Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 06:17:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548990.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_SRR1548990 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548990.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 06:17:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548990.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,910,411
Mapped reads	5,107,818 / 86.42%
Unmapped reads	802,593 / 13.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	307,537 / 5.2%
Duplication rate	5.36%
Clipped reads	237,331 / 4.02%

2.2. ACGT Content

Number/percentage of A's	61,753,961 / 30.44%
Number/percentage of C's	39,872,226 / 19.65%
Number/percentage of T's	60,442,950 / 29.79%
Number/percentage of G's	40,822,924 / 20.12%
Number/percentage of N's	1,705 / 0%
GC Percentage	39.77%

2.3. Coverage

Mean	0.0655
Standard Deviation	0.5118

2.4. Mapping Quality

Mean Mapping Quality	44.77

2.5. Mismatches and indels

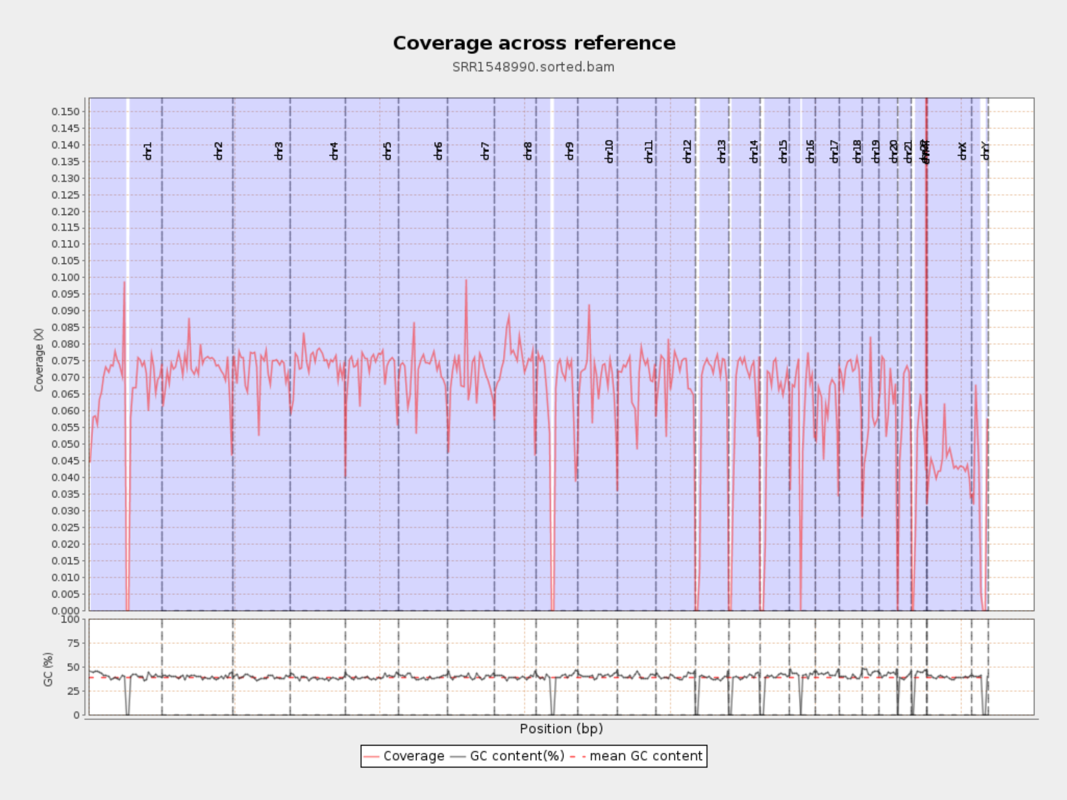
General error rate	0.31%
Mismatches	621,673
Insertions	5,712
Mapped reads with at least one insertion	0.11%
Deletions	16,857
Mapped reads with at least one deletion	0.33%
Homopolymer indels	44.32%

2.6. Chromosome stats

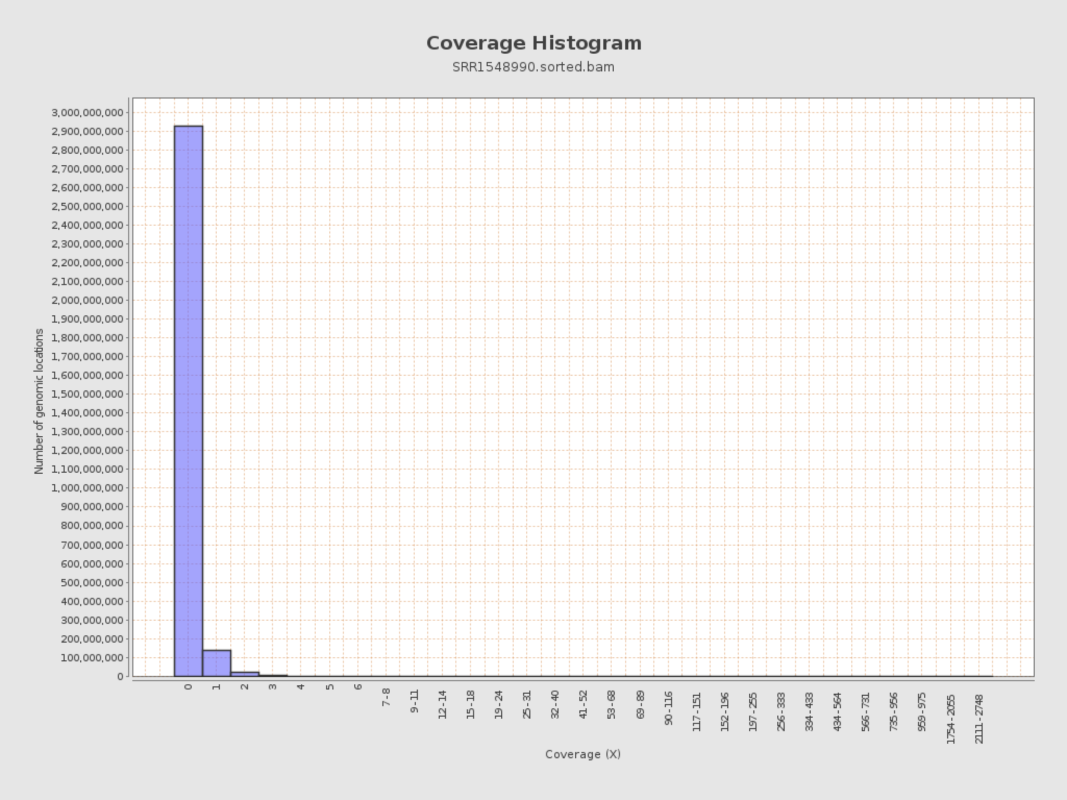
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16251724	0.0652	0.7612
chr2	243199373	17693578	0.0728	0.3988
chr3	198022430	14430694	0.0729	0.3157
chr4	191154276	14192151	0.0742	0.3366
chr5	180915260	13208911	0.073	0.3196
chr6	171115067	12311689	0.0719	0.3573
chr7	159138663	11330200	0.0712	0.5624
chr8	146364022	10900795	0.0745	1.3828

chr9	141213431	8640395	0.0612	0.3725
chr10	135534747	9538696	0.0704	0.4038
chr11	135006516	9430474	0.0699	0.3927
chr12	133851895	9412288	0.0703	0.3196
chr13	115169878	6998970	0.0608	0.2859
chr14	107349540	6364180	0.0593	0.3393
chr15	102531392	5773630	0.0563	0.2753
chr16	90354753	5377548	0.0595	0.3089
chr17	81195210	4817699	0.0593	0.3063
chr18	78077248	5606287	0.0718	0.7014
chr19	59128983	3317705	0.0561	0.5941
chr20	63025520	4069801	0.0646	0.3071
chr21	48129895	2682748	0.0557	0.3222
chr22	51304566	1995377	0.0389	0.243
chrMT	16571	13463	0.8124	1.3933
chrX	155270560	6782583	0.0437	0.2946
chrY	59373566	1773933	0.0299	0.336

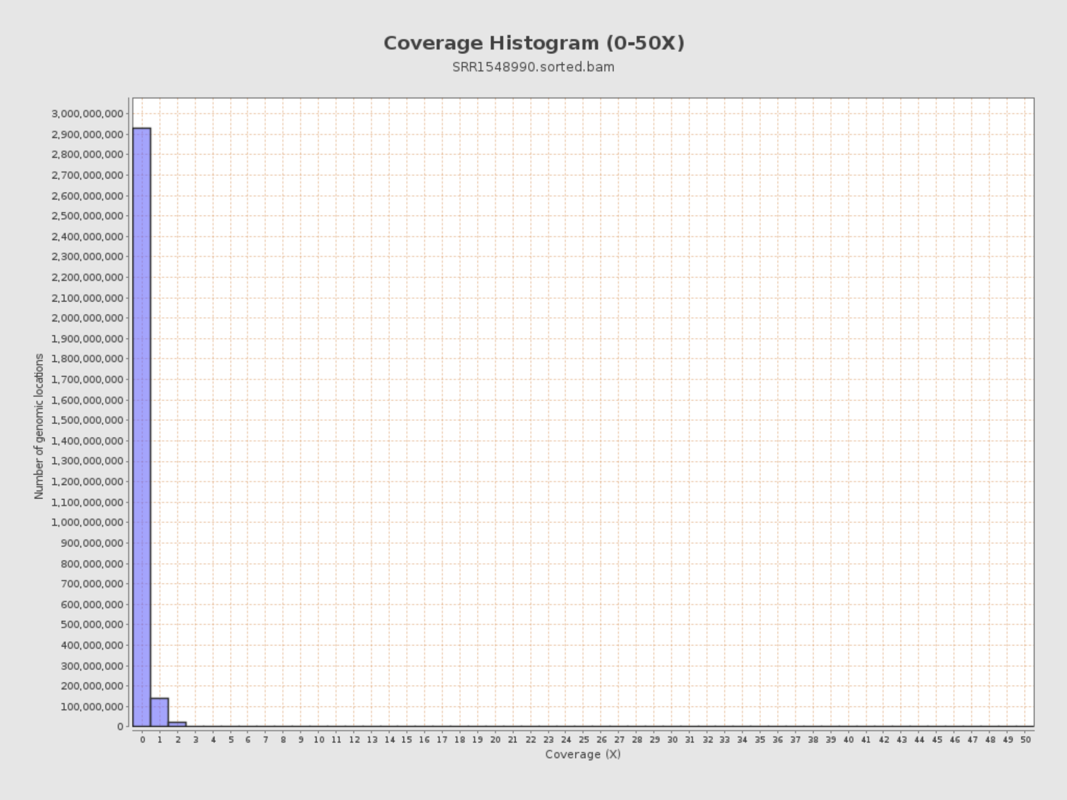
3. Results : Coverage across reference



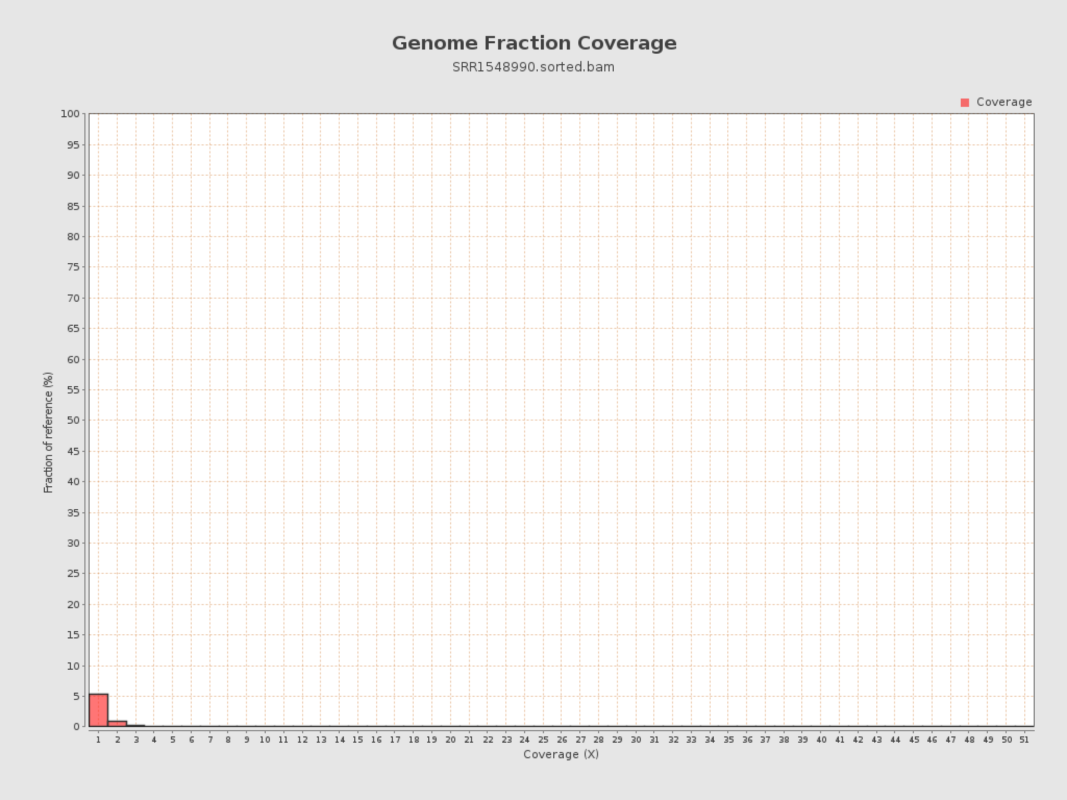
4. Results : Coverage Histogram



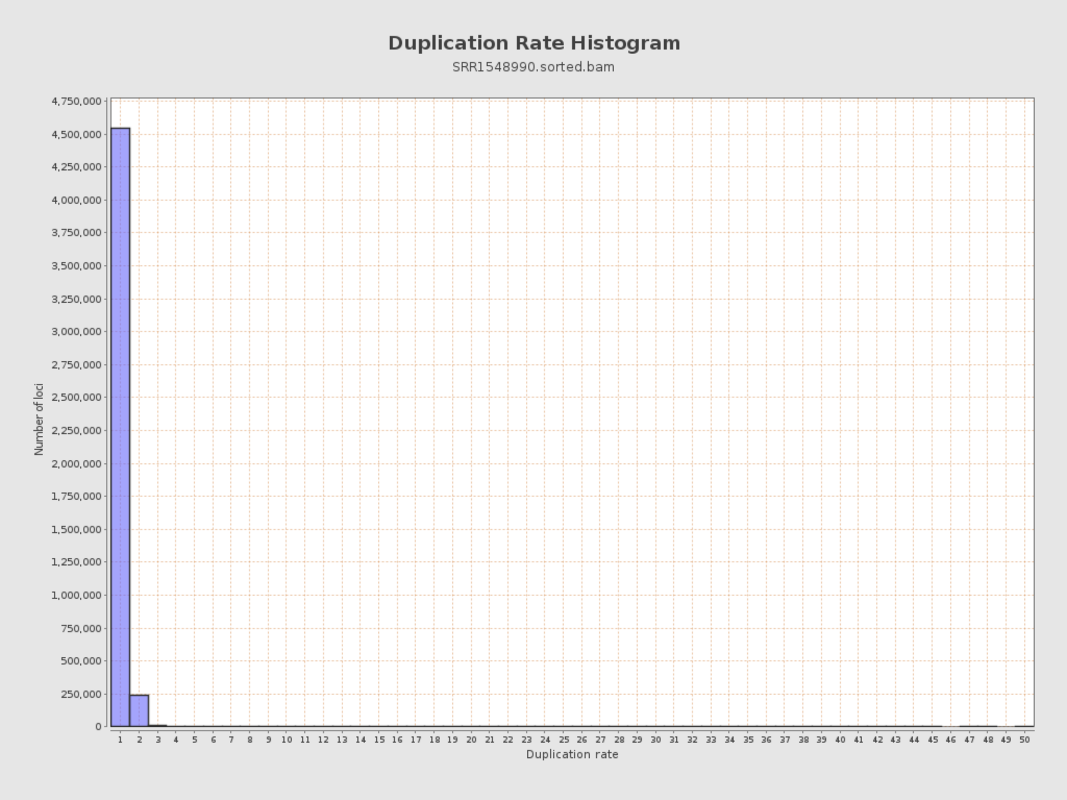
5. Results : Coverage Histogram (0-50X)



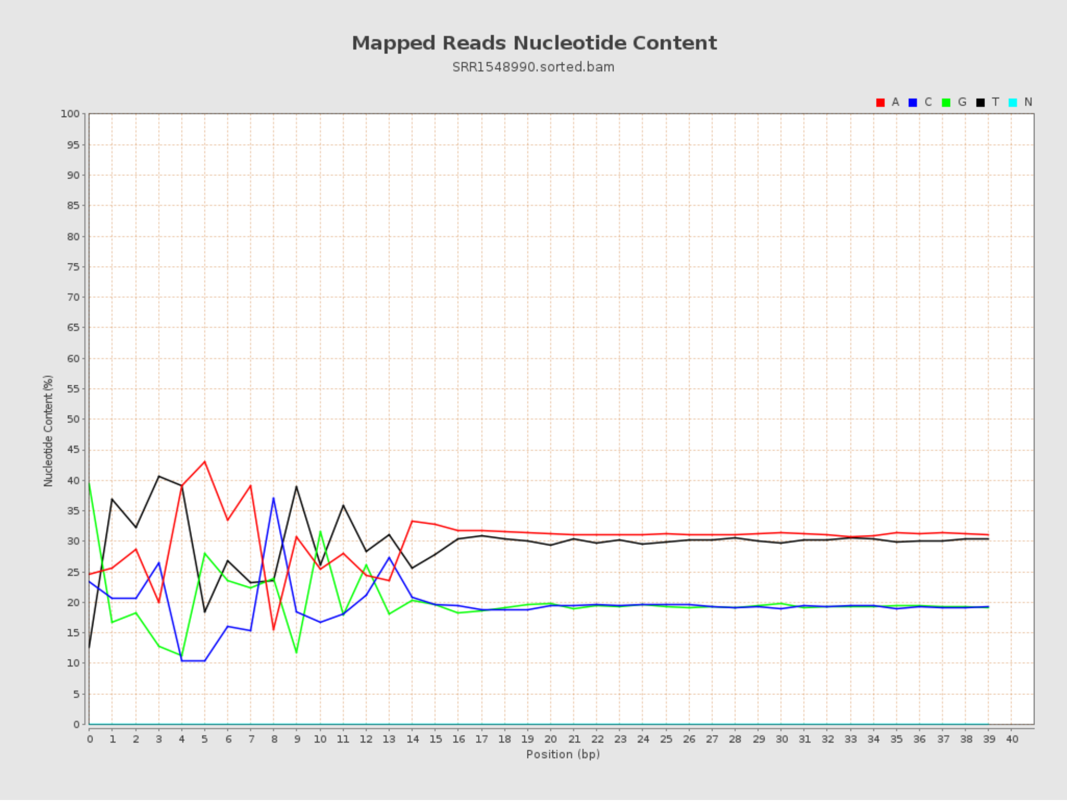
6. Results : Genome Fraction Coverage



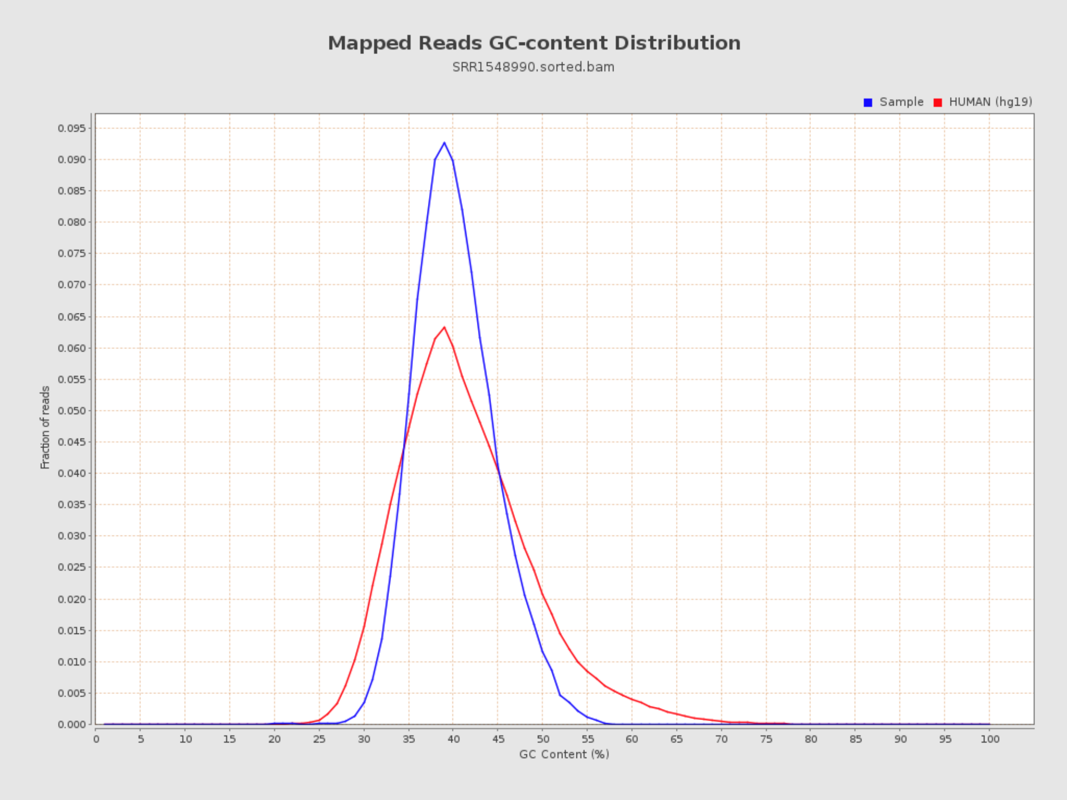
7. Results : Duplication Rate Histogram



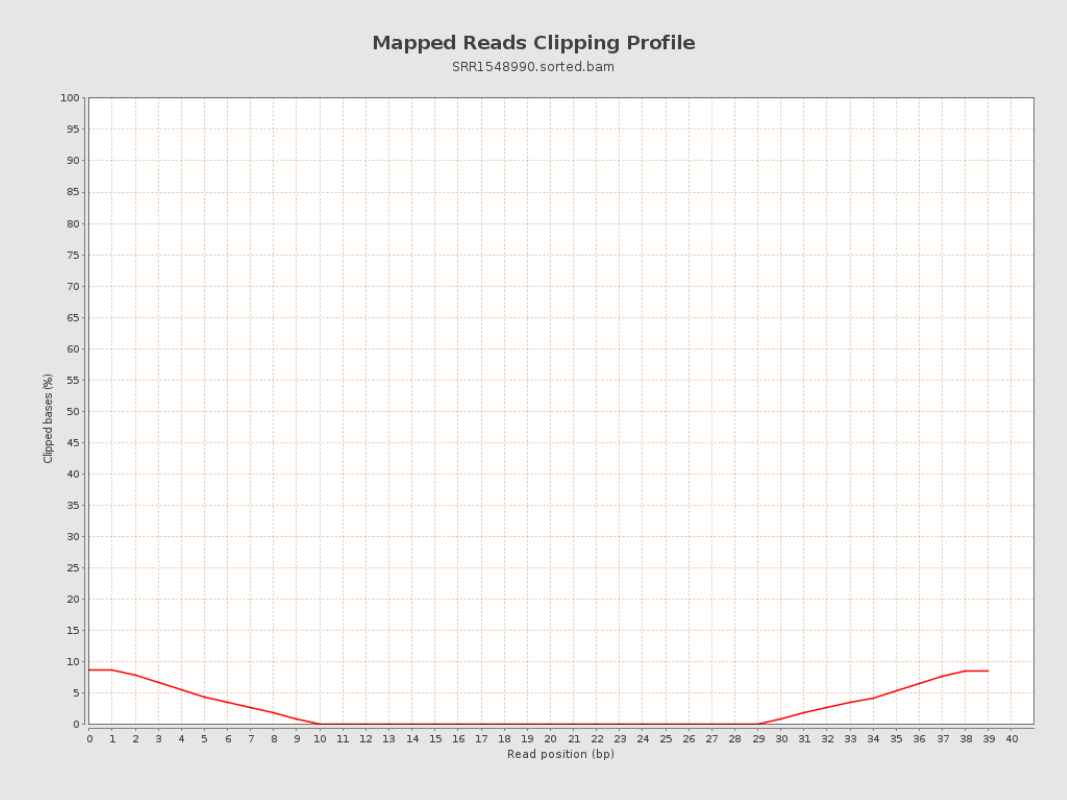
8. Results : Mapped Reads Nucleotide Content



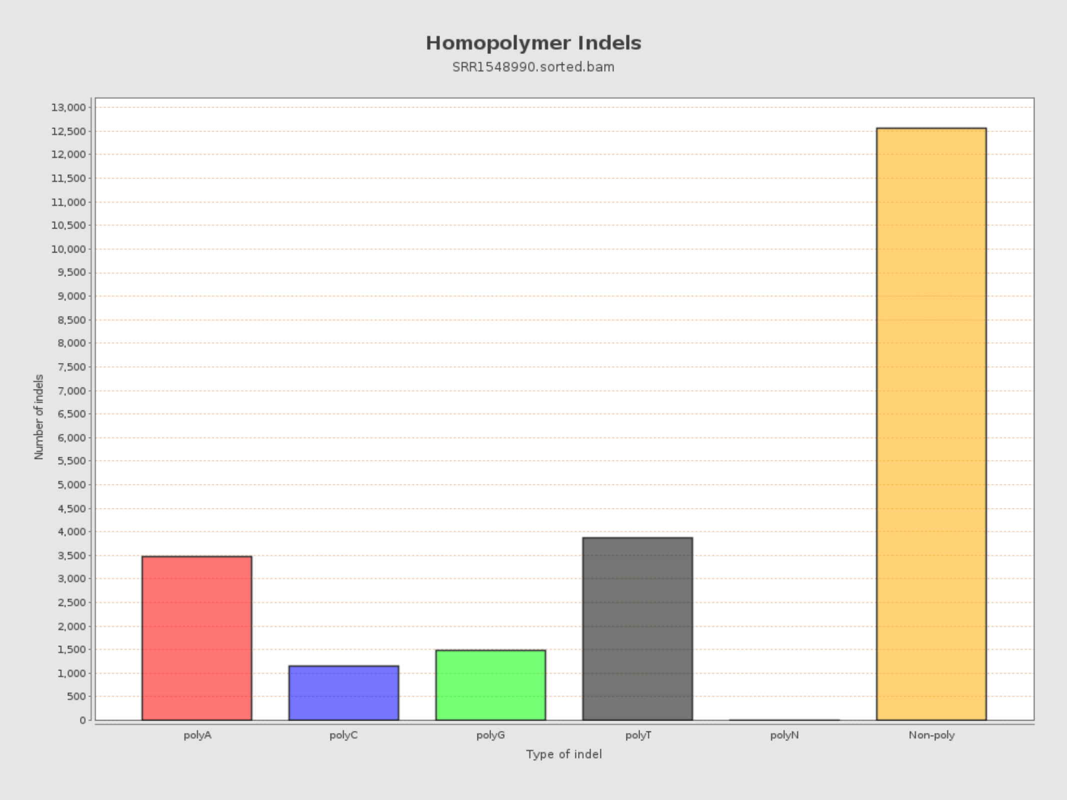
9. Results : Mapped Reads GC-content Distribution



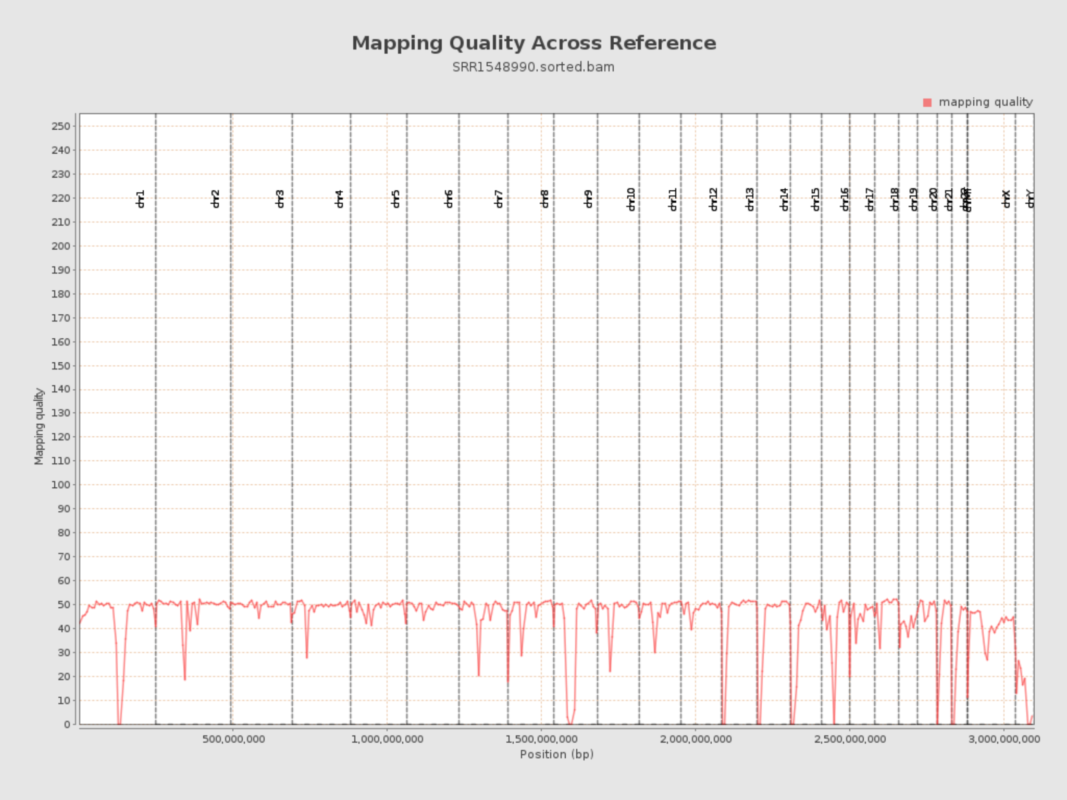
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram