Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 10:55:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008772.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_SRR6008772 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008772.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 10:55:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008772.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,195,570
Mapped reads	985,383 / 82.42%
Unmapped reads	210,187 / 17.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,330 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	24,922 / 2.08%
Duplication rate	1.74%
Clipped reads	494,496 / 41.36%

2.2. ACGT Content

Number/percentage of A's	18,536,323 / 28.83%
Number/percentage of C's	11,542,891 / 17.96%
Number/percentage of T's	19,708,764 / 30.66%
Number/percentage of G's	14,486,734 / 22.53%
Number/percentage of N's	10,975 / 0.02%
GC Percentage	40.49%

2.3. Coverage

Mean	0.0208

Standard Deviation	0.2262

2.4. Mapping Quality

Mean Mapping Quality	45.13

2.5. Mismatches and indels

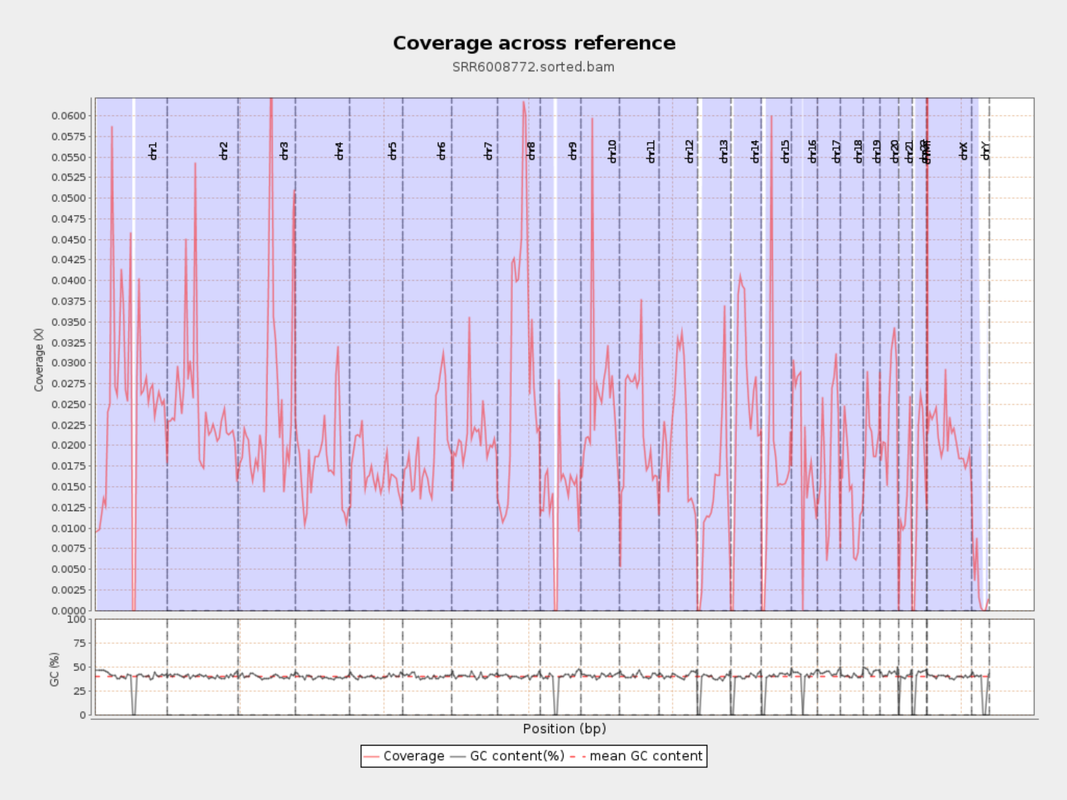
General error rate	0.86%
Mismatches	543,982
Insertions	5,557
Mapped reads with at least one insertion	0.56%
Deletions	18,398
Mapped reads with at least one deletion	1.85%
Homopolymer indels	45.18%

2.6. Chromosome stats

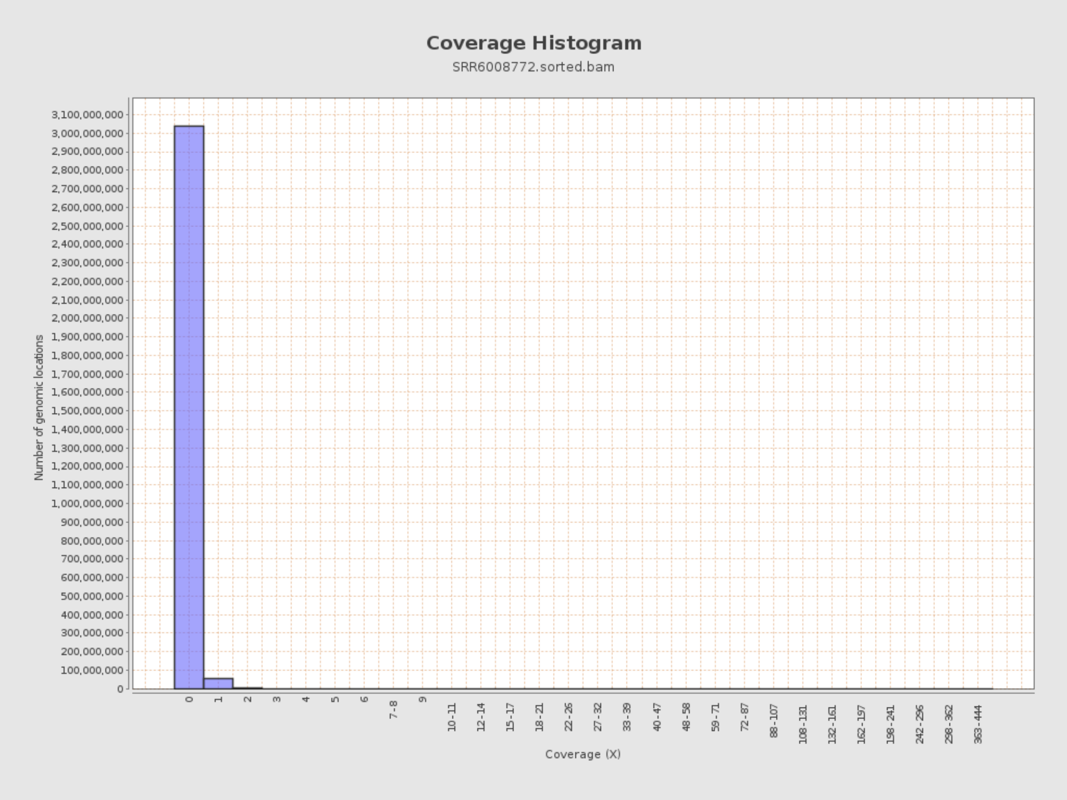
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6243203	0.025	0.3892
chr2	243199373	6023750	0.0248	0.2637
chr3	198022430	4930849	0.0249	0.1711
chr4	191154276	3433060	0.018	0.1432
chr5	180915260	3087178	0.0171	0.1368
chr6	171115067	3337914	0.0195	0.1535
chr7	159138663	3359500	0.0211	0.2414

chr8	146364022	4510576	0.0308	0.2447
chr9	141213431	1941416	0.0137	0.1873
chr10	135534747	3480642	0.0257	0.3415
chr11	135006516	3014900	0.0223	0.22
chr12	133851895	2854913	0.0213	0.1531
chr13	115169878	1575741	0.0137	0.121
chr14	107349540	2707758	0.0252	0.1688
chr15	102531392	1808785	0.0176	0.1408
chr16	90354753	1725239	0.0191	0.1743
chr17	81195210	1554359	0.0191	0.1818
chr18	78077248	1065148	0.0136	0.3667
chr19	59128983	1265945	0.0214	0.2652
chr20	63025520	1525905	0.0242	0.1644
chr21	48129895	605261	0.0126	0.1248
chr22	51304566	778965	0.0152	0.1282
chrMT	16571	57507	3.4703	2.5539
chrX	155270560	3258894	0.021	0.2154
chrY	59373566	168928	0.0028	0.0875

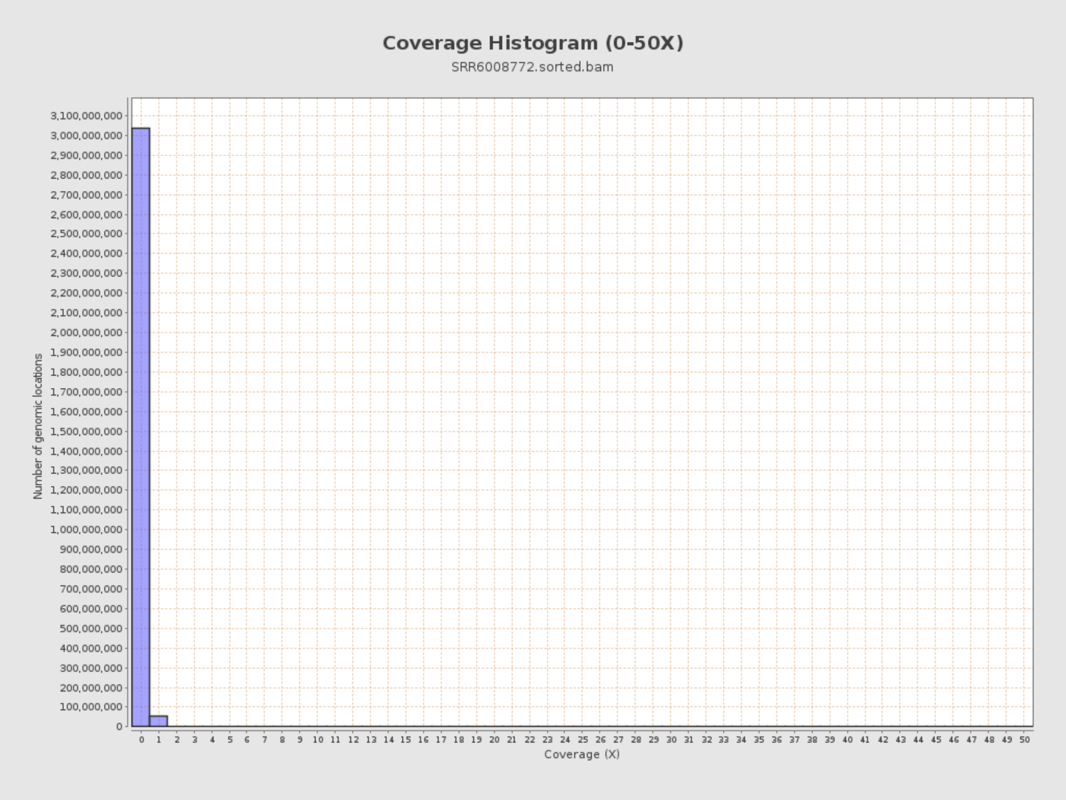
3. Results : Coverage across reference



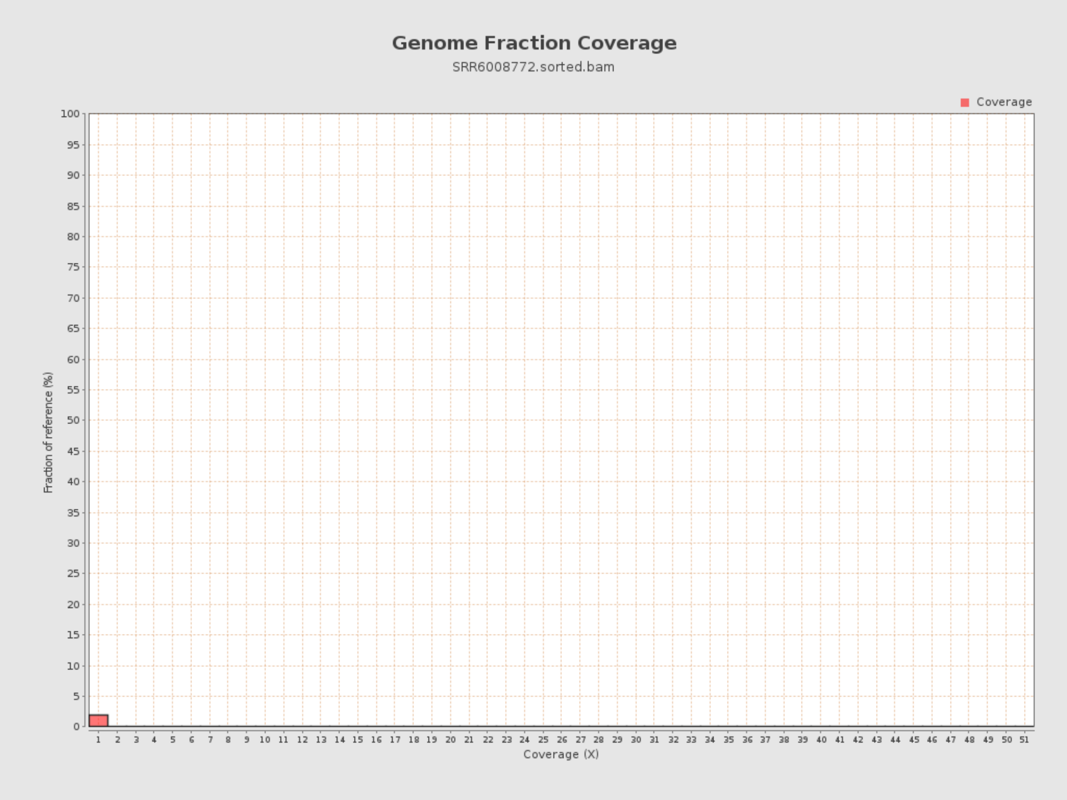
4. Results : Coverage Histogram



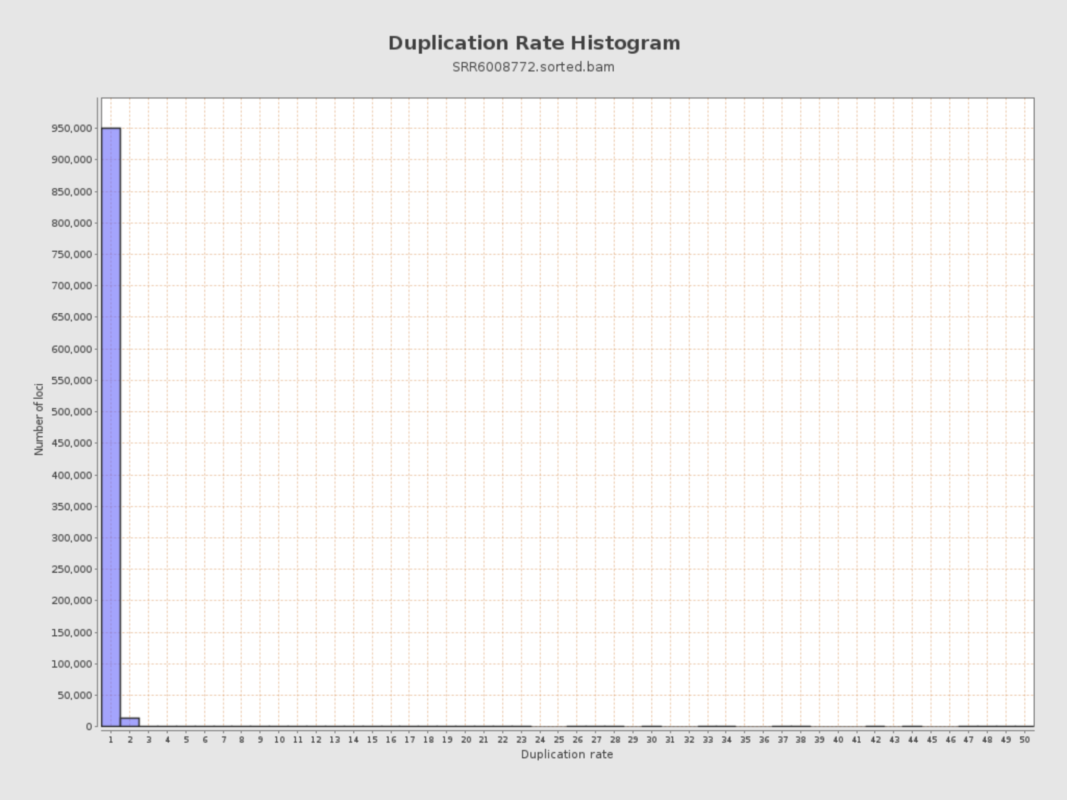
5. Results : Coverage Histogram (0-50X)



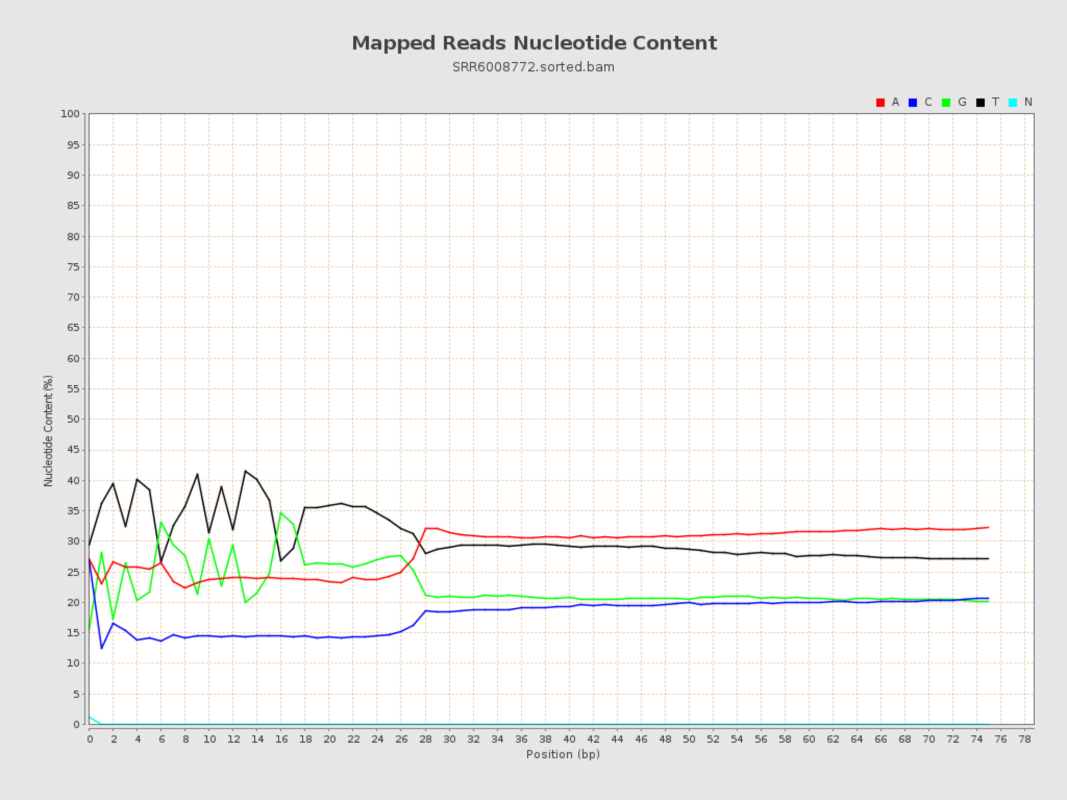
6. Results : Genome Fraction Coverage



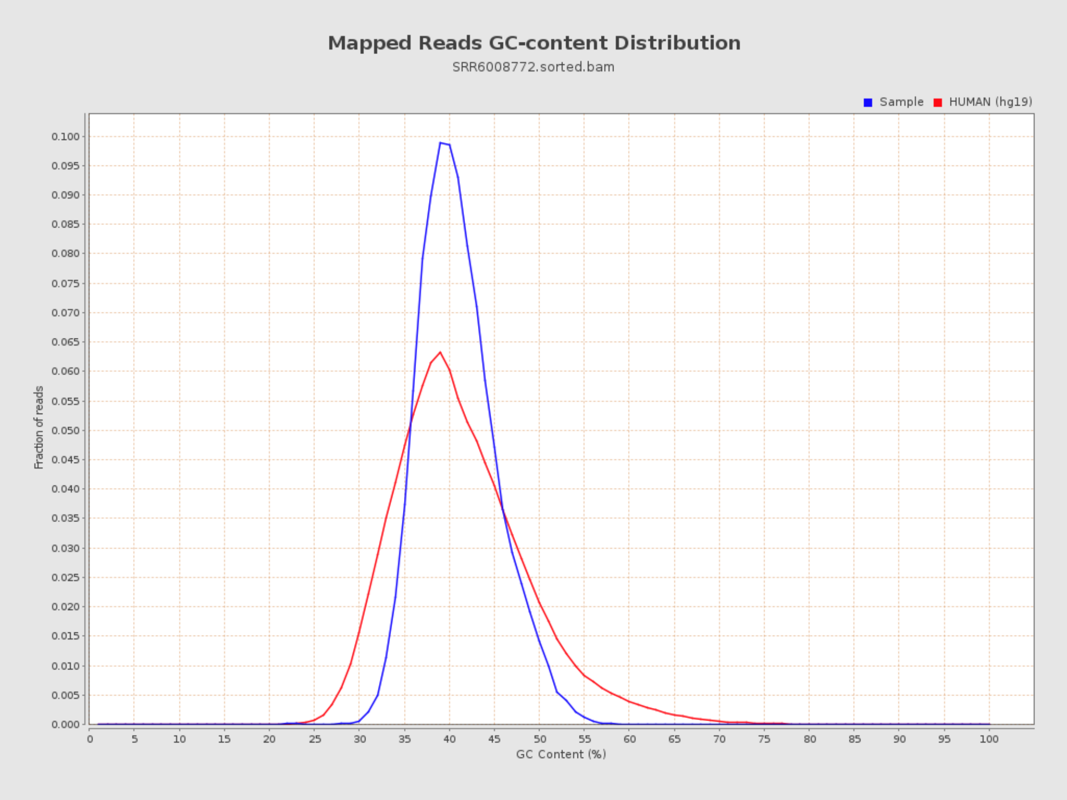
7. Results : Duplication Rate Histogram



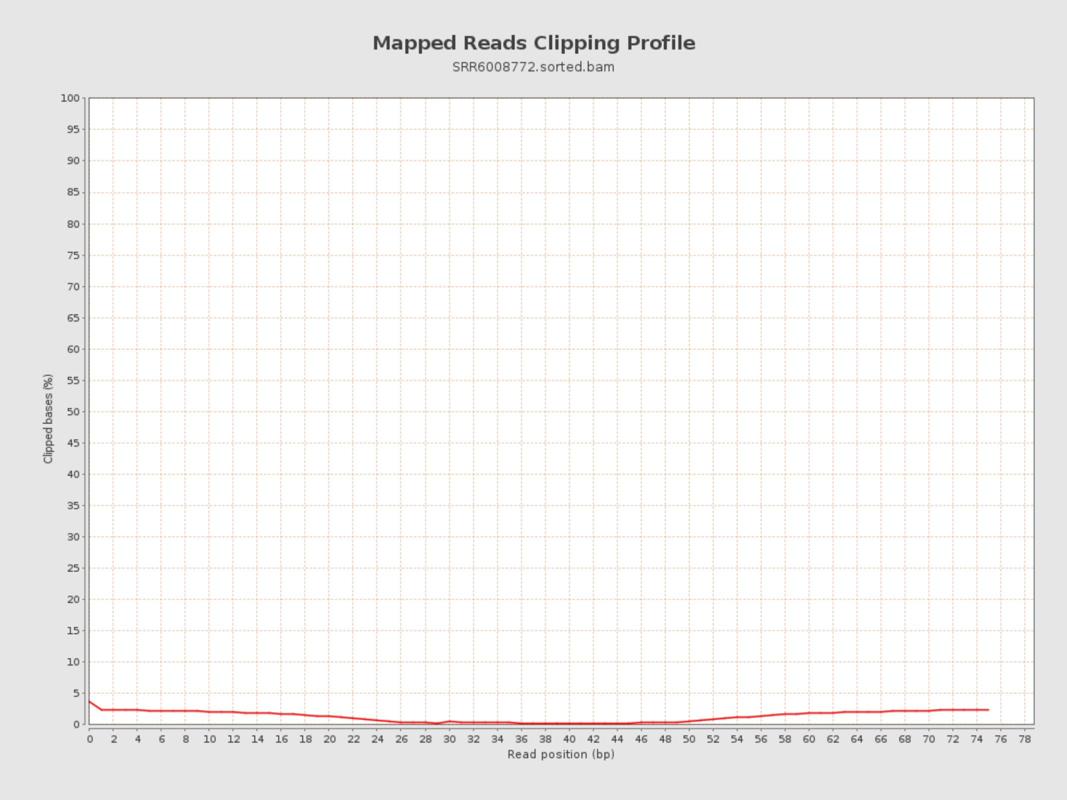
8. Results : Mapped Reads Nucleotide Content



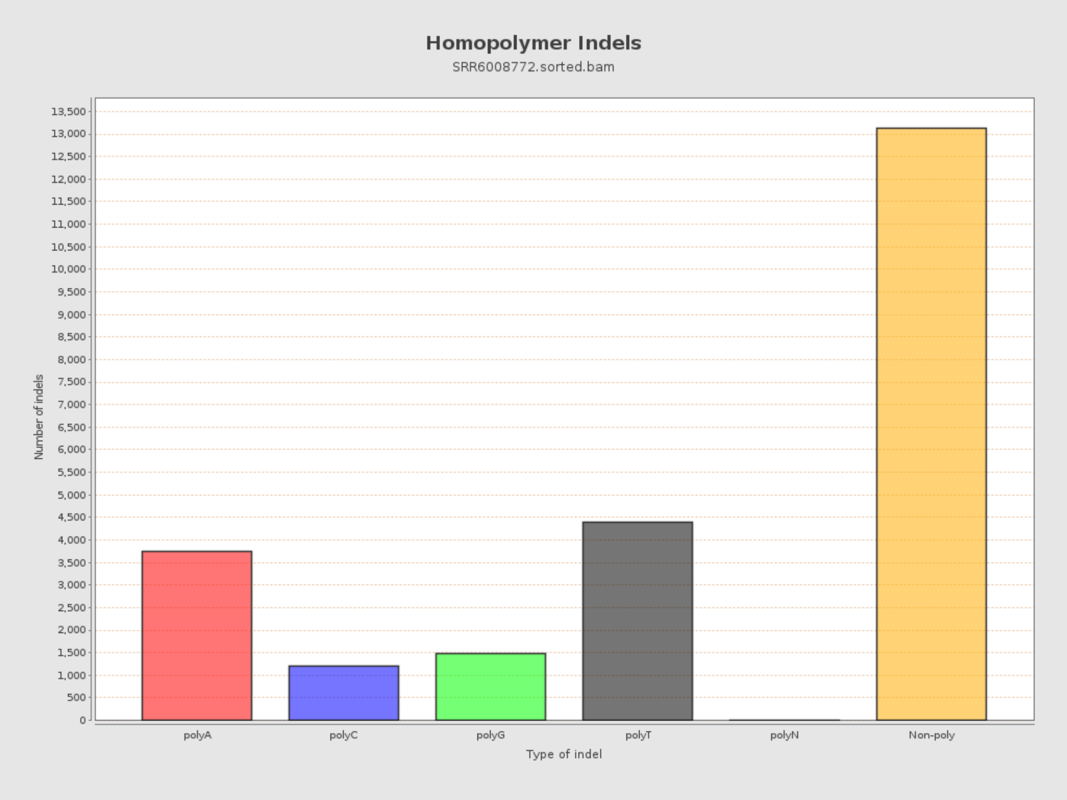
9. Results : Mapped Reads GC-content Distribution



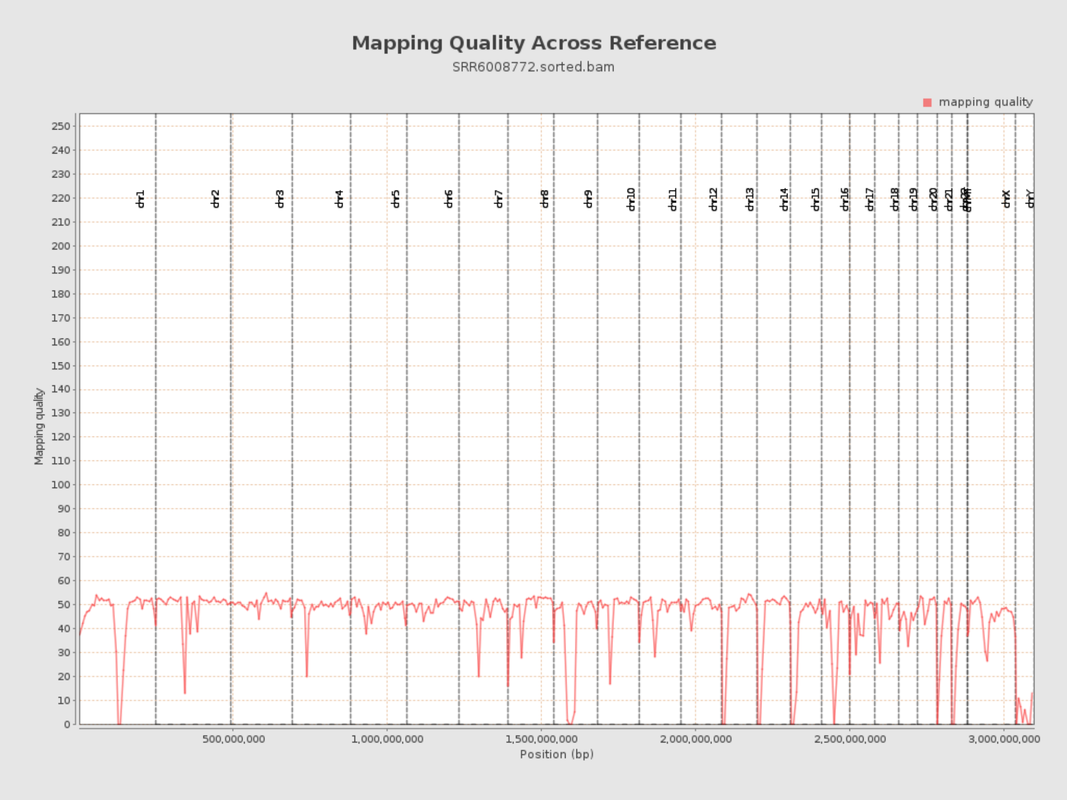
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram