Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 09:43:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008749.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_SRR6008749 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008749.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 09:43:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008749.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,730,415
Mapped reads	1,813,447 / 66.42%
Unmapped reads	916,968 / 33.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,645 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	141,741 / 5.19%
Duplication rate	6.17%
Clipped reads	1,312,463 / 48.07%

2.2. ACGT Content

Number/percentage of A's	29,839,812 / 27.65%
Number/percentage of C's	17,655,797 / 16.36%
Number/percentage of T's	34,040,720 / 31.54%
Number/percentage of G's	26,355,042 / 24.42%
Number/percentage of N's	23,997 / 0.02%
GC Percentage	40.78%

2.3. Coverage

Mean	0.0349

Standard Deviation	0.2773

2.4. Mapping Quality

Mean Mapping Quality	45.85

2.5. Mismatches and indels

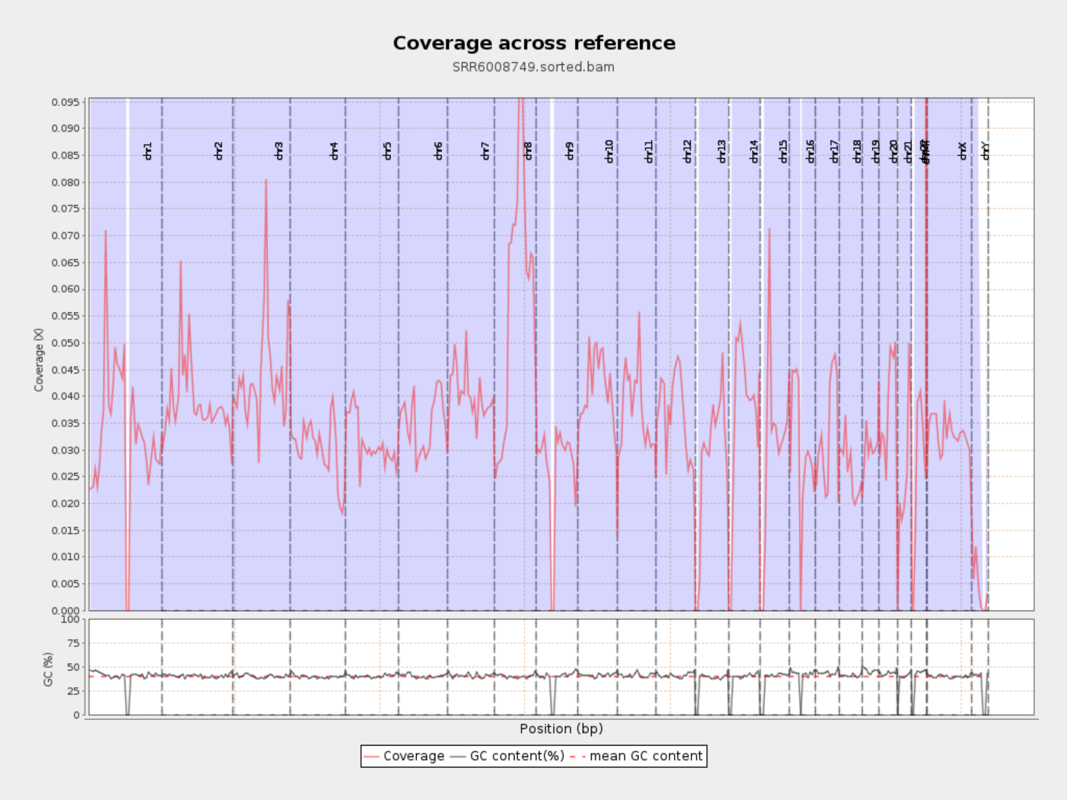
General error rate	1.15%
Mismatches	1,228,843
Insertions	8,401
Mapped reads with at least one insertion	0.46%
Deletions	39,389
Mapped reads with at least one deletion	2.15%
Homopolymer indels	49.2%

2.6. Chromosome stats

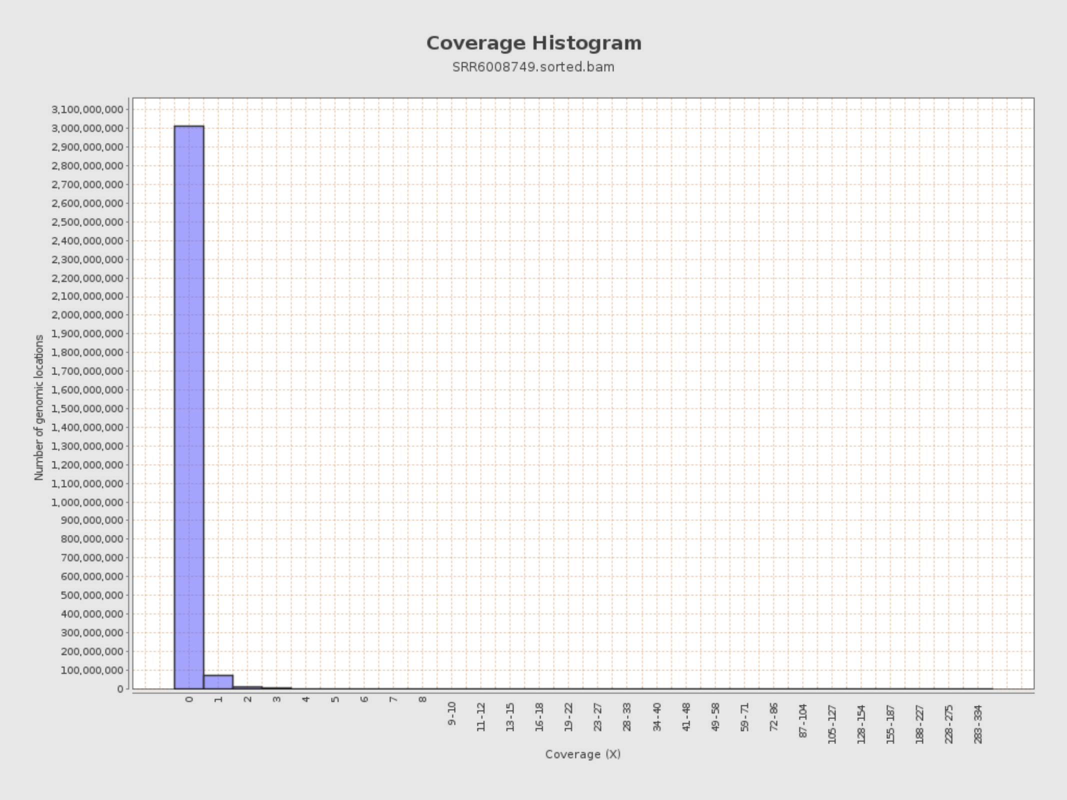
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8199694	0.0329	0.3342
chr2	243199373	9519403	0.0391	0.3107
chr3	198022430	8673294	0.0438	0.2737
chr4	191154276	5716745	0.0299	0.2264
chr5	180915260	5682777	0.0314	0.231
chr6	171115067	5989238	0.035	0.2673
chr7	159138663	6468037	0.0406	0.3603

chr8	146364022	8579932	0.0586	0.388
chr9	141213431	3725323	0.0264	0.2398
chr10	135534747	5663647	0.0418	0.295
chr11	135006516	5038056	0.0373	0.2913
chr12	133851895	4885286	0.0365	0.247
chr13	115169878	3269812	0.0284	0.218
chr14	107349540	3900782	0.0363	0.2594
chr15	102531392	3153668	0.0308	0.228
chr16	90354753	2729434	0.0302	0.2351
chr17	81195210	2673433	0.0329	0.2387
chr18	78077248	2039977	0.0261	0.3293
chr19	59128983	1809933	0.0306	0.2495
chr20	63025520	2384875	0.0378	0.2505
chr21	48129895	1196670	0.0249	0.2051
chr22	51304566	1261346	0.0246	0.1928
chrMT	16571	54310	3.2774	4.52
chrX	155270560	5103137	0.0329	0.2423
chrY	59373566	255462	0.0043	0.0921

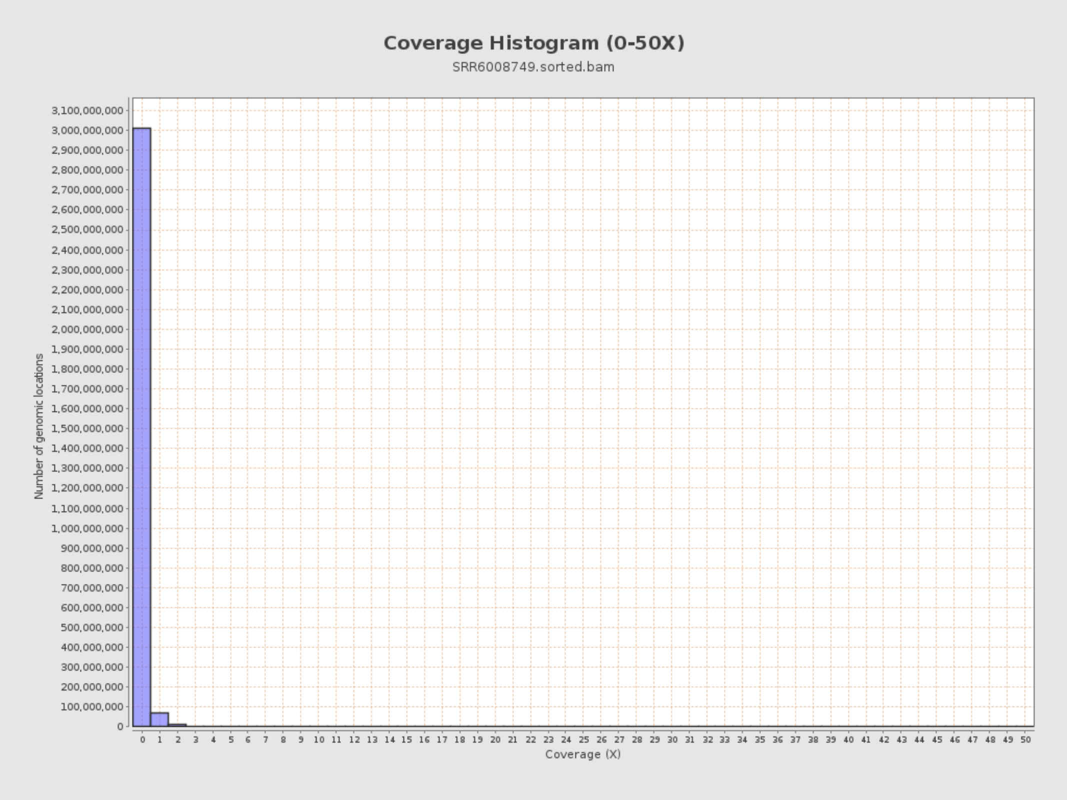
3. Results : Coverage across reference



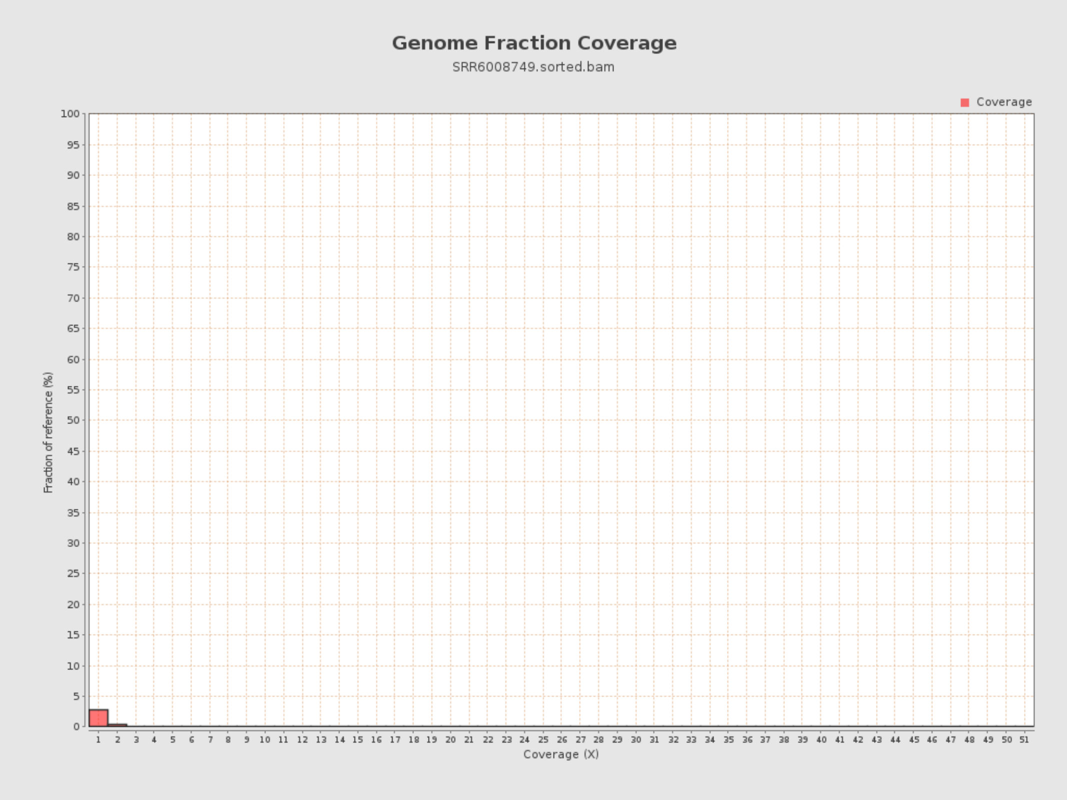
4. Results : Coverage Histogram



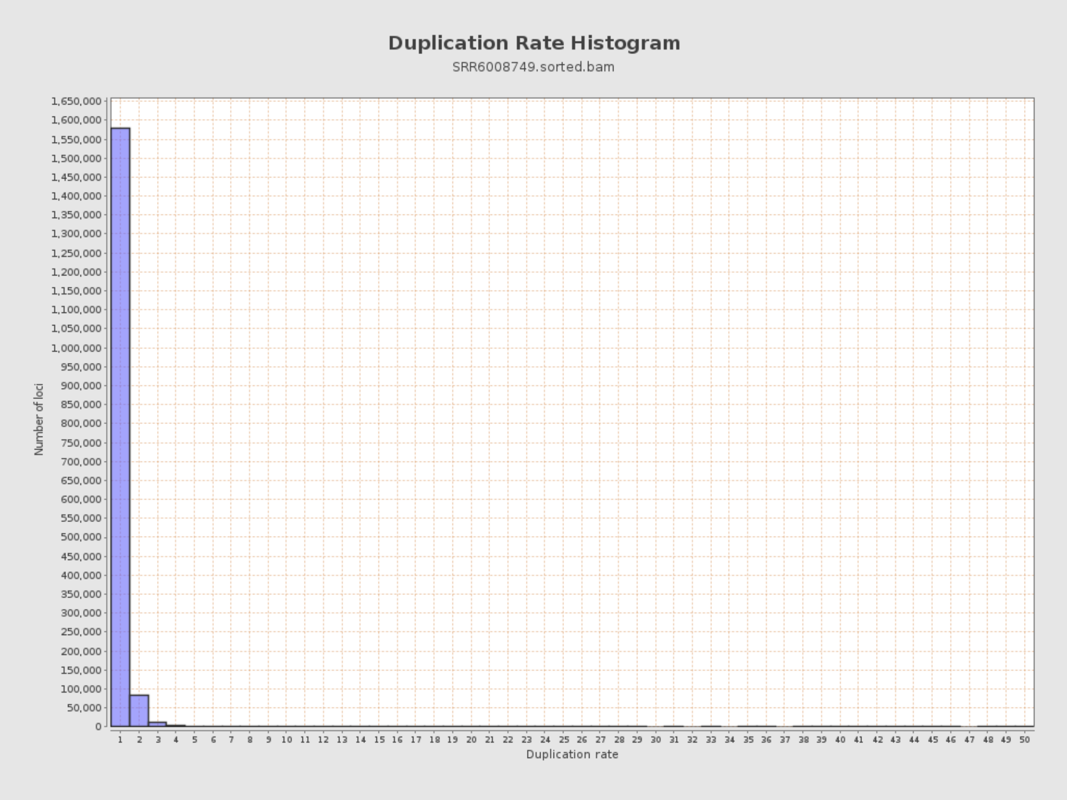
5. Results : Coverage Histogram (0-50X)



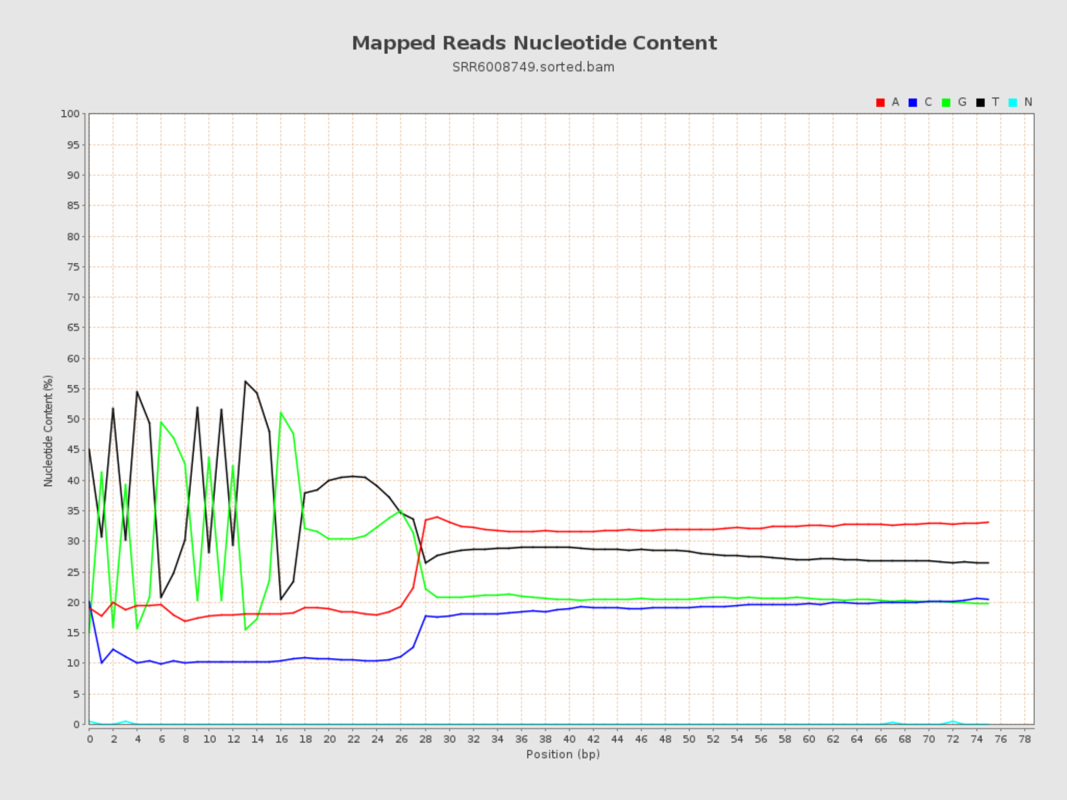
6. Results : Genome Fraction Coverage



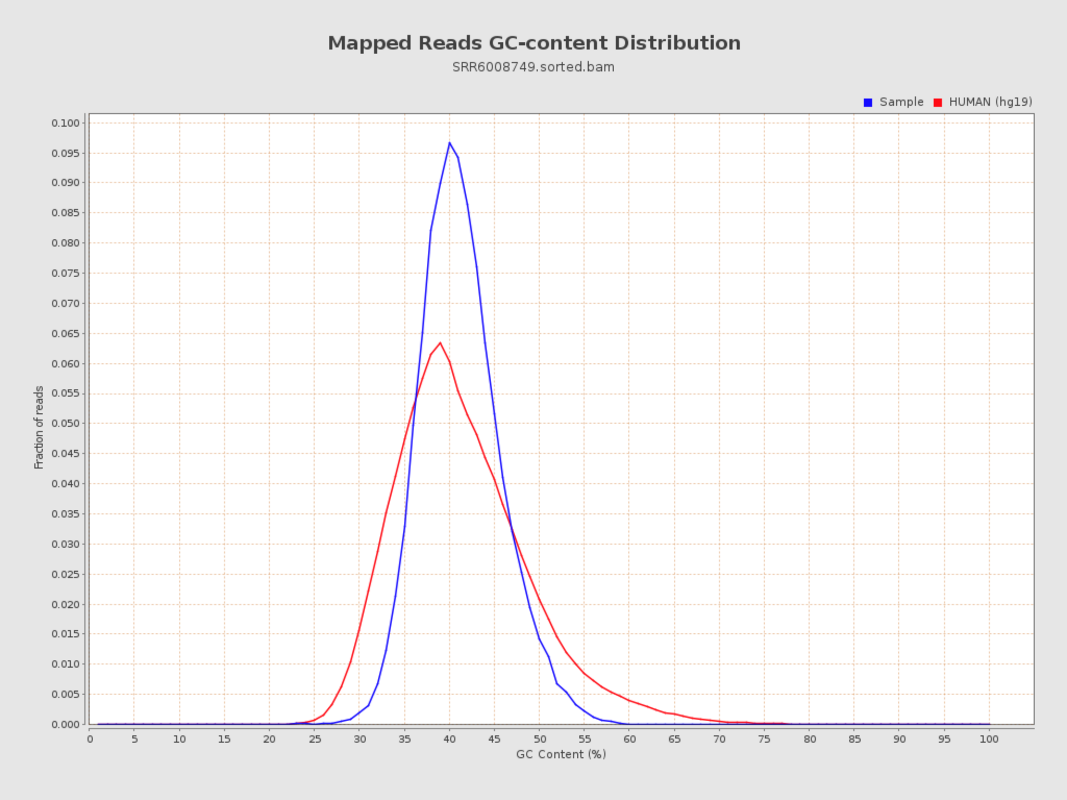
7. Results : Duplication Rate Histogram



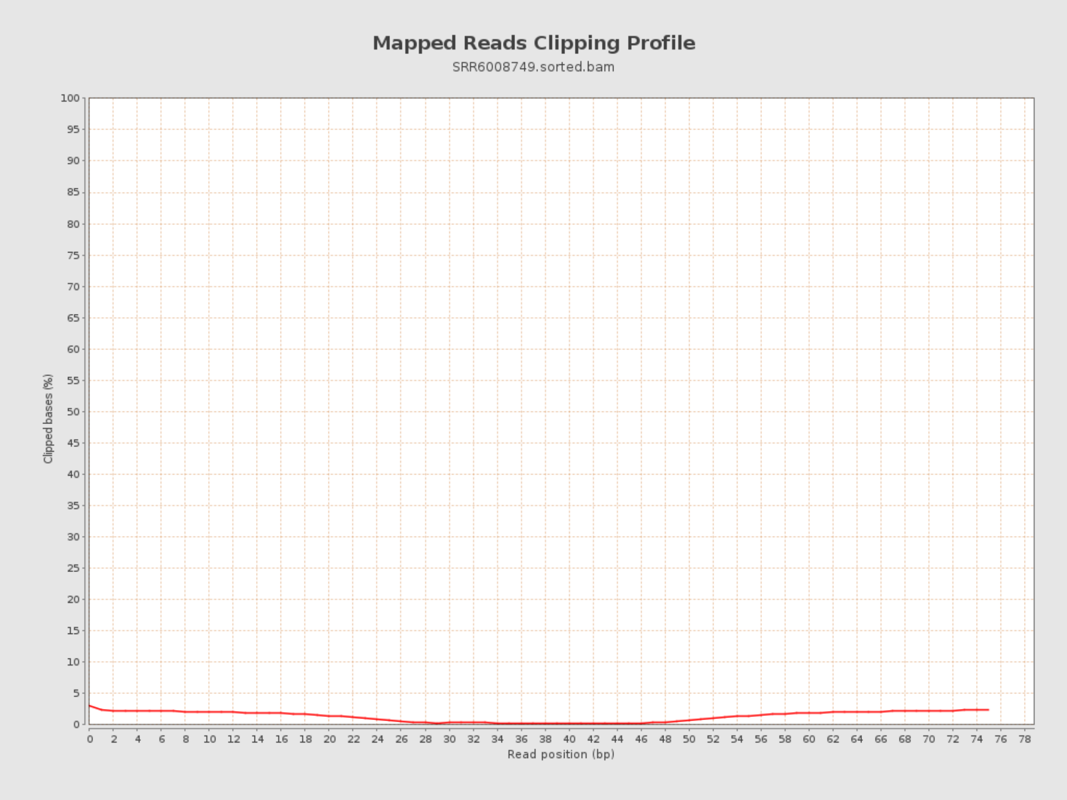
8. Results : Mapped Reads Nucleotide Content



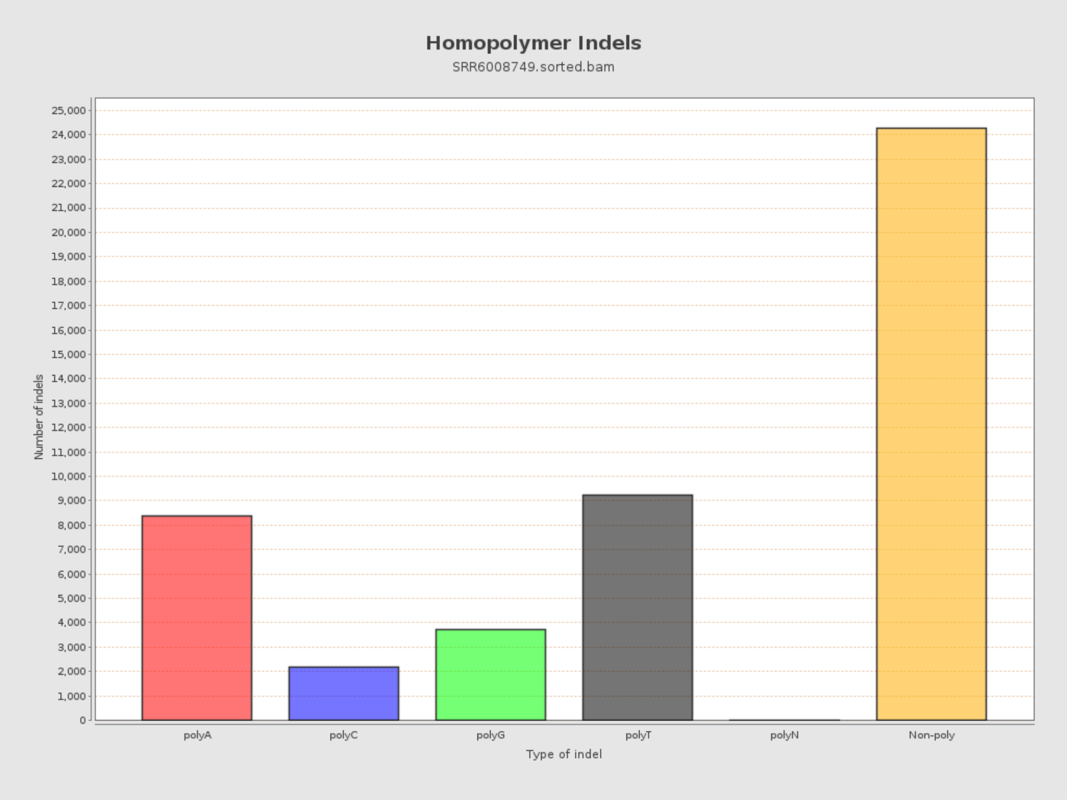
9. Results : Mapped Reads GC-content Distribution



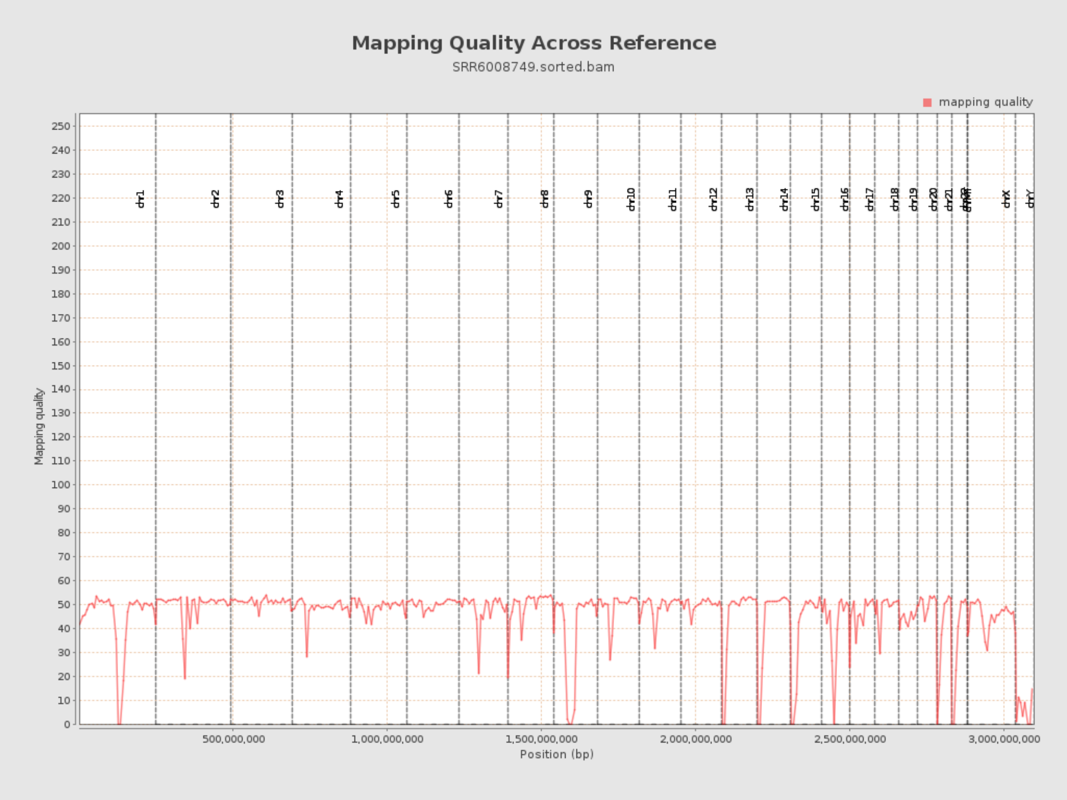
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram