Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 02:37:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240018.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_SRR6240018 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240018.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 02:37:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240018.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,660,984
Mapped reads	1,242,958 / 74.83%
Unmapped reads	418,026 / 25.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,776 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	69,001 / 4.15%
Duplication rate	4.65%
Clipped reads	789,279 / 47.52%

2.2. ACGT Content

Number/percentage of A's	20,917,557 / 27.2%
Number/percentage of C's	13,277,163 / 17.27%
Number/percentage of T's	25,070,906 / 32.6%
Number/percentage of G's	17,580,648 / 22.86%
Number/percentage of N's	51,054 / 0.07%
GC Percentage	40.13%

2.3. Coverage

Mean	0.0249

Standard Deviation	0.2466

2.4. Mapping Quality

Mean Mapping Quality	45.2

2.5. Mismatches and indels

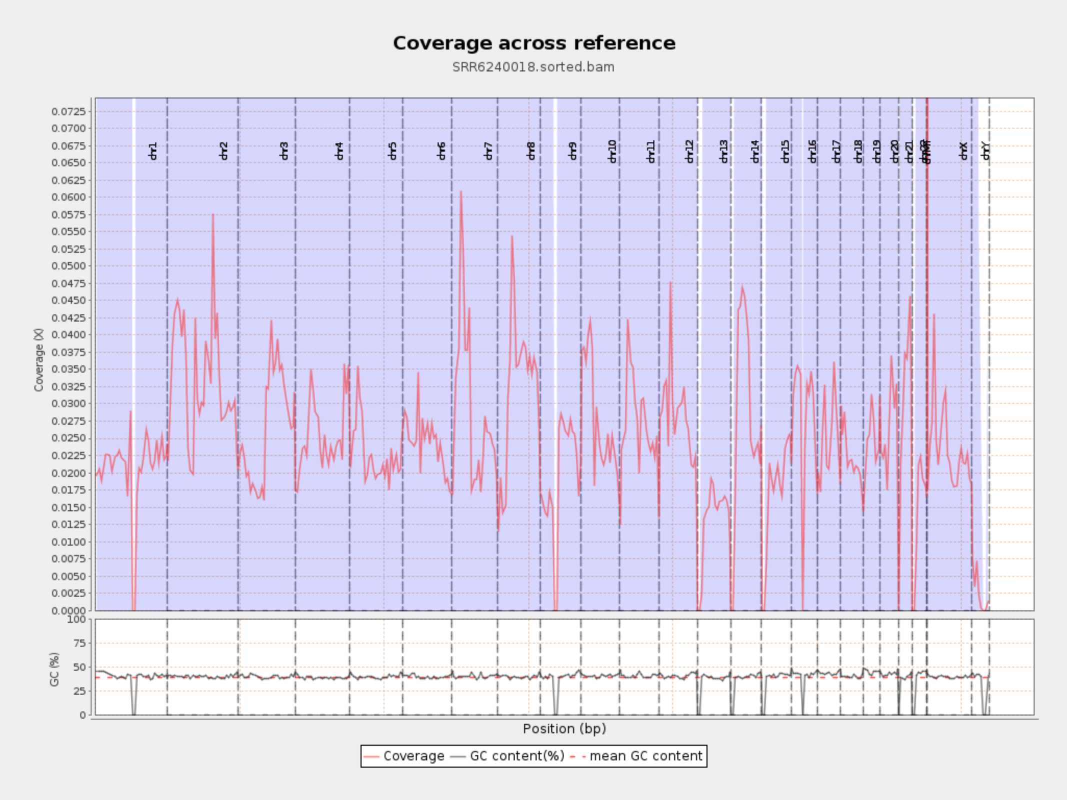
General error rate	0.98%
Mismatches	740,380
Insertions	5,581
Mapped reads with at least one insertion	0.44%
Deletions	23,881
Mapped reads with at least one deletion	1.89%
Homopolymer indels	48.78%

2.6. Chromosome stats

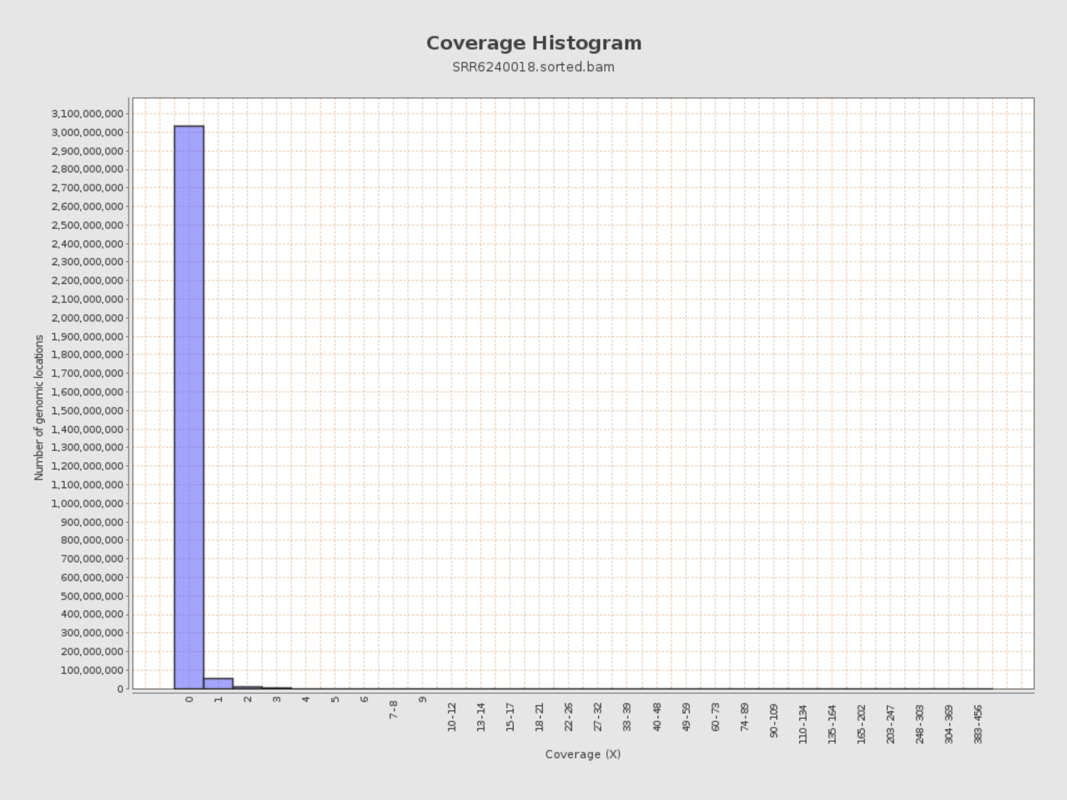
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5125155	0.0206	0.3365
chr2	243199373	8237207	0.0339	0.304
chr3	198022430	5222117	0.0264	0.1881
chr4	191154276	4858443	0.0254	0.1891
chr5	180915260	4094305	0.0226	0.1881
chr6	171115067	4169696	0.0244	0.2259
chr7	159138663	4655507	0.0293	0.3849

chr8	146364022	4773932	0.0326	0.3456
chr9	141213431	2707369	0.0192	0.2139
chr10	135534747	3787814	0.0279	0.231
chr11	135006516	3707066	0.0275	0.2491
chr12	133851895	3826980	0.0286	0.1981
chr13	115169878	1504472	0.0131	0.1313
chr14	107349540	3074285	0.0286	0.2
chr15	102531392	1726983	0.0168	0.1653
chr16	90354753	2507300	0.0277	0.1975
chr17	81195210	2044419	0.0252	0.1977
chr18	78077248	1736602	0.0222	0.3297
chr19	59128983	1457930	0.0247	0.2659
chr20	63025520	1661374	0.0264	0.191
chr21	48129895	1473859	0.0306	0.2105
chr22	51304566	725099	0.0141	0.1347
chrMT	16571	20162	1.2167	1.4073
chrX	155270560	3688188	0.0238	0.1965
chrY	59373566	151813	0.0026	0.0627

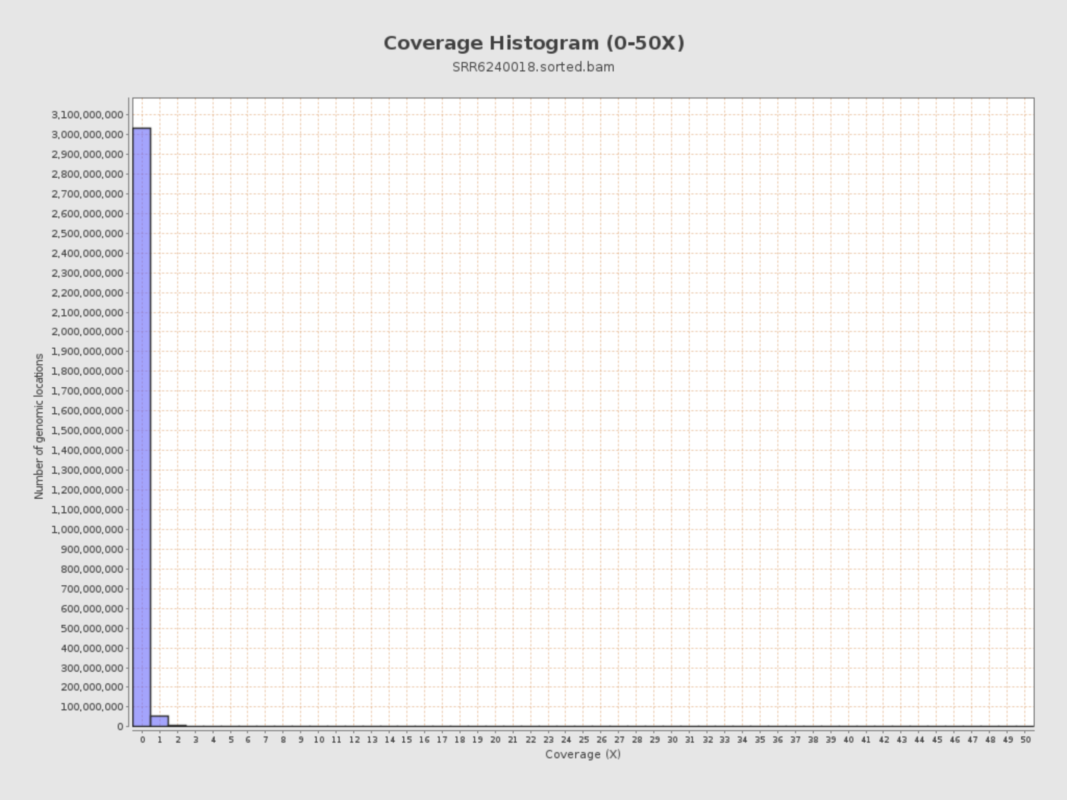
3. Results : Coverage across reference



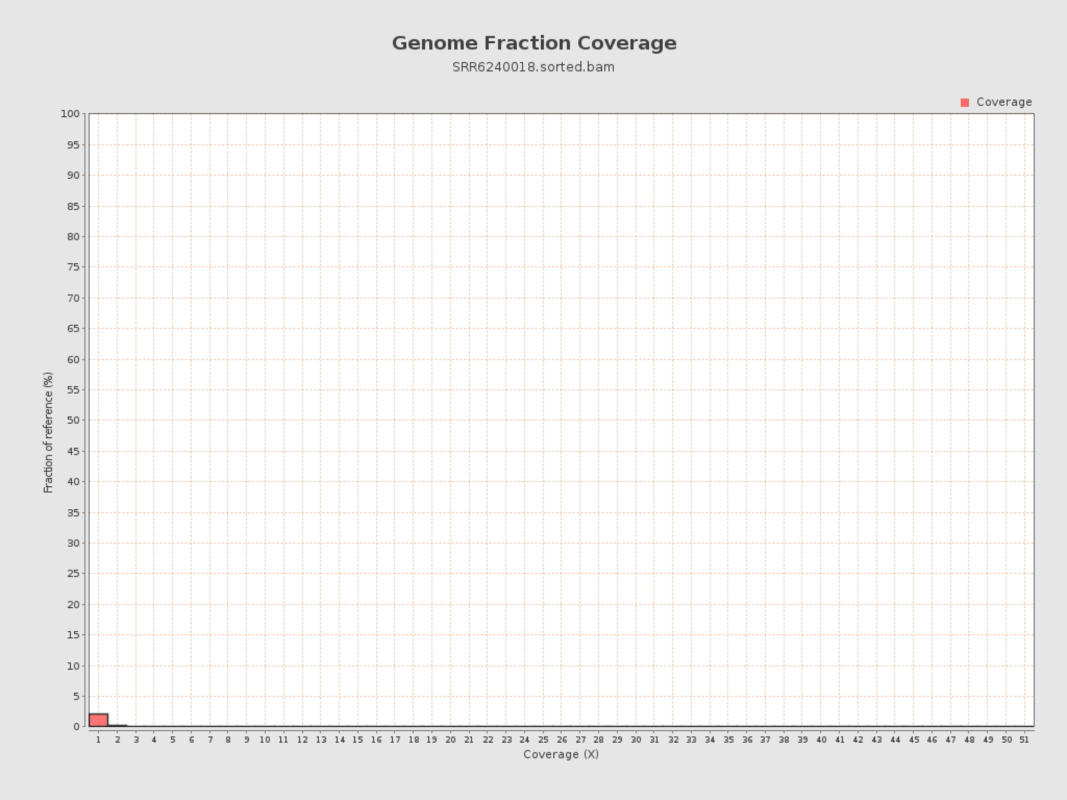
4. Results : Coverage Histogram



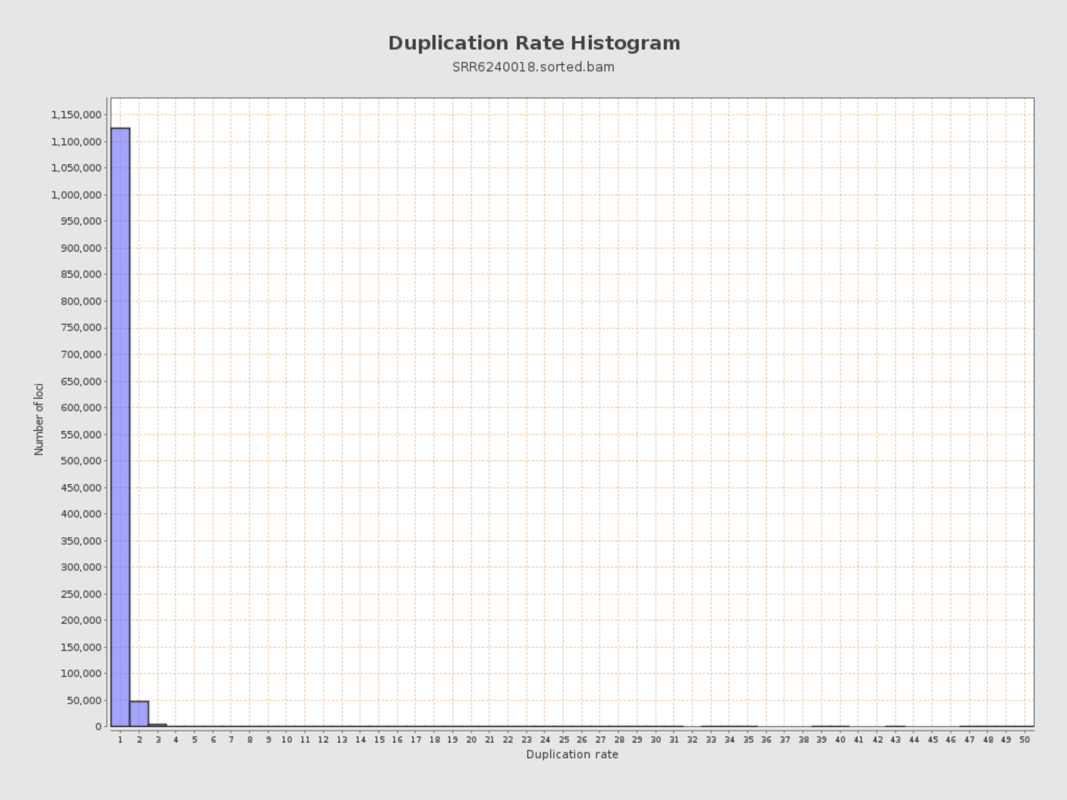
5. Results : Coverage Histogram (0-50X)



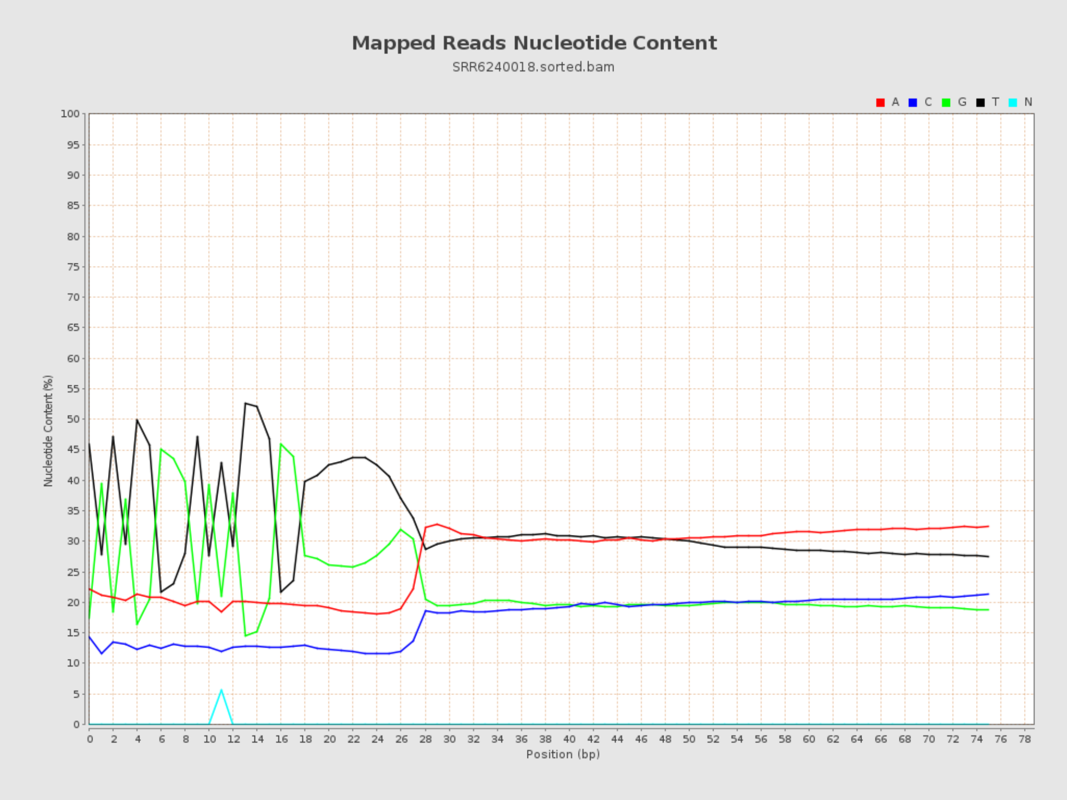
6. Results : Genome Fraction Coverage



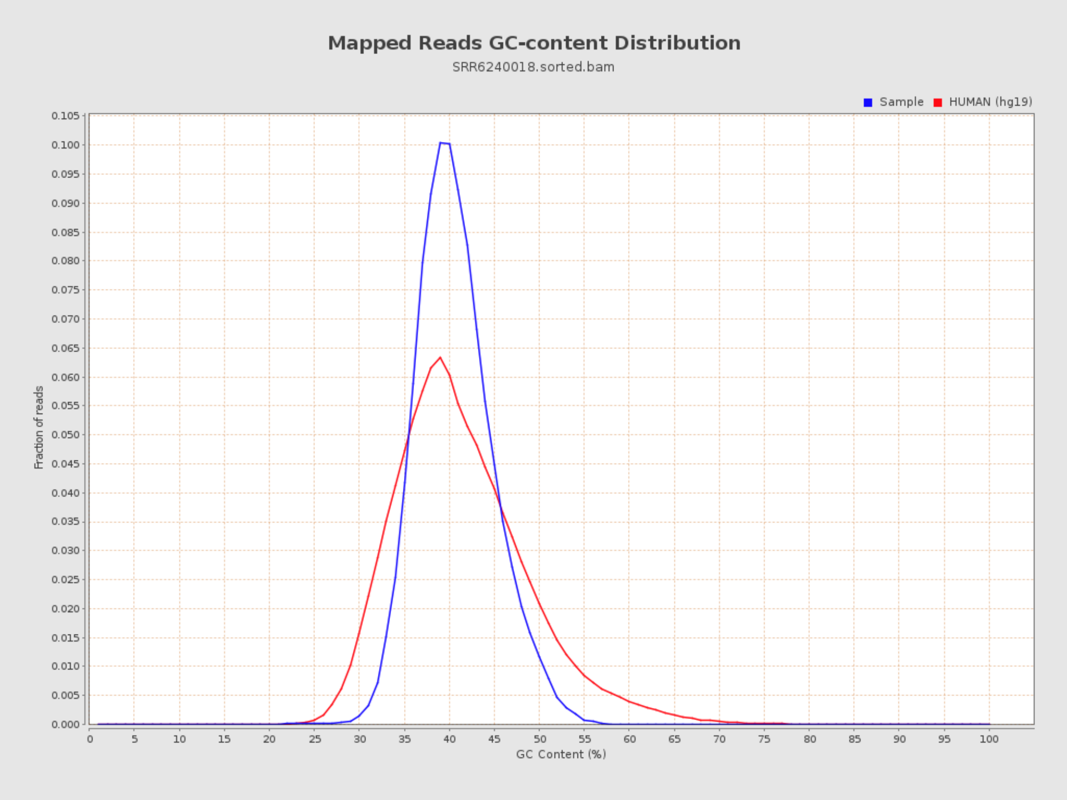
7. Results : Duplication Rate Histogram



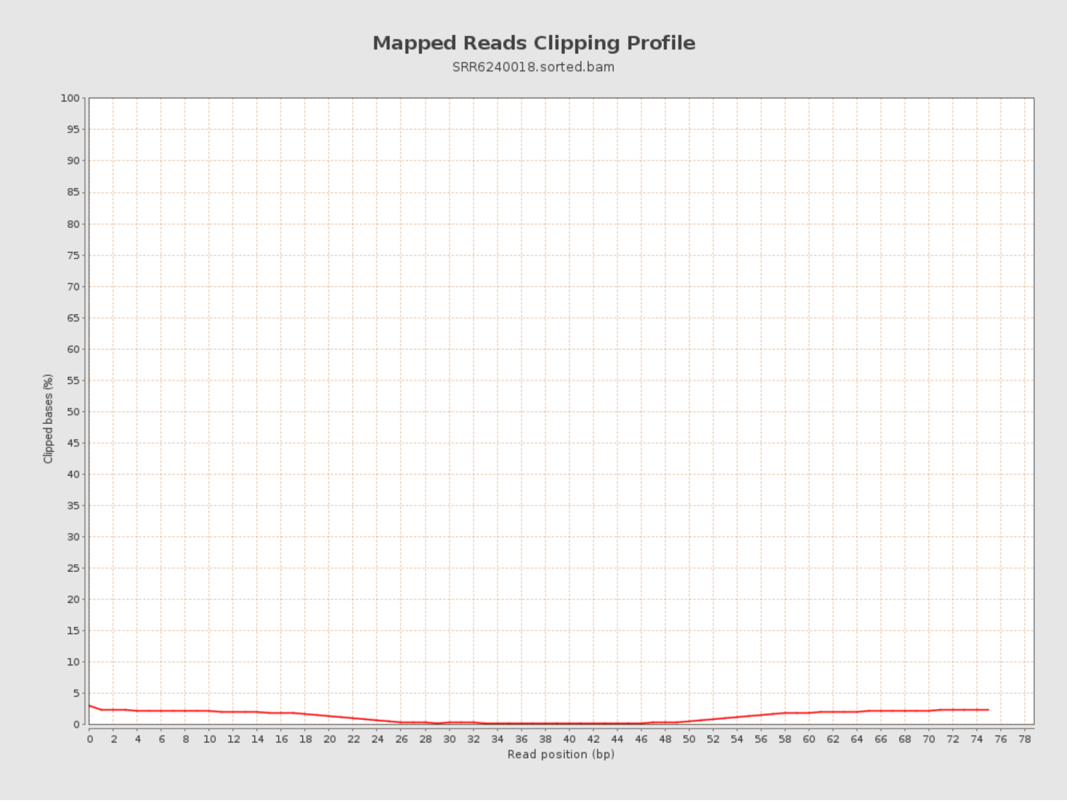
8. Results : Mapped Reads Nucleotide Content



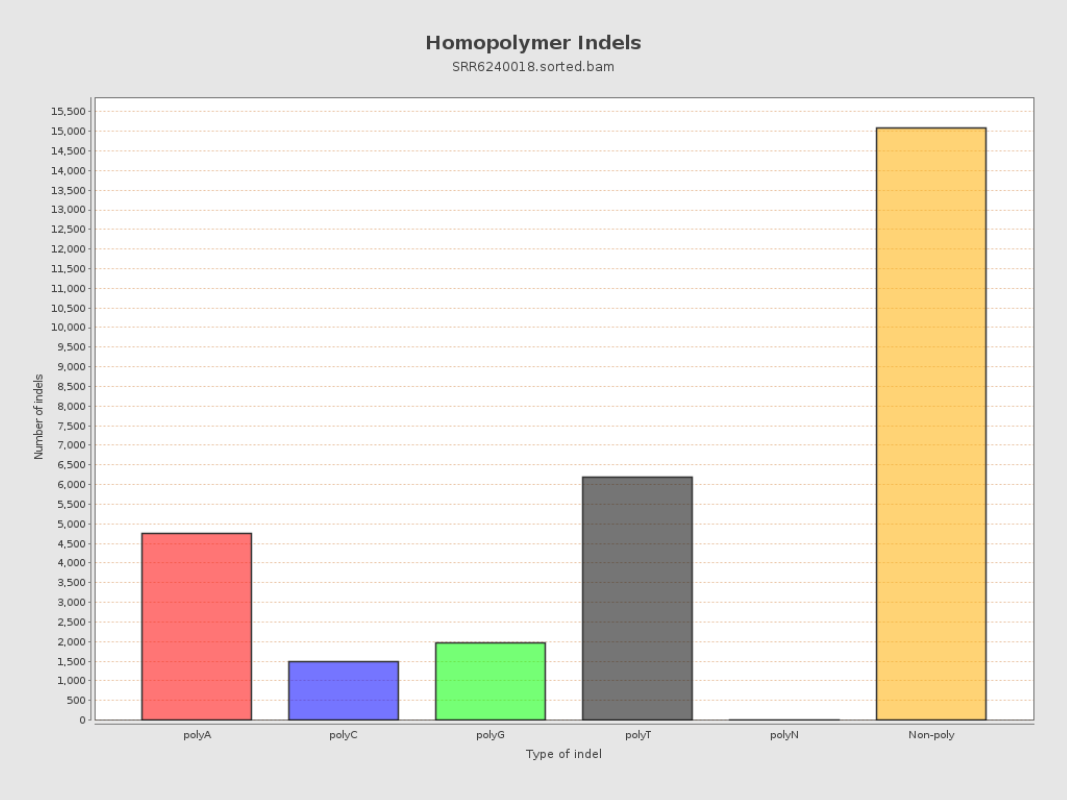
9. Results : Mapped Reads GC-content Distribution



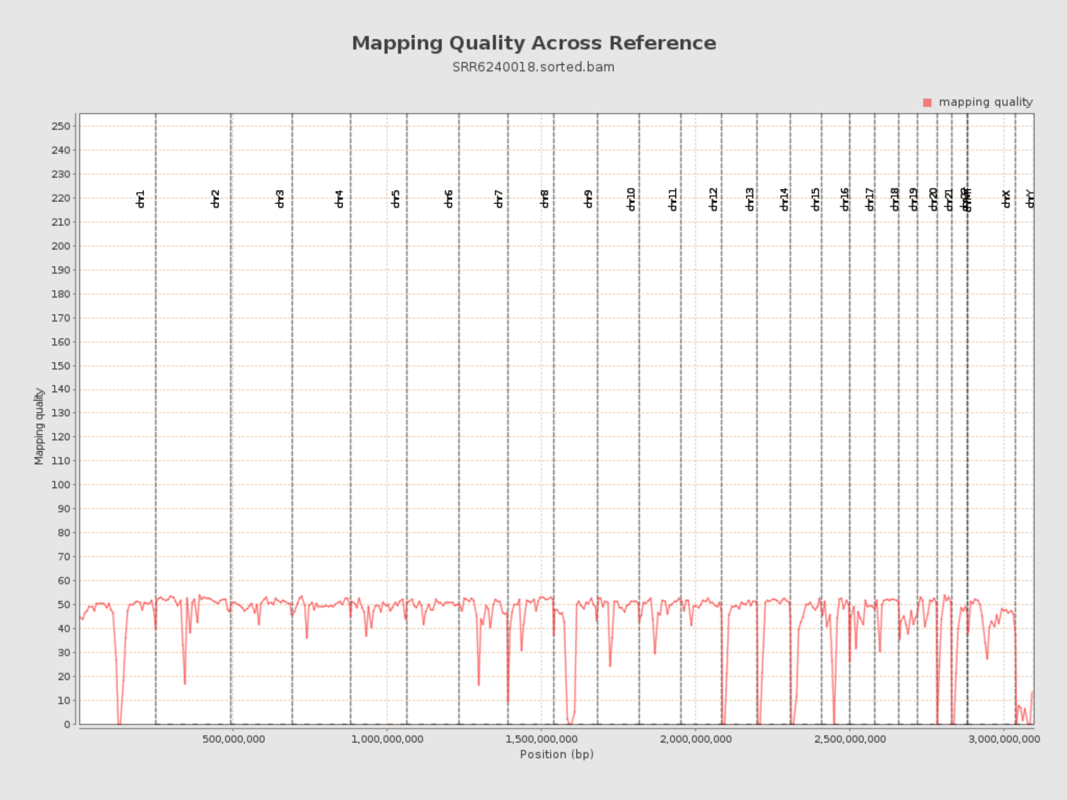
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram