Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:27:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008697.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_SRR6008697 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008697.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:27:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008697.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,671,523
Mapped reads	1,180,623 / 70.63%
Unmapped reads	490,900 / 29.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,543 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	59,308 / 3.55%
Duplication rate	4.16%
Clipped reads	843,661 / 50.47%

2.2. ACGT Content

Number/percentage of A's	19,781,743 / 28.18%
Number/percentage of C's	12,054,890 / 17.17%
Number/percentage of T's	22,010,389 / 31.35%
Number/percentage of G's	16,328,746 / 23.26%
Number/percentage of N's	26,542 / 0.04%
GC Percentage	40.43%

2.3. Coverage

Mean	0.0227

Standard Deviation	0.2005

2.4. Mapping Quality

Mean Mapping Quality	45.87

2.5. Mismatches and indels

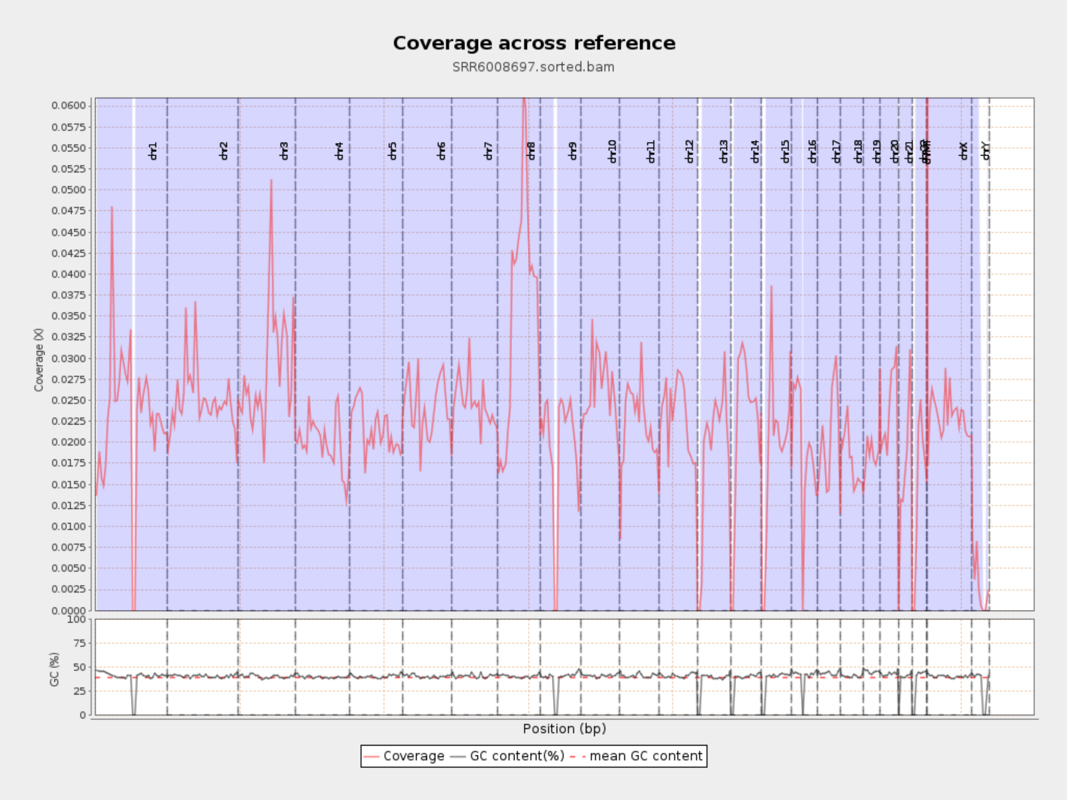
General error rate	1.04%
Mismatches	720,447
Insertions	5,571
Mapped reads with at least one insertion	0.47%
Deletions	29,319
Mapped reads with at least one deletion	2.45%
Homopolymer indels	48.33%

2.6. Chromosome stats

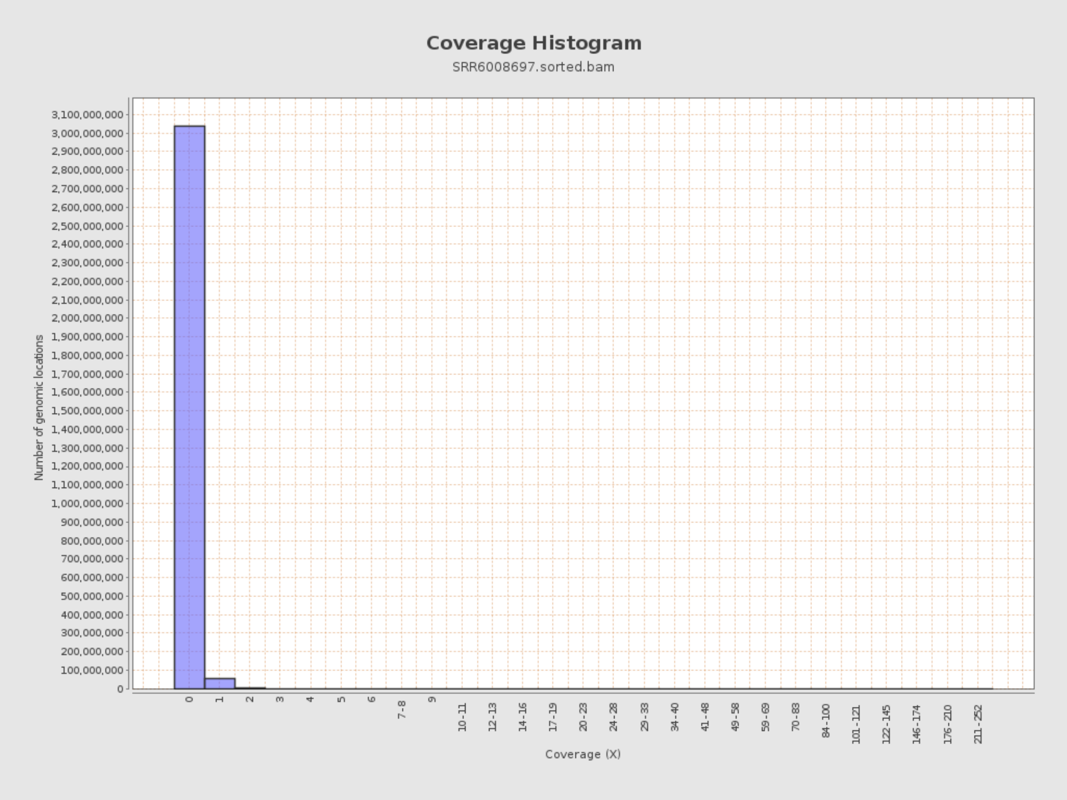
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5704841	0.0229	0.2459
chr2	243199373	6101099	0.0251	0.2323
chr3	198022430	5666498	0.0286	0.1997
chr4	191154276	3809326	0.0199	0.1678
chr5	180915260	3912549	0.0216	0.1707
chr6	171115067	4145785	0.0242	0.1958
chr7	159138663	3933987	0.0247	0.2414

chr8	146364022	5298355	0.0362	0.2624
chr9	141213431	2726263	0.0193	0.1833
chr10	135534747	3530832	0.0261	0.2094
chr11	135006516	3019832	0.0224	0.2031
chr12	133851895	3094259	0.0231	0.1774
chr13	115169878	2160460	0.0188	0.162
chr14	107349540	2379613	0.0222	0.1754
chr15	102531392	1964237	0.0192	0.1617
chr16	90354753	1716939	0.019	0.1694
chr17	81195210	1680821	0.0207	0.1766
chr18	78077248	1397166	0.0179	0.2523
chr19	59128983	1112512	0.0188	0.1878
chr20	63025520	1497148	0.0238	0.1813
chr21	48129895	826569	0.0172	0.1571
chr22	51304566	745929	0.0145	0.1378
chrMT	16571	42517	2.5657	2.9773
chrX	155270560	3604538	0.0232	0.1851
chrY	59373566	175406	0.003	0.0718

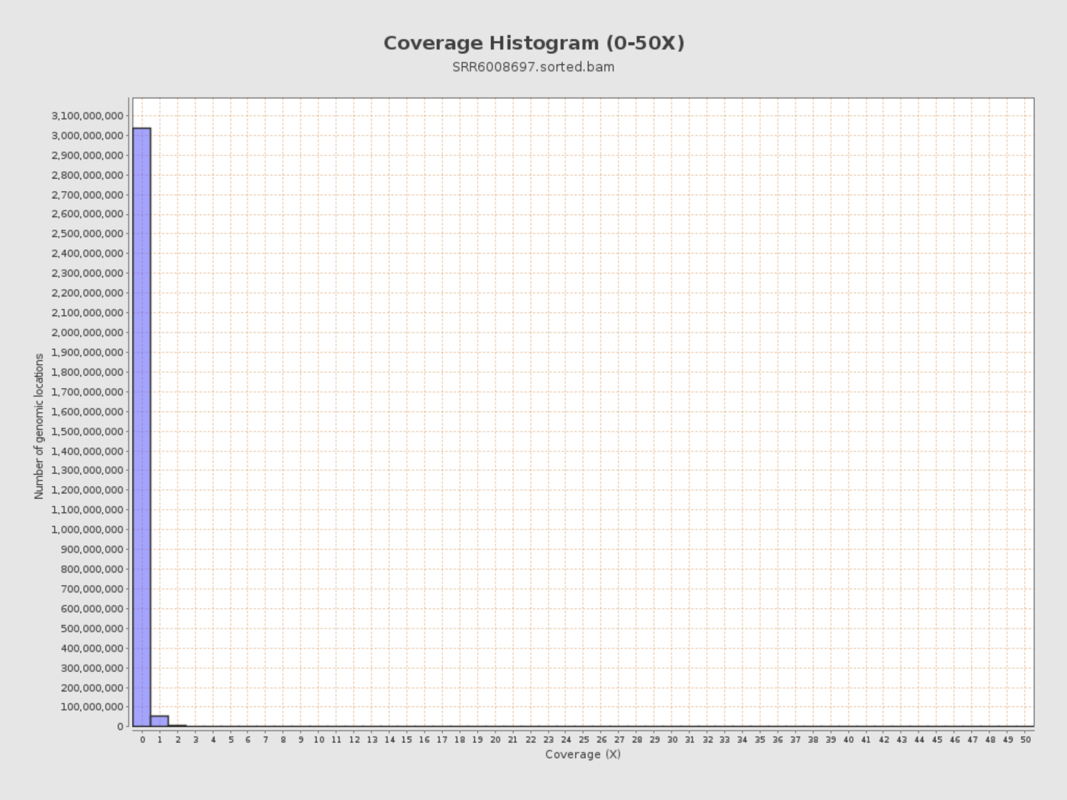
3. Results : Coverage across reference



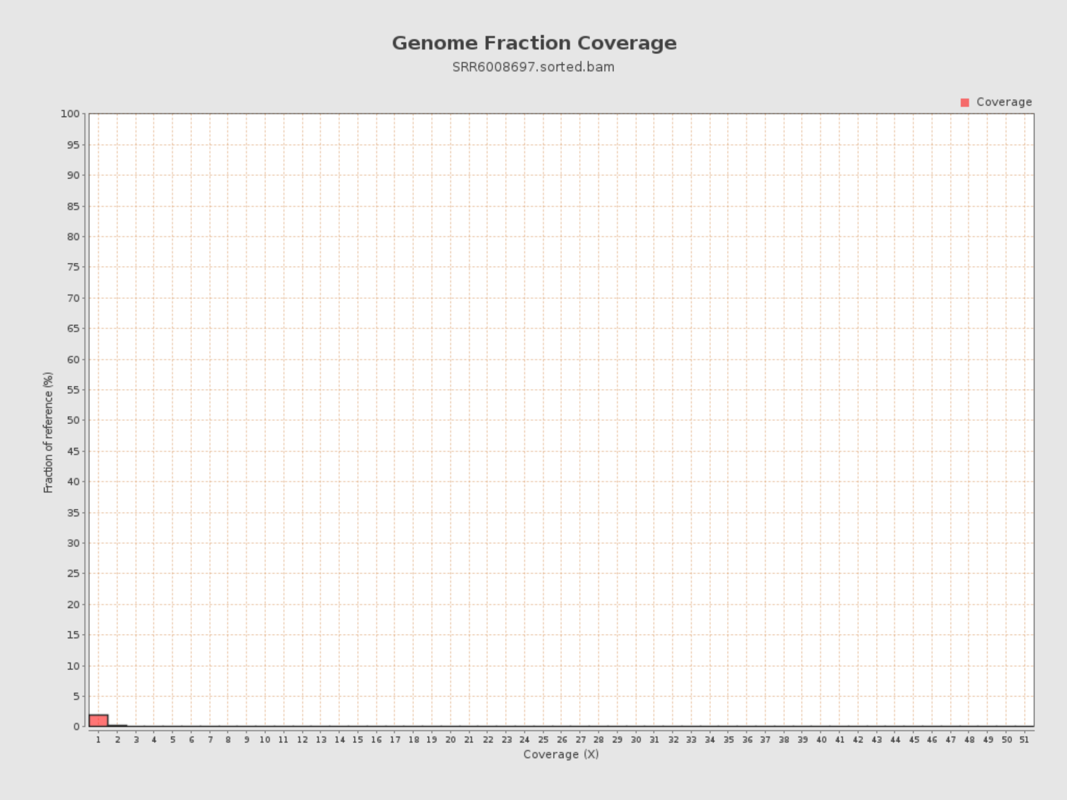
4. Results : Coverage Histogram



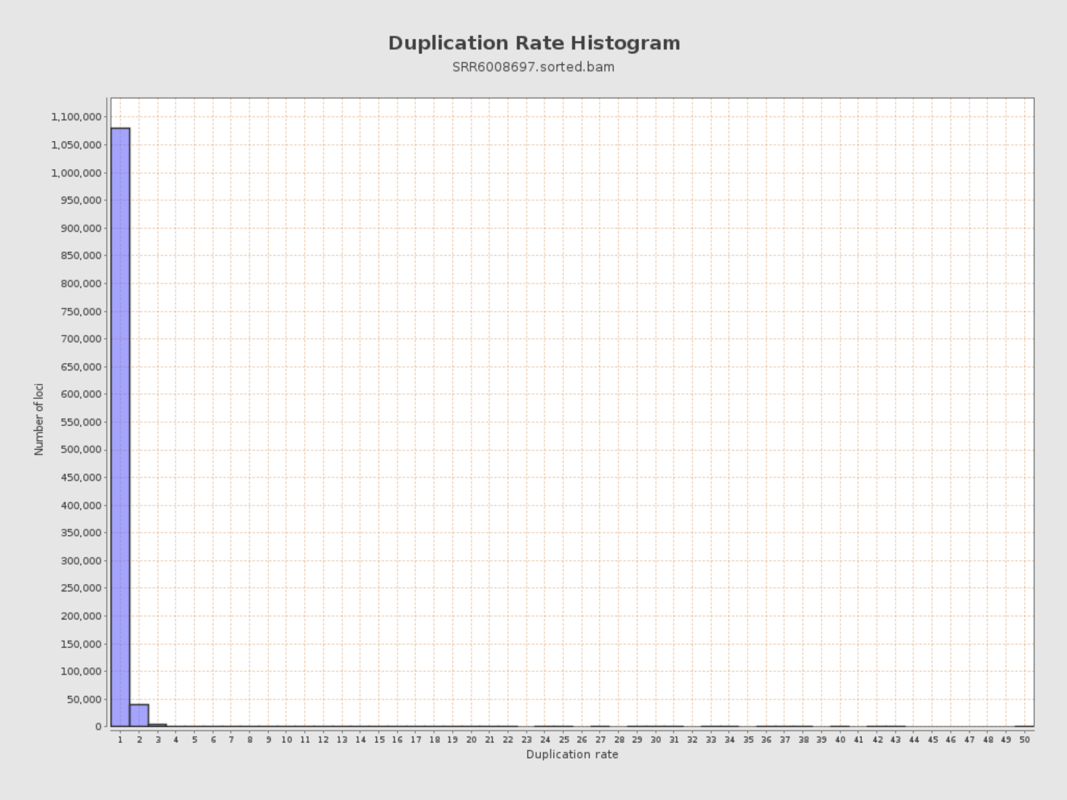
5. Results : Coverage Histogram (0-50X)



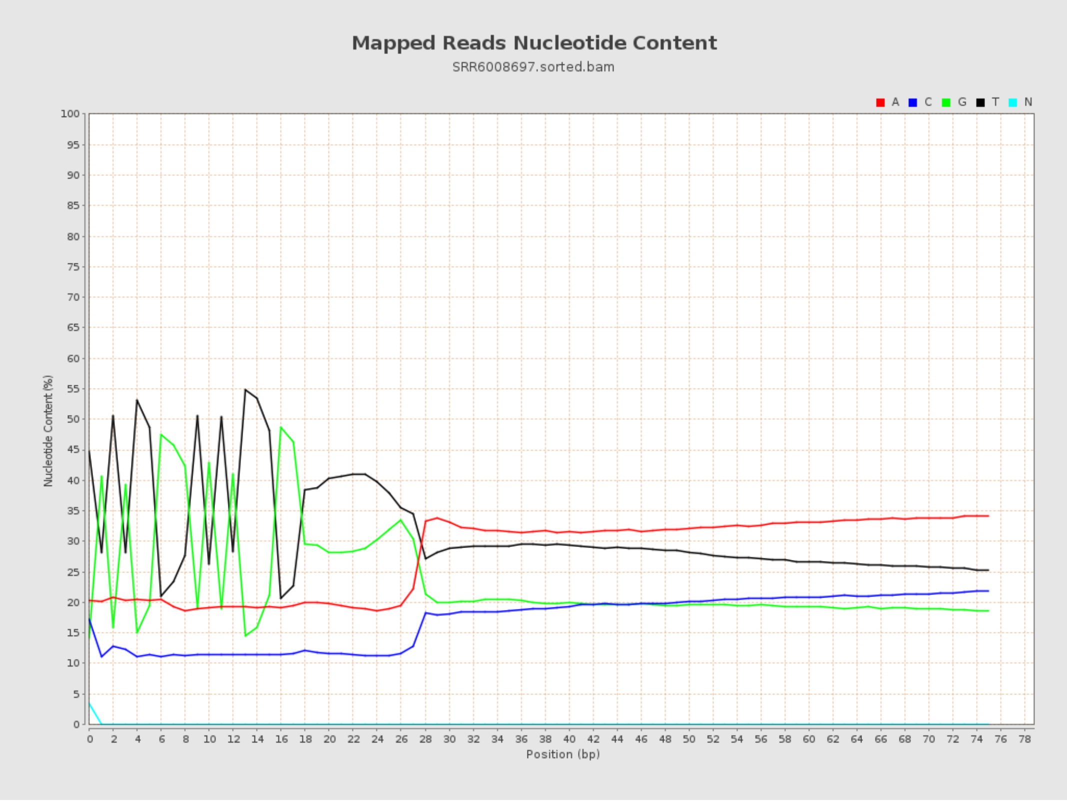
6. Results : Genome Fraction Coverage



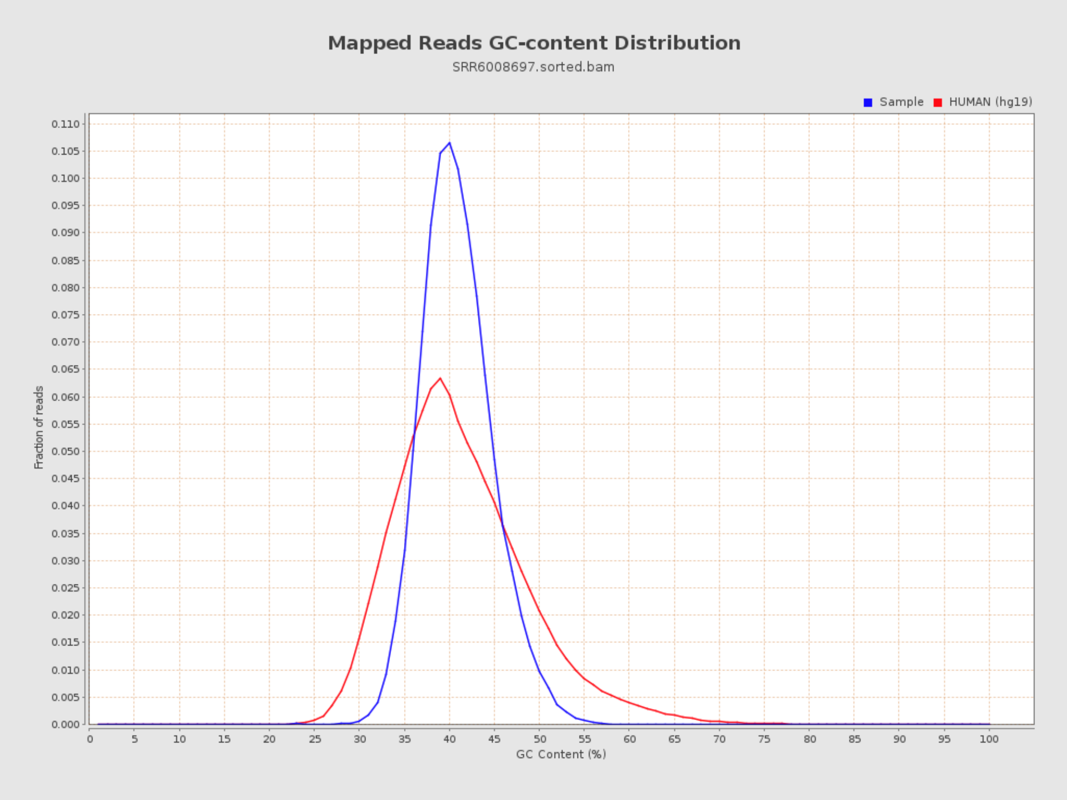
7. Results : Duplication Rate Histogram



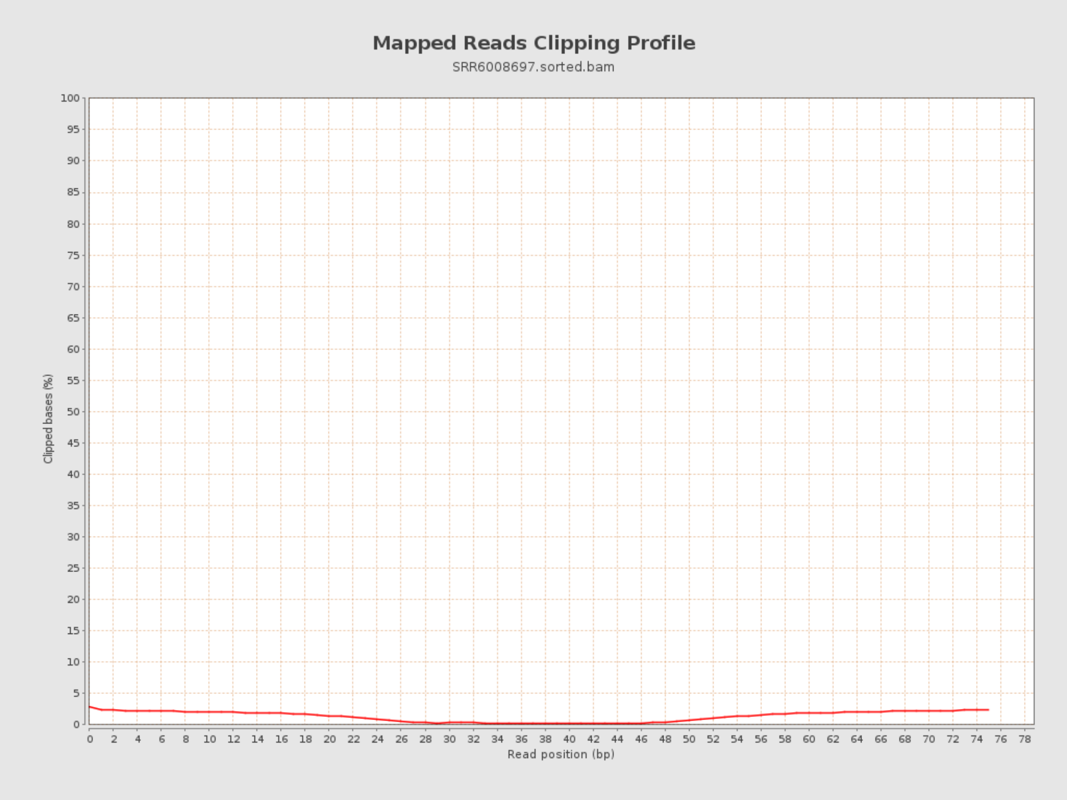
8. Results : Mapped Reads Nucleotide Content



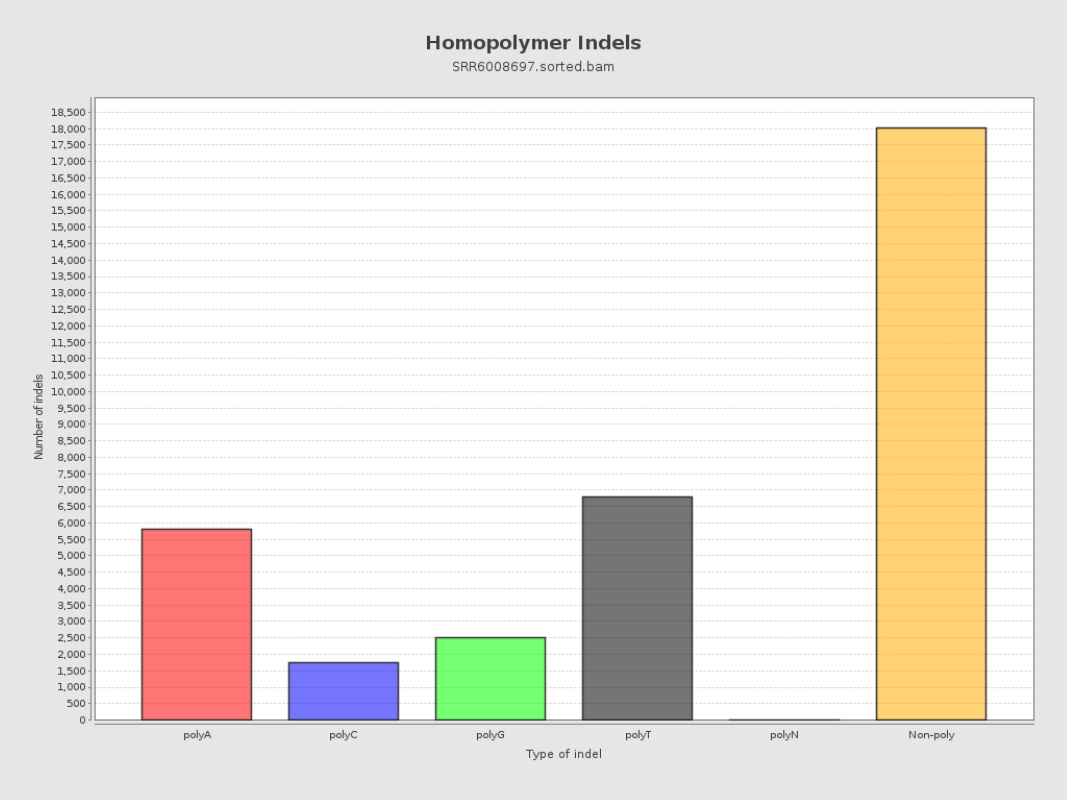
9. Results : Mapped Reads GC-content Distribution



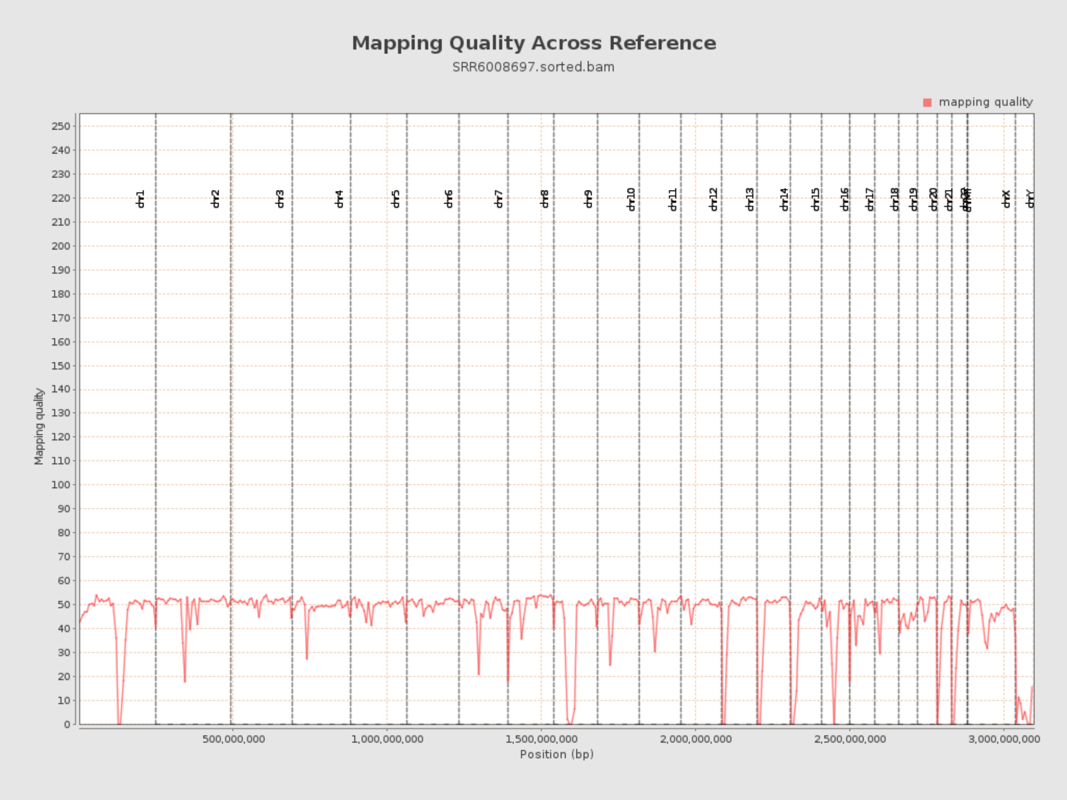
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram