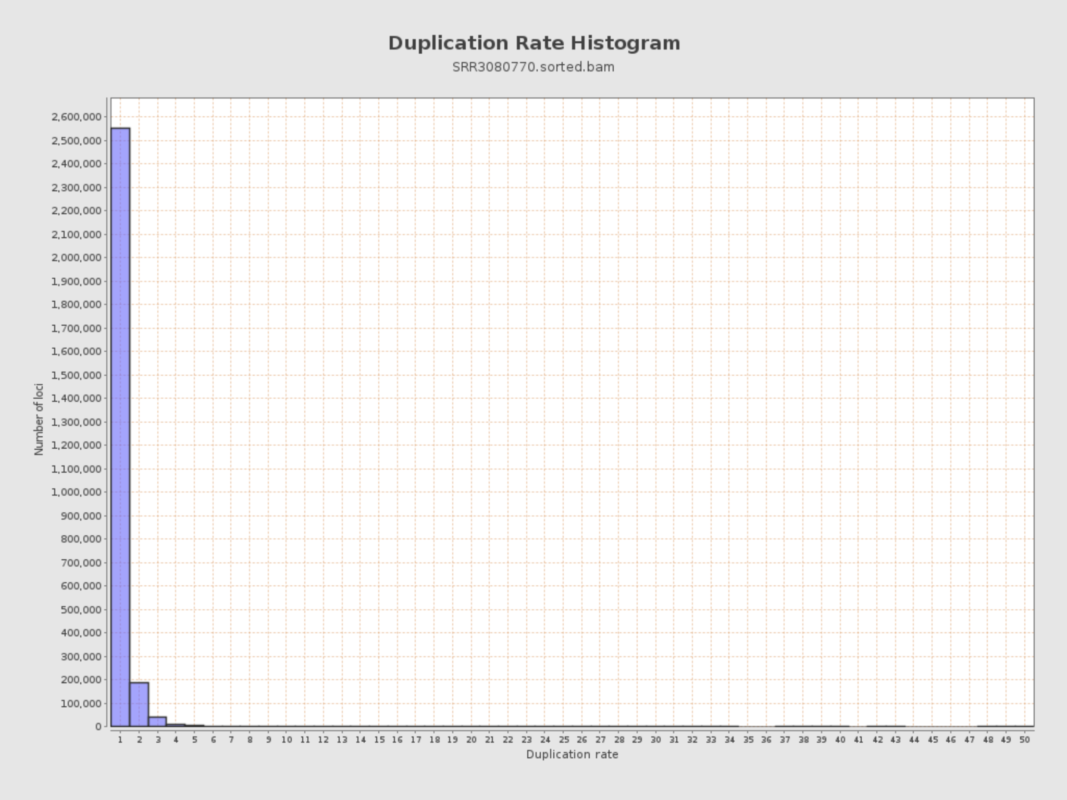
5. Results : Coverage Histogram (0-50X)



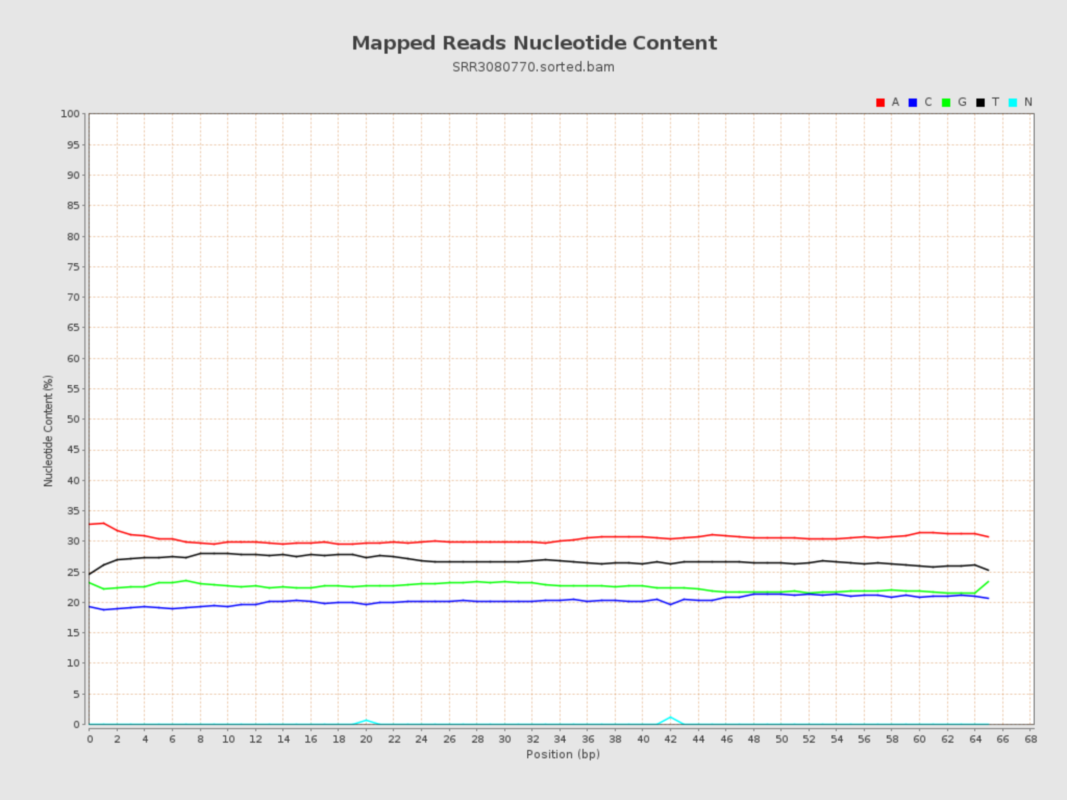
6. Results : Genome Fraction Coverage



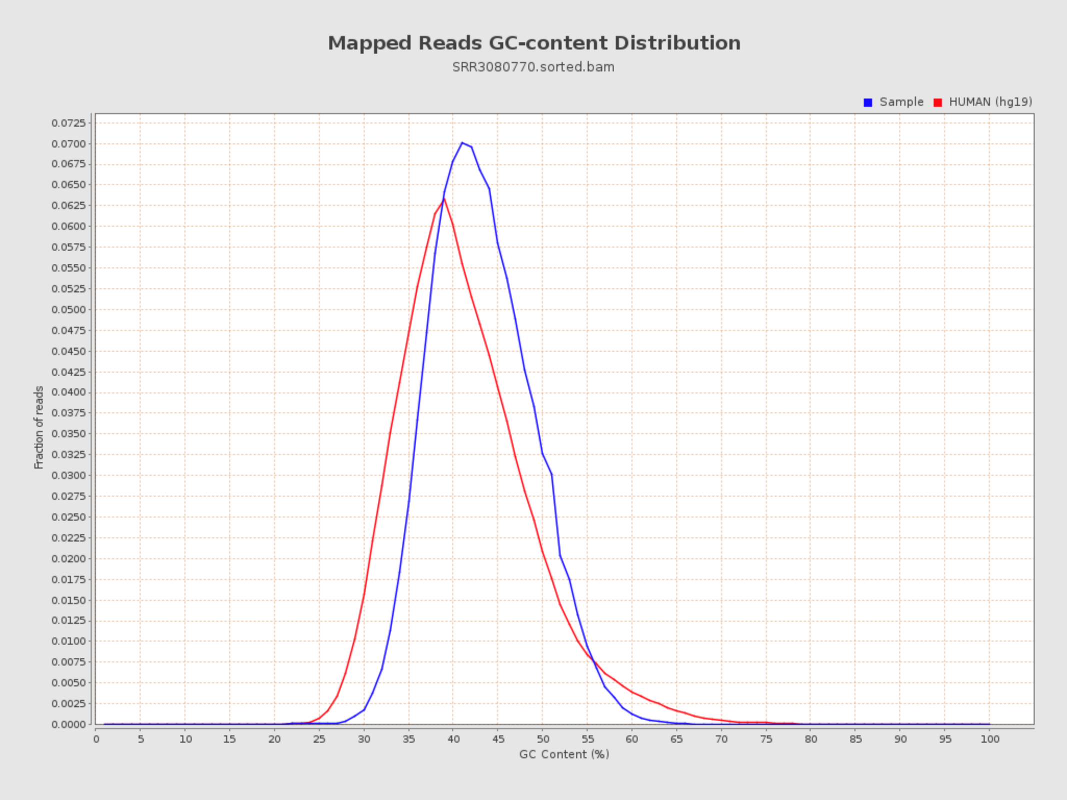
7. Results : Duplication Rate Histogram



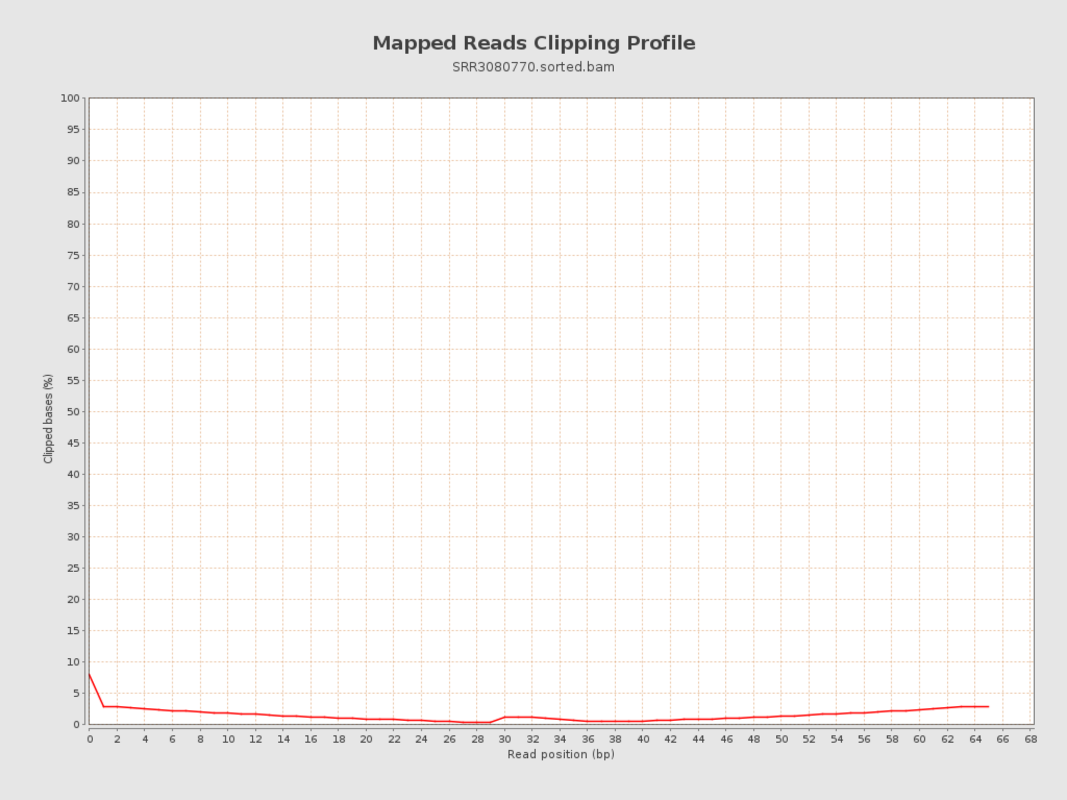
8. Results : Mapped Reads Nucleotide Content



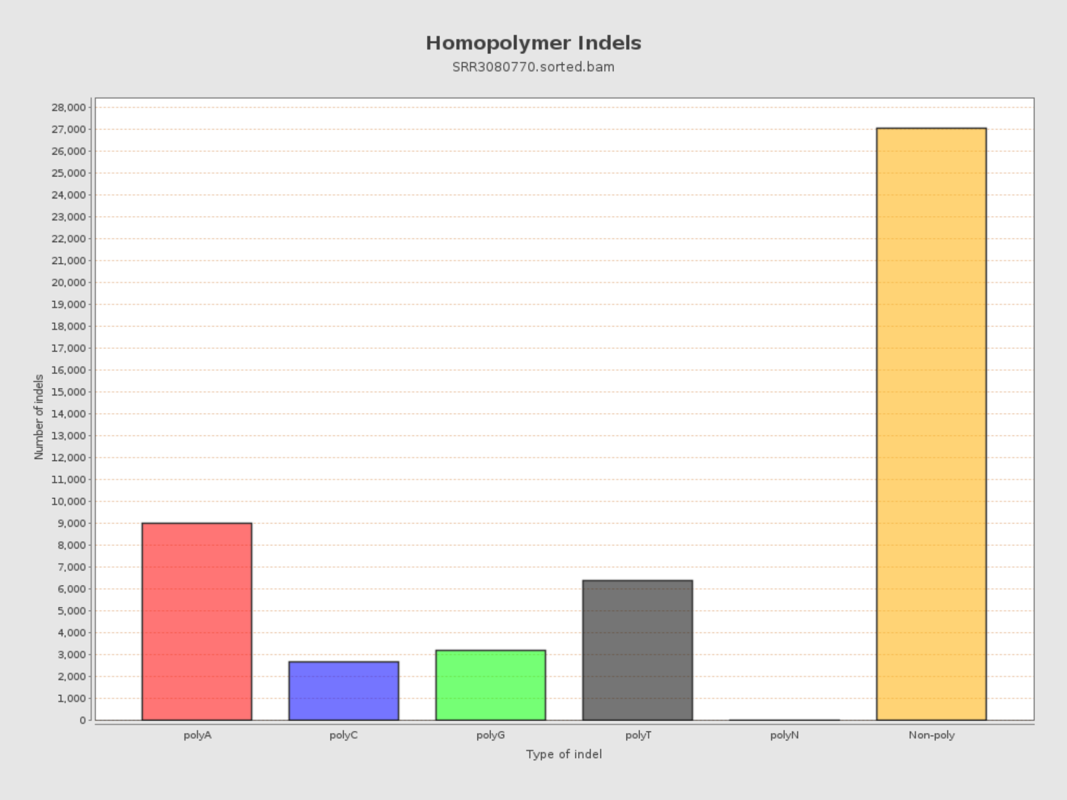
9. Results : Mapped Reads GC-content Distribution



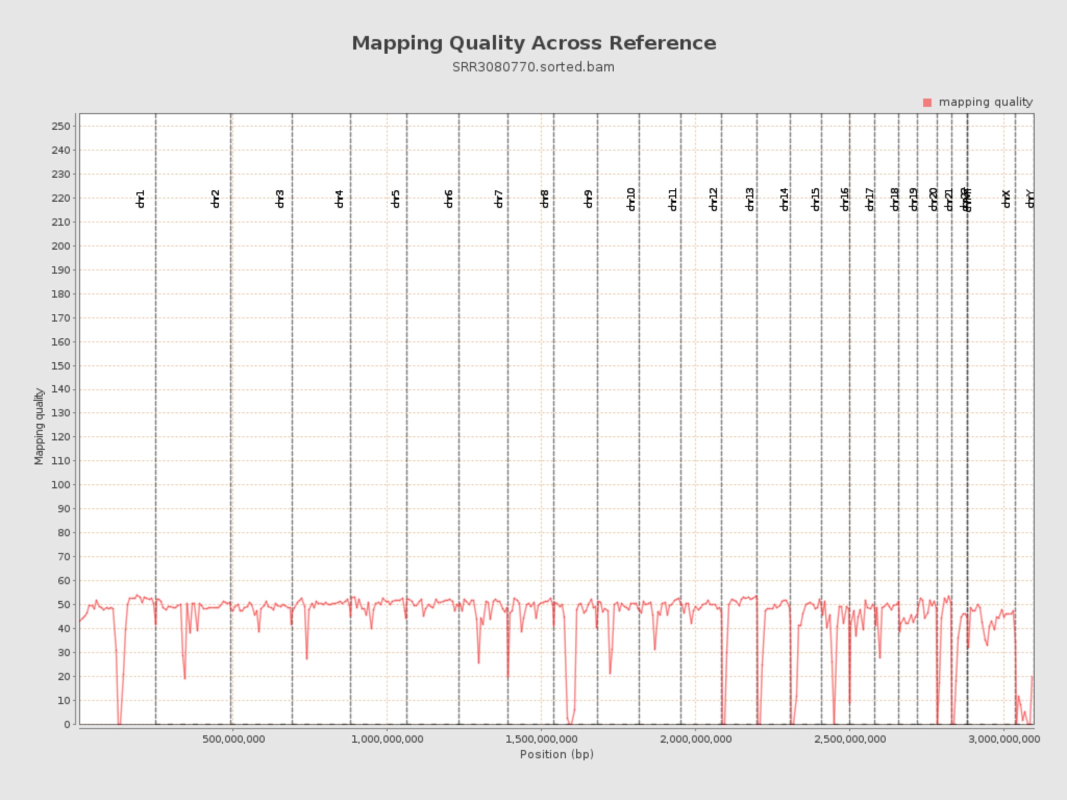
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram