Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 06:25:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240207.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_SRR6240207 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240207.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 06:25:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240207.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,587,498
Mapped reads	1,284,434 / 80.91%
Unmapped reads	303,064 / 19.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,480 / 0.28%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	114,566 / 7.22%
Duplication rate	7.39%
Clipped reads	898,318 / 56.59%

2.2. ACGT Content

Number/percentage of A's	20,625,493 / 26.53%
Number/percentage of C's	13,126,799 / 16.88%
Number/percentage of T's	25,698,418 / 33.05%
Number/percentage of G's	18,289,430 / 23.52%
Number/percentage of N's	18,132 / 0.02%
GC Percentage	40.4%

2.3. Coverage

Mean	0.0251

Standard Deviation	0.2642

2.4. Mapping Quality

Mean Mapping Quality	45.16

2.5. Mismatches and indels

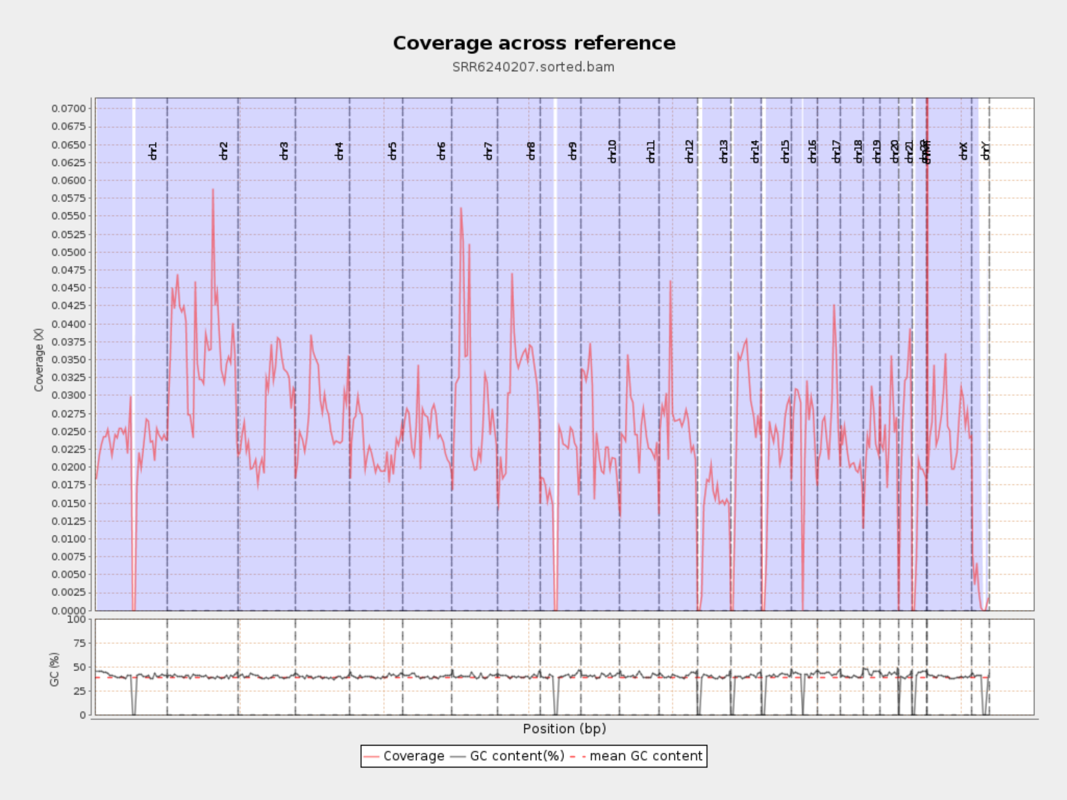
General error rate	1%
Mismatches	766,882
Insertions	5,477
Mapped reads with at least one insertion	0.42%
Deletions	28,381
Mapped reads with at least one deletion	2.18%
Homopolymer indels	51.05%

2.6. Chromosome stats

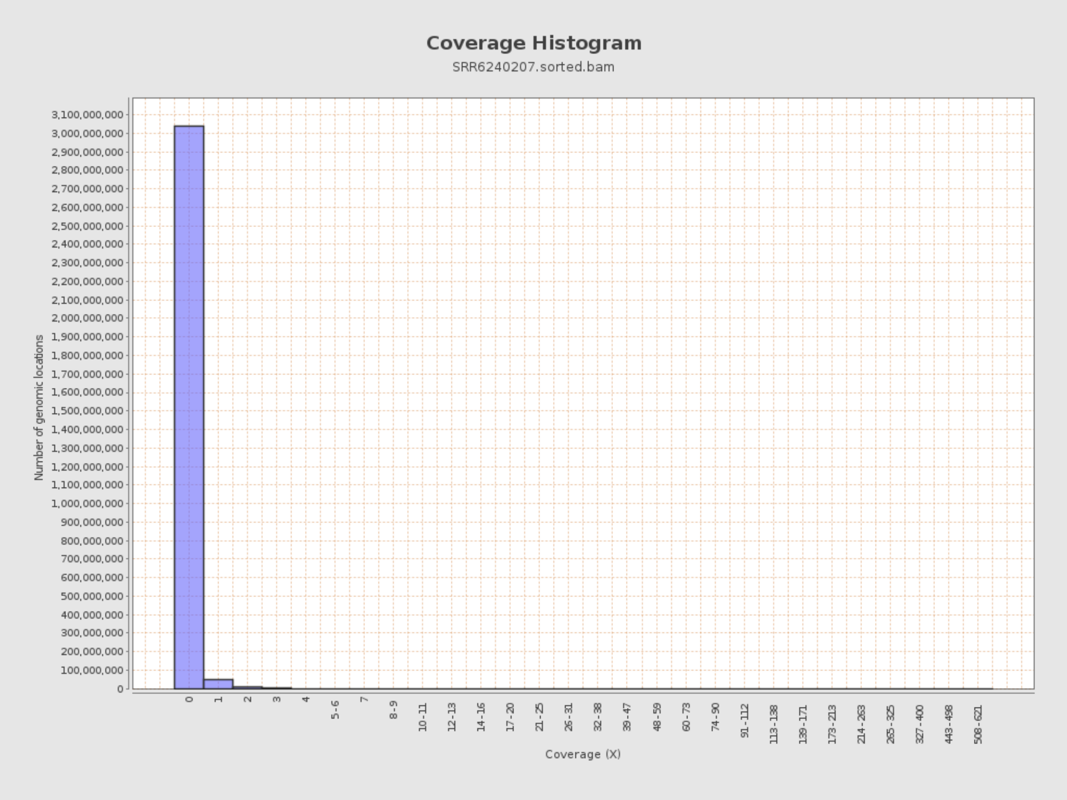
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5526386	0.0222	0.3128
chr2	243199373	9050815	0.0372	0.3151
chr3	198022430	5484431	0.0277	0.2156
chr4	191154276	5253865	0.0275	0.2186
chr5	180915260	4088912	0.0226	0.1931
chr6	171115067	4320488	0.0252	0.2334
chr7	159138663	4814811	0.0303	0.5446

chr8	146364022	4608728	0.0315	0.3123
chr9	141213431	2616388	0.0185	0.2203
chr10	135534747	3344846	0.0247	0.2228
chr11	135006516	3338531	0.0247	0.2379
chr12	133851895	3573086	0.0267	0.2082
chr13	115169878	1557954	0.0135	0.1479
chr14	107349540	2827947	0.0263	0.2121
chr15	102531392	2090176	0.0204	0.1917
chr16	90354753	2218881	0.0246	0.1998
chr17	81195210	2204569	0.0272	0.2188
chr18	78077248	1656936	0.0212	0.3142
chr19	59128983	1416952	0.024	0.2596
chr20	63025520	1549036	0.0246	0.201
chr21	48129895	1283277	0.0267	0.2109
chr22	51304566	695144	0.0135	0.1447
chrMT	16571	66699	4.025	5.0451
chrX	155270560	4062706	0.0262	0.2208
chrY	59373566	155824	0.0026	0.064

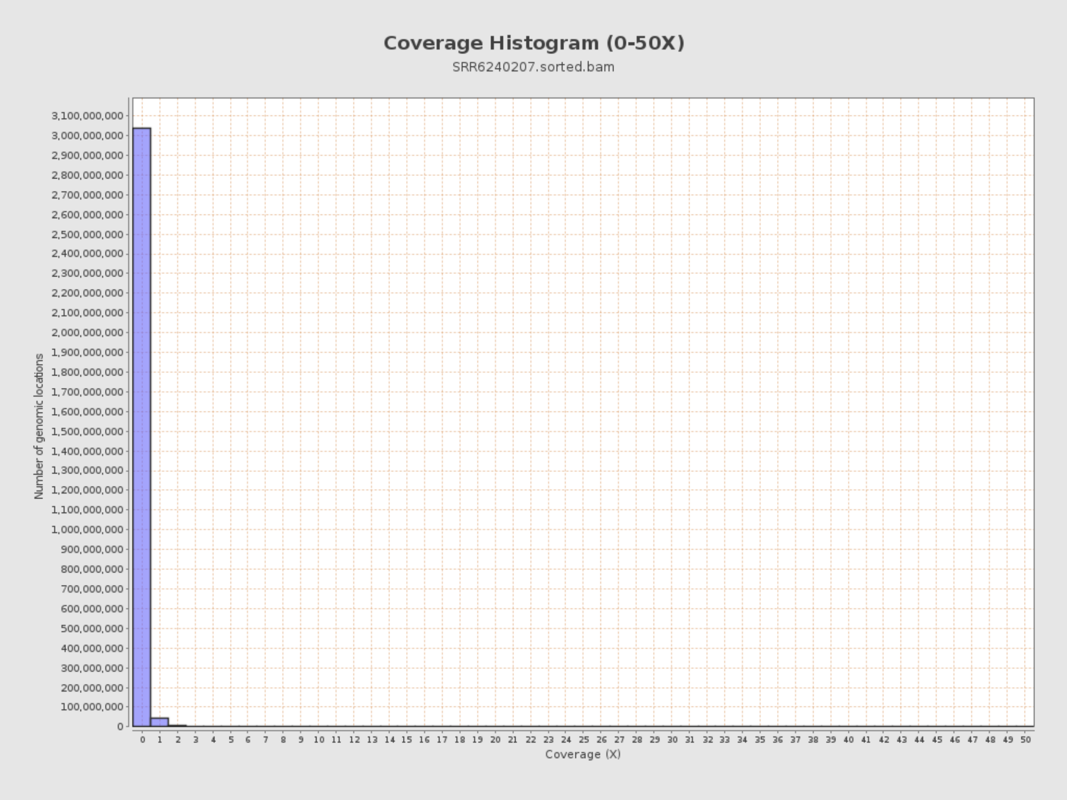
3. Results : Coverage across reference



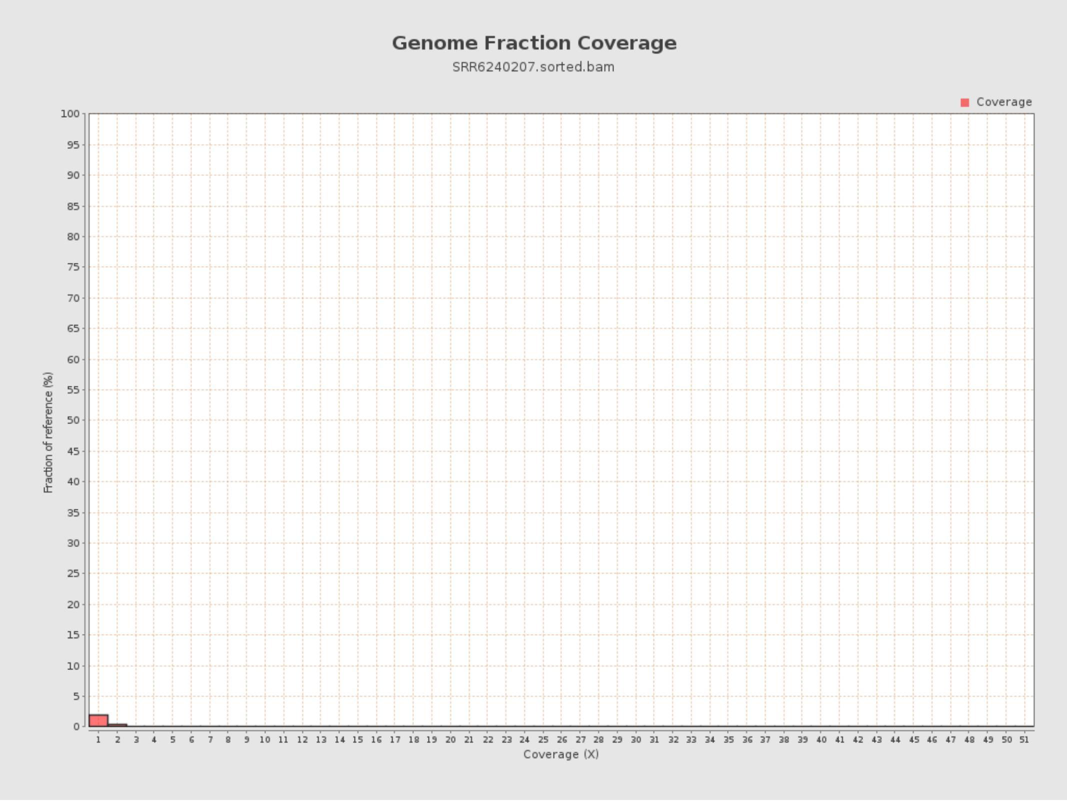
4. Results : Coverage Histogram



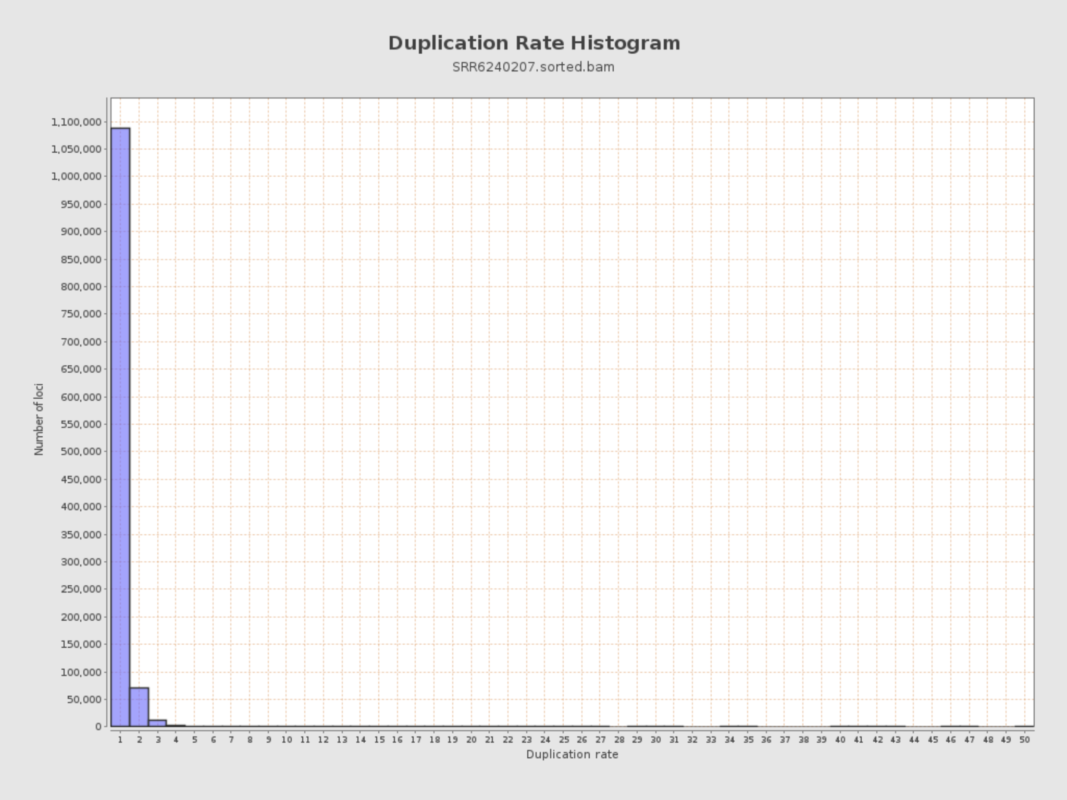
5. Results : Coverage Histogram (0-50X)



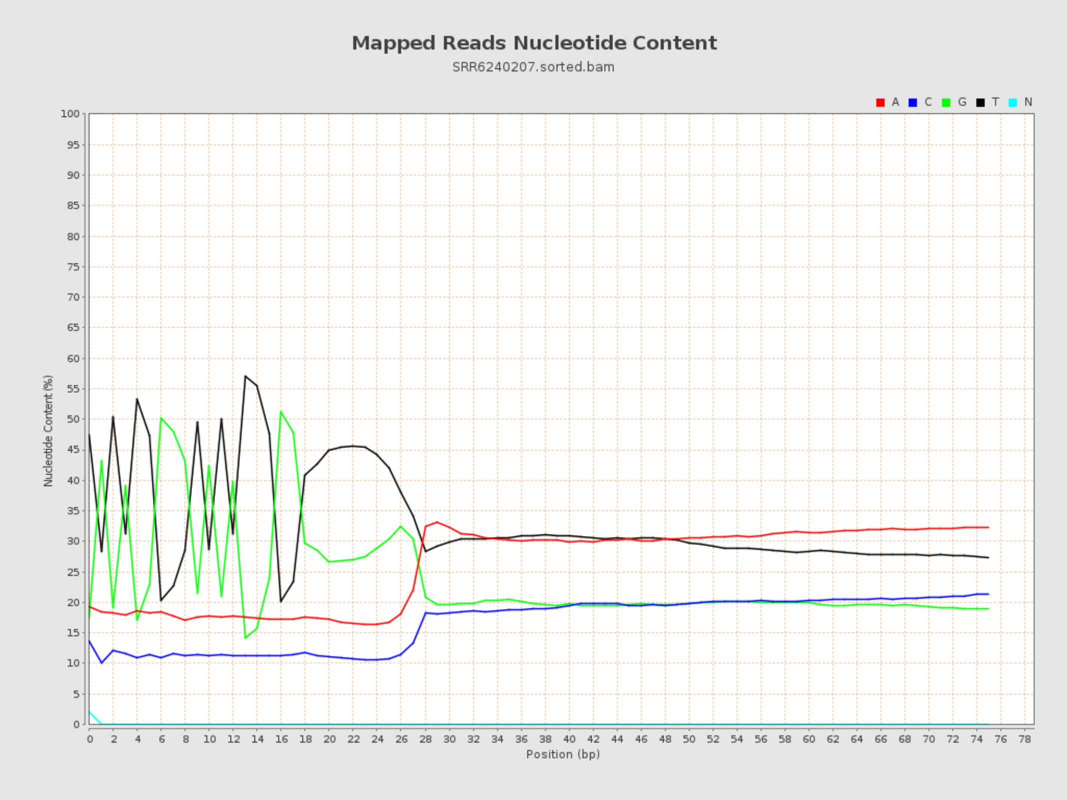
6. Results : Genome Fraction Coverage



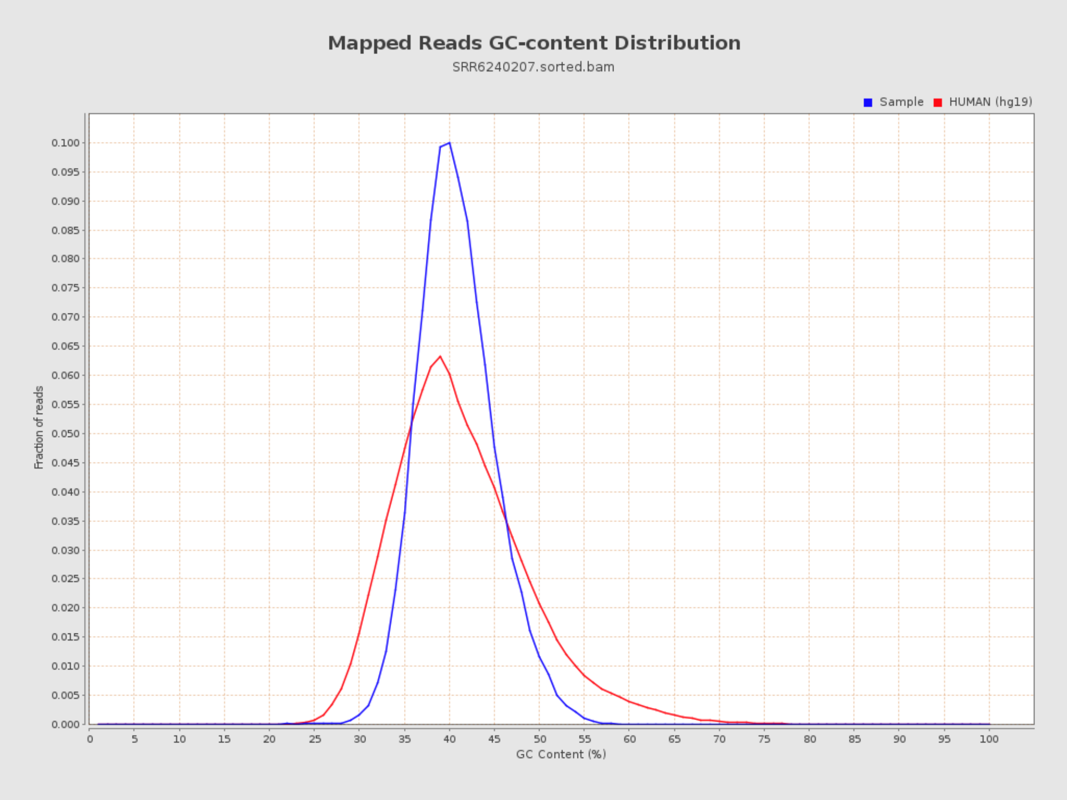
7. Results : Duplication Rate Histogram



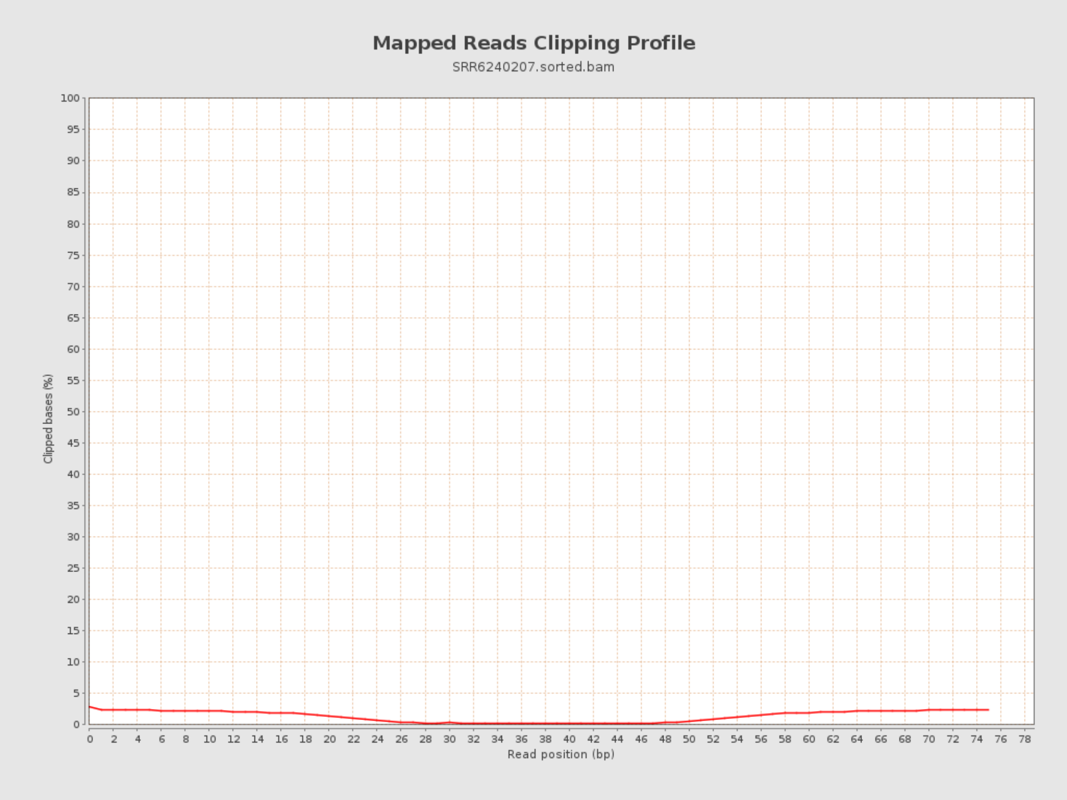
8. Results : Mapped Reads Nucleotide Content



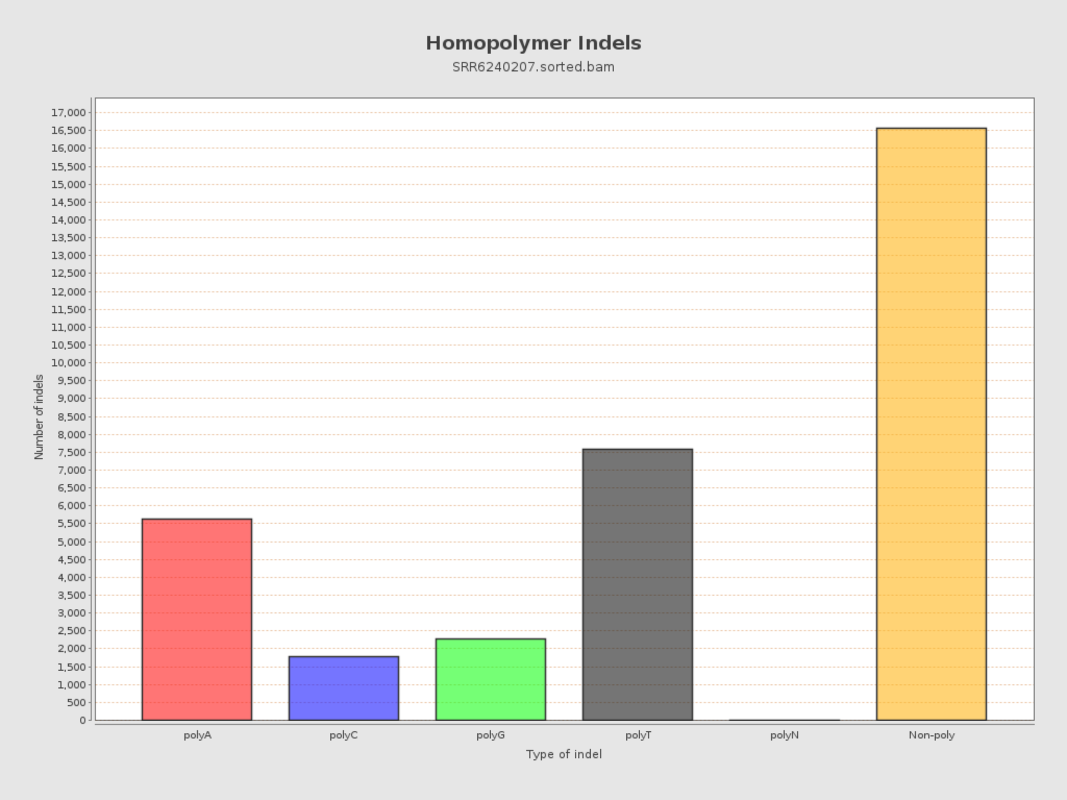
9. Results : Mapped Reads GC-content Distribution



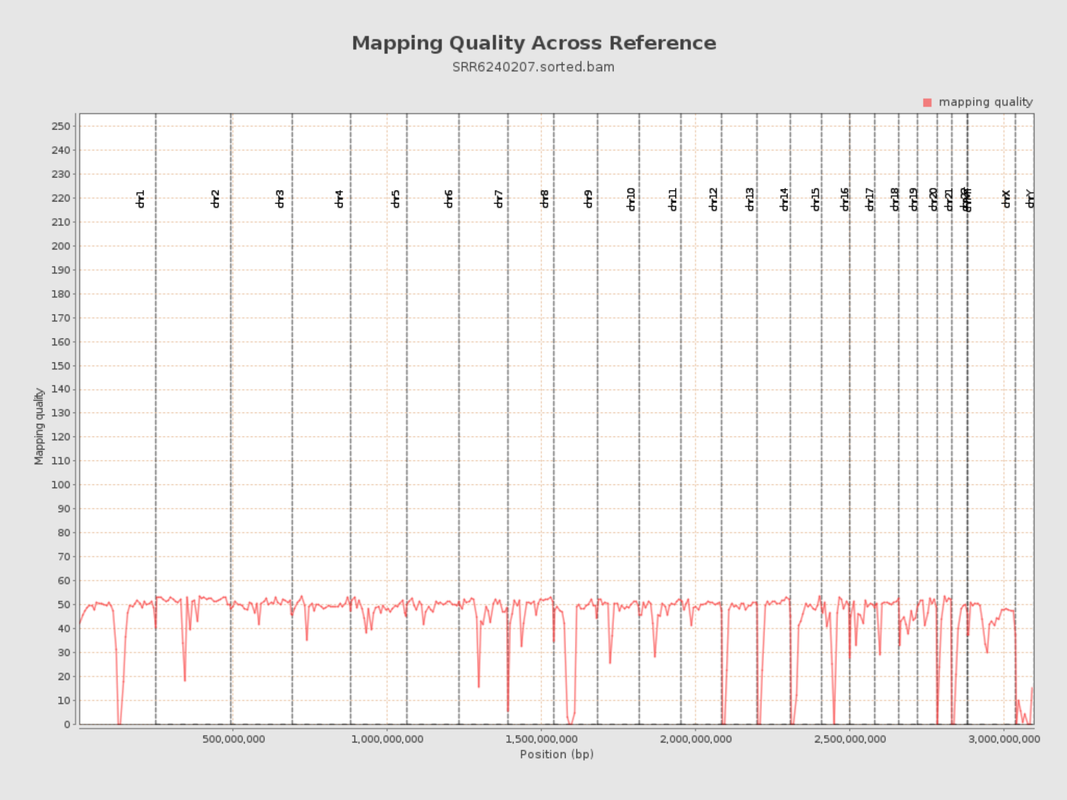
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram