

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 20:18:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505919.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_SRR1505919 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505919.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 20:18:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505919.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,539,077
Mapped reads	4,671,193 / 71.44%
Unmapped reads	1,867,884 / 28.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	235 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	200,681 / 3.07%
Duplication rate	3.11%
Clipped reads	942,398 / 14.41%

2.2. ACGT Content

Number/percentage of A's	63,157,865 / 29.39%
Number/percentage of C's	44,847,715 / 20.87%
Number/percentage of T's	61,870,526 / 28.79%
Number/percentage of G's	44,990,666 / 20.94%
Number/percentage of N's	635 / 0%
GC Percentage	41.81%

2.3. Coverage

Mean	0.0694

Standard Deviation	0.6026
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2.4. Mapping Quality

Mean Mapping Quality	43.2
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2.5. Mismatches and indels

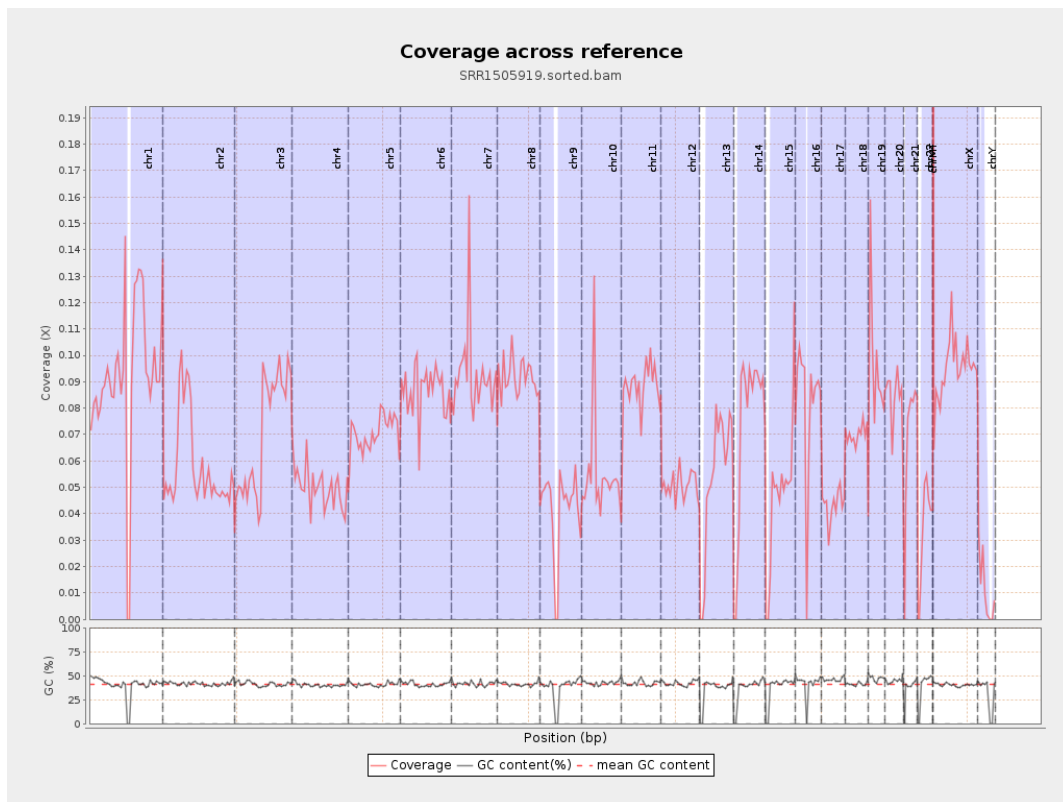
General error rate	0.51%
Mismatches	1,079,775
Insertions	9,484
Mapped reads with at least one insertion	0.2%
Deletions	31,440
Mapped reads with at least one deletion	0.67%
Homopolymer indels	44.92%

2.6. Chromosome stats

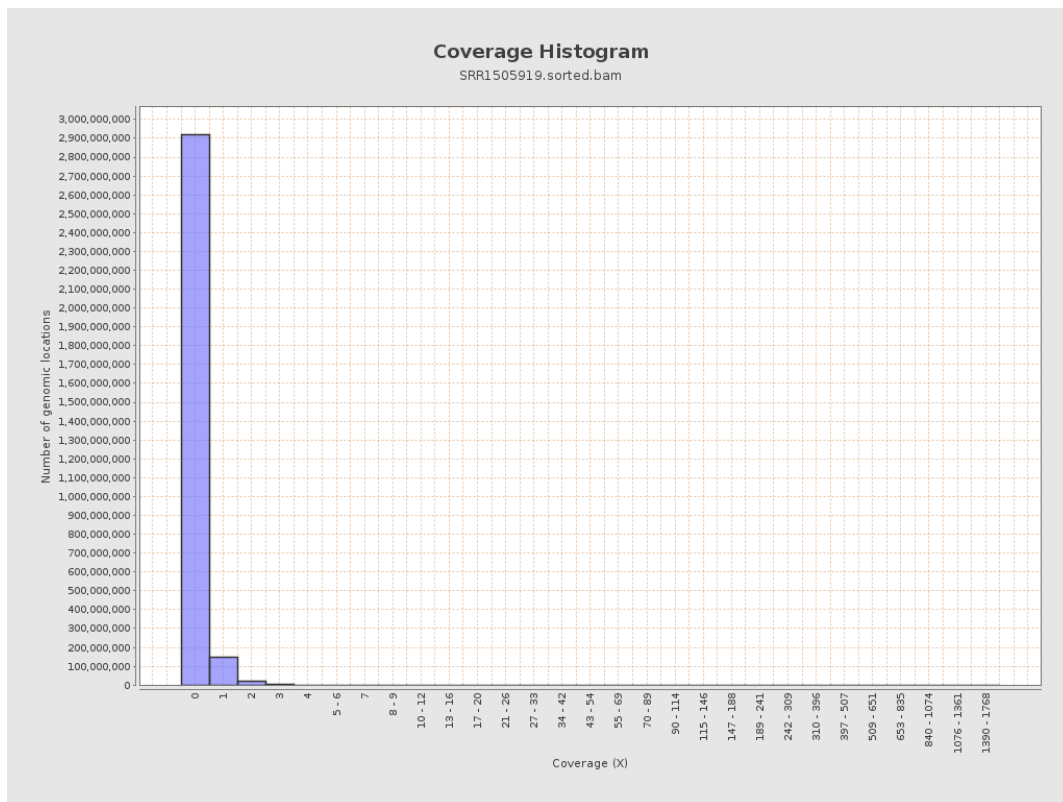
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	22982713	0.0922	1.2709
chr2	243199373	14163947	0.0582	0.412
chr3	198022430	13728644	0.0693	0.314
chr4	191154276	9563388	0.05	0.2654
chr5	180915260	12673495	0.0701	0.3171
chr6	171115067	14841188	0.0867	0.4169
chr7	159138663	14719943	0.0925	1.1109

chr8	146364022	13449797	0.0919	0.7064
chr9	141213431	5935753	0.042	0.3515
chr10	135534747	7399567	0.0546	0.6854
chr11	135006516	11865740	0.0879	0.5763
chr12	133851895	6821934	0.051	0.2862
chr13	115169878	6261137	0.0544	0.2709
chr14	107349540	8084309	0.0753	0.4558
chr15	102531392	4740142	0.0462	0.2501
chr16	90354753	7292582	0.0807	0.4341
chr17	81195210	3532698	0.0435	0.2867
chr18	78077248	5468974	0.07	0.6715
chr19	59128983	5659570	0.0957	0.9314
chr20	63025520	5289199	0.0839	0.3499
chr21	48129895	3301155	0.0686	0.3307
chr22	51304566	1738579	0.0339	0.2143
chrMT	16571	13774	0.8312	1.1424
chrX	155270560	14747500	0.095	0.4232
chrY	59373566	635480	0.0107	0.148

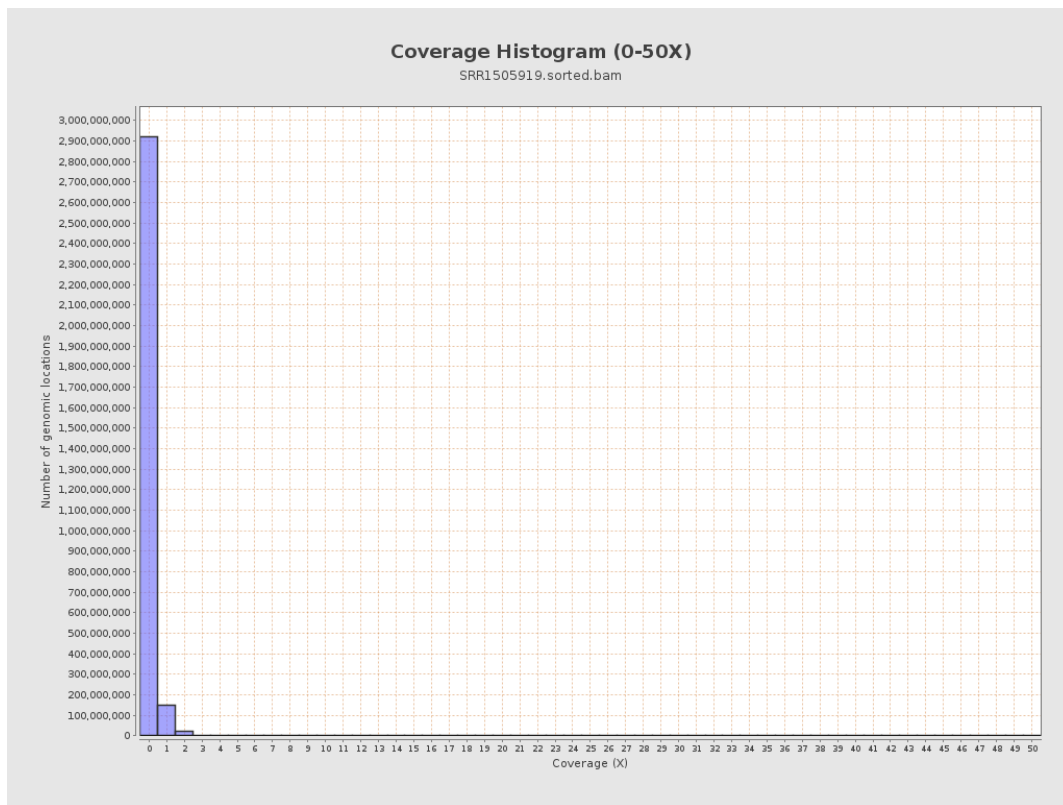
3. Results : Coverage across reference



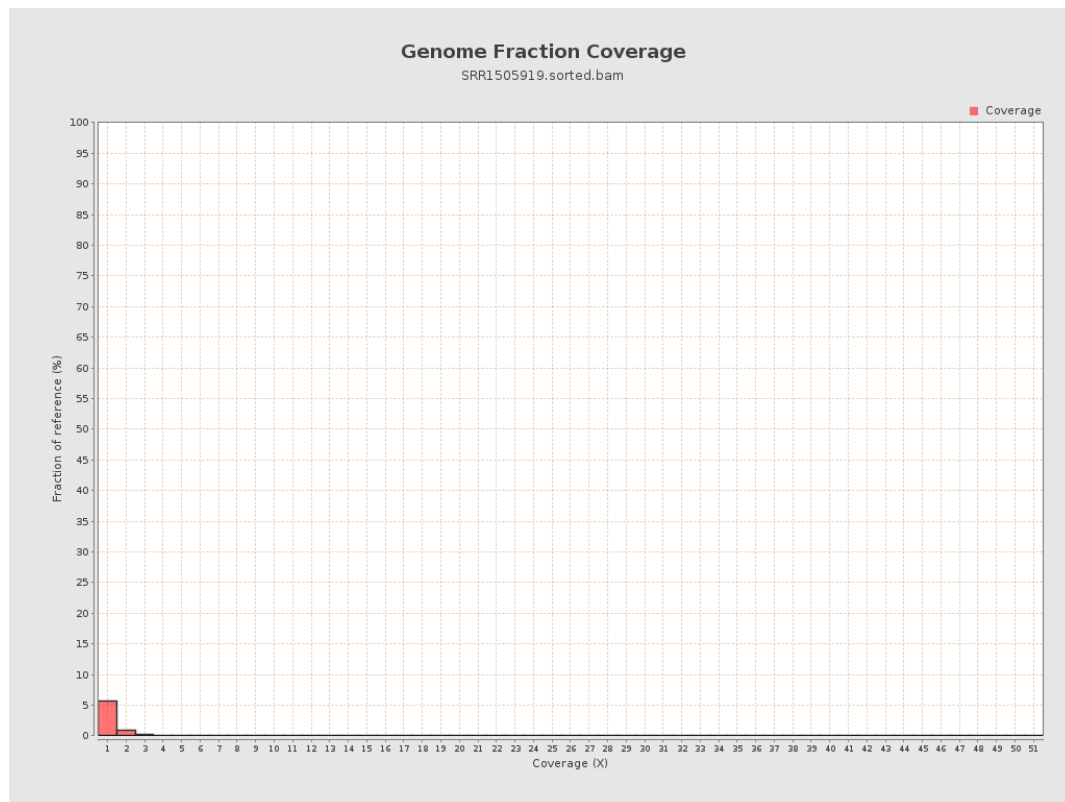
4. Results : Coverage Histogram



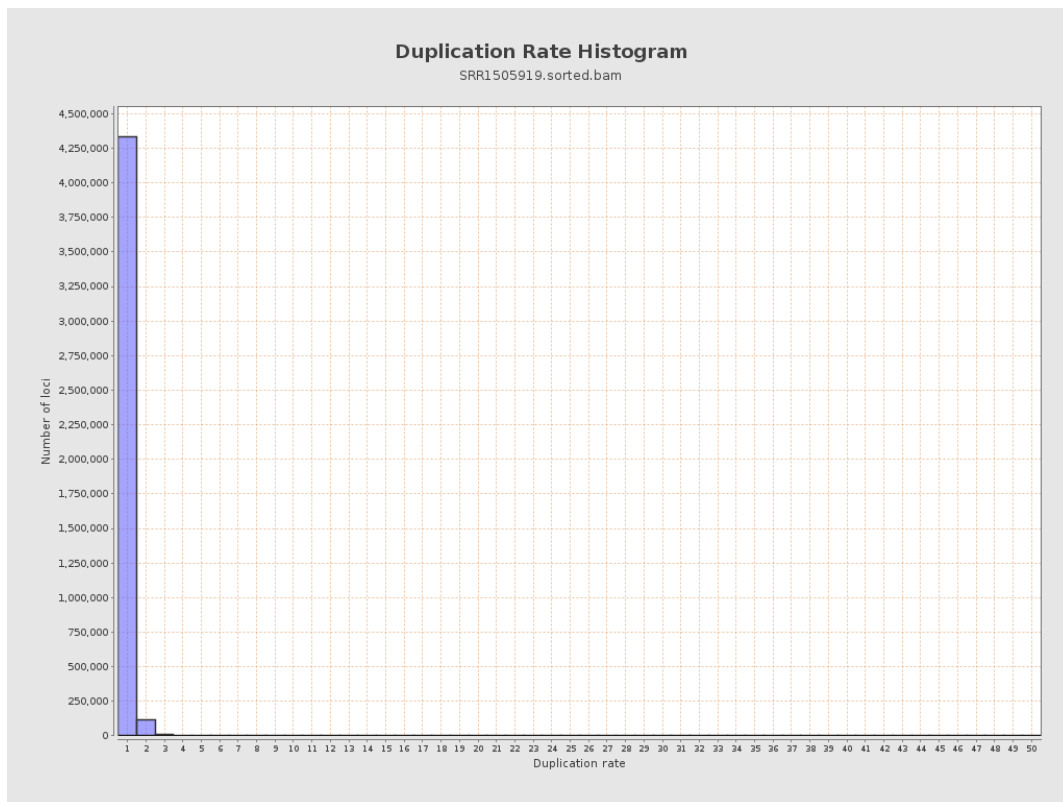
5. Results : Coverage Histogram (0-50X)



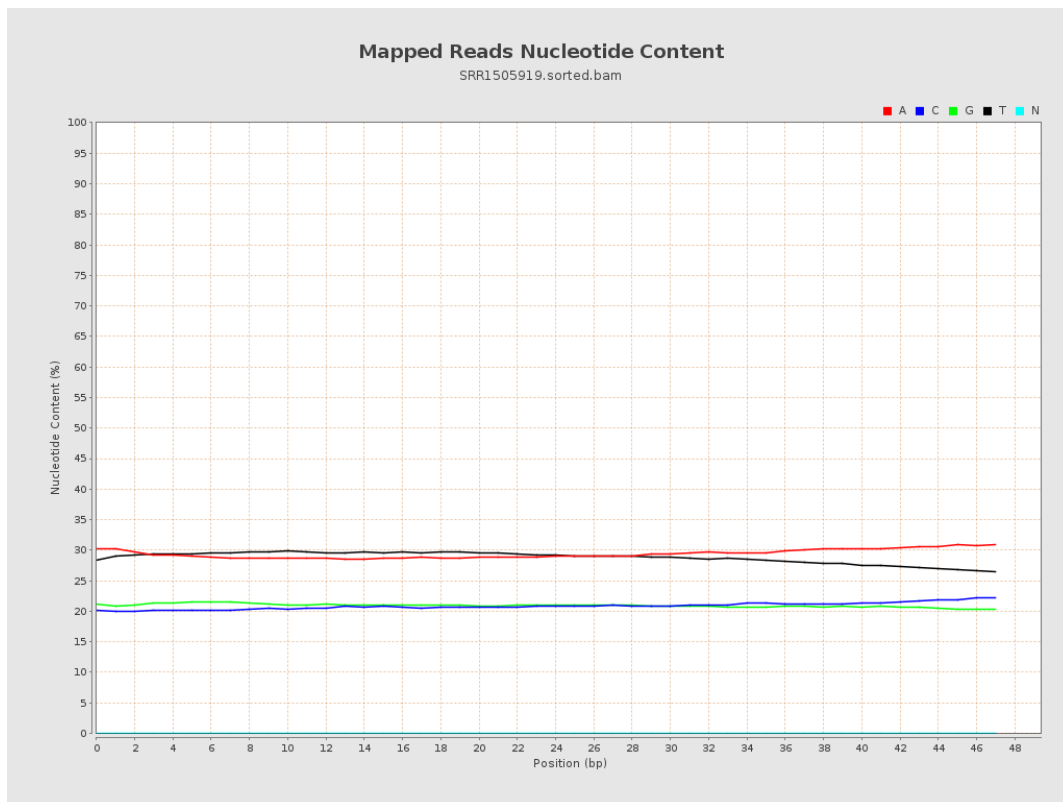
6. Results : Genome Fraction Coverage



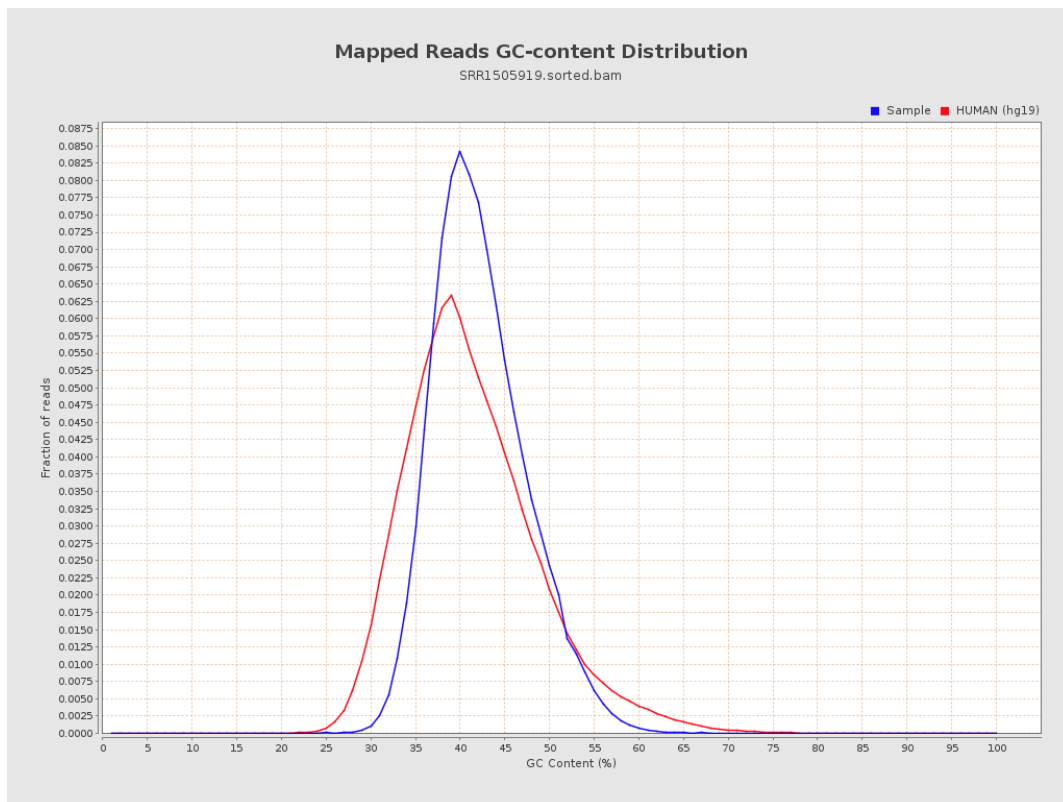
7. Results : Duplication Rate Histogram



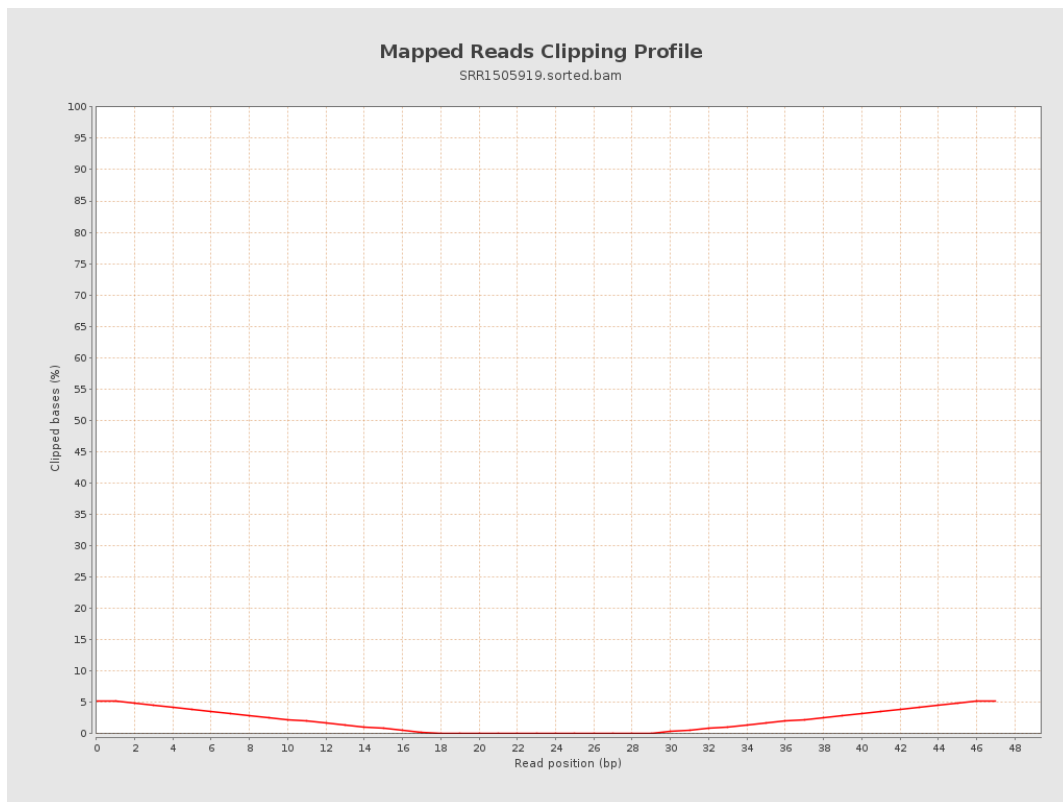
8. Results : Mapped Reads Nucleotide Content



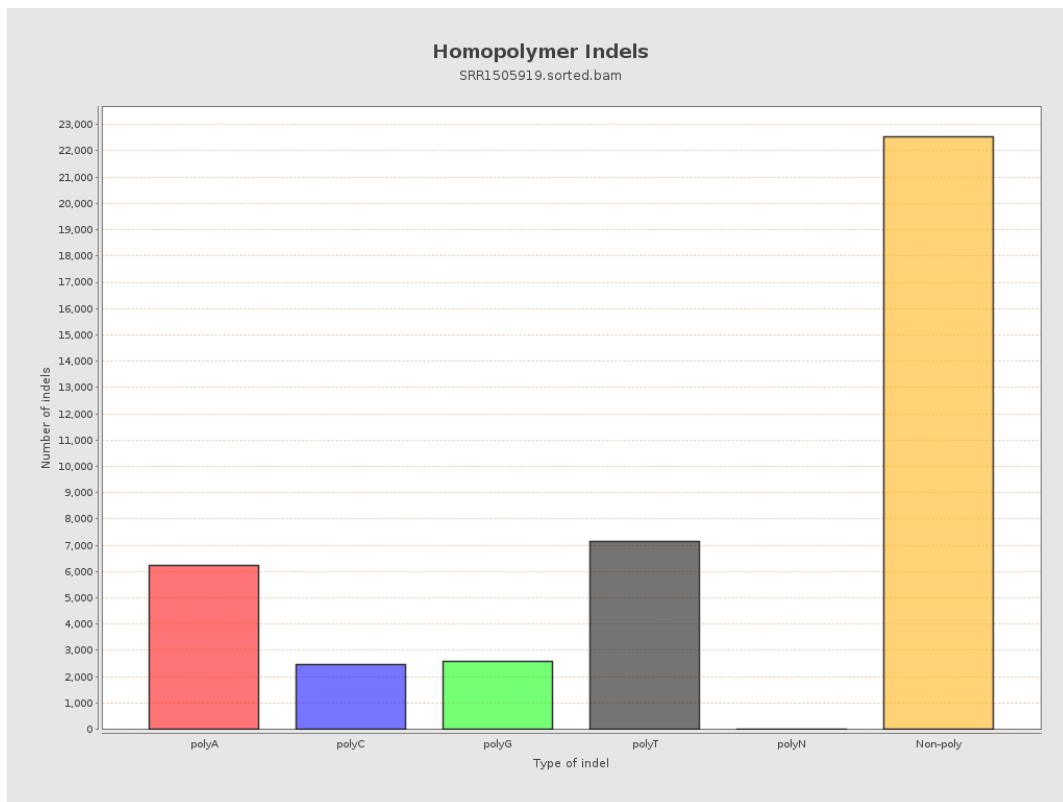
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

