Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 09:40:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008748.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_SRR6008748 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008748.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 09:40:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008748.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	985,258
Mapped reads	714,401 / 72.51%
Unmapped reads	270,857 / 27.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,593 / 0.57%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	23,712 / 2.41%
Duplication rate	2.77%
Clipped reads	416,503 / 42.27%

2.2. ACGT Content

Number/percentage of A's	13,430,469 / 29.46%
Number/percentage of C's	7,904,675 / 17.34%
Number/percentage of T's	13,797,709 / 30.27%
Number/percentage of G's	10,445,520 / 22.91%
Number/percentage of N's	7,065 / 0.02%
GC Percentage	40.25%

2.3. Coverage

Mean	0.0147

Standard Deviation	0.157

2.4. Mapping Quality

Mean Mapping Quality	46.93

2.5. Mismatches and indels

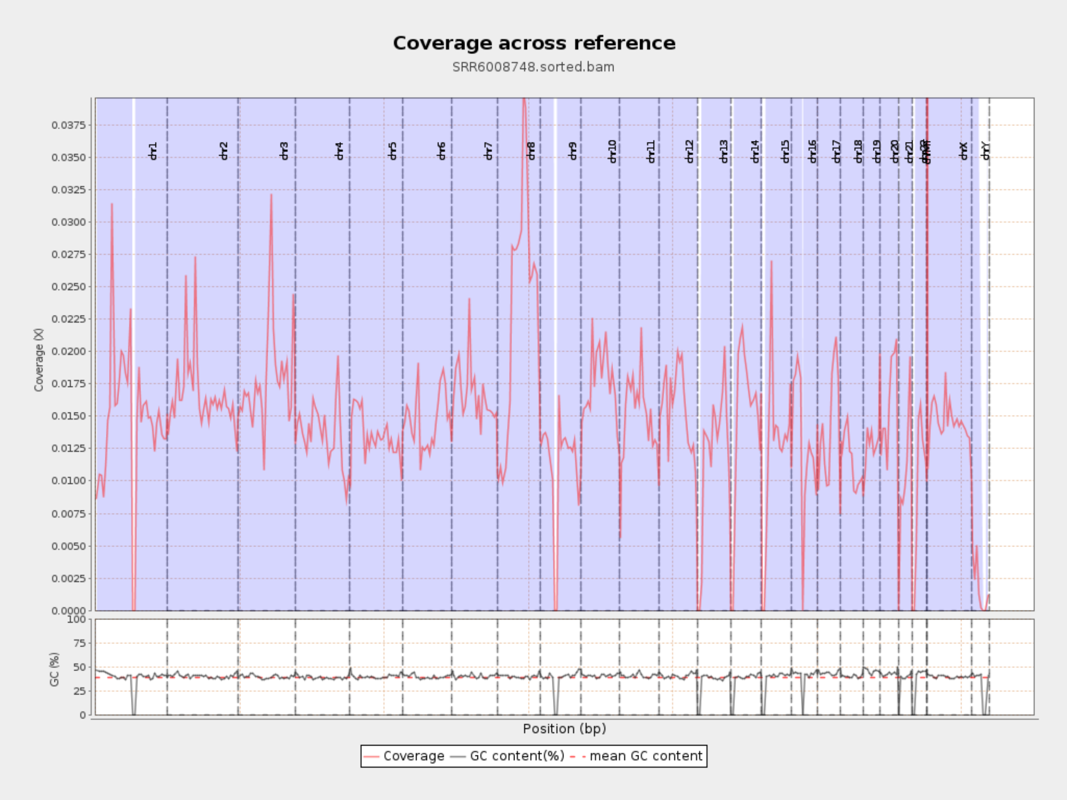
General error rate	1.09%
Mismatches	490,609
Insertions	3,788
Mapped reads with at least one insertion	0.53%
Deletions	18,459
Mapped reads with at least one deletion	2.55%
Homopolymer indels	48.69%

2.6. Chromosome stats

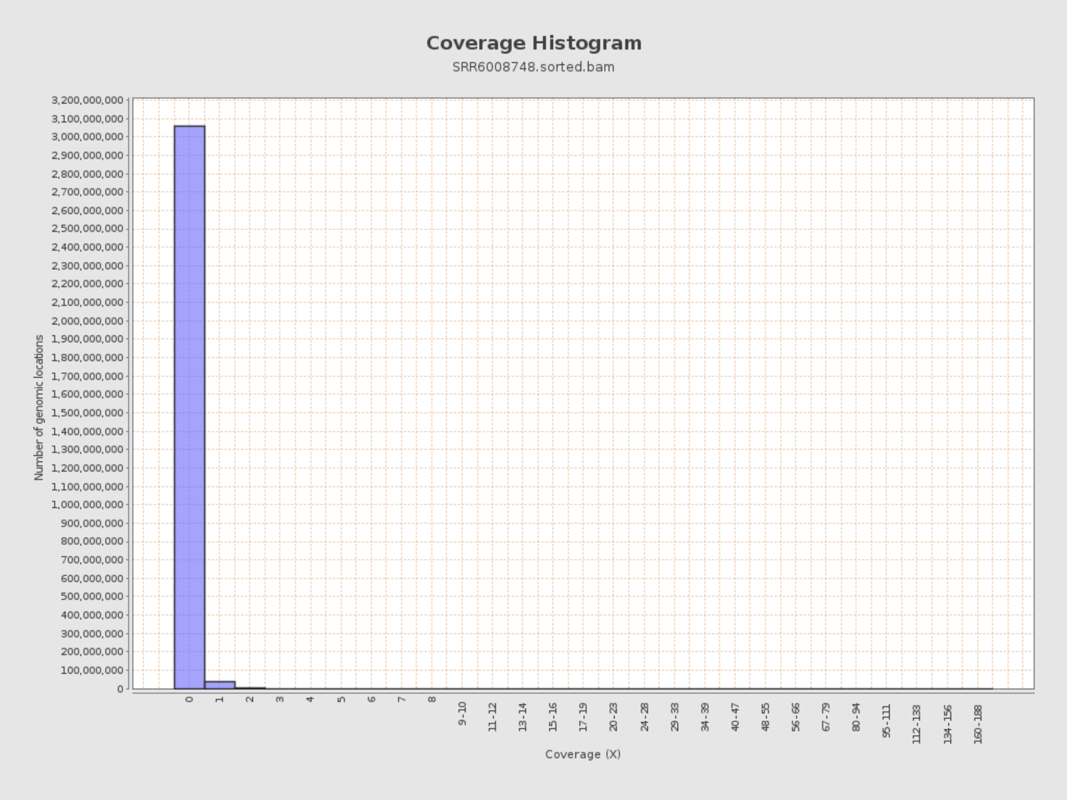
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3634344	0.0146	0.1833
chr2	243199373	4075459	0.0168	0.1841
chr3	198022430	3554737	0.018	0.153
chr4	191154276	2593420	0.0136	0.134
chr5	180915260	2472776	0.0137	0.1337
chr6	171115067	2511835	0.0147	0.1461
chr7	159138663	2659359	0.0167	0.1966

chr8	146364022	3445442	0.0235	0.2131
chr9	141213431	1576544	0.0112	0.1453
chr10	135534747	2382286	0.0176	0.1641
chr11	135006516	2046994	0.0152	0.1639
chr12	133851895	2098039	0.0157	0.1435
chr13	115169878	1373603	0.0119	0.1253
chr14	107349540	1586857	0.0148	0.1403
chr15	102531392	1263486	0.0123	0.1259
chr16	90354753	1140759	0.0126	0.1319
chr17	81195210	1149026	0.0142	0.1439
chr18	78077248	899388	0.0115	0.1926
chr19	59128983	762318	0.0129	0.1447
chr20	63025520	1001920	0.0159	0.1445
chr21	48129895	506841	0.0105	0.1223
chr22	51304566	490423	0.0096	0.1093
chrMT	16571	18183	1.0973	1.5737
chrX	155270560	2268178	0.0146	0.1413
chrY	59373566	101734	0.0017	0.0507

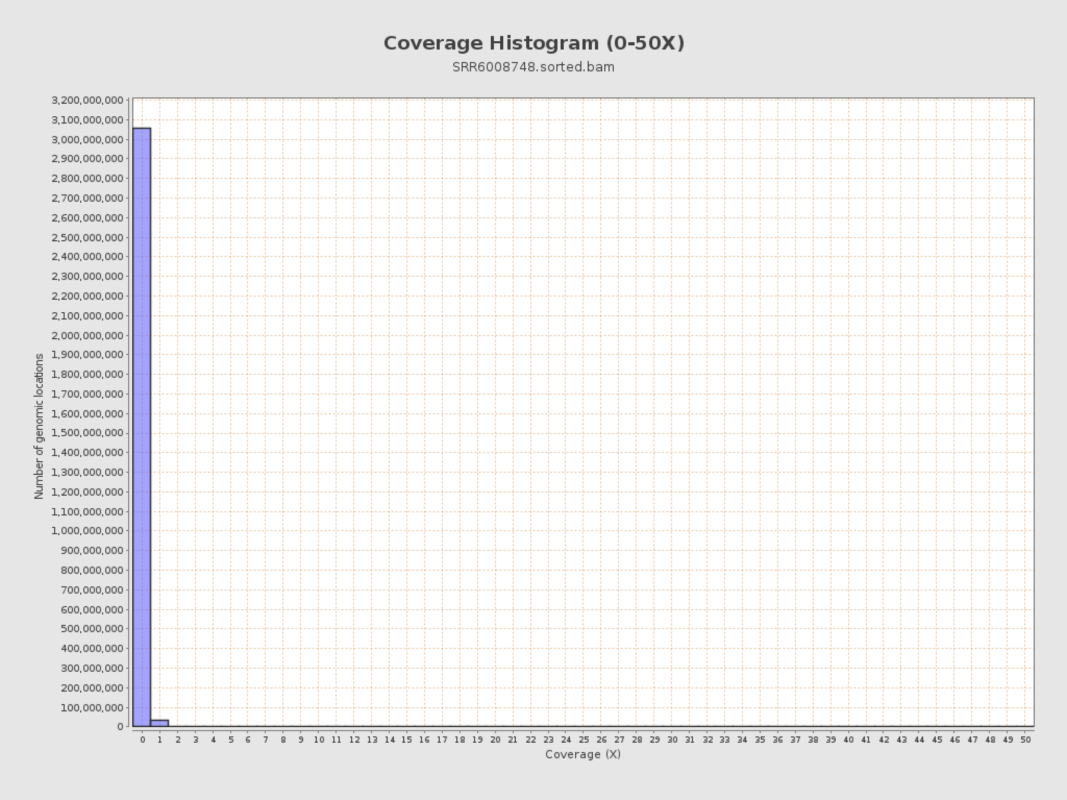
3. Results : Coverage across reference



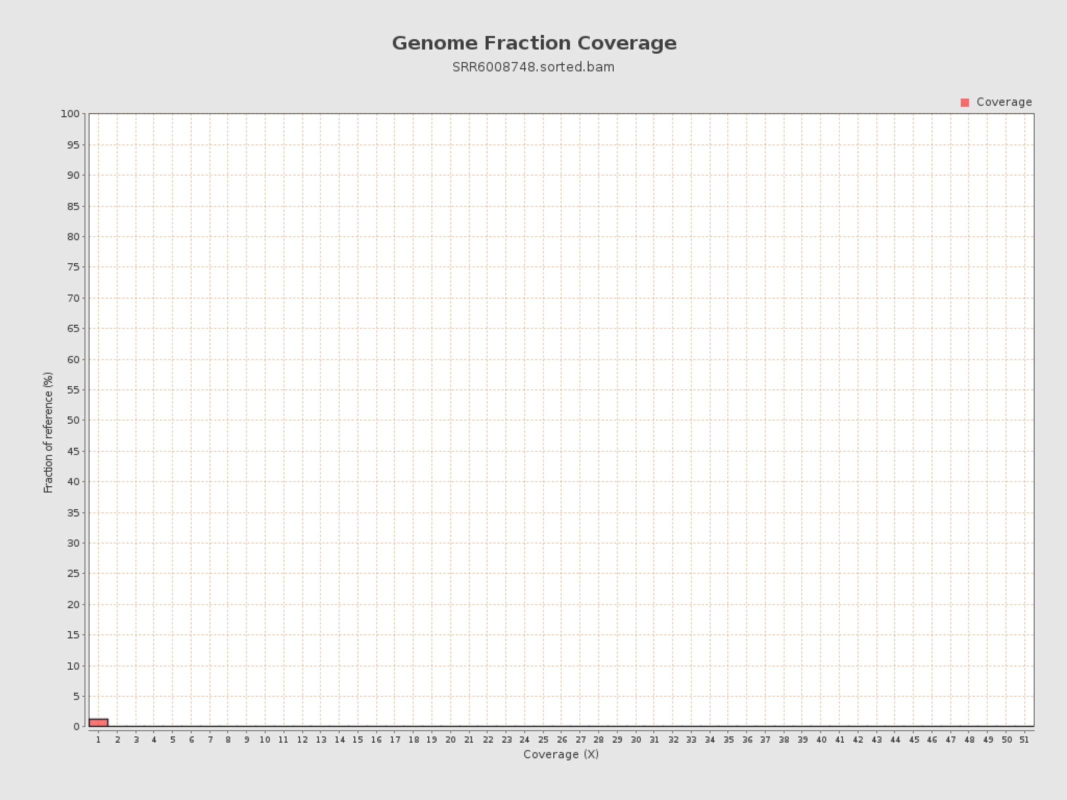
4. Results : Coverage Histogram



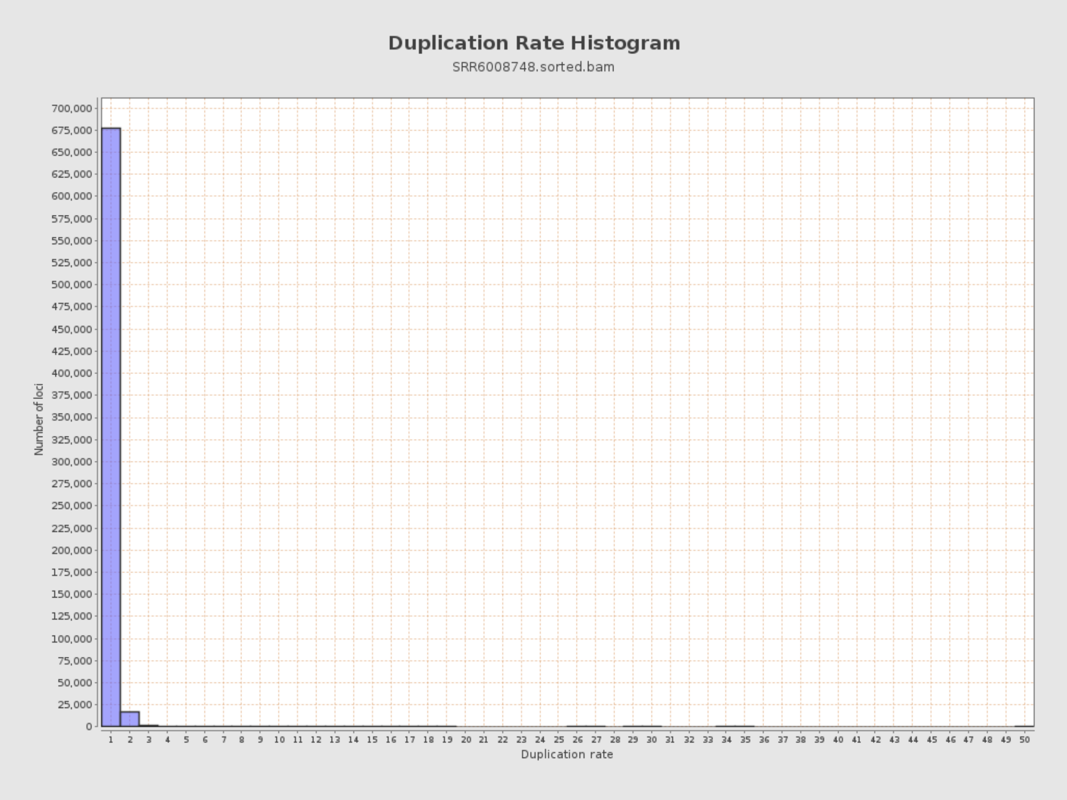
5. Results : Coverage Histogram (0-50X)



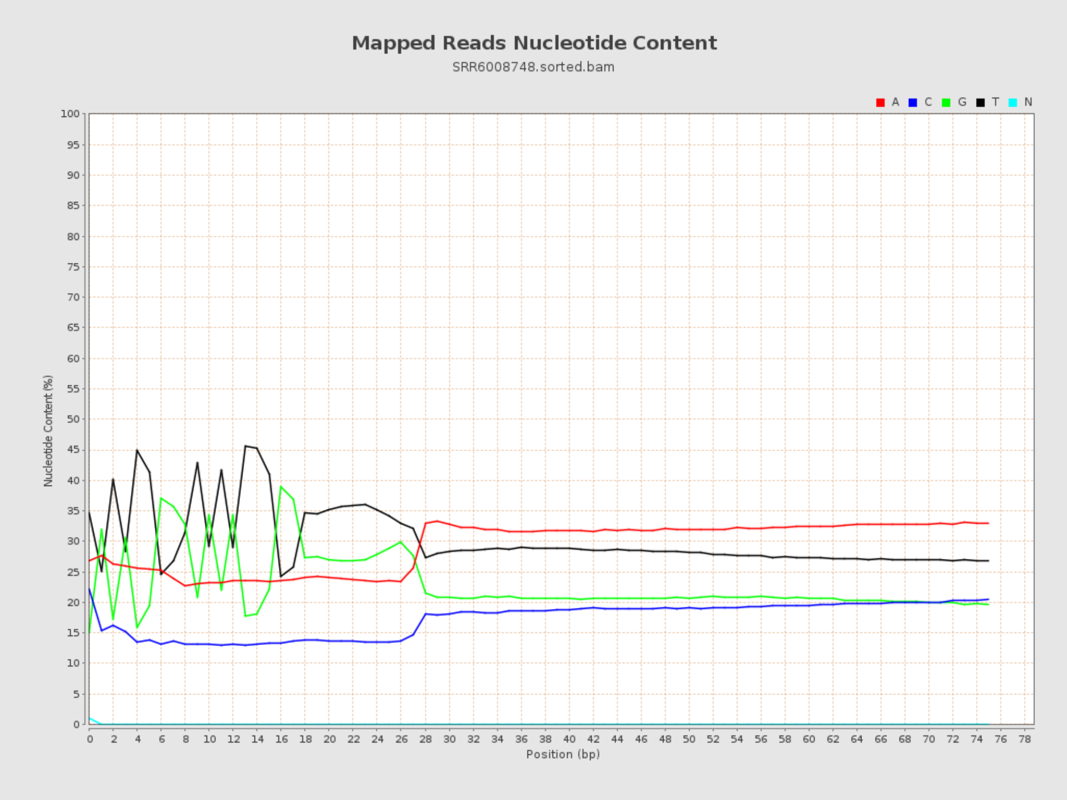
6. Results : Genome Fraction Coverage



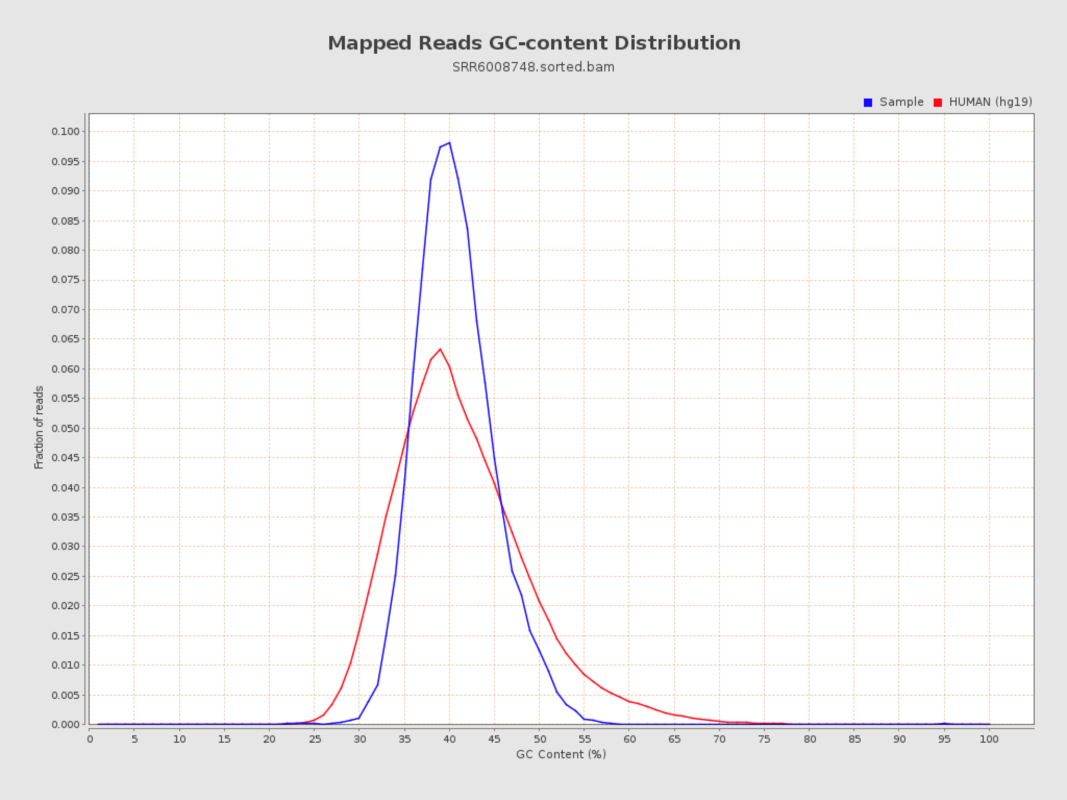
7. Results : Duplication Rate Histogram



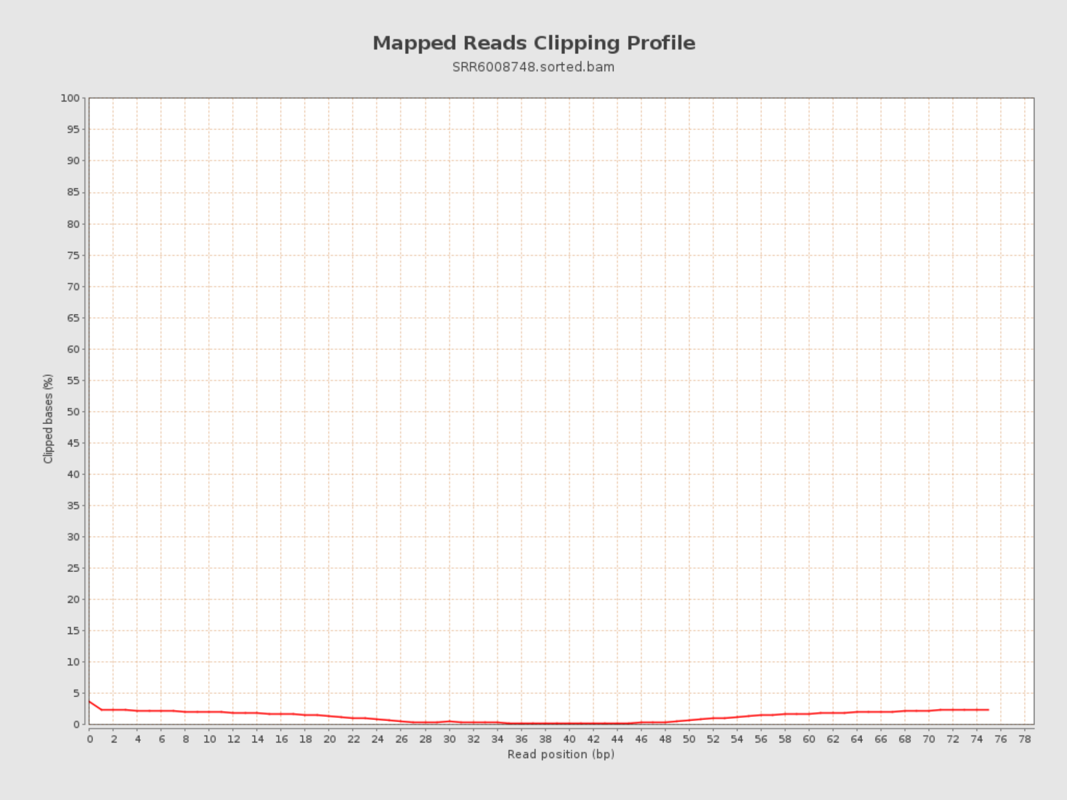
8. Results : Mapped Reads Nucleotide Content



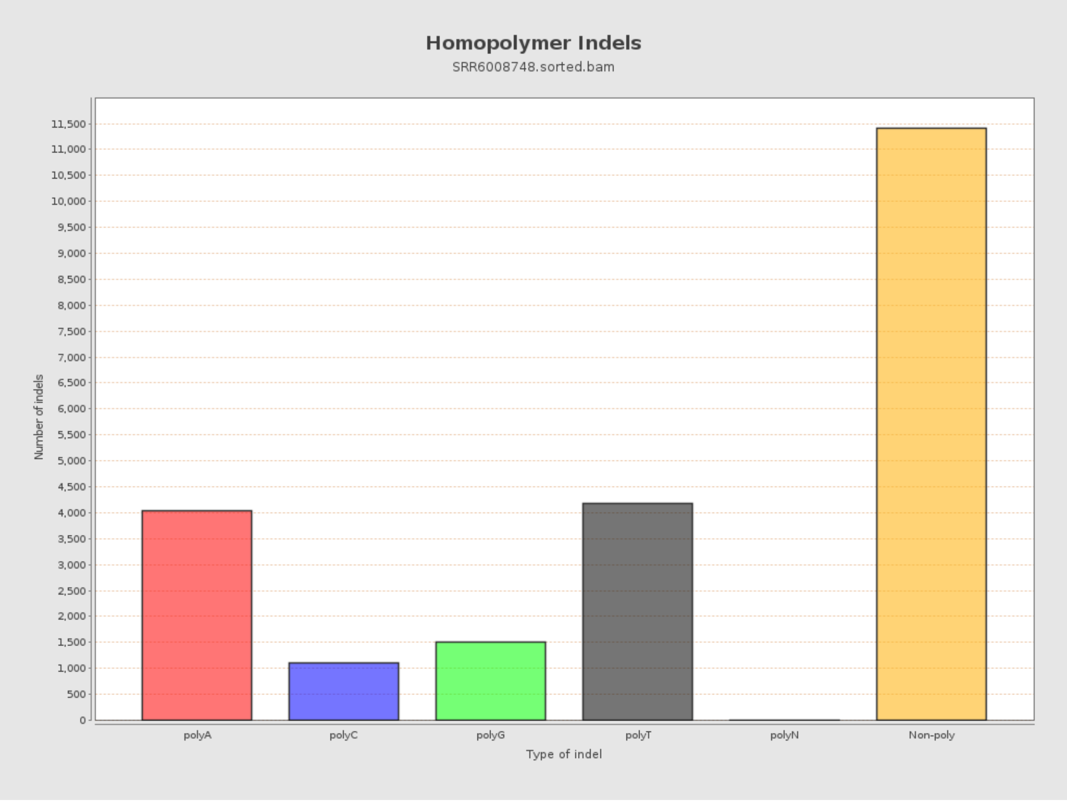
9. Results : Mapped Reads GC-content Distribution



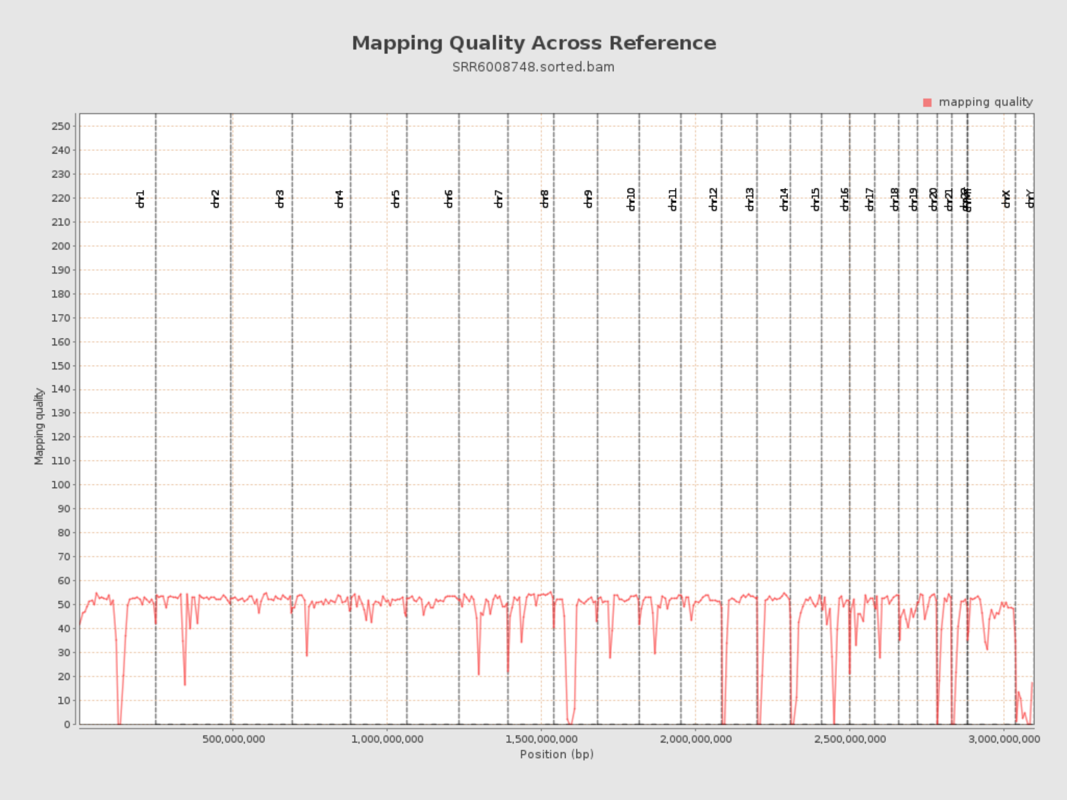
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram