Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 04:07:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240051.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_SRR6240051 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240051.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 04:07:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240051.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,870,248
Mapped reads	1,431,835 / 76.56%
Unmapped reads	438,413 / 23.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,796 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	130,648 / 6.99%
Duplication rate	7.56%
Clipped reads	990,225 / 52.95%

2.2. ACGT Content

Number/percentage of A's	23,527,652 / 27.1%
Number/percentage of C's	15,002,324 / 17.28%
Number/percentage of T's	28,324,837 / 32.63%
Number/percentage of G's	19,902,187 / 22.93%
Number/percentage of N's	55,984 / 0.06%
GC Percentage	40.21%

2.3. Coverage

Mean	0.0281

Standard Deviation	0.2891

2.4. Mapping Quality

Mean Mapping Quality	45.4

2.5. Mismatches and indels

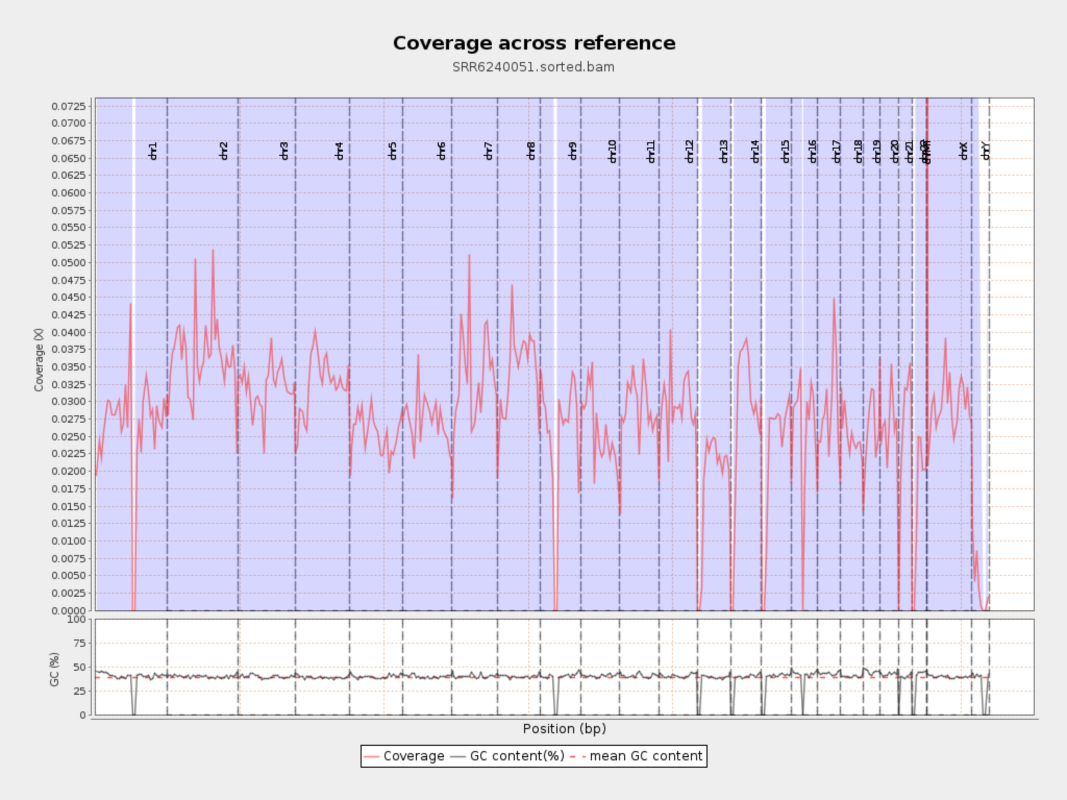
General error rate	1.02%
Mismatches	879,386
Insertions	6,145
Mapped reads with at least one insertion	0.43%
Deletions	27,972
Mapped reads with at least one deletion	1.93%
Homopolymer indels	50.39%

2.6. Chromosome stats

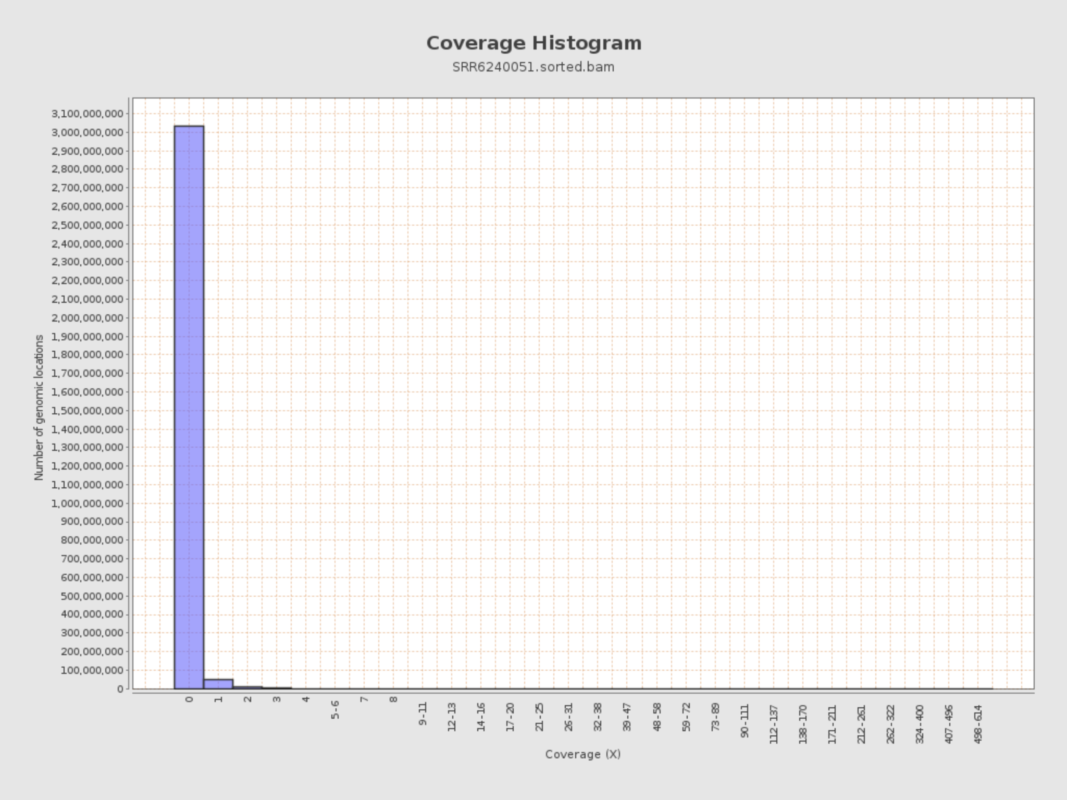
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6555532	0.0263	0.4109
chr2	243199373	8914367	0.0367	0.3314
chr3	198022430	6358172	0.0321	0.233
chr4	191154276	6201328	0.0324	0.2414
chr5	180915260	4617205	0.0255	0.207
chr6	171115067	4688148	0.0274	0.2448
chr7	159138663	5332877	0.0335	0.4724

chr8	146364022	5076531	0.0347	0.4356
chr9	141213431	3532575	0.025	0.2566
chr10	135534747	3488631	0.0257	0.2401
chr11	135006516	3941199	0.0292	0.2641
chr12	133851895	3959729	0.0296	0.2187
chr13	115169878	2126113	0.0185	0.1752
chr14	107349540	2965749	0.0276	0.2182
chr15	102531392	2294282	0.0224	0.2061
chr16	90354753	2306861	0.0255	0.2055
chr17	81195210	2360455	0.0291	0.2309
chr18	78077248	1958586	0.0251	0.3787
chr19	59128983	1560219	0.0264	0.3035
chr20	63025520	1661794	0.0264	0.2143
chr21	48129895	1266453	0.0263	0.2124
chr22	51304566	826522	0.0161	0.1573
chrMT	16571	62030	3.7433	4.2318
chrX	155270560	4605910	0.0297	0.2366
chrY	59373566	199070	0.0034	0.0764

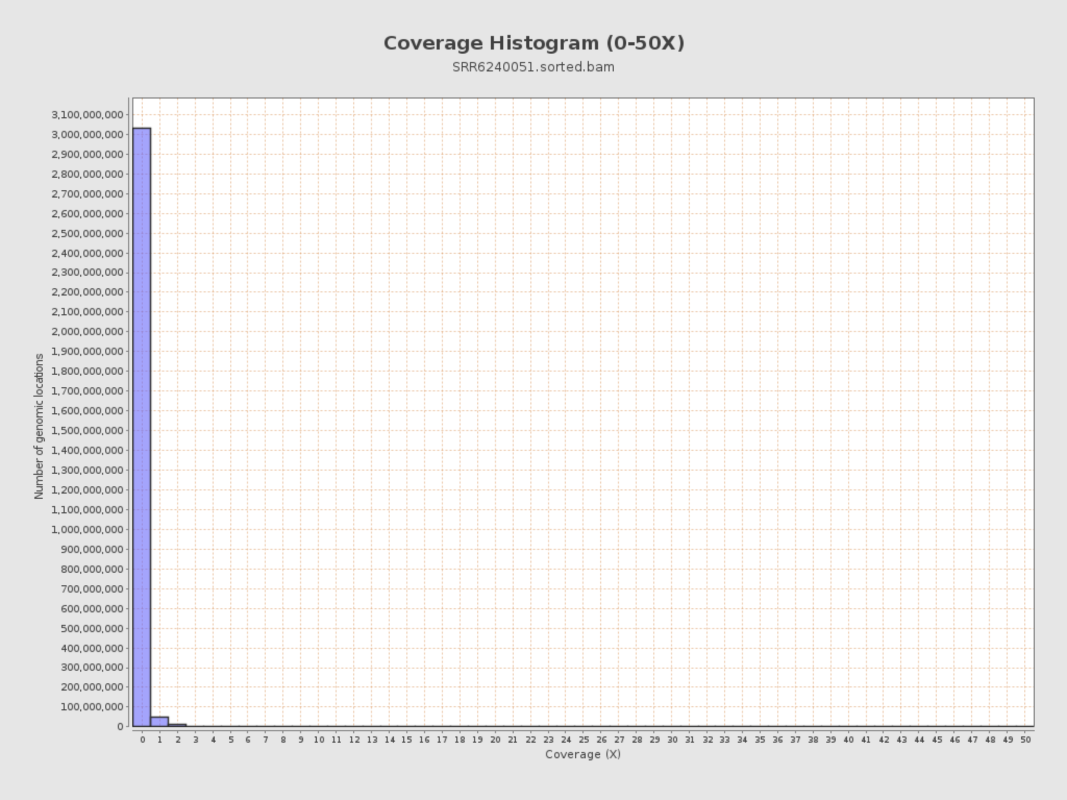
3. Results : Coverage across reference



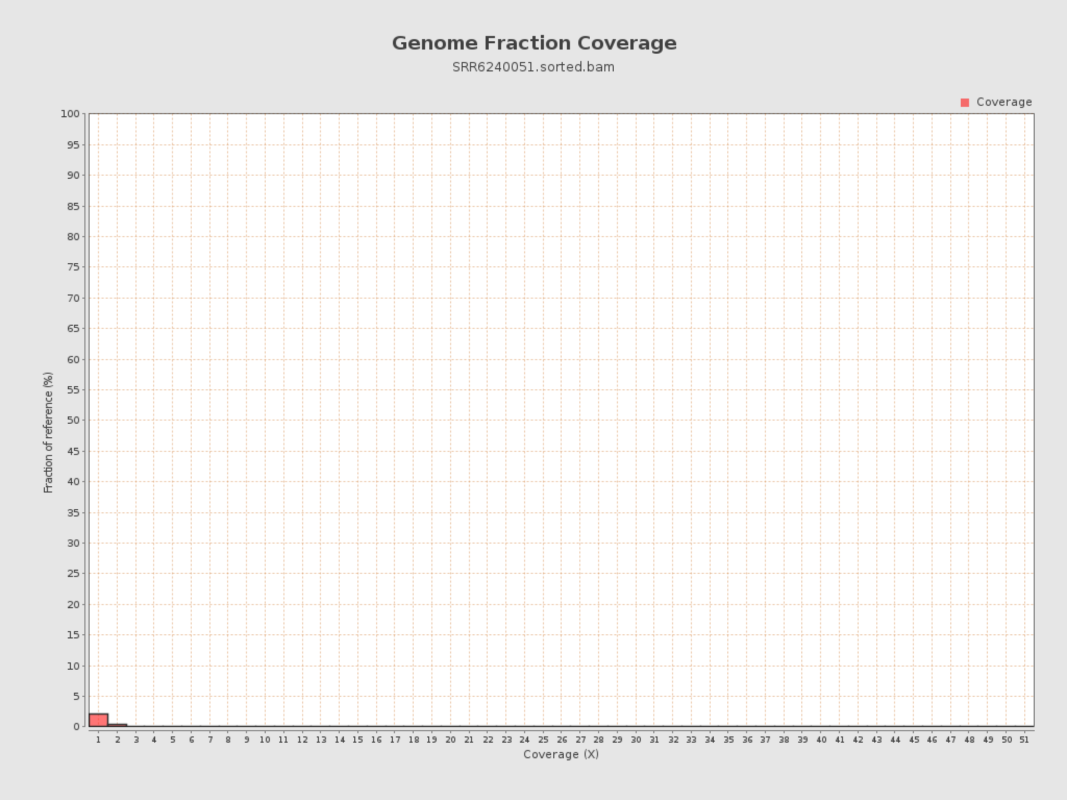
4. Results : Coverage Histogram



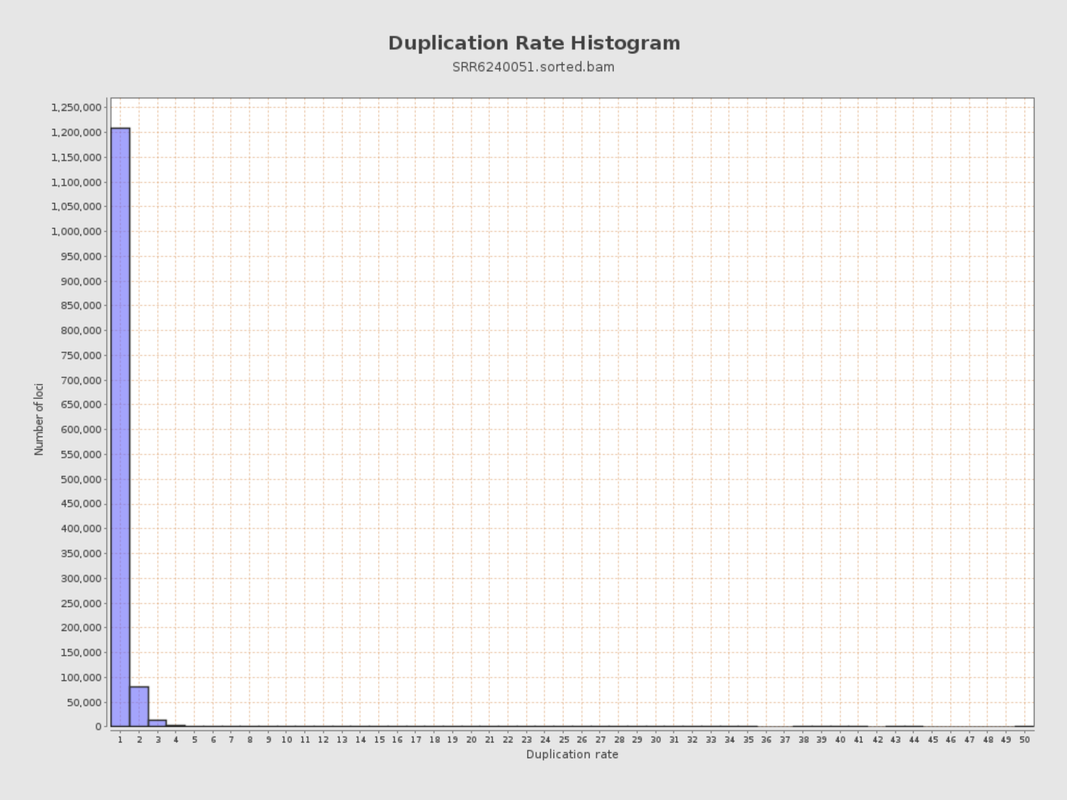
5. Results : Coverage Histogram (0-50X)



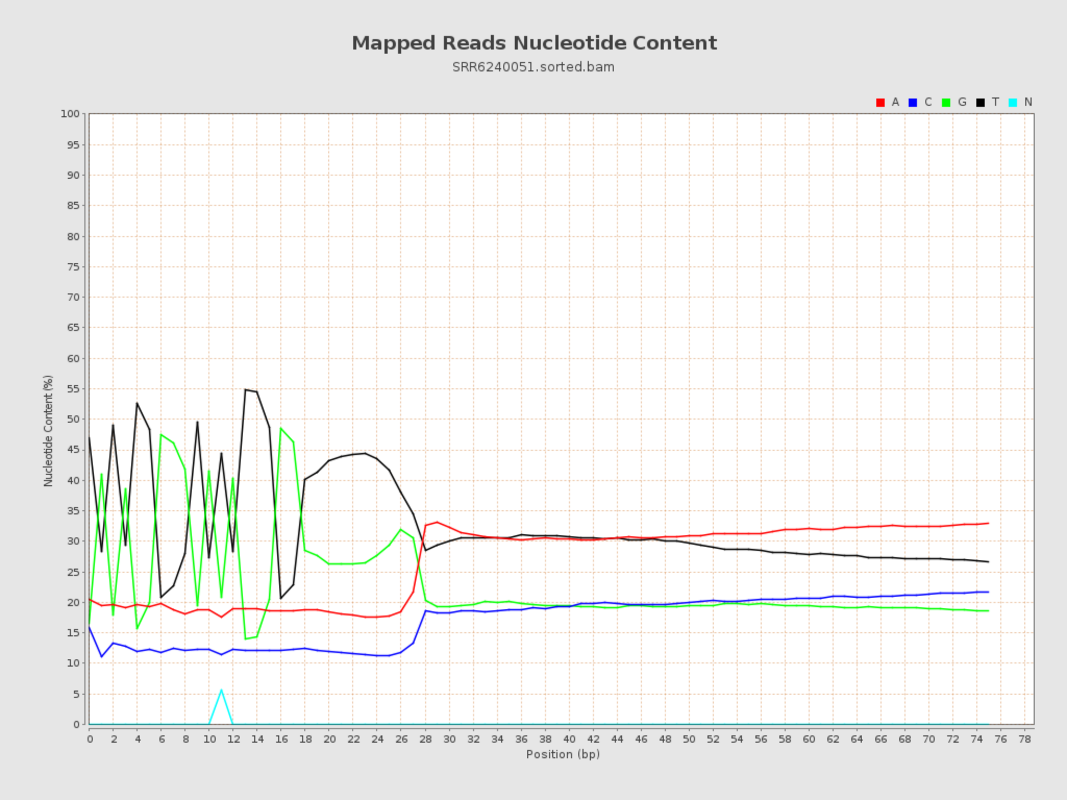
6. Results : Genome Fraction Coverage



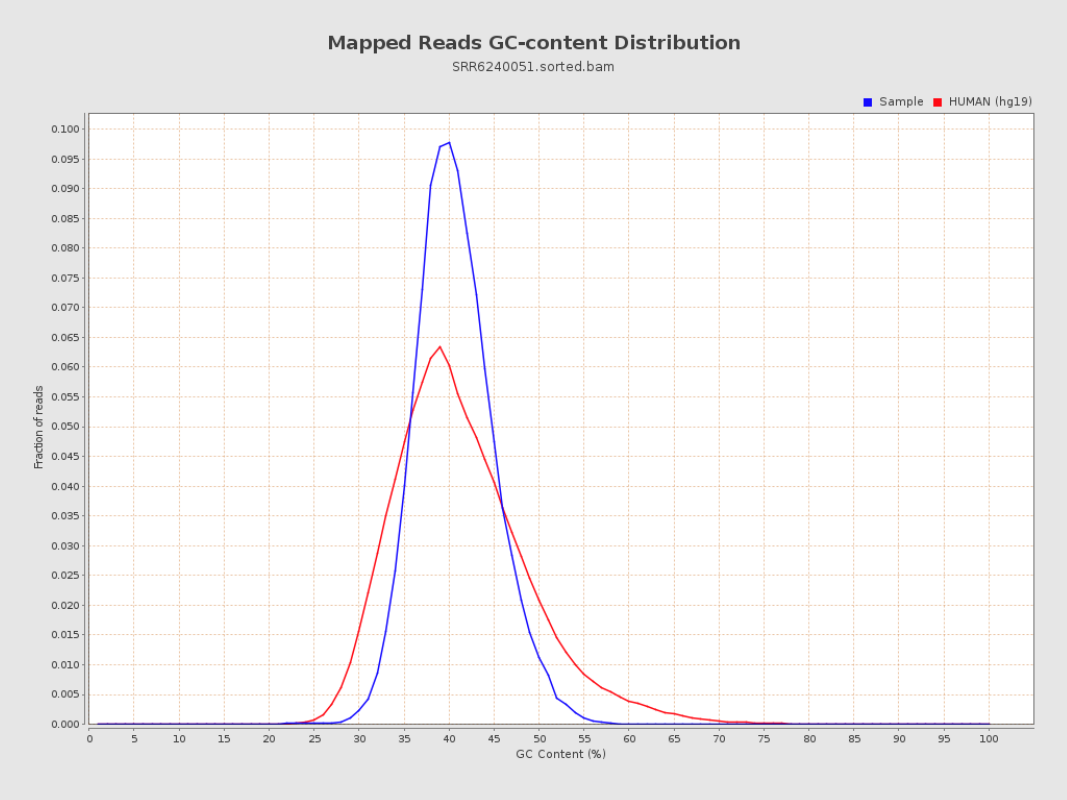
7. Results : Duplication Rate Histogram



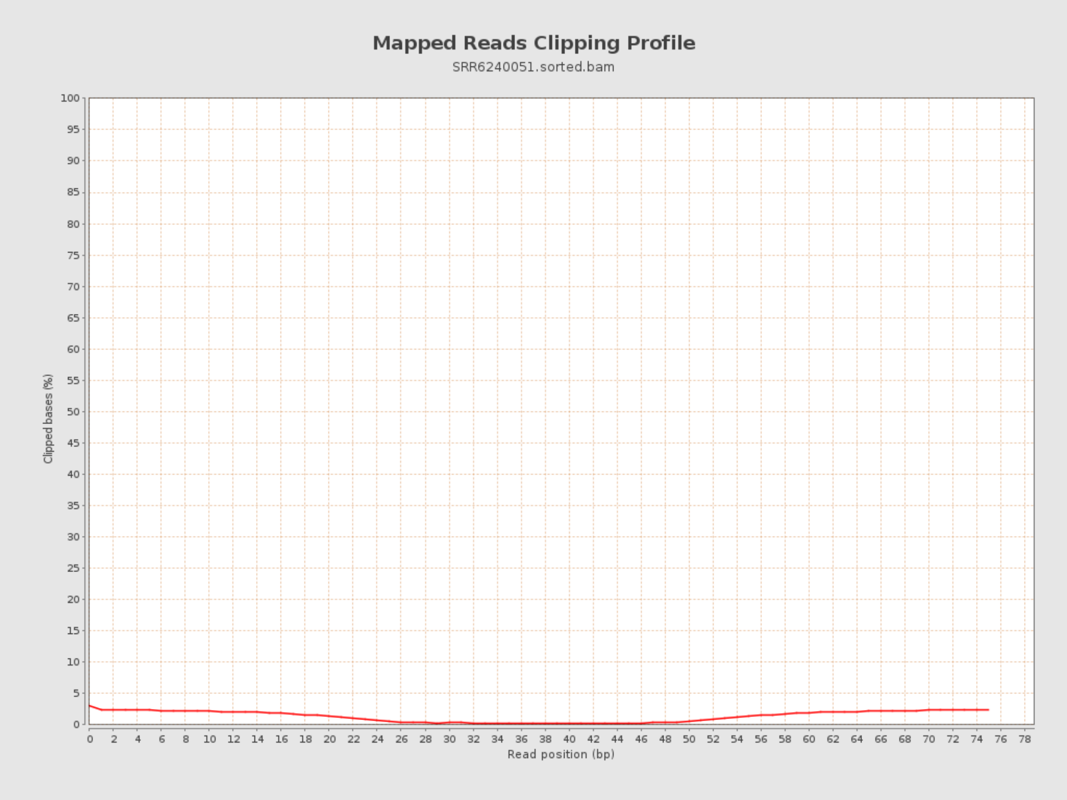
8. Results : Mapped Reads Nucleotide Content



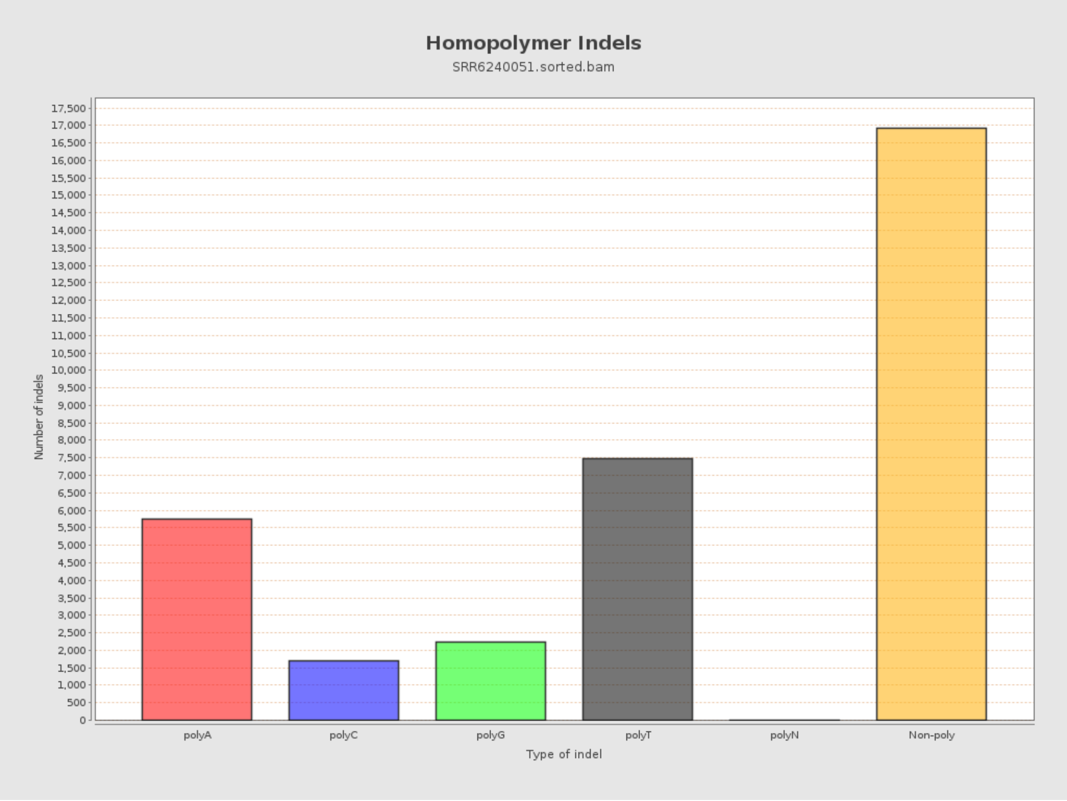
9. Results : Mapped Reads GC-content Distribution



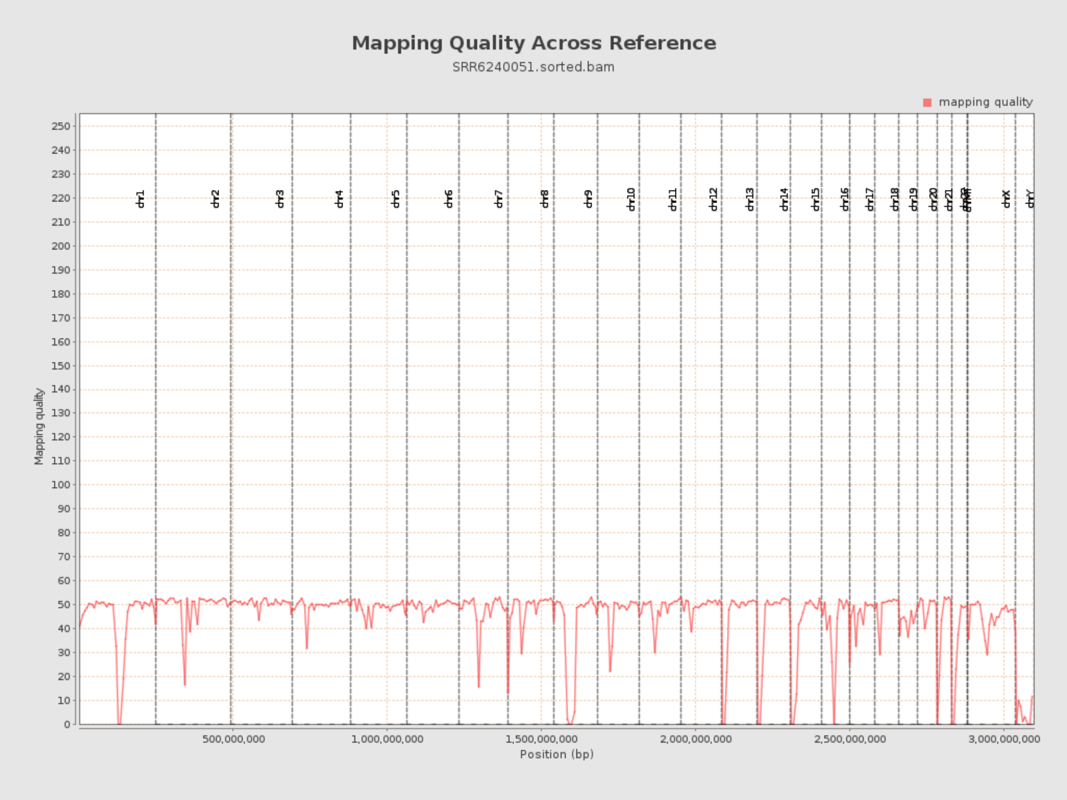
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram