Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 12:51:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008819.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_SRR6008819 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008819.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 12:51:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008819.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,375,690
Mapped reads	1,090,699 / 79.28%
Unmapped reads	284,991 / 20.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,740 / 0.93%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	26,104 / 1.9%
Duplication rate	2.02%
Clipped reads	468,969 / 34.09%

2.2. ACGT Content

Number/percentage of A's	23,338,937 / 31.39%
Number/percentage of C's	13,409,557 / 18.04%
Number/percentage of T's	21,996,372 / 29.59%
Number/percentage of G's	15,575,342 / 20.95%
Number/percentage of N's	26,072 / 0.04%
GC Percentage	38.99%

2.3. Coverage

Mean	0.024

Standard Deviation	0.2141

2.4. Mapping Quality

Mean Mapping Quality	46.92

2.5. Mismatches and indels

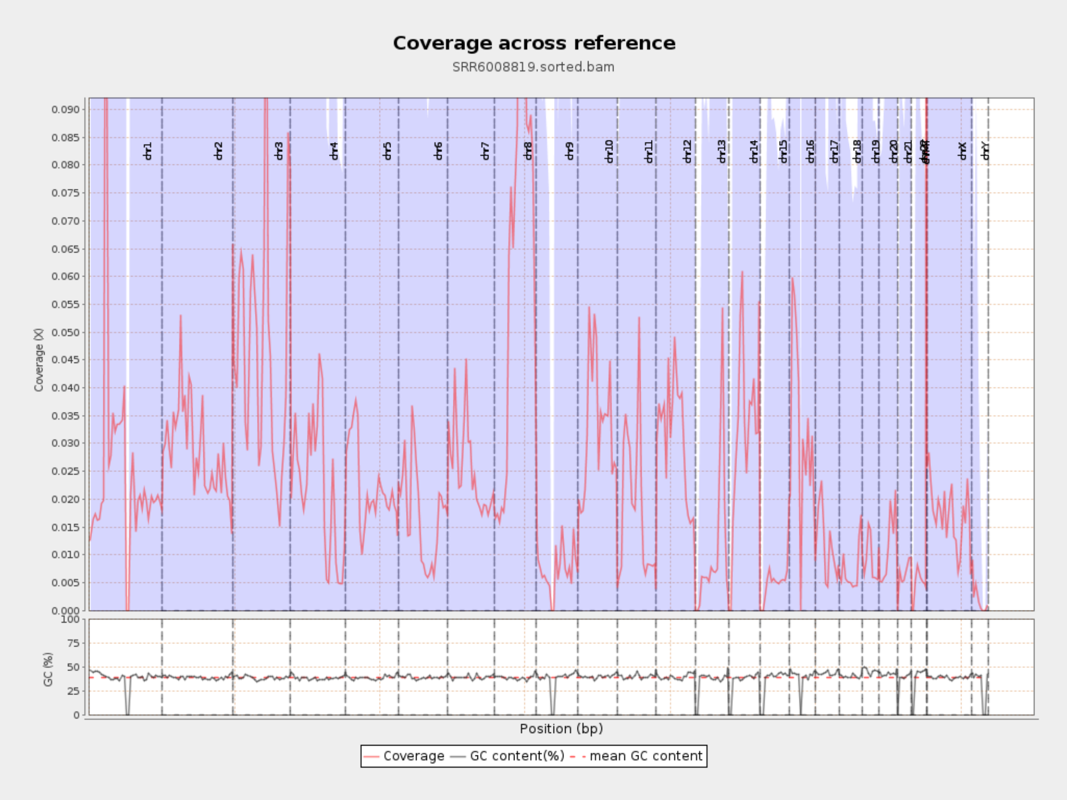
General error rate	0.98%
Mismatches	721,237
Insertions	5,143
Mapped reads with at least one insertion	0.47%
Deletions	29,172
Mapped reads with at least one deletion	2.64%
Homopolymer indels	46.11%

2.6. Chromosome stats

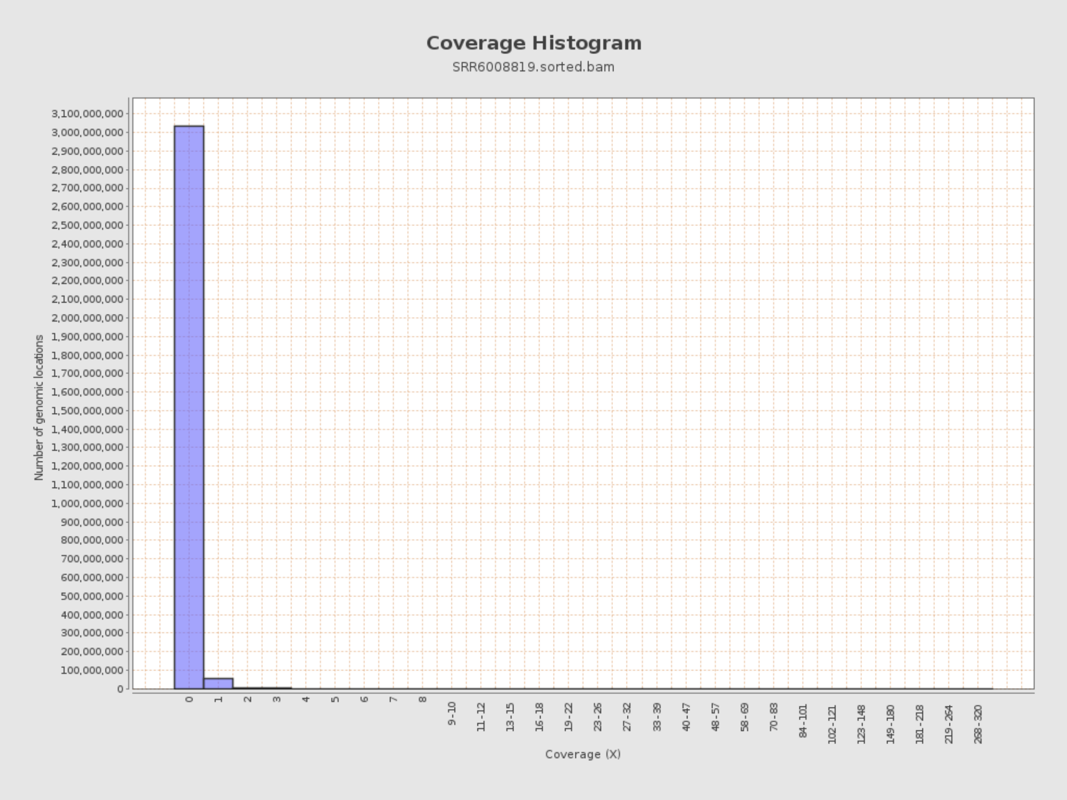
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6219570	0.025	0.3117
chr2	243199373	7077847	0.0291	0.2226
chr3	198022430	9454613	0.0477	0.2556
chr4	191154276	4206562	0.022	0.1706
chr5	180915260	4076937	0.0225	0.1708
chr6	171115067	2982275	0.0174	0.1757
chr7	159138663	4100495	0.0258	0.2674

chr8	146364022	9622969	0.0657	0.3479
chr9	141213431	1028742	0.0073	0.1086
chr10	135534747	4499798	0.0332	0.2976
chr11	135006516	2572356	0.0191	0.1742
chr12	133851895	4193754	0.0313	0.2031
chr13	115169878	1291758	0.0112	0.1228
chr14	107349540	3395541	0.0316	0.2052
chr15	102531392	530634	0.0052	0.0794
chr16	90354753	2959033	0.0327	0.2305
chr17	81195210	943957	0.0116	0.1393
chr18	78077248	553600	0.0071	0.1693
chr19	59128983	542337	0.0092	0.21
chr20	63025520	725022	0.0115	0.121
chr21	48129895	317789	0.0066	0.0911
chr22	51304566	237258	0.0046	0.0745
chrMT	16571	10347	0.6244	0.9574
chrX	155270560	2725712	0.0176	0.1543
chrY	59373566	124179	0.0021	0.0519

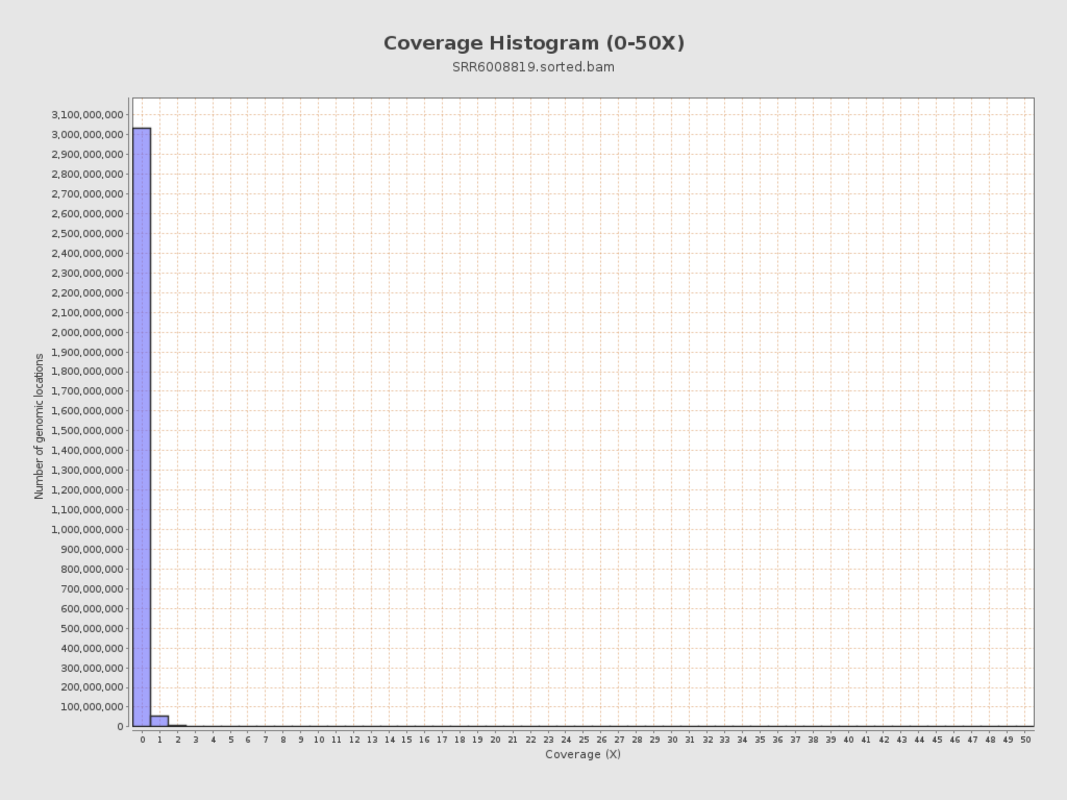
3. Results : Coverage across reference



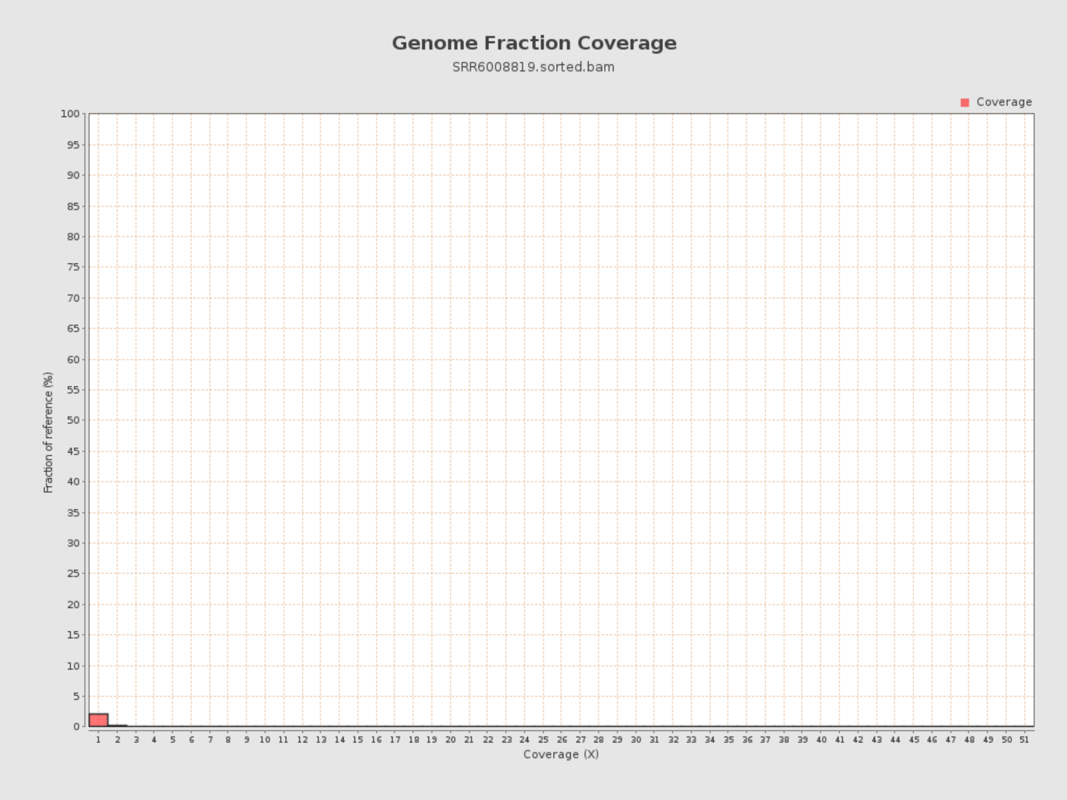
4. Results : Coverage Histogram



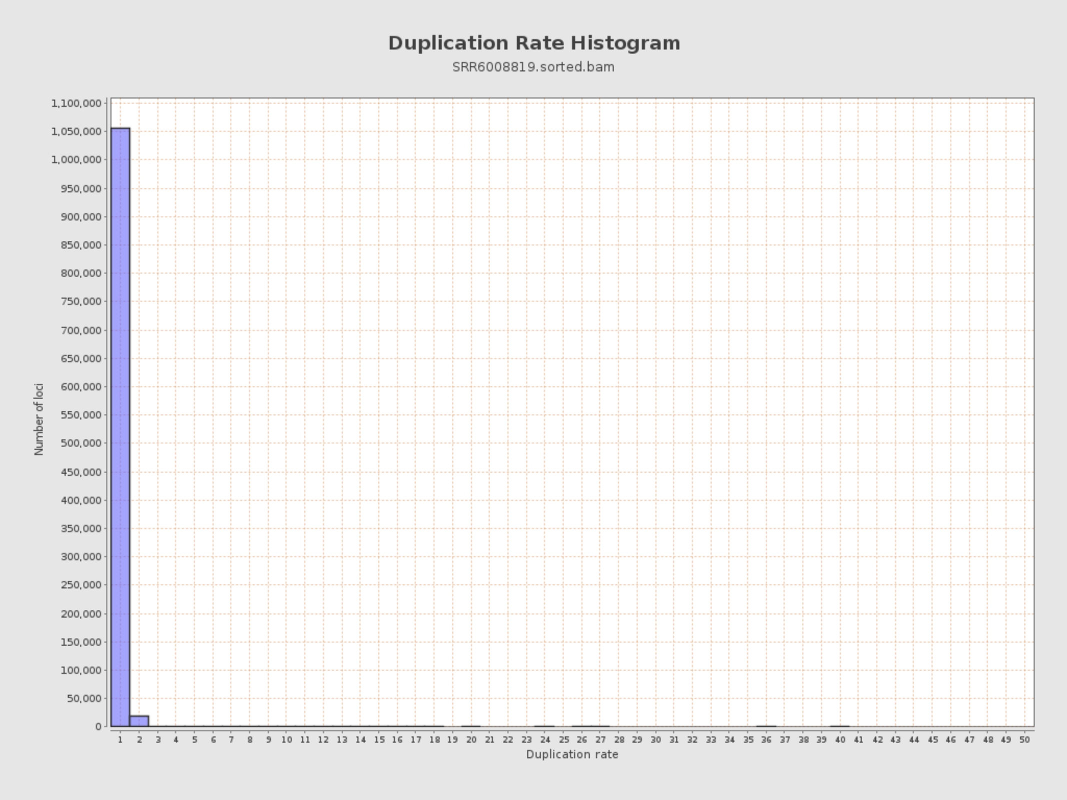
5. Results : Coverage Histogram (0-50X)



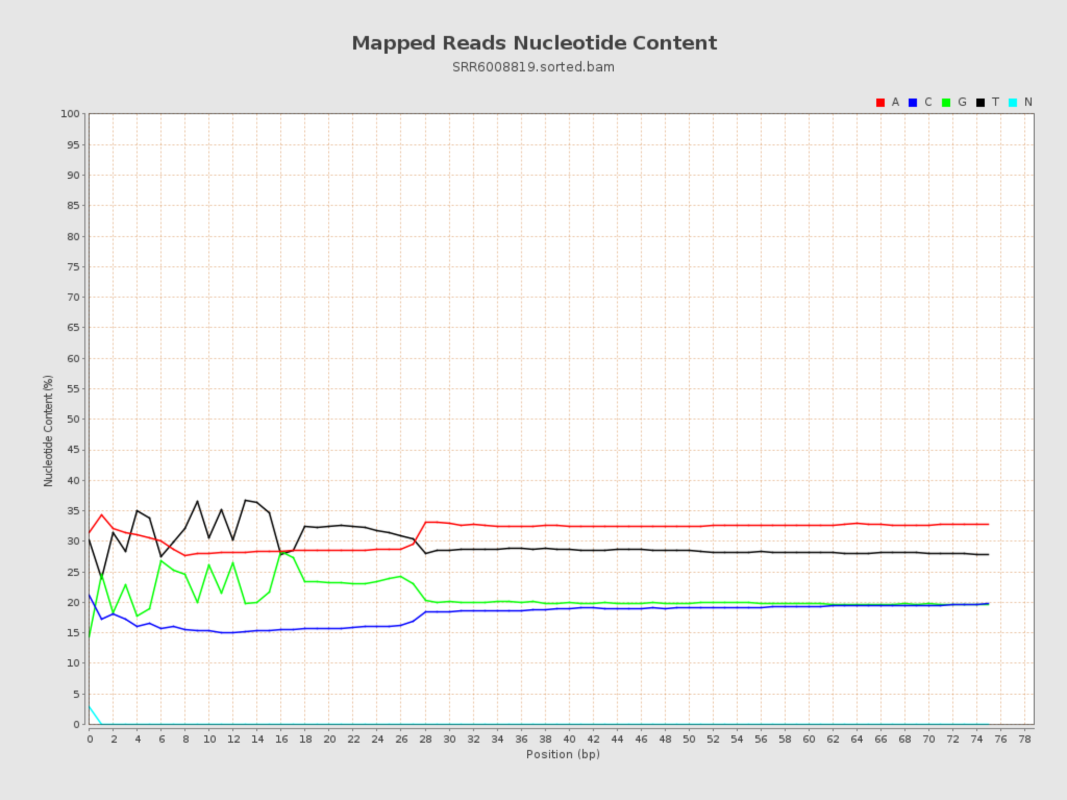
6. Results : Genome Fraction Coverage



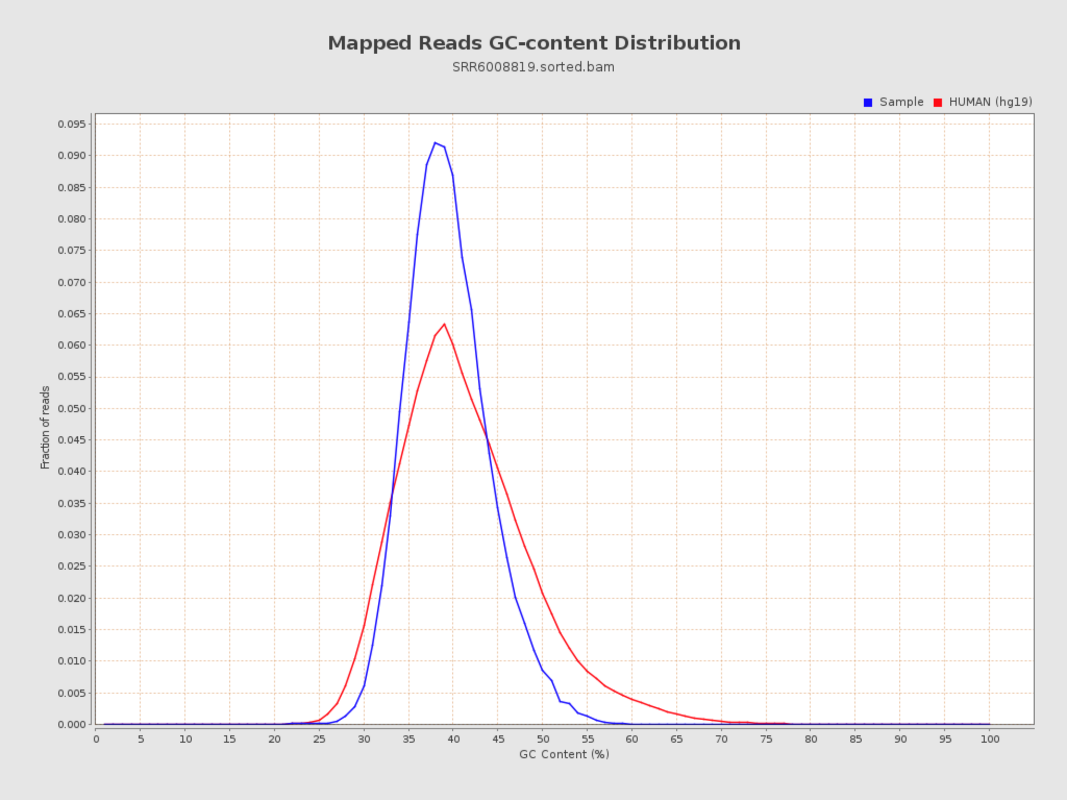
7. Results : Duplication Rate Histogram



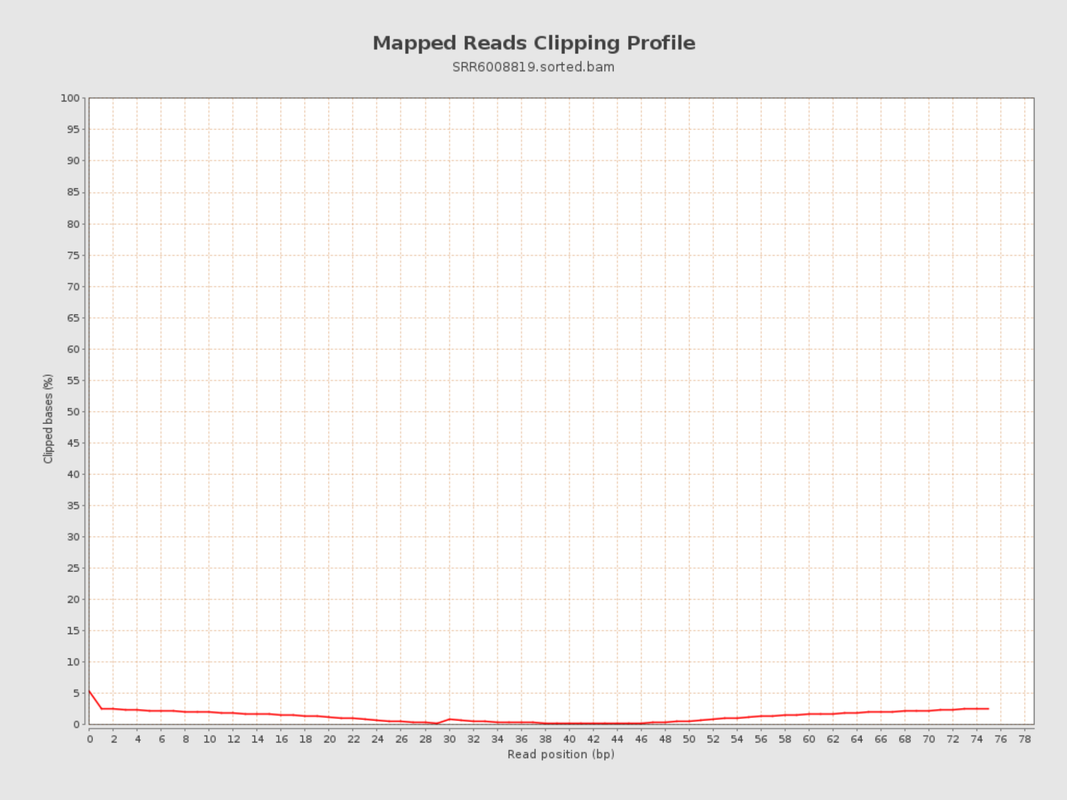
8. Results : Mapped Reads Nucleotide Content



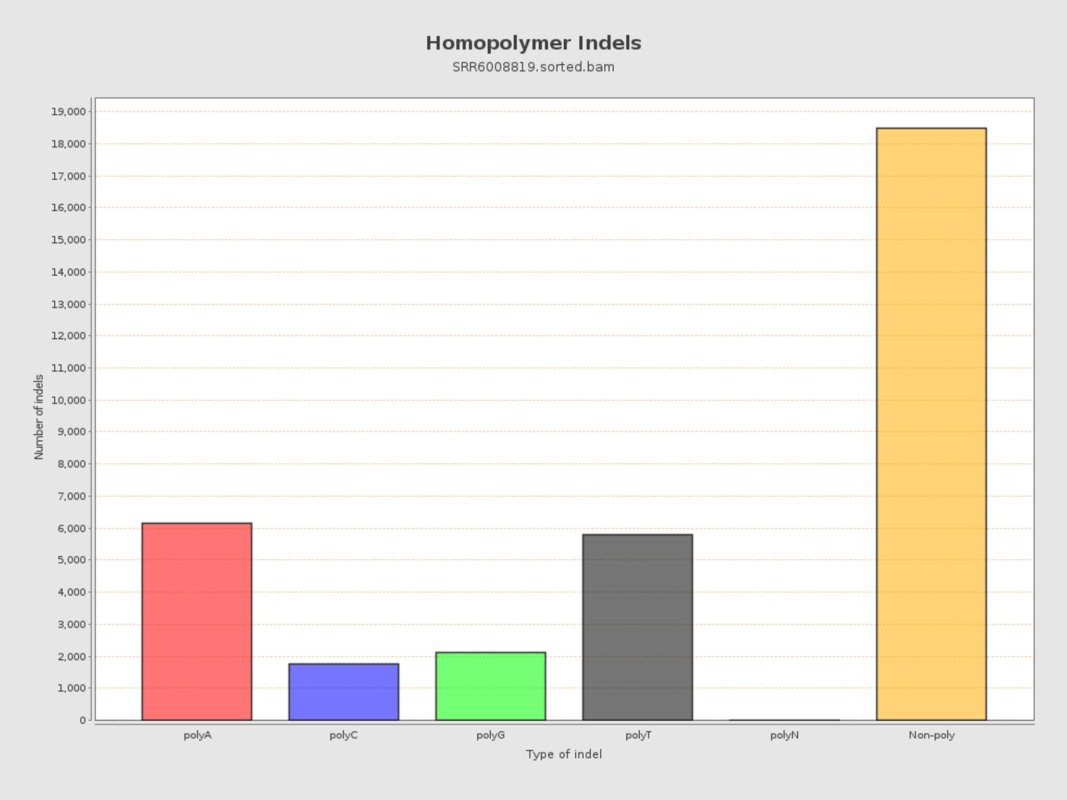
9. Results : Mapped Reads GC-content Distribution



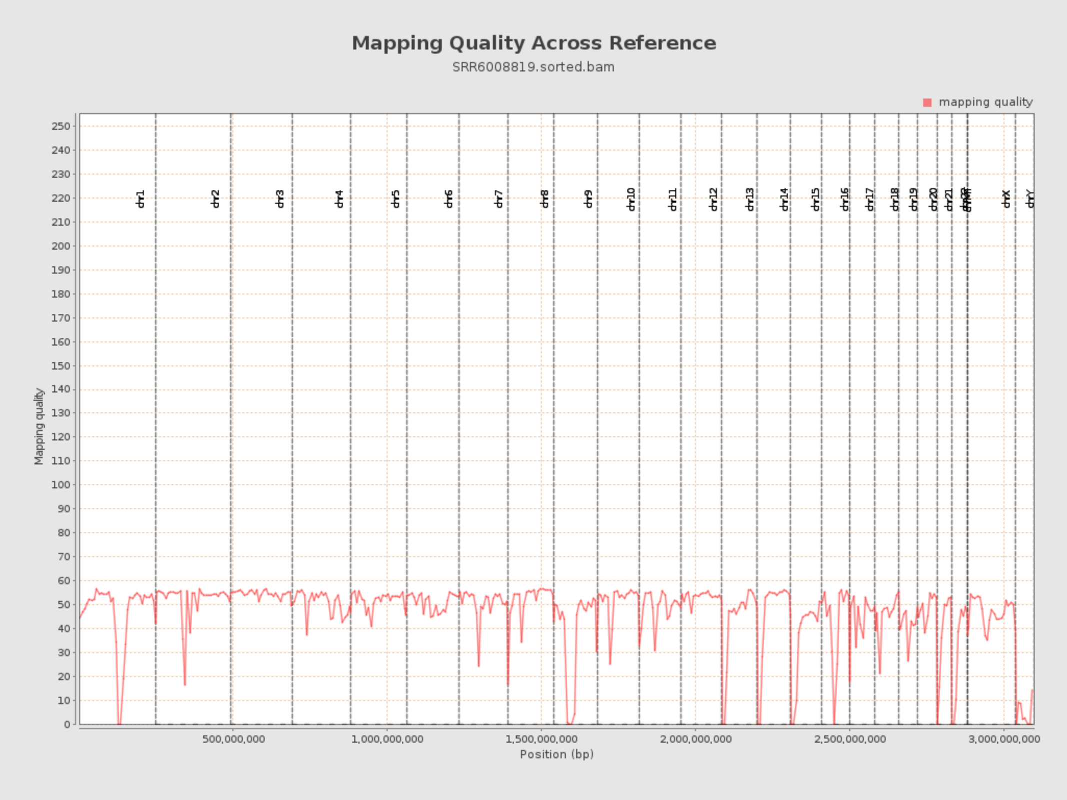
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram