Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 16:17:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548949.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_SRR1548949 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548949.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 16:17:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548949.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,679,862
Mapped reads	6,528,123 / 85%
Unmapped reads	1,151,739 / 15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	341,466 / 4.45%
Duplication rate	3.06%
Clipped reads	625,490 / 8.14%

2.2. ACGT Content

Number/percentage of A's	71,329,936 / 27.69%
Number/percentage of C's	56,769,852 / 22.04%
Number/percentage of T's	72,840,873 / 28.28%
Number/percentage of G's	56,651,957 / 21.99%
Number/percentage of N's	364 / 0%
GC Percentage	44.03%

2.3. Coverage

Mean	0.0832
Standard Deviation	0.9187

2.4. Mapping Quality

Mean Mapping Quality	34

2.5. Mismatches and indels

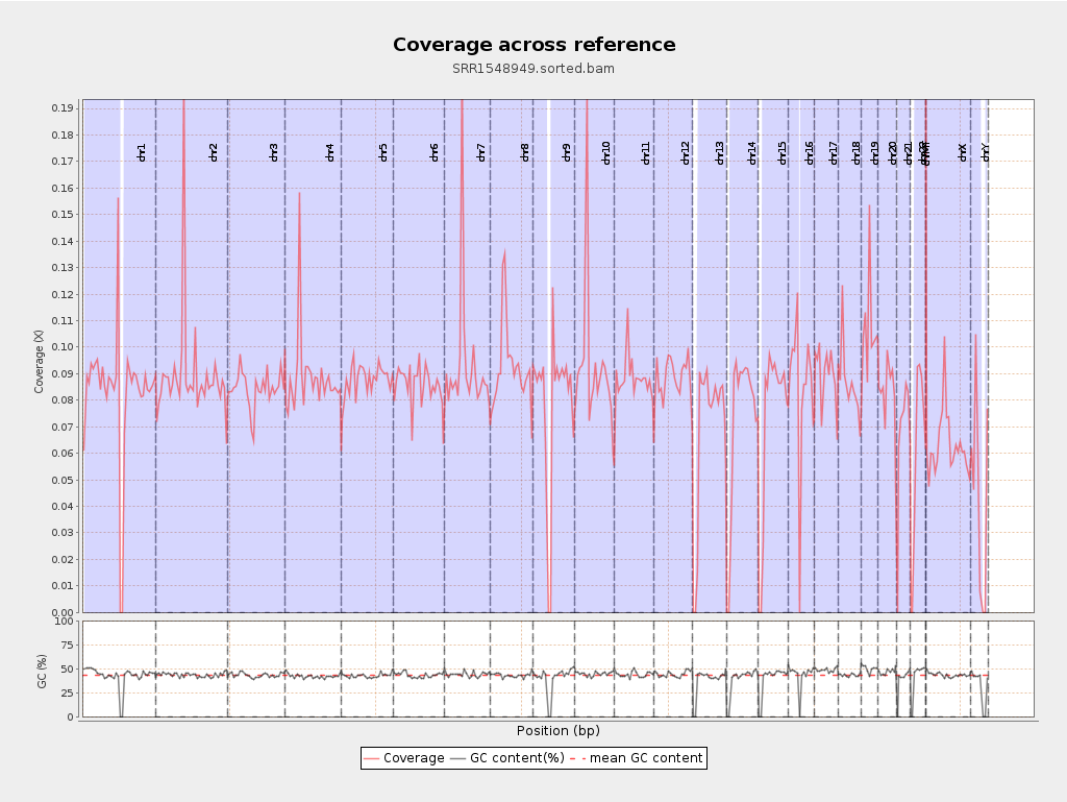
General error rate	0.35%
Mismatches	901,187
Insertions	9,696
Mapped reads with at least one insertion	0.15%
Deletions	18,904
Mapped reads with at least one deletion	0.29%
Homopolymer indels	37.45%

2.6. Chromosome stats

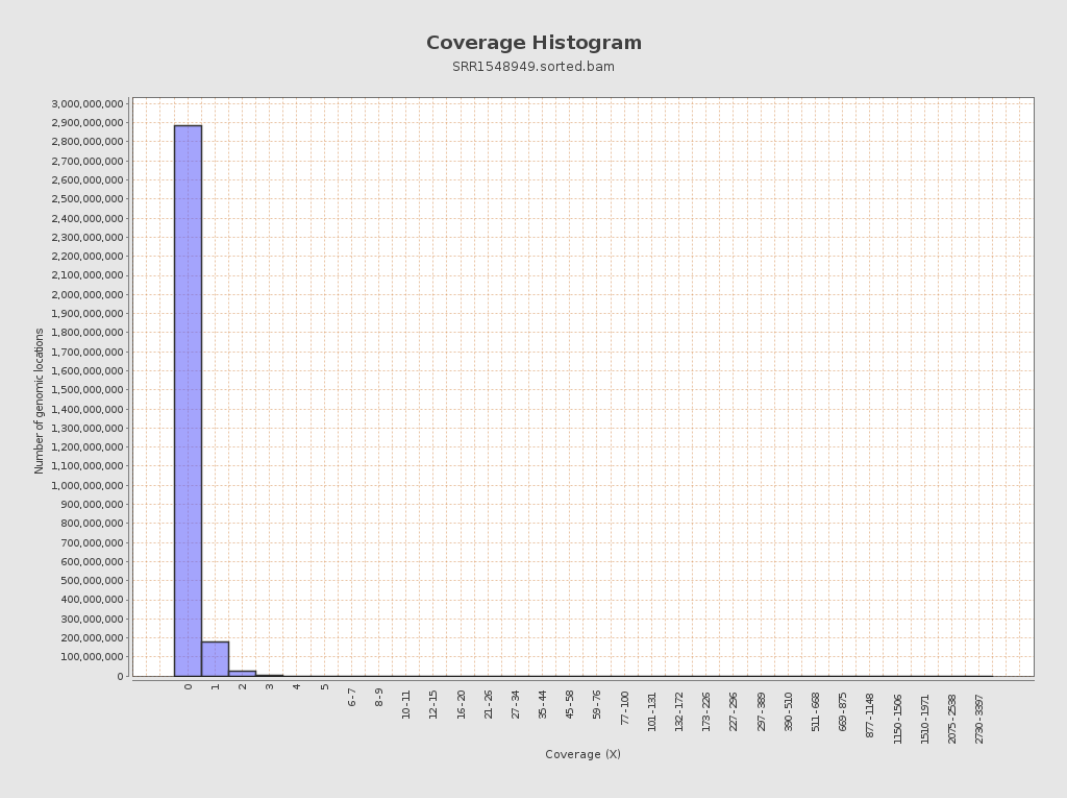
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20716821	0.0831	1.6641
chr2	243199373	21749881	0.0894	0.9541
chr3	198022430	16709748	0.0844	0.3484
chr4	191154276	16906952	0.0884	0.4591
chr5	180915260	15878879	0.0878	0.3785
chr6	171115067	14675033	0.0858	0.3768
chr7	159138663	14826268	0.0932	1.2618
chr8	146364022	13516355	0.0923	1.7551

chr9	141213431	11128063	0.0788	0.9822
chr10	135534747	12502409	0.0922	0.7875
chr11	135006516	11858954	0.0878	0.6038
chr12	133851895	11907605	0.089	0.3982
chr13	115169878	7965318	0.0692	0.3018
chr14	107349540	7868801	0.0733	0.5219
chr15	102531392	7316804	0.0714	0.3213
chr16	90354753	7542697	0.0835	0.4886
chr17	81195210	7356827	0.0906	0.3931
chr18	78077248	6807457	0.0872	1.7559
chr19	59128983	6336030	0.1072	1.729
chr20	63025520	5264246	0.0835	0.4052
chr21	48129895	3266168	0.0679	0.5233
chr22	51304566	3096149	0.0603	0.4371
chrMT	16571	3762	0.227	0.5222
chrX	155270560	9794891	0.0631	0.5199
chrY	59373566	2620958	0.0441	0.4894

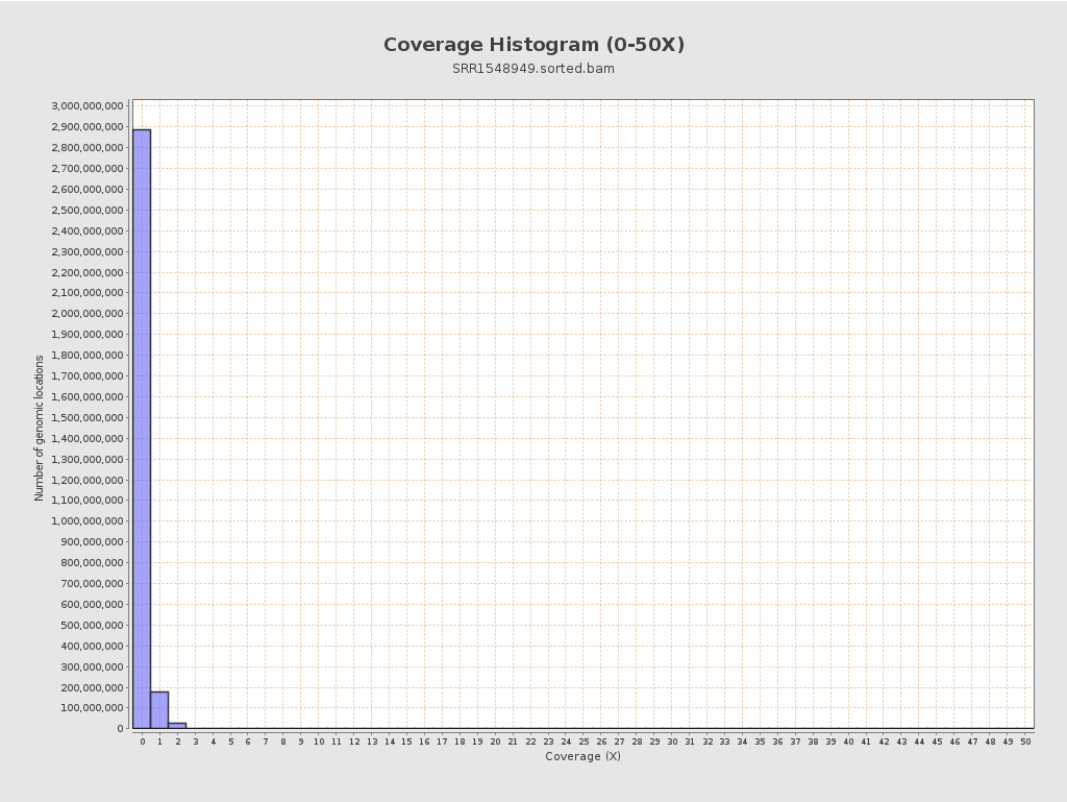
3. Results : Coverage across reference



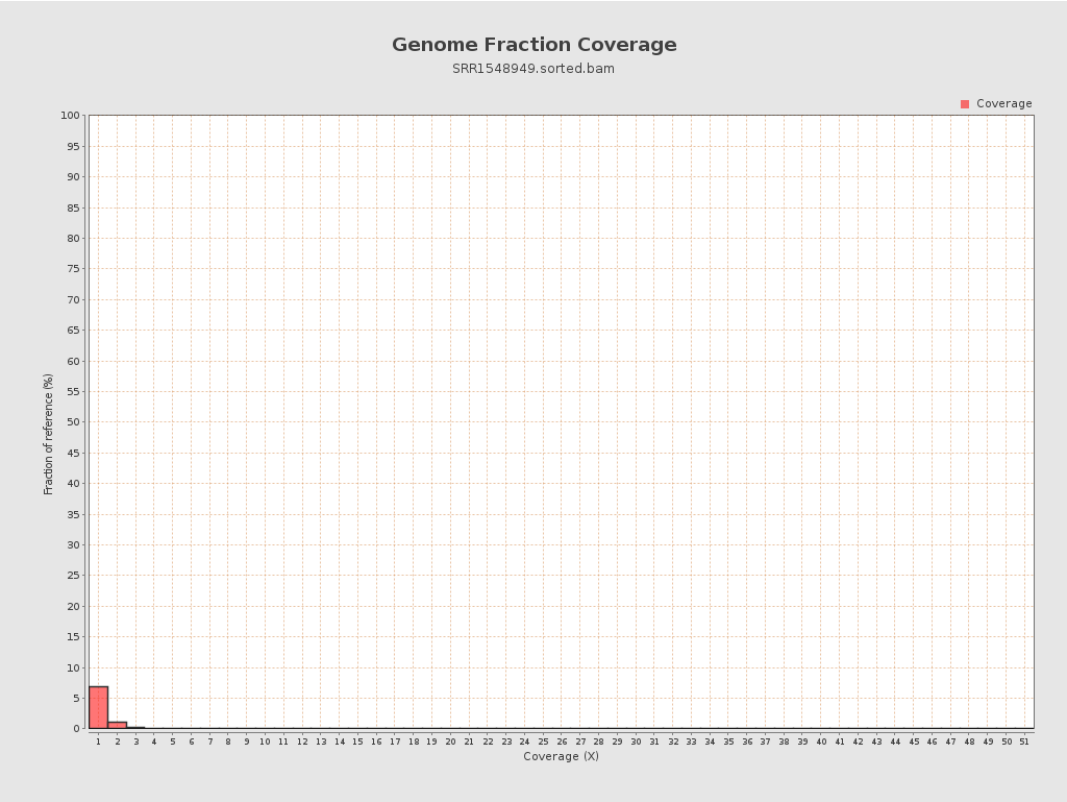
4. Results : Coverage Histogram



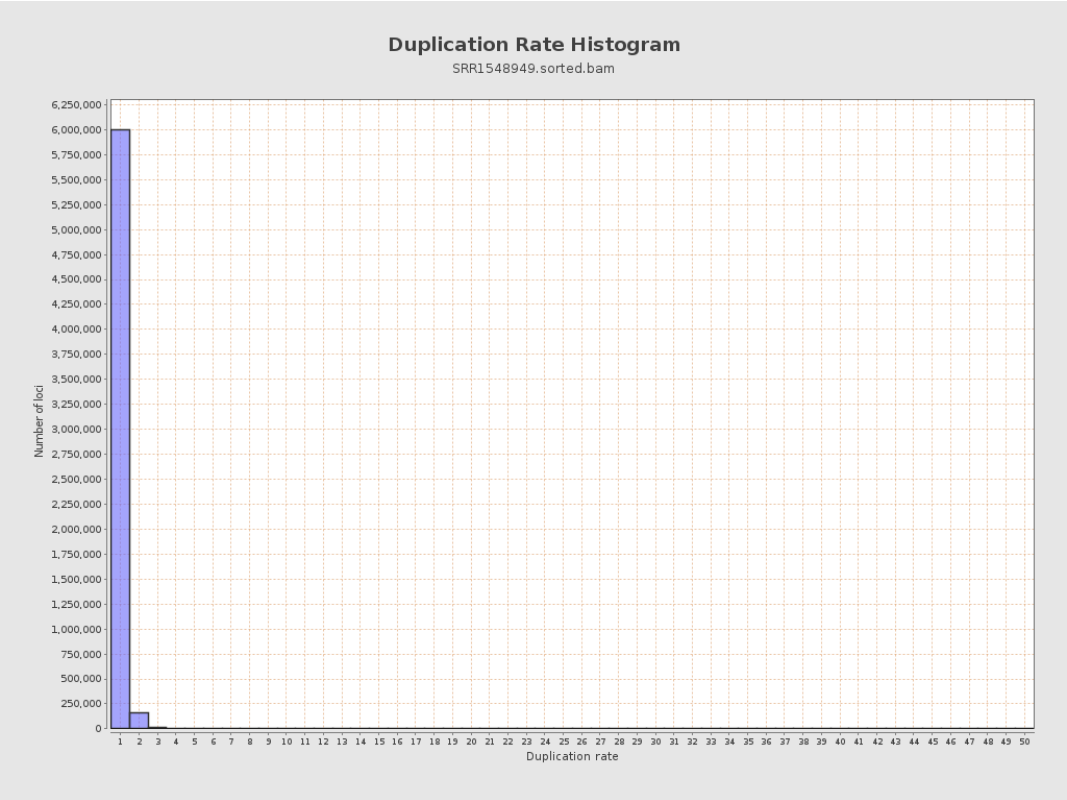
5. Results : Coverage Histogram (0-50X)



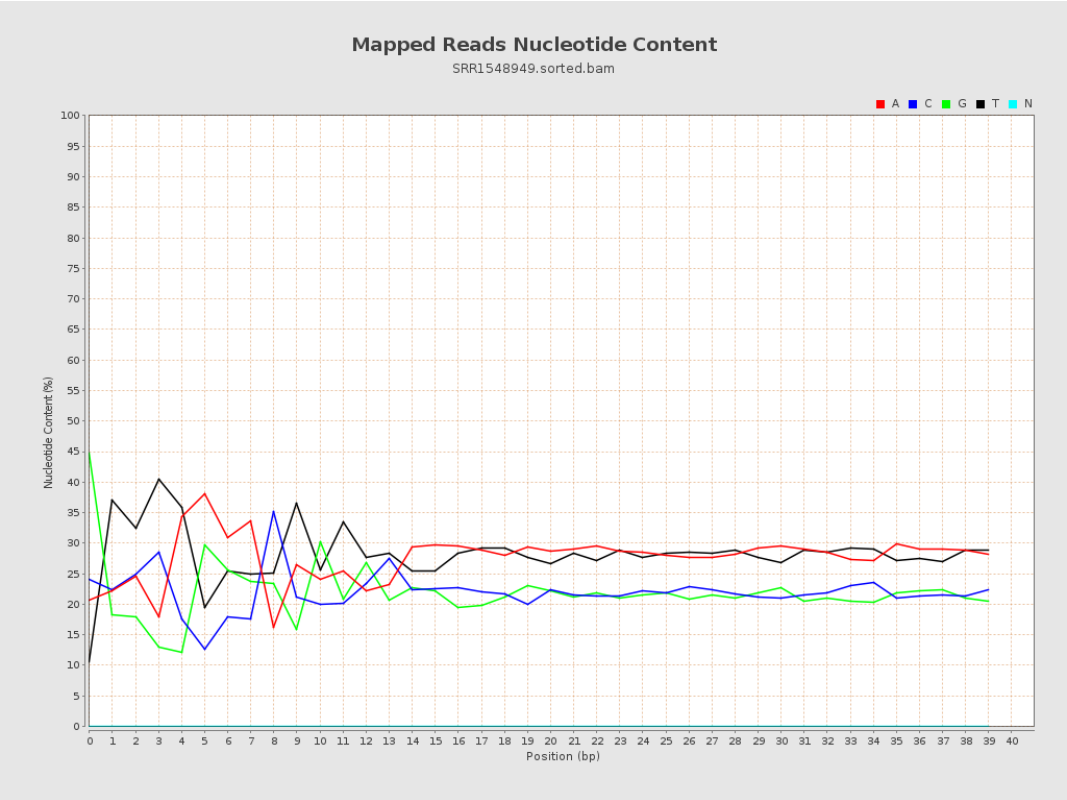
6. Results : Genome Fraction Coverage



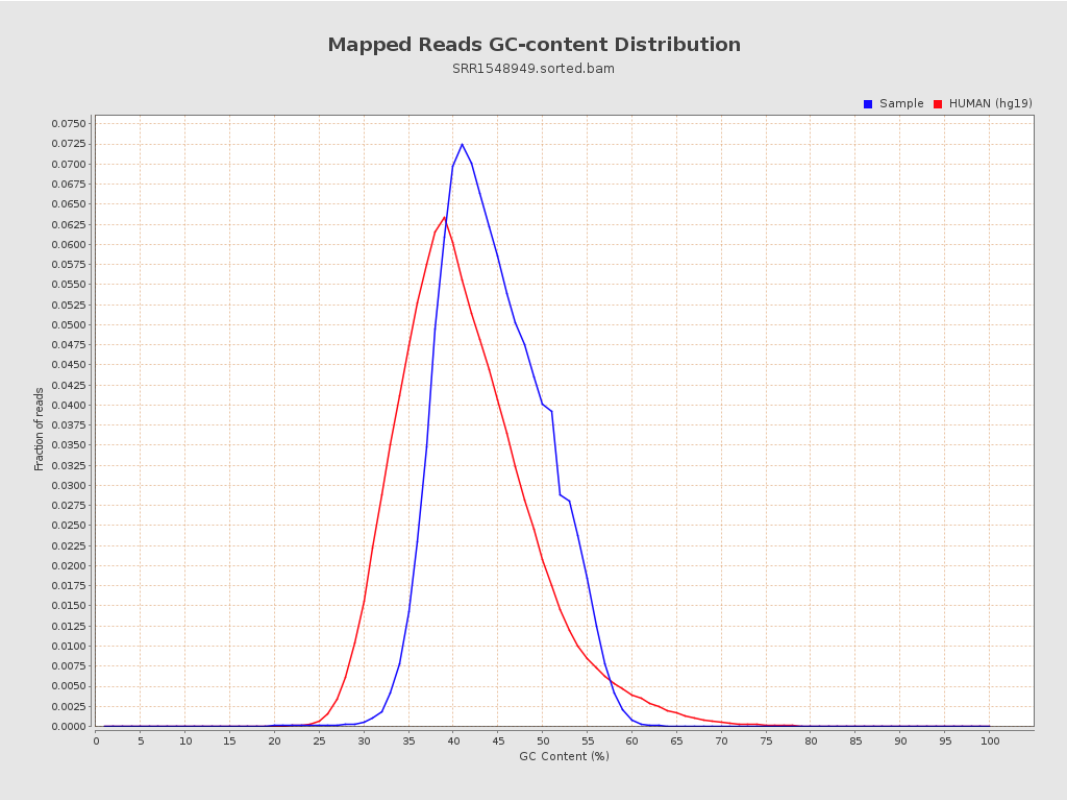
7. Results : Duplication Rate Histogram



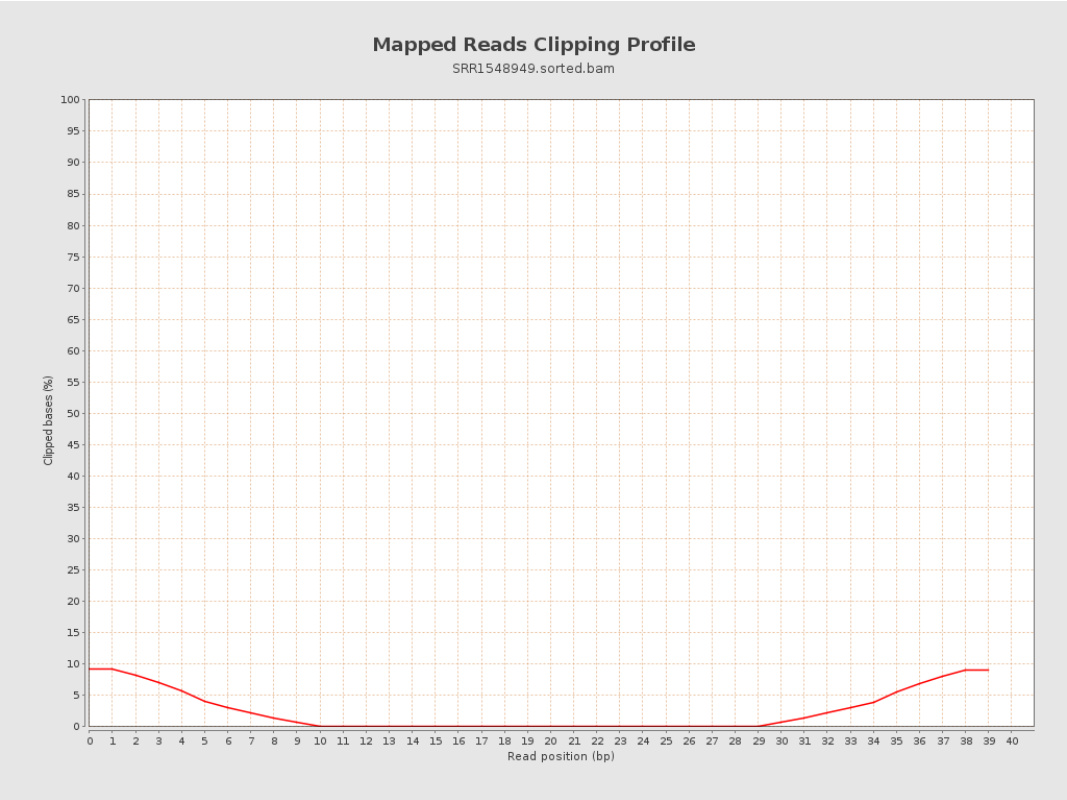
8. Results : Mapped Reads Nucleotide Content



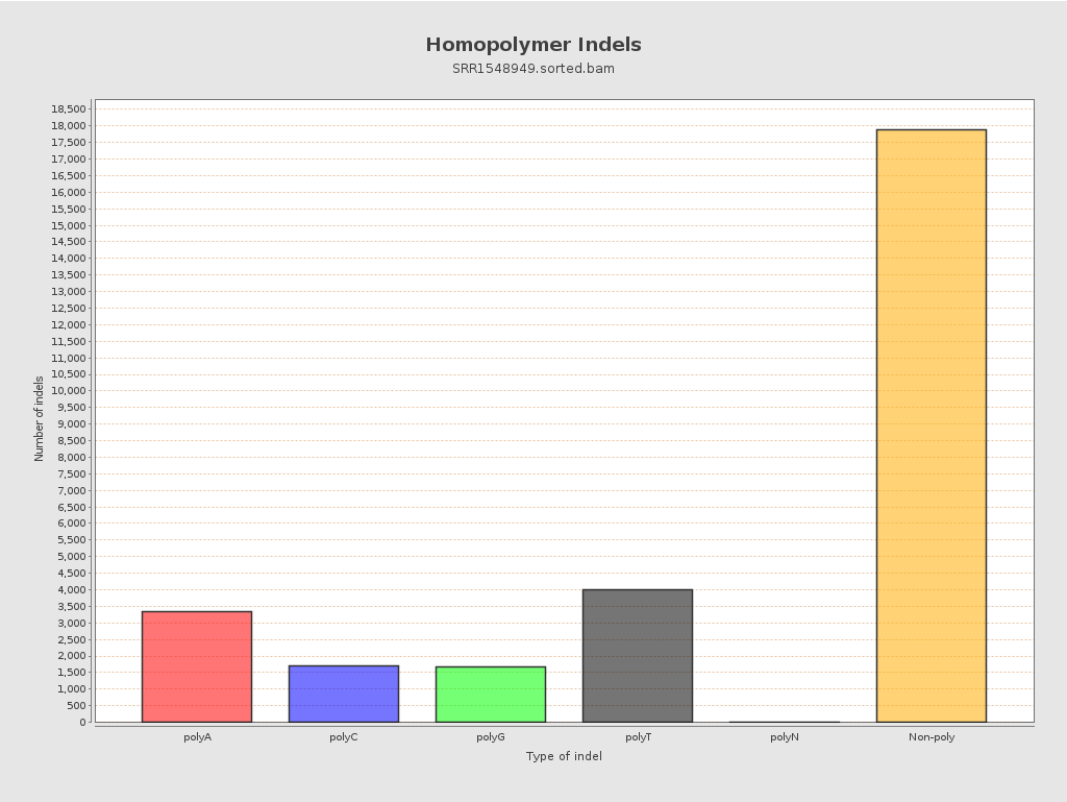
9. Results : Mapped Reads GC-content Distribution



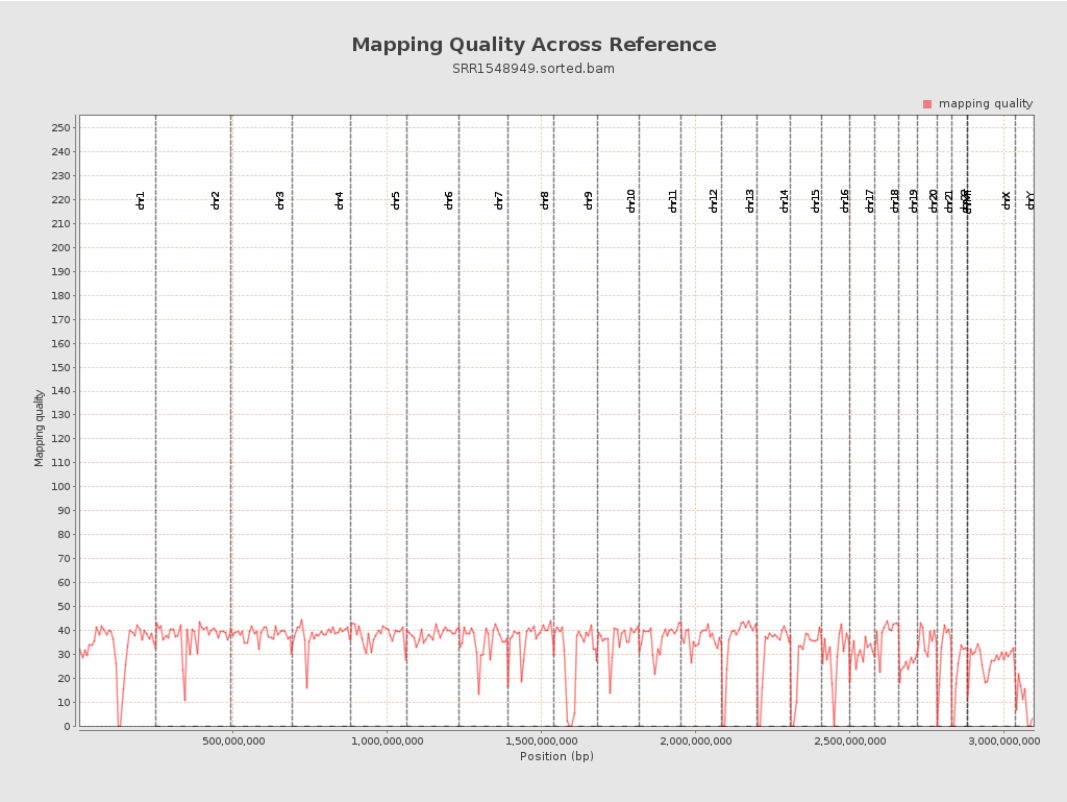
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram