Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 06:07:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240200.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_SRR6240200 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240200.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 06:07:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240200.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,975,038
Mapped reads	1,470,062 / 74.43%
Unmapped reads	504,976 / 25.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,078 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	95,940 / 4.86%
Duplication rate	5.47%
Clipped reads	931,223 / 47.15%

2.2. ACGT Content

Number/percentage of A's	24,789,085 / 27.15%
Number/percentage of C's	15,682,478 / 17.17%
Number/percentage of T's	29,703,850 / 32.53%
Number/percentage of G's	21,120,761 / 23.13%
Number/percentage of N's	21,438 / 0.02%
GC Percentage	40.3%

2.3. Coverage

Mean	0.0295

Standard Deviation	0.2856

2.4. Mapping Quality

Mean Mapping Quality	45.33

2.5. Mismatches and indels

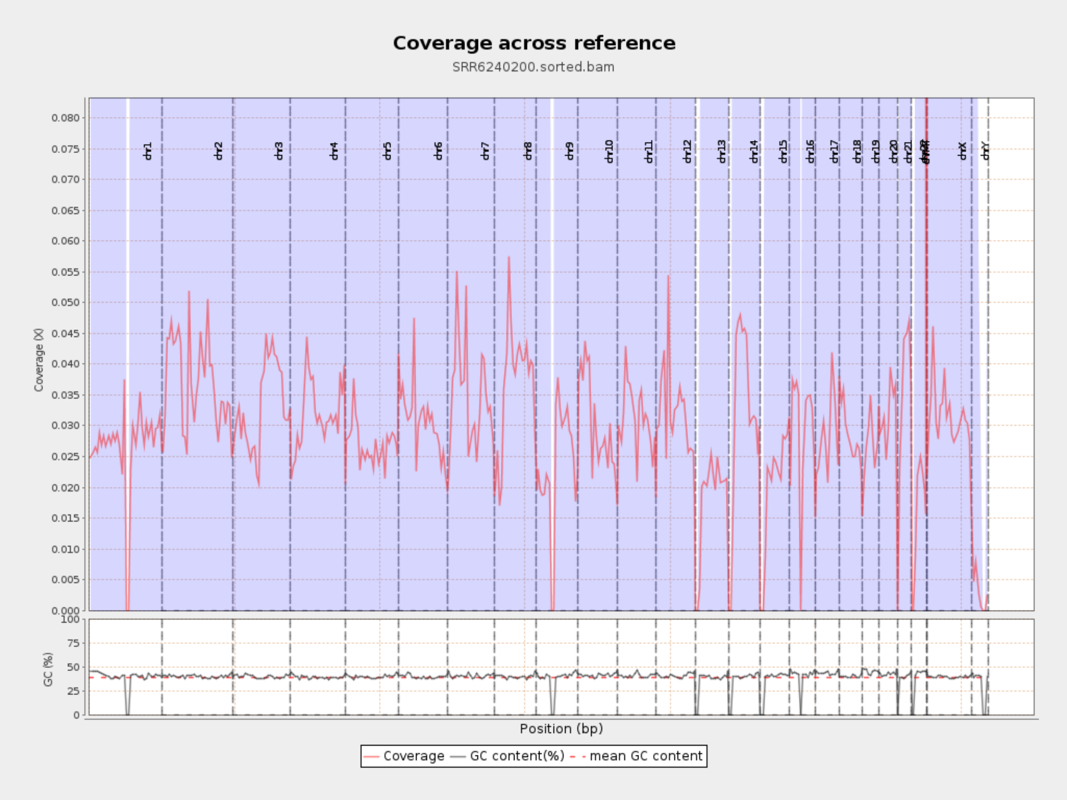
General error rate	0.94%
Mismatches	847,228
Insertions	6,374
Mapped reads with at least one insertion	0.43%
Deletions	28,990
Mapped reads with at least one deletion	1.95%
Homopolymer indels	48.47%

2.6. Chromosome stats

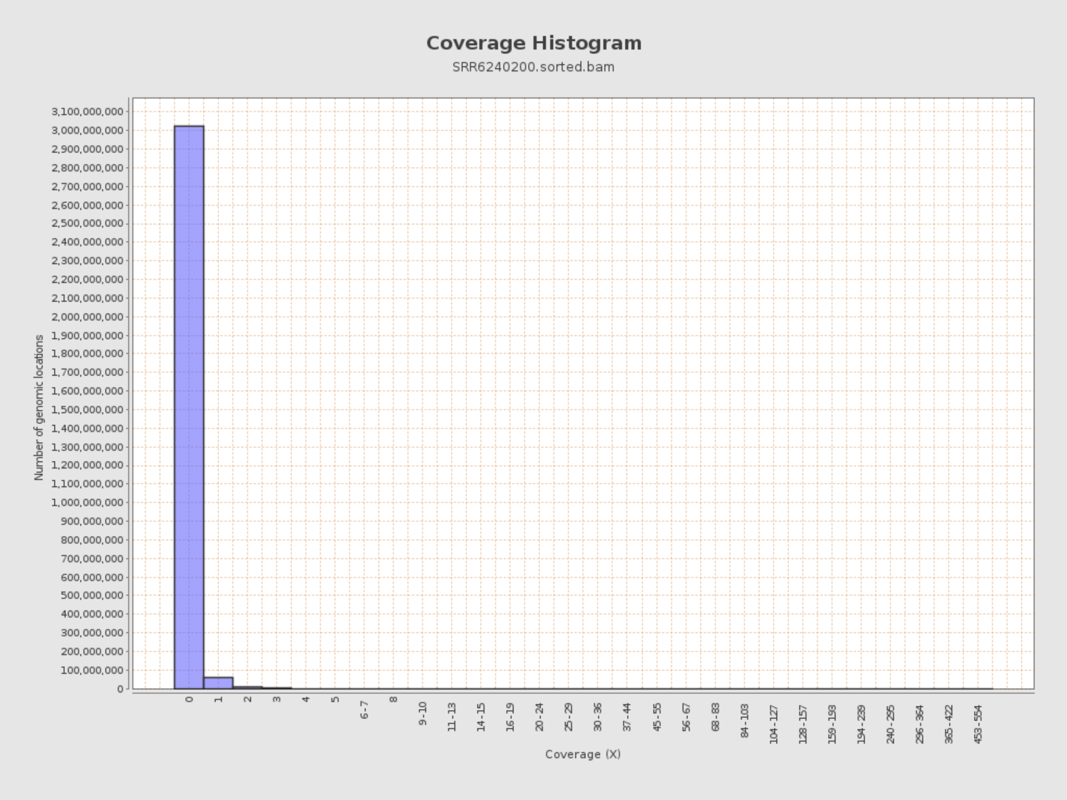
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6620017	0.0266	0.4007
chr2	243199373	9038530	0.0372	0.3486
chr3	198022430	6554465	0.0331	0.2188
chr4	191154276	6087207	0.0318	0.2229
chr5	180915260	4892126	0.027	0.1985
chr6	171115067	5292061	0.0309	0.2648
chr7	159138663	5588911	0.0351	0.457

chr8	146364022	5398473	0.0369	0.4073
chr9	141213431	3304736	0.0234	0.2507
chr10	135534747	4169848	0.0308	0.2567
chr11	135006516	4205388	0.0311	0.2723
chr12	133851895	4338977	0.0324	0.2187
chr13	115169878	2061737	0.0179	0.1592
chr14	107349540	3444333	0.0321	0.2232
chr15	102531392	2047026	0.02	0.1848
chr16	90354753	2658238	0.0294	0.2104
chr17	81195210	2286177	0.0282	0.2131
chr18	78077248	2250868	0.0288	0.4022
chr19	59128983	1604554	0.0271	0.3111
chr20	63025520	1976895	0.0314	0.2139
chr21	48129895	1669235	0.0347	0.2319
chr22	51304566	786105	0.0153	0.1434
chrMT	16571	34162	2.0616	2.4955
chrX	155270560	4864893	0.0313	0.229
chrY	59373566	192358	0.0032	0.0722

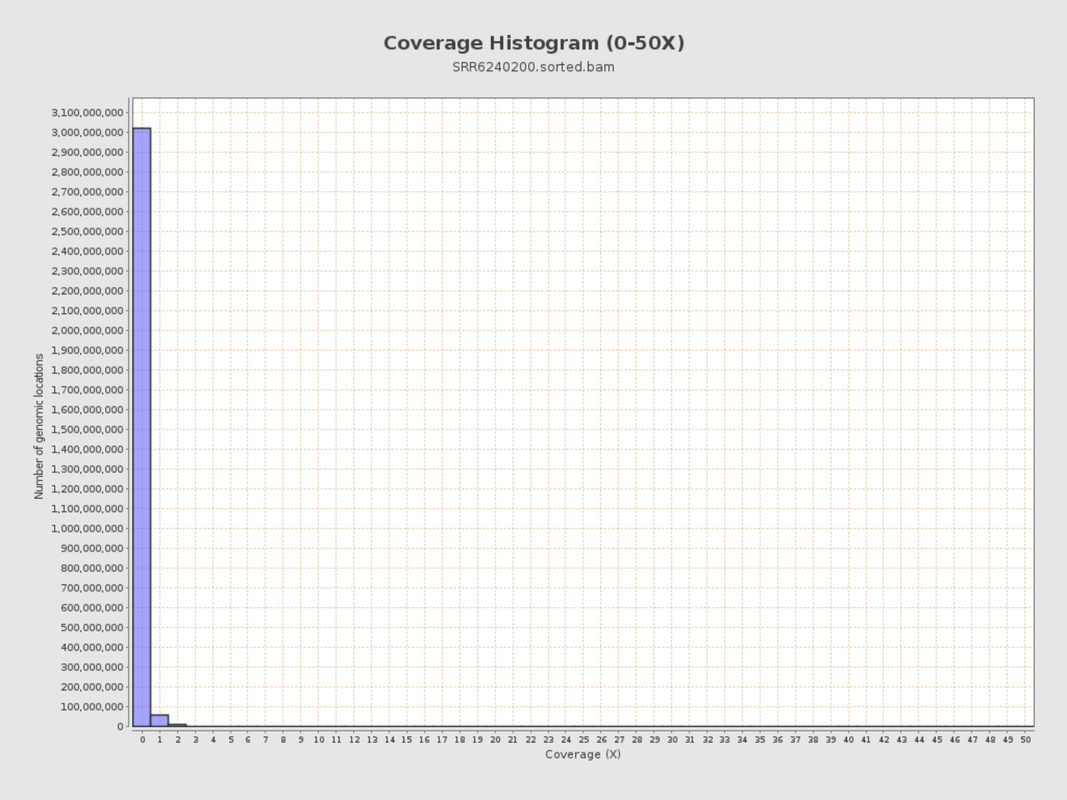
3. Results : Coverage across reference



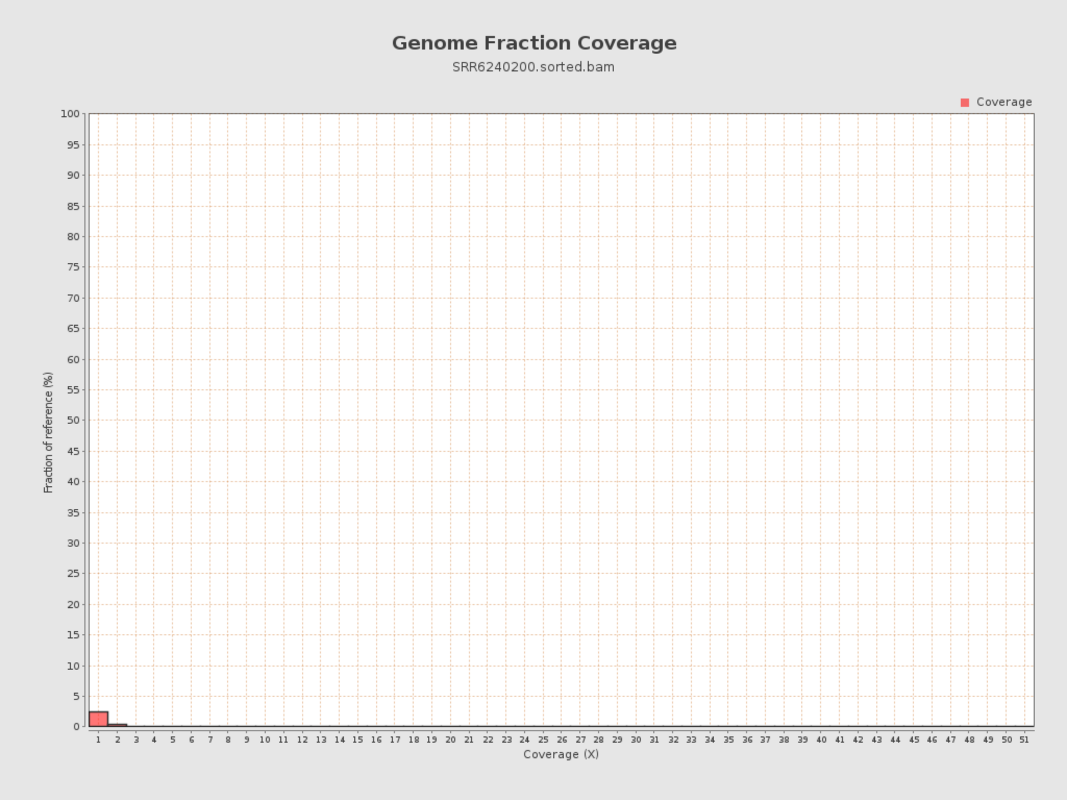
4. Results : Coverage Histogram



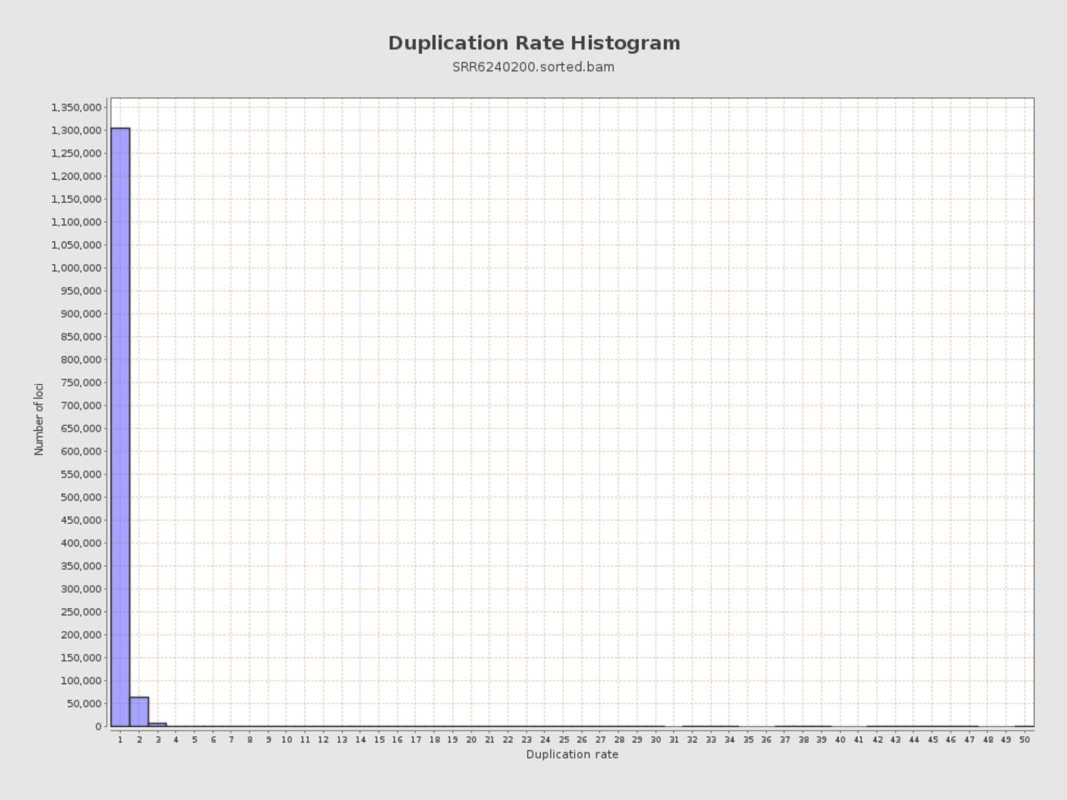
5. Results : Coverage Histogram (0-50X)



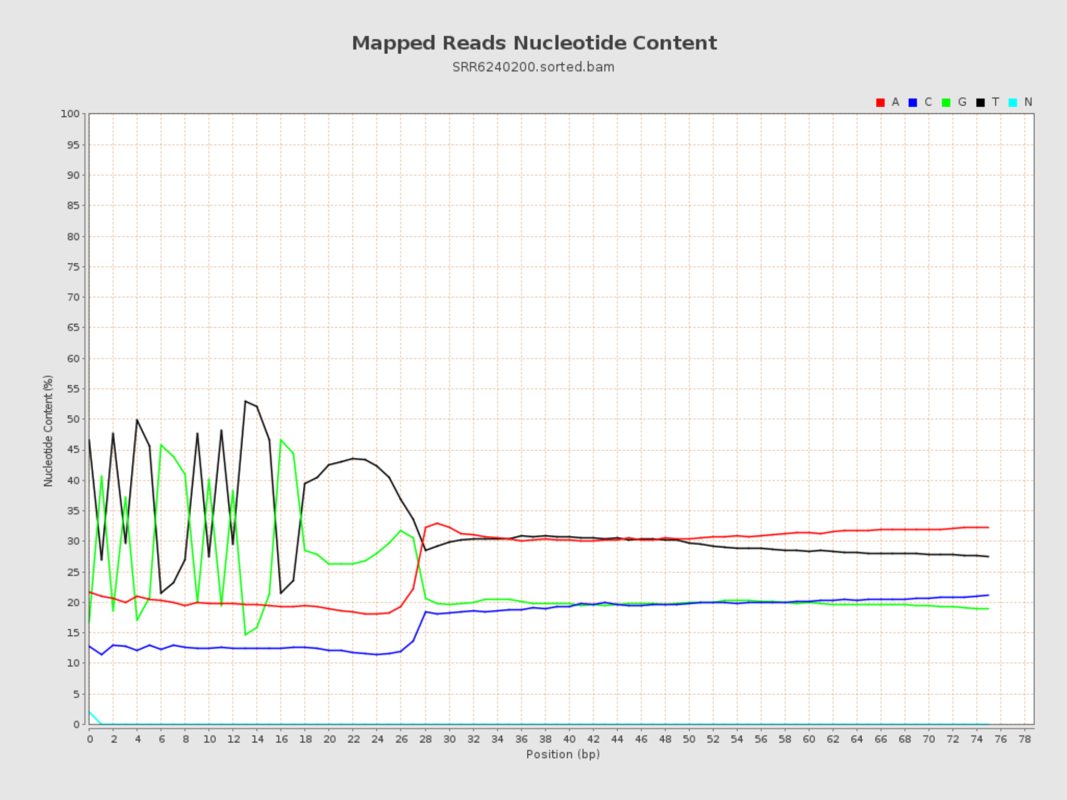
6. Results : Genome Fraction Coverage



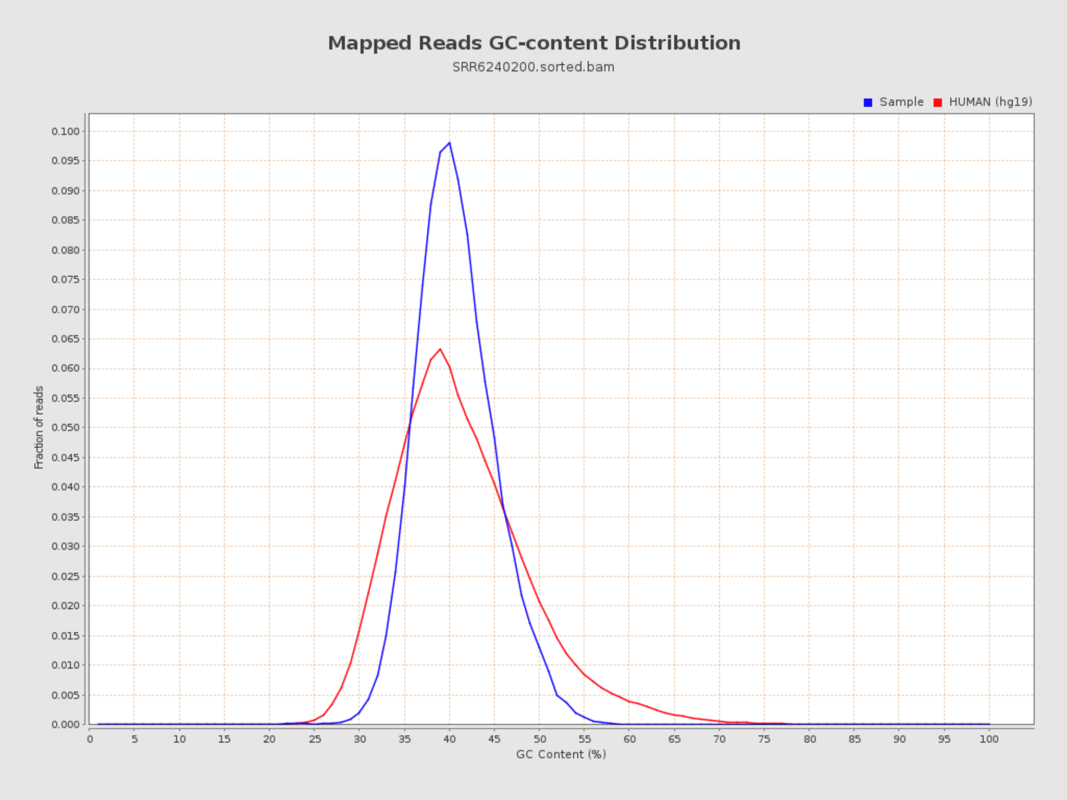
7. Results : Duplication Rate Histogram



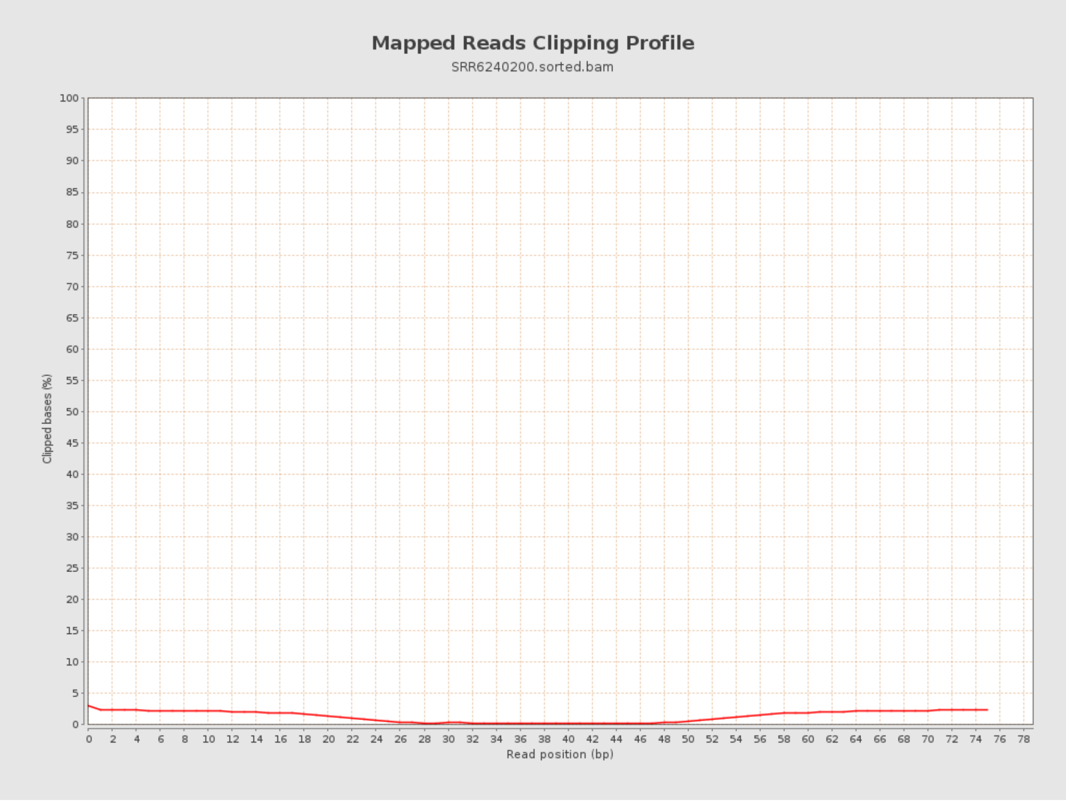
8. Results : Mapped Reads Nucleotide Content



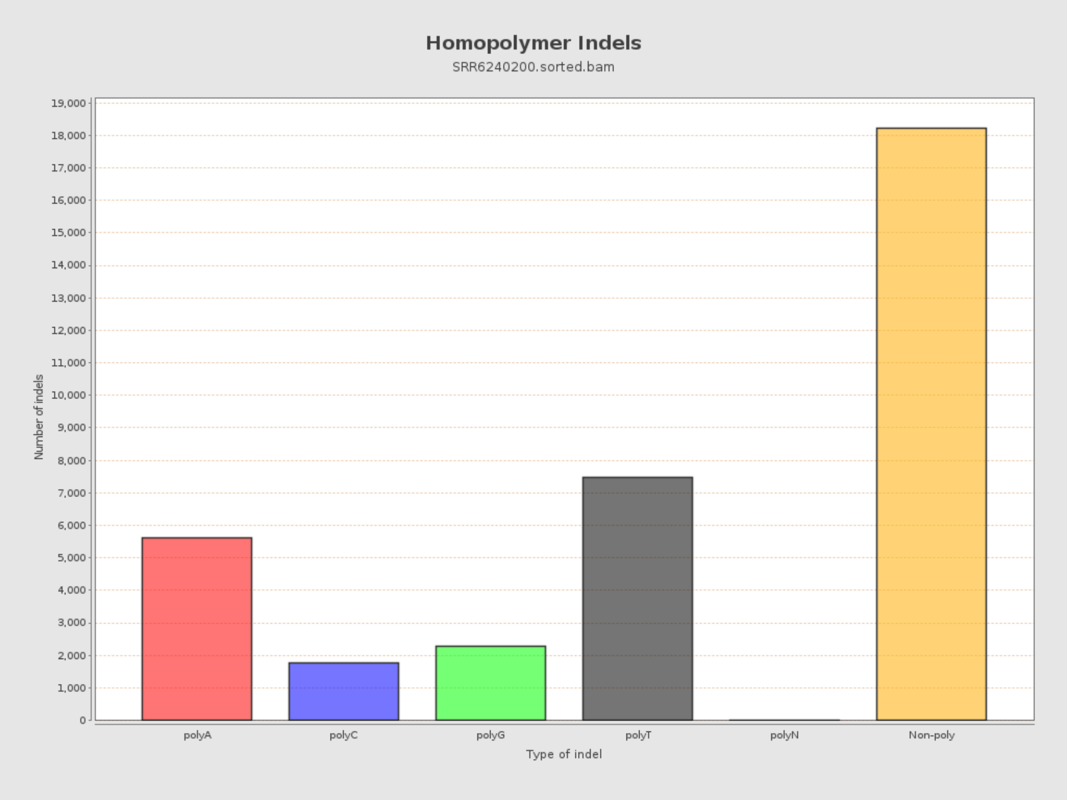
9. Results : Mapped Reads GC-content Distribution



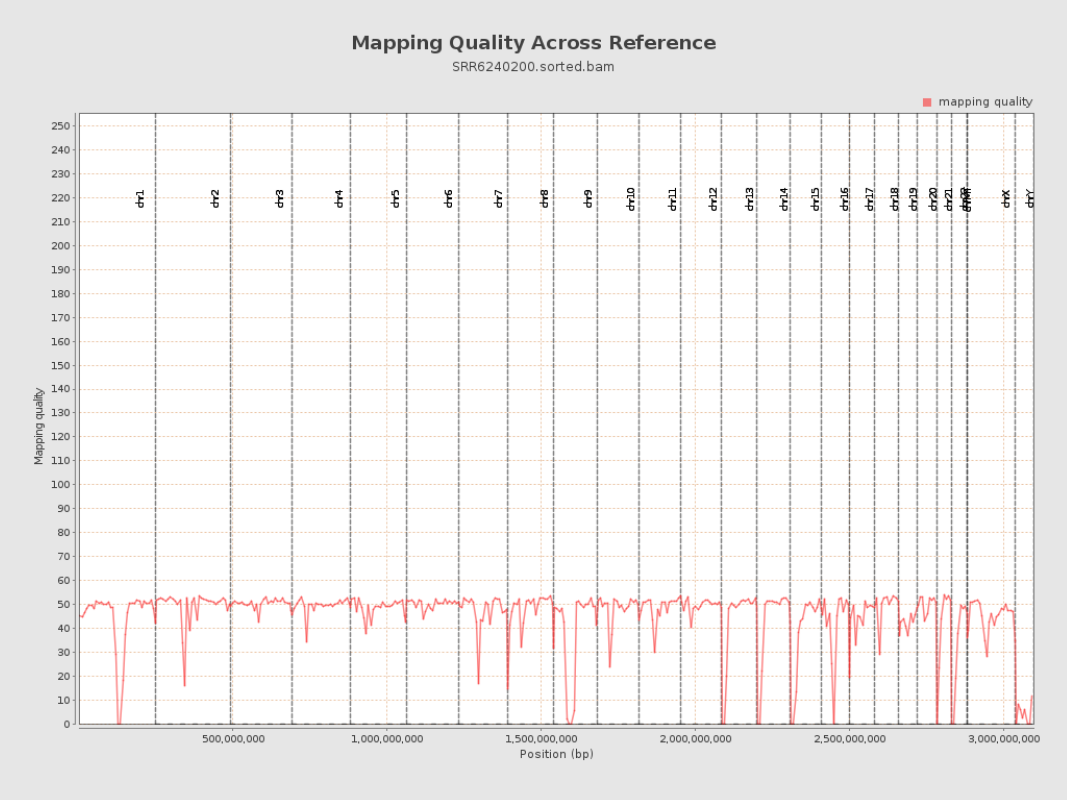
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram