Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 19:16:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6003988.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_SRR6003988 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6003988.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 19:16:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6003988.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,353,811
Mapped reads	2,311,753 / 68.93%
Unmapped reads	1,042,058 / 31.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,496 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	447,380 / 13.34%
Duplication rate	15.04%
Clipped reads	1,533,097 / 45.71%

2.2. ACGT Content

Number/percentage of A's	36,683,773 / 25.88%
Number/percentage of C's	23,078,342 / 16.28%
Number/percentage of T's	49,820,924 / 35.15%
Number/percentage of G's	32,143,263 / 22.68%
Number/percentage of N's	14,155 / 0.01%
GC Percentage	38.96%

2.3. Coverage

Mean	0.0458

Standard Deviation	0.4747

2.4. Mapping Quality

Mean Mapping Quality	45.31

2.5. Mismatches and indels

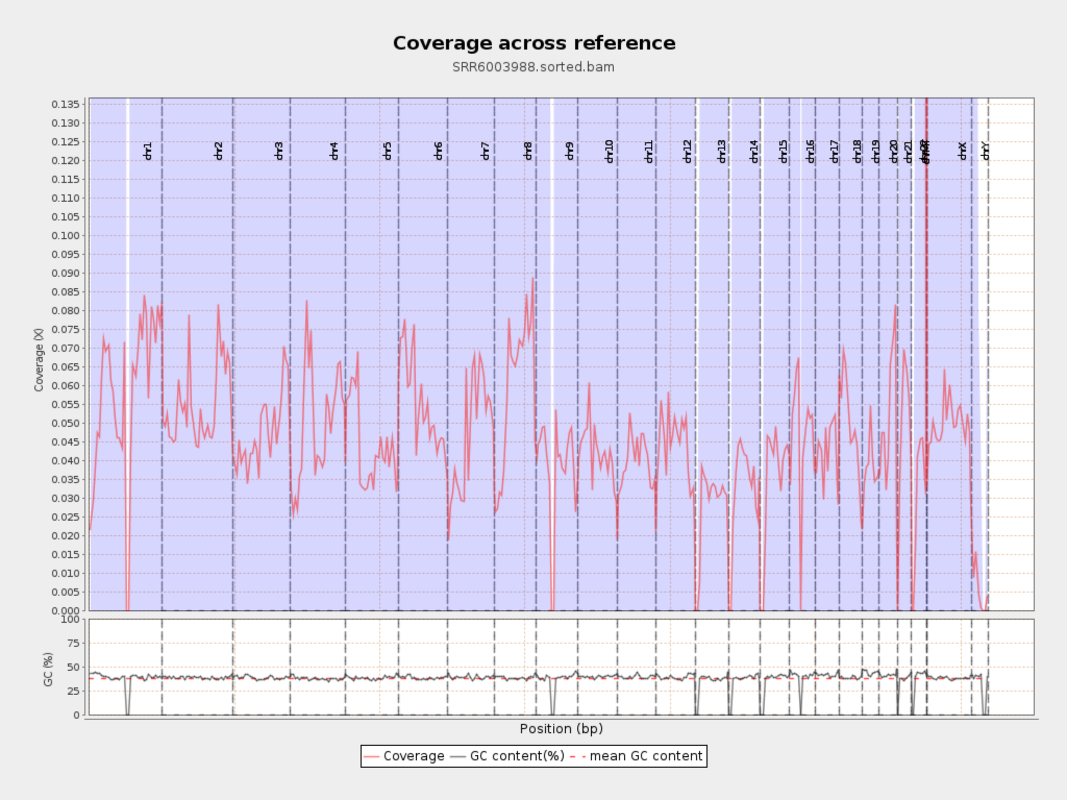
General error rate	1.11%
Mismatches	1,554,010
Insertions	12,274
Mapped reads with at least one insertion	0.53%
Deletions	44,684
Mapped reads with at least one deletion	1.91%
Homopolymer indels	48.92%

2.6. Chromosome stats

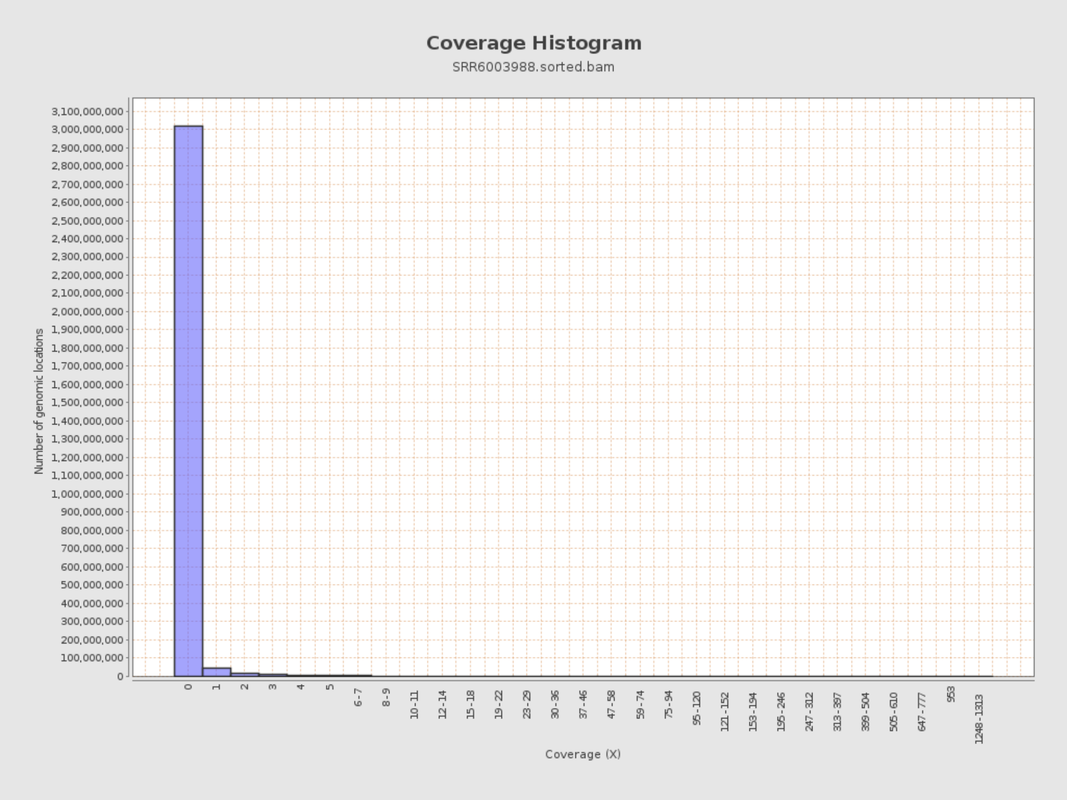
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14321426	0.0575	0.6892
chr2	243199373	13288222	0.0546	0.7037
chr3	198022430	9438968	0.0477	0.3682
chr4	191154276	9465166	0.0495	0.3831
chr5	180915260	7954655	0.044	0.3526
chr6	171115067	9459029	0.0553	0.4606
chr7	159138663	7559622	0.0475	0.5101

chr8	146364022	8775339	0.06	0.625
chr9	141213431	5337860	0.0378	0.4278
chr10	135534747	5755405	0.0425	0.3954
chr11	135006516	5353600	0.0397	0.3956
chr12	133851895	5926129	0.0443	0.3575
chr13	115169878	3151510	0.0274	0.276
chr14	107349540	3406684	0.0317	0.3153
chr15	102531392	3548579	0.0346	0.3125
chr16	90354753	4256393	0.0471	0.3666
chr17	81195210	3391875	0.0418	0.3424
chr18	78077248	3952433	0.0506	0.7783
chr19	59128983	2281112	0.0386	0.4812
chr20	63025520	3282023	0.0521	0.3841
chr21	48129895	2336068	0.0485	0.3756
chr22	51304566	1484983	0.0289	0.2658
chrMT	16571	97553	5.887	7.5525
chrX	155270560	7653917	0.0493	0.4144
chrY	59373566	334079	0.0056	0.1198

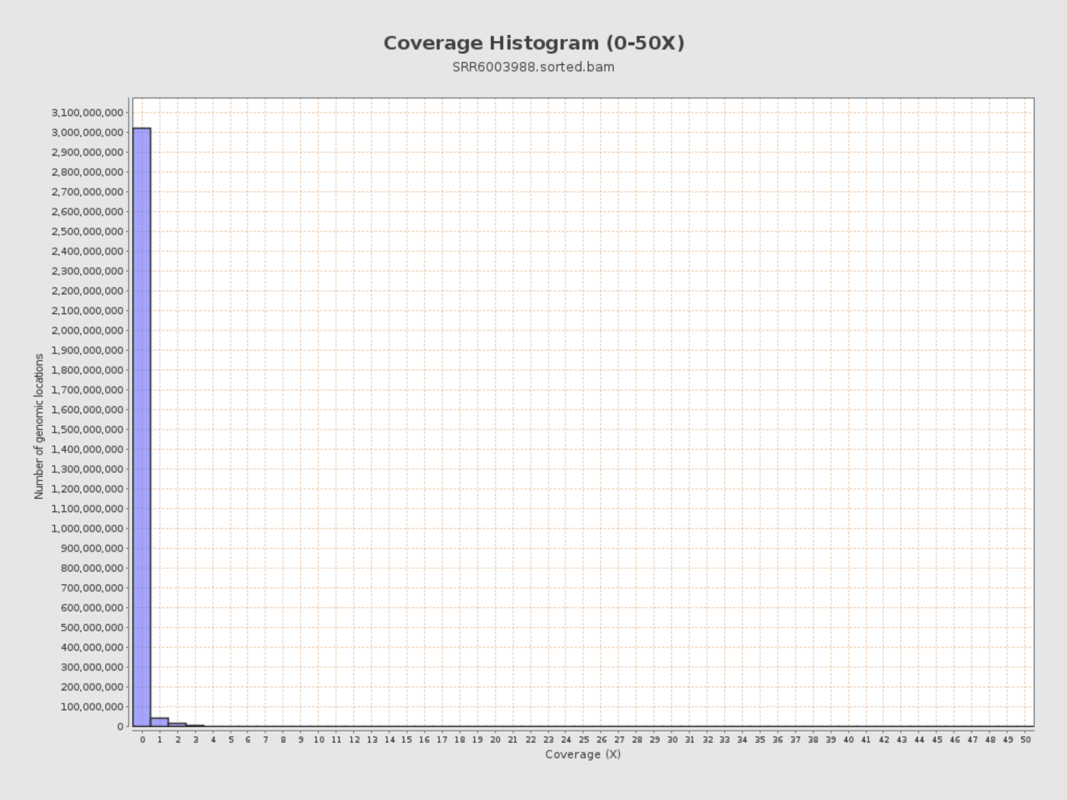
3. Results : Coverage across reference



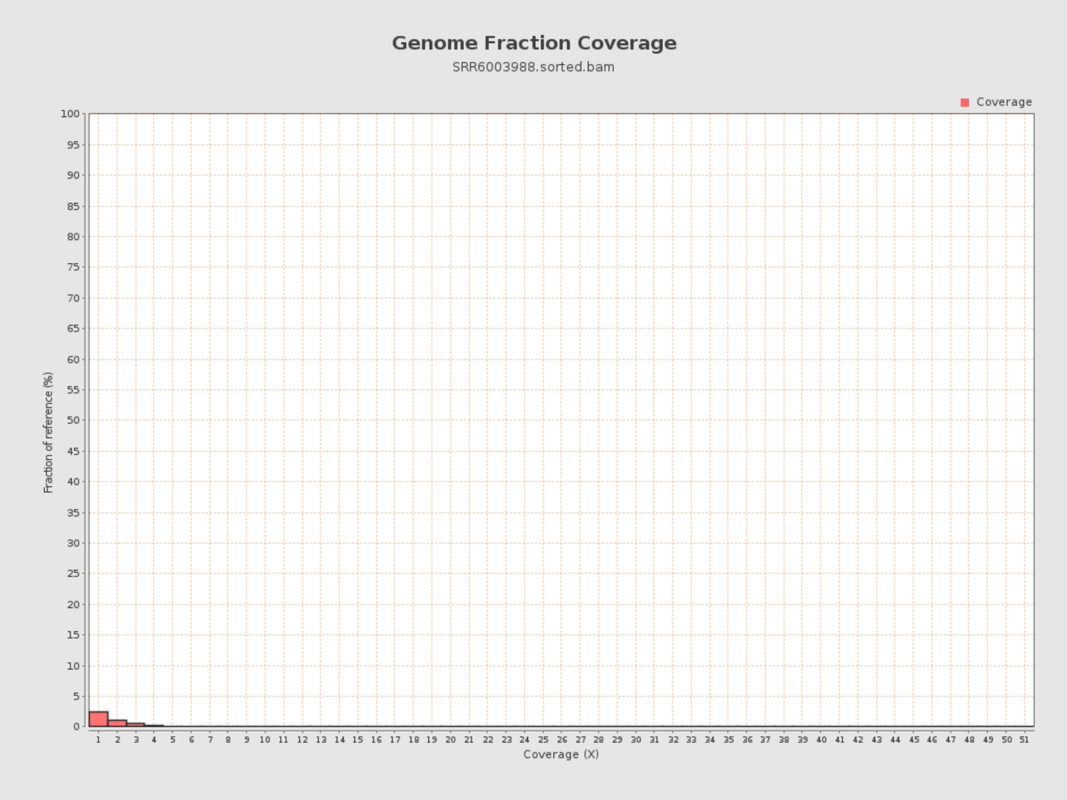
4. Results : Coverage Histogram



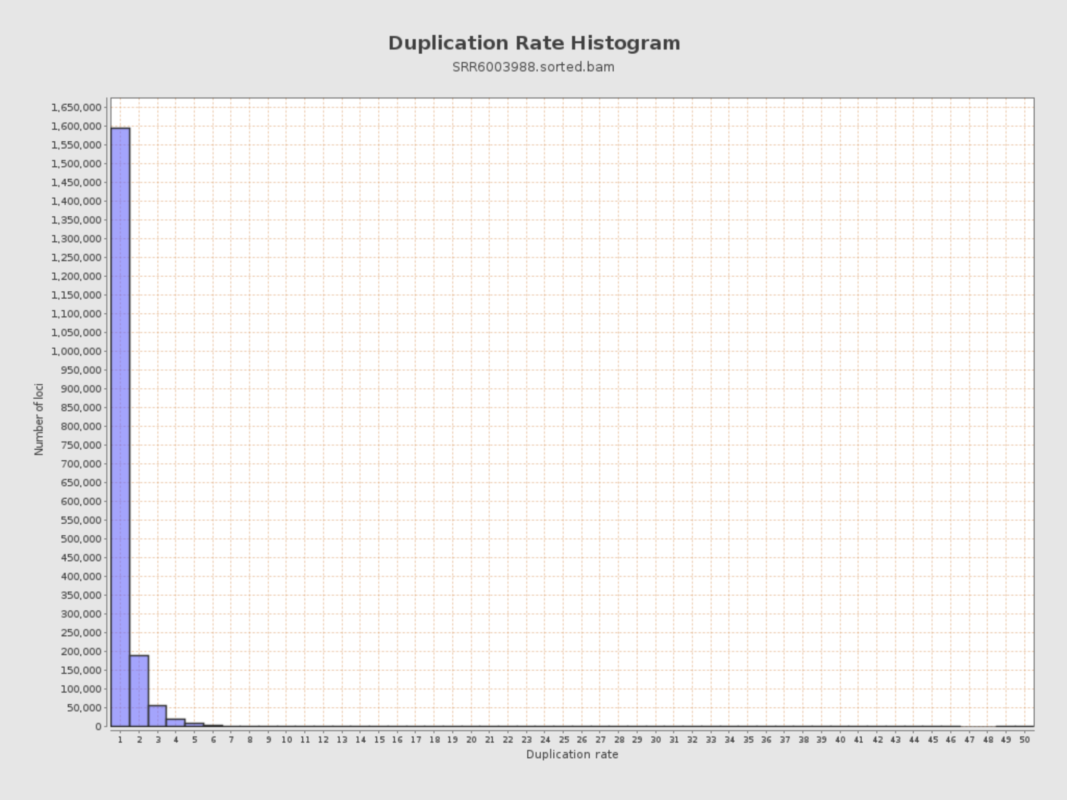
5. Results : Coverage Histogram (0-50X)



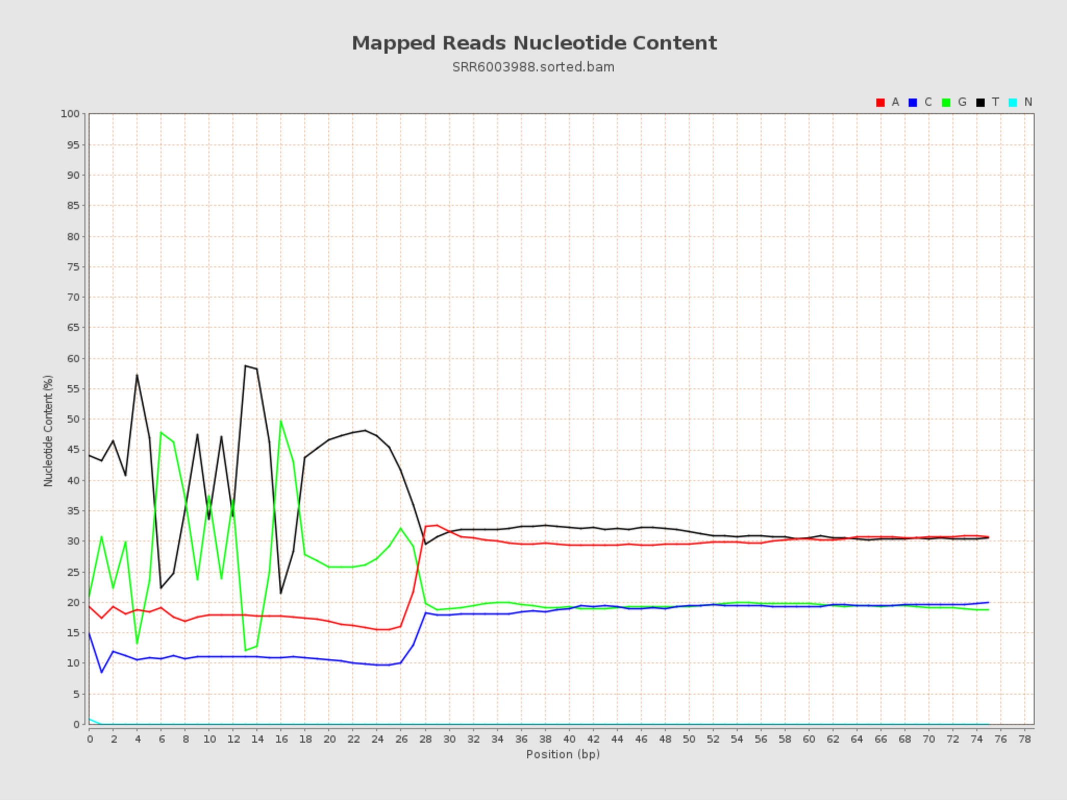
6. Results : Genome Fraction Coverage



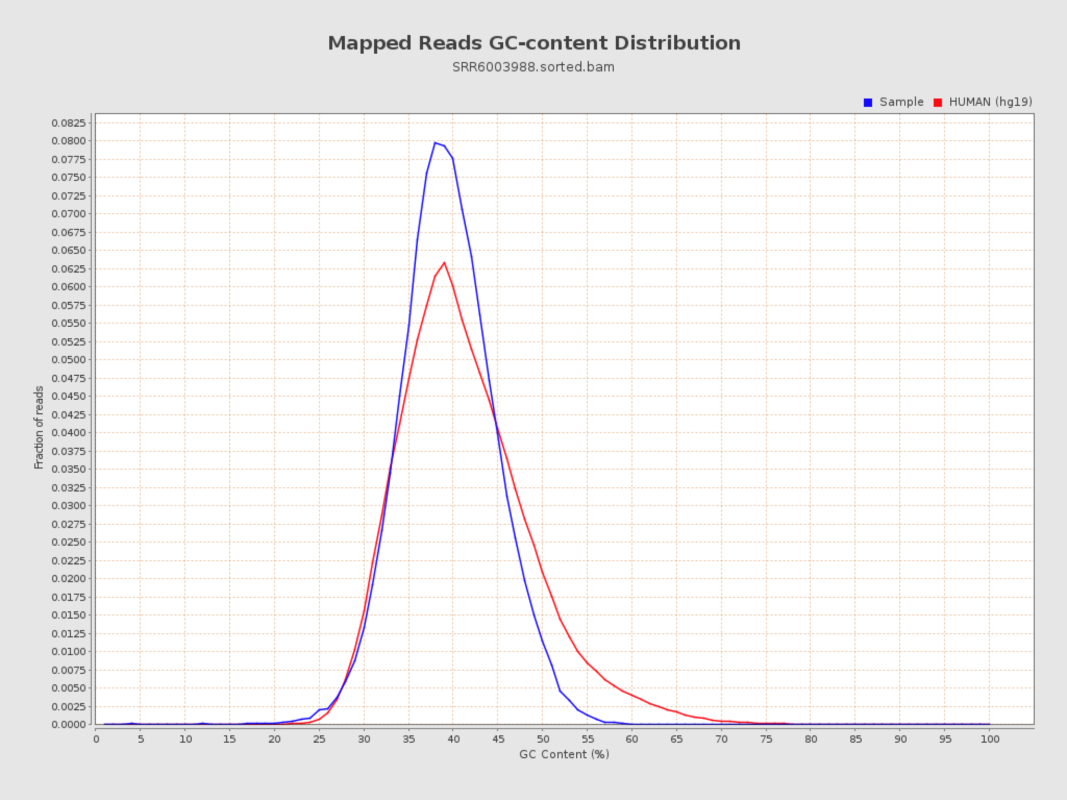
7. Results : Duplication Rate Histogram



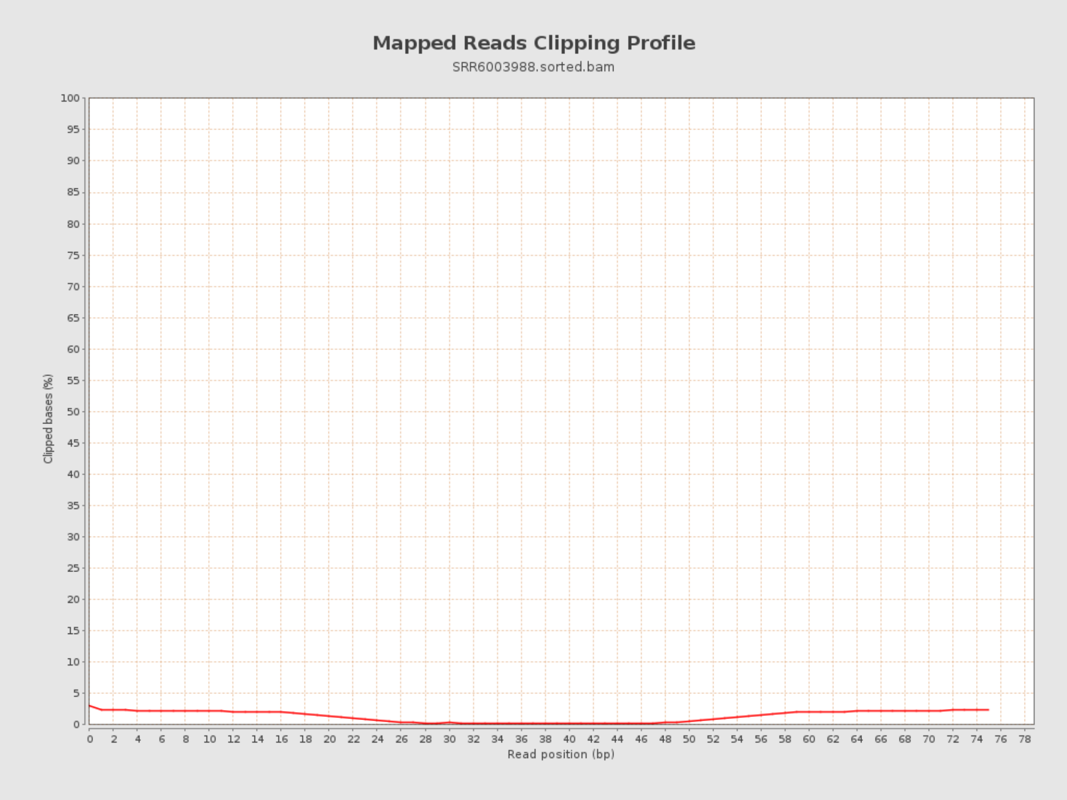
8. Results : Mapped Reads Nucleotide Content



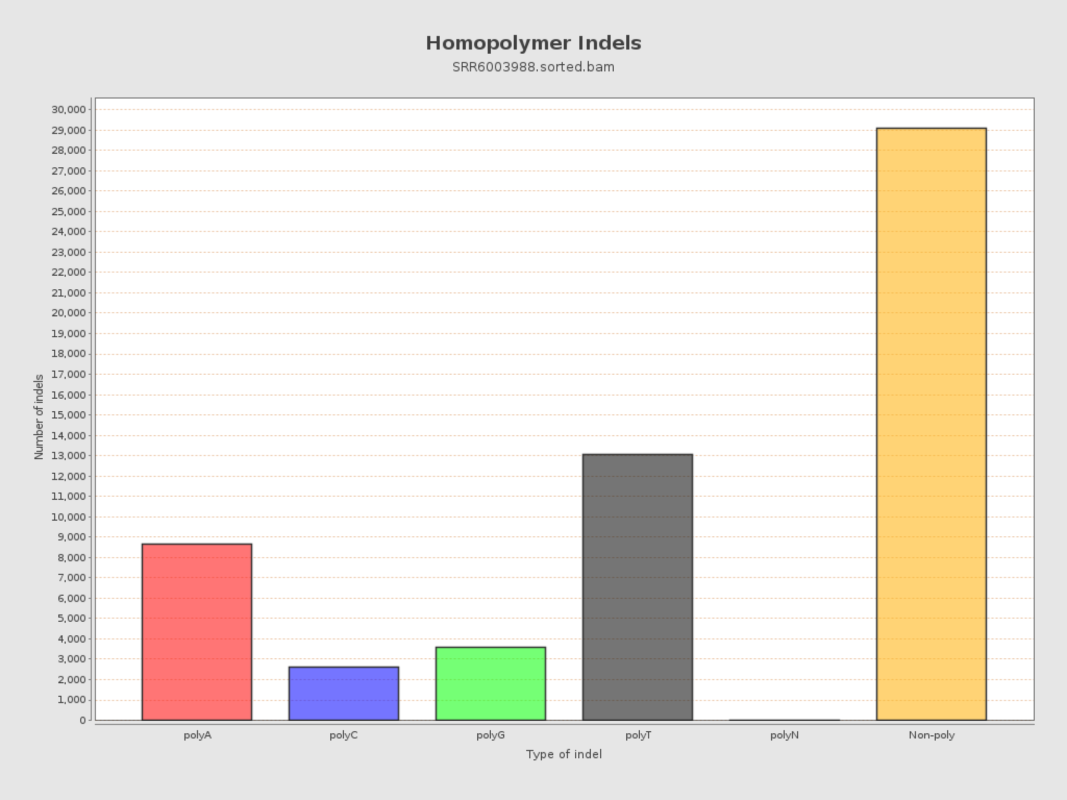
9. Results : Mapped Reads GC-content Distribution



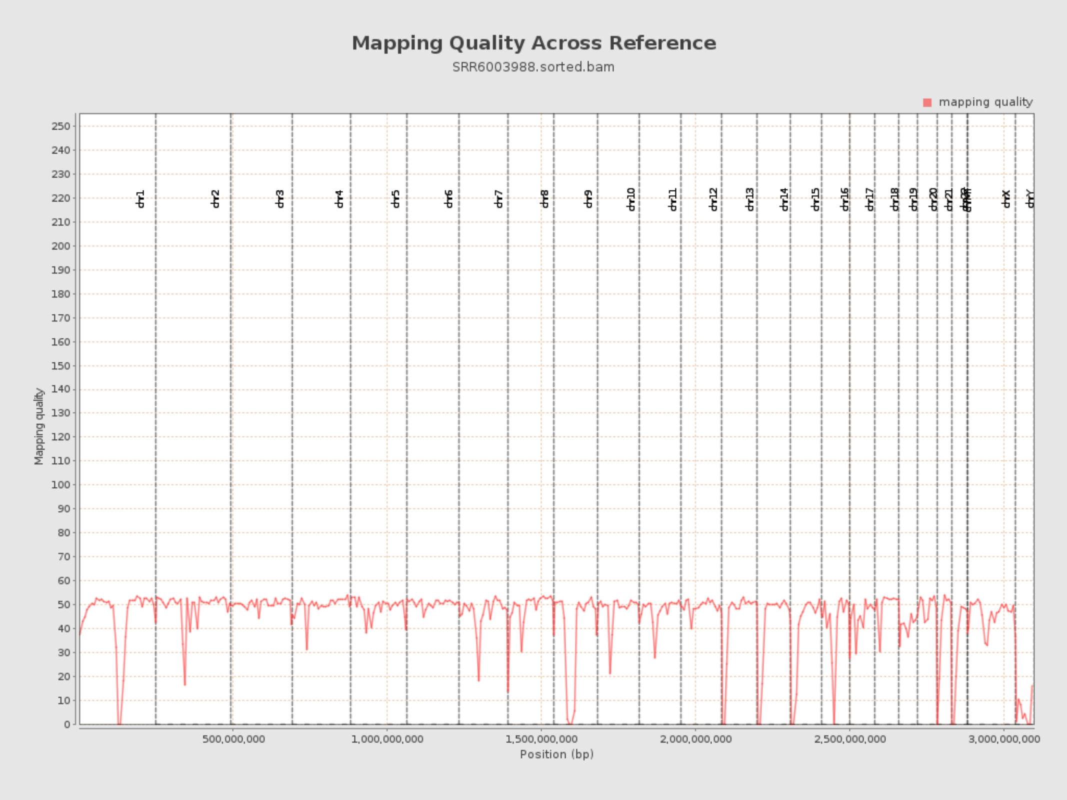
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram