Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 05:47:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240192.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_SRR6240192 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240192.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 05:47:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240192.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,956,079
Mapped reads	1,498,352 / 76.6%
Unmapped reads	457,727 / 23.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,438 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	197,502 / 10.1%
Duplication rate	10.77%
Clipped reads	1,005,964 / 51.43%

2.2. ACGT Content

Number/percentage of A's	24,725,906 / 26.97%
Number/percentage of C's	15,945,991 / 17.4%
Number/percentage of T's	30,026,447 / 32.76%
Number/percentage of G's	20,944,170 / 22.85%
Number/percentage of N's	23,778 / 0.03%
GC Percentage	40.24%

2.3. Coverage

Mean	0.0296

Standard Deviation	0.3148

2.4. Mapping Quality

Mean Mapping Quality	45.35

2.5. Mismatches and indels

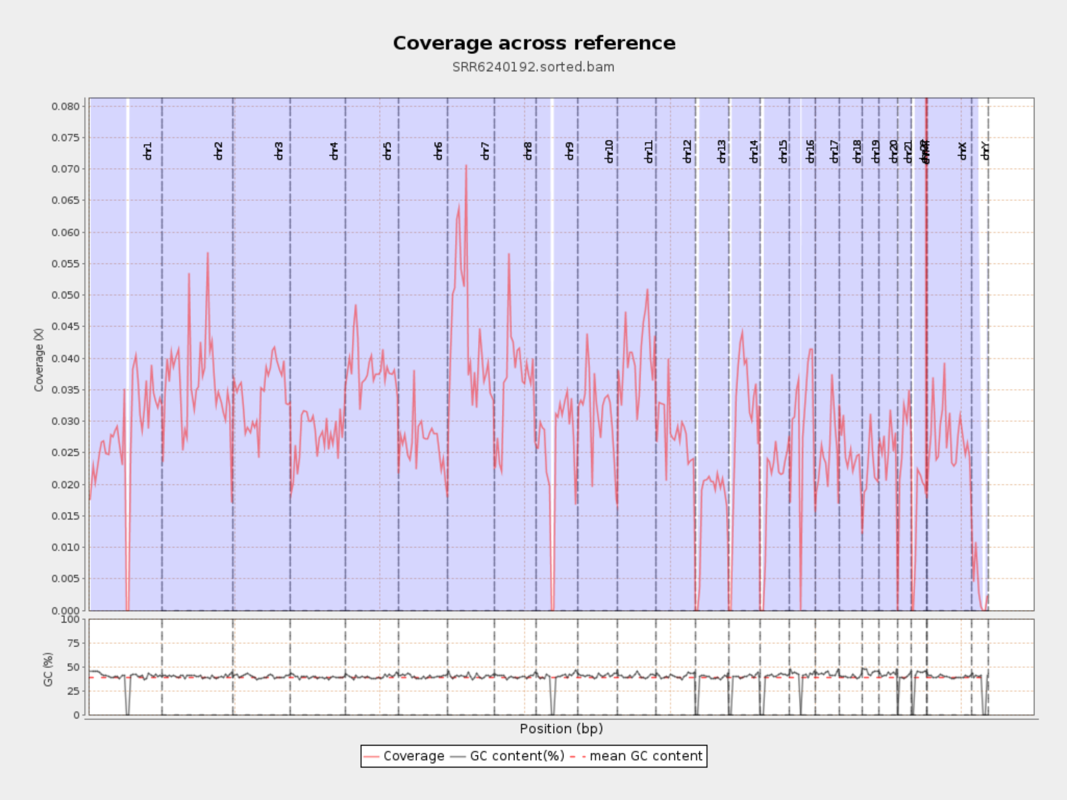
General error rate	0.95%
Mismatches	857,303
Insertions	6,505
Mapped reads with at least one insertion	0.43%
Deletions	30,812
Mapped reads with at least one deletion	2.03%
Homopolymer indels	48.63%

2.6. Chromosome stats

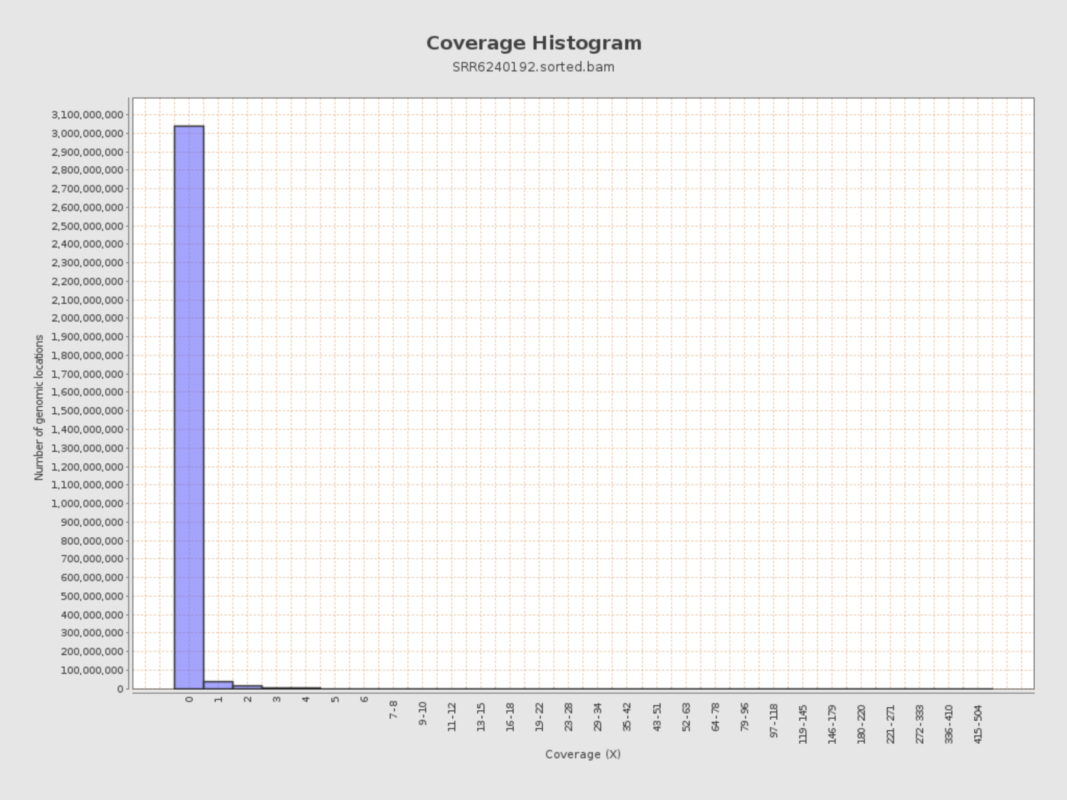
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6856236	0.0275	0.3892
chr2	243199373	8773410	0.0361	0.37
chr3	198022430	6808750	0.0344	0.2662
chr4	191154276	5267824	0.0276	0.2479
chr5	180915260	6970882	0.0385	0.2806
chr6	171115067	4539006	0.0265	0.2719
chr7	159138663	7013645	0.0441	0.566

chr8	146364022	5277751	0.0361	0.4054
chr9	141213431	3588229	0.0254	0.2779
chr10	135534747	4311300	0.0318	0.2866
chr11	135006516	5386778	0.0399	0.3365
chr12	133851895	3760219	0.0281	0.2461
chr13	115169878	1904800	0.0165	0.188
chr14	107349540	3212782	0.0299	0.2579
chr15	102531392	1949605	0.019	0.2042
chr16	90354753	2702344	0.0299	0.2556
chr17	81195210	2009498	0.0247	0.2441
chr18	78077248	1954848	0.025	0.3952
chr19	59128983	1331739	0.0225	0.3017
chr20	63025520	1622774	0.0257	0.2371
chr21	48129895	1238941	0.0257	0.2368
chr22	51304566	748014	0.0146	0.173
chrMT	16571	56768	3.4257	4.1838
chrX	155270560	4224942	0.0272	0.2524
chrY	59373566	207074	0.0035	0.0888

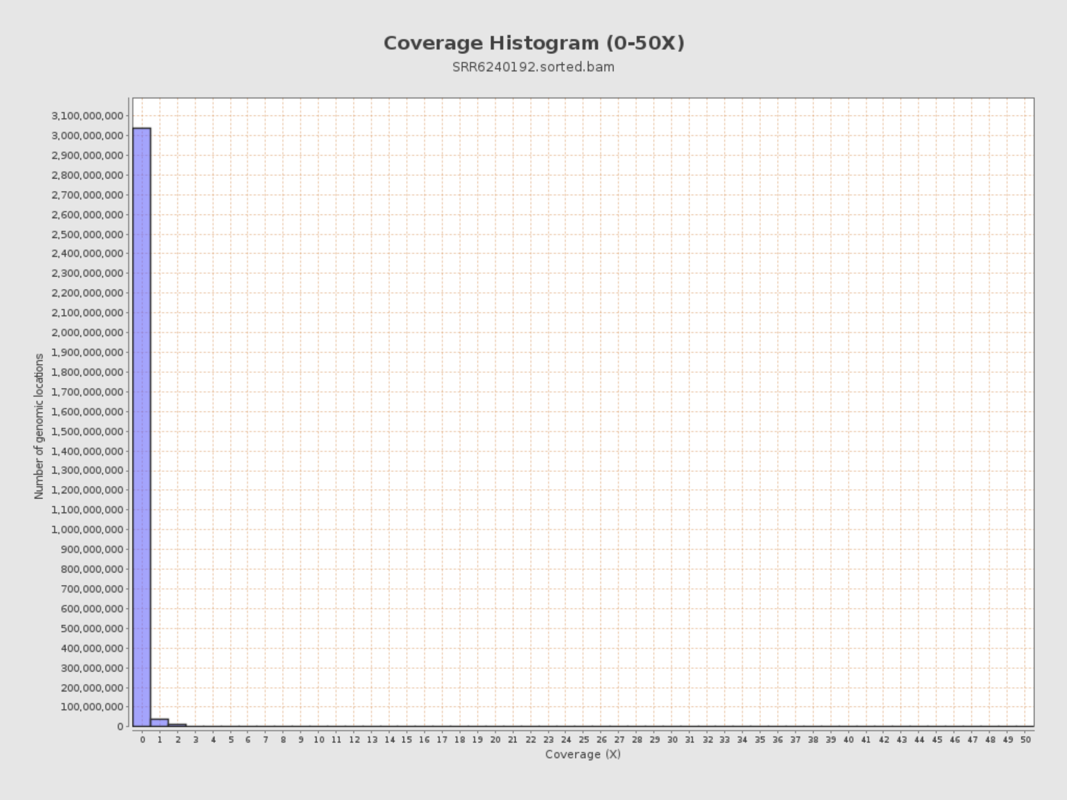
3. Results : Coverage across reference



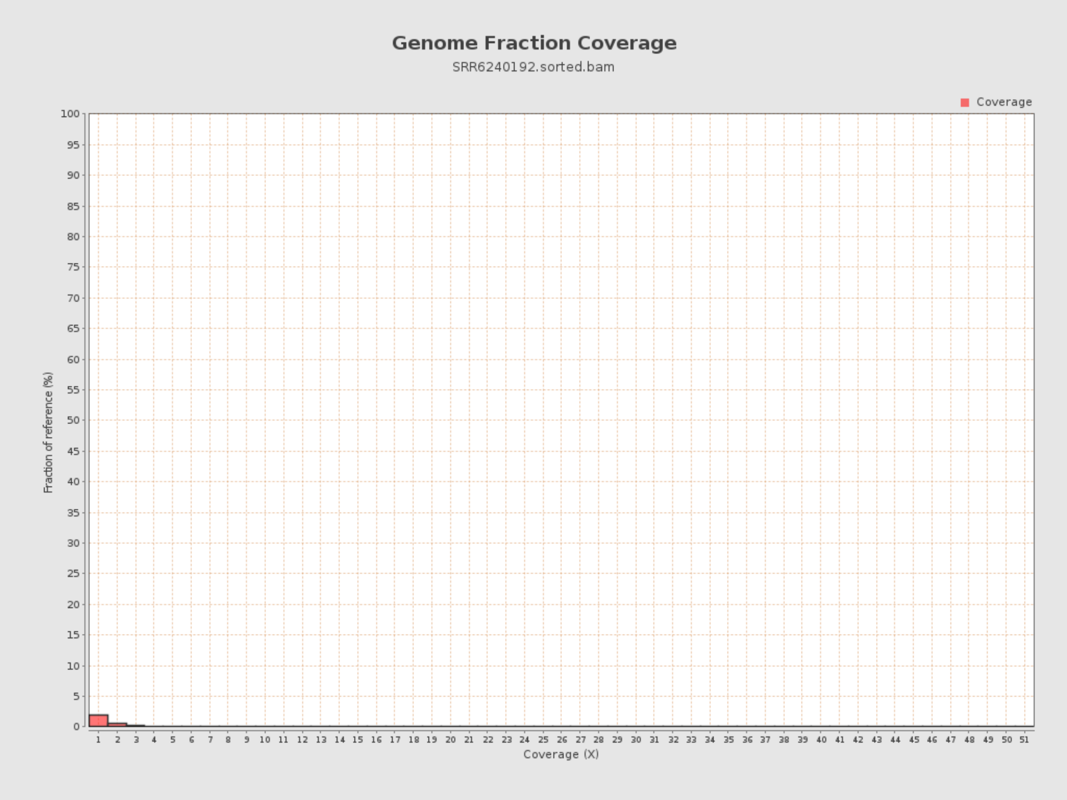
4. Results : Coverage Histogram



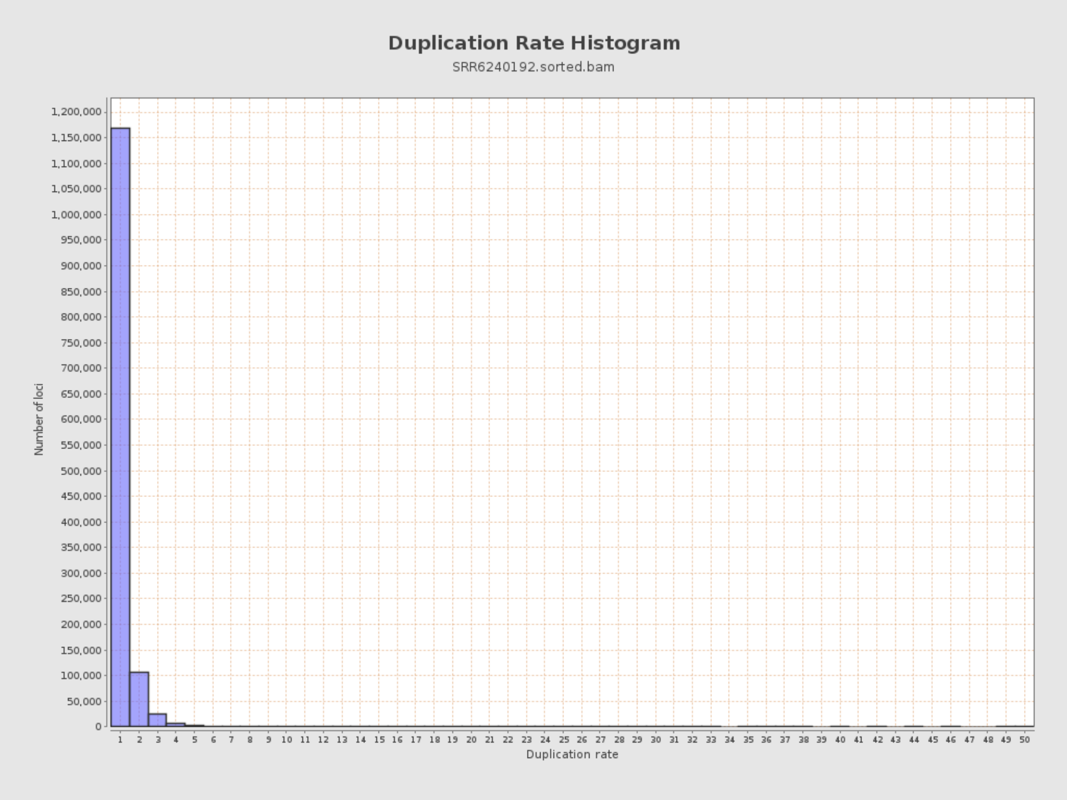
5. Results : Coverage Histogram (0-50X)



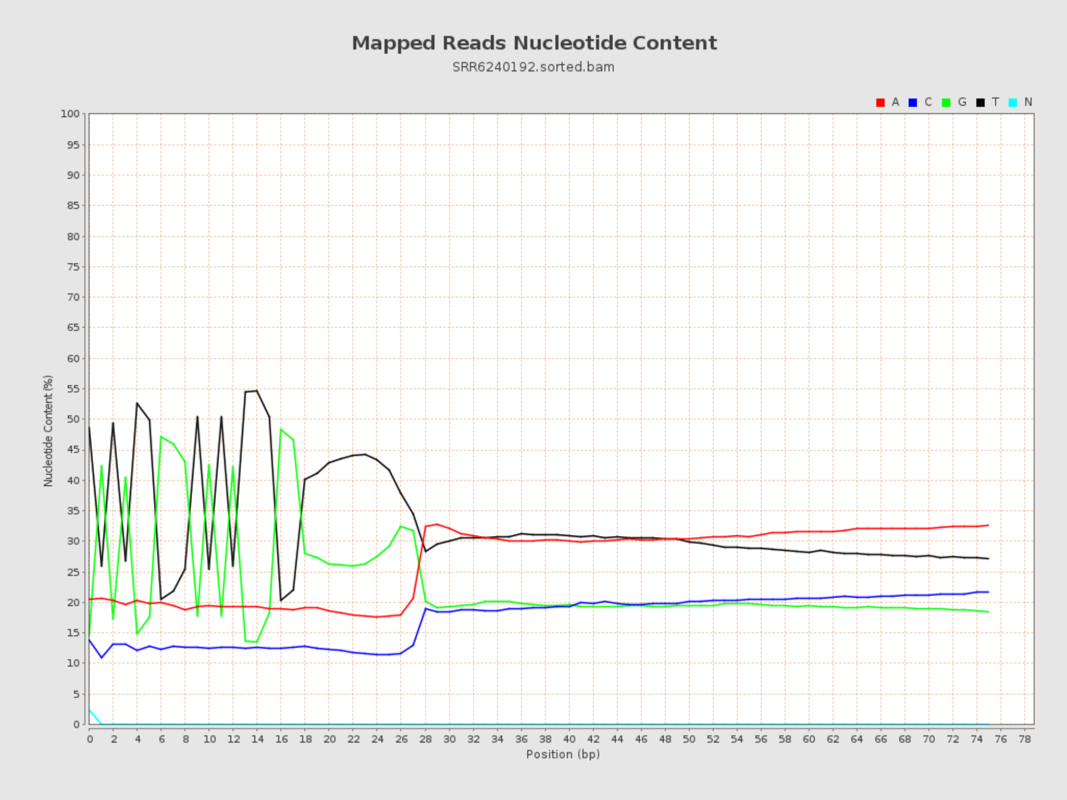
6. Results : Genome Fraction Coverage



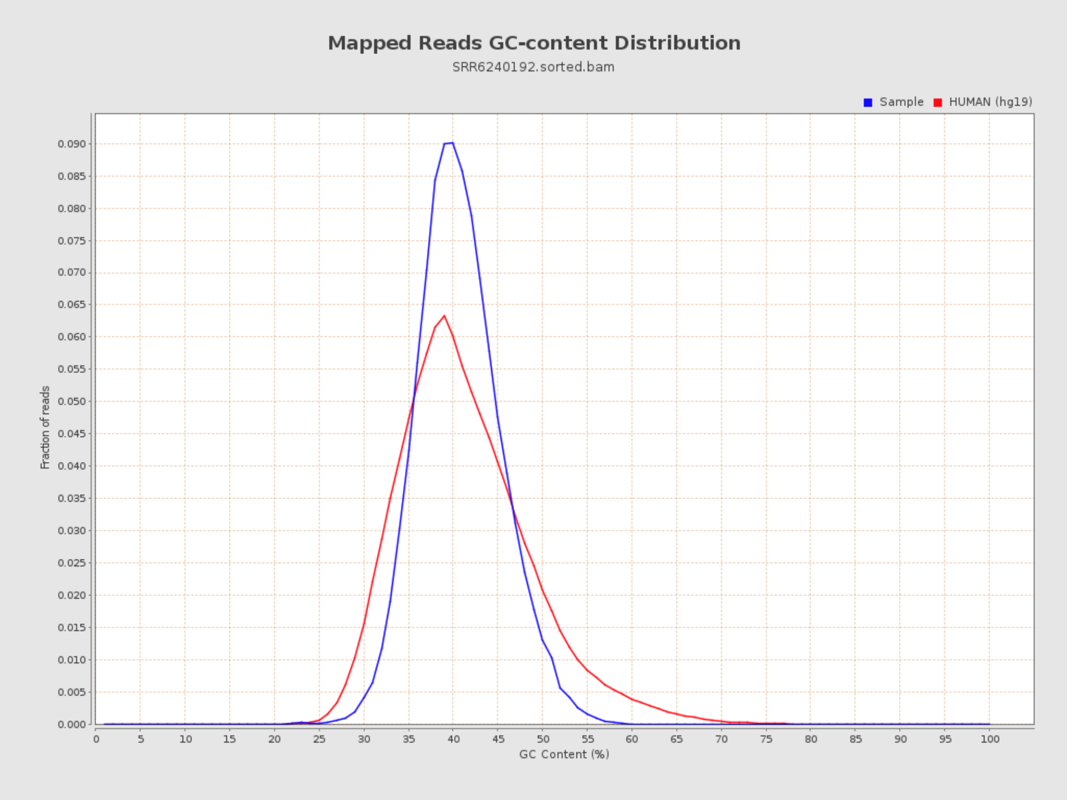
7. Results : Duplication Rate Histogram



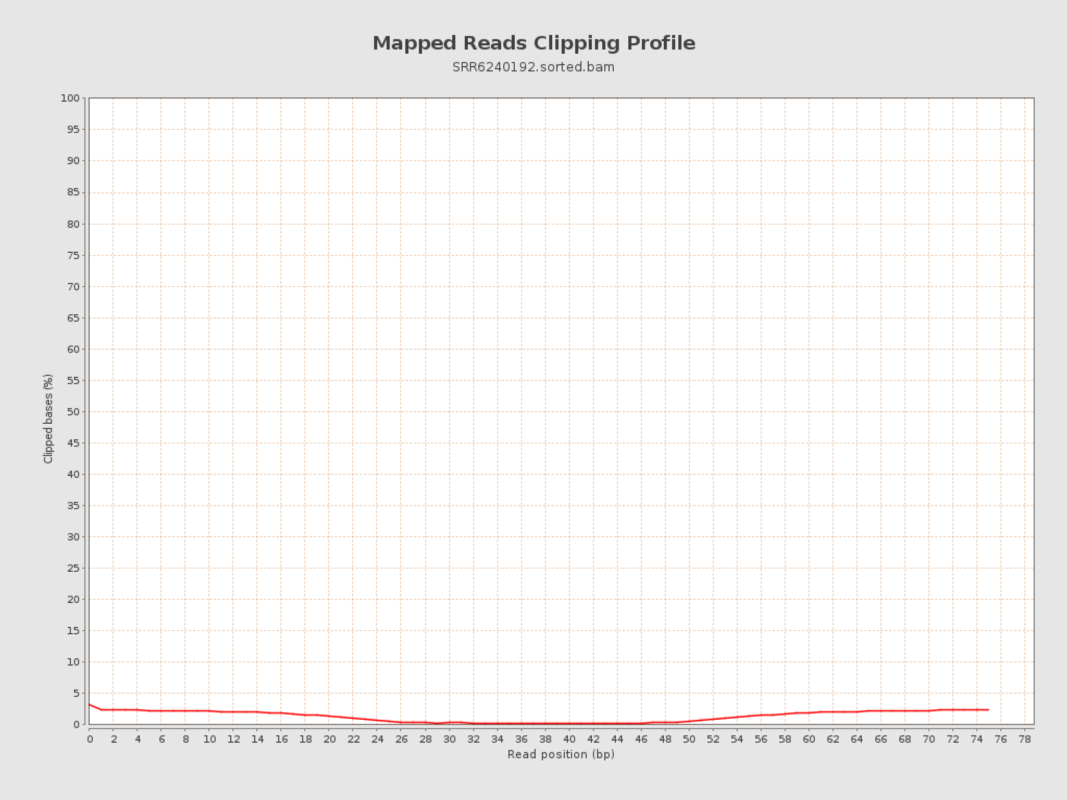
8. Results : Mapped Reads Nucleotide Content



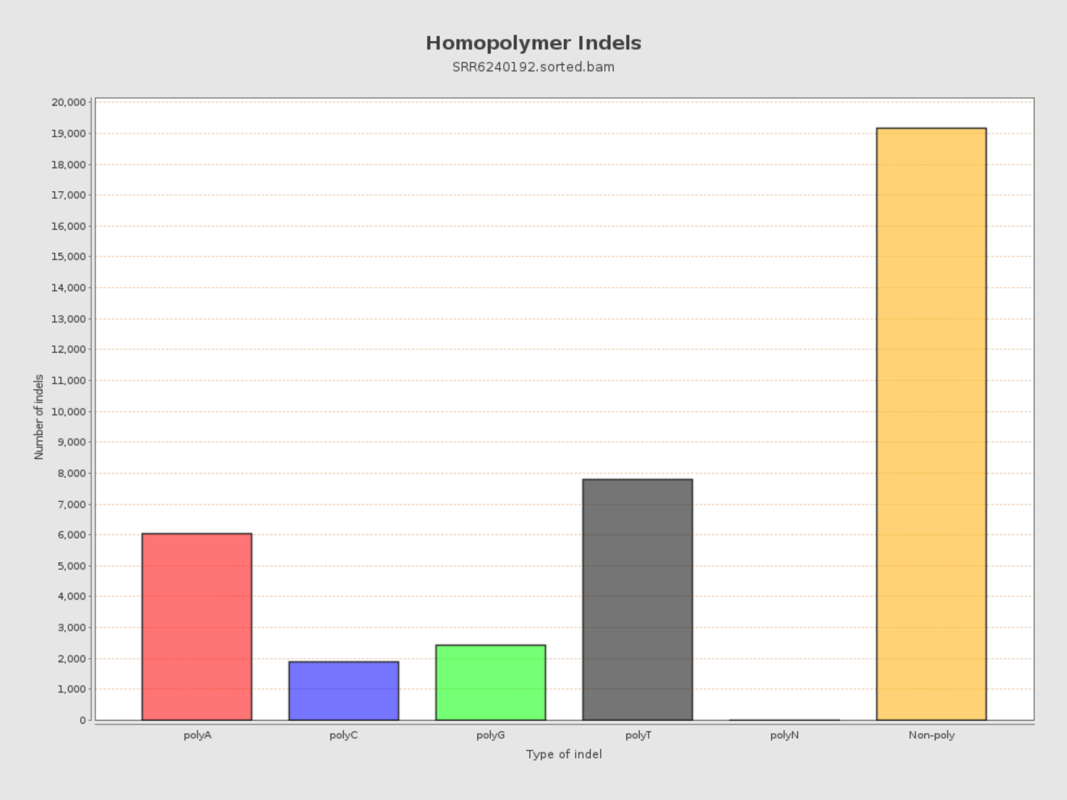
9. Results : Mapped Reads GC-content Distribution



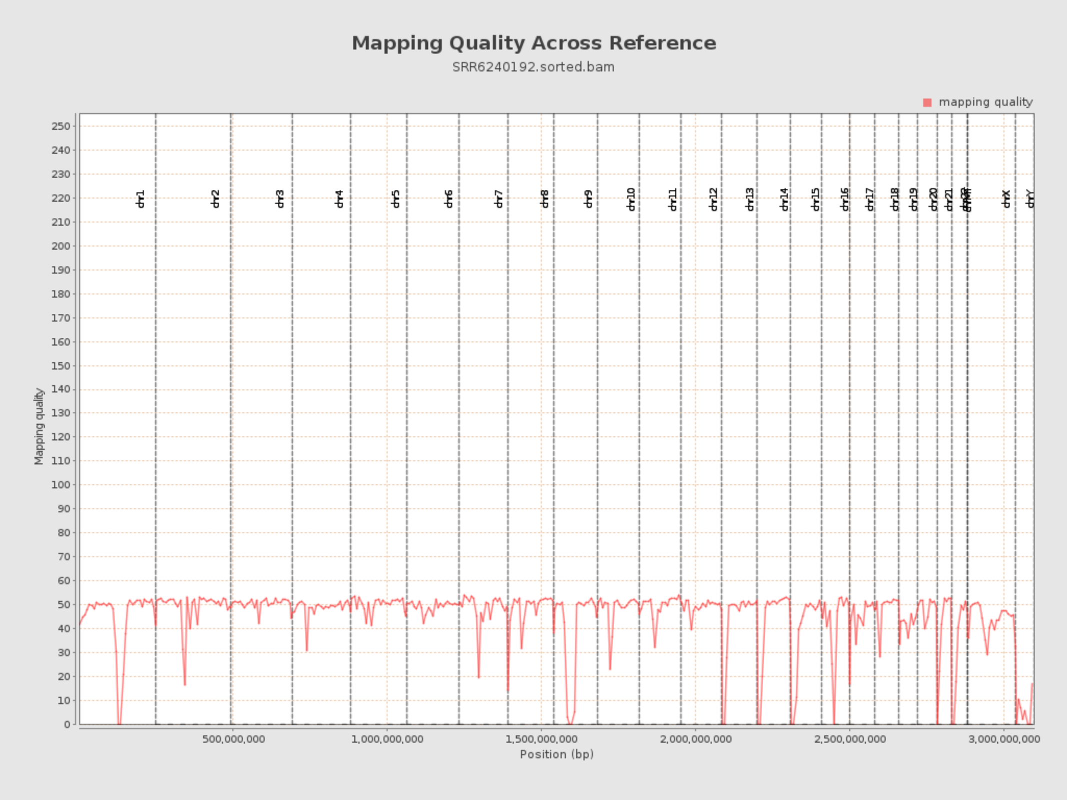
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram