Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 03:23:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240035.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_SRR6240035 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240035.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 03:23:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240035.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,710,089
Mapped reads	1,354,833 / 79.23%
Unmapped reads	355,256 / 20.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,070 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	121,070 / 7.08%
Duplication rate	7.49%
Clipped reads	936,786 / 54.78%

2.2. ACGT Content

Number/percentage of A's	21,929,445 / 26.67%
Number/percentage of C's	13,998,097 / 17.03%
Number/percentage of T's	27,087,740 / 32.95%
Number/percentage of G's	19,145,771 / 23.29%
Number/percentage of N's	57,115 / 0.07%
GC Percentage	40.31%

2.3. Coverage

Mean	0.0266

Standard Deviation	0.2763

2.4. Mapping Quality

Mean Mapping Quality	45.41

2.5. Mismatches and indels

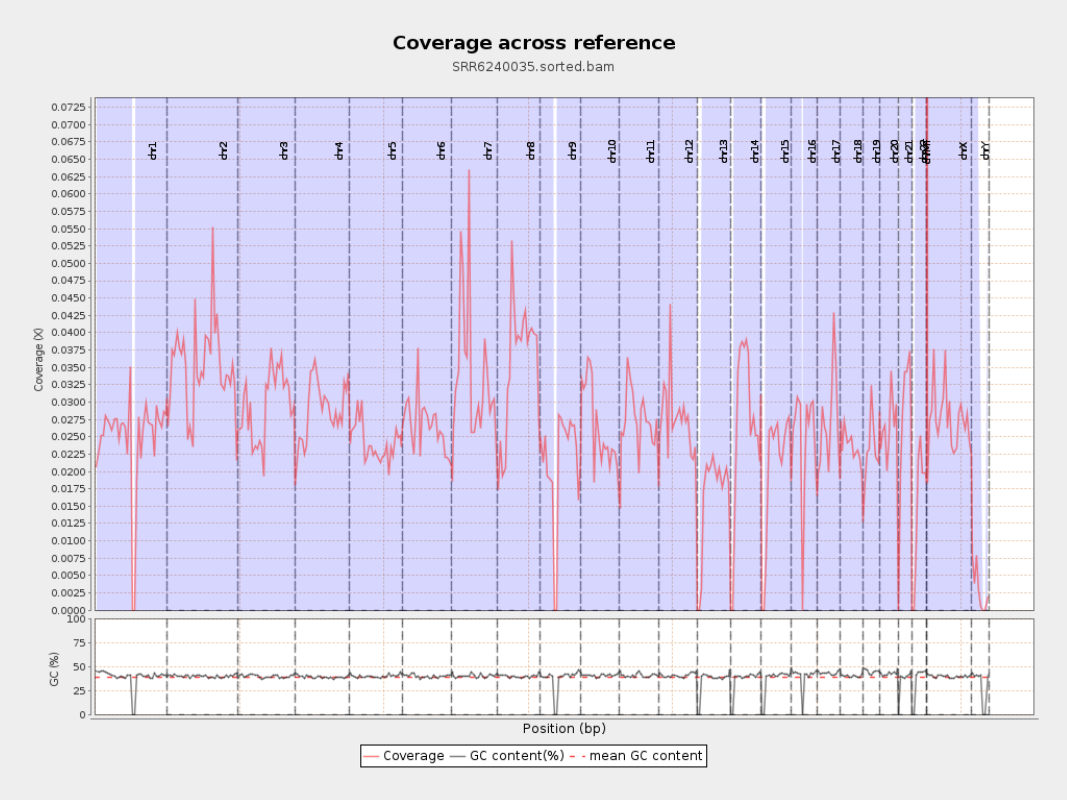
General error rate	1.03%
Mismatches	837,056
Insertions	5,789
Mapped reads with at least one insertion	0.42%
Deletions	29,287
Mapped reads with at least one deletion	2.14%
Homopolymer indels	50.71%

2.6. Chromosome stats

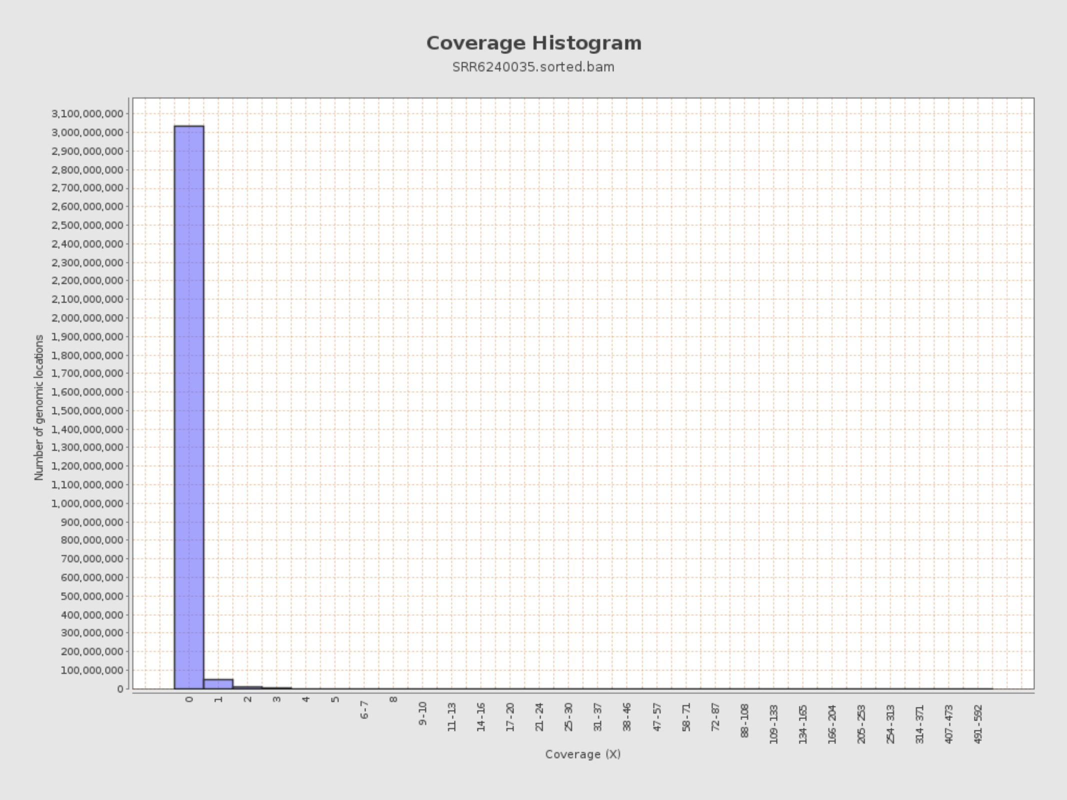
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6144628	0.0247	0.36
chr2	243199373	8564969	0.0352	0.3048
chr3	198022430	5860228	0.0296	0.2186
chr4	191154276	5508013	0.0288	0.2195
chr5	180915260	4372199	0.0242	0.1964
chr6	171115067	4559818	0.0266	0.2371
chr7	159138663	5390018	0.0339	0.5857

chr8	146364022	5189251	0.0355	0.3316
chr9	141213431	2992583	0.0212	0.2364
chr10	135534747	3575237	0.0264	0.2325
chr11	135006516	3694790	0.0274	0.2479
chr12	133851895	3692624	0.0276	0.2094
chr13	115169878	1884331	0.0164	0.1616
chr14	107349540	2852598	0.0266	0.2147
chr15	102531392	2095023	0.0204	0.1893
chr16	90354753	2178982	0.0241	0.1958
chr17	81195210	2216409	0.0273	0.2228
chr18	78077248	1841634	0.0236	0.3161
chr19	59128983	1391192	0.0235	0.2756
chr20	63025520	1635548	0.026	0.2043
chr21	48129895	1334913	0.0277	0.2151
chr22	51304566	775550	0.0151	0.1506
chrMT	16571	48577	2.9314	4.2867
chrX	155270560	4297366	0.0277	0.2235
chrY	59373566	171352	0.0029	0.0673

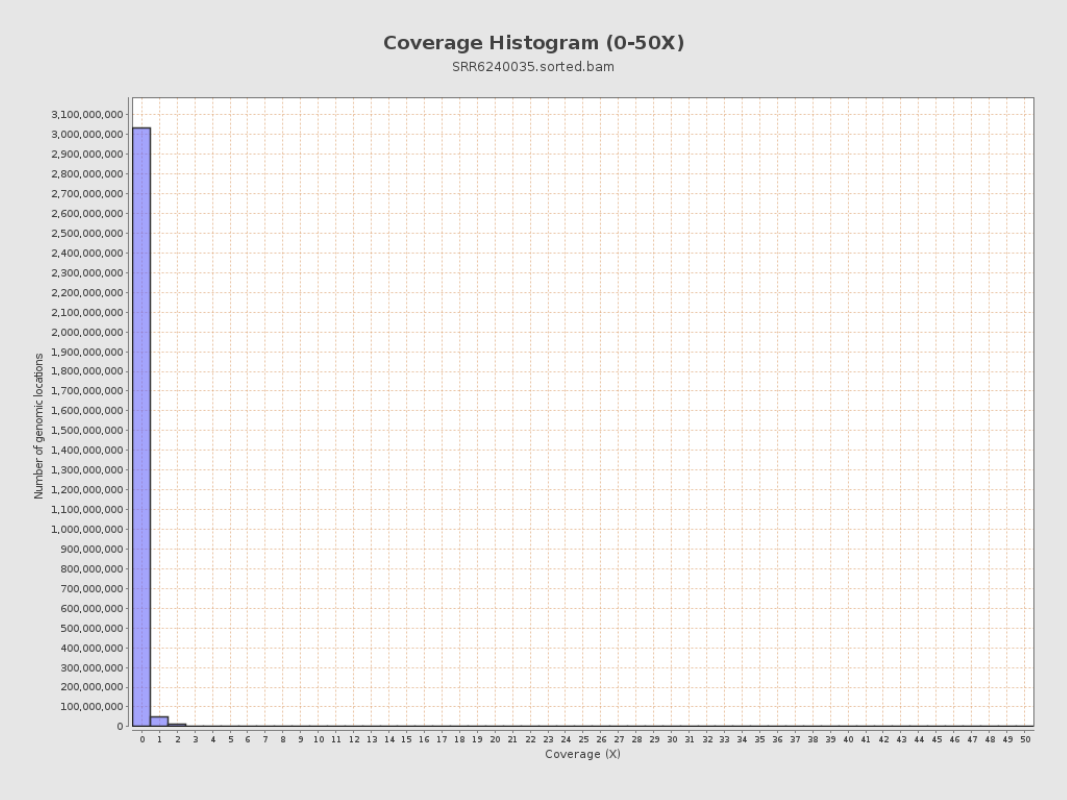
3. Results : Coverage across reference



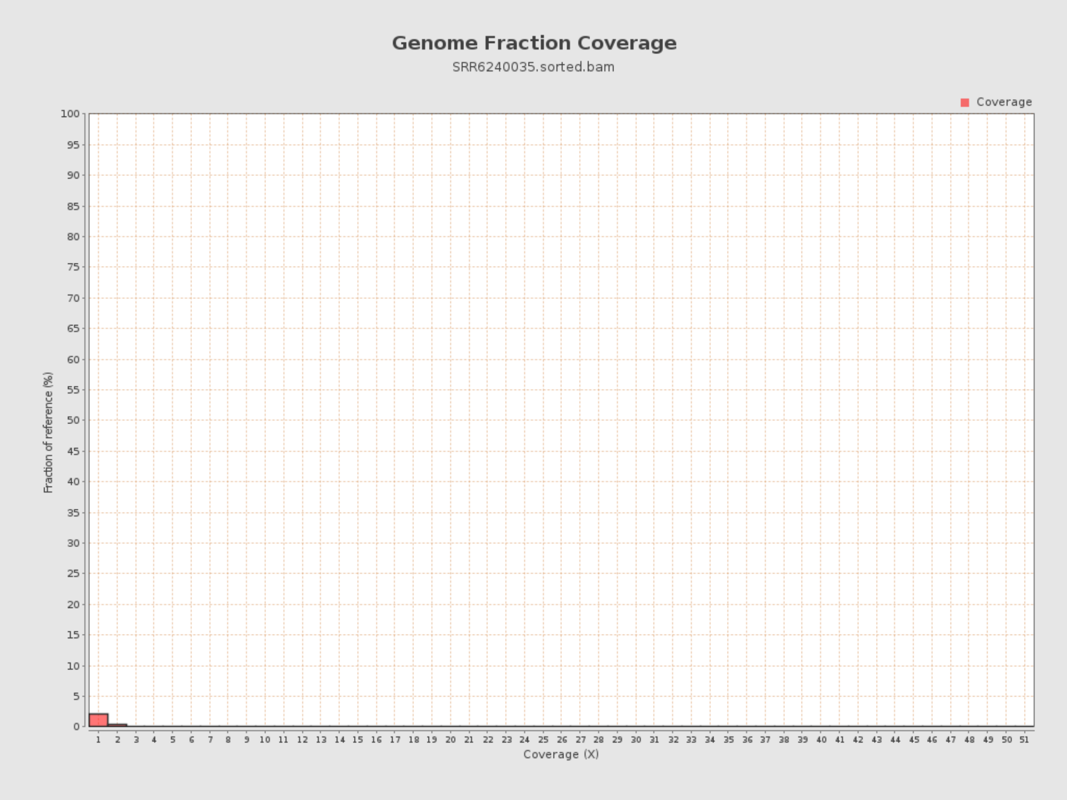
4. Results : Coverage Histogram



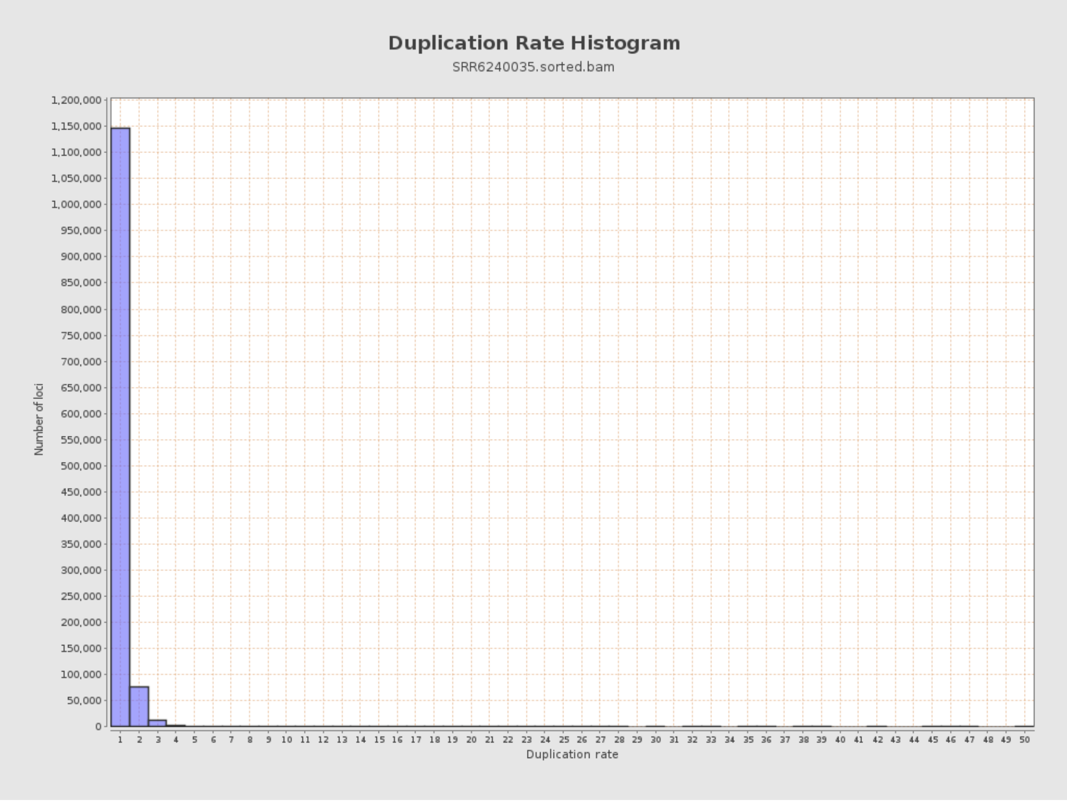
5. Results : Coverage Histogram (0-50X)



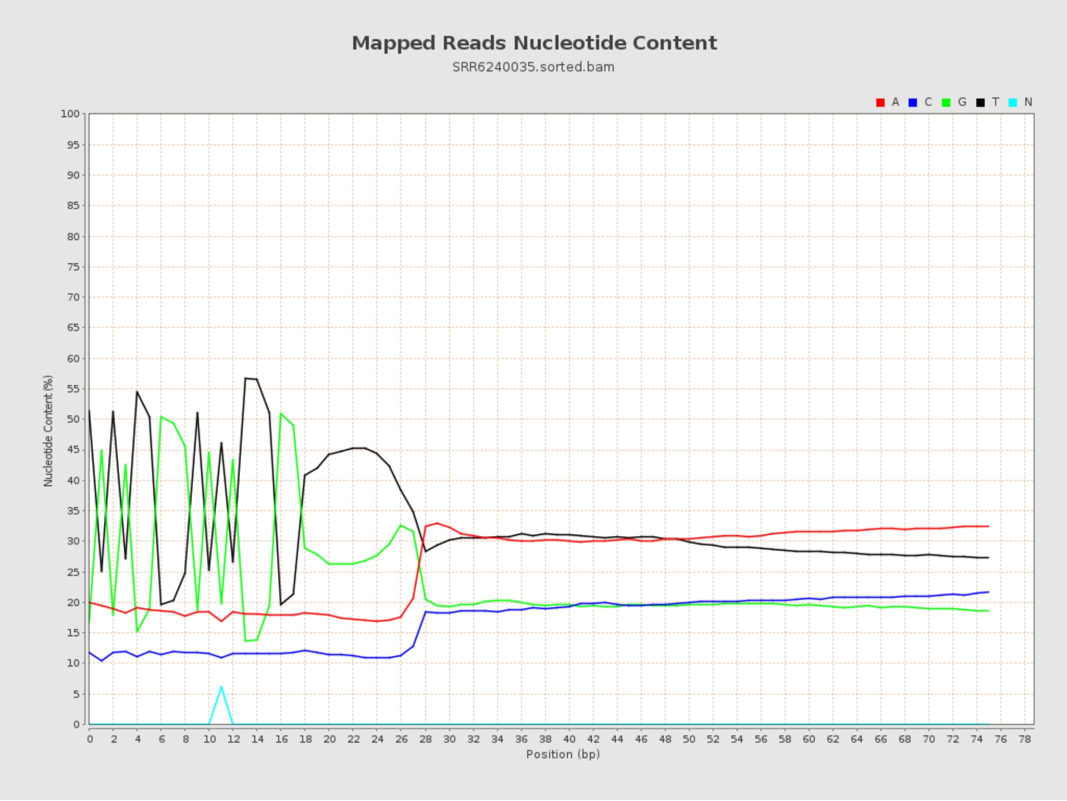
6. Results : Genome Fraction Coverage



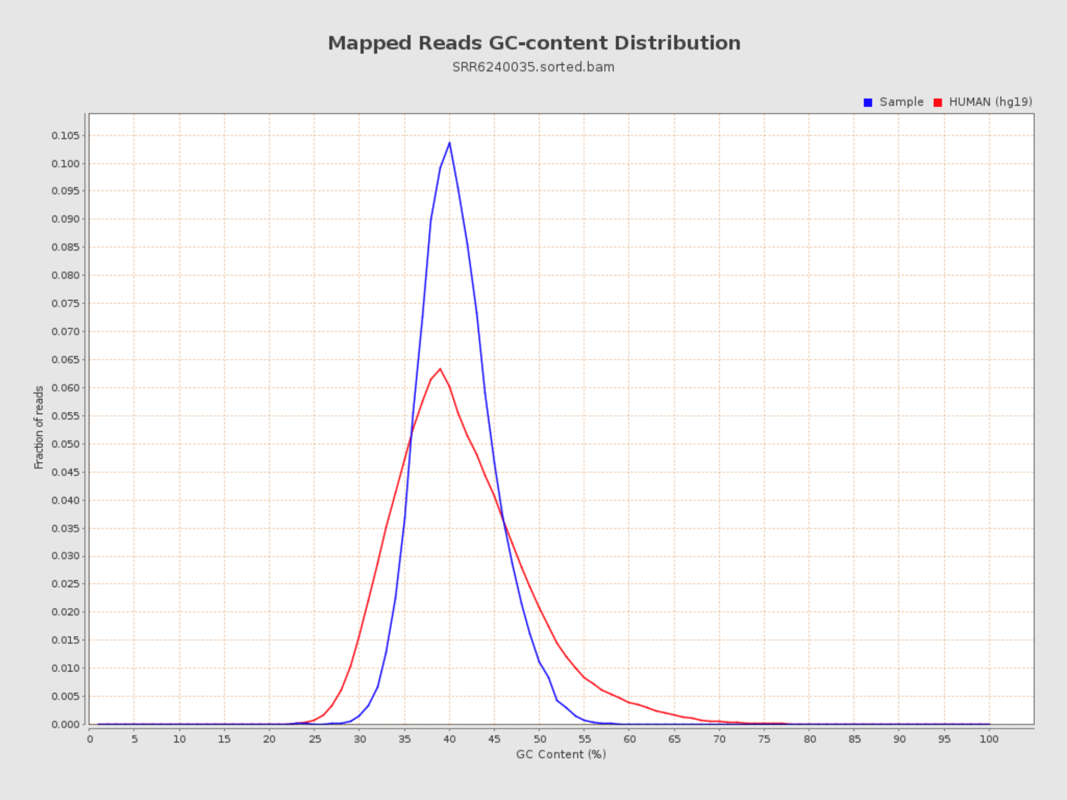
7. Results : Duplication Rate Histogram



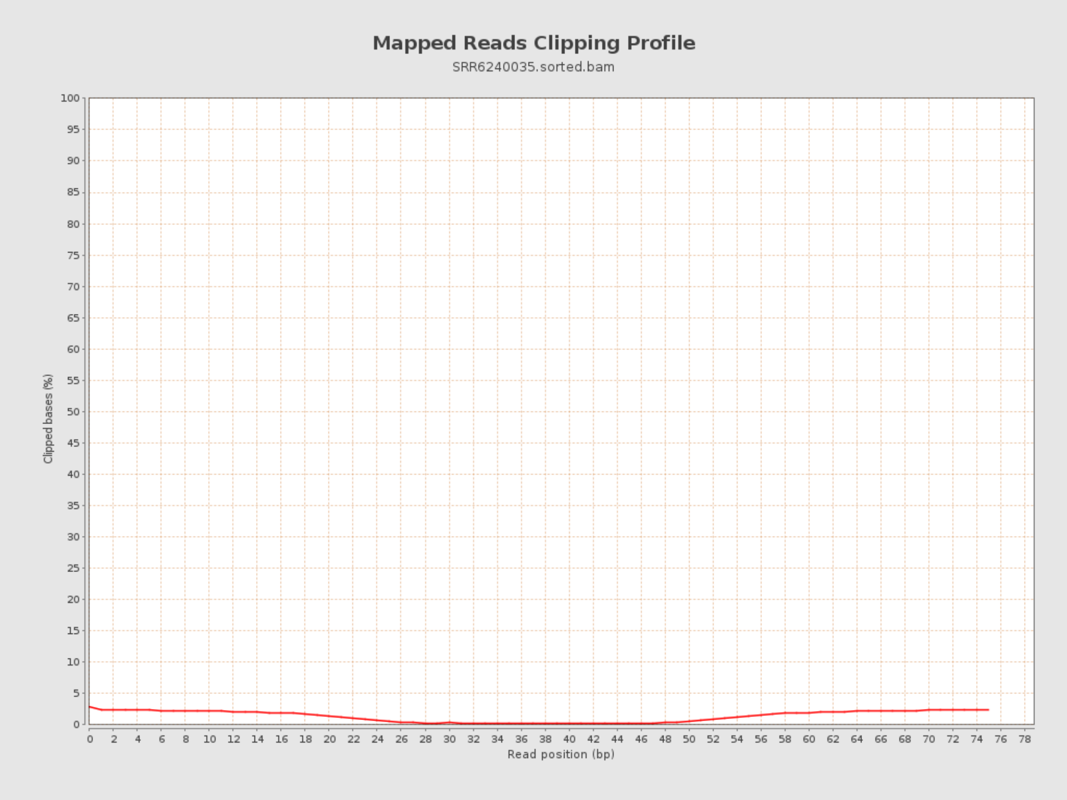
8. Results : Mapped Reads Nucleotide Content



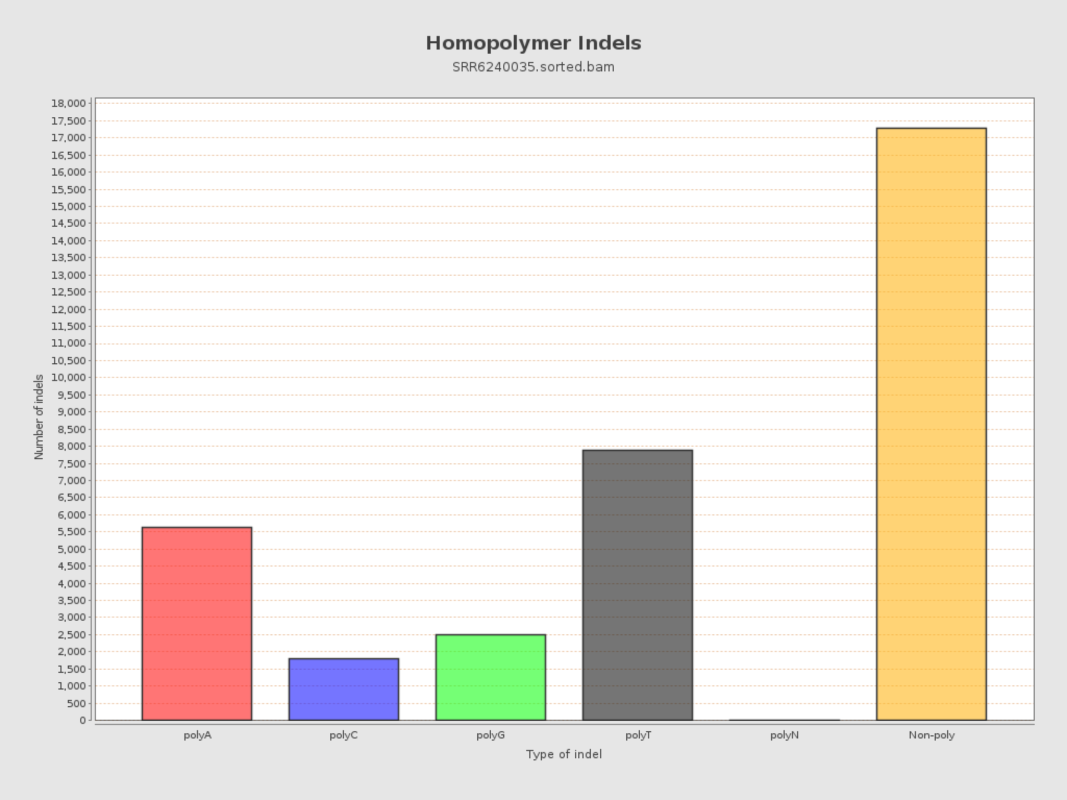
9. Results : Mapped Reads GC-content Distribution



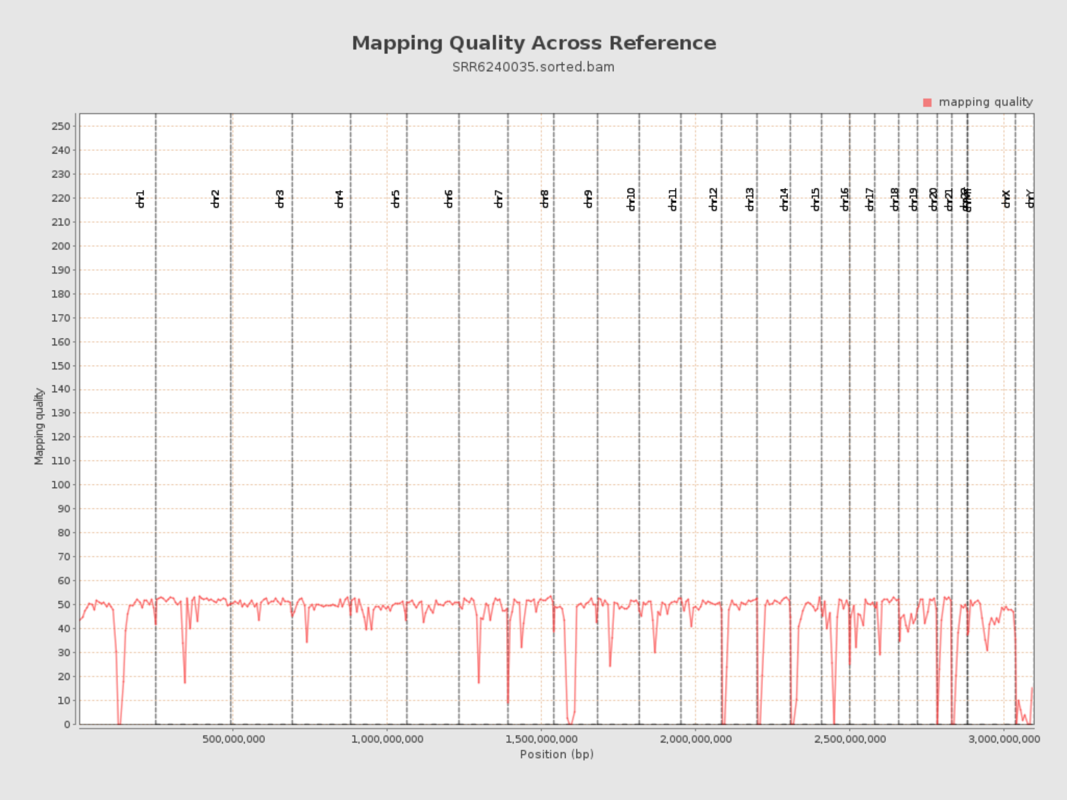
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram