Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 03:09:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548924.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_SRR1548924 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548924.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 03:09:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548924.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,002,677
Mapped reads	6,108,896 / 87.24%
Unmapped reads	893,781 / 12.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	183,648 / 2.62%
Duplication rate	2.12%
Clipped reads	431,195 / 6.16%

2.2. ACGT Content

Number/percentage of A's	72,066,748 / 29.79%
Number/percentage of C's	48,887,440 / 20.21%
Number/percentage of T's	72,108,394 / 29.8%
Number/percentage of G's	48,869,746 / 20.2%
Number/percentage of N's	2,226 / 0%
GC Percentage	40.41%

2.3. Coverage

Mean	0.0782
Standard Deviation	0.8705

2.4. Mapping Quality

Mean Mapping Quality	42.33

2.5. Mismatches and indels

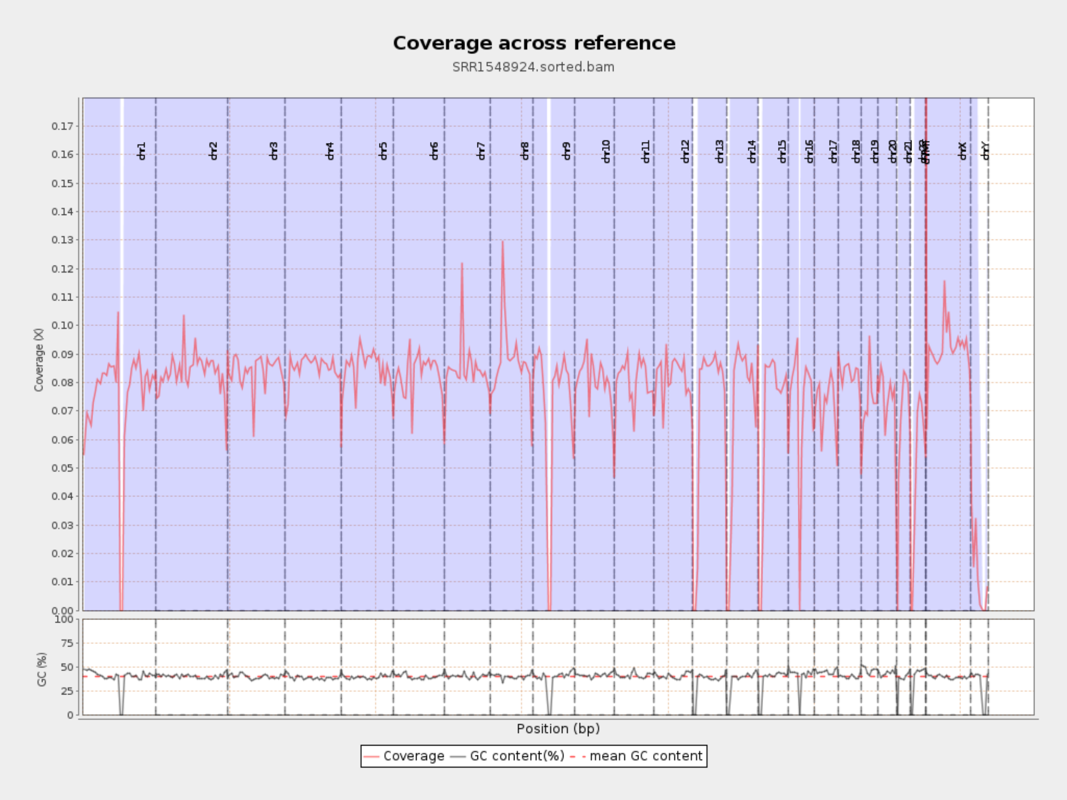
General error rate	0.28%
Mismatches	664,695
Insertions	7,554
Mapped reads with at least one insertion	0.12%
Deletions	20,605
Mapped reads with at least one deletion	0.34%
Homopolymer indels	42.18%

2.6. Chromosome stats

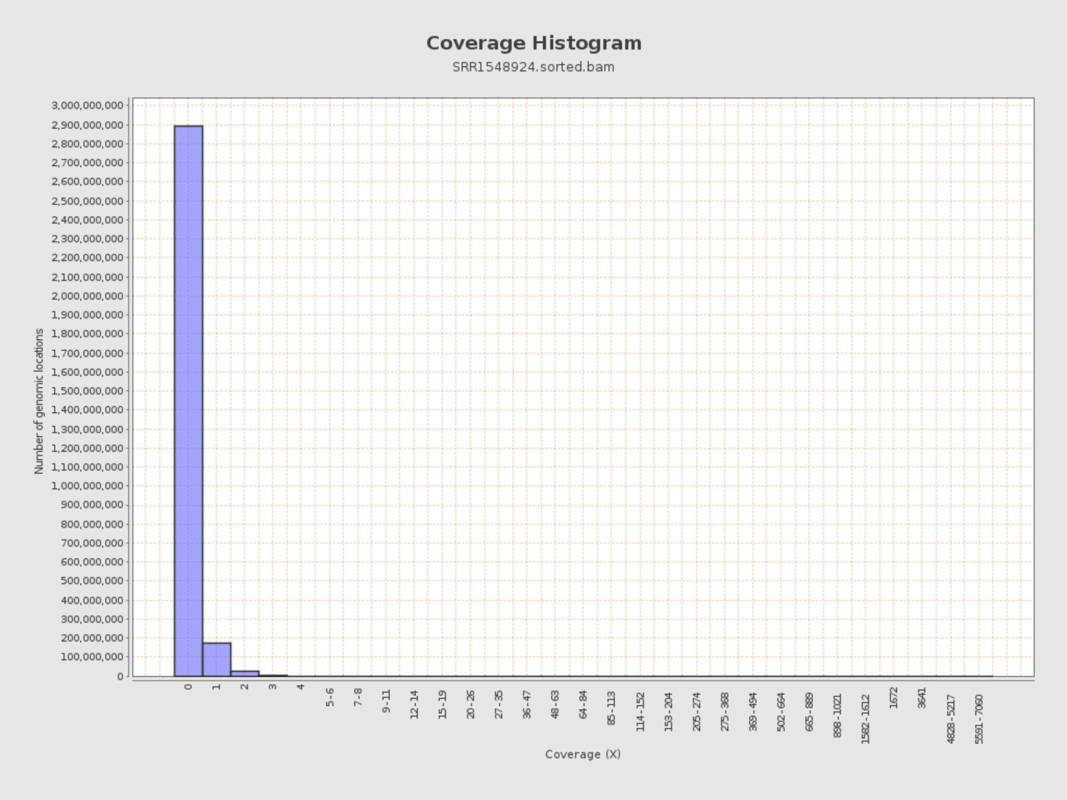
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18588159	0.0746	0.7981
chr2	243199373	20383018	0.0838	0.4482
chr3	198022430	16671770	0.0842	0.3359
chr4	191154276	16283299	0.0852	0.3456
chr5	180915260	15339601	0.0848	0.3412
chr6	171115067	14243755	0.0832	0.3642
chr7	159138663	13458987	0.0846	0.6485
chr8	146364022	12829257	0.0877	3.4183

chr9	141213431	10207308	0.0723	0.4374
chr10	135534747	11022821	0.0813	0.4107
chr11	135006516	10875768	0.0806	0.477
chr12	133851895	10948289	0.0818	0.3398
chr13	115169878	8155751	0.0708	0.3045
chr14	107349540	7536246	0.0702	0.3523
chr15	102531392	6892007	0.0672	0.2981
chr16	90354753	6402022	0.0709	0.3315
chr17	81195210	5928344	0.073	0.3285
chr18	78077248	6504725	0.0833	0.7871
chr19	59128983	4355214	0.0737	0.734
chr20	63025520	4717823	0.0749	0.3232
chr21	48129895	3089326	0.0642	0.3218
chr22	51304566	2507220	0.0489	0.2768
chrMT	16571	7447	0.4494	0.7845
chrX	155270560	14280911	0.092	0.4133
chrY	59373566	733046	0.0123	0.1696

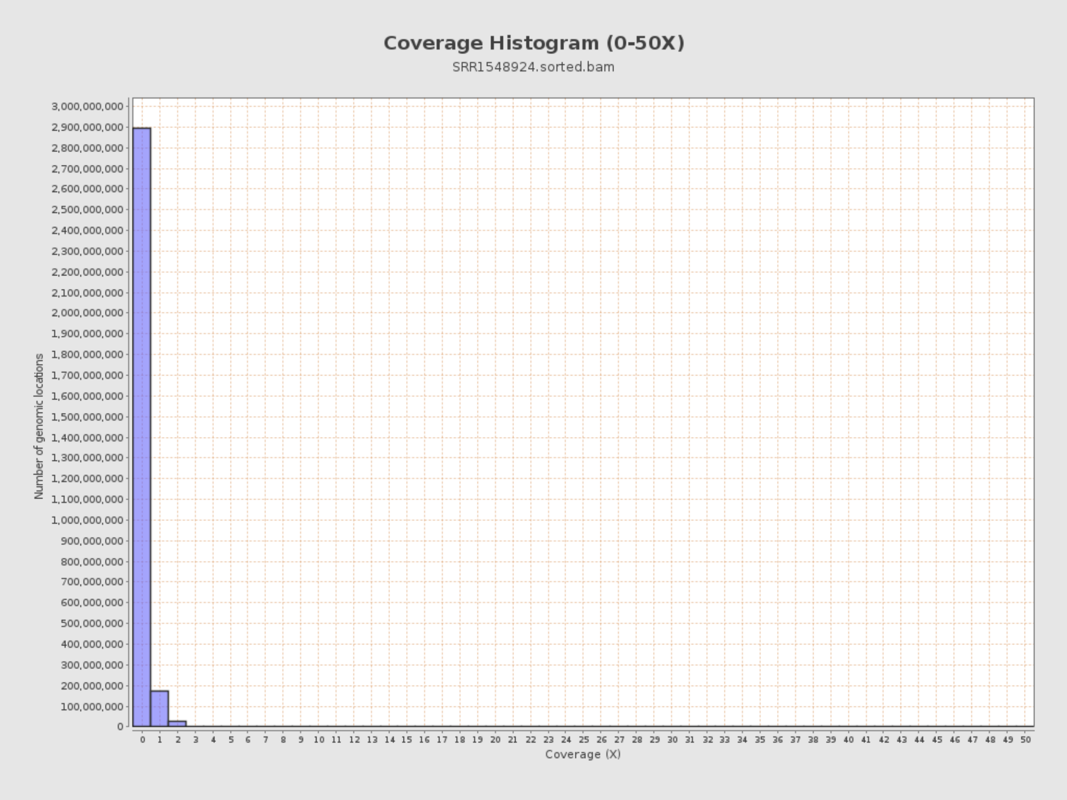
3. Results : Coverage across reference



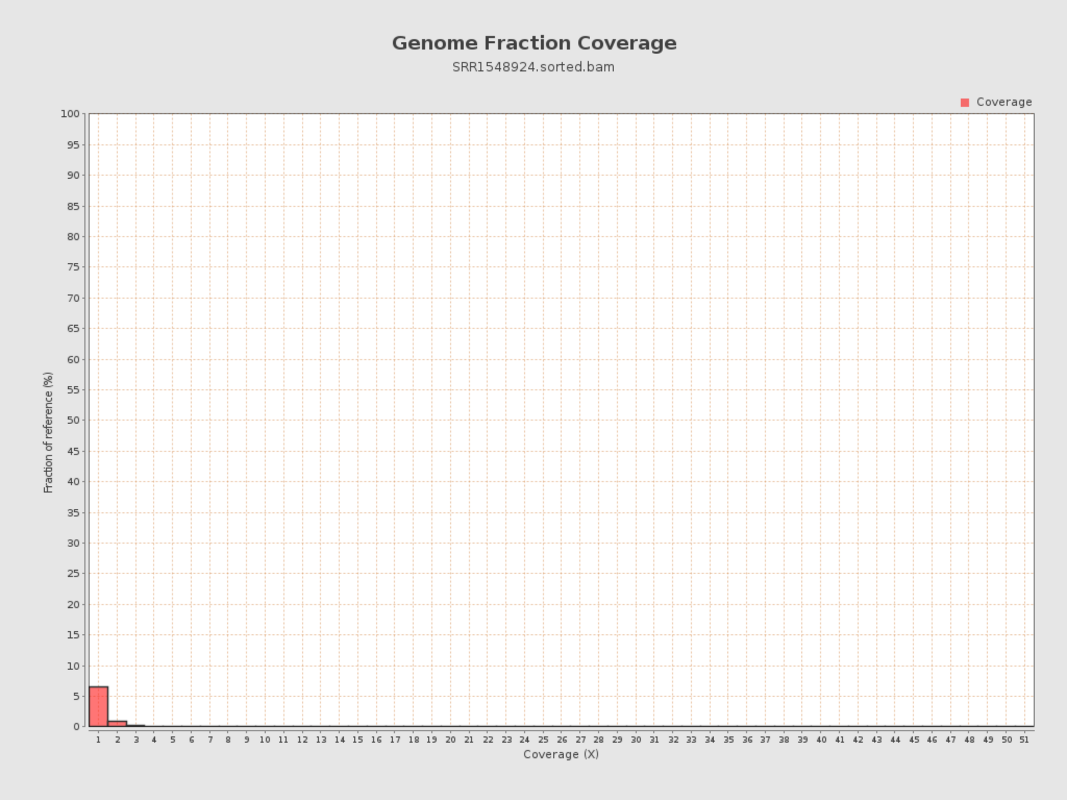
4. Results : Coverage Histogram



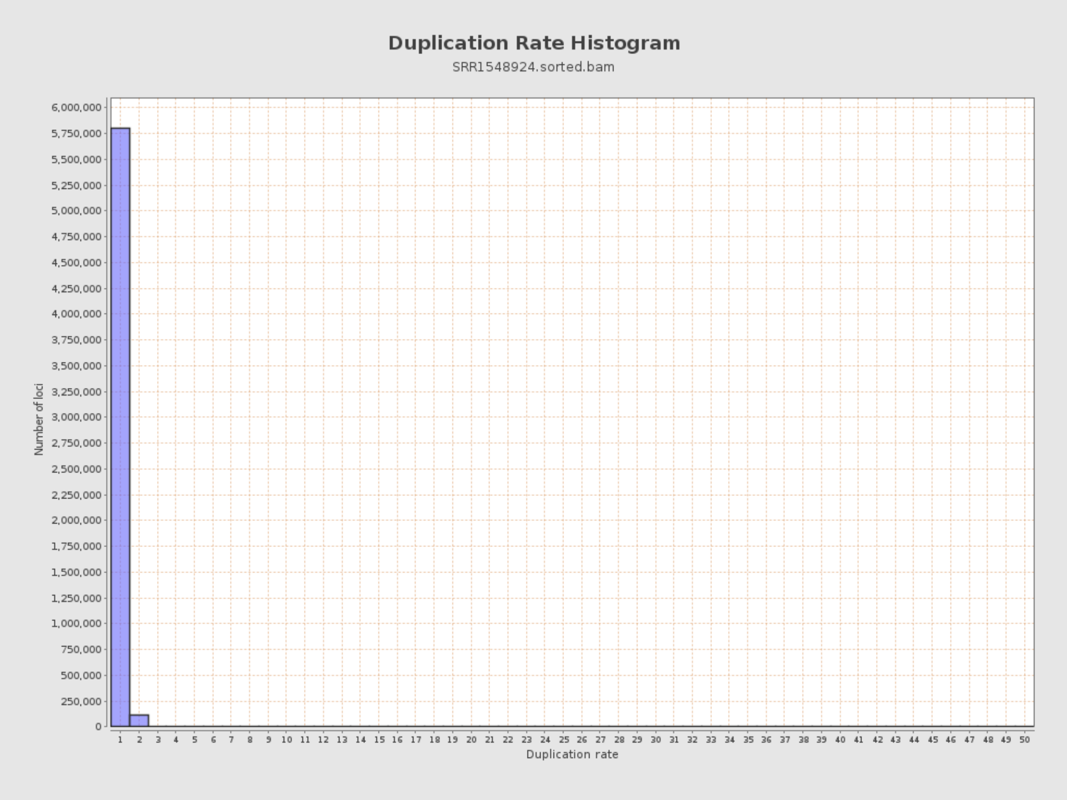
5. Results : Coverage Histogram (0-50X)



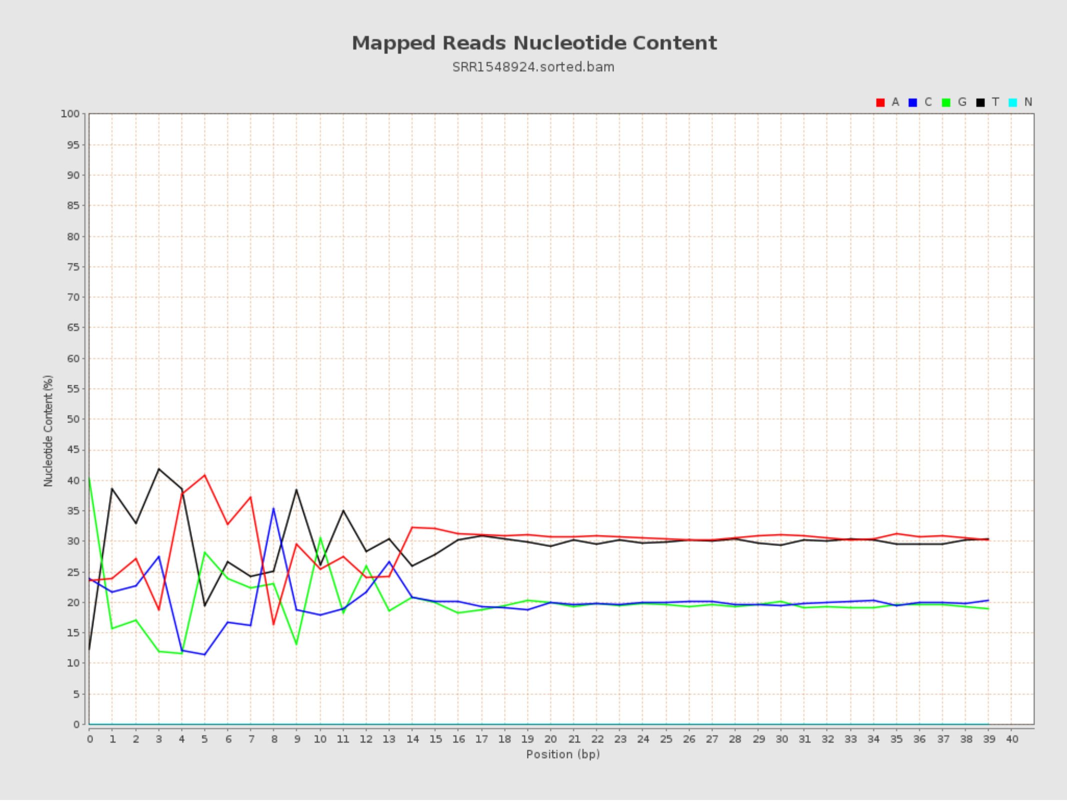
6. Results : Genome Fraction Coverage



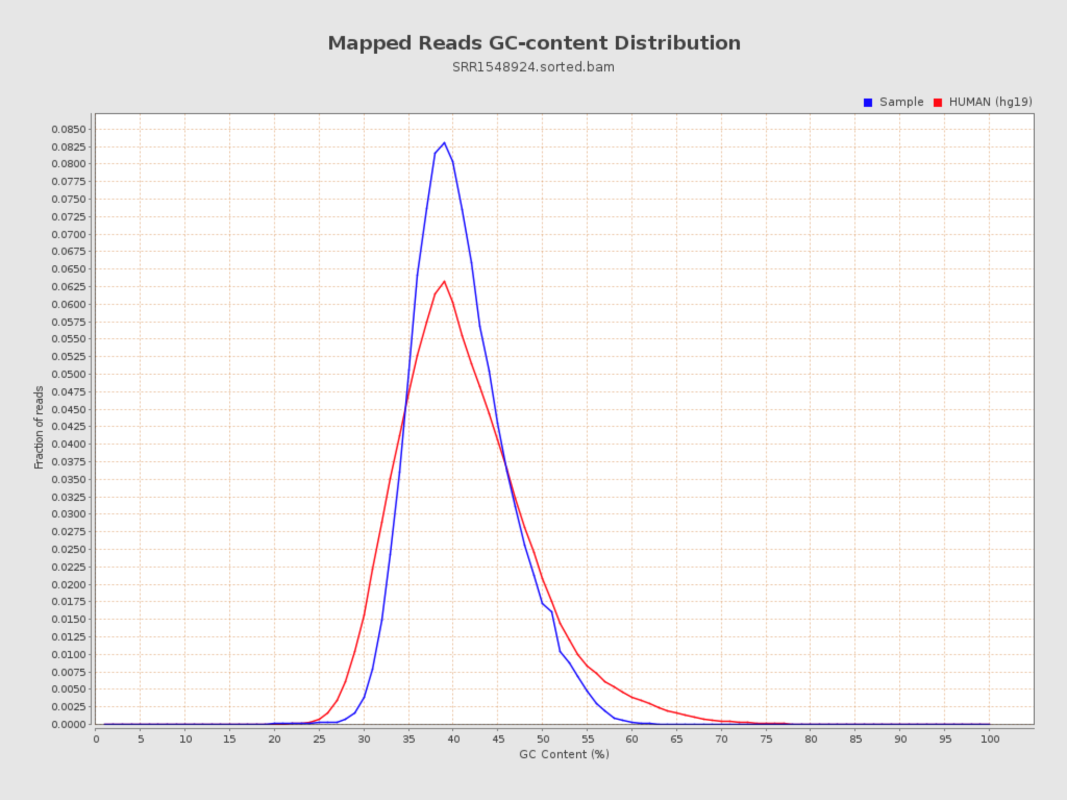
7. Results : Duplication Rate Histogram



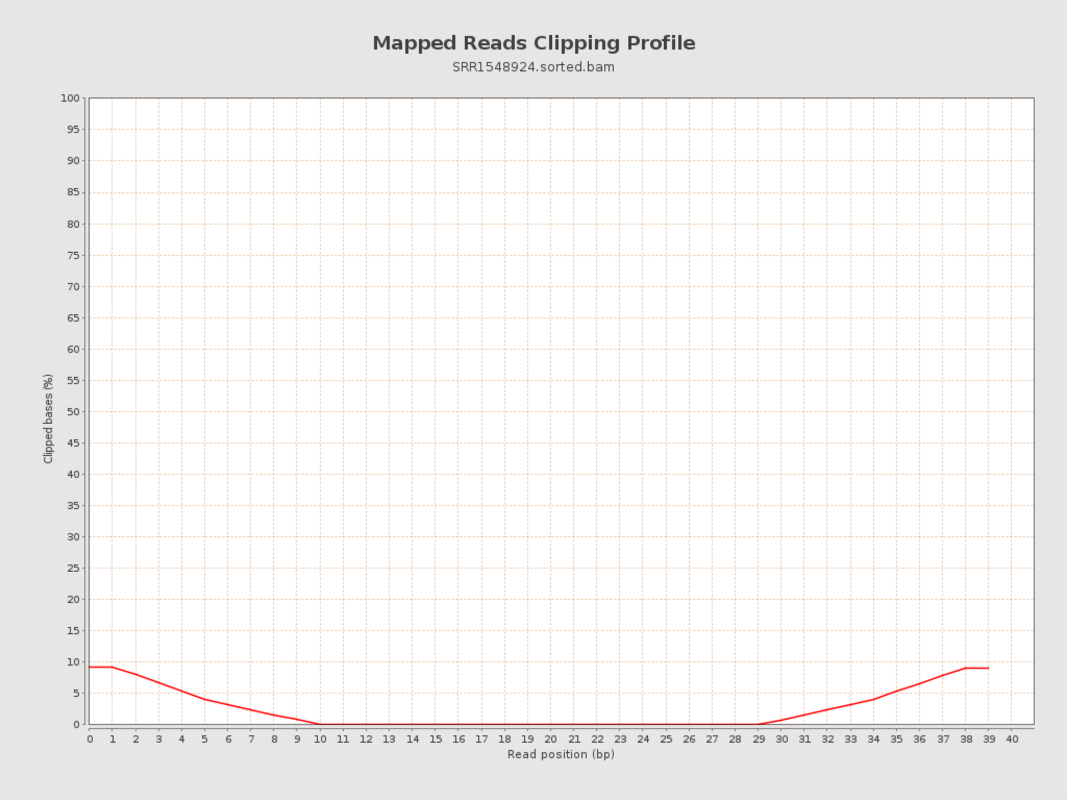
8. Results : Mapped Reads Nucleotide Content



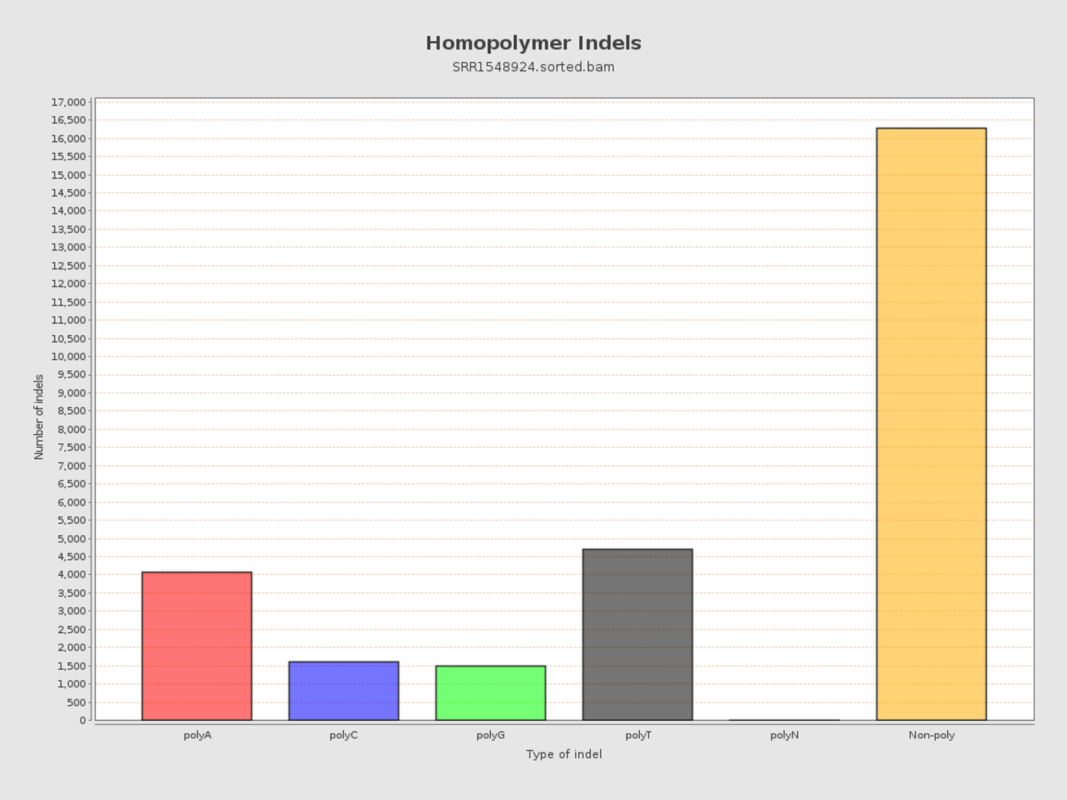
9. Results : Mapped Reads GC-content Distribution



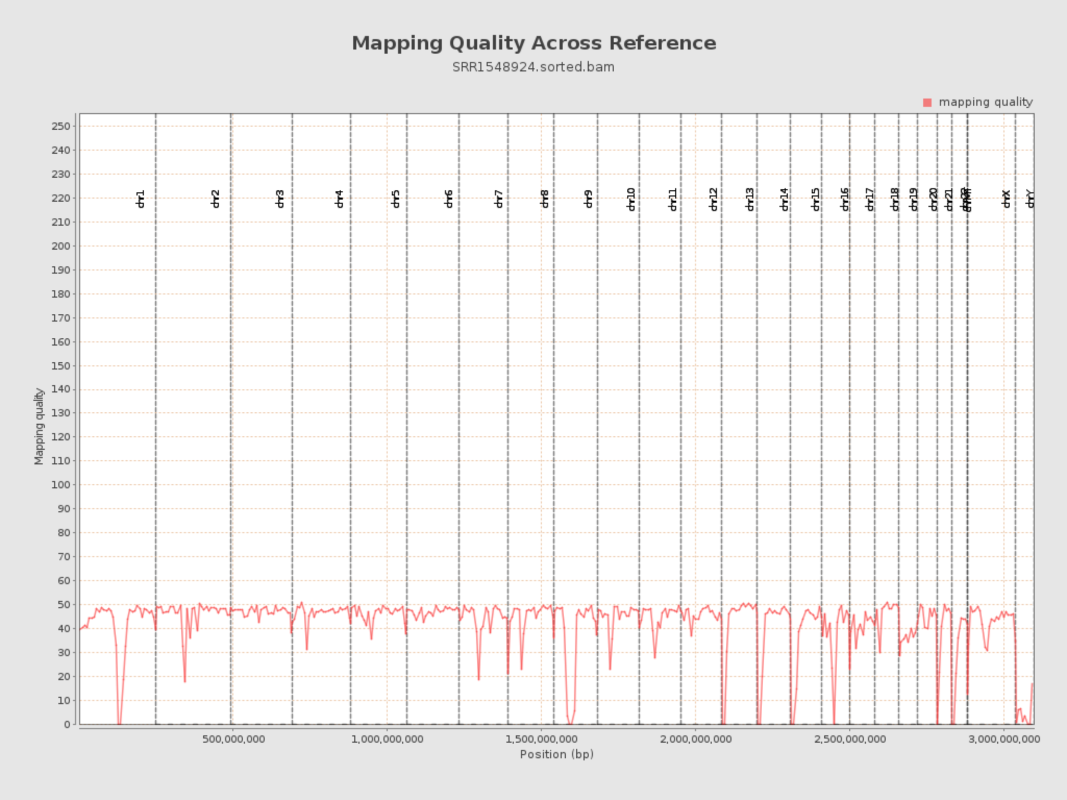
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram