Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 08:28:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008722.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_SRR6008722 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008722.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 08:28:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008722.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,582,349
Mapped reads	1,023,667 / 64.69%
Unmapped reads	558,682 / 35.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,468 / 0.28%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	26,350 / 1.67%
Duplication rate	2.05%
Clipped reads	564,337 / 35.66%

2.2. ACGT Content

Number/percentage of A's	18,727,050 / 28.89%
Number/percentage of C's	11,017,342 / 16.99%
Number/percentage of T's	19,873,186 / 30.66%
Number/percentage of G's	15,194,258 / 23.44%
Number/percentage of N's	16,318 / 0.03%
GC Percentage	40.43%

2.3. Coverage

Mean	0.021

Standard Deviation	0.1946

2.4. Mapping Quality

Mean Mapping Quality	45.97

2.5. Mismatches and indels

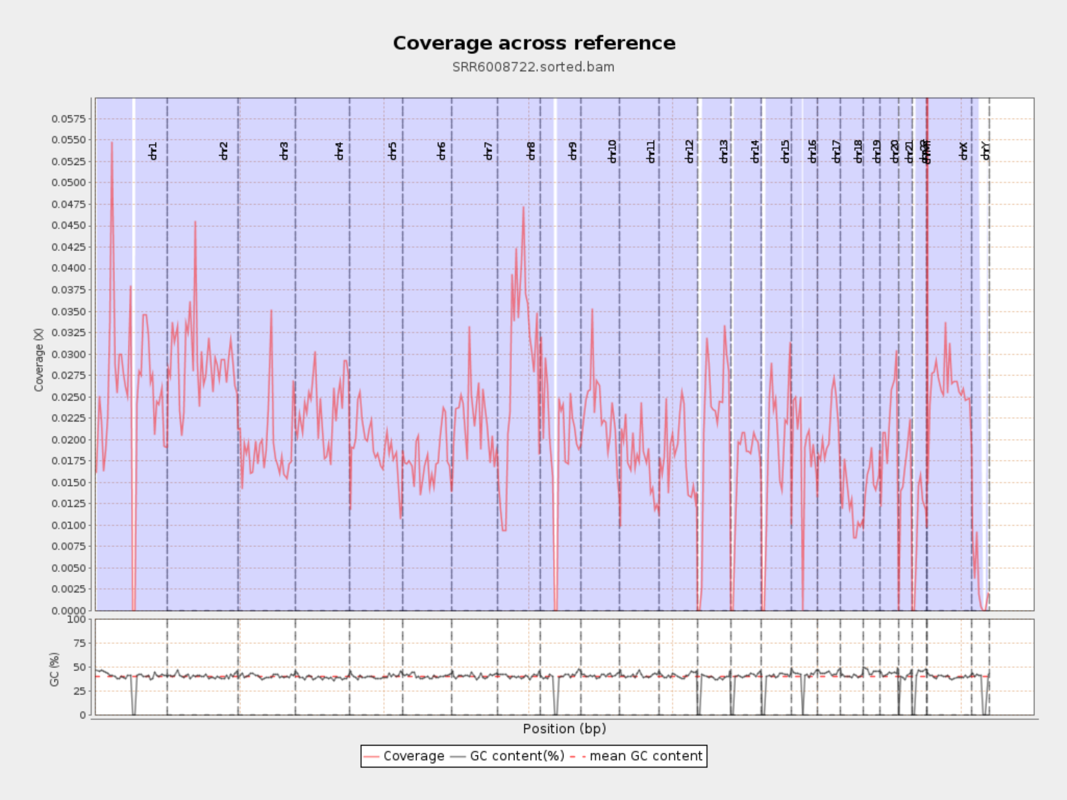
General error rate	1.07%
Mismatches	681,263
Insertions	5,564
Mapped reads with at least one insertion	0.54%
Deletions	22,872
Mapped reads with at least one deletion	2.21%
Homopolymer indels	46.87%

2.6. Chromosome stats

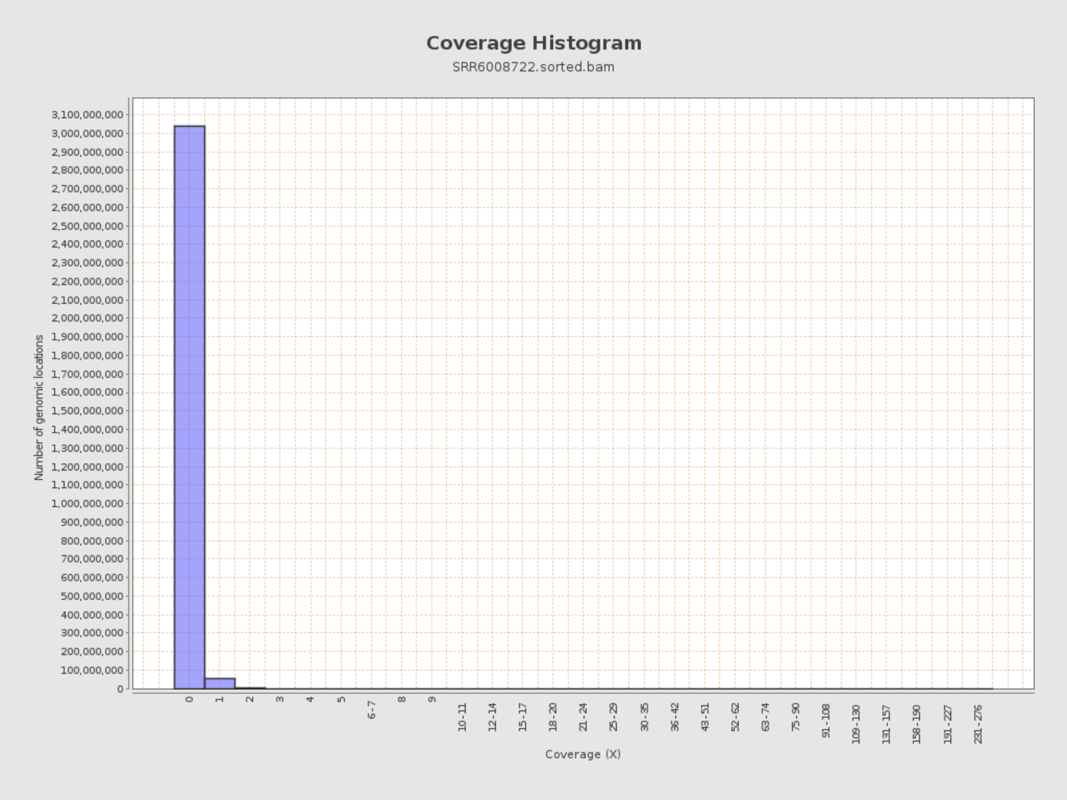
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6293544	0.0252	0.2861
chr2	243199373	7101490	0.0292	0.2684
chr3	198022430	3794065	0.0192	0.1487
chr4	191154276	4505939	0.0236	0.1684
chr5	180915260	3458071	0.0191	0.1476
chr6	171115067	2992233	0.0175	0.1515
chr7	159138663	3546443	0.0223	0.2239

chr8	146364022	4191062	0.0286	0.2464
chr9	141213431	2822376	0.02	0.1947
chr10	135534747	3118212	0.023	0.2094
chr11	135006516	2373821	0.0176	0.162
chr12	133851895	2439827	0.0182	0.146
chr13	115169878	2486779	0.0216	0.1565
chr14	107349540	1743914	0.0162	0.1411
chr15	102531392	1905022	0.0186	0.1474
chr16	90354753	1666451	0.0184	0.1542
chr17	81195210	1699210	0.0209	0.1609
chr18	78077248	917237	0.0117	0.2498
chr19	59128983	919220	0.0155	0.1851
chr20	63025520	1385041	0.022	0.16
chr21	48129895	740567	0.0154	0.141
chr22	51304566	495780	0.0097	0.1044
chrMT	16571	21703	1.3097	1.4591
chrX	155270560	4068244	0.0262	0.1808
chrY	59373566	178514	0.003	0.0783

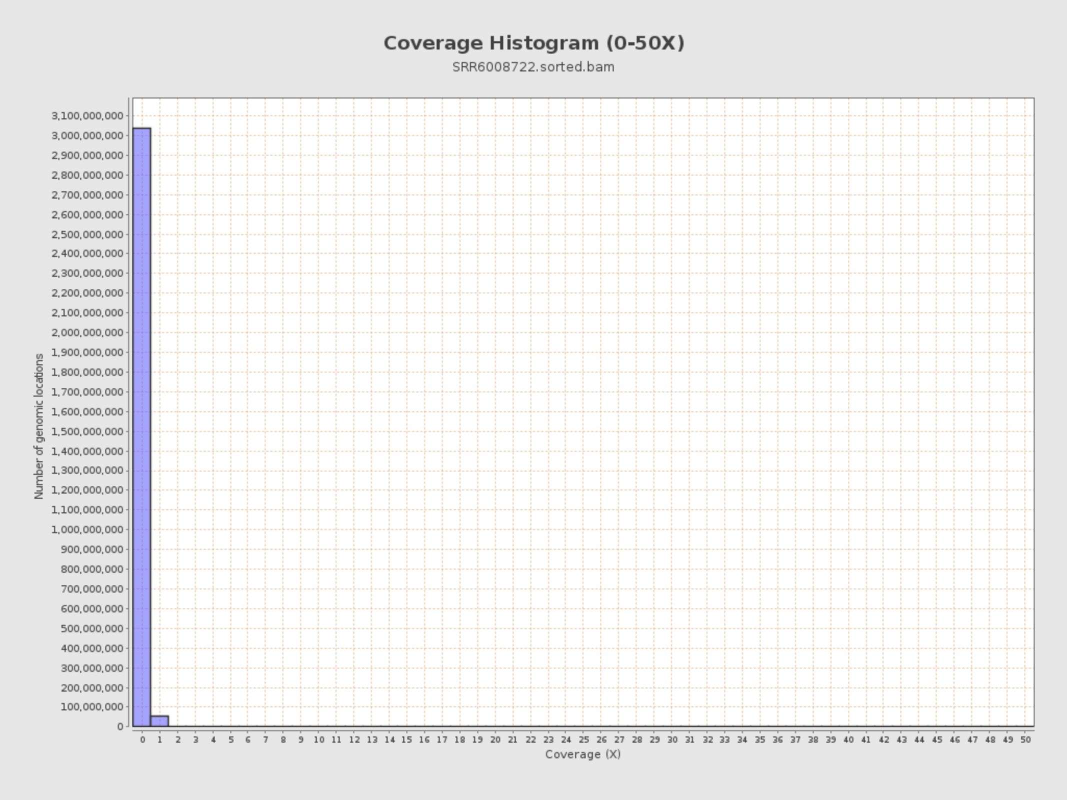
3. Results : Coverage across reference



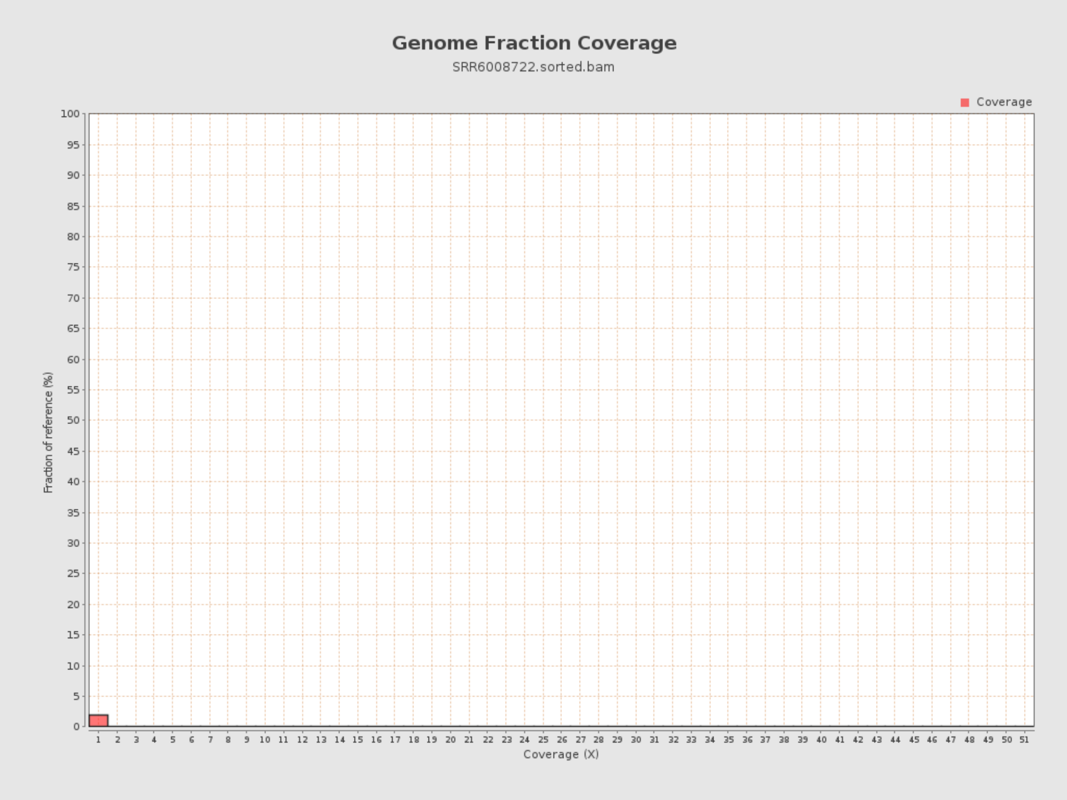
4. Results : Coverage Histogram



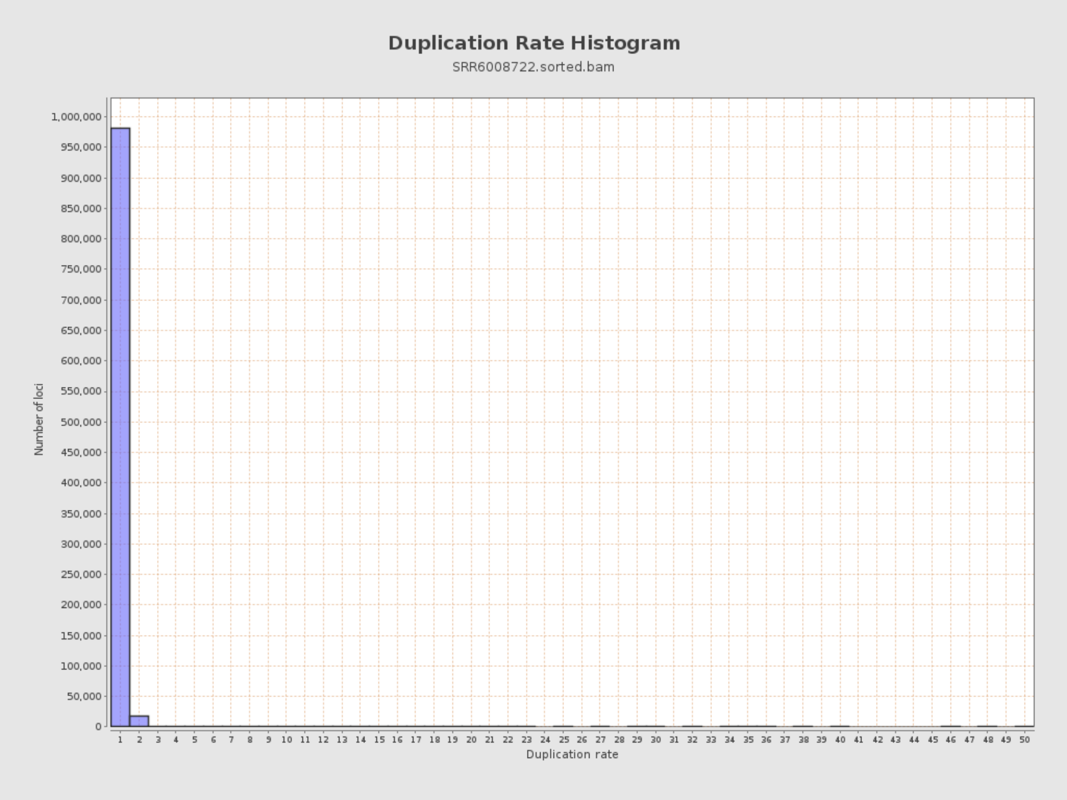
5. Results : Coverage Histogram (0-50X)



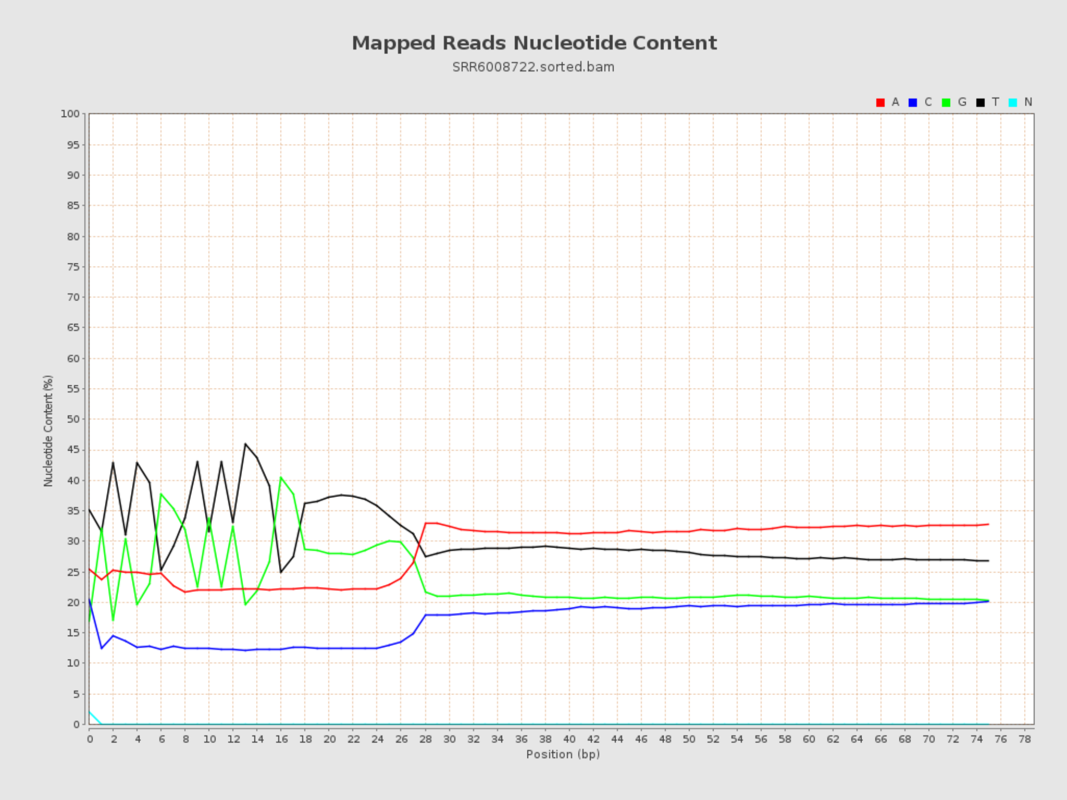
6. Results : Genome Fraction Coverage



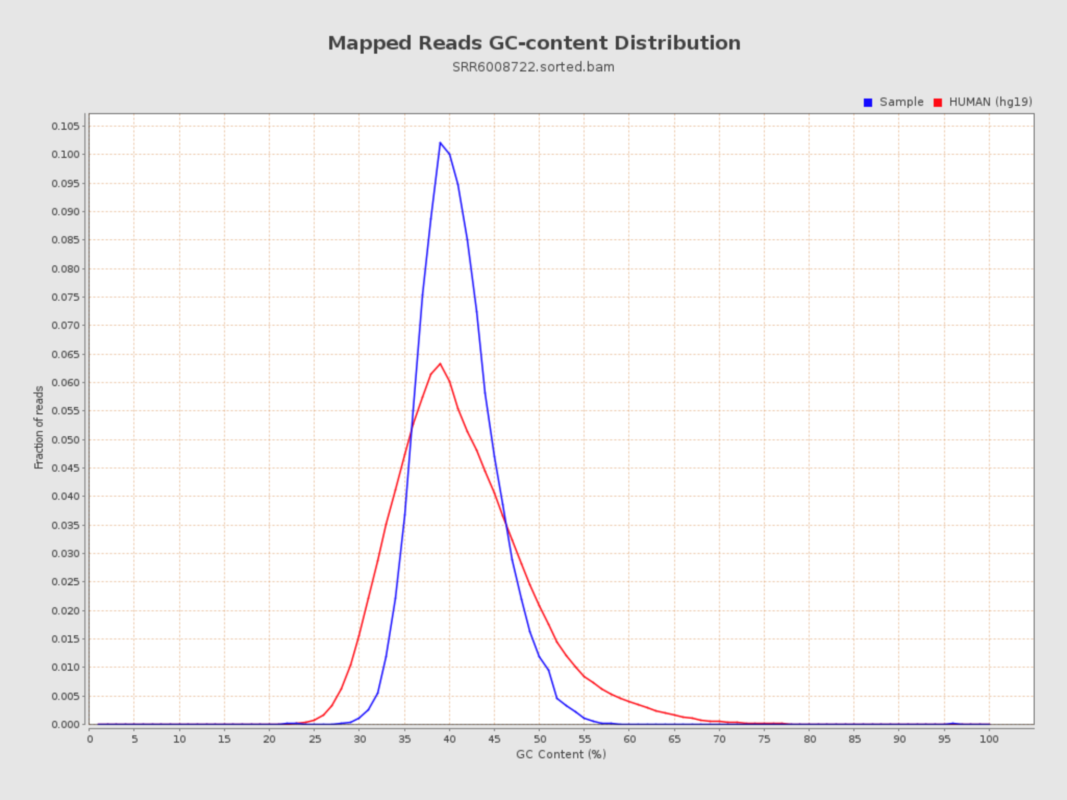
7. Results : Duplication Rate Histogram



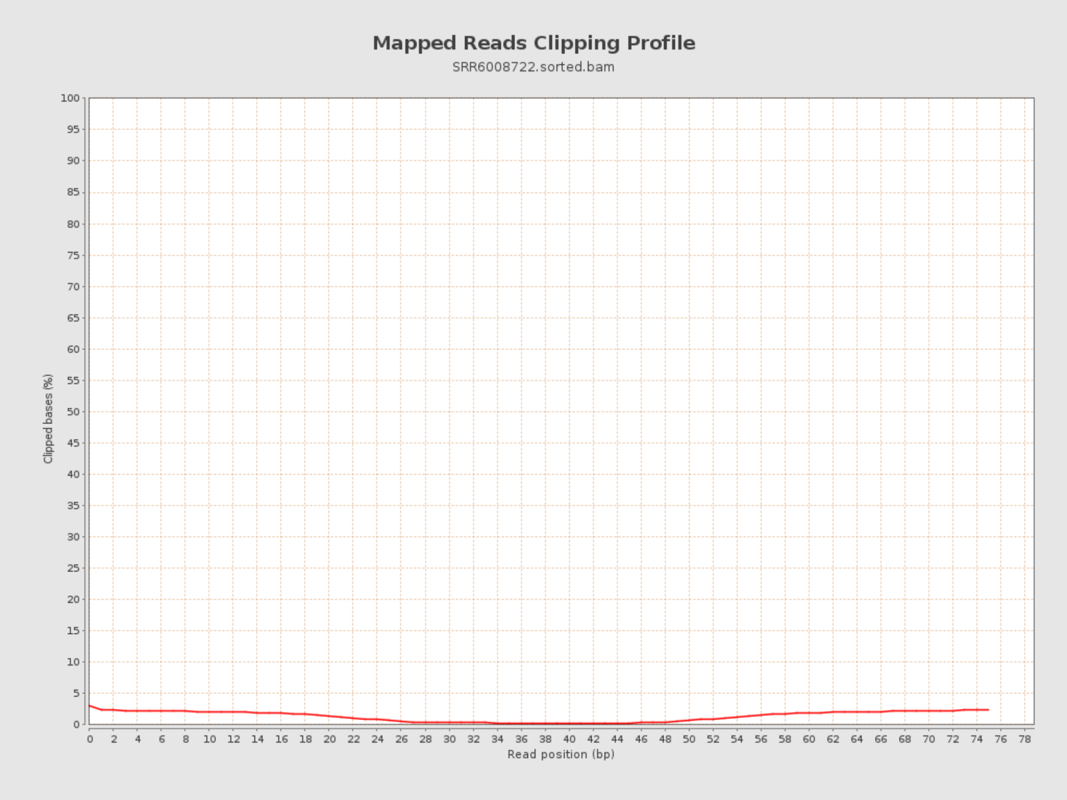
8. Results : Mapped Reads Nucleotide Content



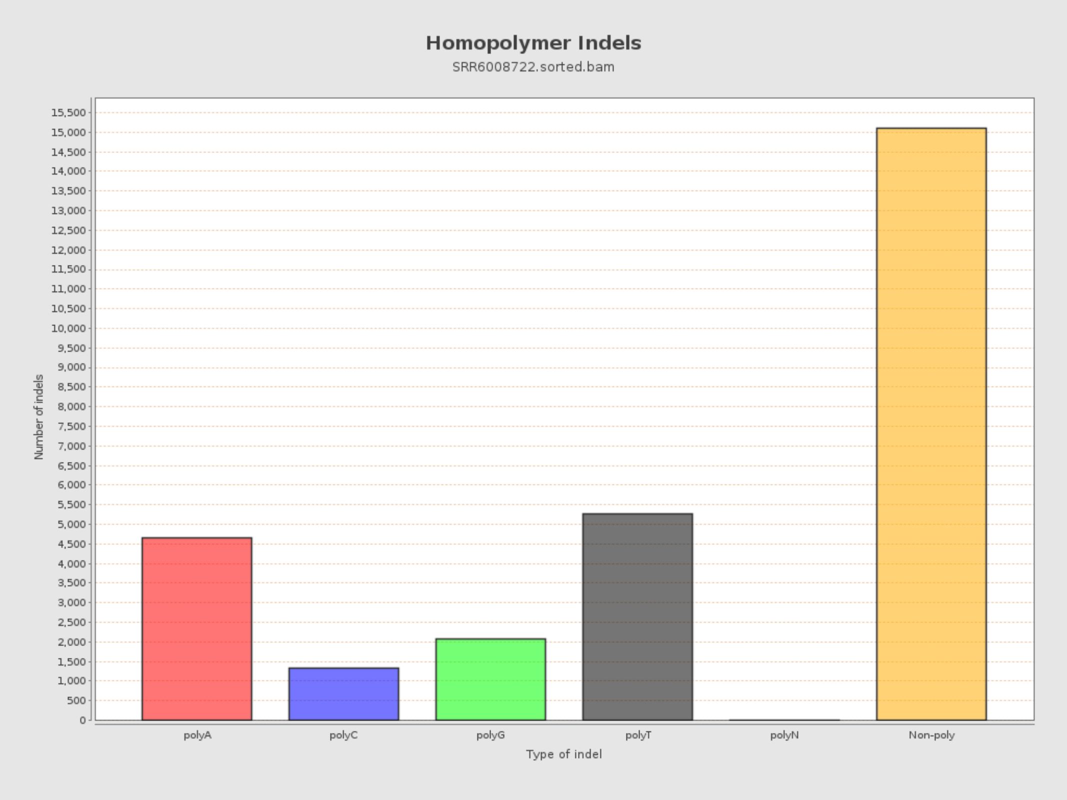
9. Results : Mapped Reads GC-content Distribution



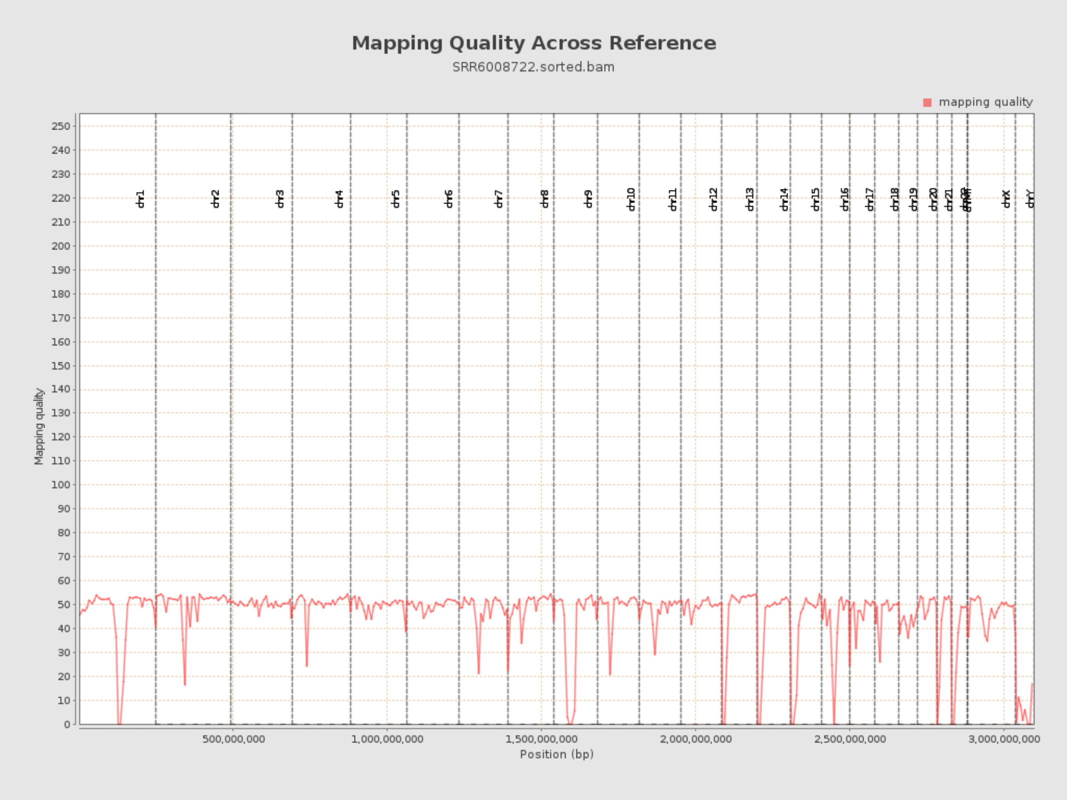
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram