Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 18:24:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013260.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_SRR6013260 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013260.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 18:24:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013260.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,757,067
Mapped reads	1,474,727 / 83.93%
Unmapped reads	282,340 / 16.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,200 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	126,517 / 7.2%
Duplication rate	6.96%
Clipped reads	749,520 / 42.66%

2.2. ACGT Content

Number/percentage of A's	26,256,452 / 27.39%
Number/percentage of C's	16,801,654 / 17.53%
Number/percentage of T's	31,562,893 / 32.92%
Number/percentage of G's	21,249,317 / 22.16%
Number/percentage of N's	1,336 / 0%
GC Percentage	39.69%

2.3. Coverage

Mean	0.031

Standard Deviation	0.3532

2.4. Mapping Quality

Mean Mapping Quality	46.12

2.5. Mismatches and indels

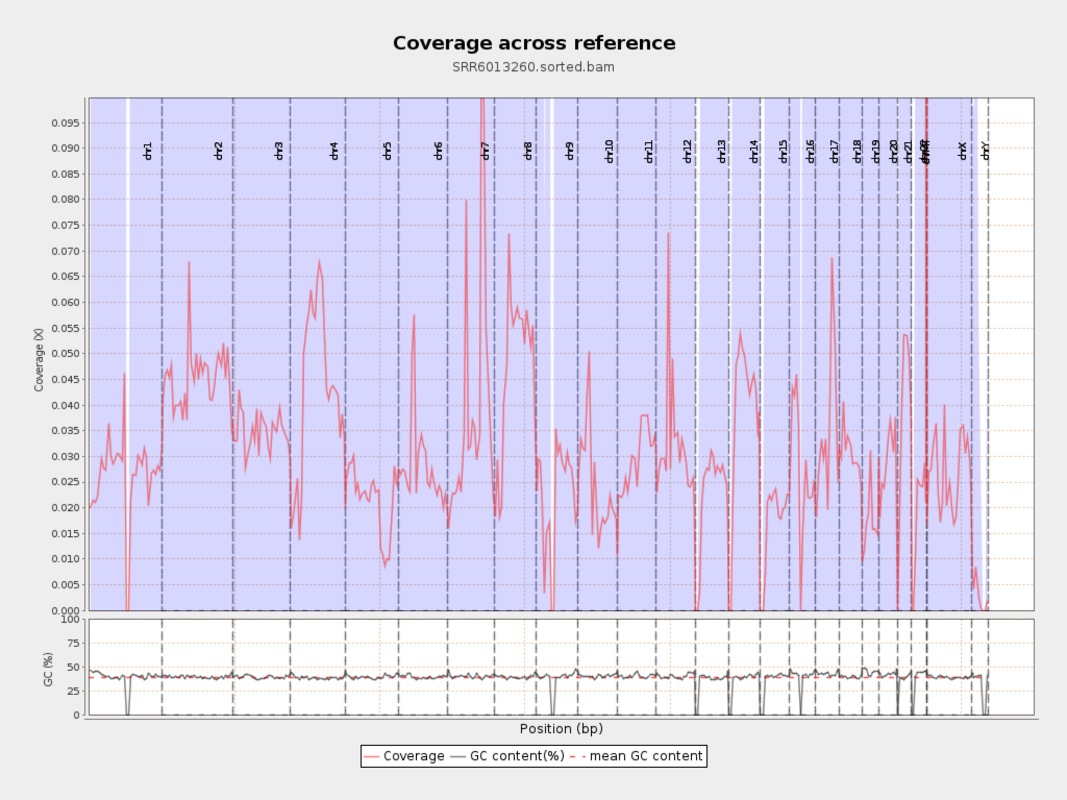
General error rate	0.84%
Mismatches	789,458
Insertions	7,103
Mapped reads with at least one insertion	0.48%
Deletions	28,835
Mapped reads with at least one deletion	1.93%
Homopolymer indels	49.86%

2.6. Chromosome stats

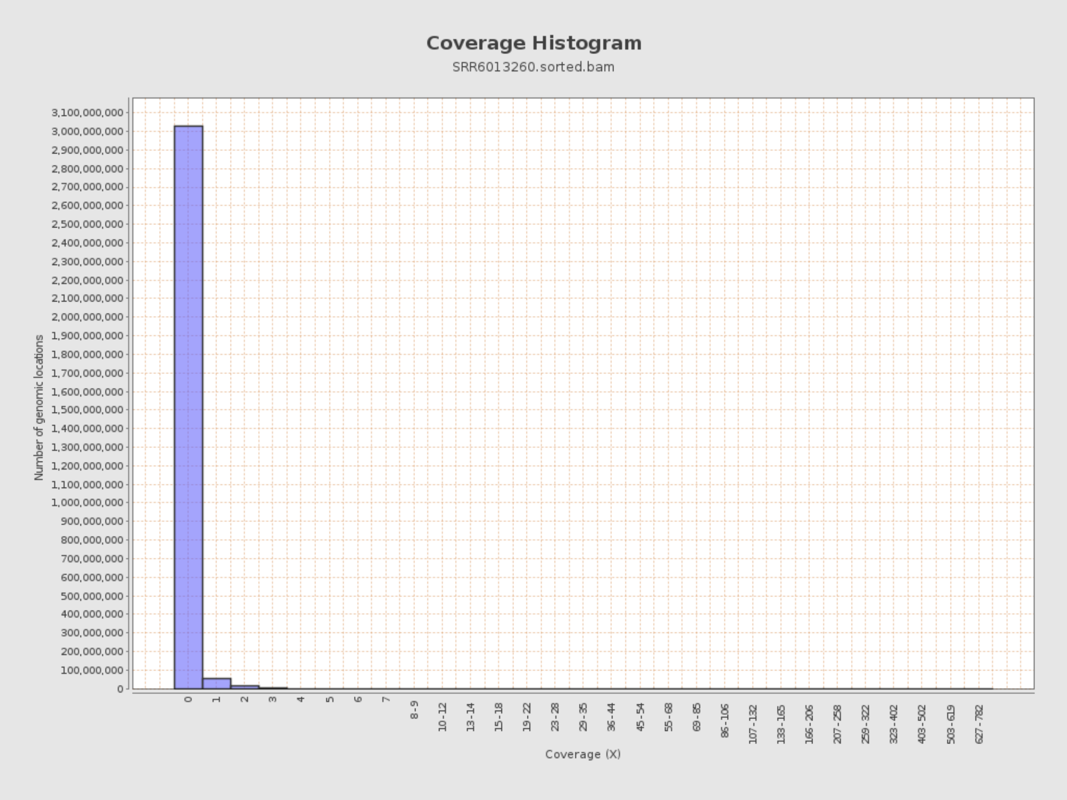
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6519688	0.0262	0.4713
chr2	243199373	11027754	0.0453	0.4162
chr3	198022430	6907452	0.0349	0.2433
chr4	191154276	8236161	0.0431	0.2804
chr5	180915260	3876885	0.0214	0.1896
chr6	171115067	4863063	0.0284	0.2686
chr7	159138663	6553768	0.0412	0.7383

chr8	146364022	6938269	0.0474	0.5393
chr9	141213431	3117794	0.0221	0.2794
chr10	135534747	3335332	0.0246	0.328
chr11	135006516	3980501	0.0295	0.2719
chr12	133851895	4308064	0.0322	0.2371
chr13	115169878	2563557	0.0223	0.1958
chr14	107349540	4142919	0.0386	0.2643
chr15	102531392	1748294	0.0171	0.1728
chr16	90354753	2489582	0.0276	0.2277
chr17	81195210	2823499	0.0348	0.2568
chr18	78077248	2411909	0.0309	0.5171
chr19	59128983	1056635	0.0179	0.348
chr20	63025520	1832969	0.0291	0.2243
chr21	48129895	1856849	0.0386	0.2602
chr22	51304566	913499	0.0178	0.1691
chrMT	16571	104141	6.2845	5.0784
chrX	155270560	4142901	0.0267	0.2284
chrY	59373566	170723	0.0029	0.0755

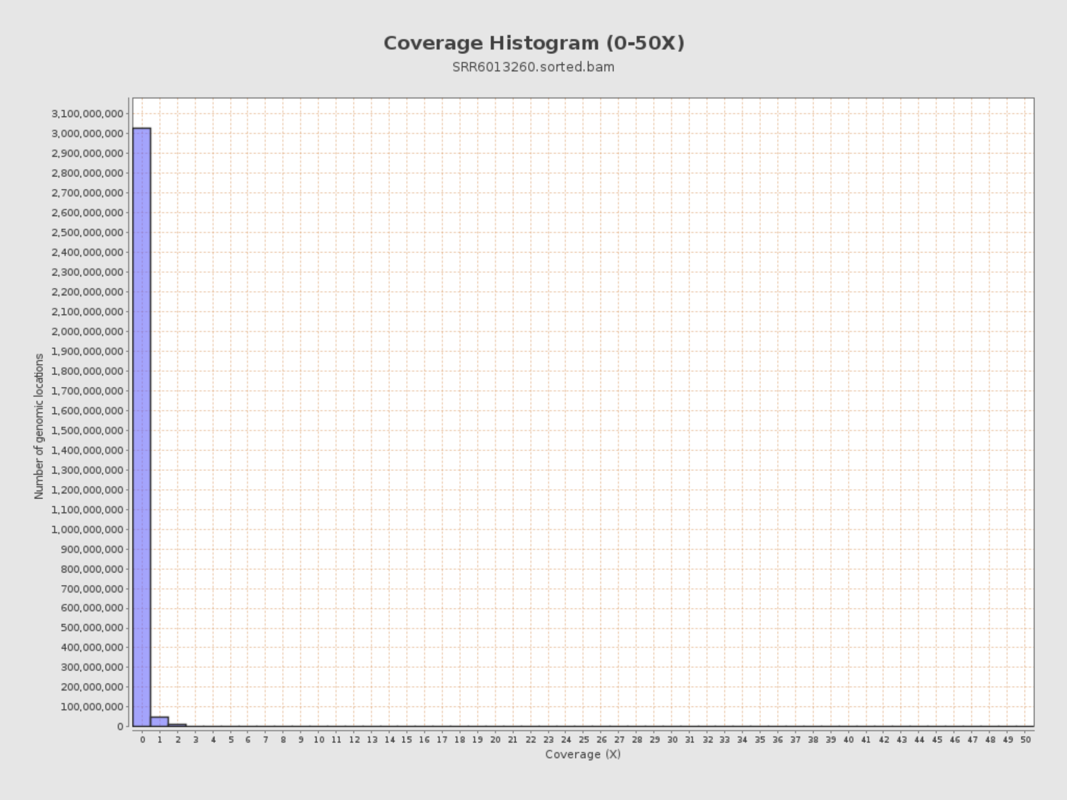
3. Results : Coverage across reference



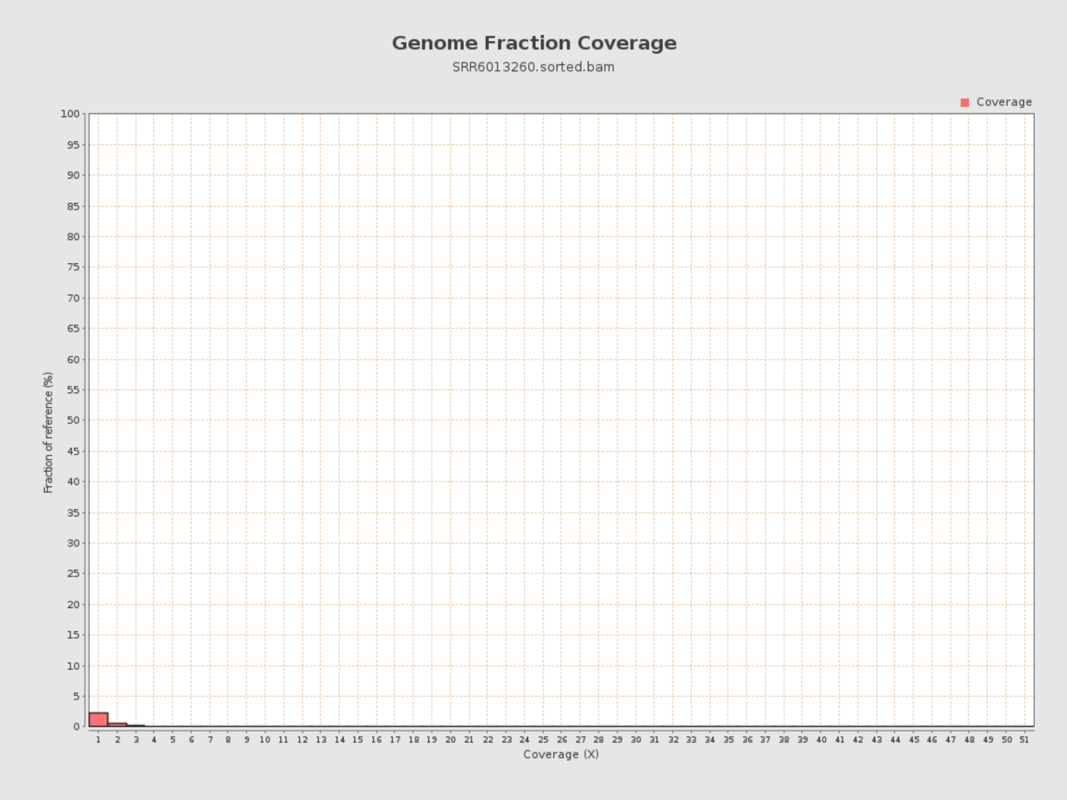
4. Results : Coverage Histogram



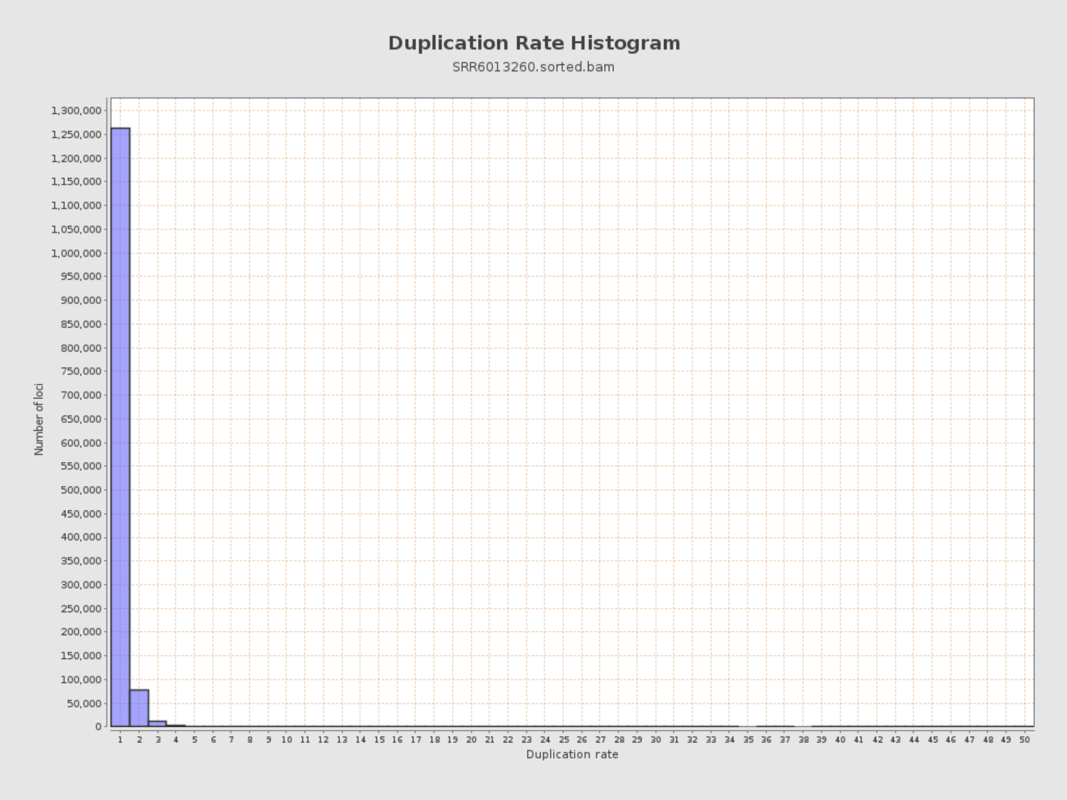
5. Results : Coverage Histogram (0-50X)



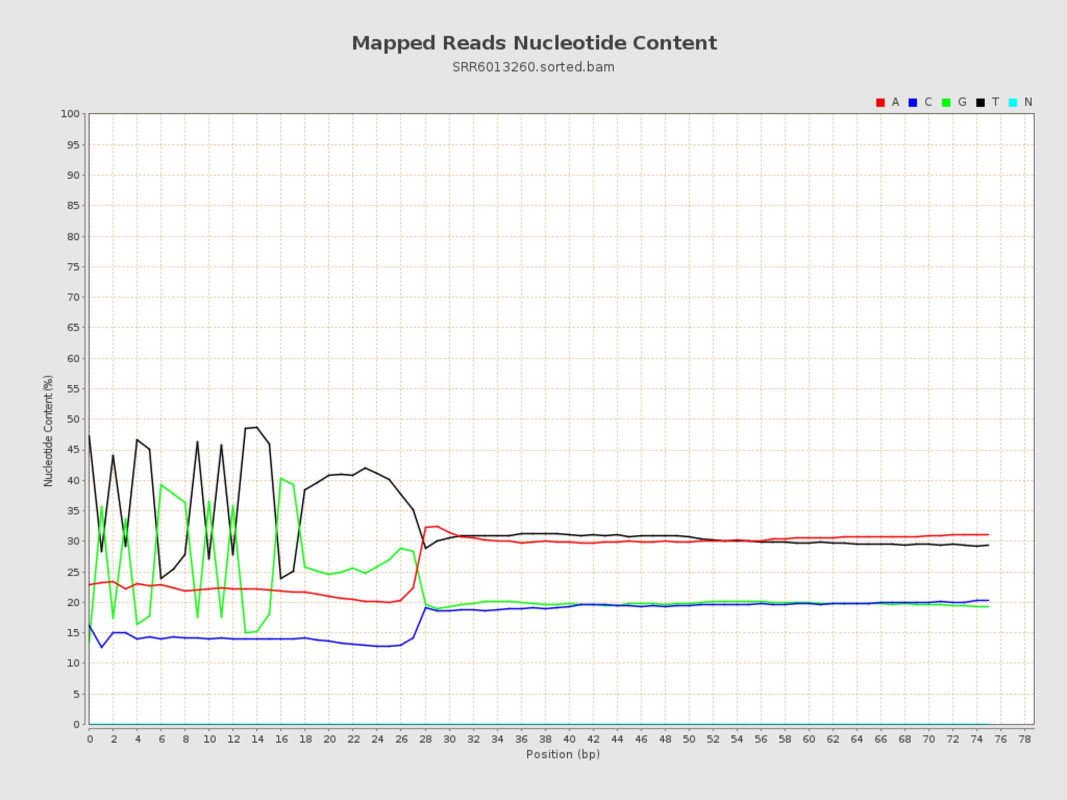
6. Results : Genome Fraction Coverage



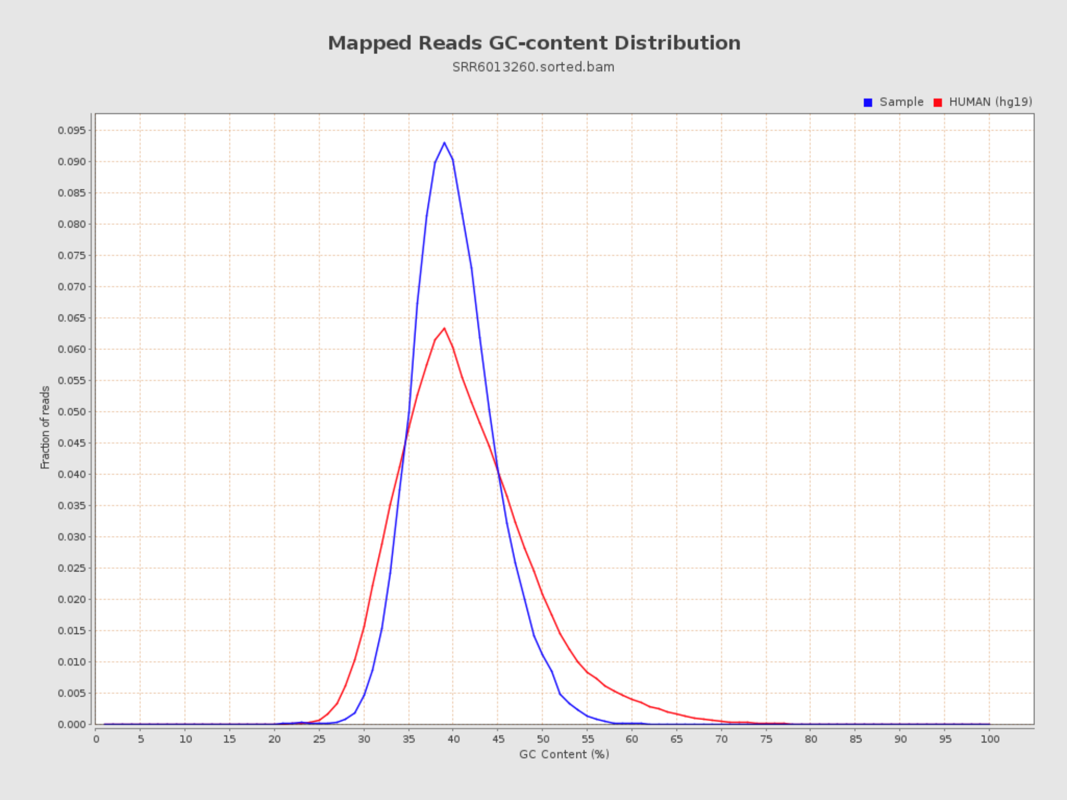
7. Results : Duplication Rate Histogram



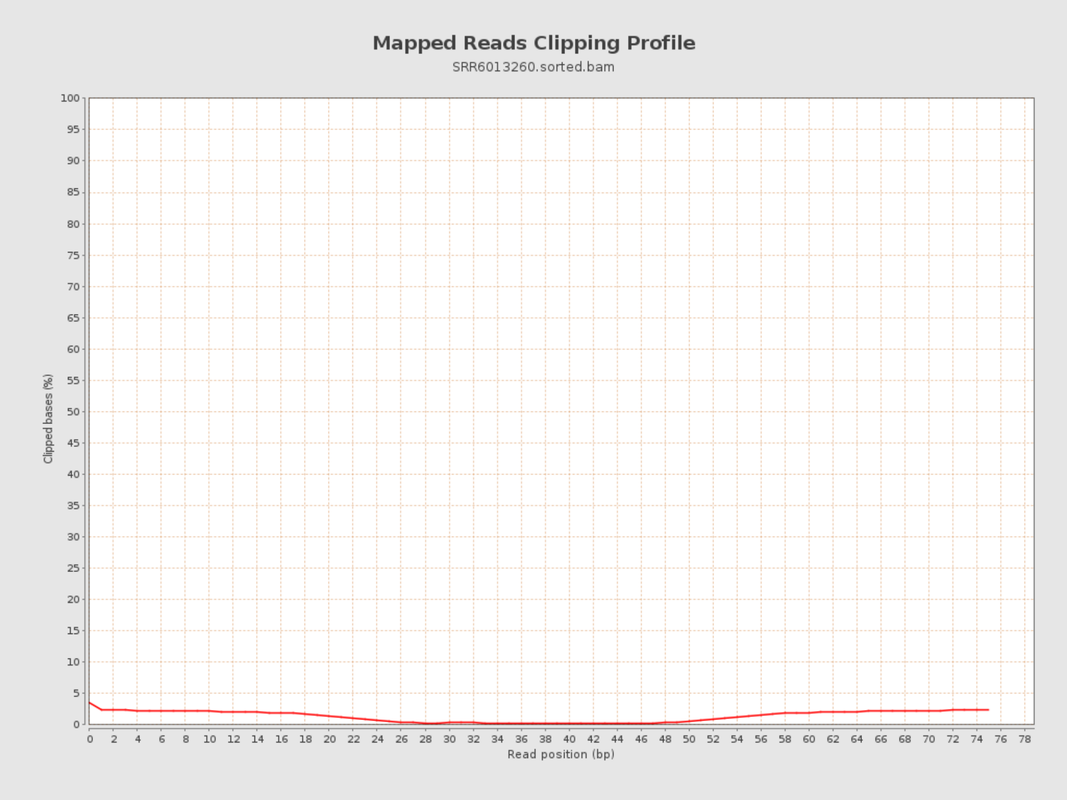
8. Results : Mapped Reads Nucleotide Content



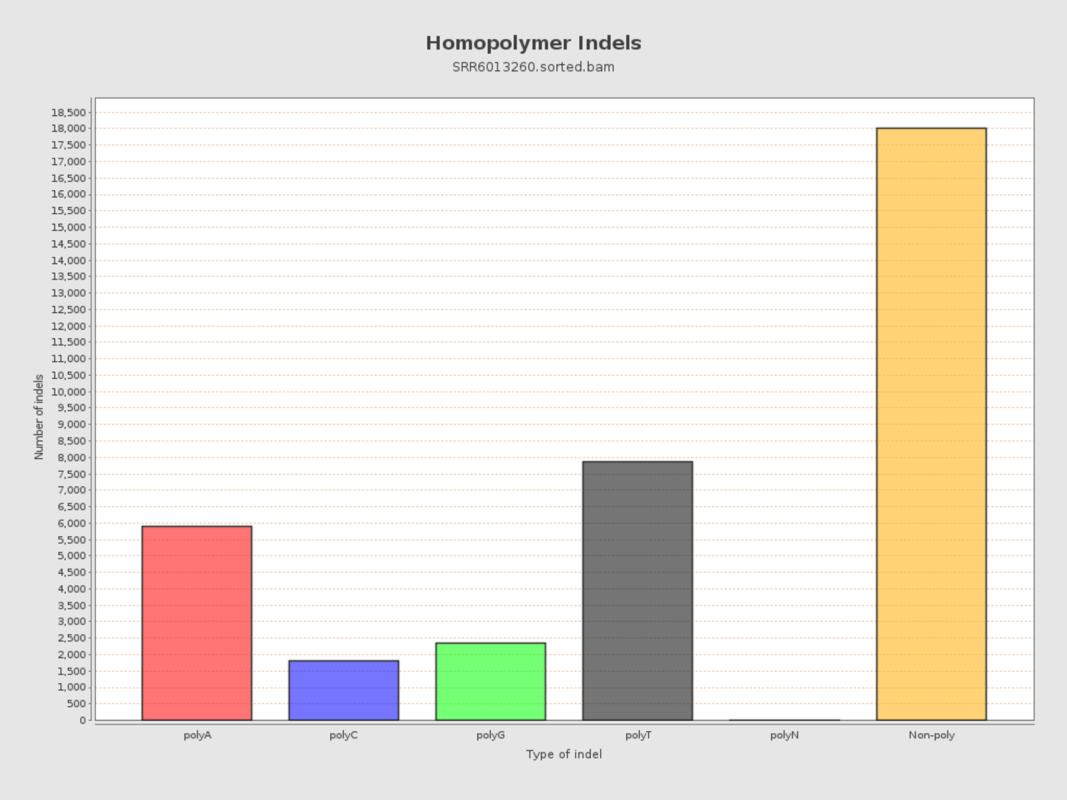
9. Results : Mapped Reads GC-content Distribution



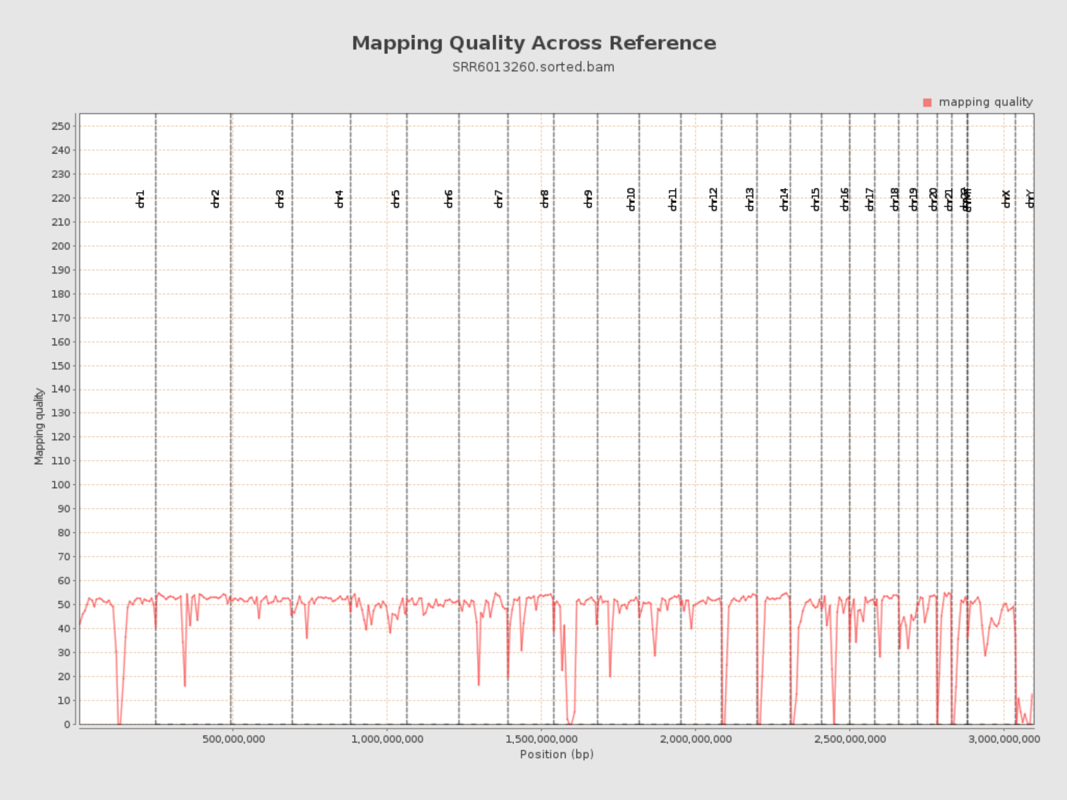
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram