Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 06:31:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240209.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_SRR6240209 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240209.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 06:31:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240209.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,107,866
Mapped reads	1,559,757 / 74%
Unmapped reads	548,109 / 26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,528 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	164,026 / 7.78%
Duplication rate	8.95%
Clipped reads	1,094,303 / 51.92%

2.2. ACGT Content

Number/percentage of A's	24,836,094 / 26.36%
Number/percentage of C's	16,405,655 / 17.41%
Number/percentage of T's	30,786,099 / 32.67%
Number/percentage of G's	22,179,760 / 23.54%
Number/percentage of N's	20,903 / 0.02%
GC Percentage	40.95%

2.3. Coverage

Mean	0.0305

Standard Deviation	0.2915

2.4. Mapping Quality

Mean Mapping Quality	44.9

2.5. Mismatches and indels

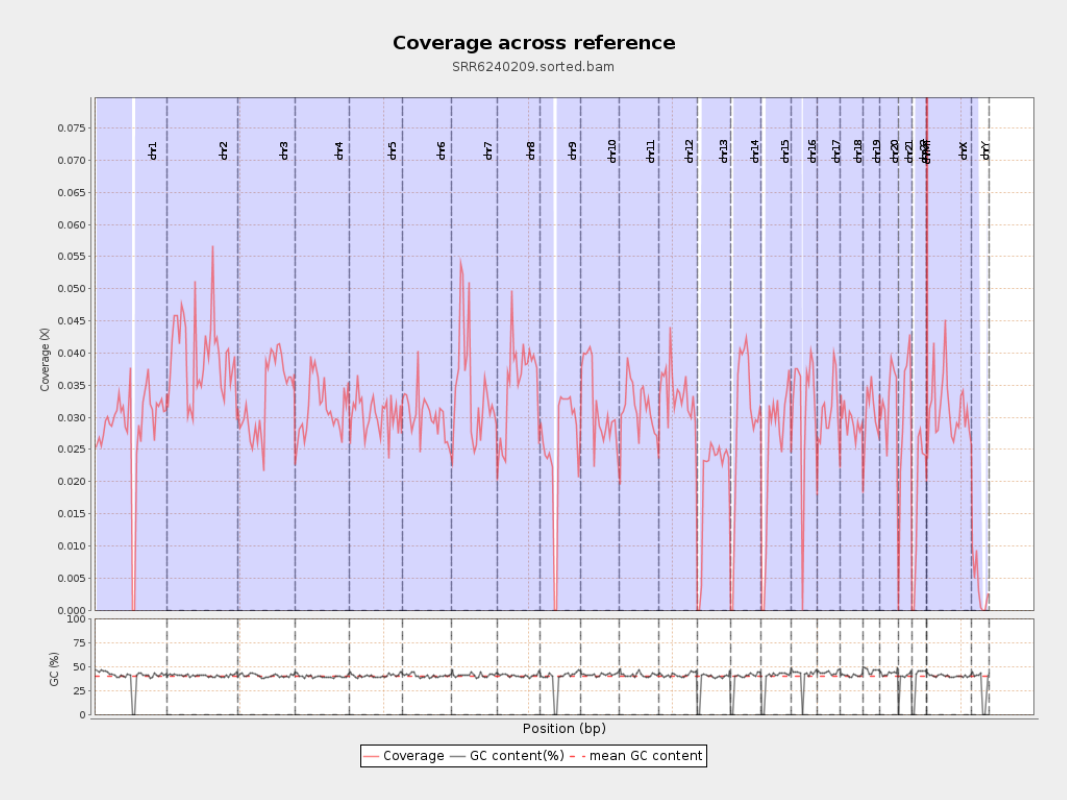
General error rate	0.96%
Mismatches	890,622
Insertions	6,456
Mapped reads with at least one insertion	0.41%
Deletions	28,289
Mapped reads with at least one deletion	1.8%
Homopolymer indels	49.04%

2.6. Chromosome stats

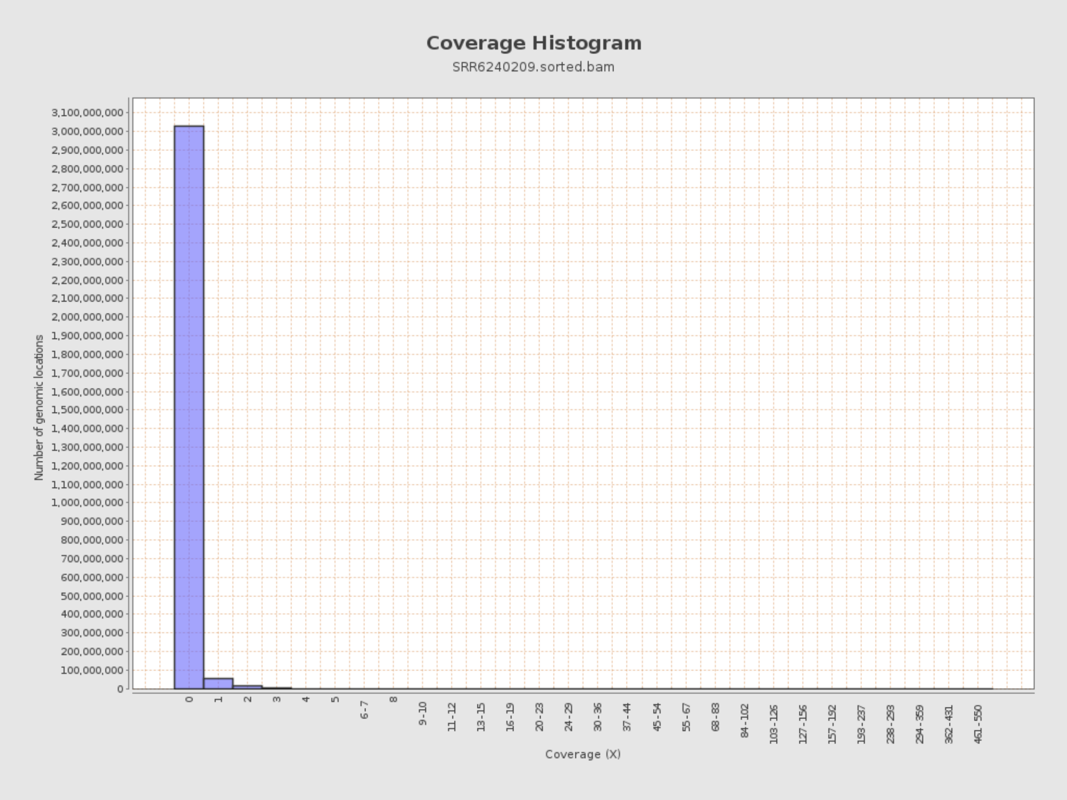
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7071809	0.0284	0.3922
chr2	243199373	9631336	0.0396	0.389
chr3	198022430	6576150	0.0332	0.2387
chr4	191154276	5977120	0.0313	0.2378
chr5	180915260	5530765	0.0306	0.2302
chr6	171115067	5168603	0.0302	0.2674
chr7	159138663	5462791	0.0343	0.4435

chr8	146364022	5172312	0.0353	0.33
chr9	141213431	3597703	0.0255	0.2656
chr10	135534747	4290418	0.0317	0.269
chr11	135006516	4248622	0.0315	0.269
chr12	133851895	4518190	0.0338	0.2422
chr13	115169878	2308302	0.02	0.1859
chr14	107349540	3158079	0.0294	0.2338
chr15	102531392	2576198	0.0251	0.2152
chr16	90354753	2812506	0.0311	0.2345
chr17	81195210	2503543	0.0308	0.2452
chr18	78077248	2291231	0.0293	0.3799
chr19	59128983	1819856	0.0308	0.3072
chr20	63025520	2037756	0.0323	0.2406
chr21	48129895	1457803	0.0303	0.2317
chr22	51304566	913274	0.0178	0.1697
chrMT	16571	37340	2.2533	2.7855
chrX	155270560	4904996	0.0316	0.2489
chrY	59373566	209771	0.0035	0.0796

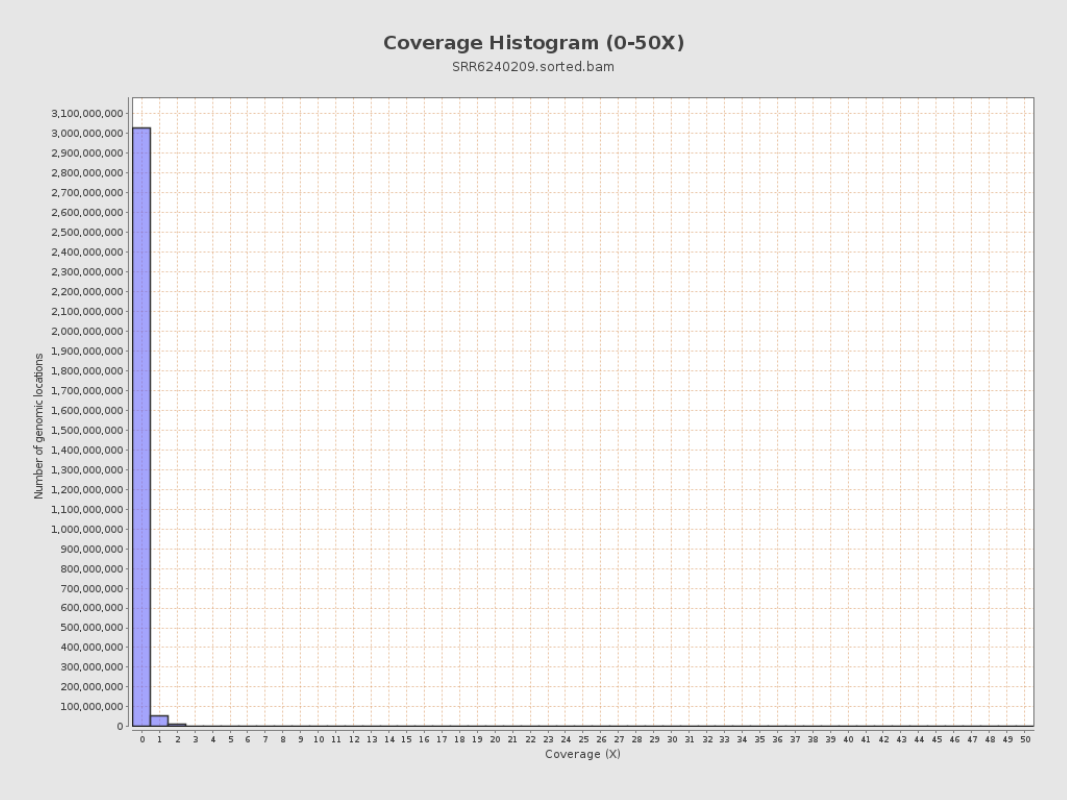
3. Results : Coverage across reference



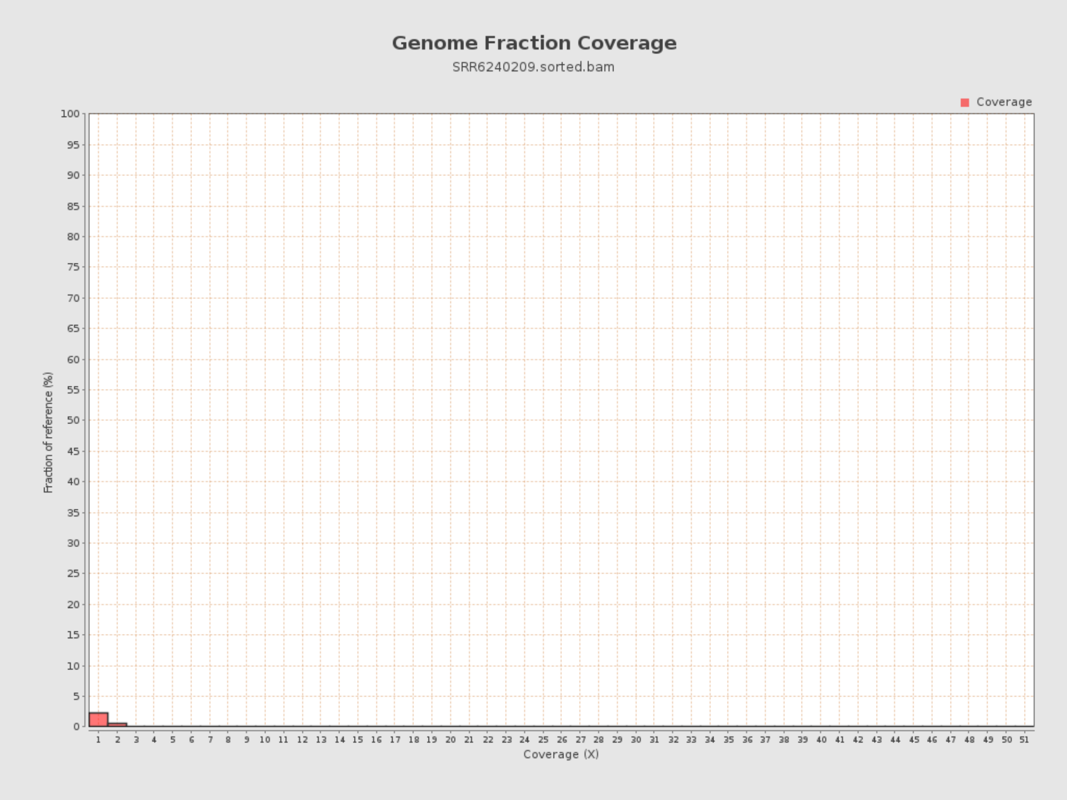
4. Results : Coverage Histogram



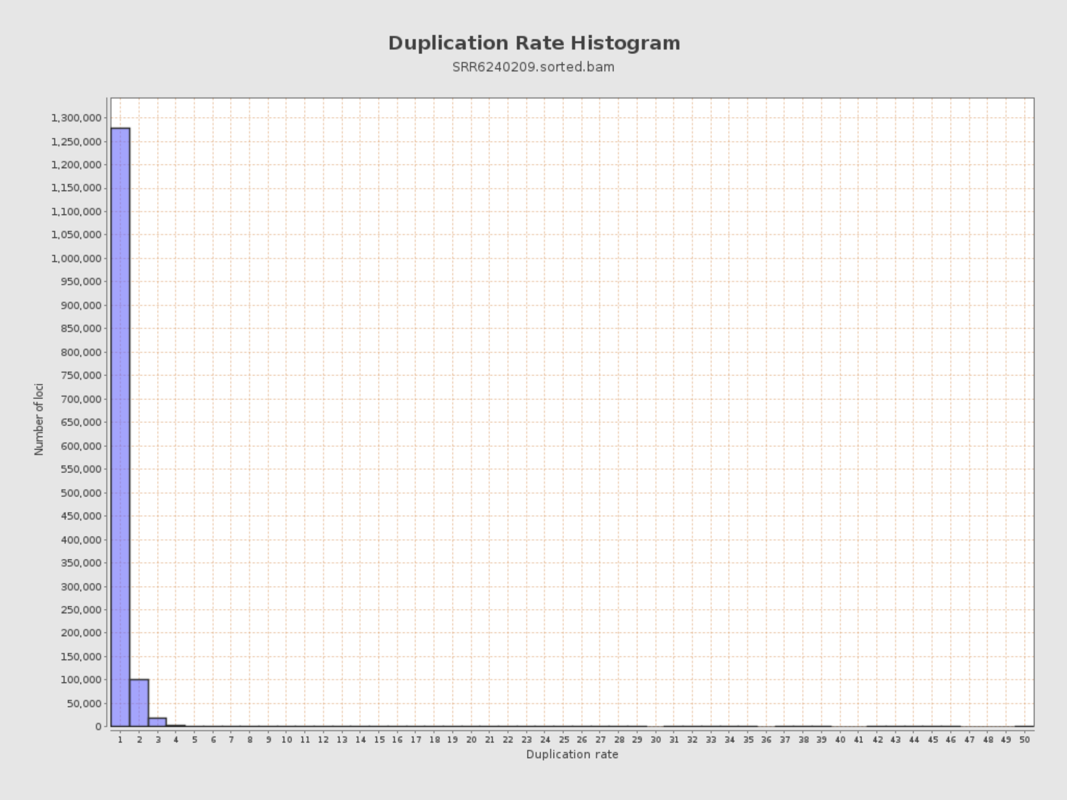
5. Results : Coverage Histogram (0-50X)



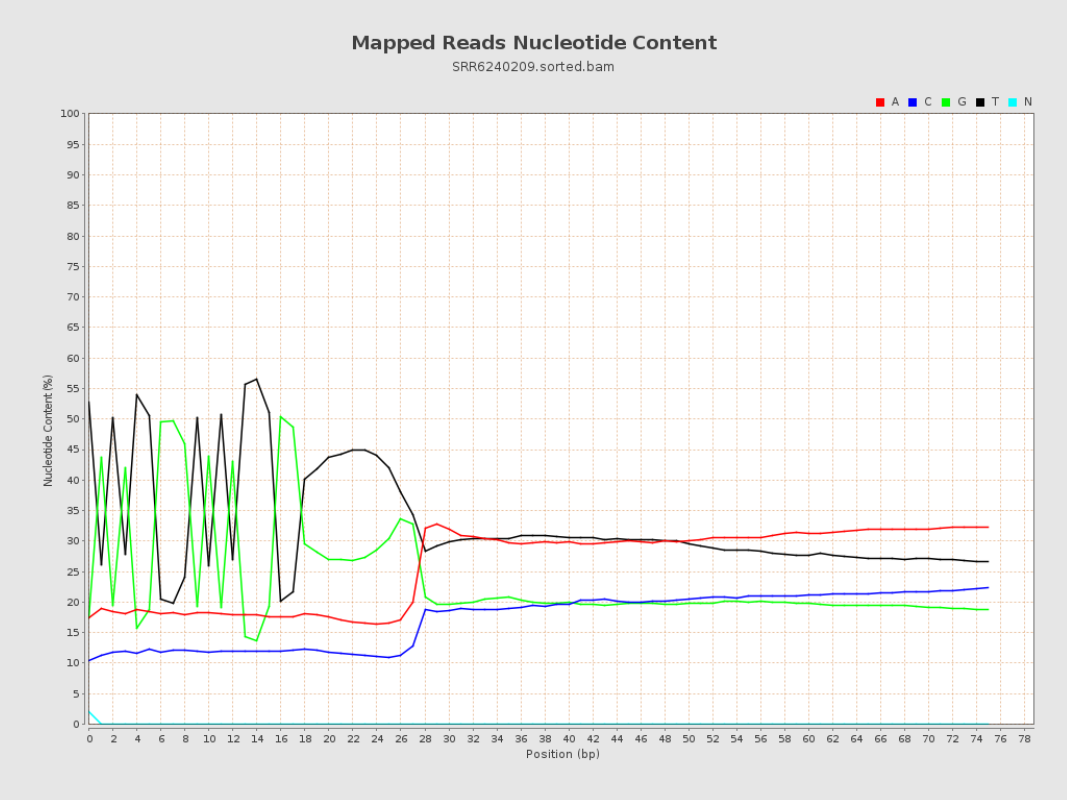
6. Results : Genome Fraction Coverage



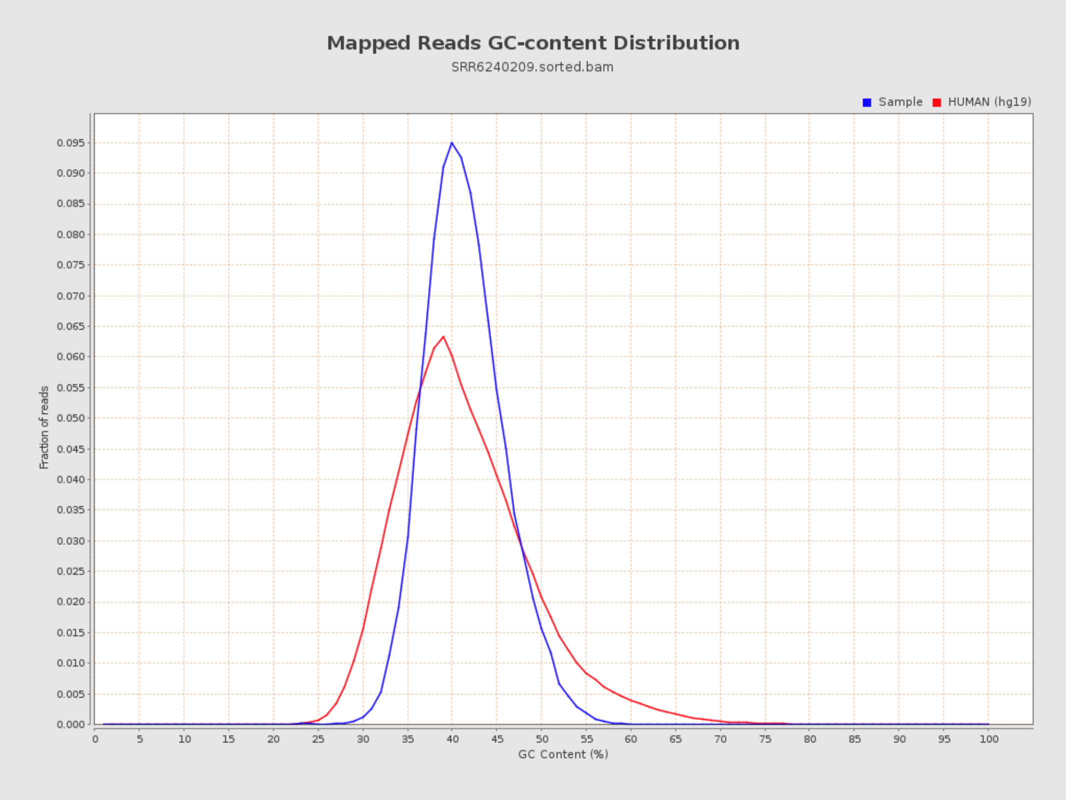
7. Results : Duplication Rate Histogram



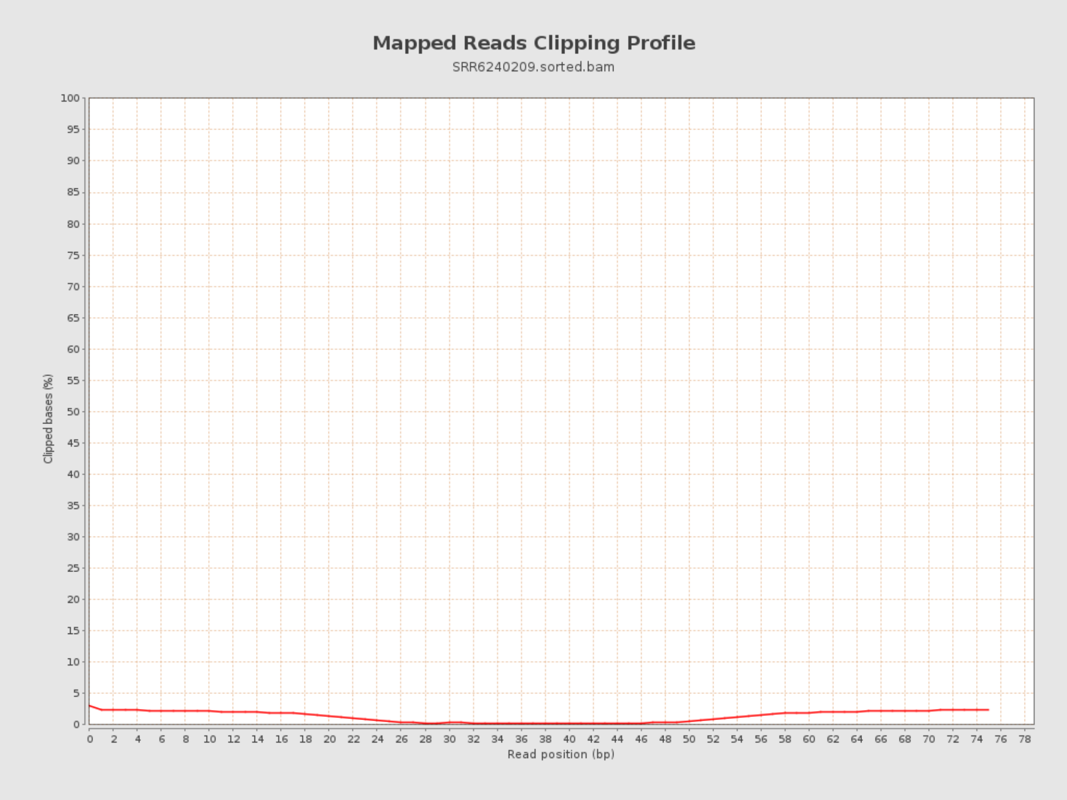
8. Results : Mapped Reads Nucleotide Content



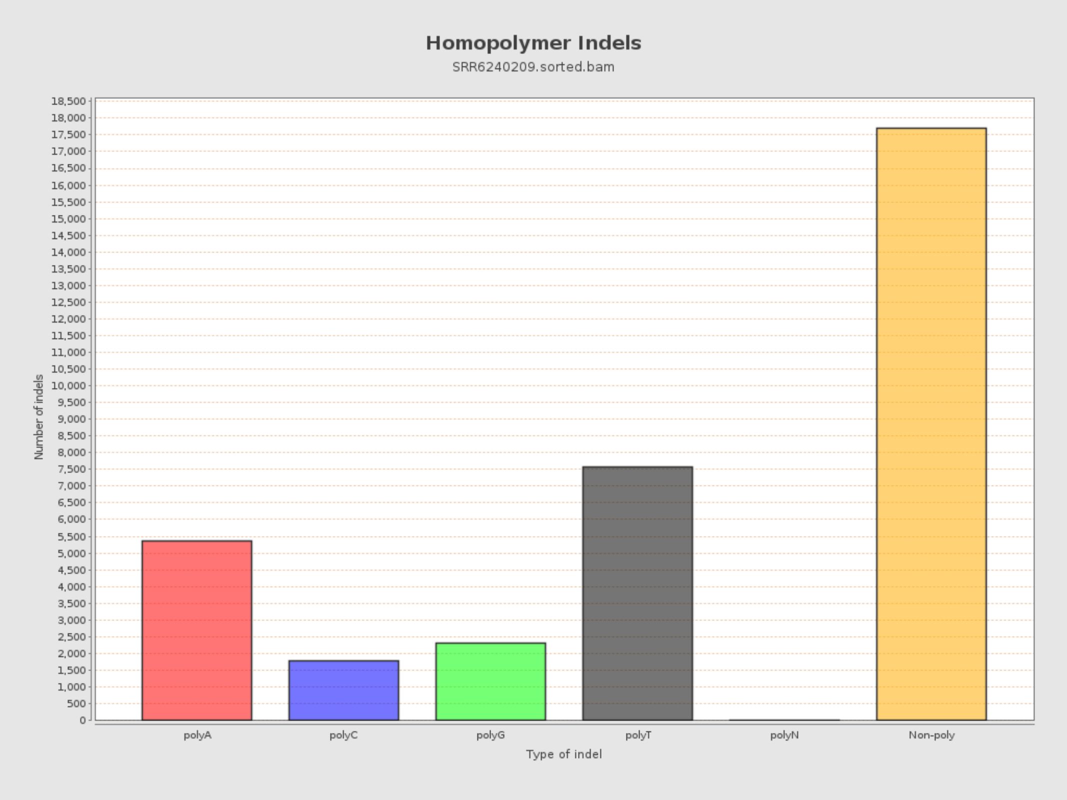
9. Results : Mapped Reads GC-content Distribution



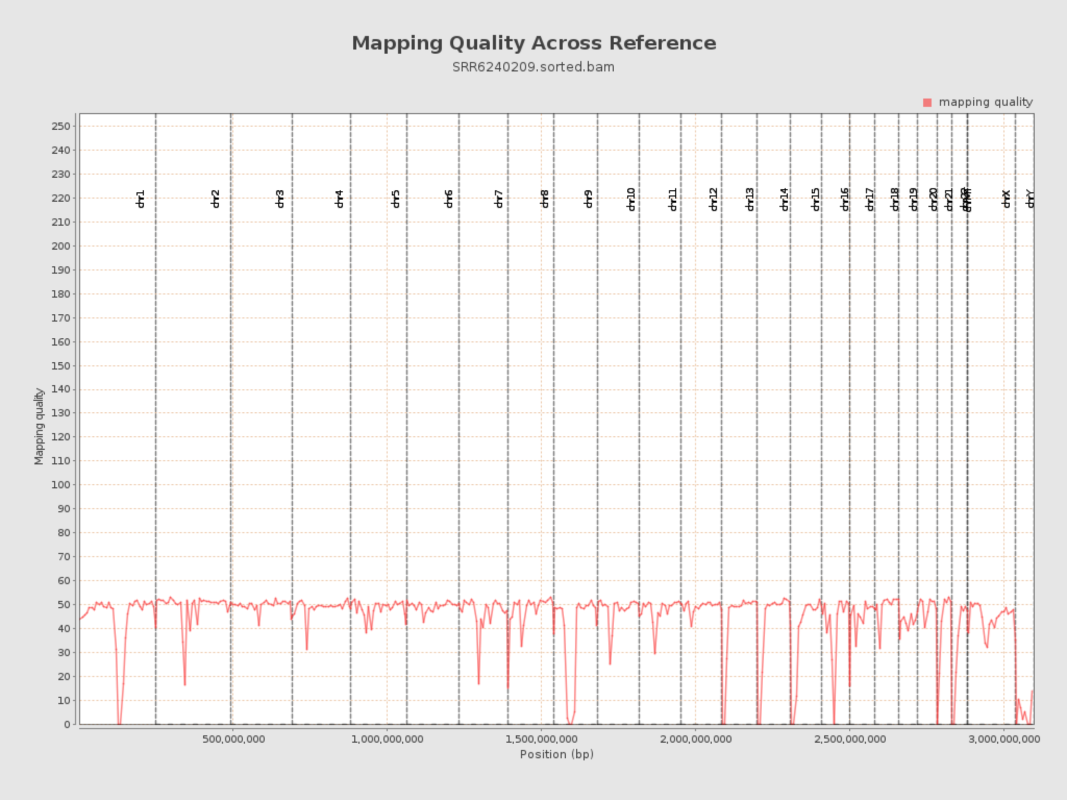
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram