Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 06:51:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548993.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_SRR1548993 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548993.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 06:51:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548993.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,712,624
Mapped reads	7,545,429 / 86.6%
Unmapped reads	1,167,195 / 13.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	634,045 / 7.28%
Duplication rate	7.65%
Clipped reads	402,625 / 4.62%

2.2. ACGT Content

Number/percentage of A's	89,902,225 / 30.03%
Number/percentage of C's	59,275,692 / 19.8%
Number/percentage of T's	90,243,281 / 30.14%
Number/percentage of G's	59,958,521 / 20.03%
Number/percentage of N's	2,917 / 0%
GC Percentage	39.83%

2.3. Coverage

Mean	0.0967
Standard Deviation	0.7759

2.4. Mapping Quality

Mean Mapping Quality	44.03

2.5. Mismatches and indels

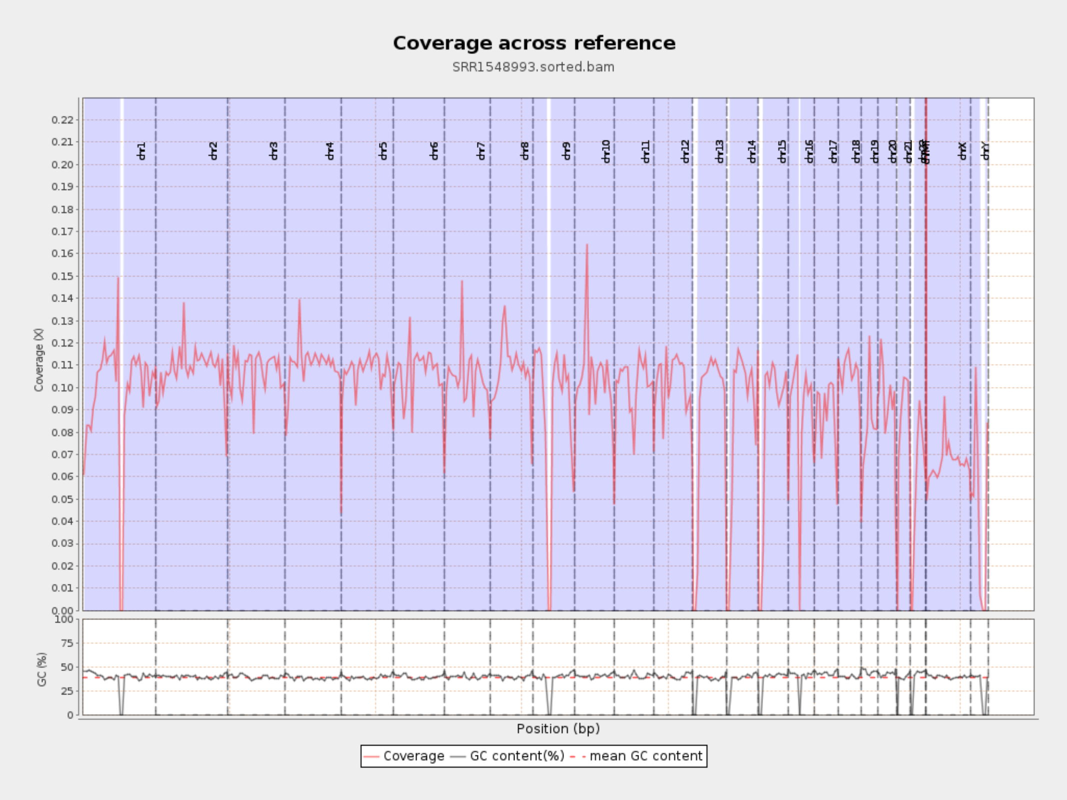
General error rate	0.3%
Mismatches	880,383
Insertions	9,306
Mapped reads with at least one insertion	0.12%
Deletions	24,792
Mapped reads with at least one deletion	0.33%
Homopolymer indels	43.16%

2.6. Chromosome stats

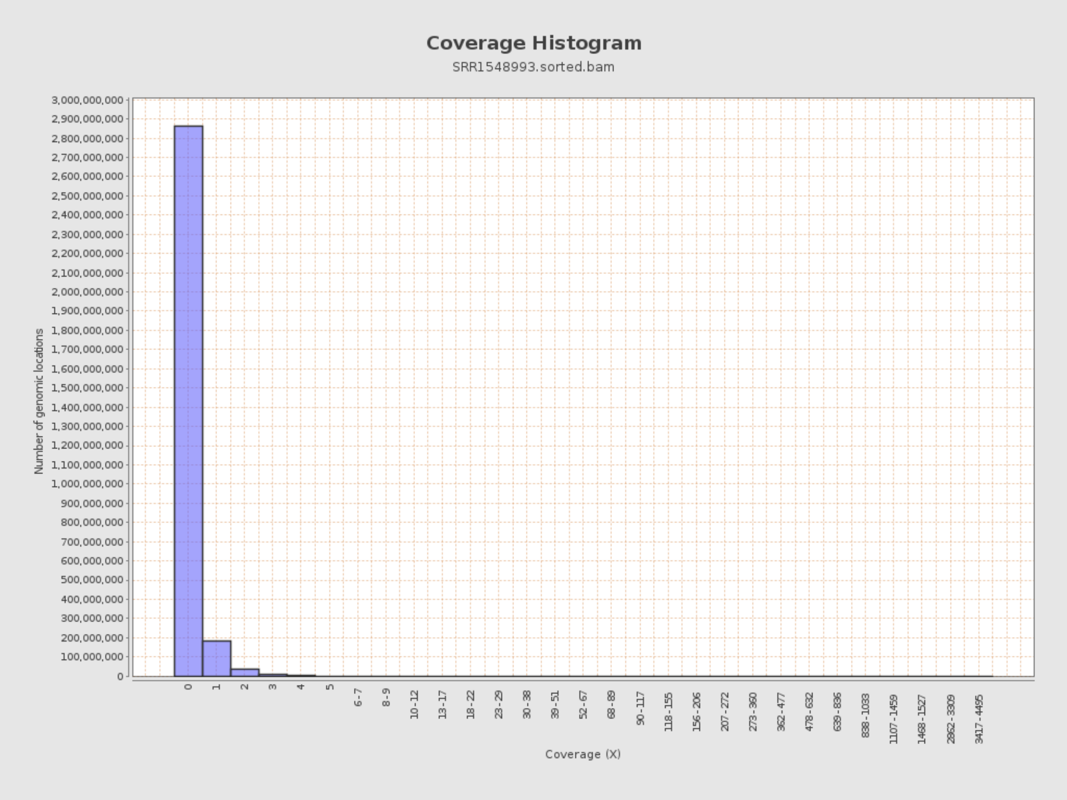
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24293826	0.0975	1.1954
chr2	243199373	26353825	0.1084	0.5823
chr3	198022430	21297174	0.1075	0.4019
chr4	191154276	21122819	0.1105	0.4553
chr5	180915260	19298391	0.1067	0.407
chr6	171115067	18341396	0.1072	0.4772
chr7	159138663	16502012	0.1037	0.8041
chr8	146364022	15772130	0.1078	2.2366

chr9	141213431	12773603	0.0905	0.5248
chr10	135534747	14274113	0.1053	0.641
chr11	135006516	13658474	0.1012	0.5188
chr12	133851895	13730082	0.1026	0.4127
chr13	115169878	10097333	0.0877	0.3586
chr14	107349540	9340122	0.087	0.4477
chr15	102531392	8445106	0.0824	0.3467
chr16	90354753	7787535	0.0862	0.4069
chr17	81195210	7163453	0.0882	0.3987
chr18	78077248	8376931	0.1073	1.1167
chr19	59128983	4903292	0.0829	0.9478
chr20	63025520	6009540	0.0954	0.4074
chr21	48129895	3936669	0.0818	0.4411
chr22	51304566	2889669	0.0563	0.3237
chrMT	16571	11627	0.7016	1.2212
chrX	155270560	10296817	0.0663	0.4311
chrY	59373566	2738688	0.0461	0.4841

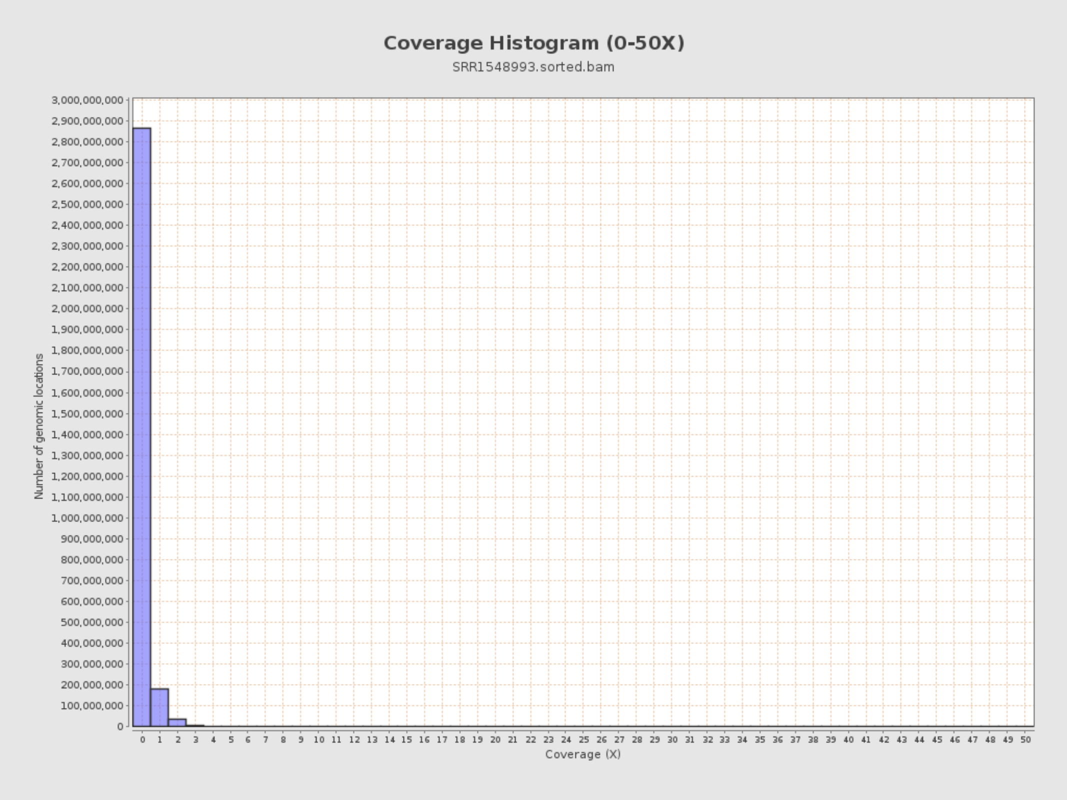
3. Results : Coverage across reference



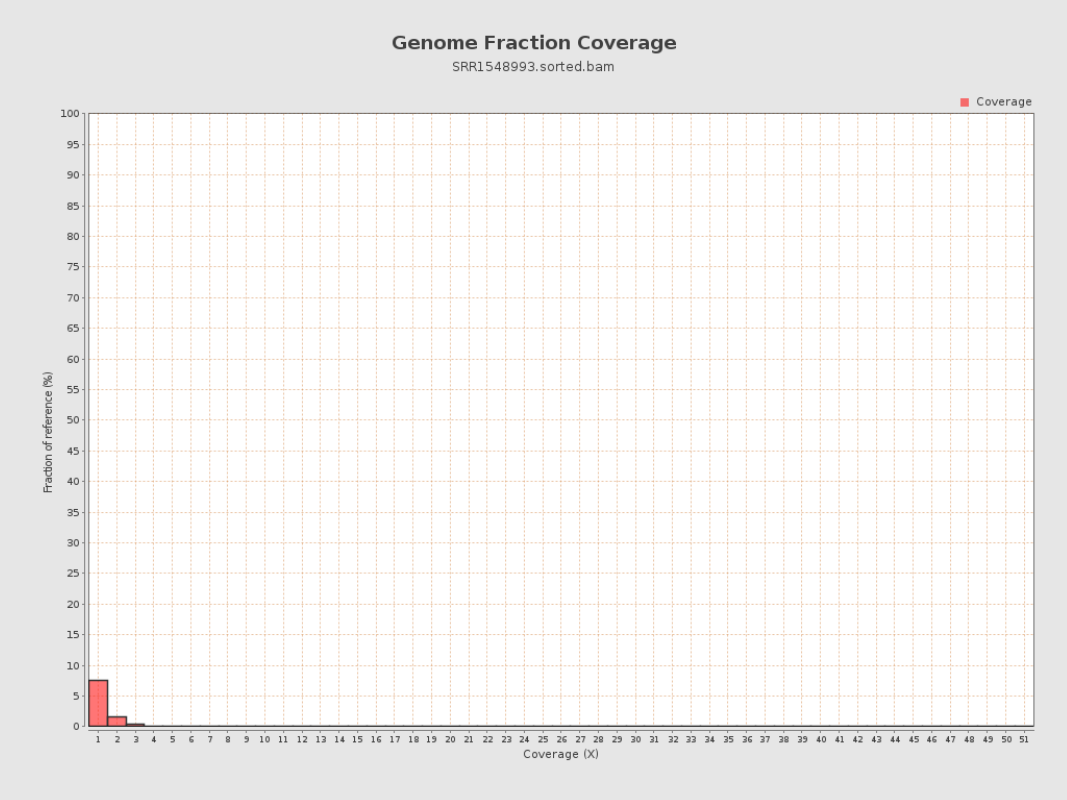
4. Results : Coverage Histogram



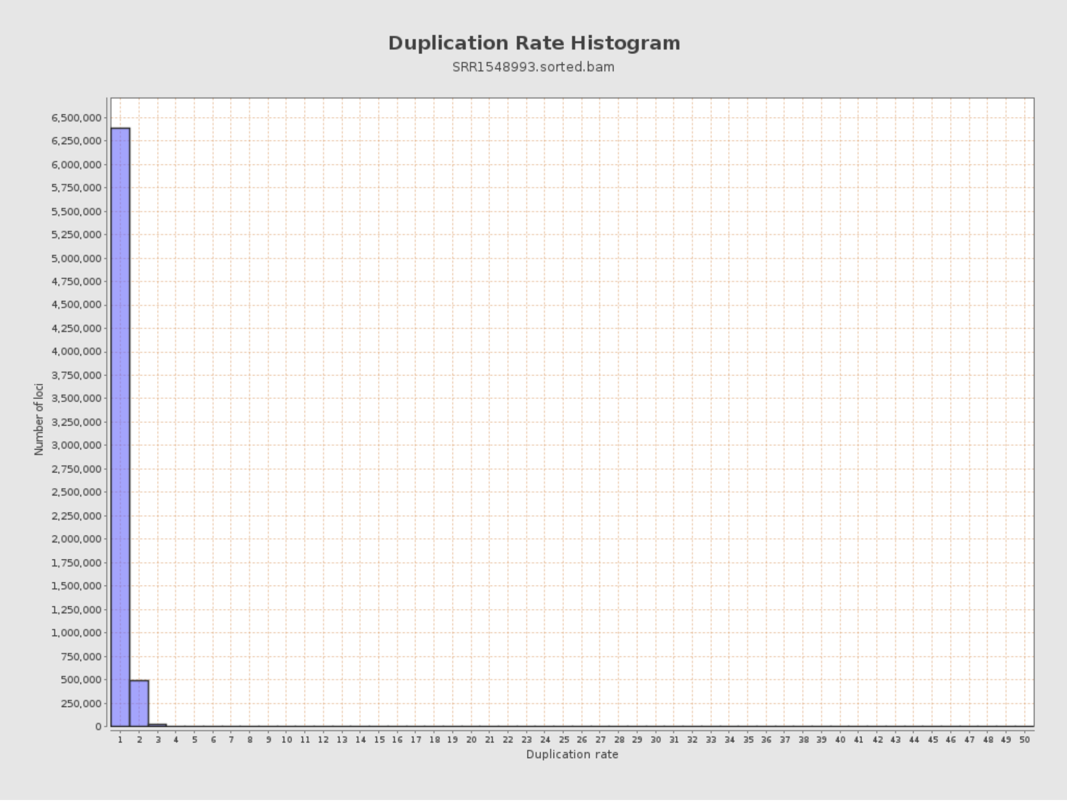
5. Results : Coverage Histogram (0-50X)



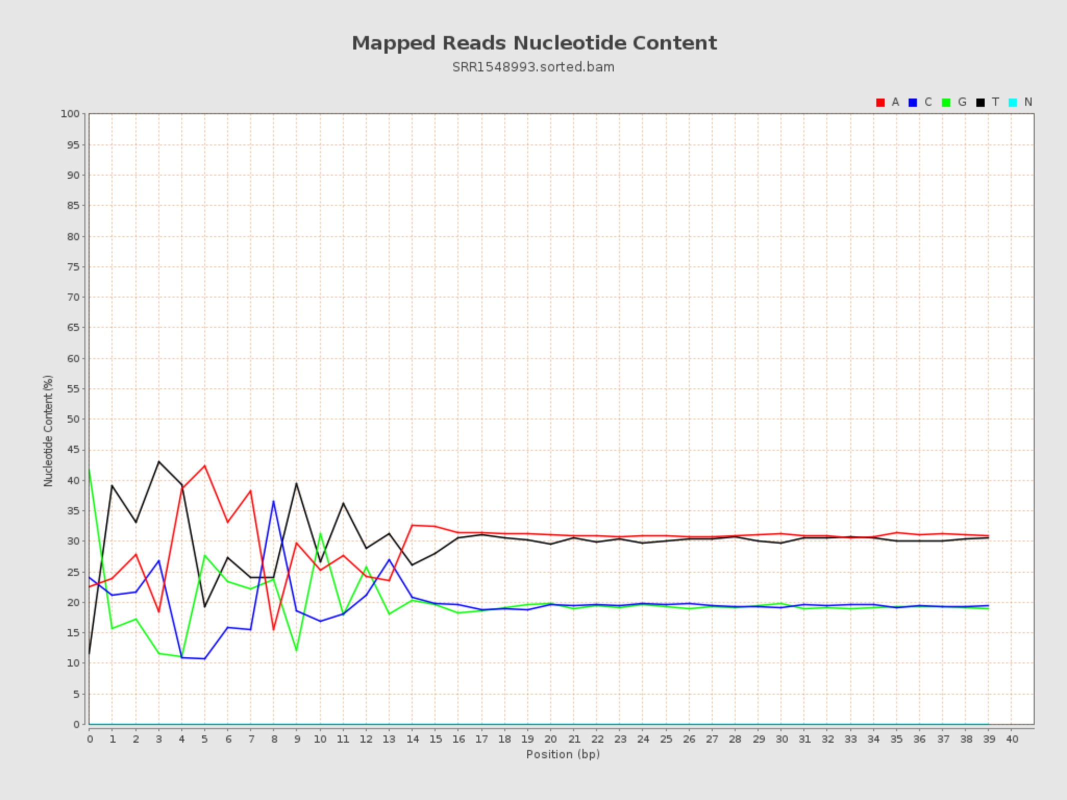
6. Results : Genome Fraction Coverage



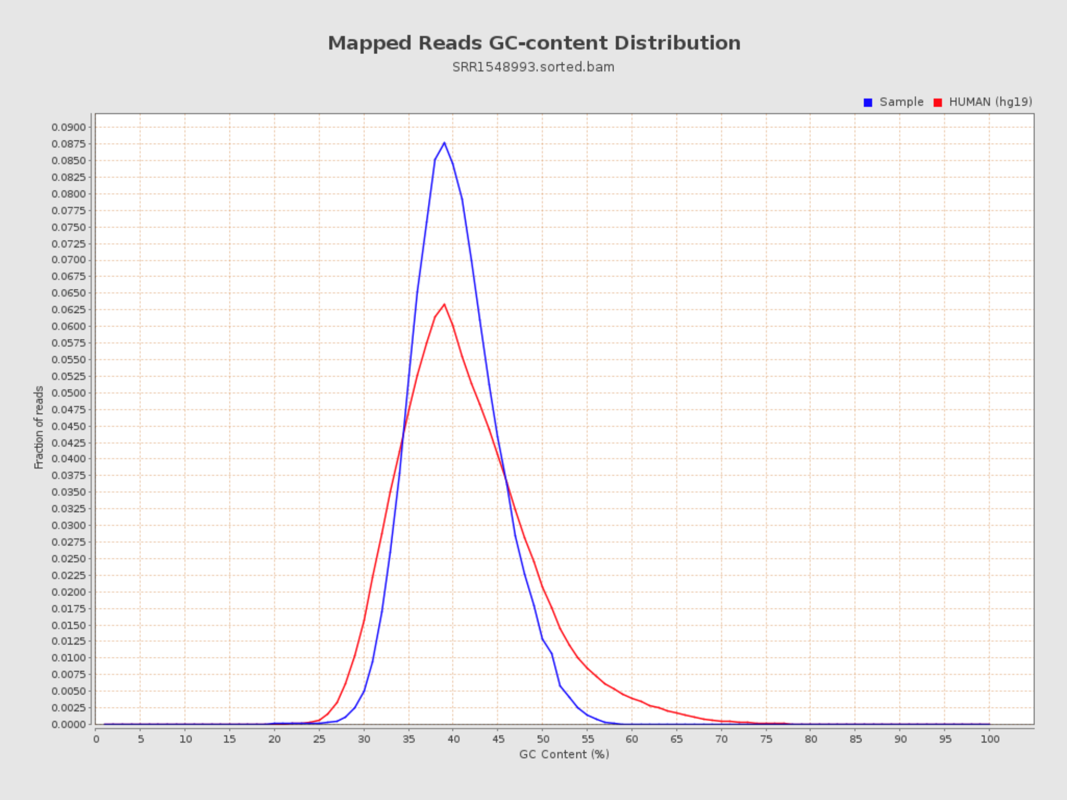
7. Results : Duplication Rate Histogram



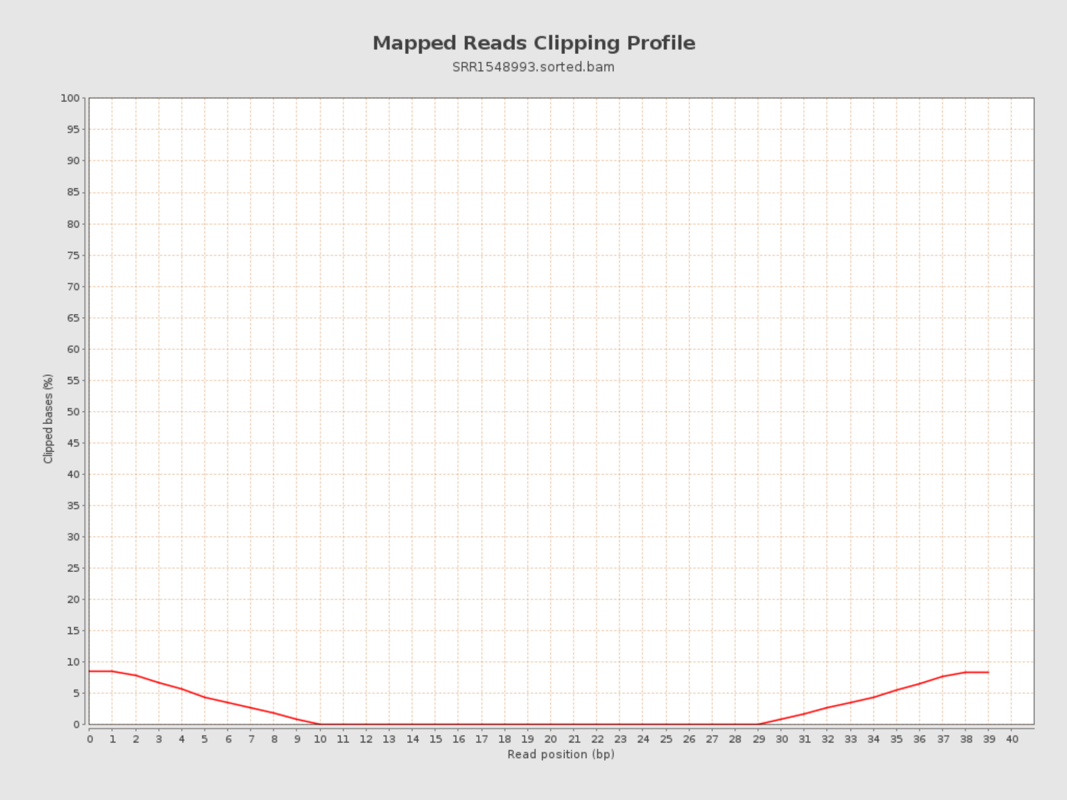
8. Results : Mapped Reads Nucleotide Content



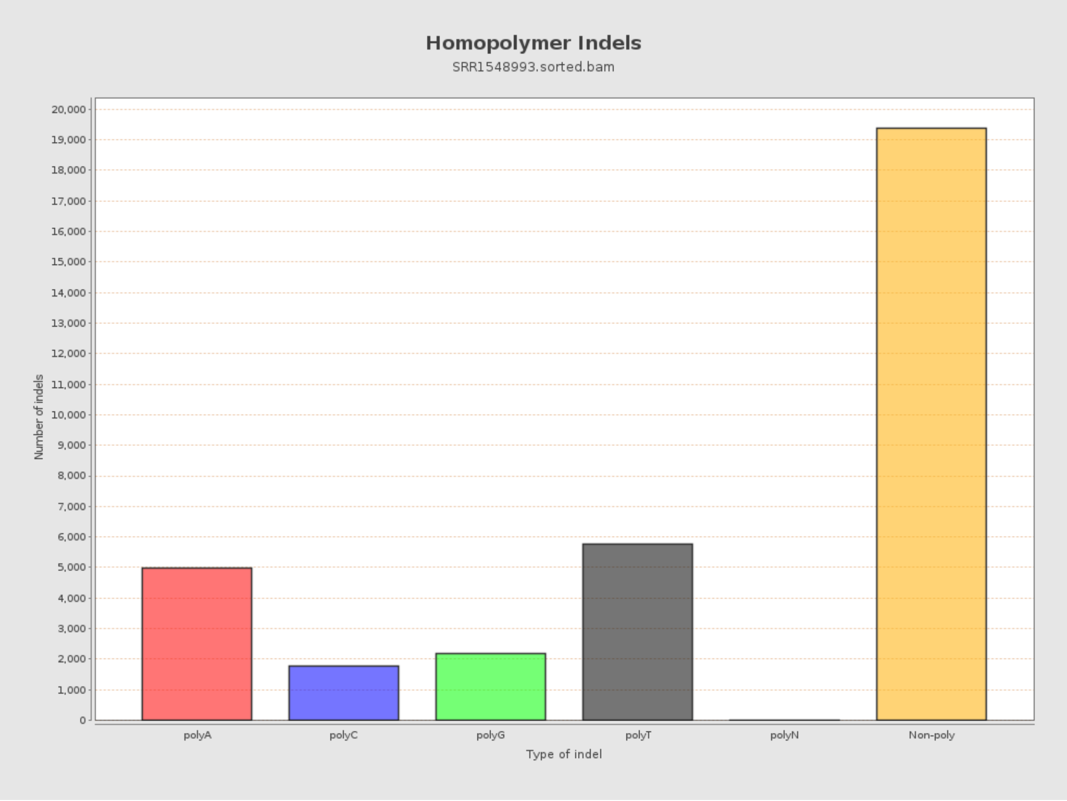
9. Results : Mapped Reads GC-content Distribution



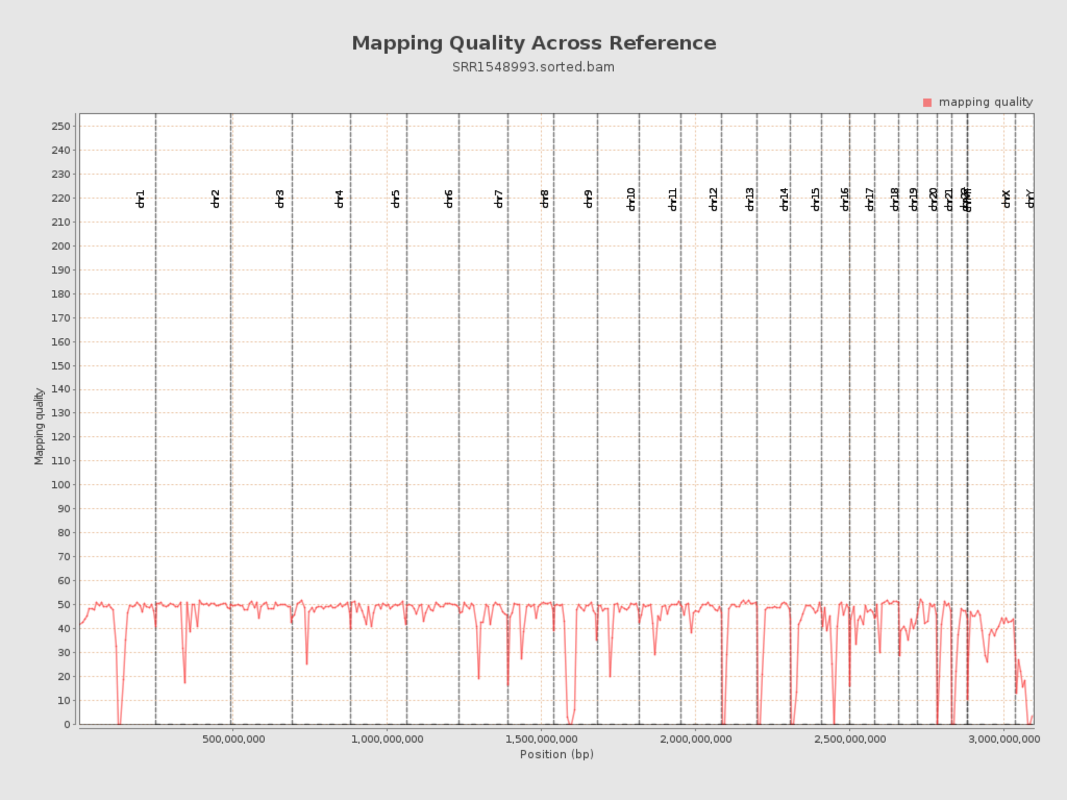
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram