Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 19:19:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6003989.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_SRR6003989 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6003989.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 19:19:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6003989.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,994,538
Mapped reads	2,353,523 / 78.59%
Unmapped reads	641,015 / 21.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,651 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	97,462 / 3.25%
Duplication rate	2.8%
Clipped reads	1,046,529 / 34.95%

2.2. ACGT Content

Number/percentage of A's	44,659,029 / 28.32%
Number/percentage of C's	27,991,017 / 17.75%
Number/percentage of T's	50,874,257 / 32.26%
Number/percentage of G's	34,160,935 / 21.66%
Number/percentage of N's	16,745 / 0.01%
GC Percentage	39.41%

2.3. Coverage

Mean	0.051

Standard Deviation	0.5616

2.4. Mapping Quality

Mean Mapping Quality	44.5

2.5. Mismatches and indels

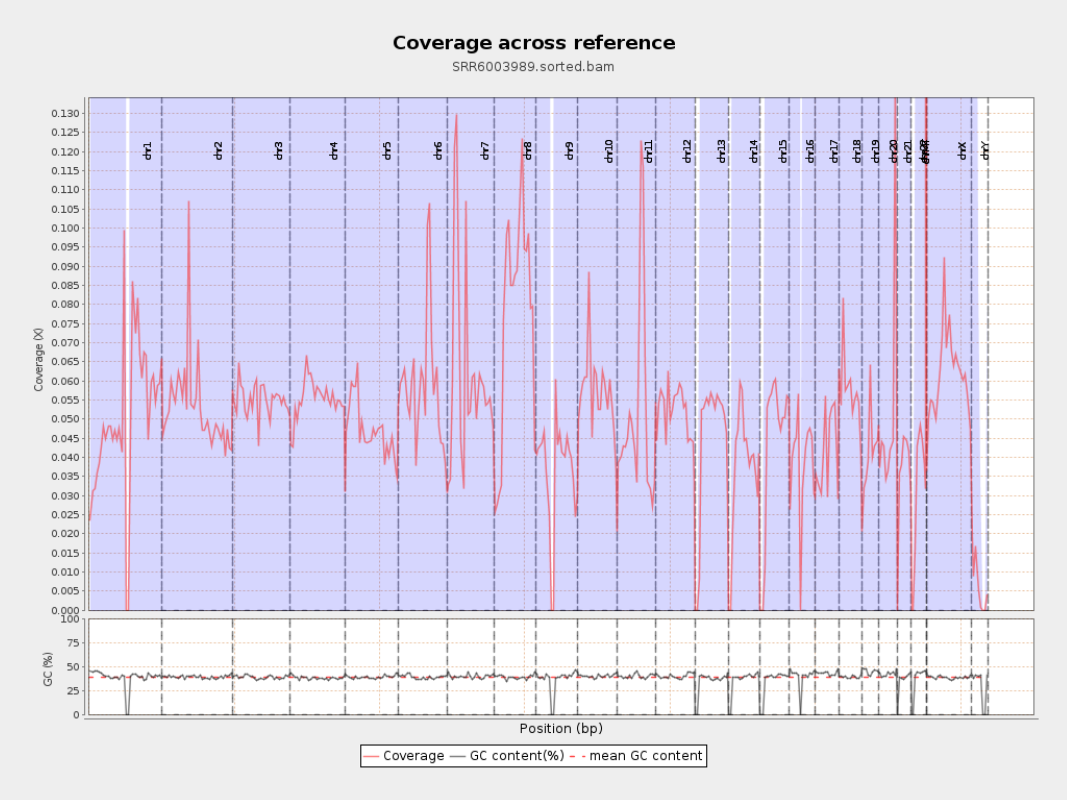
General error rate	1.03%
Mismatches	1,601,939
Insertions	14,783
Mapped reads with at least one insertion	0.62%
Deletions	42,789
Mapped reads with at least one deletion	1.8%
Homopolymer indels	46.59%

2.6. Chromosome stats

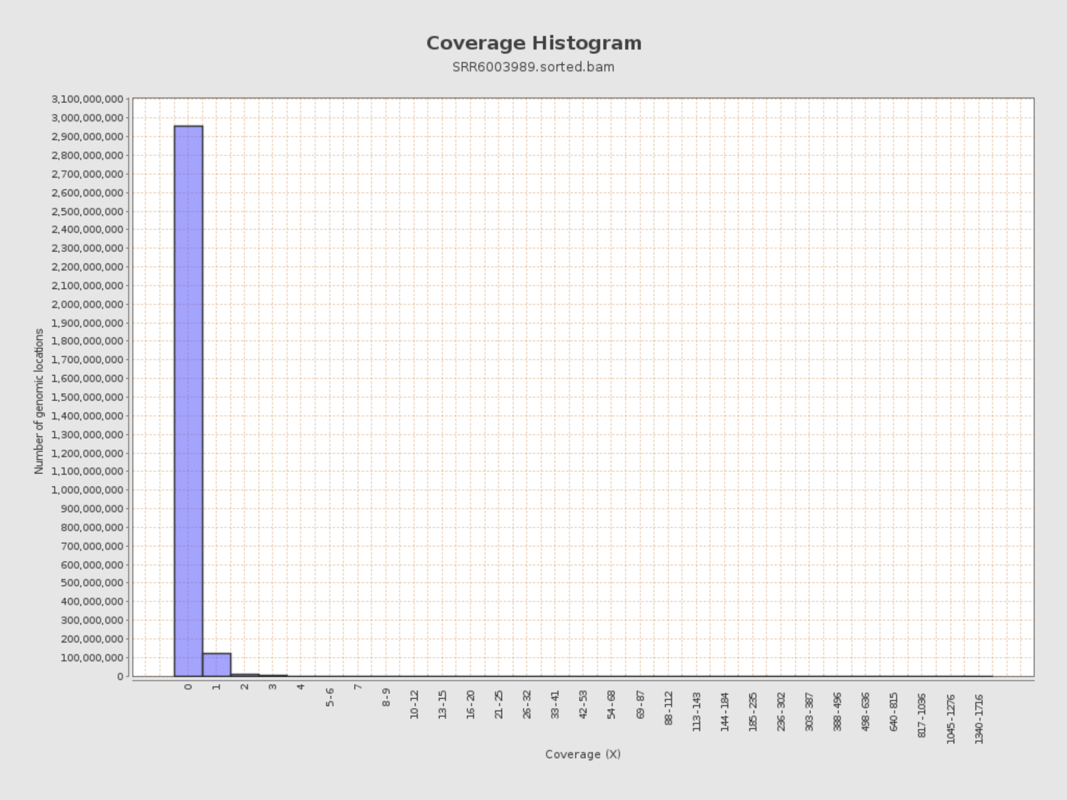
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12519002	0.0502	1.0993
chr2	243199373	12917806	0.0531	0.5769
chr3	198022430	10911900	0.0551	0.2599
chr4	191154276	10578923	0.0553	0.2676
chr5	180915260	8560043	0.0473	0.2466
chr6	171115067	10057114	0.0588	0.3255
chr7	159138663	10067635	0.0633	0.8085

chr8	146364022	11210018	0.0766	1.078
chr9	141213431	5137291	0.0364	0.4702
chr10	135534747	7781000	0.0574	0.4483
chr11	135006516	6960733	0.0516	0.4132
chr12	133851895	6960691	0.052	0.268
chr13	115169878	5091709	0.0442	0.2311
chr14	107349540	3939712	0.0367	0.2613
chr15	102531392	4422564	0.0431	0.2366
chr16	90354753	3471184	0.0384	0.277
chr17	81195210	3389193	0.0417	0.2585
chr18	78077248	4522412	0.0579	1.0119
chr19	59128983	2462580	0.0416	0.7231
chr20	63025520	3427372	0.0544	0.2804
chr21	48129895	1742297	0.0362	0.2375
chr22	51304566	1532973	0.0299	0.1872
chrMT	16571	152163	9.1825	7.035
chrX	155270560	9581566	0.0617	0.3366
chrY	59373566	375035	0.0063	0.1163

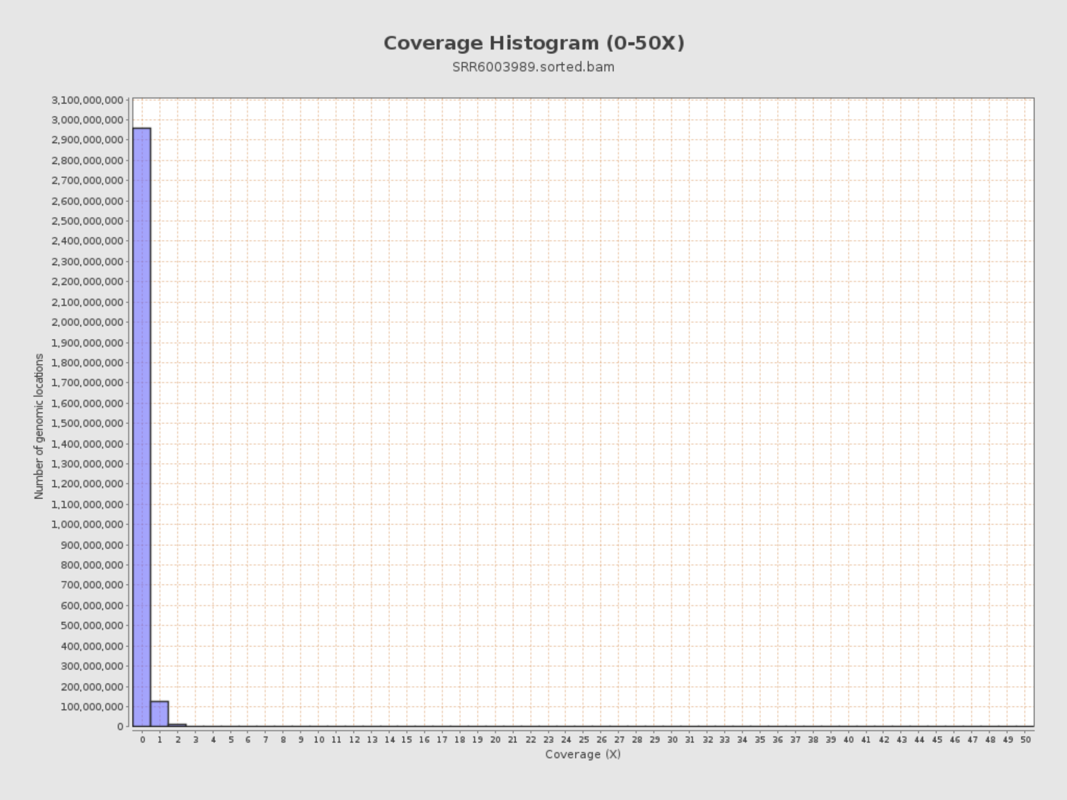
3. Results : Coverage across reference



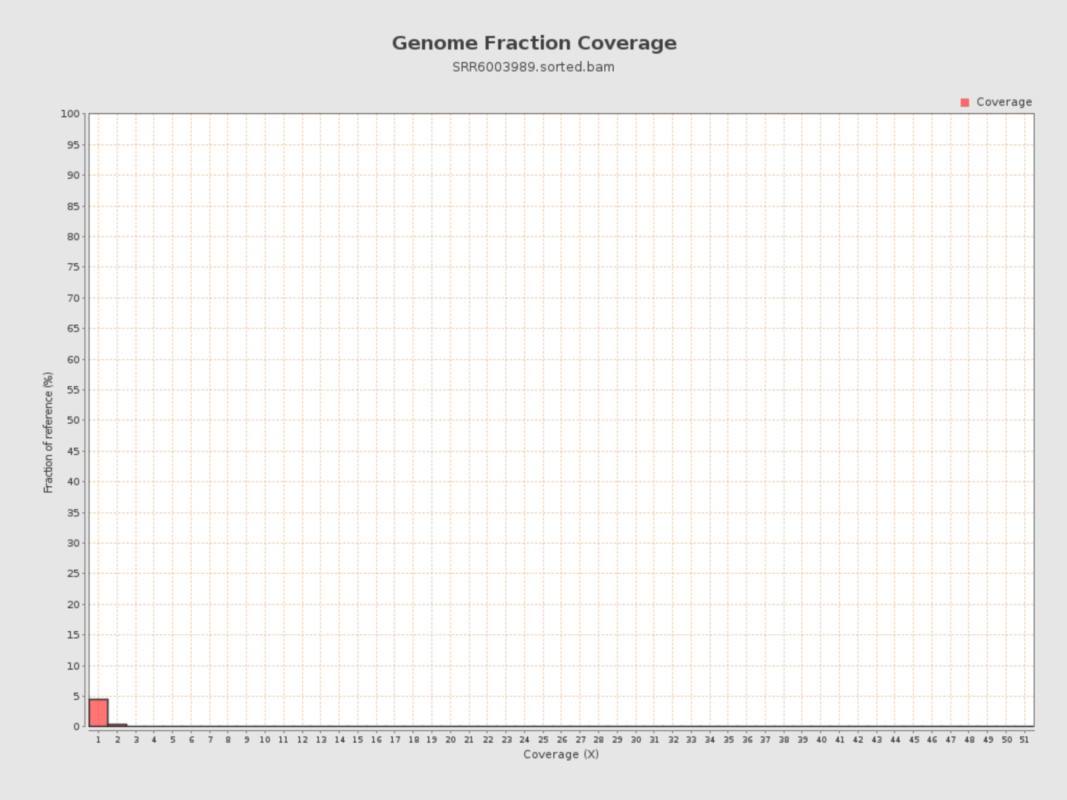
4. Results : Coverage Histogram



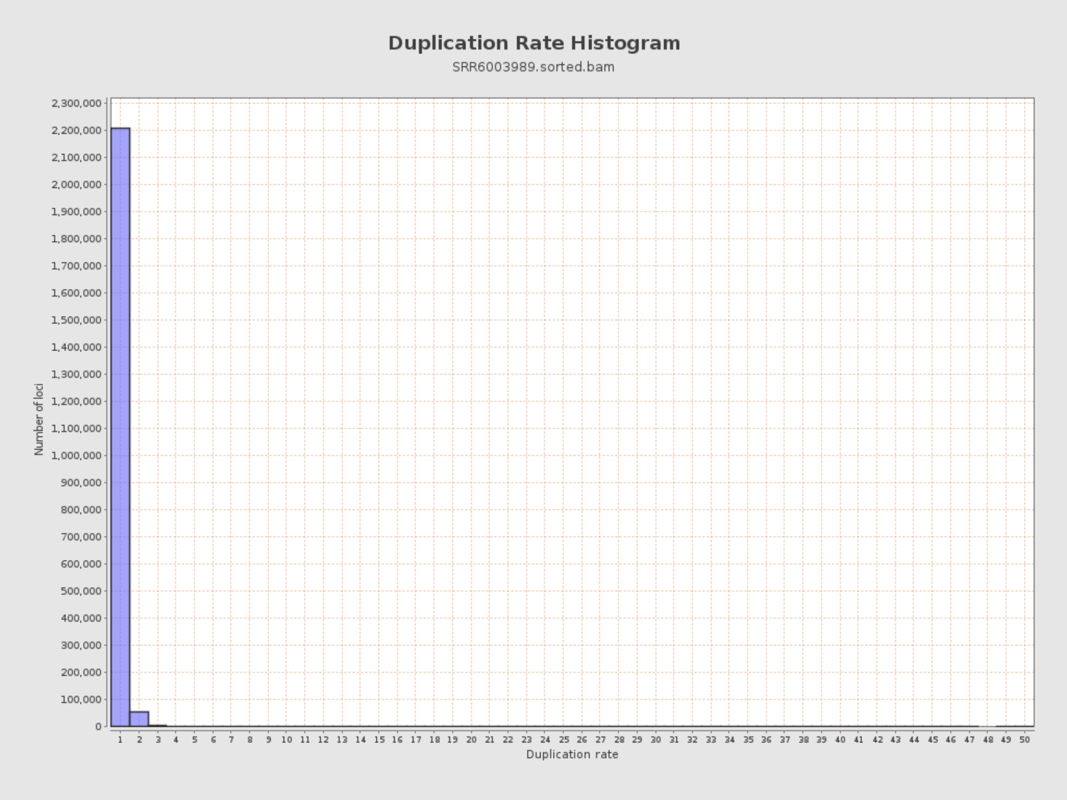
5. Results : Coverage Histogram (0-50X)



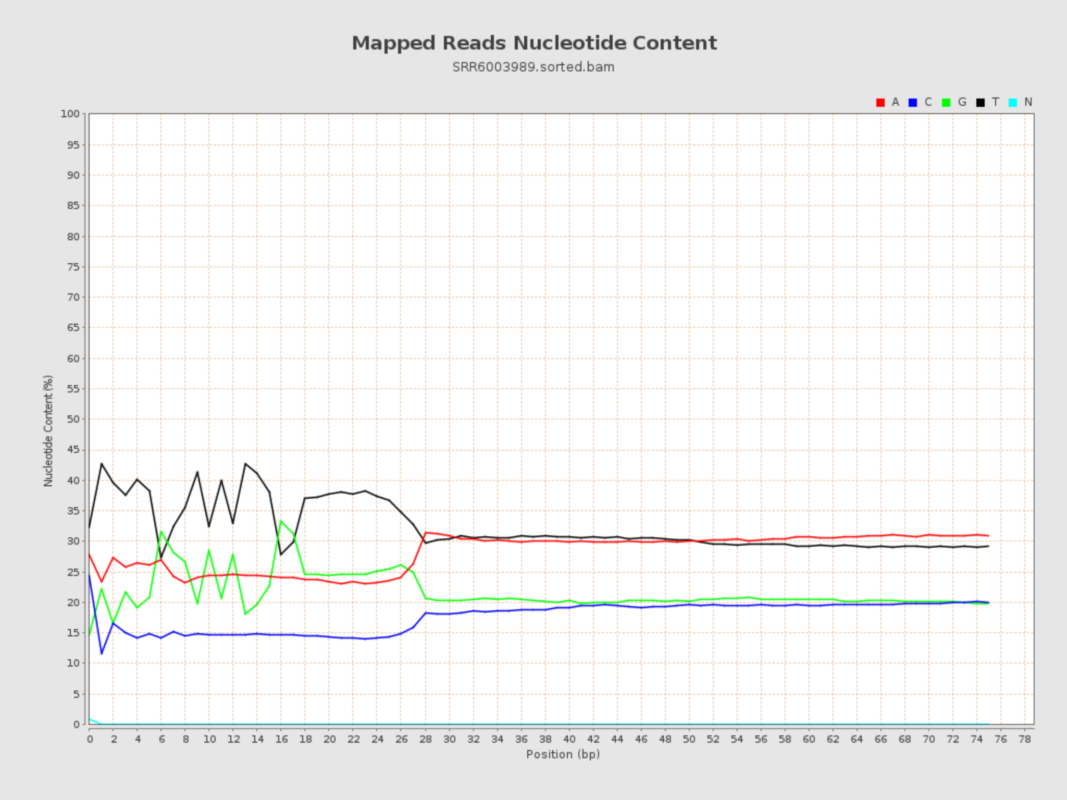
6. Results : Genome Fraction Coverage



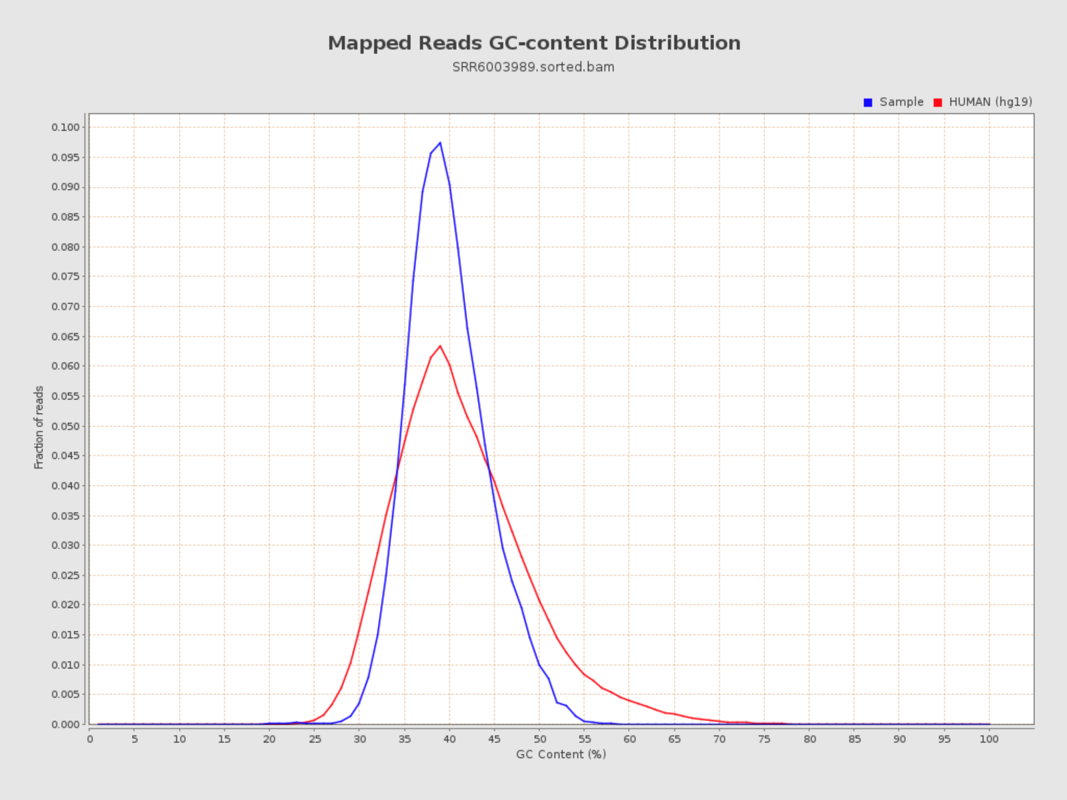
7. Results : Duplication Rate Histogram



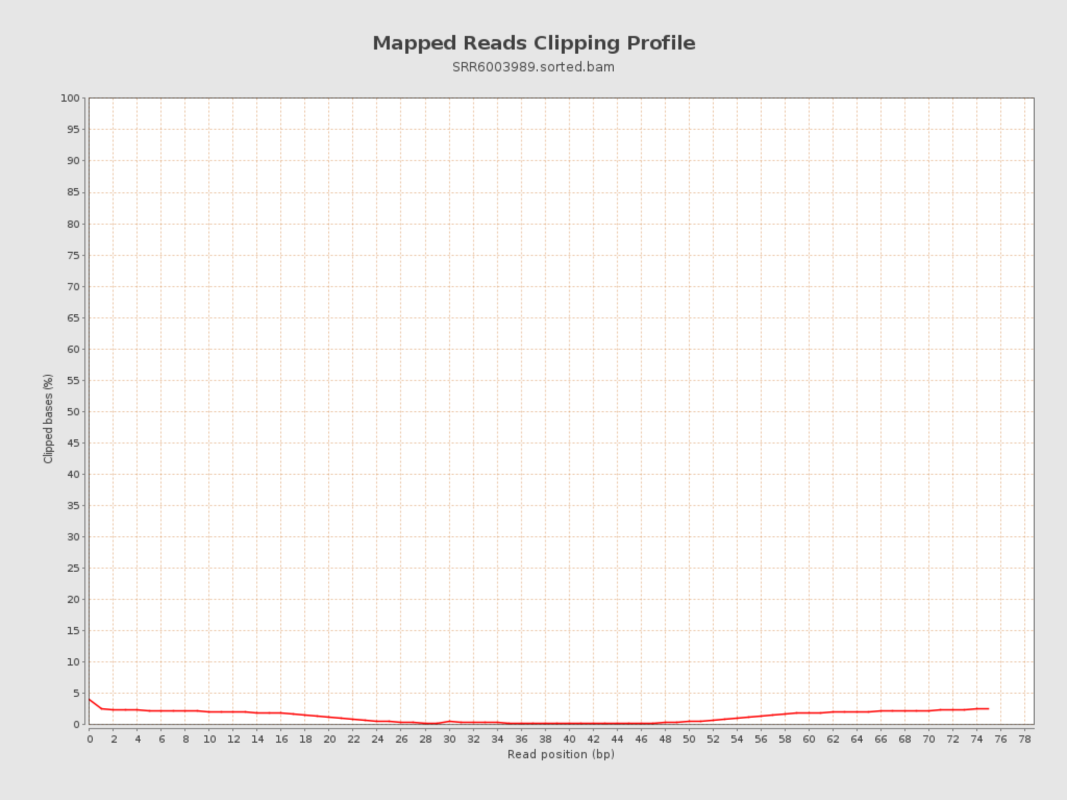
8. Results : Mapped Reads Nucleotide Content



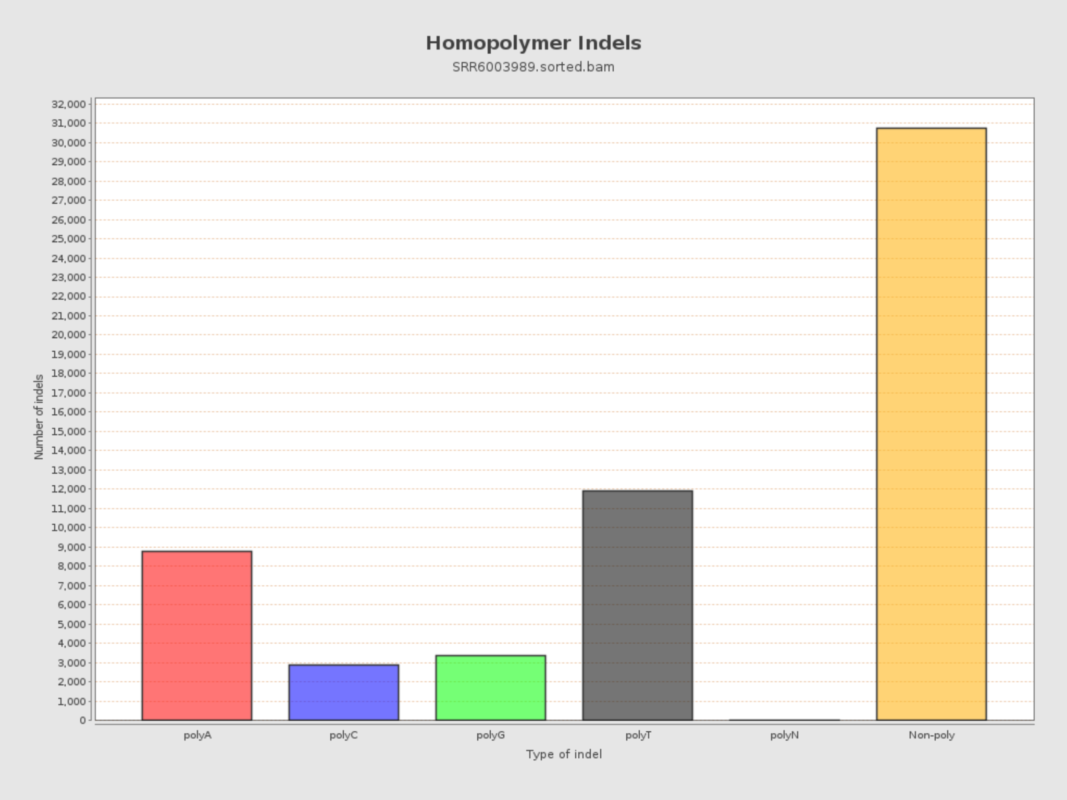
9. Results : Mapped Reads GC-content Distribution



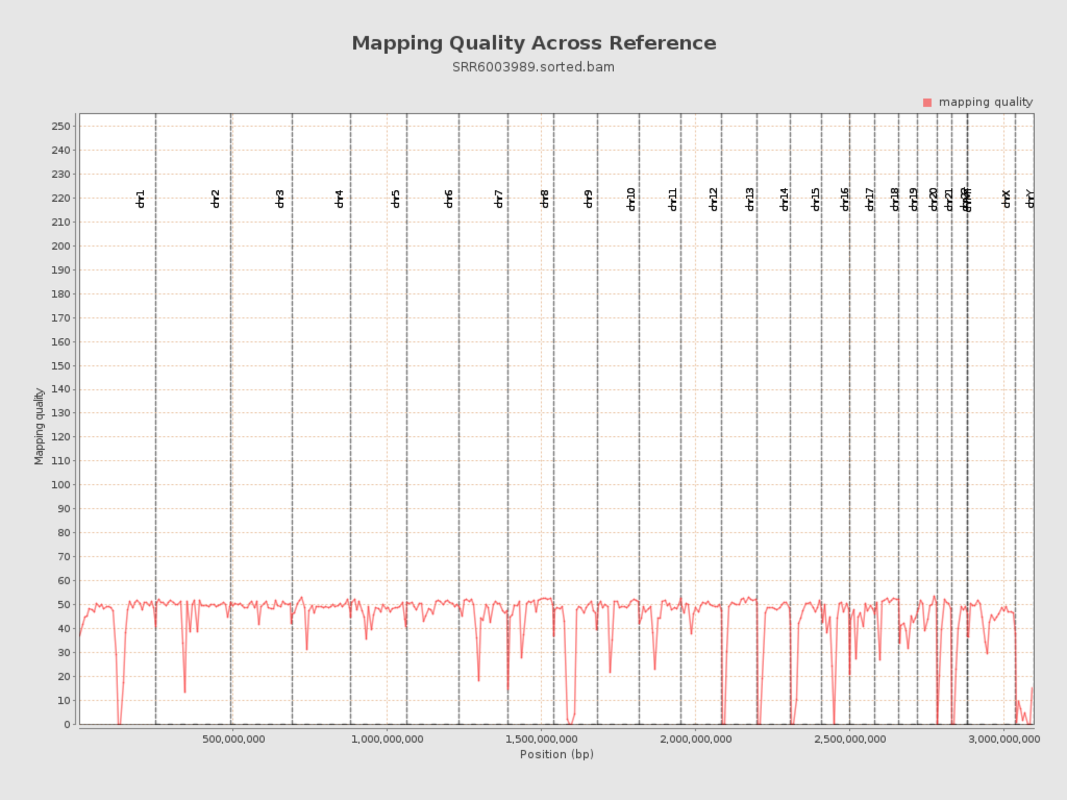
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram