Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 12:03:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080663.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_SRR3080663 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080663.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 12:03:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080663.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,391,622
Mapped reads	1,270,099 / 91.27%
Unmapped reads	121,523 / 8.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,989 / 0.93%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	48,929 / 3.52%
Duplication rate	2.95%
Clipped reads	555,100 / 39.89%

2.2. ACGT Content

Number/percentage of A's	23,293,906 / 27.43%
Number/percentage of C's	15,822,030 / 18.63%
Number/percentage of T's	26,738,186 / 31.48%
Number/percentage of G's	19,072,287 / 22.46%
Number/percentage of N's	3,627 / 0%
GC Percentage	41.09%

2.3. Coverage

Mean	0.0274

Standard Deviation	0.3036

2.4. Mapping Quality

Mean Mapping Quality	45.36

2.5. Mismatches and indels

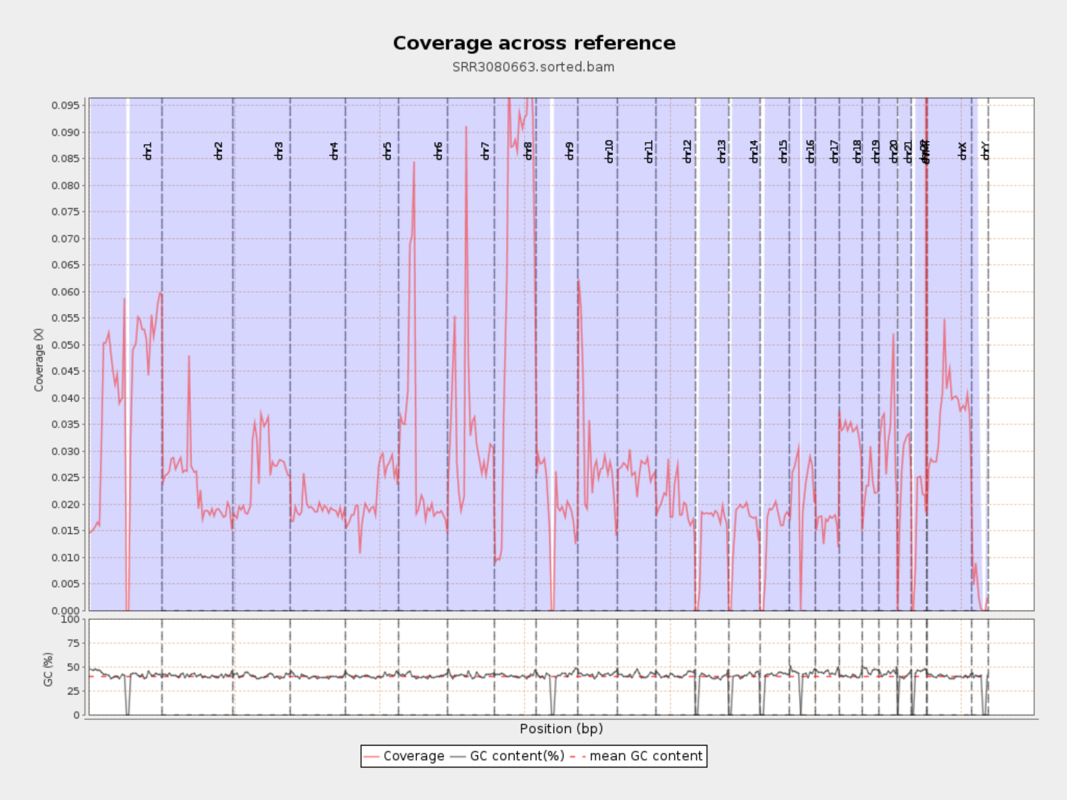
General error rate	0.71%
Mismatches	590,614
Insertions	6,552
Mapped reads with at least one insertion	0.51%
Deletions	19,292
Mapped reads with at least one deletion	1.5%
Homopolymer indels	47.38%

2.6. Chromosome stats

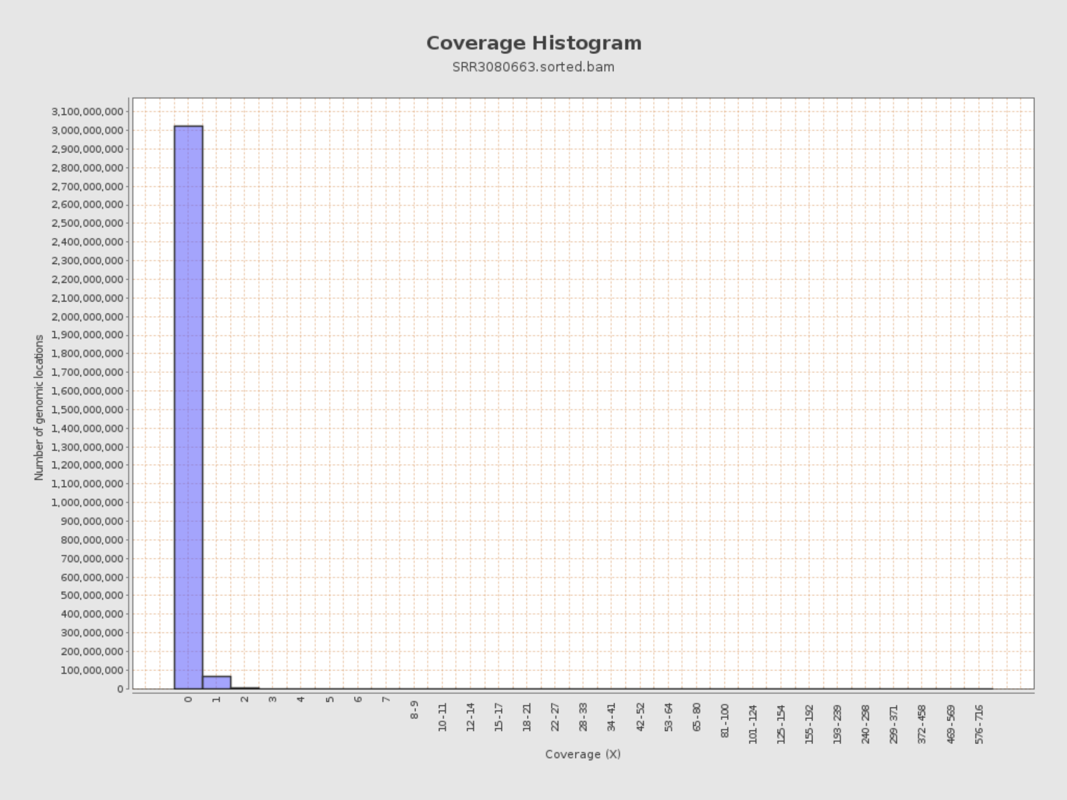
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10184207	0.0409	0.421
chr2	243199373	5691361	0.0234	0.3374
chr3	198022430	5212736	0.0263	0.1773
chr4	191154276	3646680	0.0191	0.1591
chr5	180915260	3913077	0.0216	0.1612
chr6	171115067	5104368	0.0298	0.2613
chr7	159138663	5504337	0.0346	0.8023

chr8	146364022	10157854	0.0694	0.3771
chr9	141213431	2699985	0.0191	0.2116
chr10	135534747	4067416	0.03	0.2299
chr11	135006516	3559407	0.0264	0.2131
chr12	133851895	2684351	0.0201	0.158
chr13	115169878	1726314	0.015	0.1335
chr14	107349540	1651899	0.0154	0.1455
chr15	102531392	1504880	0.0147	0.1382
chr16	90354753	2093023	0.0232	0.1763
chr17	81195210	1327233	0.0163	0.1518
chr18	78077248	2659800	0.0341	0.3514
chr19	59128983	1389909	0.0235	0.2672
chr20	63025520	2138391	0.0339	0.207
chr21	48129895	1208569	0.0251	0.1803
chr22	51304566	822122	0.016	0.1371
chrMT	16571	106050	6.3997	3.8544
chrX	155270560	5710778	0.0368	0.2265
chrY	59373566	196820	0.0033	0.0789

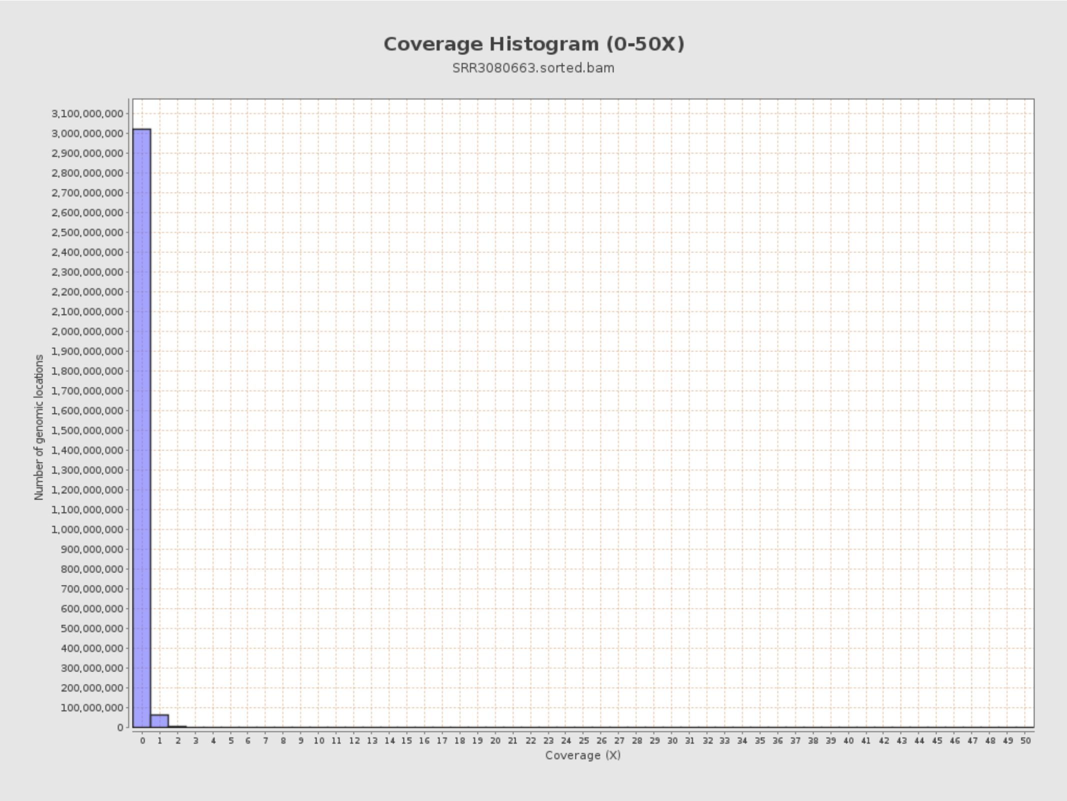
3. Results : Coverage across reference



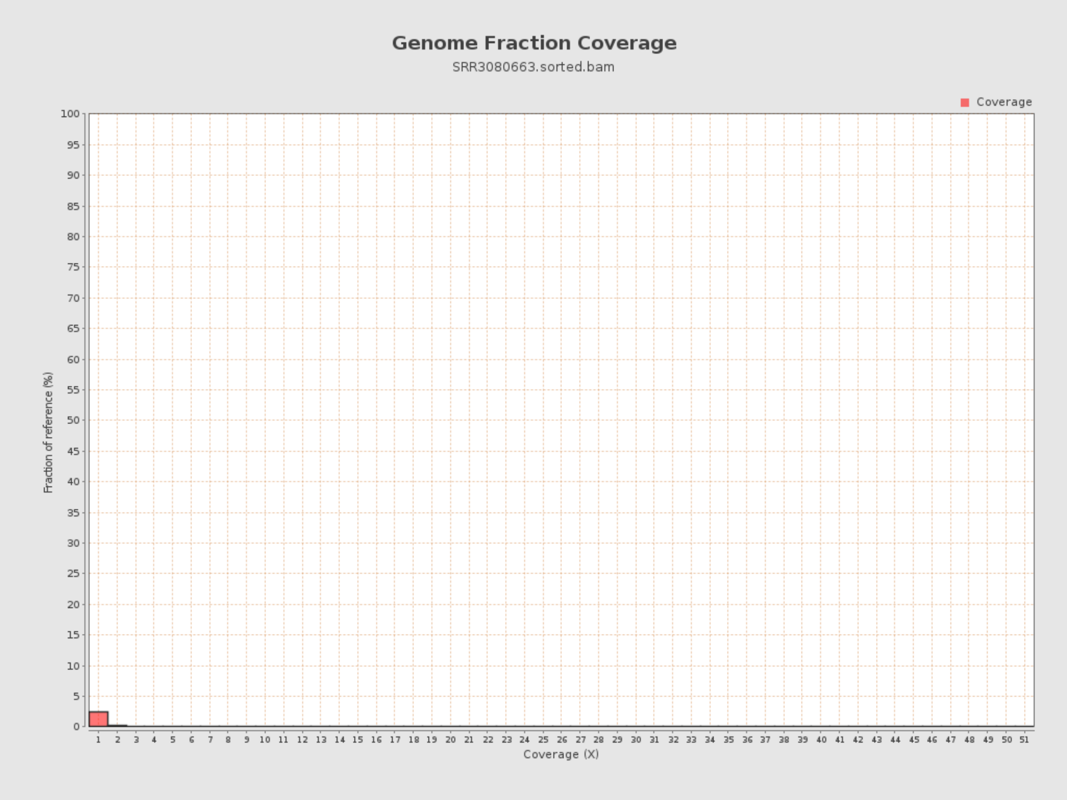
4. Results : Coverage Histogram



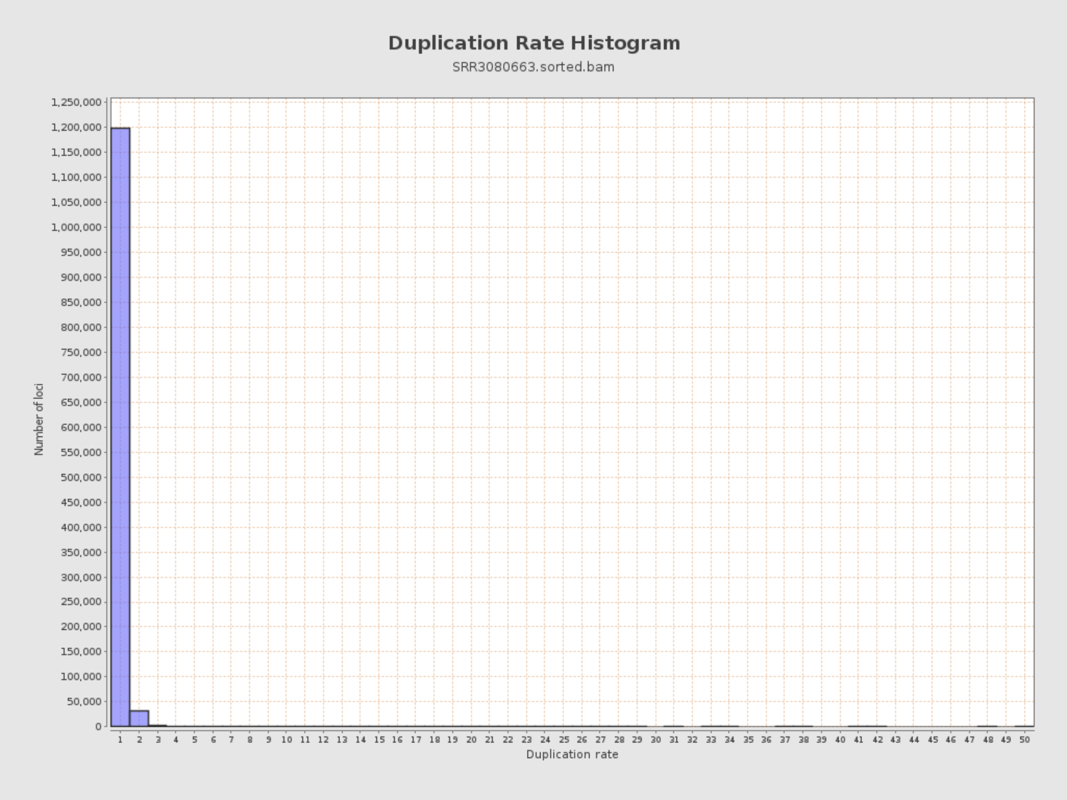
5. Results : Coverage Histogram (0-50X)



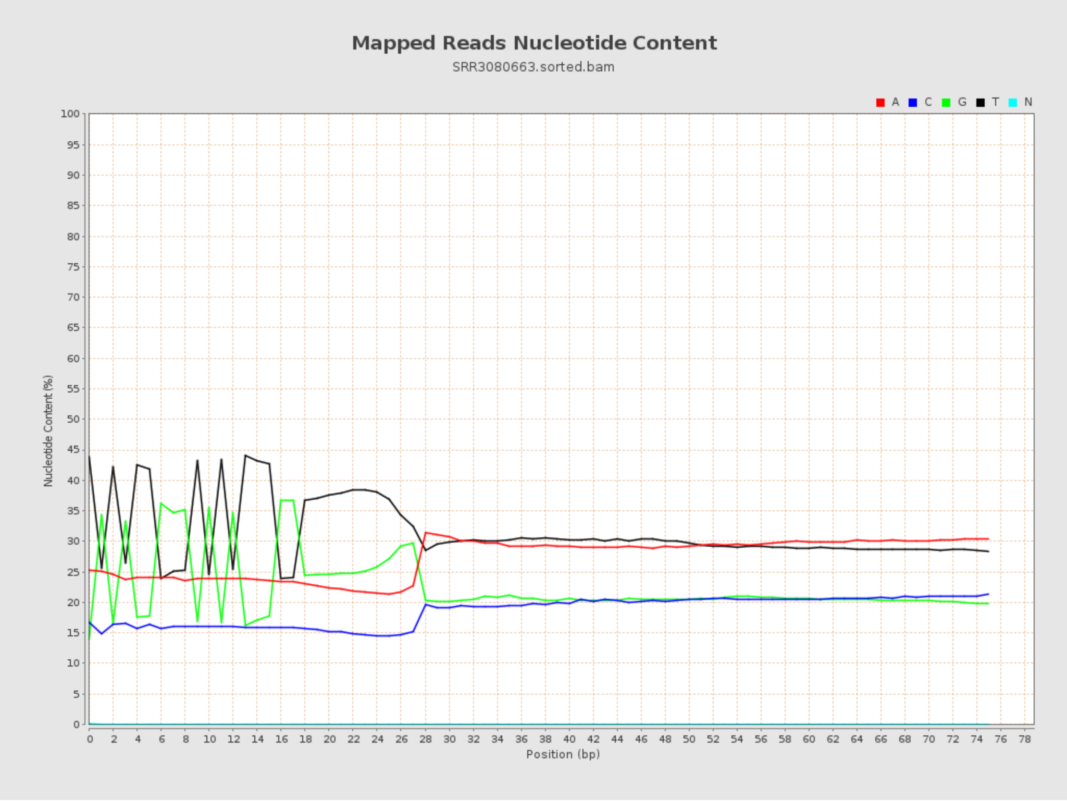
6. Results : Genome Fraction Coverage



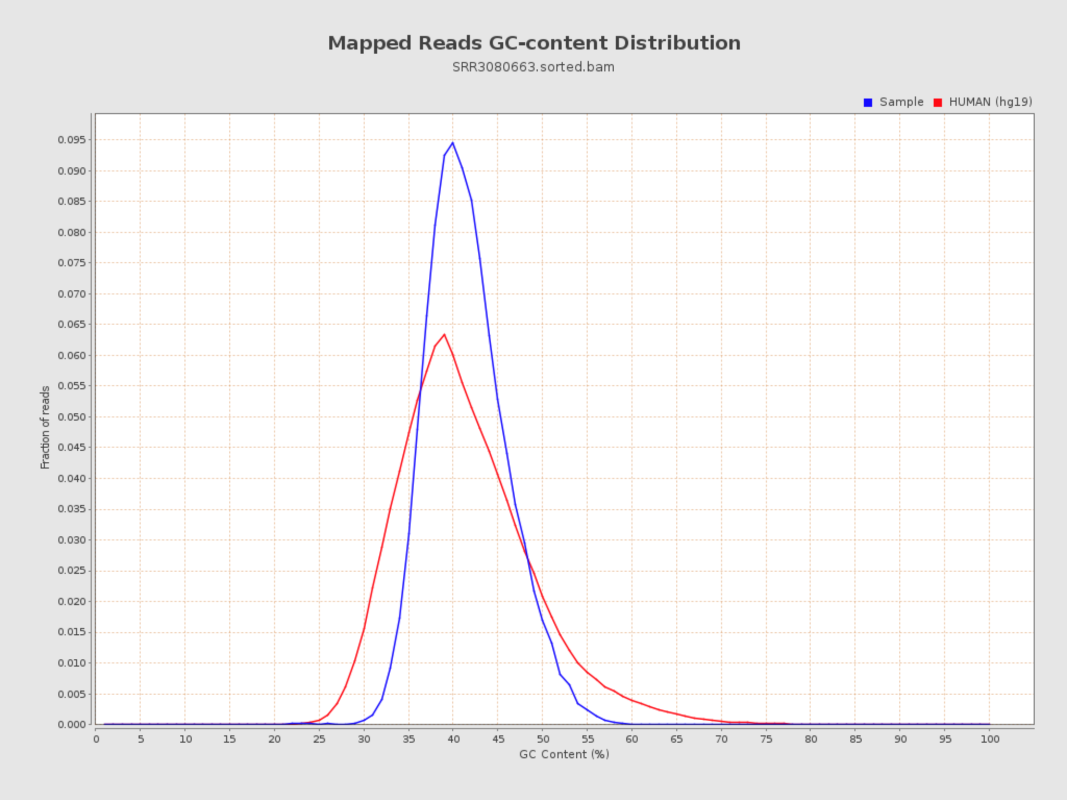
7. Results : Duplication Rate Histogram



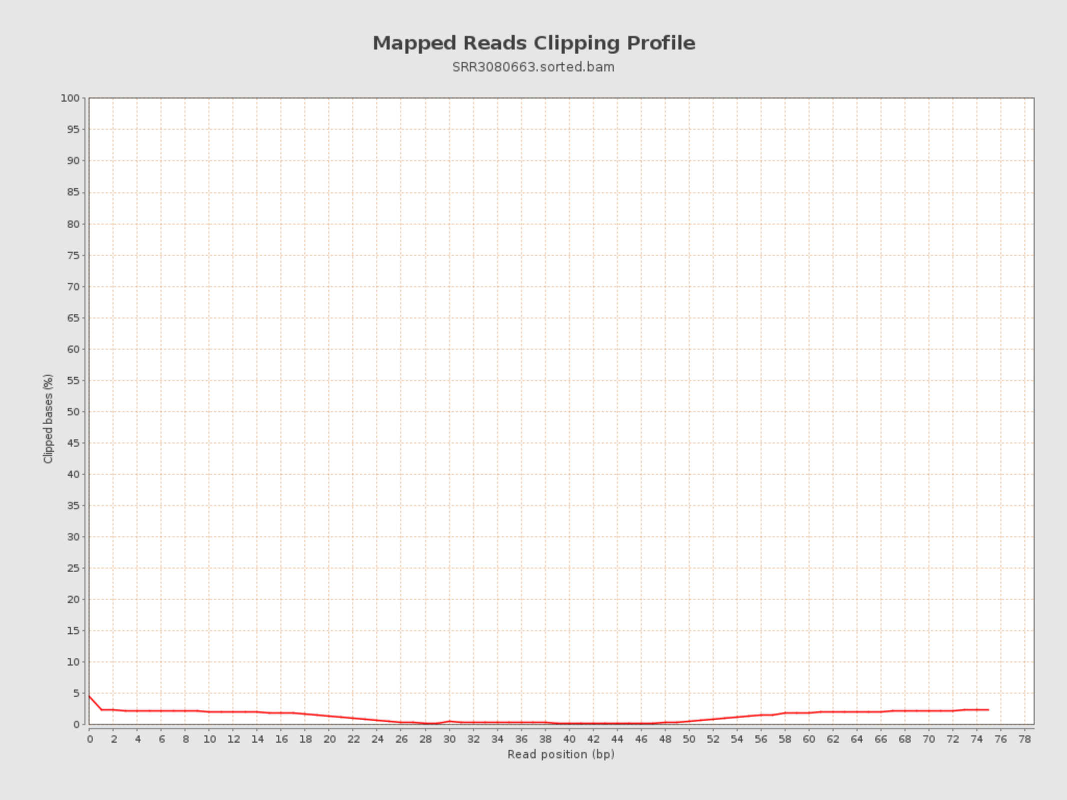
8. Results : Mapped Reads Nucleotide Content



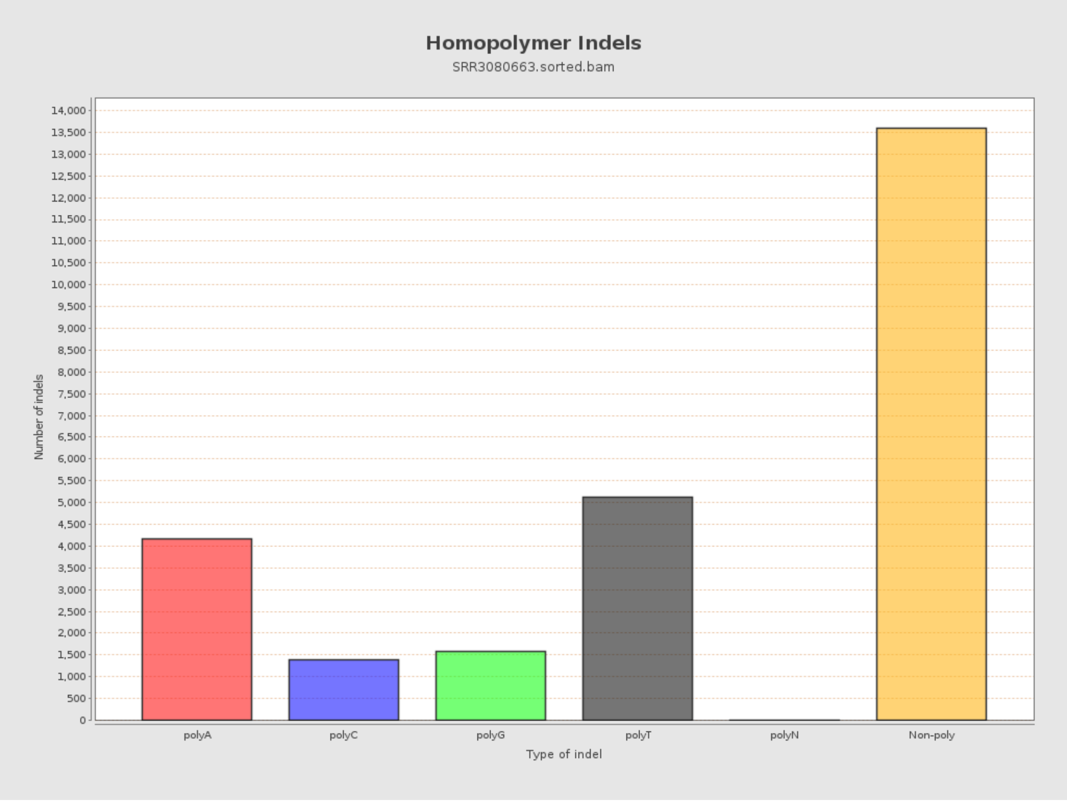
9. Results : Mapped Reads GC-content Distribution



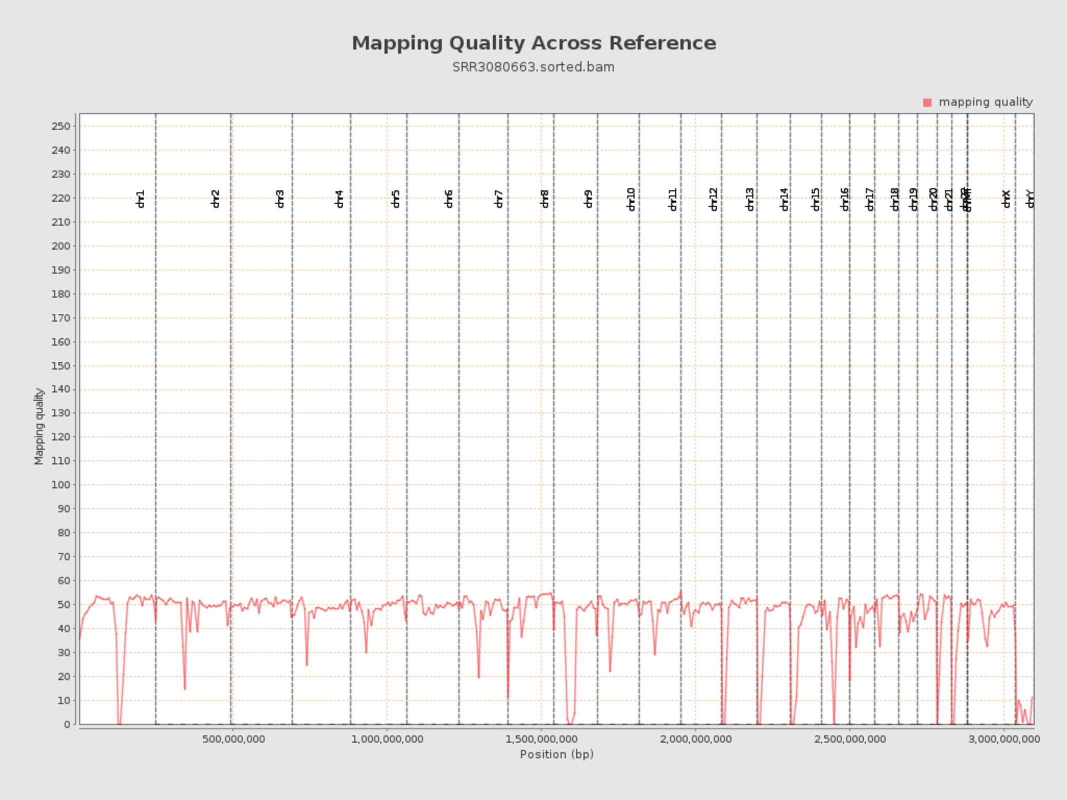
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram