Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 08:53:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008730.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_SRR6008730 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008730.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 08:53:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008730.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,300,963
Mapped reads	2,925,667 / 88.63%
Unmapped reads	375,296 / 11.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,145 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	154,363 / 4.68%
Duplication rate	4.05%
Clipped reads	1,705,459 / 51.67%

2.2. ACGT Content

Number/percentage of A's	48,821,429 / 26.2%
Number/percentage of C's	34,267,648 / 18.39%
Number/percentage of T's	57,656,778 / 30.95%
Number/percentage of G's	45,436,690 / 24.39%
Number/percentage of N's	133,152 / 0.07%
GC Percentage	42.78%

2.3. Coverage

Mean	0.0602

Standard Deviation	0.4972

2.4. Mapping Quality

Mean Mapping Quality	43.33

2.5. Mismatches and indels

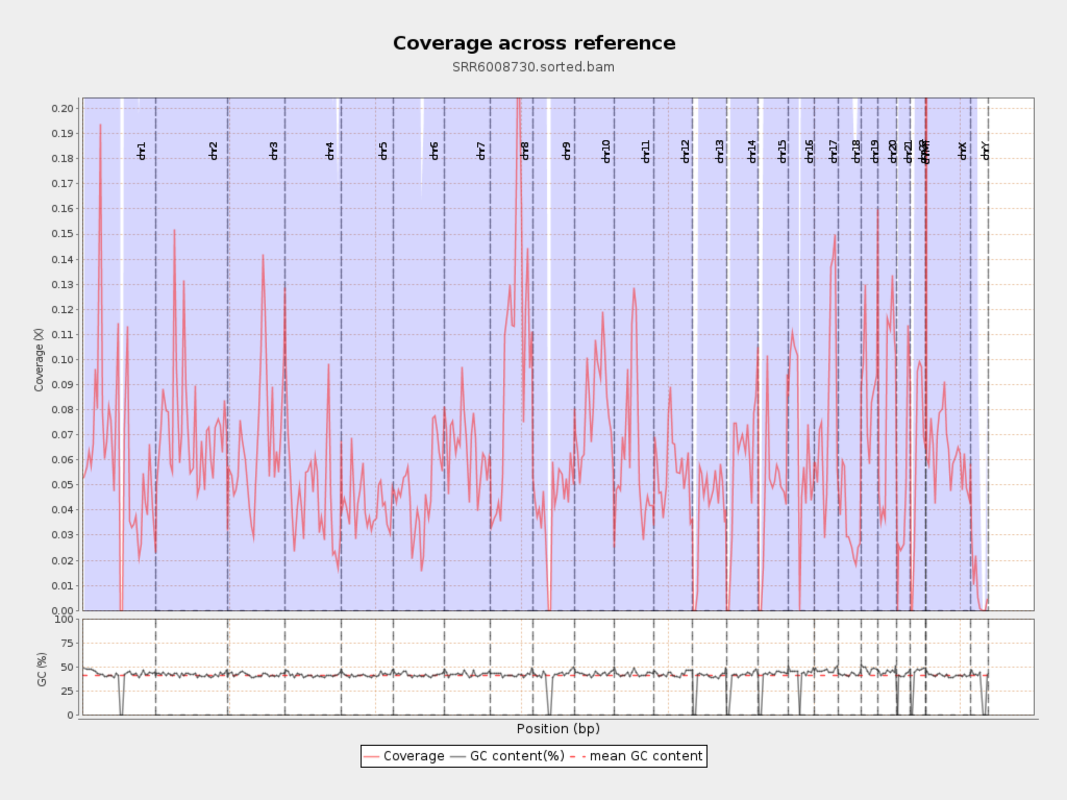
General error rate	0.85%
Mismatches	1,567,401
Insertions	13,698
Mapped reads with at least one insertion	0.46%
Deletions	63,596
Mapped reads with at least one deletion	2.15%
Homopolymer indels	44.26%

2.6. Chromosome stats

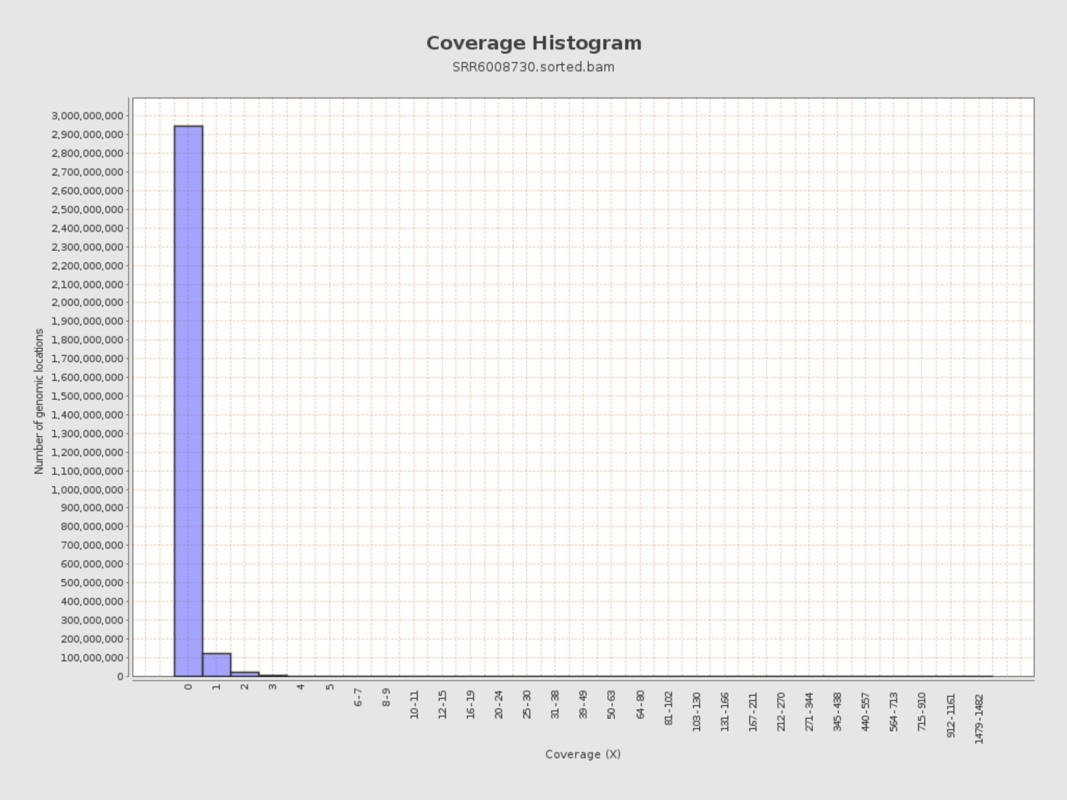
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14932693	0.0599	0.9072
chr2	243199373	17691992	0.0727	0.8122
chr3	198022430	13314731	0.0672	0.3136
chr4	191154276	8933931	0.0467	0.2756
chr5	180915260	7674813	0.0424	0.2517
chr6	171115067	8050116	0.047	0.321
chr7	159138663	10400275	0.0654	0.5508

chr8	146364022	14918773	0.1019	0.5896
chr9	141213431	5886129	0.0417	0.4168
chr10	135534747	11026363	0.0814	0.4348
chr11	135006516	8442338	0.0625	0.4722
chr12	133851895	7669096	0.0573	0.2956
chr13	115169878	4699293	0.0408	0.2419
chr14	107349540	6168086	0.0575	0.3015
chr15	102531392	4743049	0.0463	0.2814
chr16	90354753	6119735	0.0677	0.375
chr17	81195210	6786129	0.0836	0.4242
chr18	78077248	2649948	0.0339	0.6167
chr19	59128983	5391383	0.0912	0.634
chr20	63025520	5100930	0.0809	0.3554
chr21	48129895	2305340	0.0479	0.2787
chr22	51304566	3117905	0.0608	0.2974
chrMT	16571	136686	8.2485	6.5497
chrX	155270560	9767697	0.0629	0.3497
chrY	59373566	495697	0.0083	0.1837

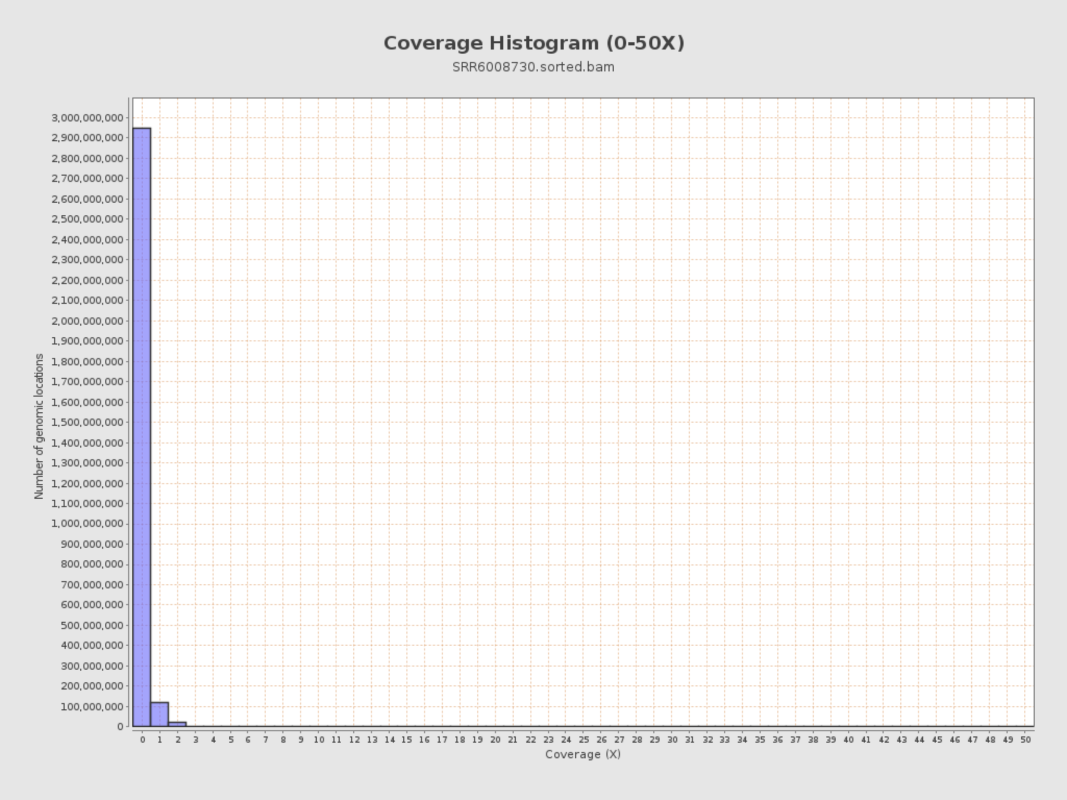
3. Results : Coverage across reference



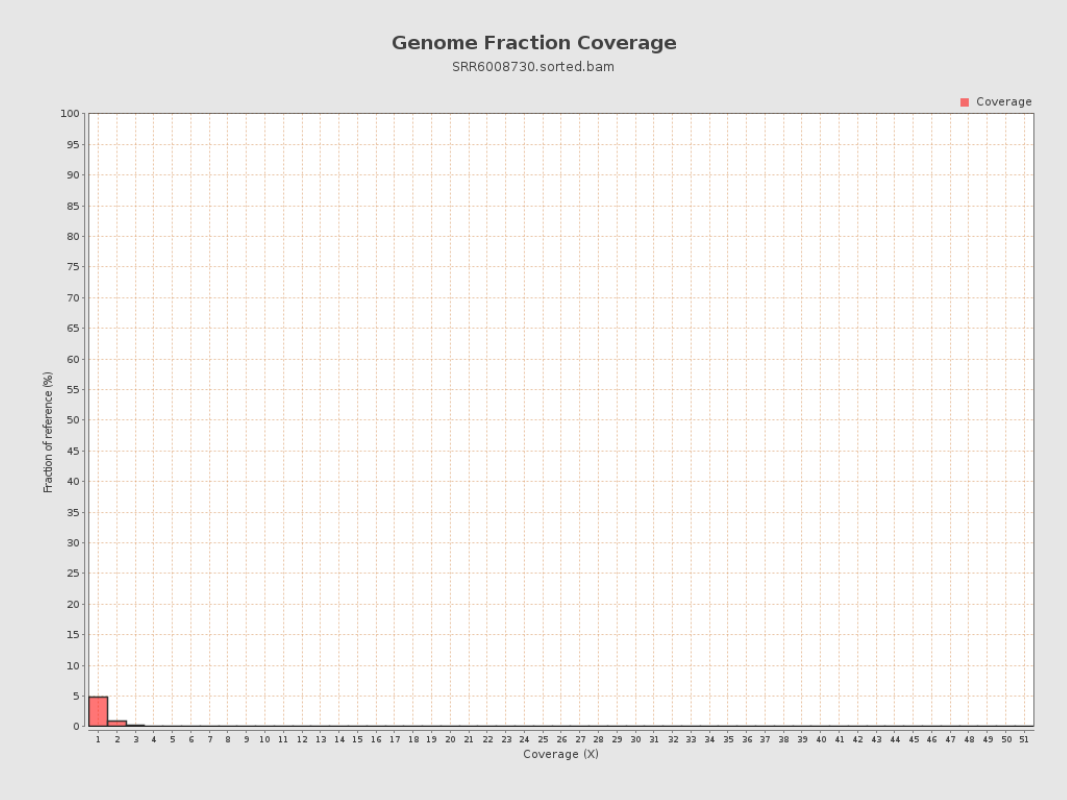
4. Results : Coverage Histogram



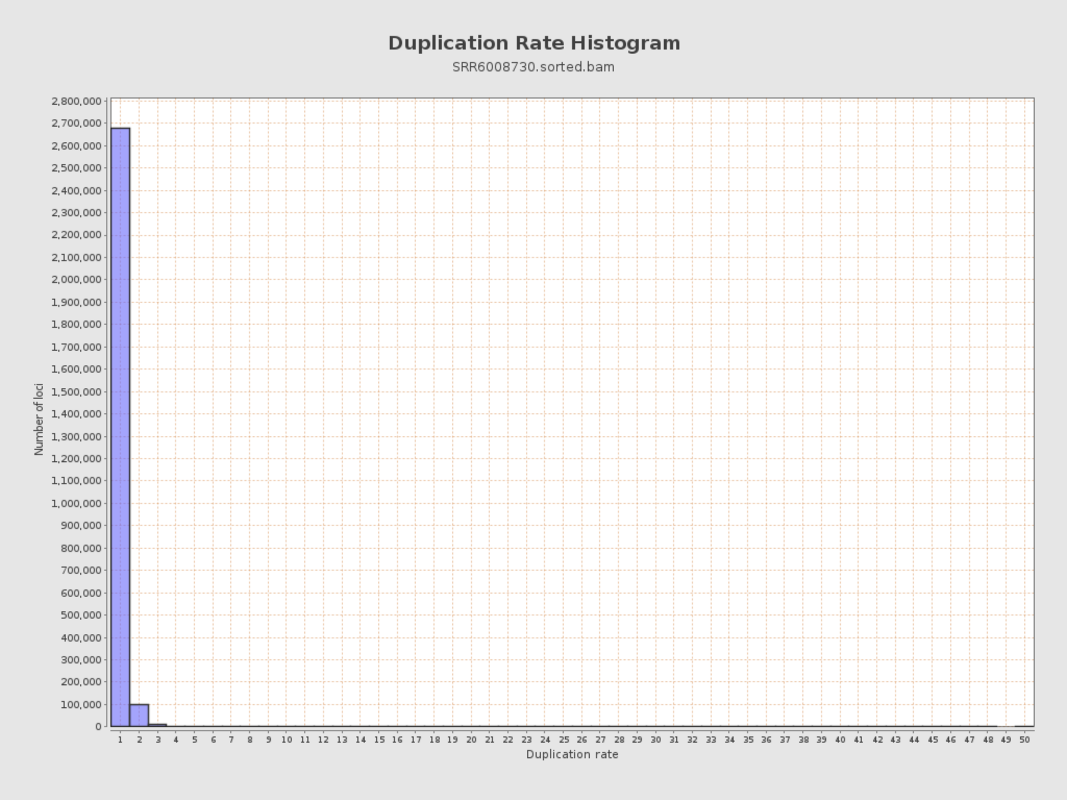
5. Results : Coverage Histogram (0-50X)



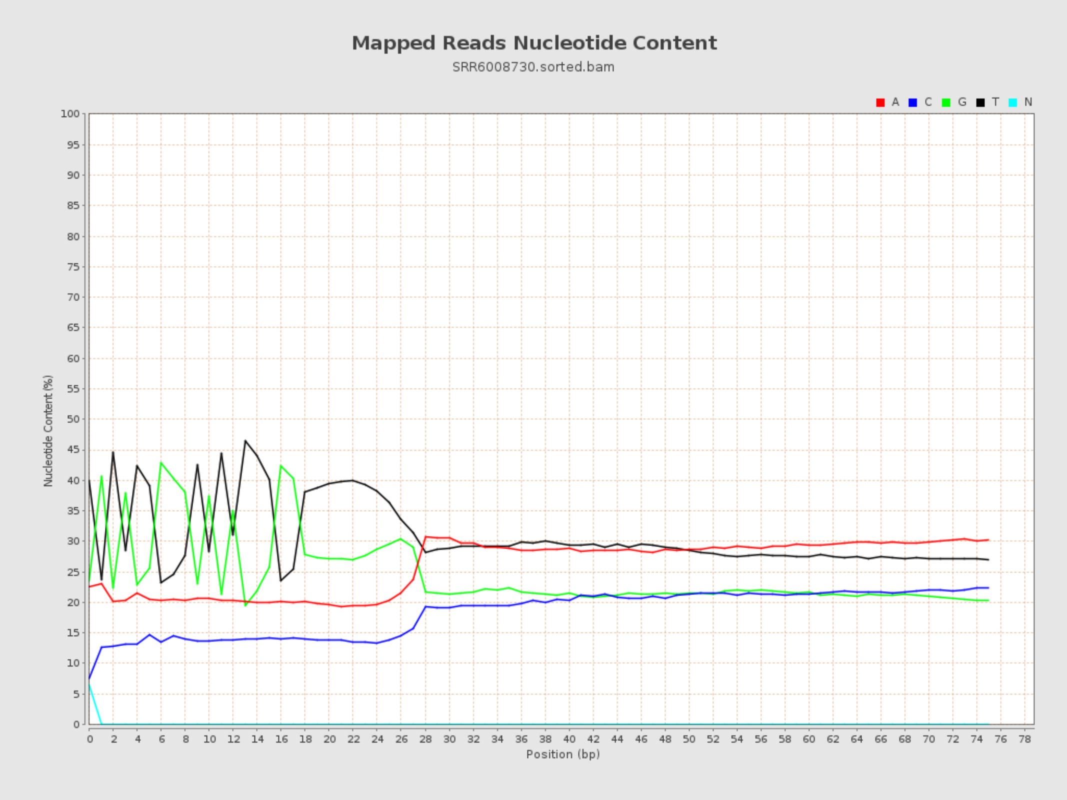
6. Results : Genome Fraction Coverage



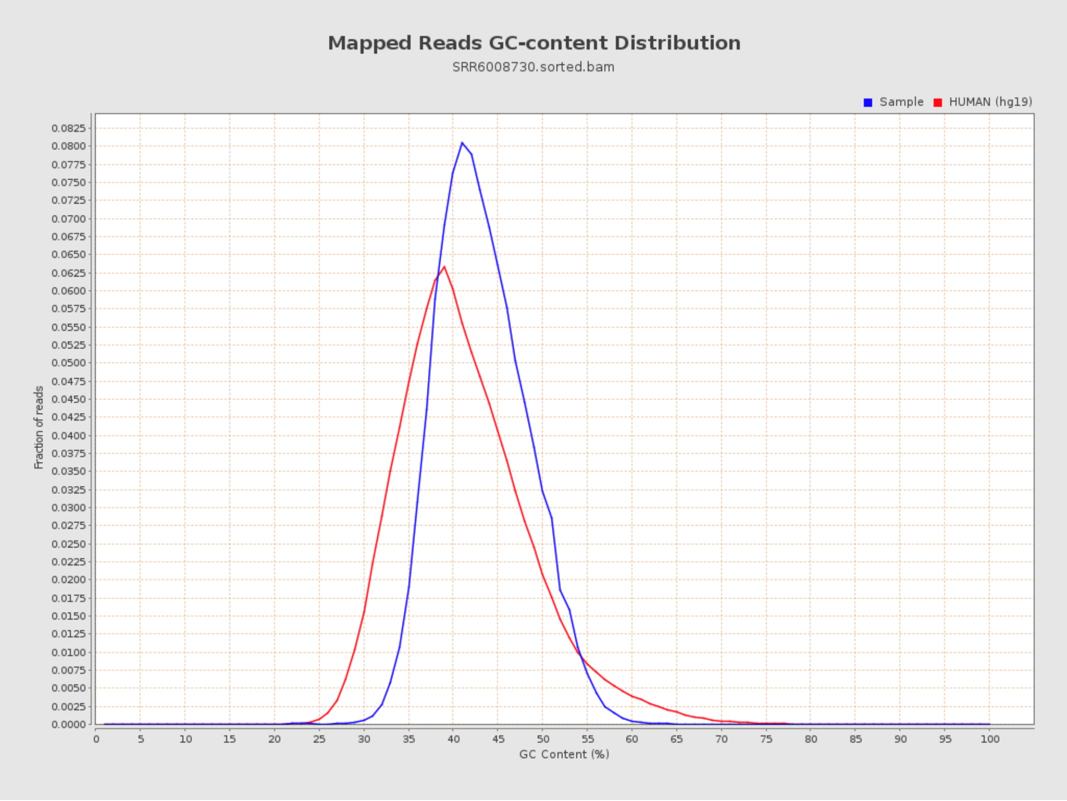
7. Results : Duplication Rate Histogram



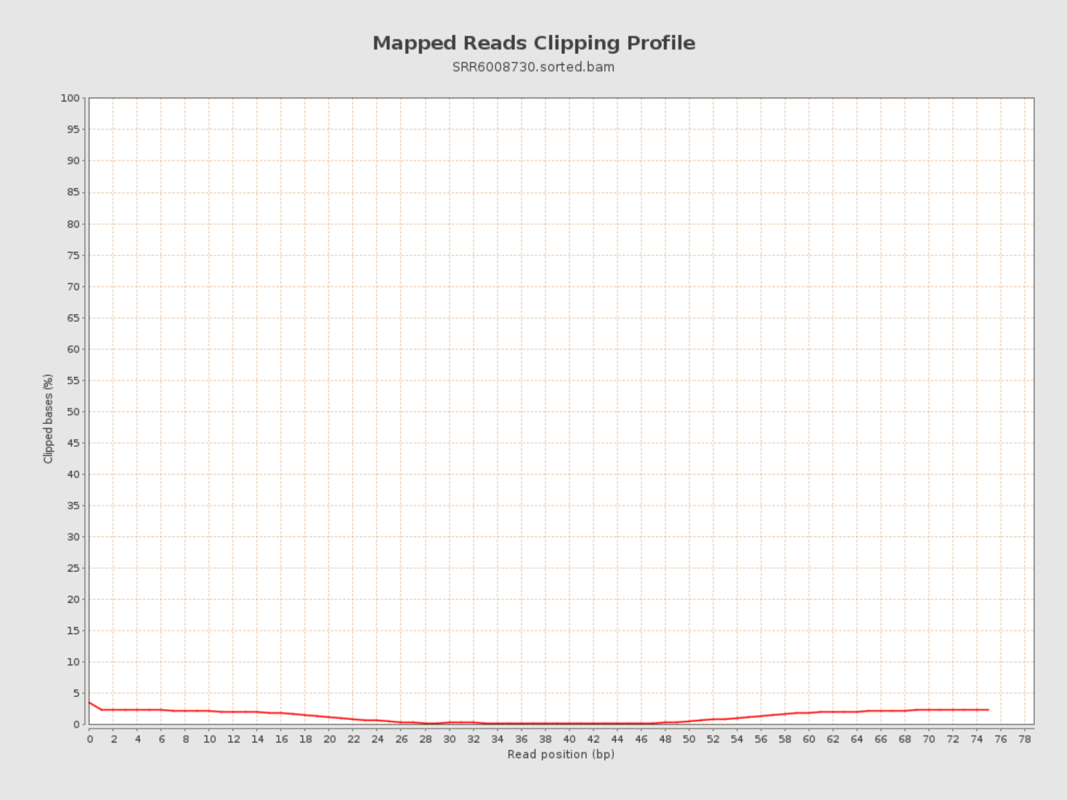
8. Results : Mapped Reads Nucleotide Content



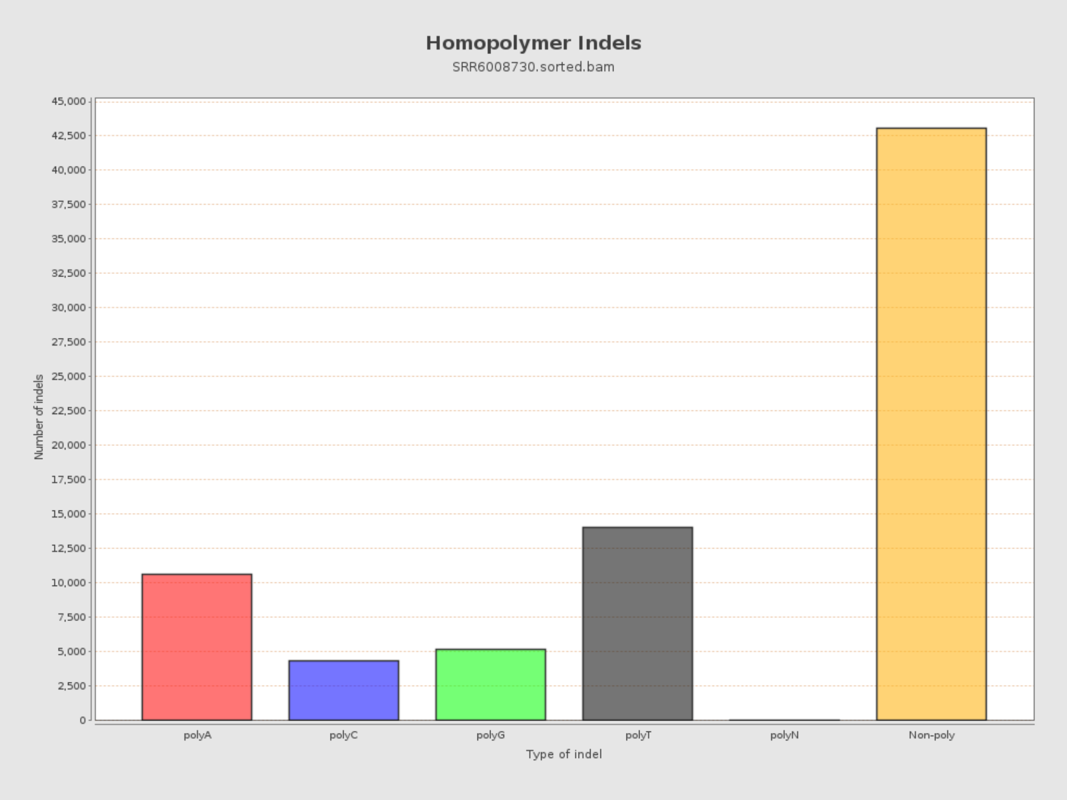
9. Results : Mapped Reads GC-content Distribution



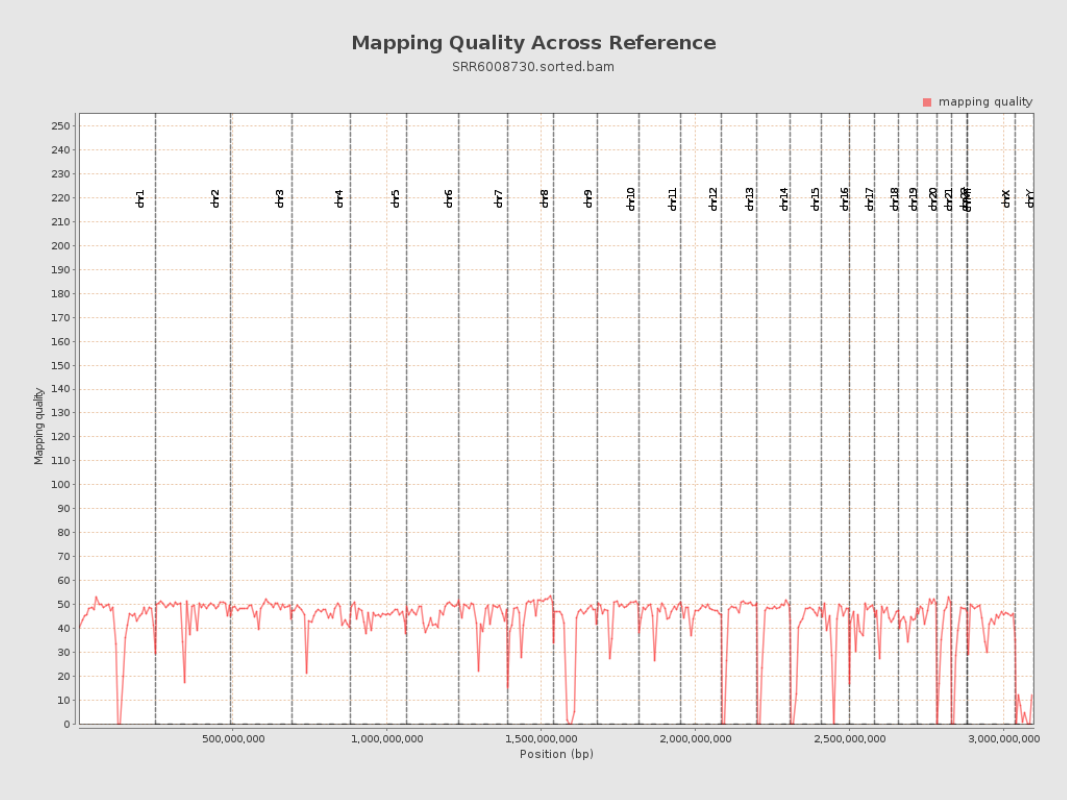
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram