Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:13:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818919.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_SRR1818919 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818919.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:13:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818919.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,053,549
Mapped reads	1,994,412 / 97.12%
Unmapped reads	59,137 / 2.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,842 / 1.4%
Read min/max/mean length	30 / 101 / 101.54
Duplicated reads (estimated)	498,626 / 24.28%
Duplication rate	21.11%
Clipped reads	2,015,019 / 98.12%

2.2. ACGT Content

Number/percentage of A's	51,747,523 / 28.02%
Number/percentage of C's	38,535,560 / 20.86%
Number/percentage of T's	53,004,912 / 28.7%
Number/percentage of G's	41,400,982 / 22.42%
Number/percentage of N's	2,551 / 0%
GC Percentage	43.28%

2.3. Coverage

Mean	0.0597

Standard Deviation	0.745

2.4. Mapping Quality

Mean Mapping Quality	49.33

2.5. Mismatches and indels

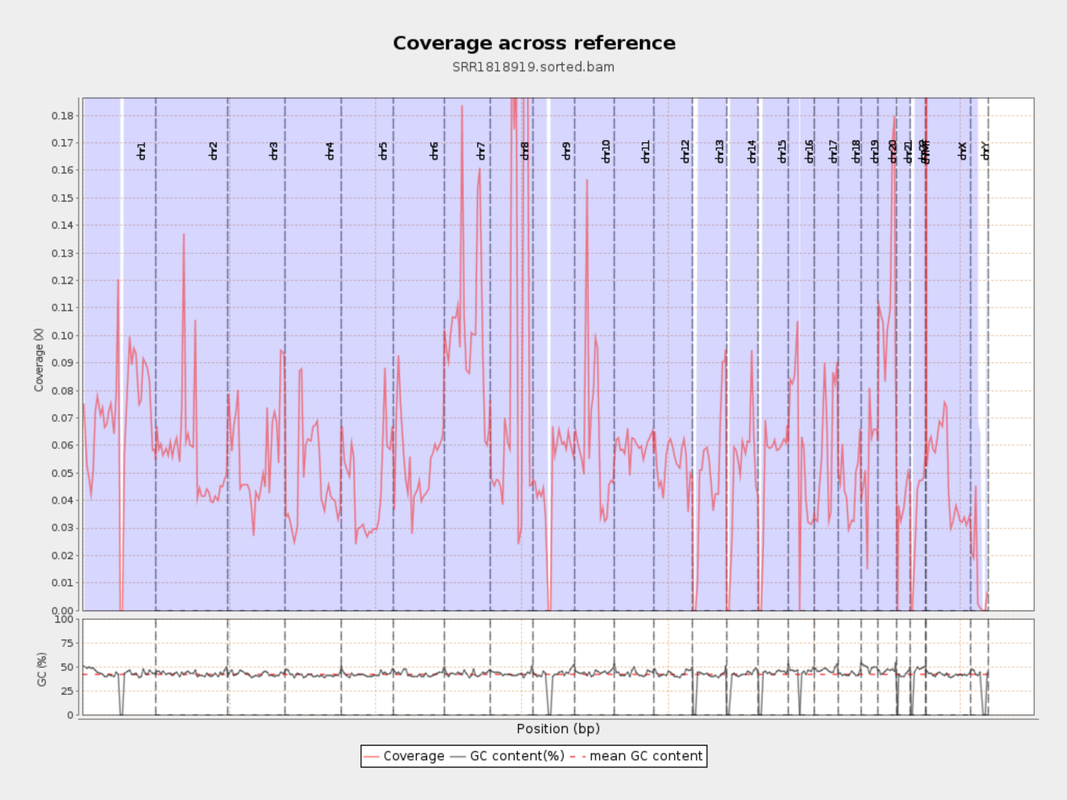
General error rate	0.64%
Mismatches	1,111,808
Insertions	25,298
Mapped reads with at least one insertion	1.23%
Deletions	59,847
Mapped reads with at least one deletion	2.93%
Homopolymer indels	41.76%

2.6. Chromosome stats

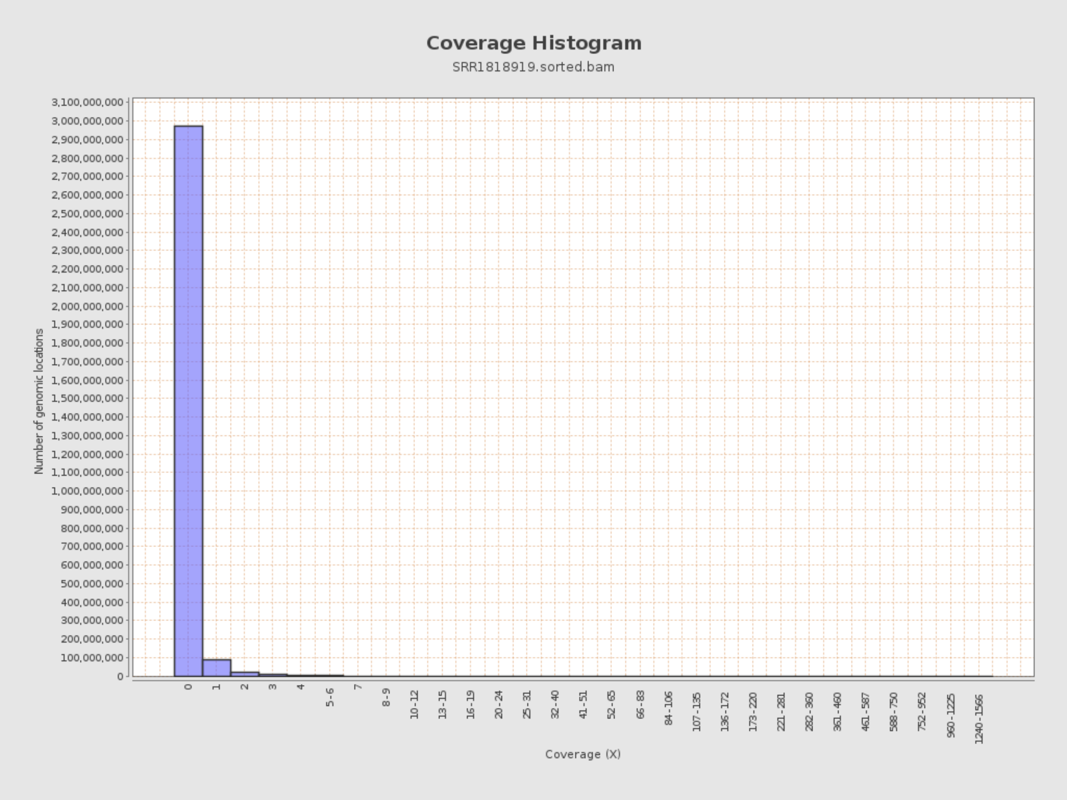
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17498909	0.0702	1.1778
chr2	243199373	13812423	0.0568	1.0033
chr3	198022430	11452831	0.0578	0.3372
chr4	191154276	9299273	0.0486	0.4193
chr5	180915260	8191724	0.0453	0.3097
chr6	171115067	9111706	0.0532	0.359
chr7	159138663	16448908	0.1034	1.6996

chr8	146364022	15967172	0.1091	0.6063
chr9	141213431	6791632	0.0481	0.5638
chr10	135534747	8509856	0.0628	0.9702
chr11	135006516	8090043	0.0599	0.4326
chr12	133851895	7173161	0.0536	0.3286
chr13	115169878	5634776	0.0489	0.3049
chr14	107349540	5394916	0.0503	0.3394
chr15	102531392	5100093	0.0497	0.3099
chr16	90354753	5076328	0.0562	0.6772
chr17	81195210	4727930	0.0582	0.45
chr18	78077248	3522018	0.0451	0.6973
chr19	59128983	3230774	0.0546	1.0629
chr20	63025520	7541754	0.1197	0.5229
chr21	48129895	1803208	0.0375	0.3305
chr22	51304566	1699744	0.0331	0.2781
chrMT	16571	456333	27.538	18.2164
chrX	155270560	7581475	0.0488	0.3867
chrY	59373566	691642	0.0116	0.8393

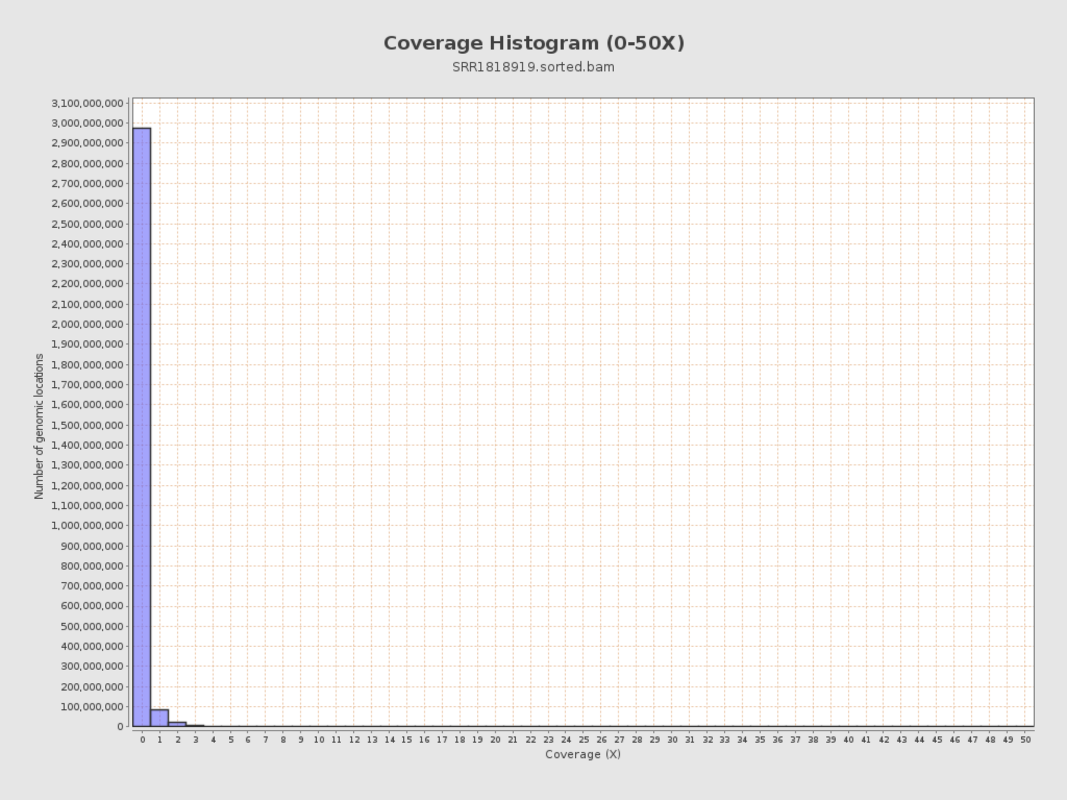
3. Results : Coverage across reference



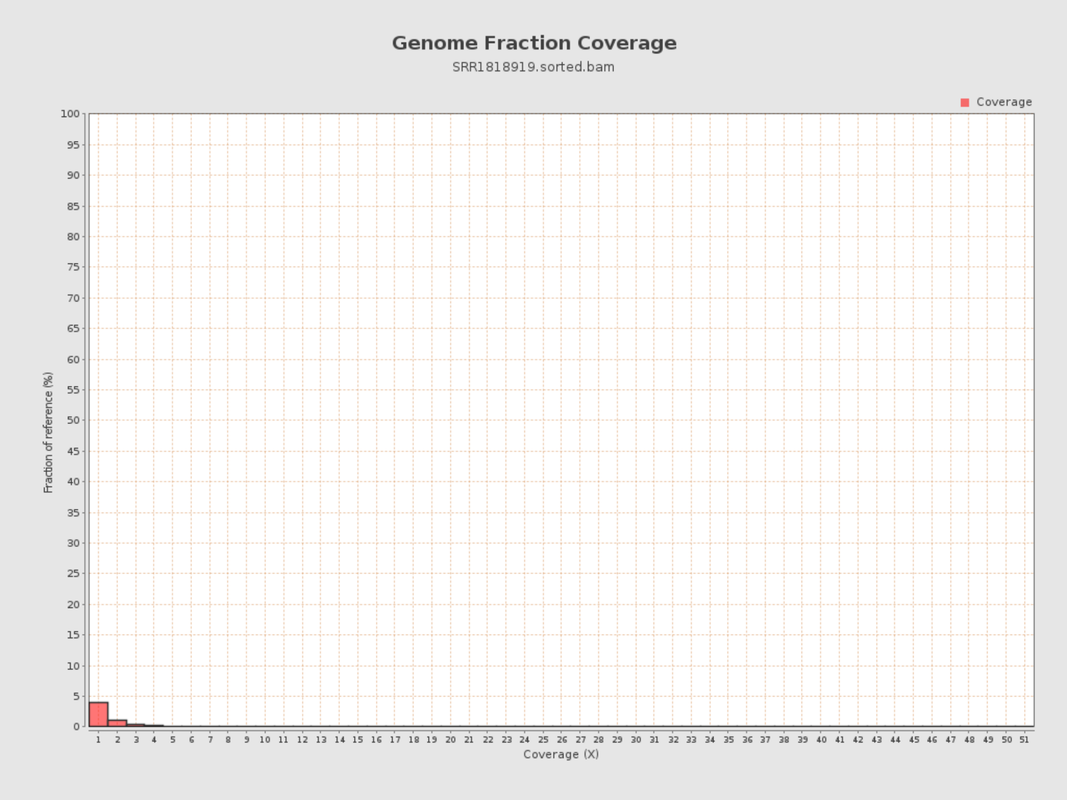
4. Results : Coverage Histogram



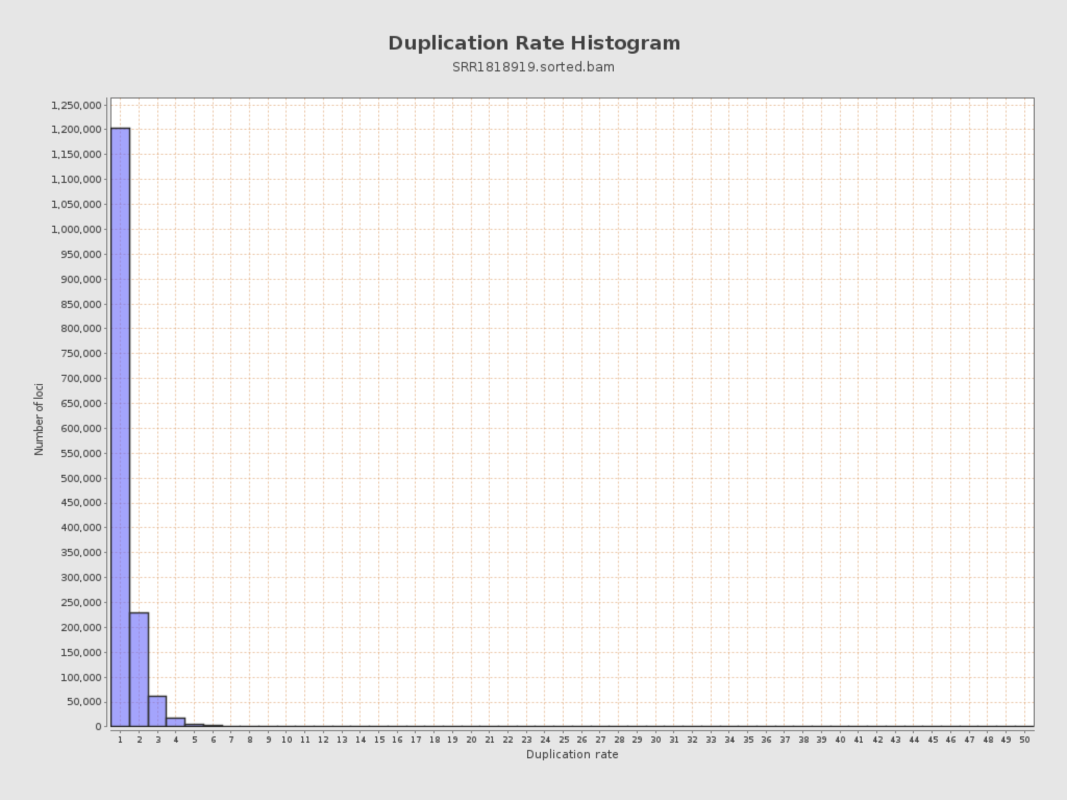
5. Results : Coverage Histogram (0-50X)



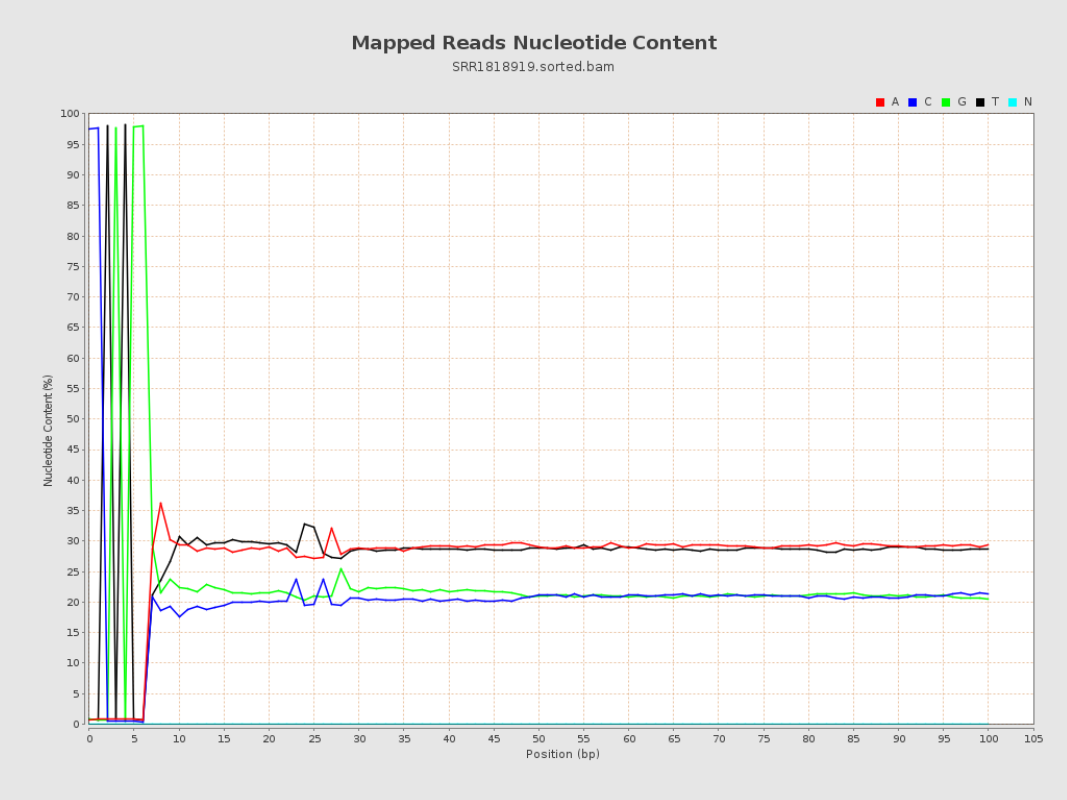
6. Results : Genome Fraction Coverage



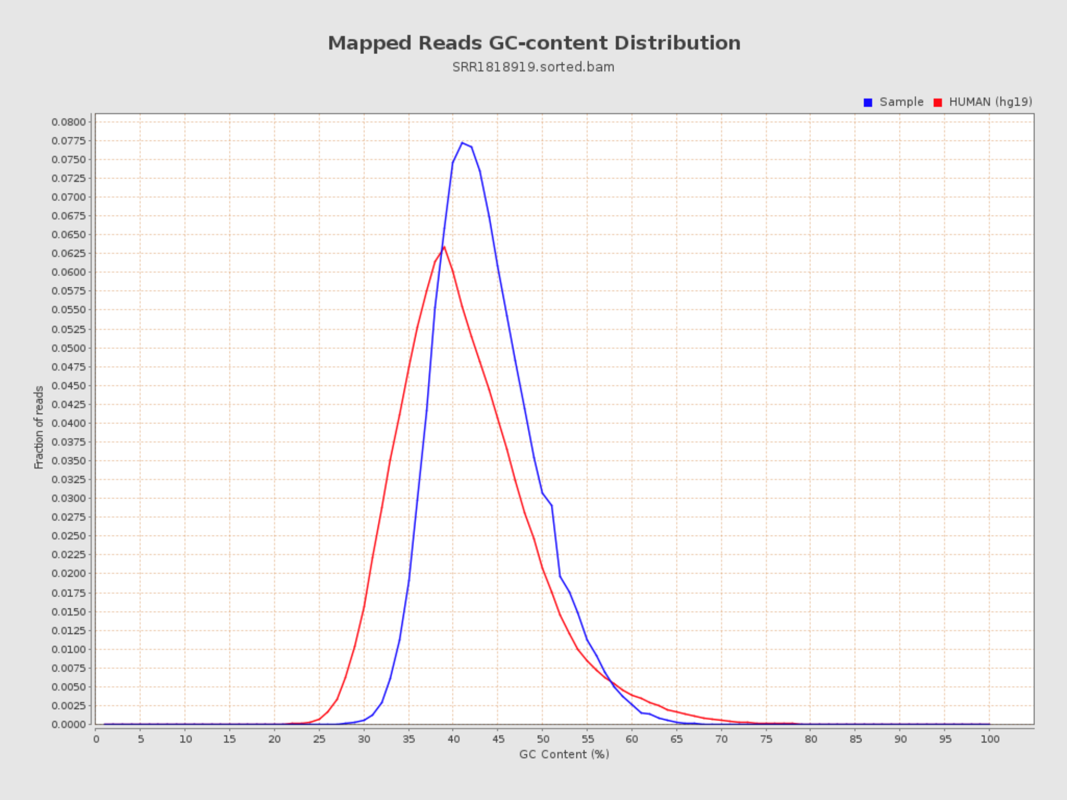
7. Results : Duplication Rate Histogram



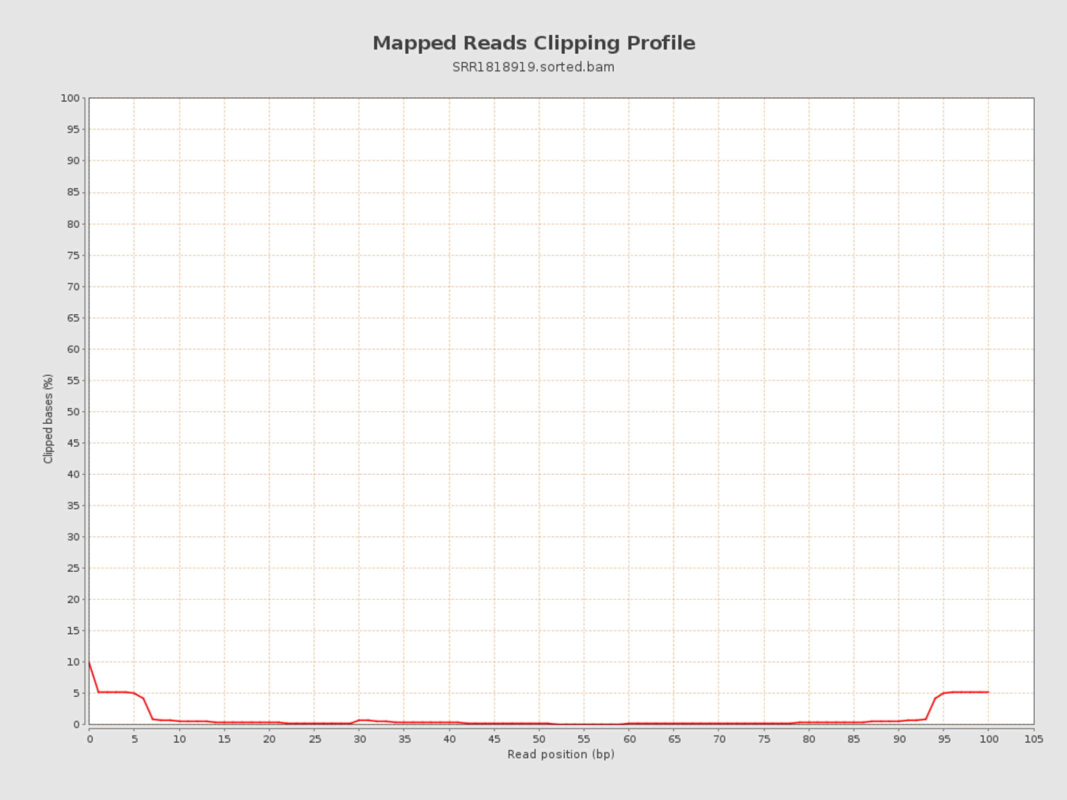
8. Results : Mapped Reads Nucleotide Content



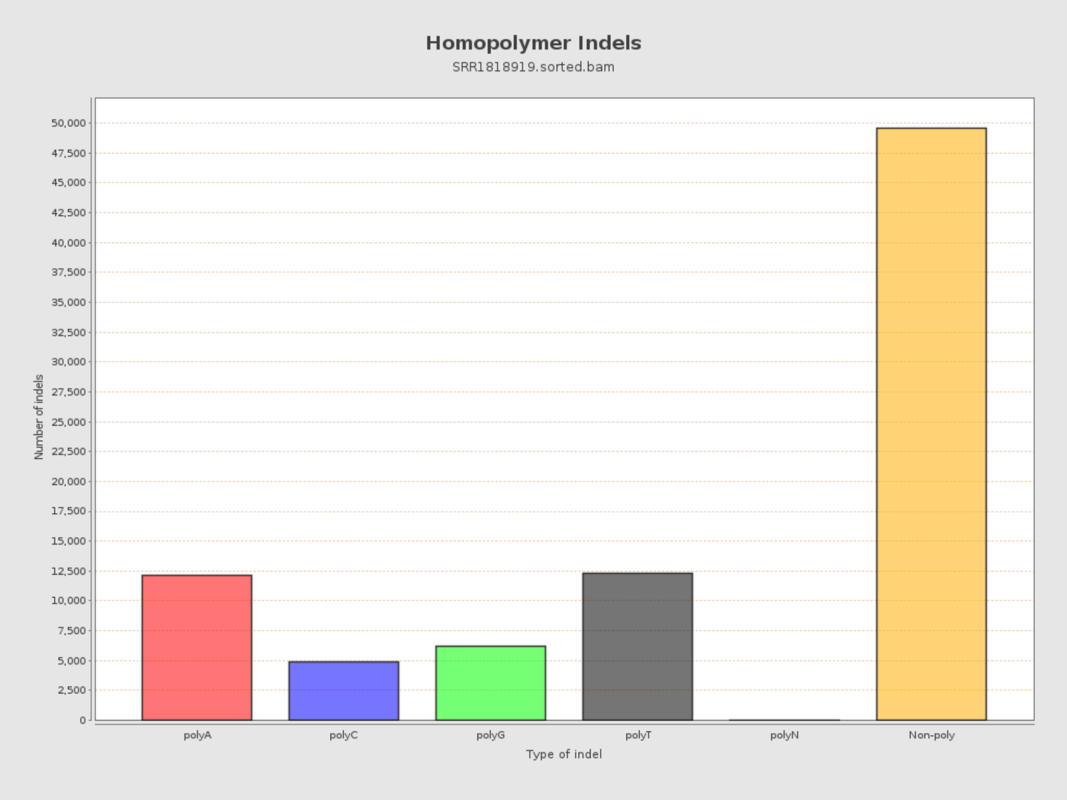
9. Results : Mapped Reads GC-content Distribution



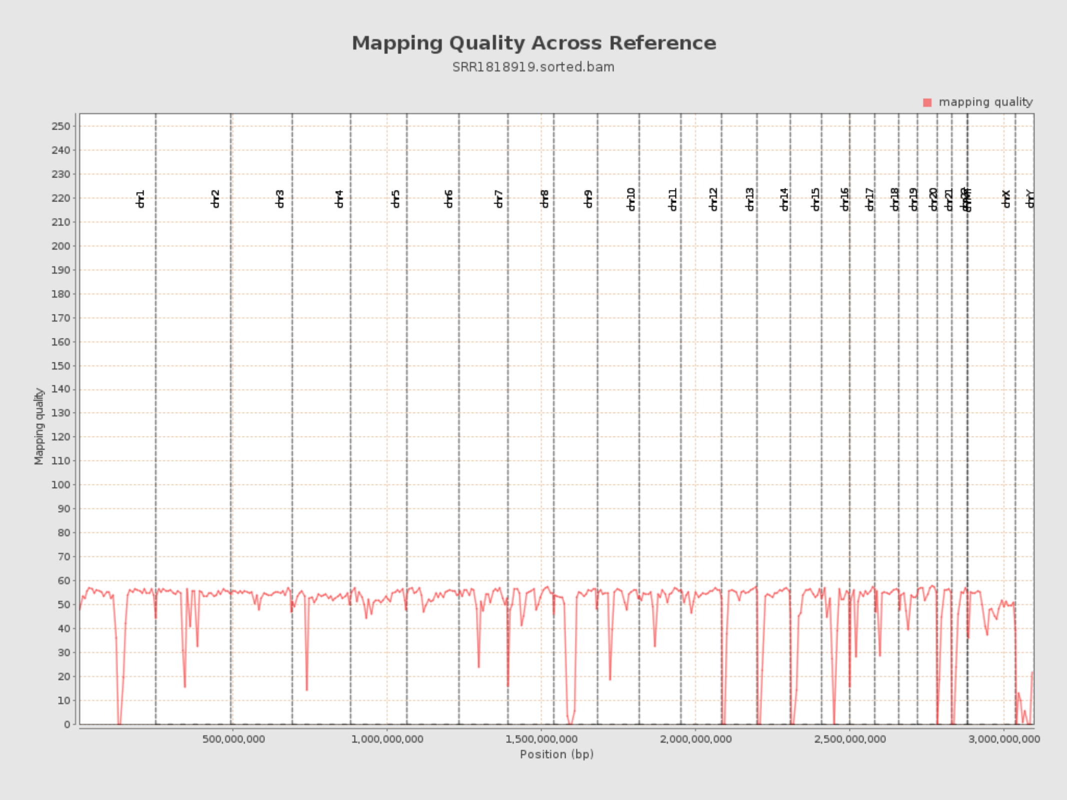
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram