Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 12:58:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008822.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_SRR6008822 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008822.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 12:58:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008822.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,292,738
Mapped reads	1,765,981 / 77.02%
Unmapped reads	526,757 / 22.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,505 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	107,872 / 4.7%
Duplication rate	5%
Clipped reads	896,002 / 39.08%

2.2. ACGT Content

Number/percentage of A's	31,492,767 / 27.52%
Number/percentage of C's	21,550,246 / 18.83%
Number/percentage of T's	35,736,772 / 31.23%
Number/percentage of G's	25,479,419 / 22.27%
Number/percentage of N's	162,953 / 0.14%
GC Percentage	41.1%

2.3. Coverage

Mean	0.037

Standard Deviation	0.3513

2.4. Mapping Quality

Mean Mapping Quality	34.45

2.5. Mismatches and indels

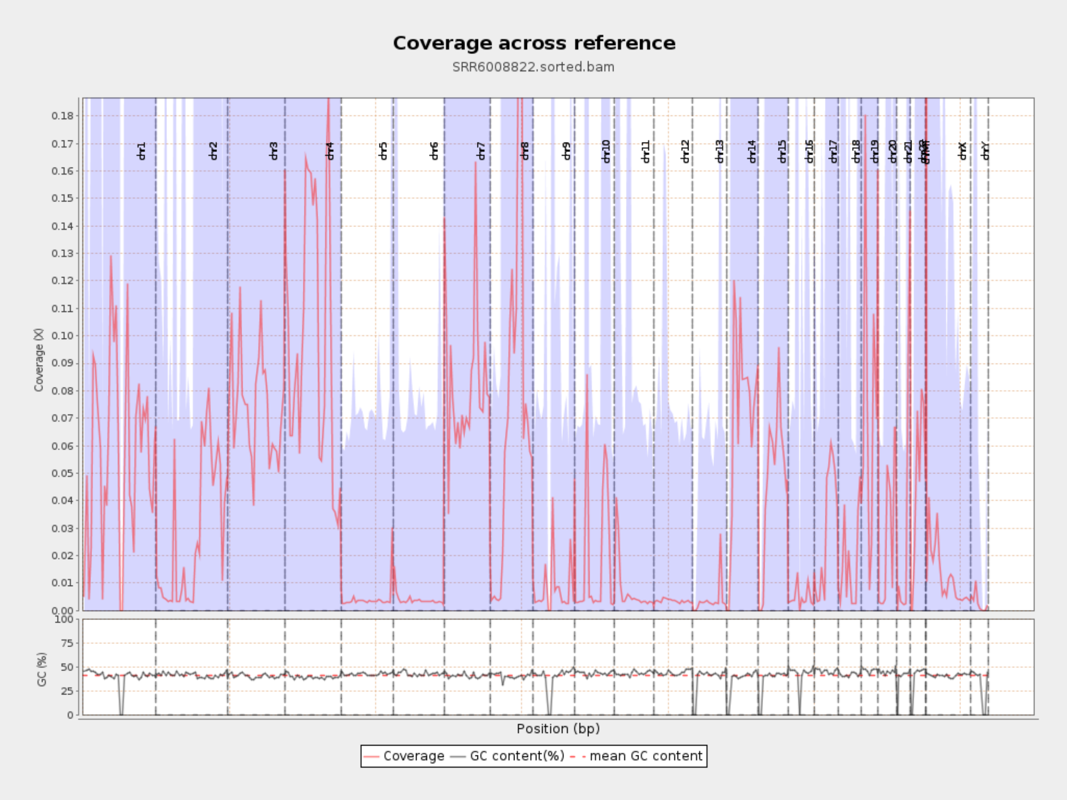
General error rate	0.81%
Mismatches	915,562
Insertions	7,585
Mapped reads with at least one insertion	0.43%
Deletions	32,295
Mapped reads with at least one deletion	1.81%
Homopolymer indels	46.06%

2.6. Chromosome stats

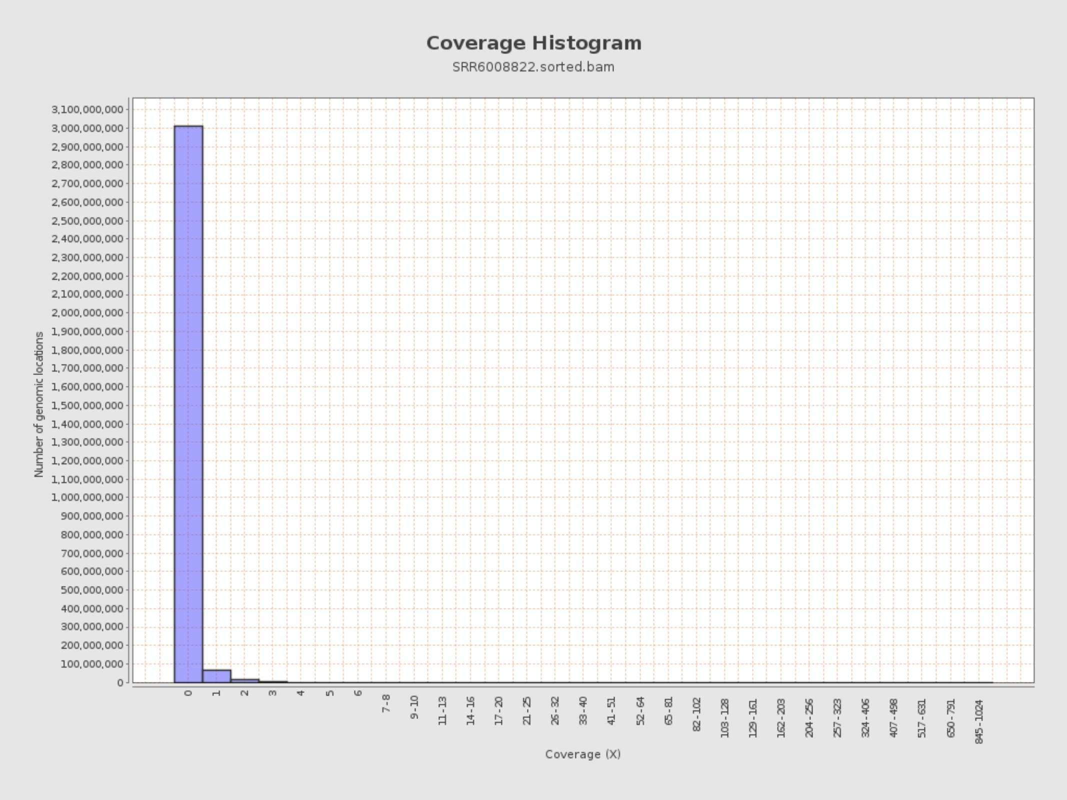
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14062709	0.0564	0.3998
chr2	243199373	6606773	0.0272	0.2924
chr3	198022430	14789996	0.0747	0.3824
chr4	191154276	19280319	0.1009	0.4155
chr5	180915260	815328	0.0045	0.0819
chr6	171115067	684689	0.004	0.0939
chr7	159138663	13195791	0.0829	0.4278

chr8	146364022	10625672	0.0726	0.6684
chr9	141213431	1146551	0.0081	0.1649
chr10	135534747	2481274	0.0183	0.8176
chr11	135006516	1046525	0.0078	0.1542
chr12	133851895	471005	0.0035	0.084
chr13	115169878	470064	0.0041	0.0796
chr14	107349540	7689214	0.0716	0.3501
chr15	102531392	4764117	0.0465	0.2873
chr16	90354753	417314	0.0046	0.173
chr17	81195210	2501097	0.0308	0.2215
chr18	78077248	1248748	0.016	0.3277
chr19	59128983	4421941	0.0748	0.3803
chr20	63025520	1629330	0.0259	0.2124
chr21	48129895	1542781	0.0321	0.2428
chr22	51304566	2372483	0.0462	0.2718
chrMT	16571	75792	4.5738	4.0842
chrX	155270560	1963527	0.0126	0.1517
chrY	59373566	176914	0.003	0.1243

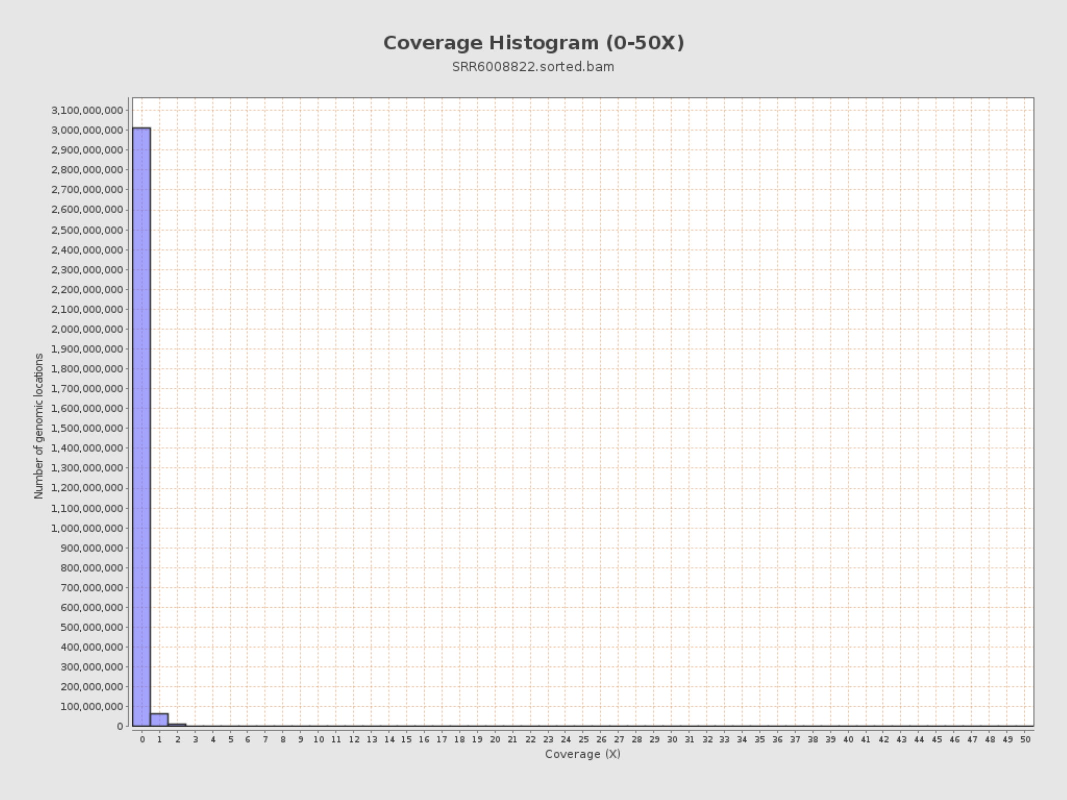
3. Results : Coverage across reference



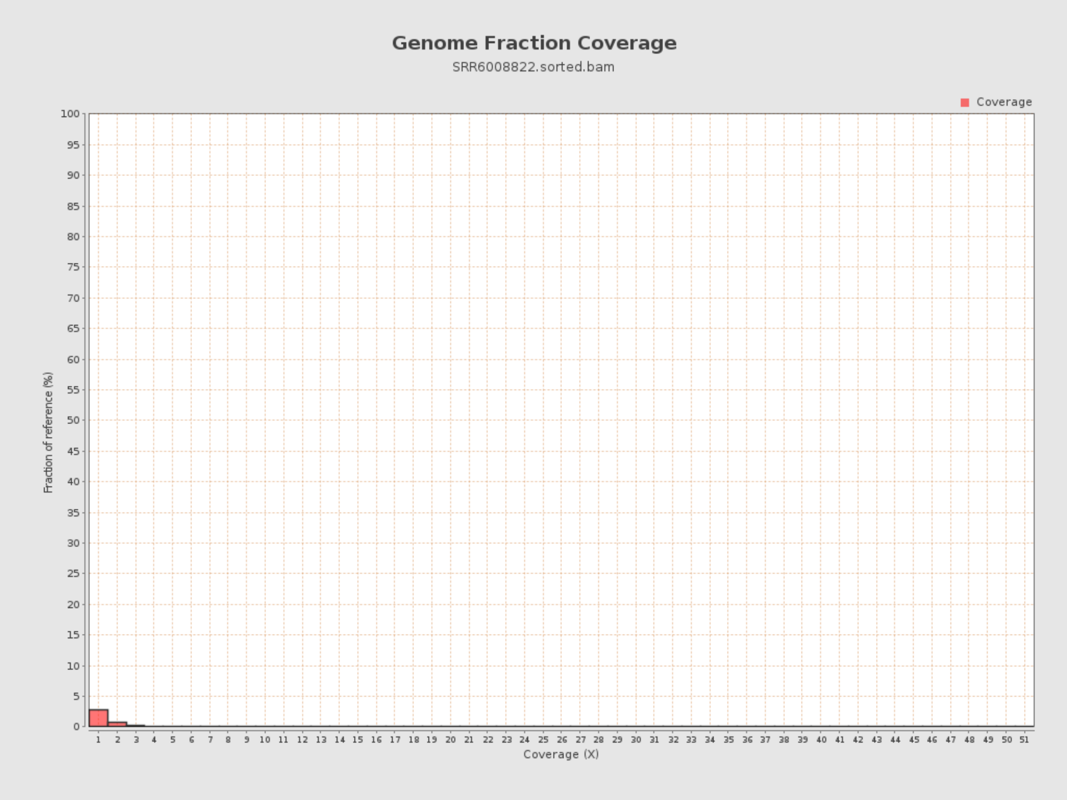
4. Results : Coverage Histogram



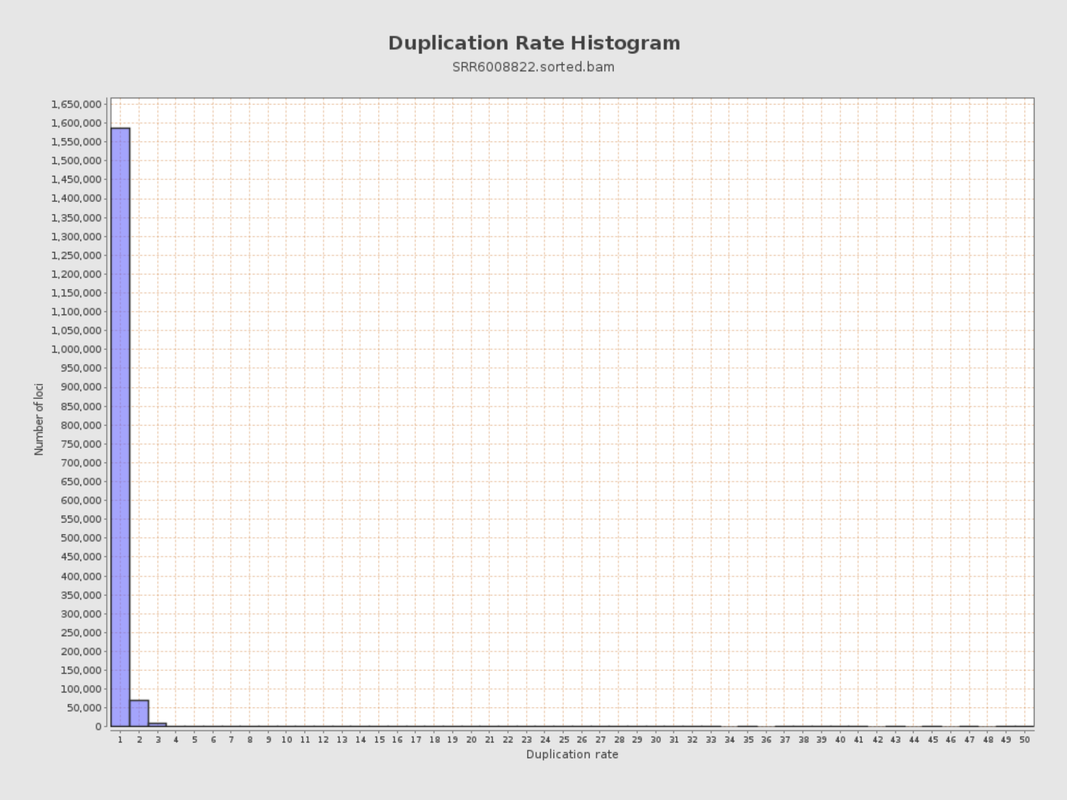
5. Results : Coverage Histogram (0-50X)



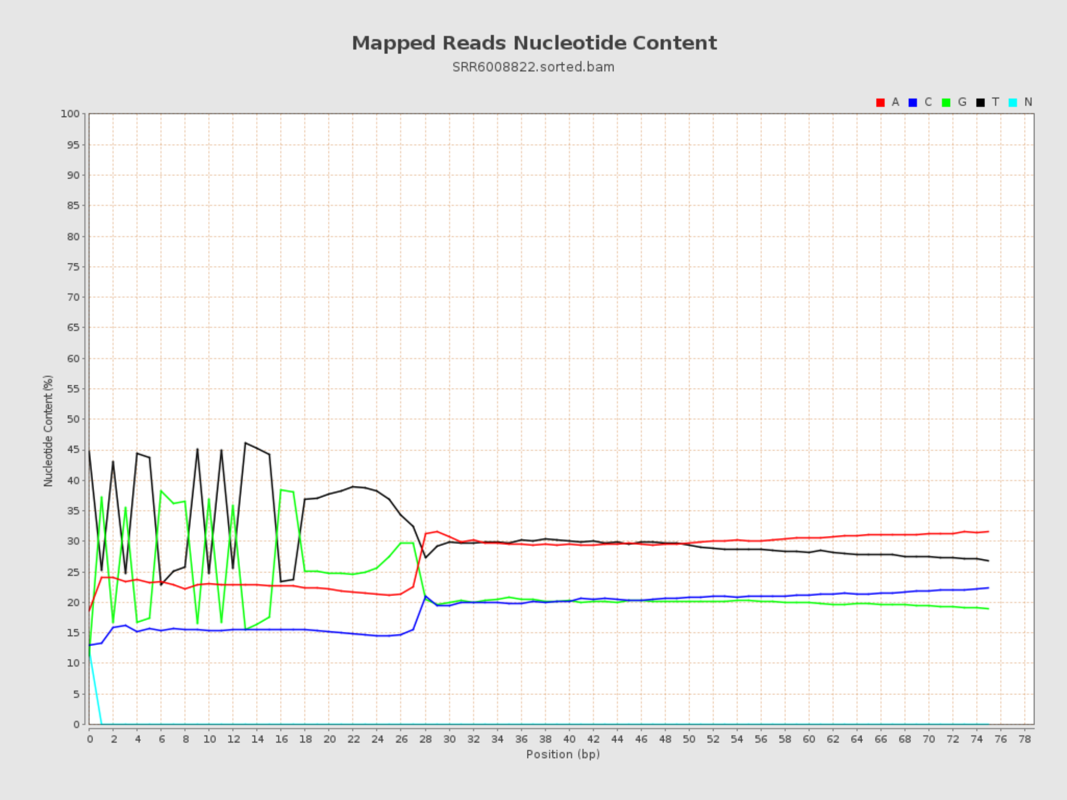
6. Results : Genome Fraction Coverage



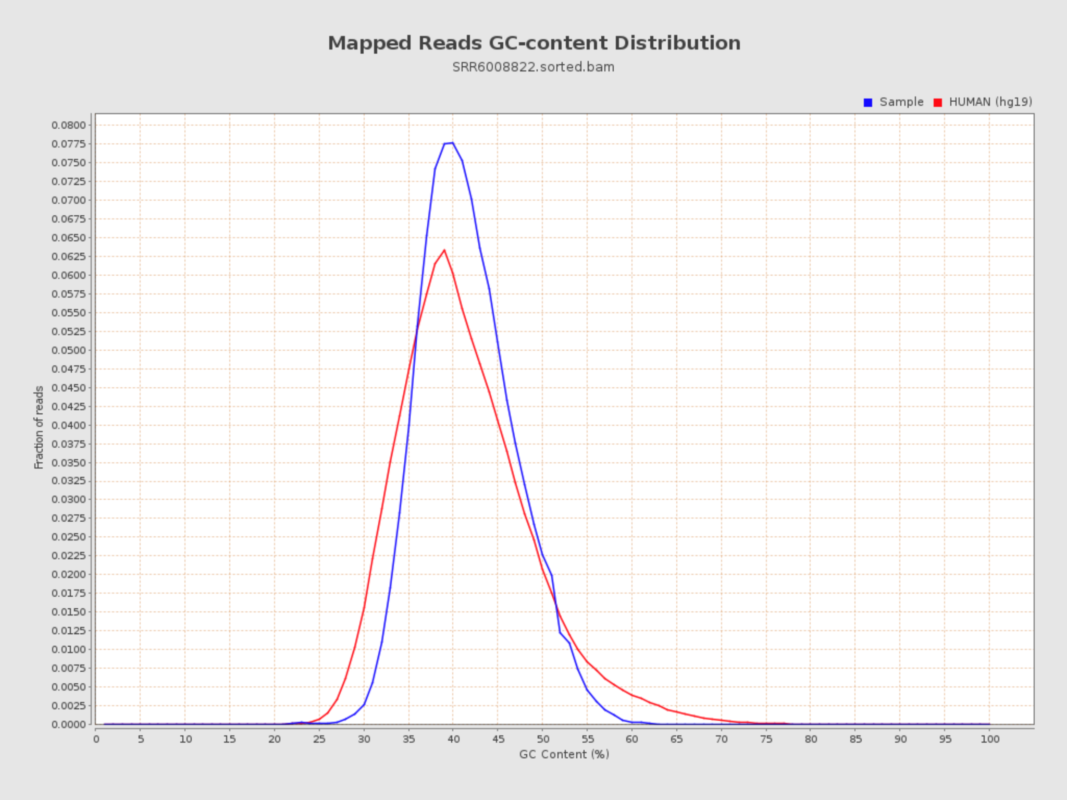
7. Results : Duplication Rate Histogram



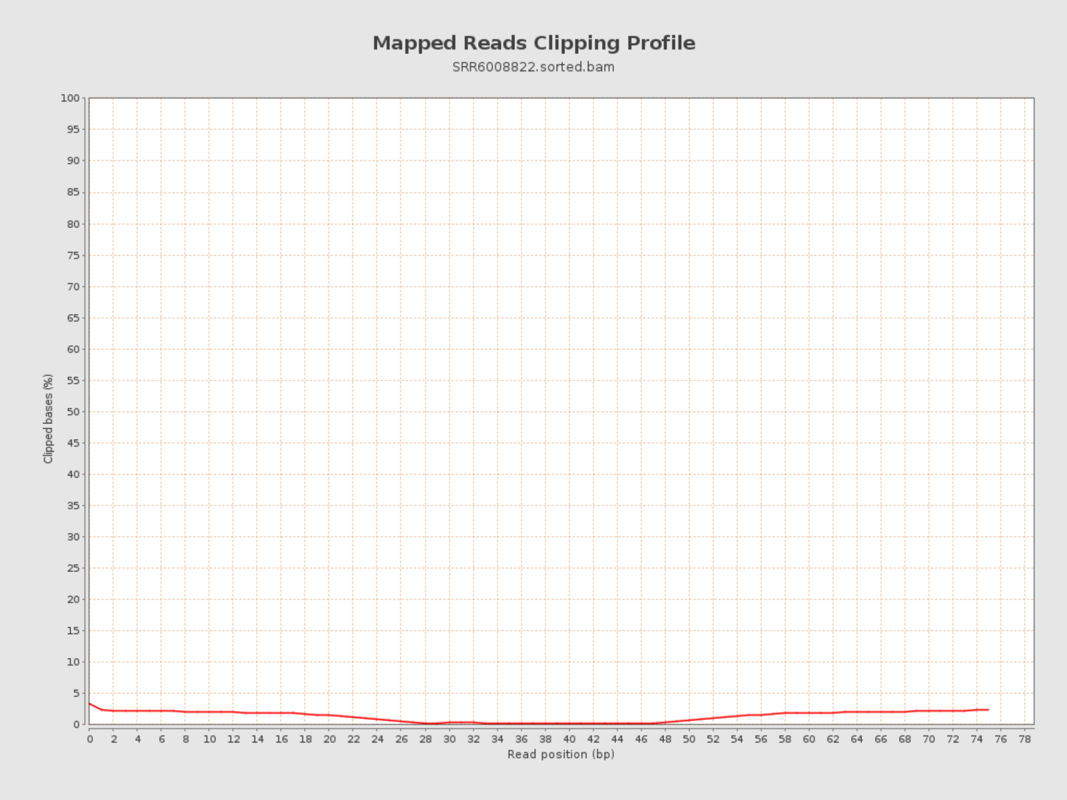
8. Results : Mapped Reads Nucleotide Content



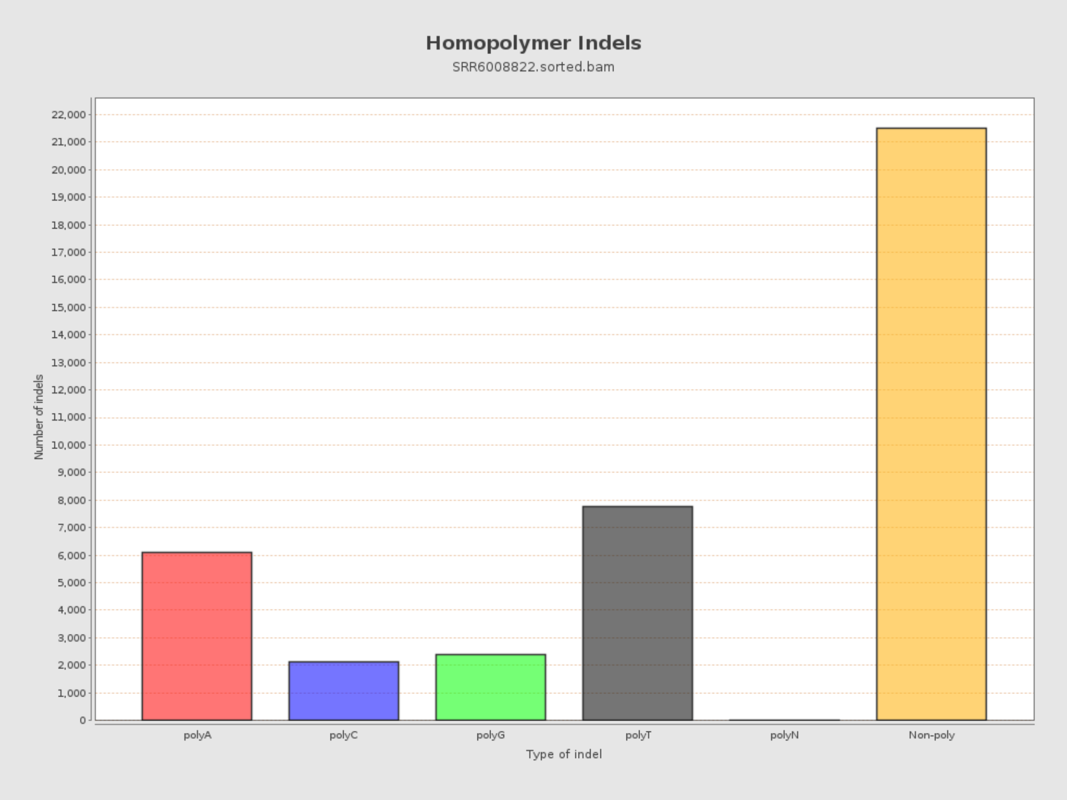
9. Results : Mapped Reads GC-content Distribution



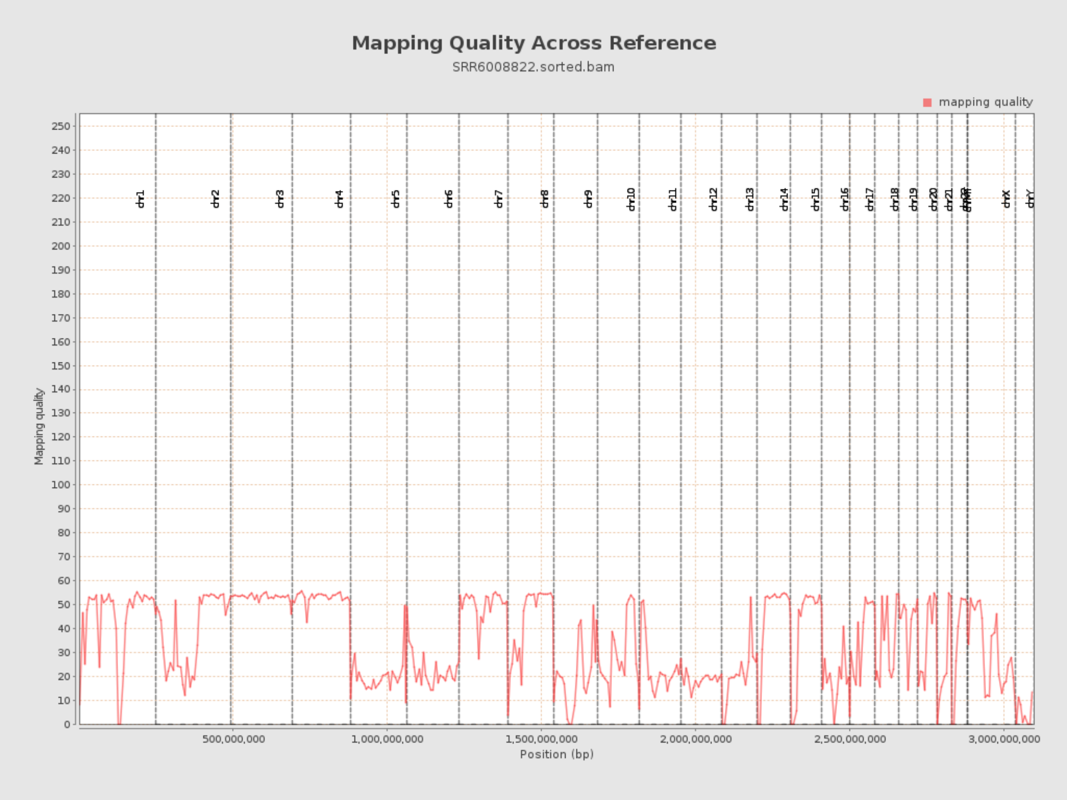
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram