Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:32:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818990.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_SRR1818990 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818990.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:32:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818990.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,408,771
Mapped reads	2,373,019 / 98.52%
Unmapped reads	35,752 / 1.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,978 / 1.37%
Read min/max/mean length	30 / 101 / 101.53
Duplicated reads (estimated)	1,032,747 / 42.87%
Duplication rate	36.6%
Clipped reads	2,392,294 / 99.32%

2.2. ACGT Content

Number/percentage of A's	63,632,953 / 28.98%
Number/percentage of C's	47,704,233 / 21.72%
Number/percentage of T's	61,449,175 / 27.98%
Number/percentage of G's	46,798,495 / 21.31%
Number/percentage of N's	11,464 / 0.01%
GC Percentage	43.03%

2.3. Coverage

Mean	0.071

Standard Deviation	0.8166

2.4. Mapping Quality

Mean Mapping Quality	49.21

2.5. Mismatches and indels

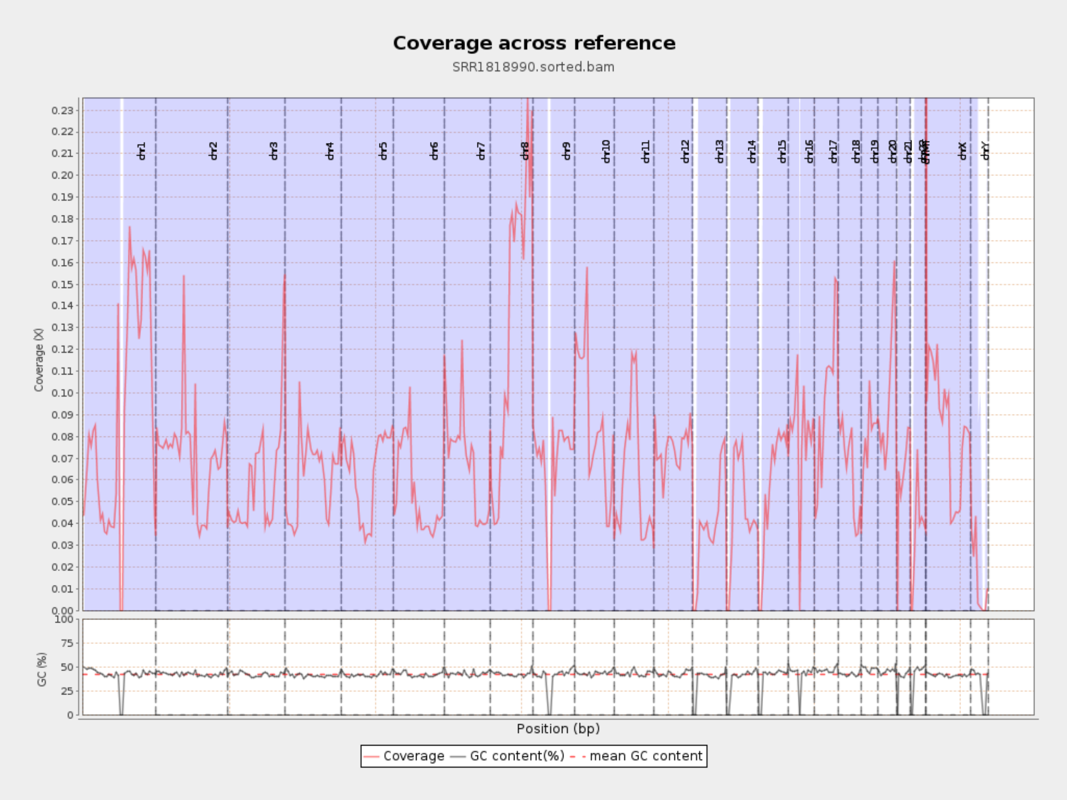
General error rate	0.66%
Mismatches	1,376,371
Insertions	33,388
Mapped reads with at least one insertion	1.37%
Deletions	69,360
Mapped reads with at least one deletion	2.86%
Homopolymer indels	41.77%

2.6. Chromosome stats

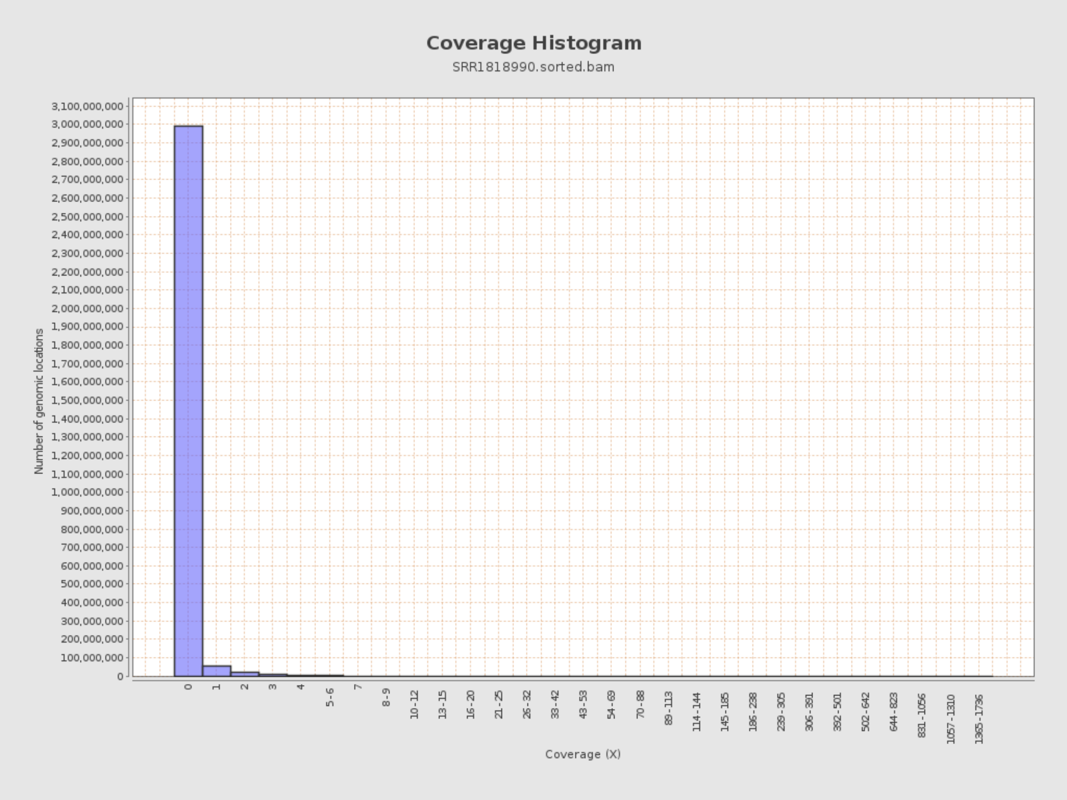
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22380493	0.0898	1.4786
chr2	243199373	17518718	0.072	1.0957
chr3	198022430	11691482	0.059	0.4394
chr4	191154276	11895968	0.0622	0.5326
chr5	180915260	11569481	0.0639	0.4821
chr6	171115067	9196081	0.0537	0.5356
chr7	159138663	10868297	0.0683	1.0544

chr8	146364022	19974568	0.1365	0.7662
chr9	141213431	9404117	0.0666	0.7938
chr10	135534747	11682040	0.0862	0.9929
chr11	135006516	8211711	0.0608	0.5769
chr12	133851895	10076479	0.0753	0.5184
chr13	115169878	4551709	0.0395	0.3605
chr14	107349540	5039835	0.0469	0.4218
chr15	102531392	5744979	0.056	0.433
chr16	90354753	7166102	0.0793	0.9271
chr17	81195210	7824000	0.0964	0.6653
chr18	78077248	5074357	0.065	0.9135
chr19	59128983	4702303	0.0795	1.2714
chr20	63025520	6389007	0.1014	0.6266
chr21	48129895	3022784	0.0628	0.516
chr22	51304566	1776864	0.0346	0.3833
chrMT	16571	25009	1.5092	2.2454
chrX	155270560	13107148	0.0844	0.6209
chrY	59373566	832695	0.014	0.8544

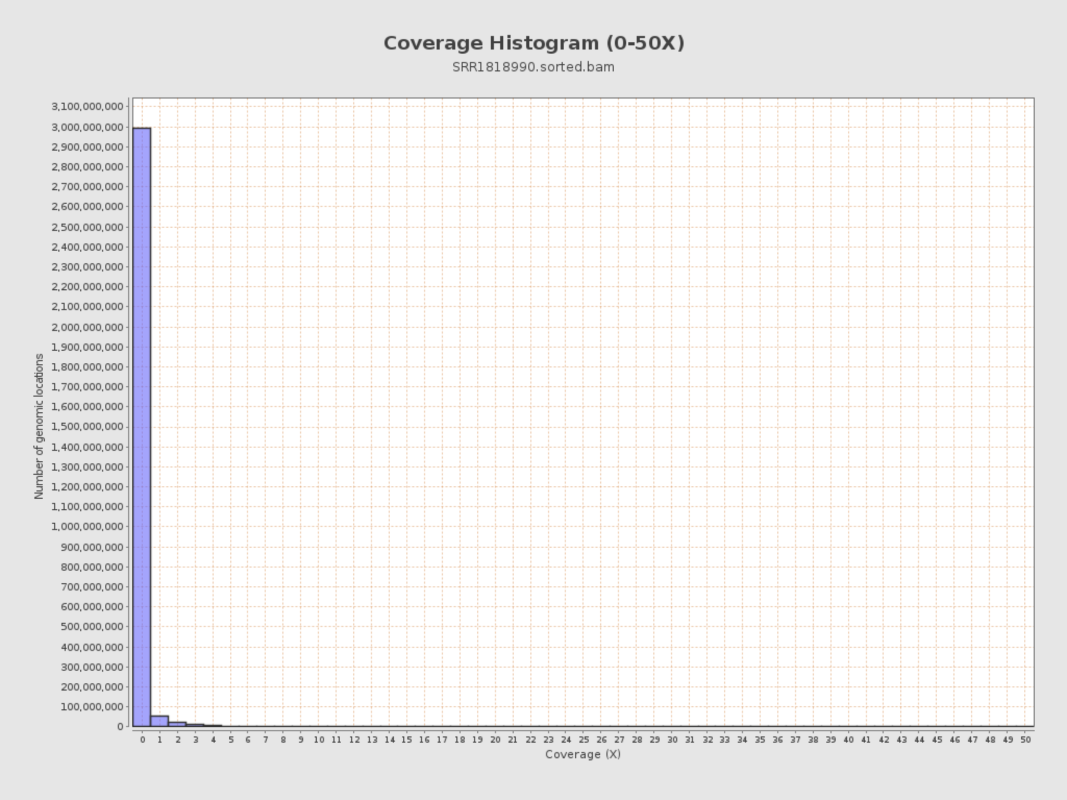
3. Results : Coverage across reference



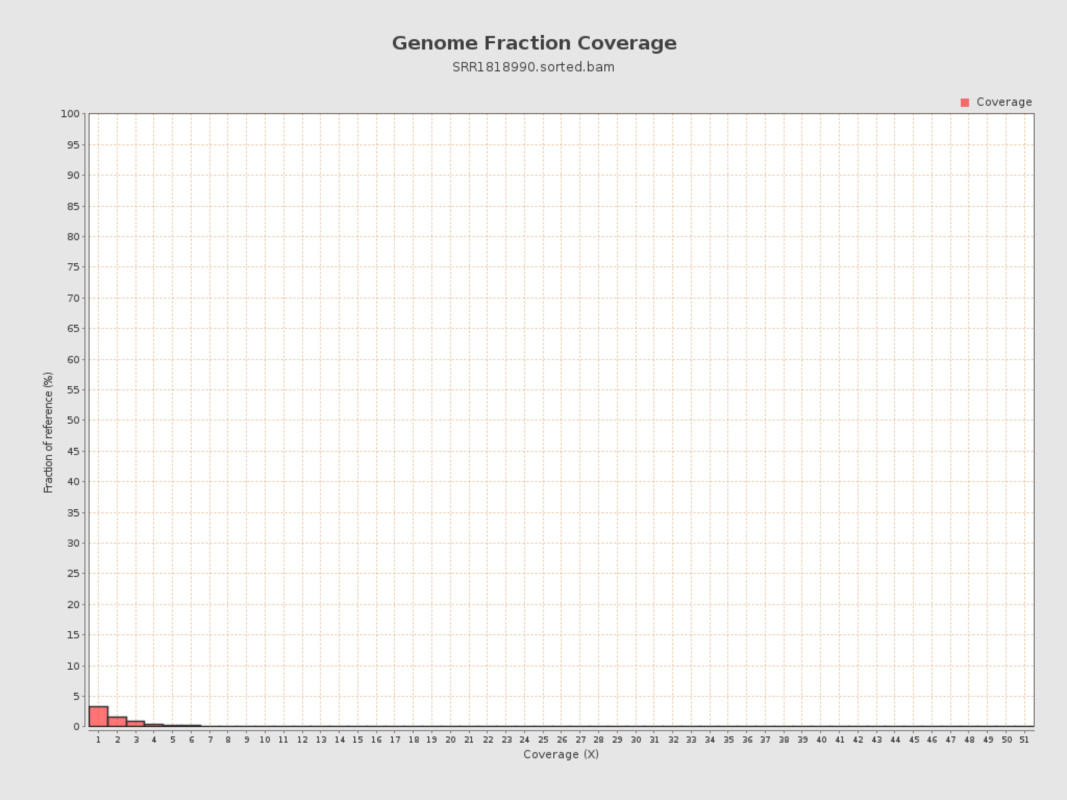
4. Results : Coverage Histogram



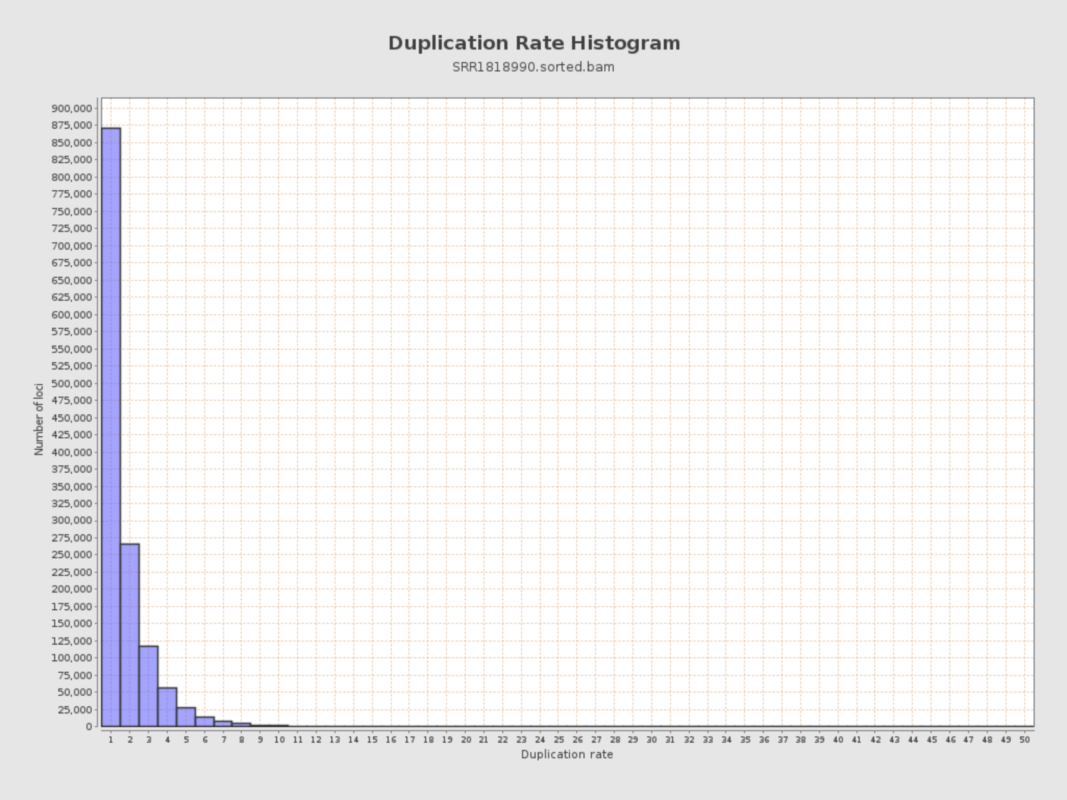
5. Results : Coverage Histogram (0-50X)



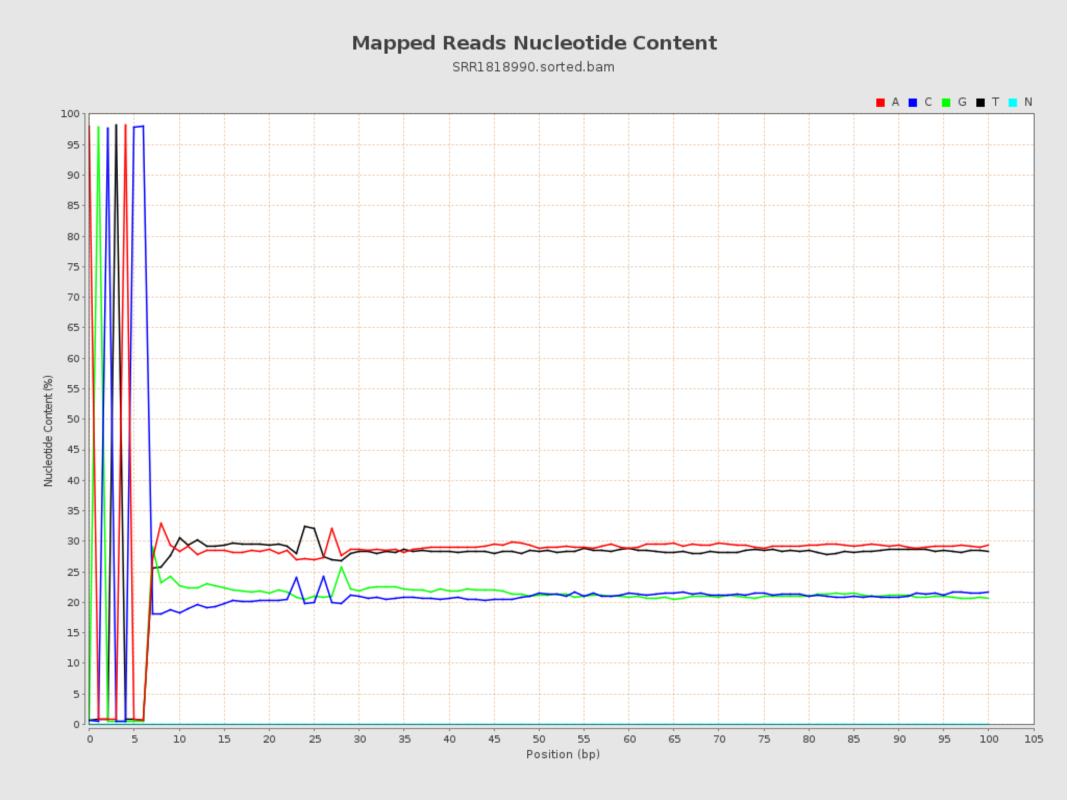
6. Results : Genome Fraction Coverage



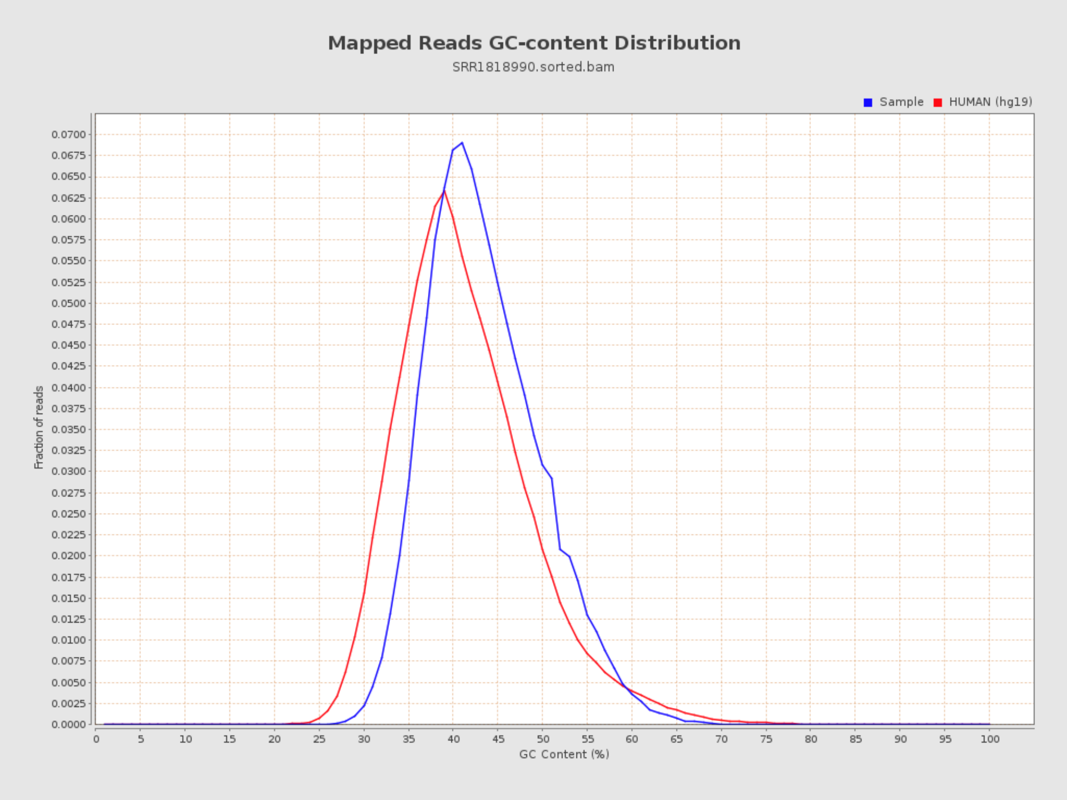
7. Results : Duplication Rate Histogram



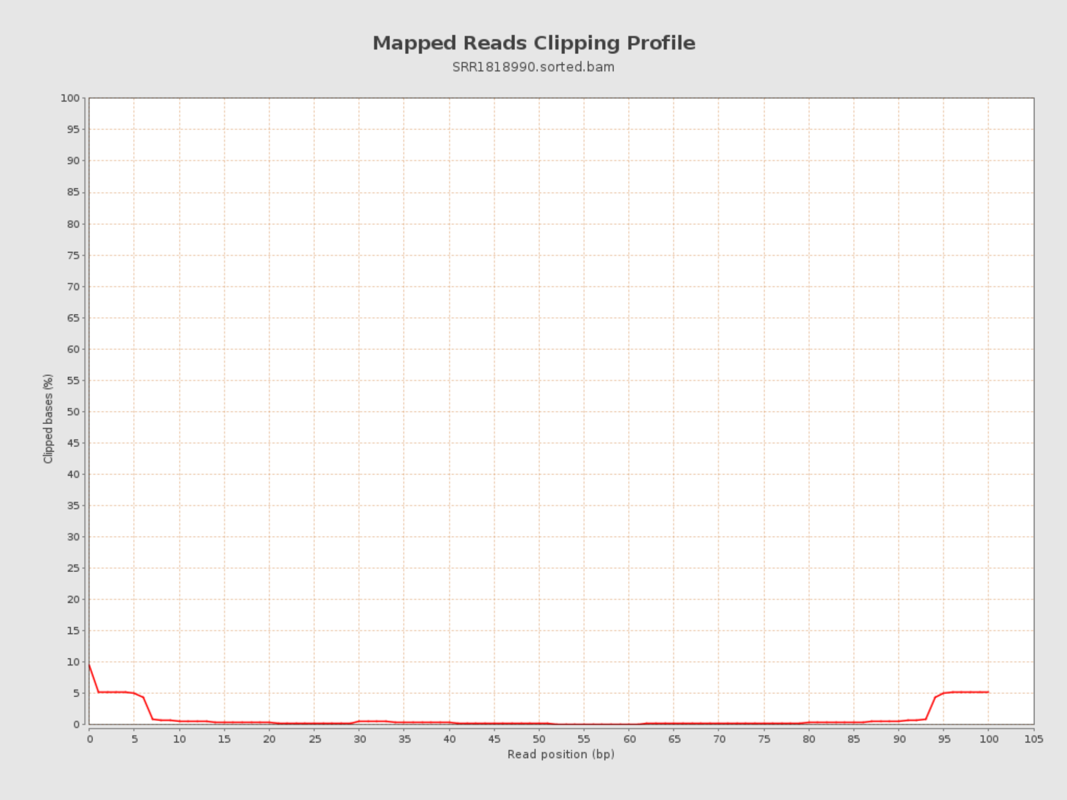
8. Results : Mapped Reads Nucleotide Content



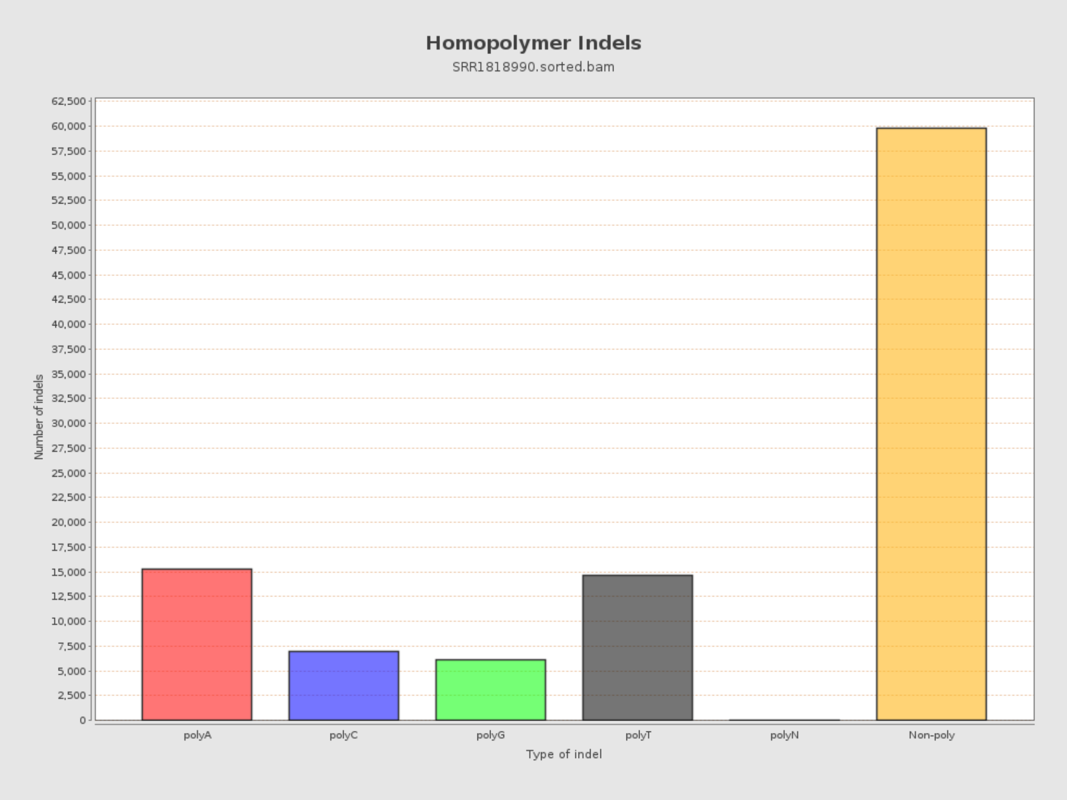
9. Results : Mapped Reads GC-content Distribution



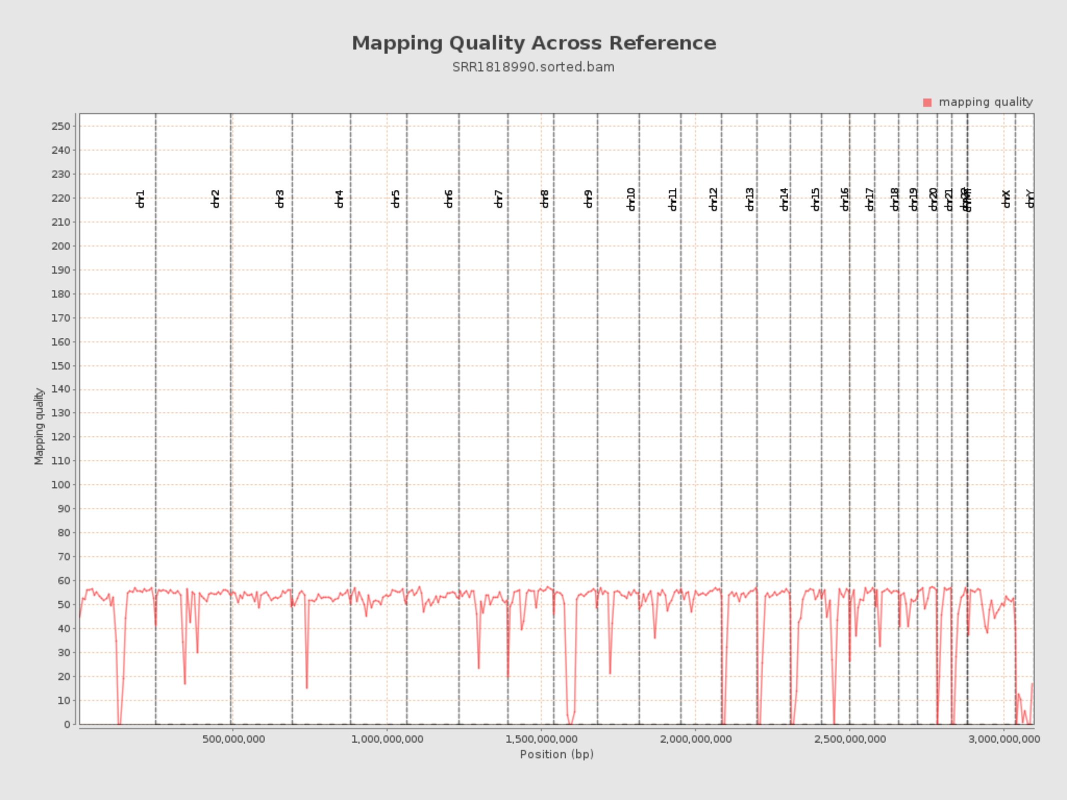
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram