Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:02:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080760.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_SRR3080760 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080760.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:02:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080760.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,881,354
Mapped reads	6,626,429 / 67.06%
Unmapped reads	3,254,925 / 32.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	52,047 / 0.53%
Read min/max/mean length	30 / 66 / 66.17
Duplicated reads (estimated)	1,025,053 / 10.37%
Duplication rate	11.68%
Clipped reads	1,077,427 / 10.9%

2.2. ACGT Content

Number/percentage of A's	129,574,882 / 30.72%
Number/percentage of C's	85,136,488 / 20.18%
Number/percentage of T's	110,923,610 / 26.3%
Number/percentage of G's	96,031,811 / 22.77%
Number/percentage of N's	135,777 / 0.03%
GC Percentage	42.95%

2.3. Coverage

Mean	0.1363

Standard Deviation	0.8647

2.4. Mapping Quality

Mean Mapping Quality	44.45

2.5. Mismatches and indels

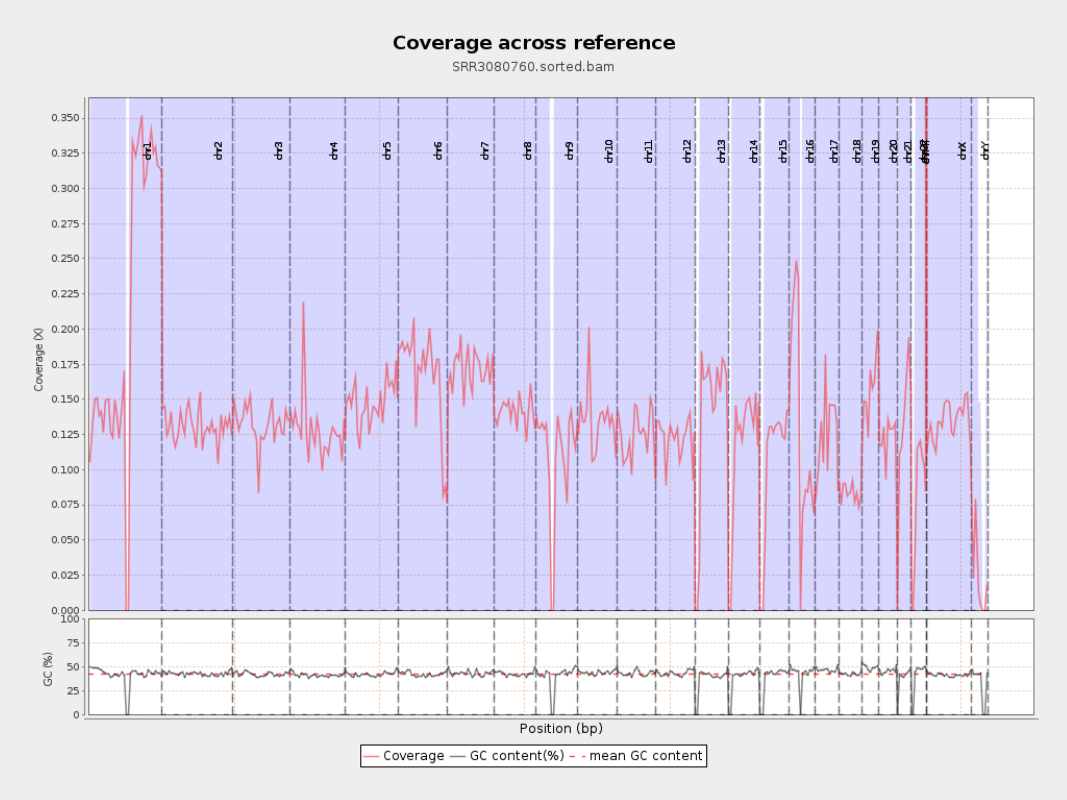
General error rate	0.88%
Mismatches	3,637,563
Insertions	31,362
Mapped reads with at least one insertion	0.47%
Deletions	79,996
Mapped reads with at least one deletion	1.19%
Homopolymer indels	42.57%

2.6. Chromosome stats

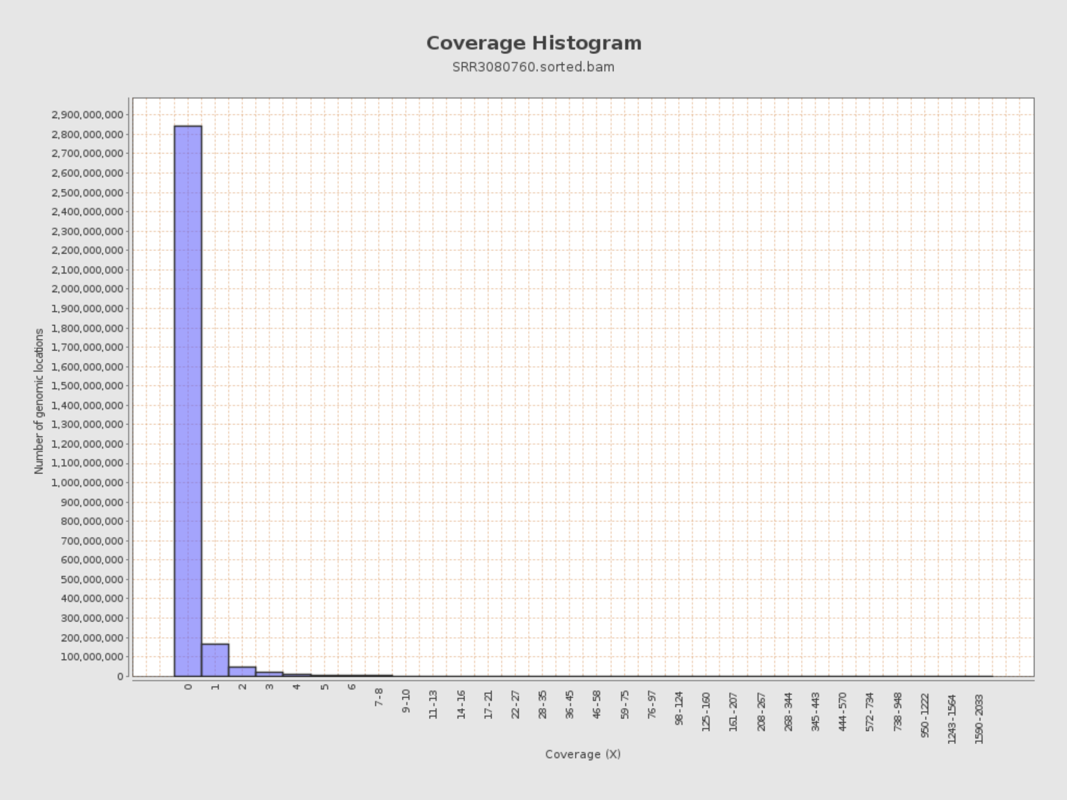
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	52127263	0.2091	1.214
chr2	243199373	31916268	0.1312	0.7865
chr3	198022430	26161706	0.1321	0.5768
chr4	191154276	24454957	0.1279	0.7111
chr5	180915260	26790811	0.1481	0.6225
chr6	171115067	28689786	0.1677	1.2806
chr7	159138663	27353828	0.1719	1.1746

chr8	146364022	20647047	0.1411	1.2296
chr9	141213431	15165152	0.1074	0.6608
chr10	135534747	18215298	0.1344	0.9314
chr11	135006516	16818395	0.1246	0.8231
chr12	133851895	16350592	0.1222	0.6039
chr13	115169878	15863340	0.1377	0.5979
chr14	107349540	12238903	0.114	0.6388
chr15	102531392	10772288	0.1051	0.521
chr16	90354753	11831596	0.1309	0.6465
chr17	81195210	10185783	0.1254	0.6066
chr18	78077248	6496755	0.0832	0.9961
chr19	59128983	9322114	0.1577	1.3751
chr20	63025520	7657487	0.1215	0.5927
chr21	48129895	6370597	0.1324	0.7143
chr22	51304566	3941119	0.0768	0.4425
chrMT	16571	332807	20.0837	14.2749
chrX	155270560	20900200	0.1346	0.625
chrY	59373566	1346838	0.0227	0.6193

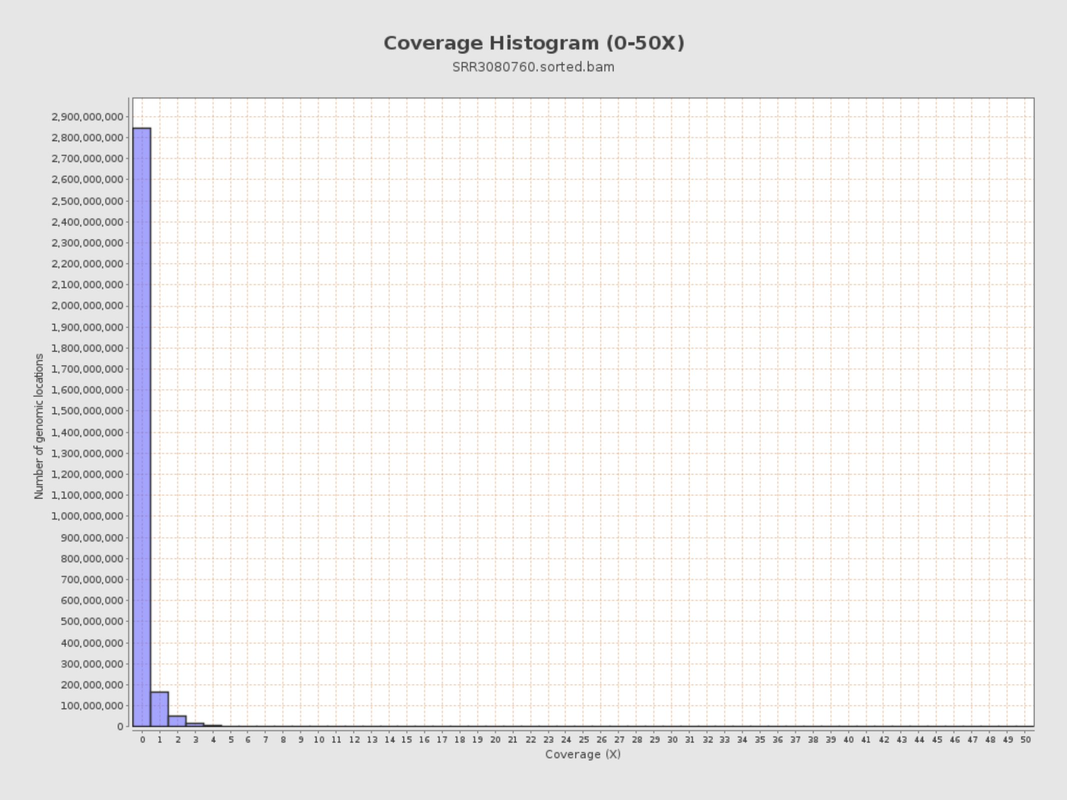
3. Results : Coverage across reference



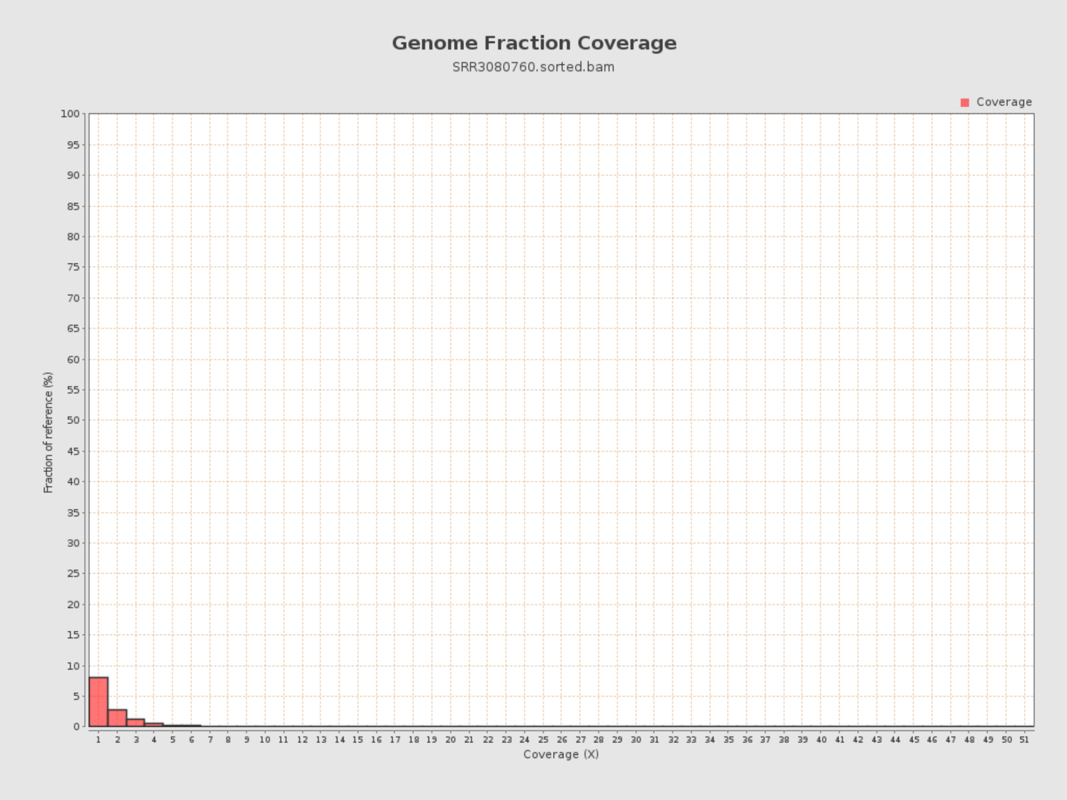
4. Results : Coverage Histogram



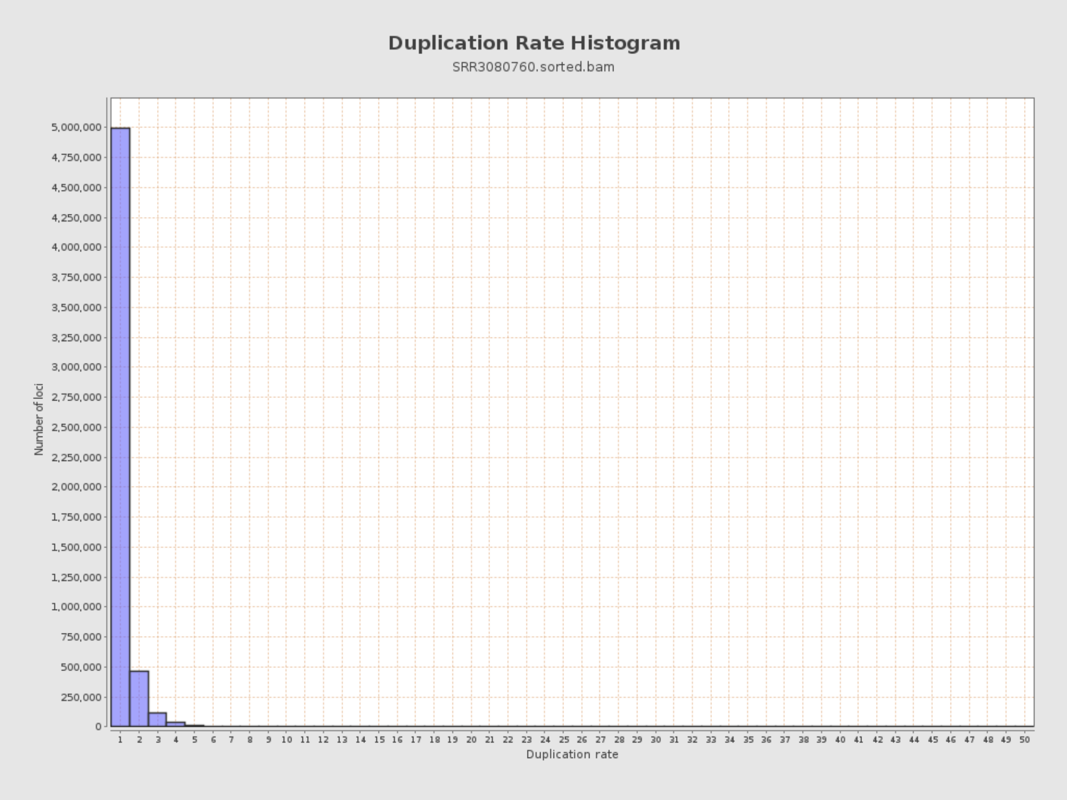
5. Results : Coverage Histogram (0-50X)



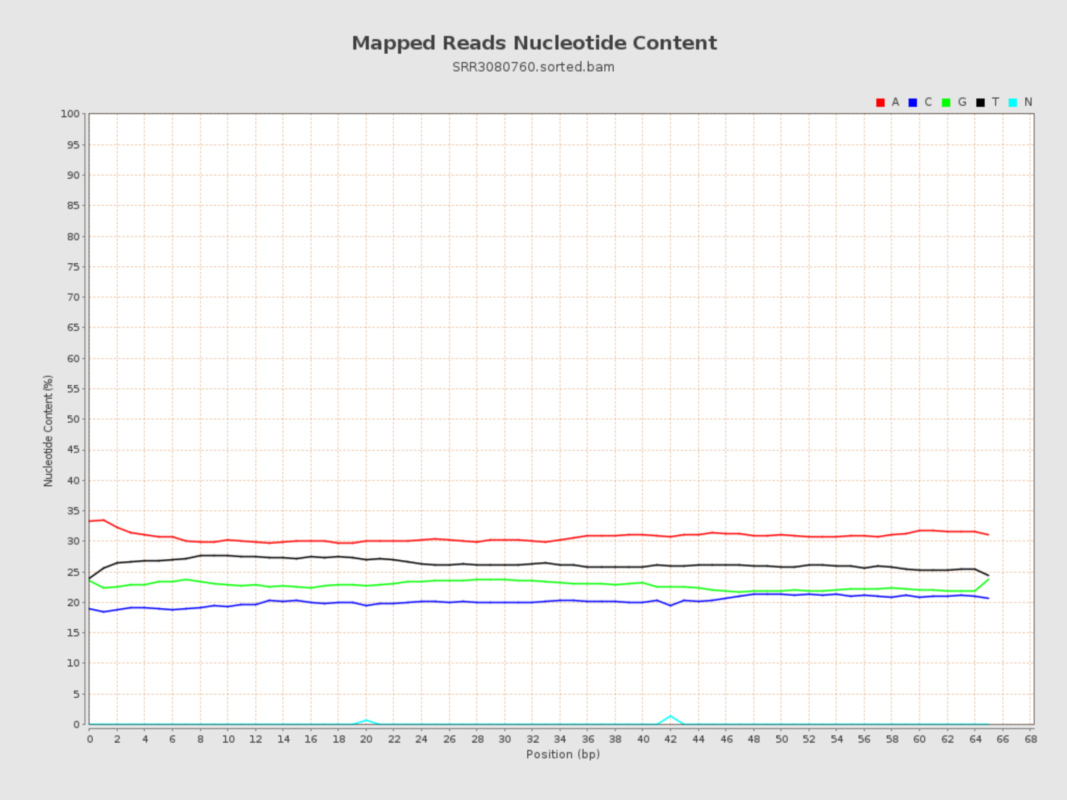
6. Results : Genome Fraction Coverage



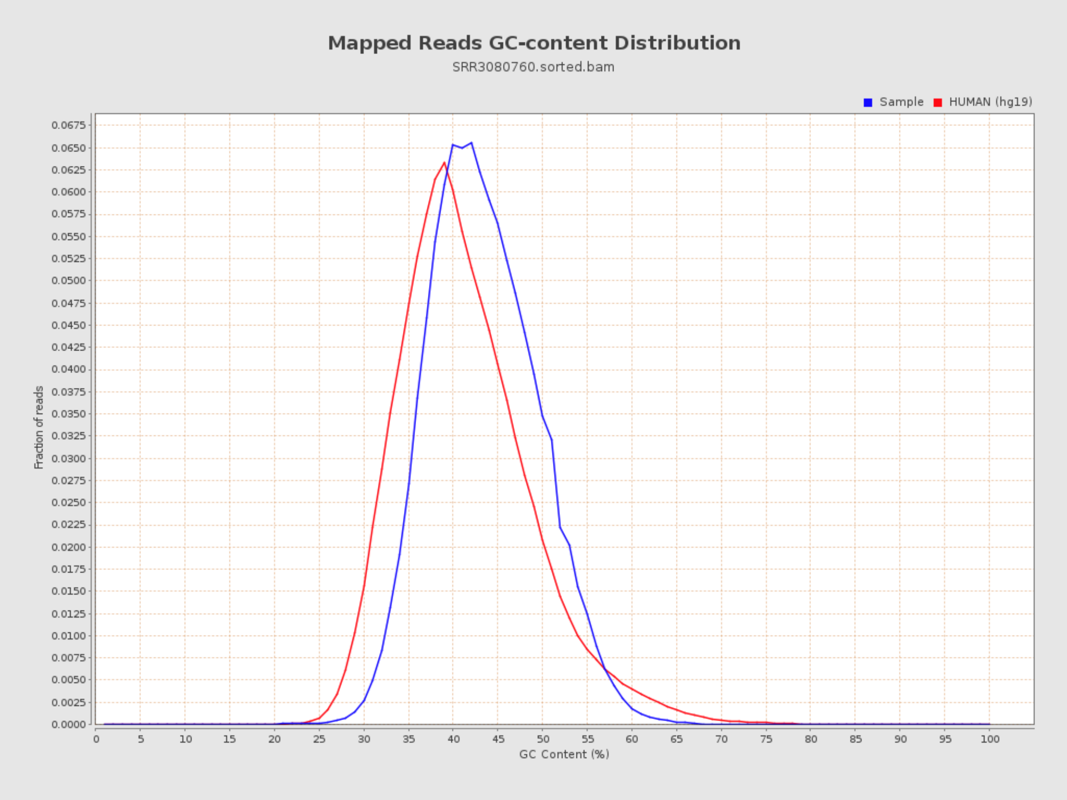
7. Results : Duplication Rate Histogram



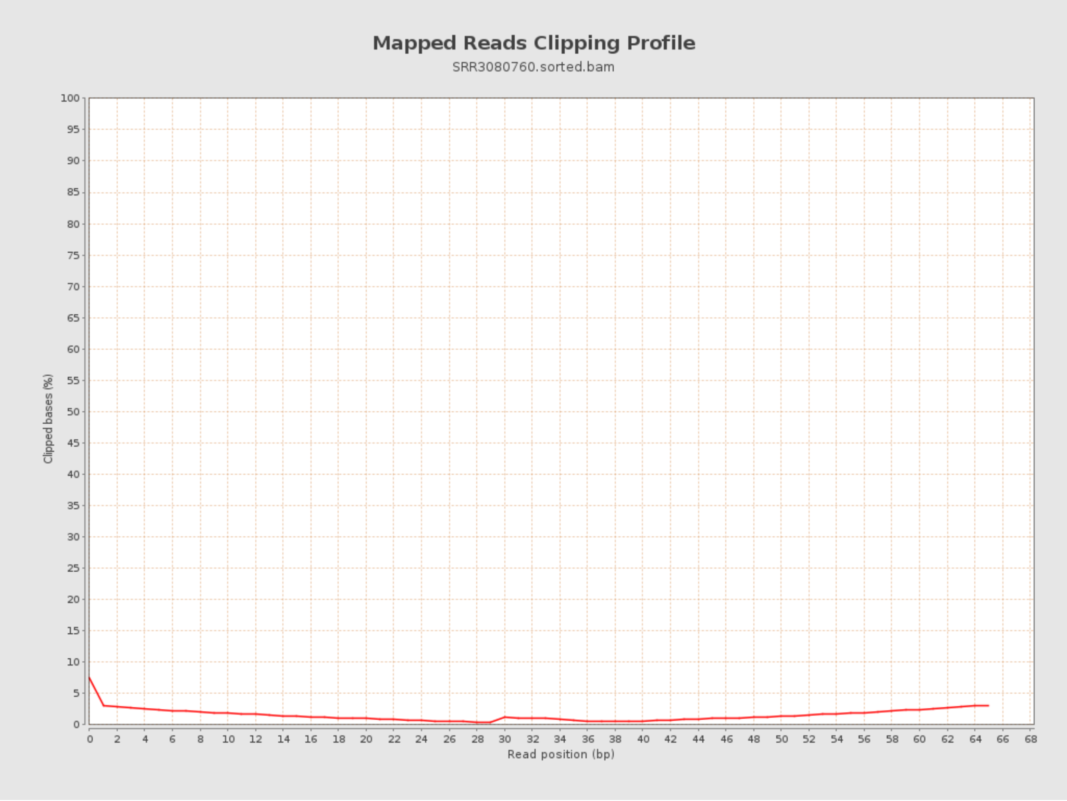
8. Results : Mapped Reads Nucleotide Content



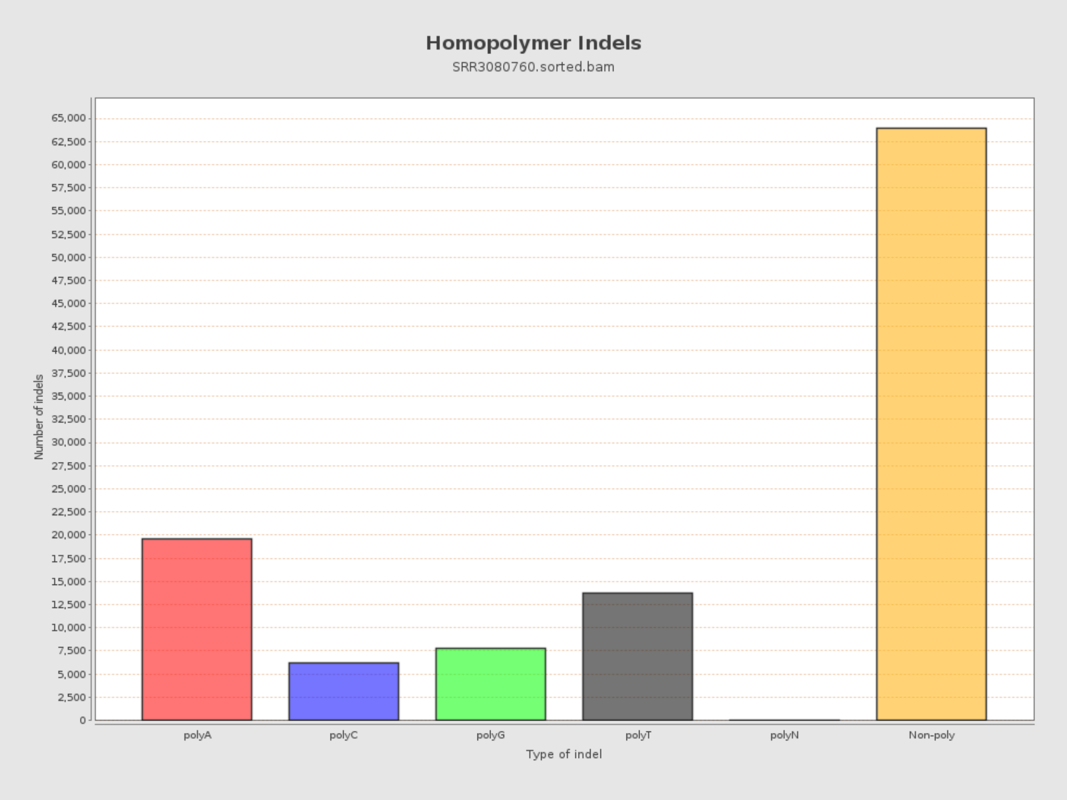
9. Results : Mapped Reads GC-content Distribution



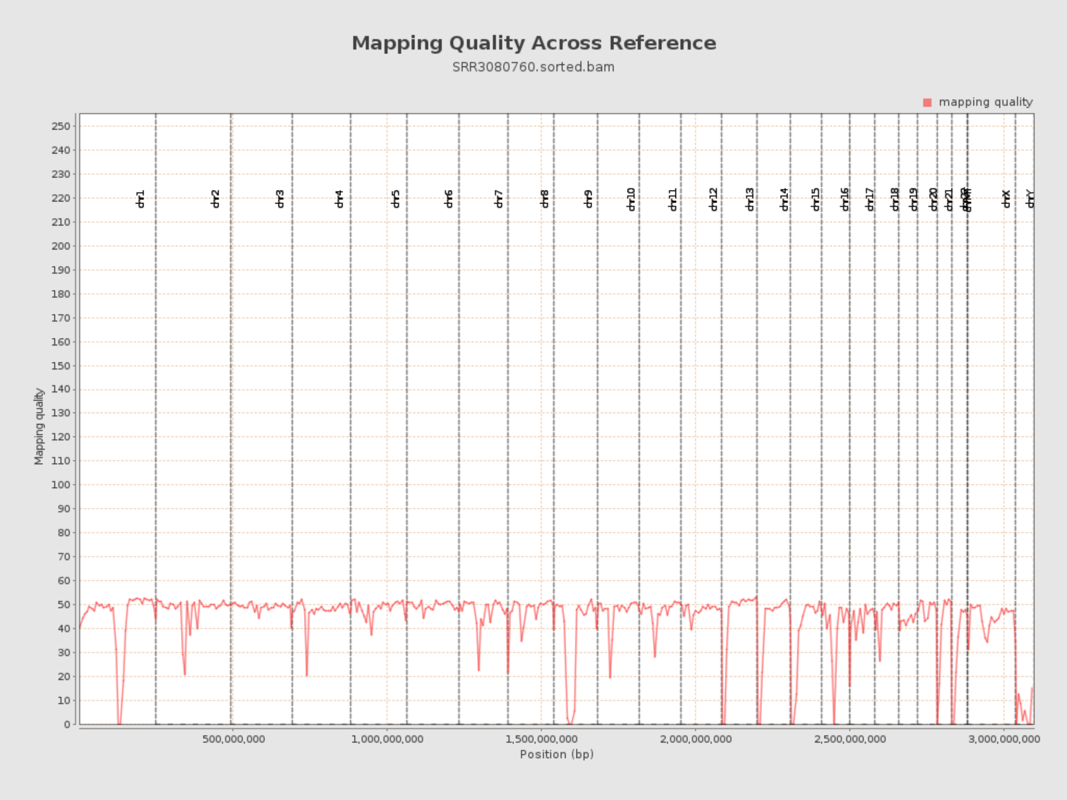
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram