Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 06:44:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240213.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_SRR6240213 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240213.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 06:44:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240213.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,026,785
Mapped reads	1,547,633 / 76.36%
Unmapped reads	479,152 / 23.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,286 / 0.7%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	86,201 / 4.25%
Duplication rate	4.51%
Clipped reads	721,526 / 35.6%

2.2. ACGT Content

Number/percentage of A's	29,477,356 / 28.67%
Number/percentage of C's	18,925,942 / 18.41%
Number/percentage of T's	32,736,373 / 31.84%
Number/percentage of G's	21,673,992 / 21.08%
Number/percentage of N's	9,884 / 0.01%
GC Percentage	39.49%

2.3. Coverage

Mean	0.0332

Standard Deviation	0.3469

2.4. Mapping Quality

Mean Mapping Quality	47.06

2.5. Mismatches and indels

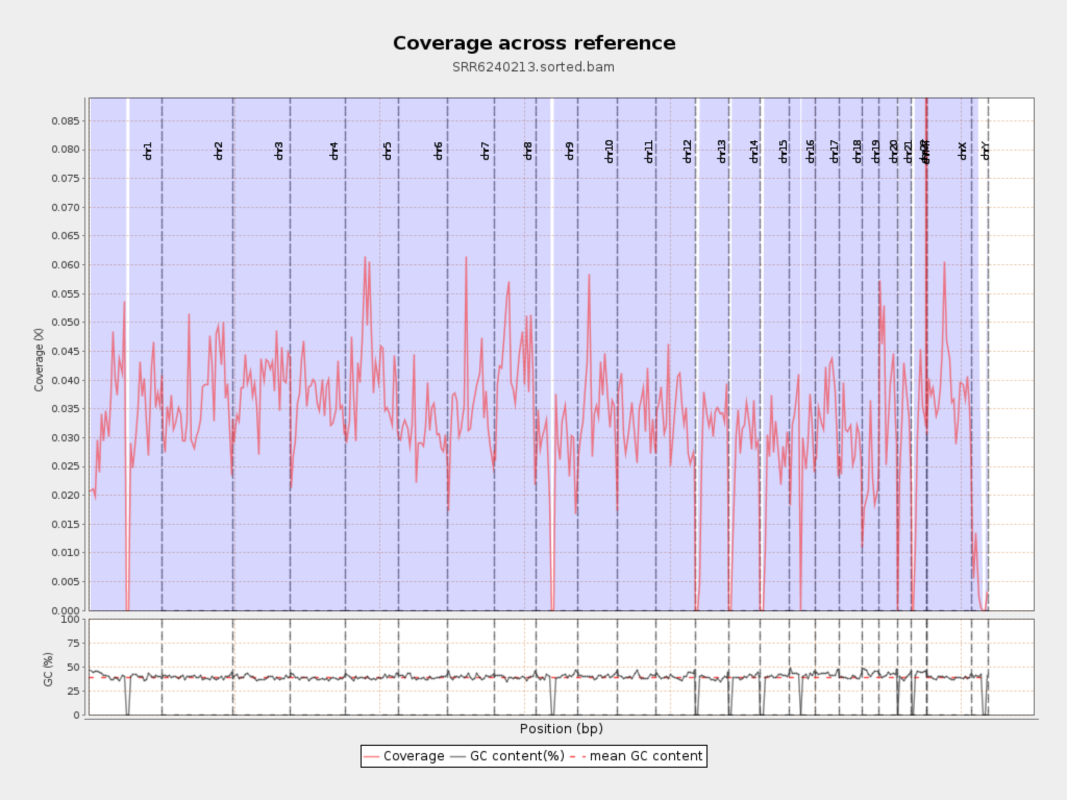
General error rate	0.82%
Mismatches	831,472
Insertions	7,485
Mapped reads with at least one insertion	0.48%
Deletions	27,642
Mapped reads with at least one deletion	1.77%
Homopolymer indels	46.55%

2.6. Chromosome stats

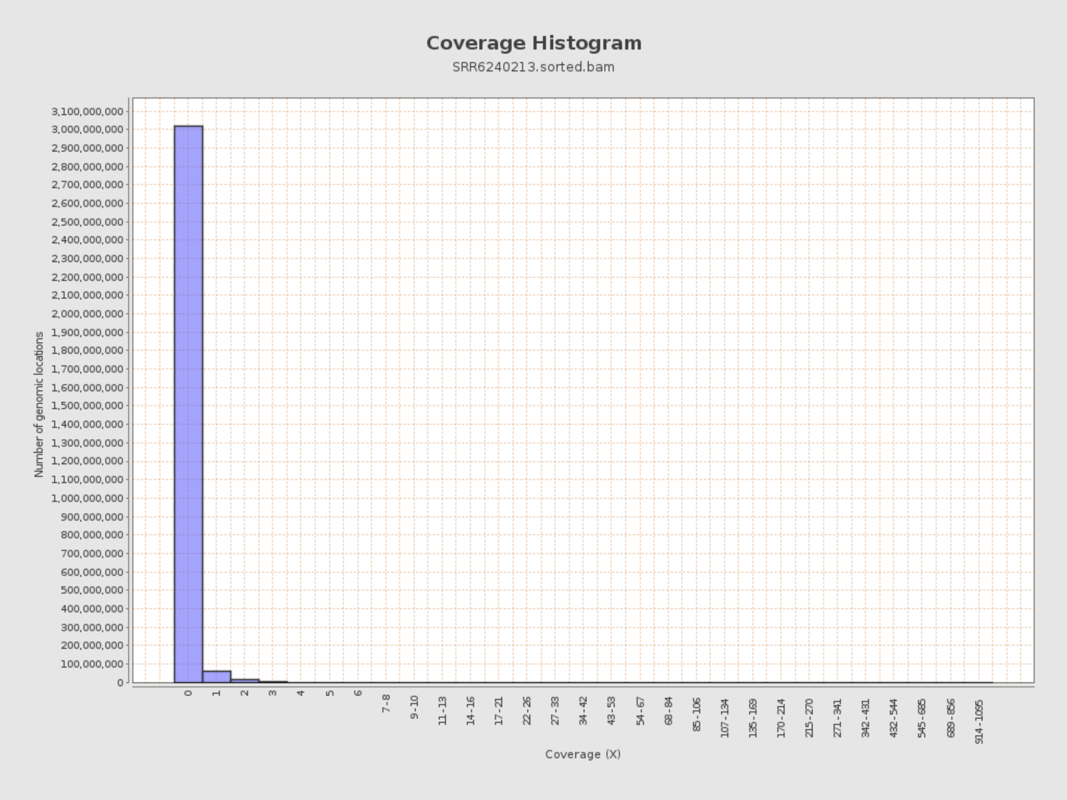
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8133349	0.0326	0.5268
chr2	243199373	8815427	0.0362	0.3363
chr3	198022430	7789517	0.0393	0.2503
chr4	191154276	6925724	0.0362	0.2482
chr5	180915260	7495308	0.0414	0.2591
chr6	171115067	5364335	0.0313	0.2559
chr7	159138663	5640509	0.0354	0.4218

chr8	146364022	6169507	0.0422	0.7013
chr9	141213431	3679158	0.0261	0.2888
chr10	135534747	4937449	0.0364	0.3287
chr11	135006516	4426763	0.0328	0.3059
chr12	133851895	4485579	0.0335	0.2341
chr13	115169878	3217418	0.0279	0.2118
chr14	107349540	2807838	0.0262	0.2962
chr15	102531392	2388222	0.0233	0.1928
chr16	90354753	2591527	0.0287	0.2324
chr17	81195210	2844320	0.035	0.2515
chr18	78077248	2332310	0.0299	0.5425
chr19	59128983	1300544	0.022	0.3874
chr20	63025520	2534411	0.0402	0.2538
chr21	48129895	1419497	0.0295	0.2228
chr22	51304566	1268080	0.0247	0.193
chrMT	16571	24320	1.4676	1.8219
chrX	155270560	6030662	0.0388	0.2788
chrY	59373566	249688	0.0042	0.1098

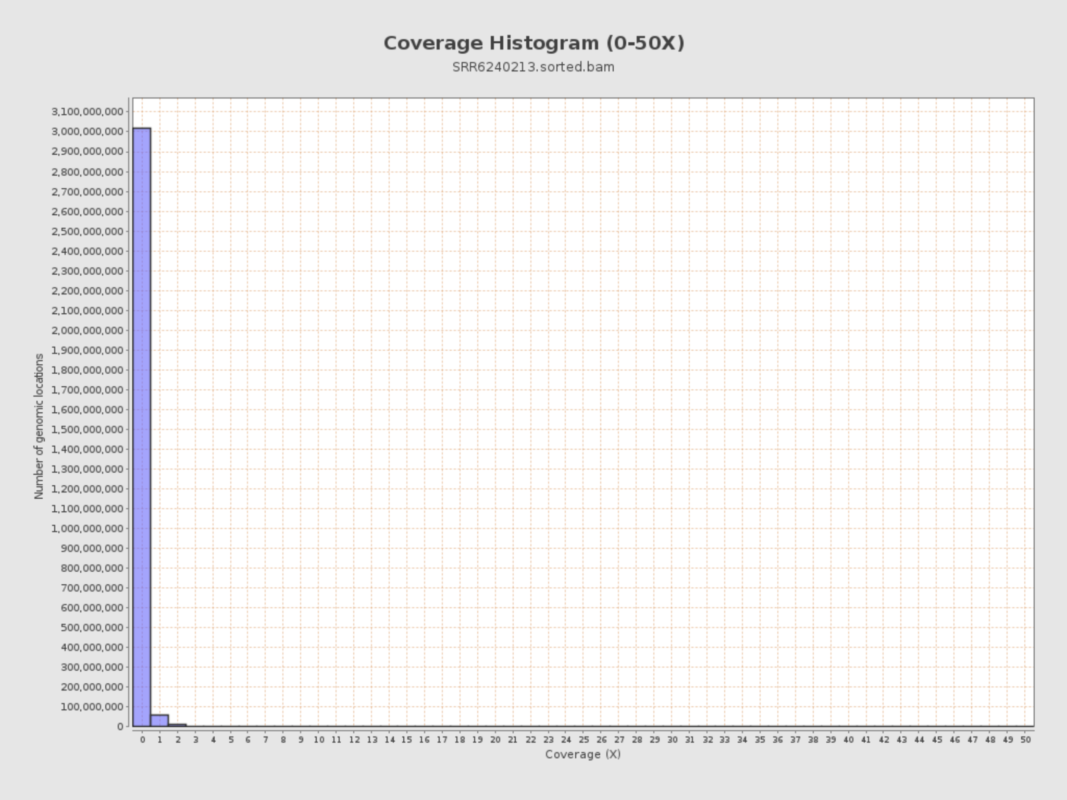
3. Results : Coverage across reference



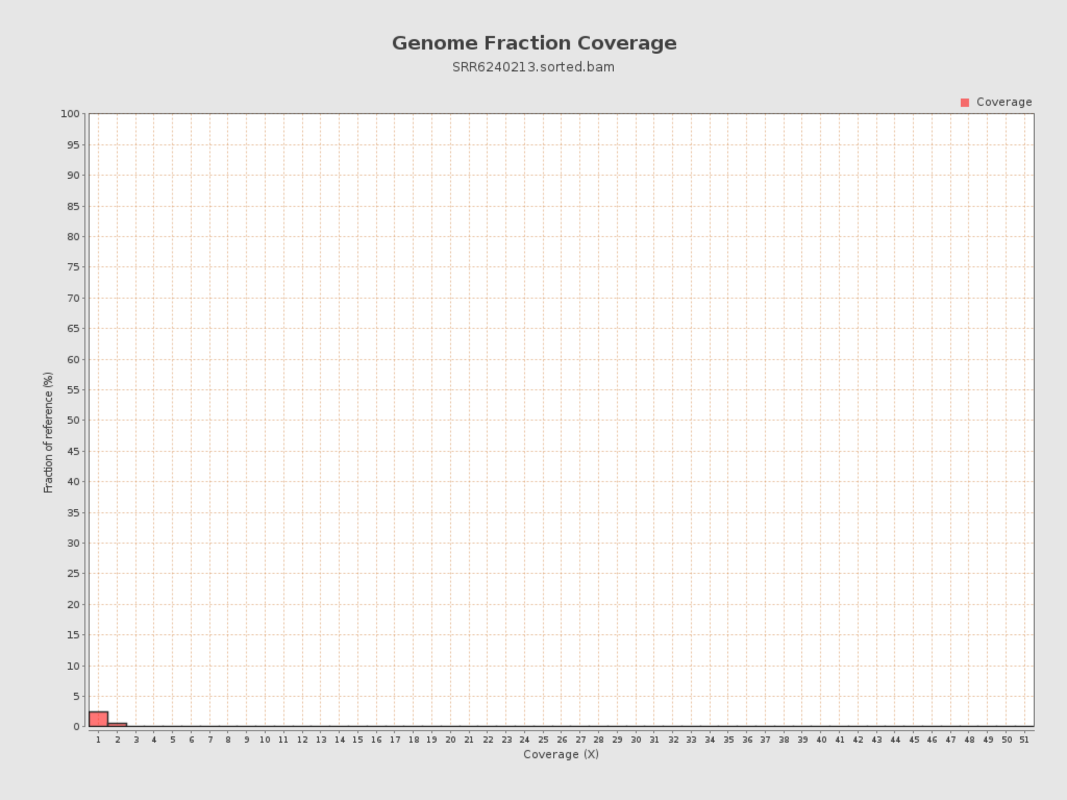
4. Results : Coverage Histogram



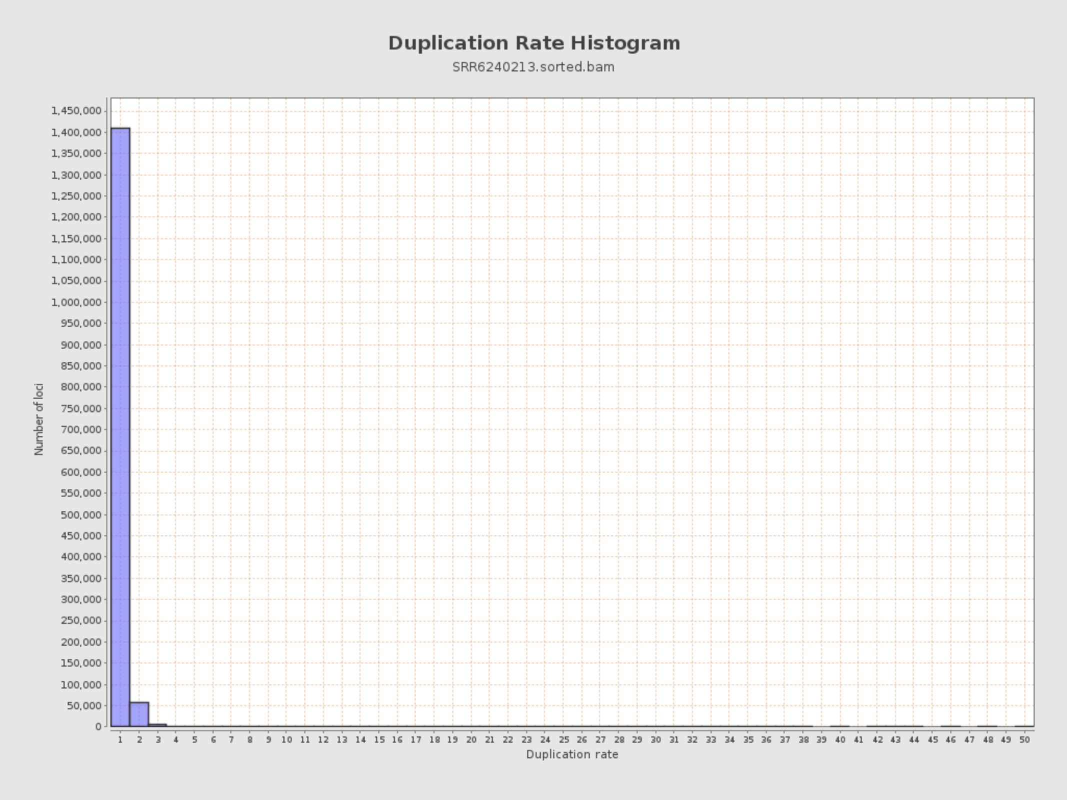
5. Results : Coverage Histogram (0-50X)



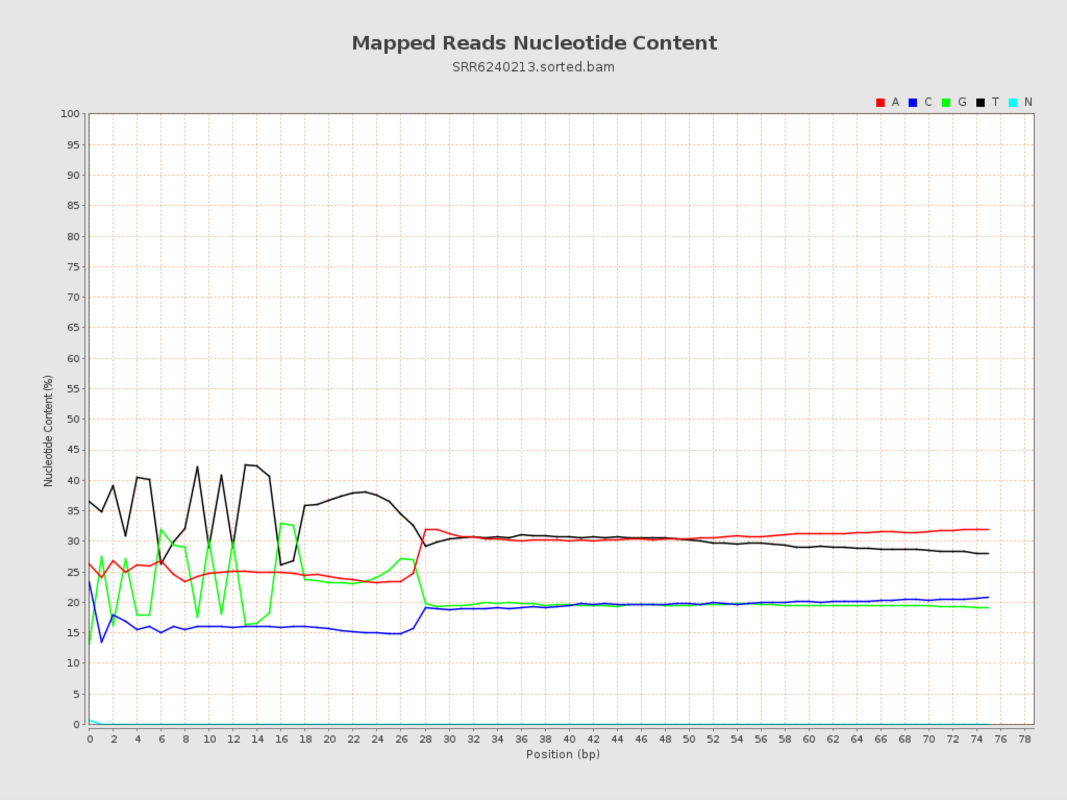
6. Results : Genome Fraction Coverage



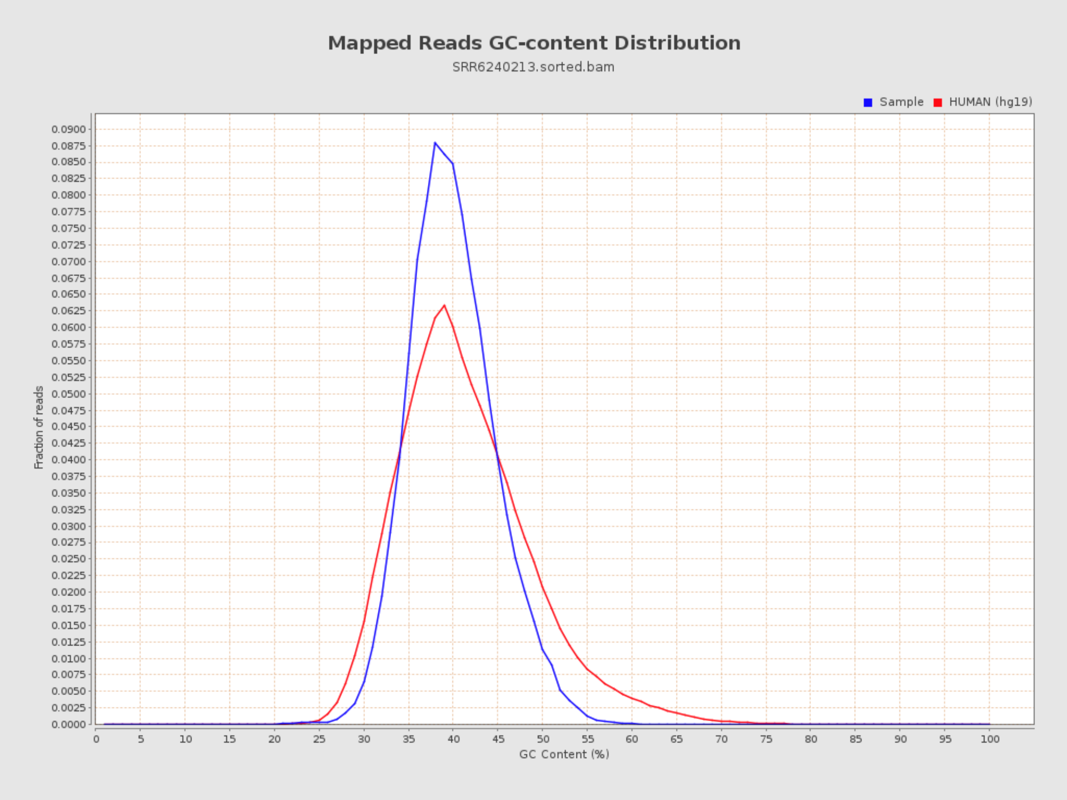
7. Results : Duplication Rate Histogram



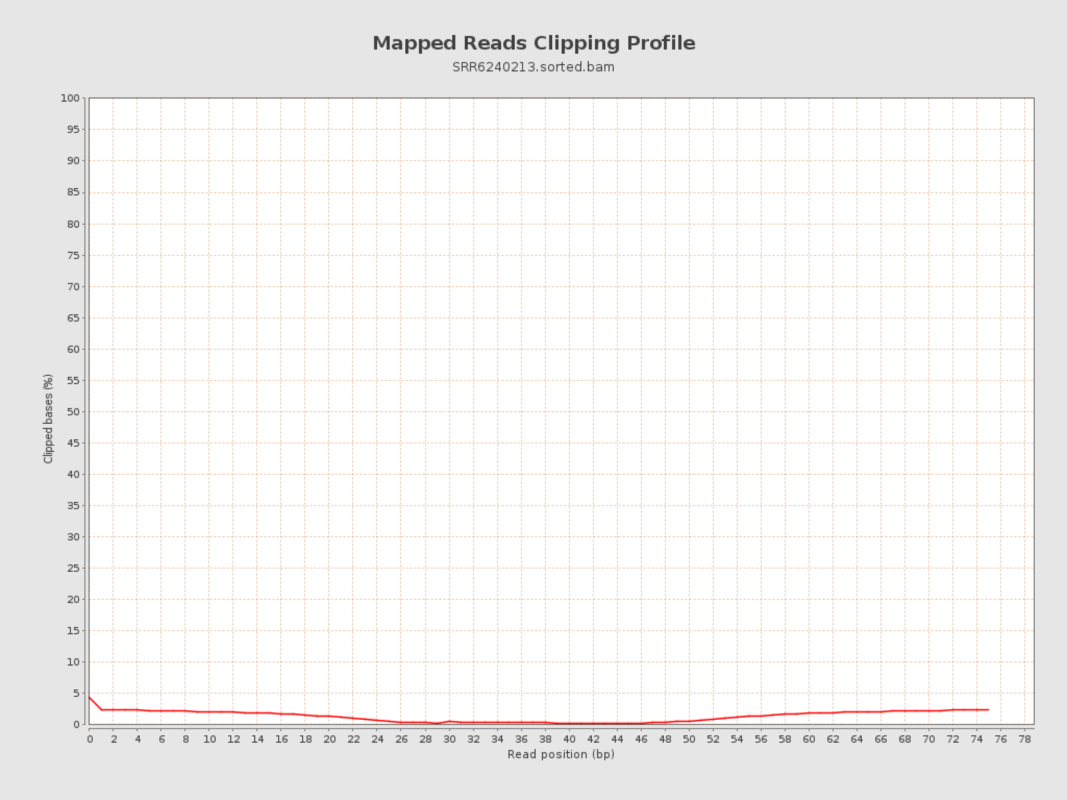
8. Results : Mapped Reads Nucleotide Content



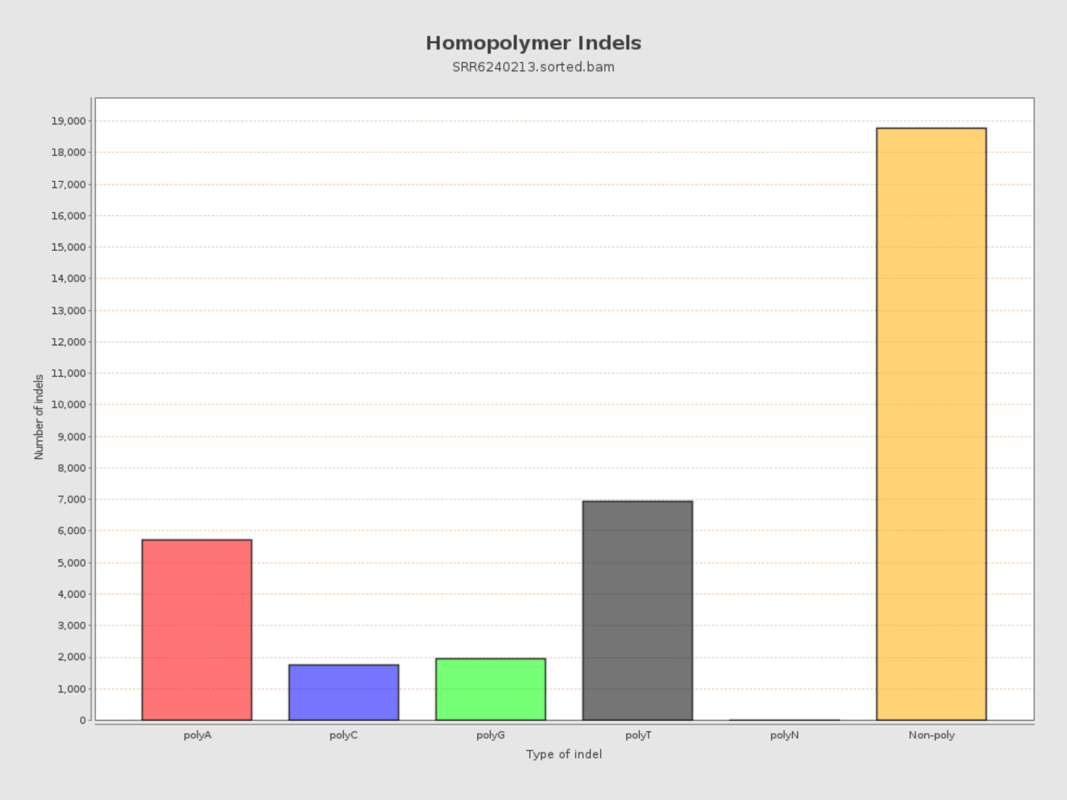
9. Results : Mapped Reads GC-content Distribution



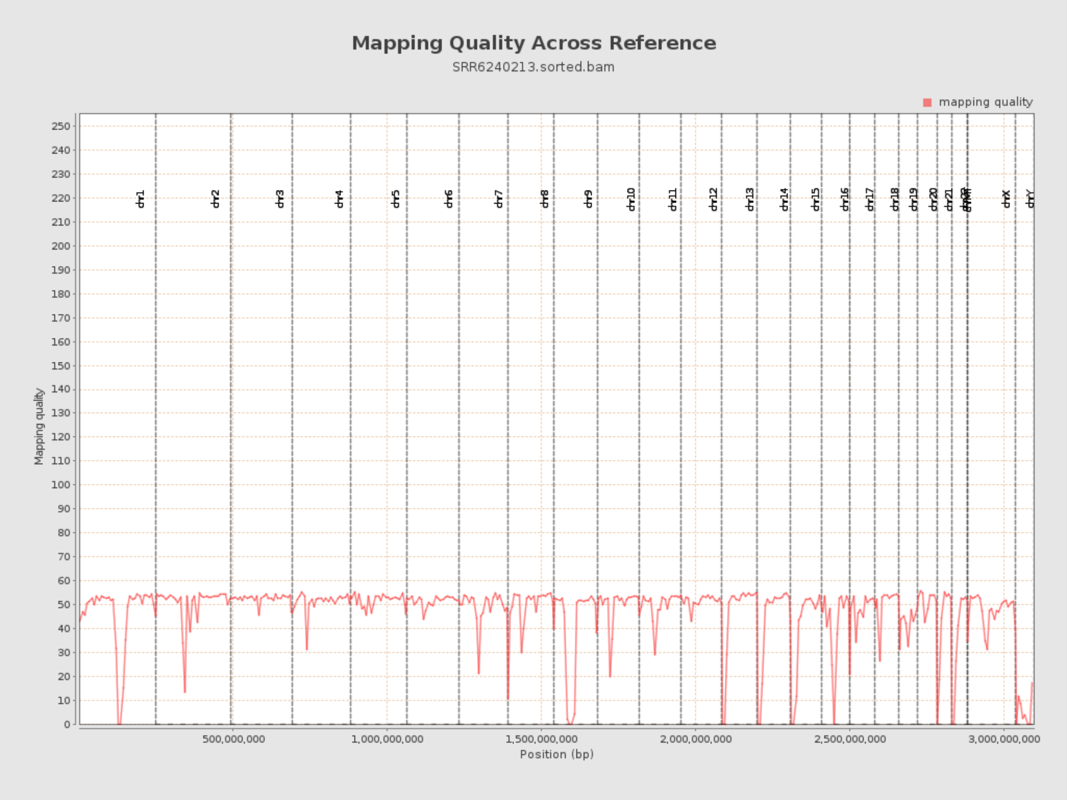
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram