

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 20:50:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505953.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_SRR1505953 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505953.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 20:50:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505953.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,833,191
Mapped reads	5,127,386 / 75.04%
Unmapped reads	1,705,805 / 24.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	244 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	323,380 / 4.73%
Duplication rate	4.73%
Clipped reads	804,628 / 11.78%

2.2. ACGT Content

Number/percentage of A's	70,366,915 / 29.54%
Number/percentage of C's	49,253,568 / 20.68%
Number/percentage of T's	69,201,760 / 29.05%
Number/percentage of G's	49,390,841 / 20.73%
Number/percentage of N's	695 / 0%
GC Percentage	41.41%

2.3. Coverage

Mean	0.077

Standard Deviation	0.6938
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2.4. Mapping Quality

Mean Mapping Quality	44.28
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2.5. Mismatches and indels

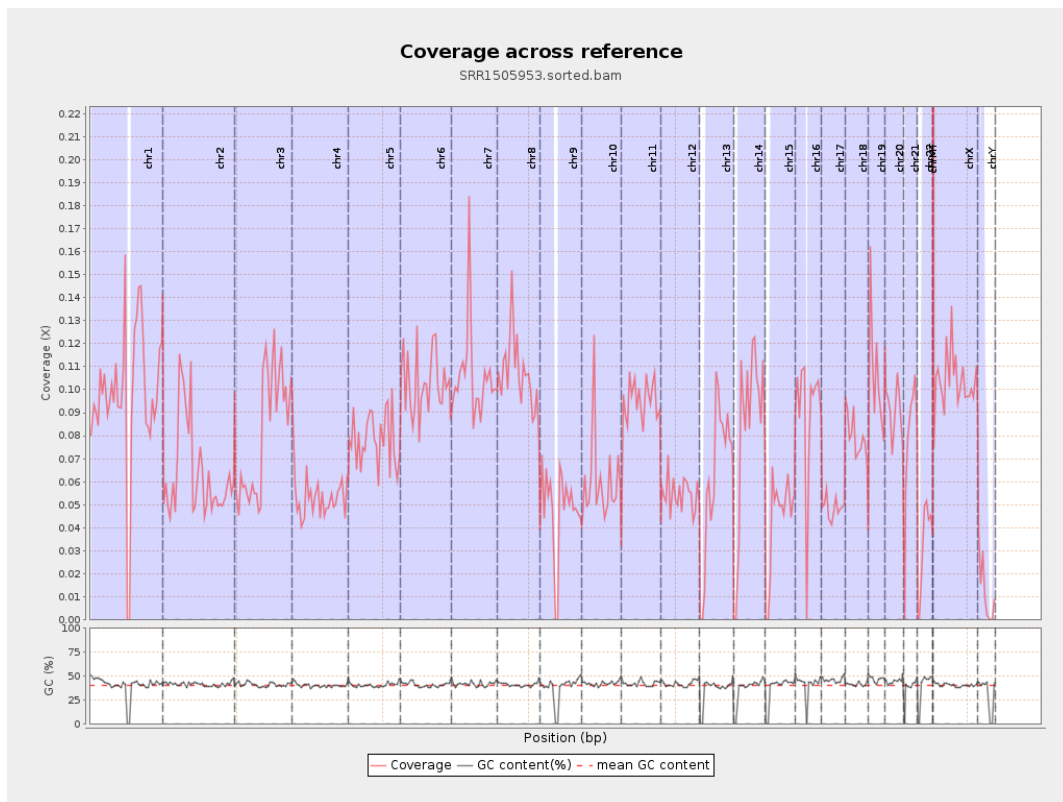
General error rate	0.5%
Mismatches	1,169,500
Insertions	10,090
Mapped reads with at least one insertion	0.2%
Deletions	35,118
Mapped reads with at least one deletion	0.68%
Homopolymer indels	45.77%

2.6. Chromosome stats

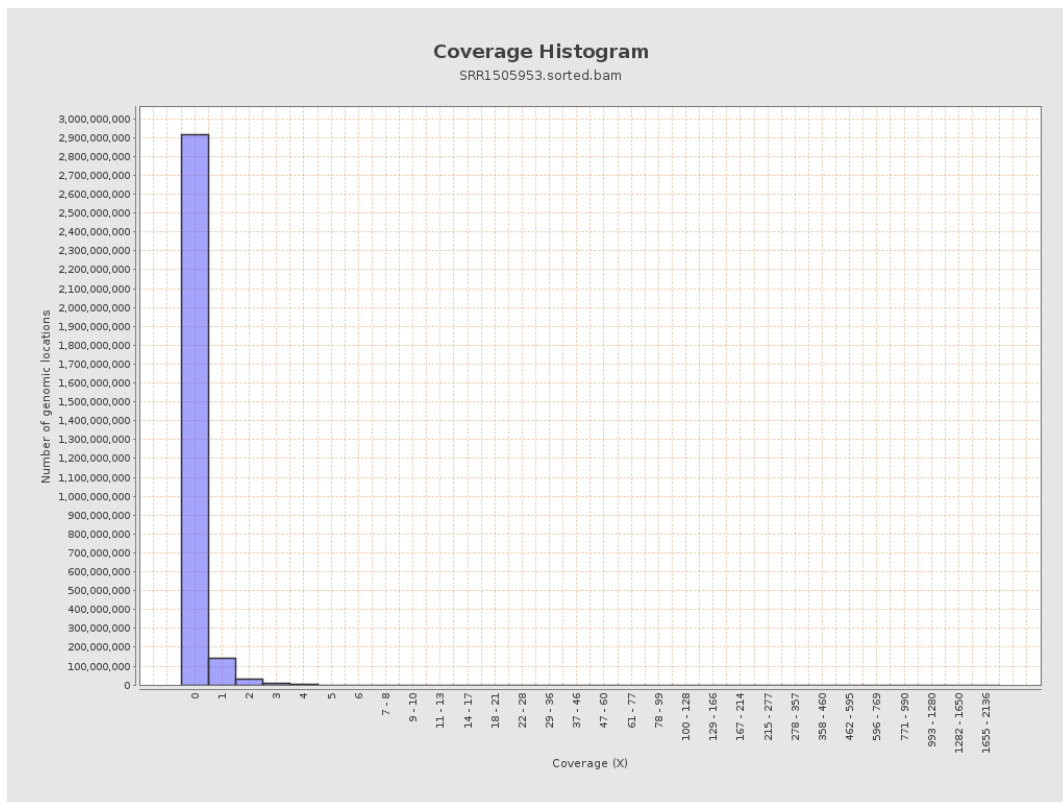
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24431383	0.098	1.5354
chr2	243199373	15515266	0.0638	0.476
chr3	198022430	16016652	0.0809	0.3633
chr4	191154276	10181739	0.0533	0.2956
chr5	180915260	14133620	0.0781	0.3564
chr6	171115067	17552866	0.1026	0.5491
chr7	159138663	16846949	0.1059	1.1922

chr8	146364022	15543452	0.1062	0.8763
chr9	141213431	6826392	0.0483	0.3927
chr10	135534747	8043934	0.0593	0.6827
chr11	135006516	12760262	0.0945	0.576
chr12	133851895	7292237	0.0545	0.3128
chr13	115169878	7305366	0.0634	0.3145
chr14	107349540	9061445	0.0844	0.5171
chr15	102531392	4418214	0.0431	0.2563
chr16	90354753	8057076	0.0892	0.4361
chr17	81195210	3941964	0.0485	0.3154
chr18	78077248	6226353	0.0797	0.6995
chr19	59128983	6207141	0.105	1.1842
chr20	63025520	5684403	0.0902	0.392
chr21	48129895	3751873	0.078	0.377
chr22	51304566	1677390	0.0327	0.2235
chrMT	16571	31107	1.8772	1.9377
chrX	155270560	16051068	0.1034	0.4589
chrY	59373566	704572	0.0119	0.1664

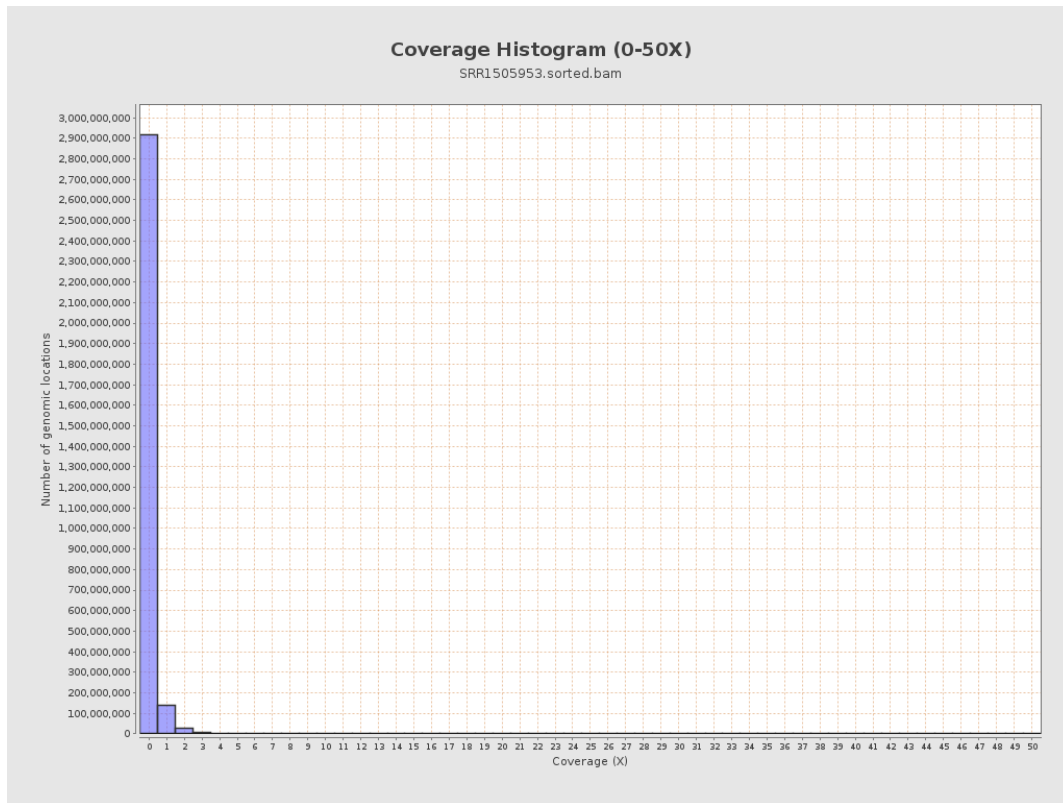
3. Results : Coverage across reference



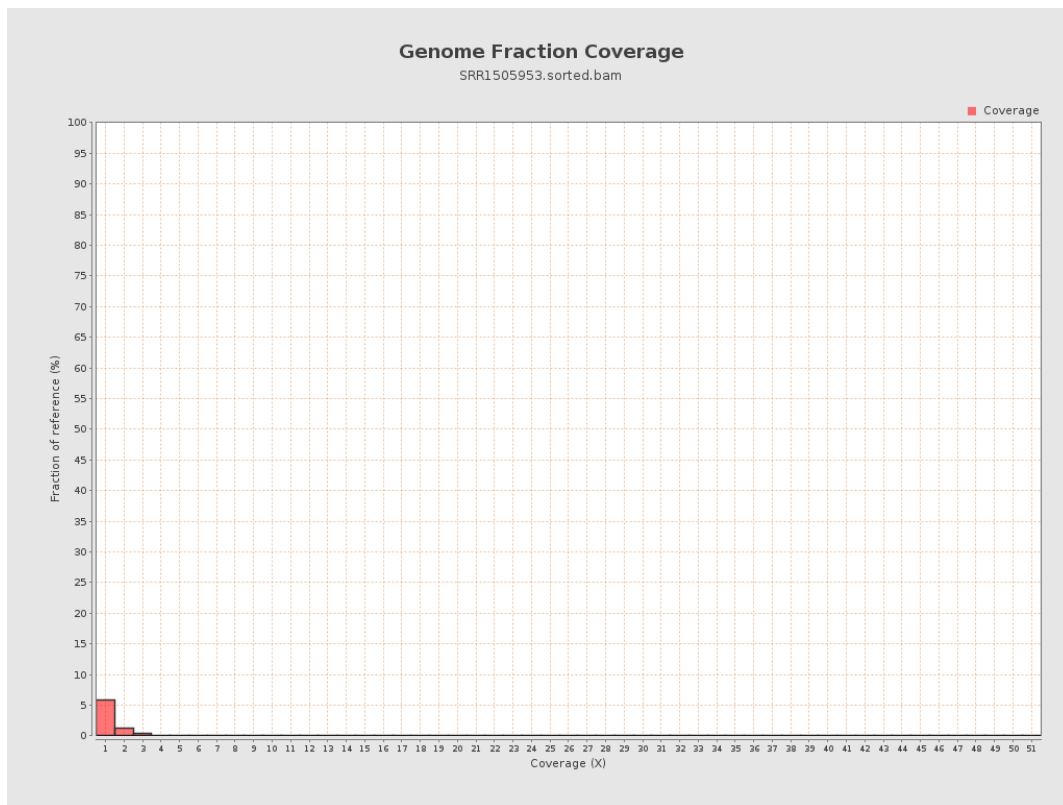
4. Results : Coverage Histogram



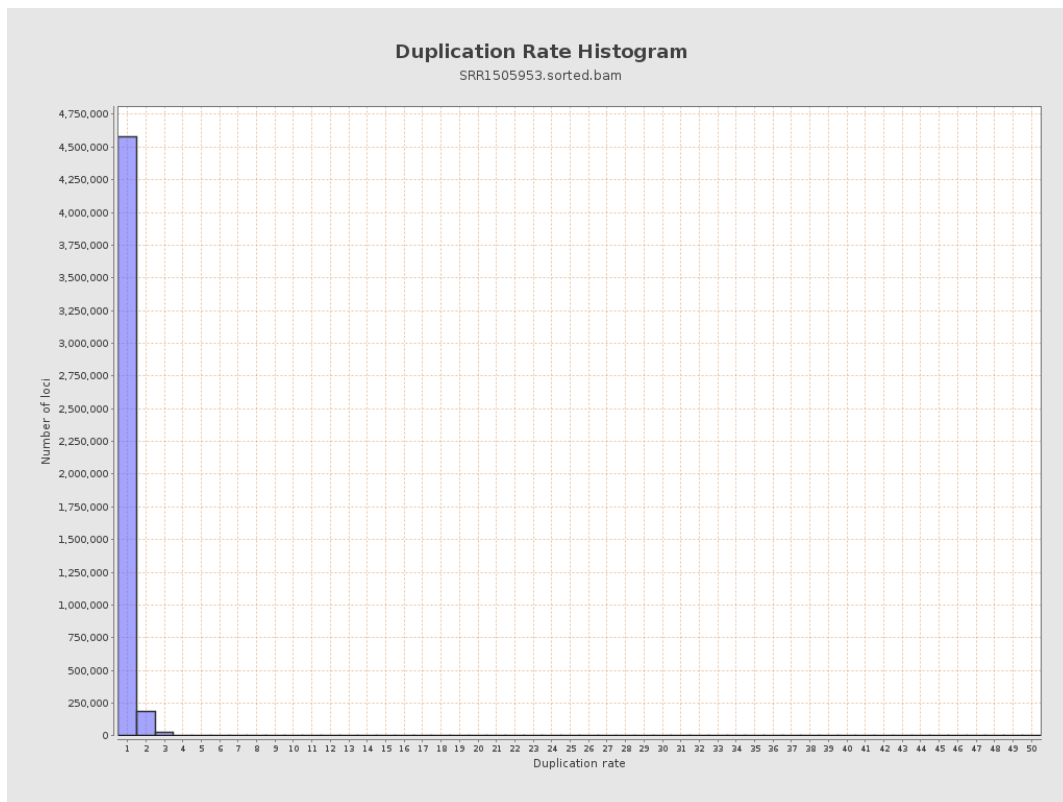
5. Results : Coverage Histogram (0-50X)



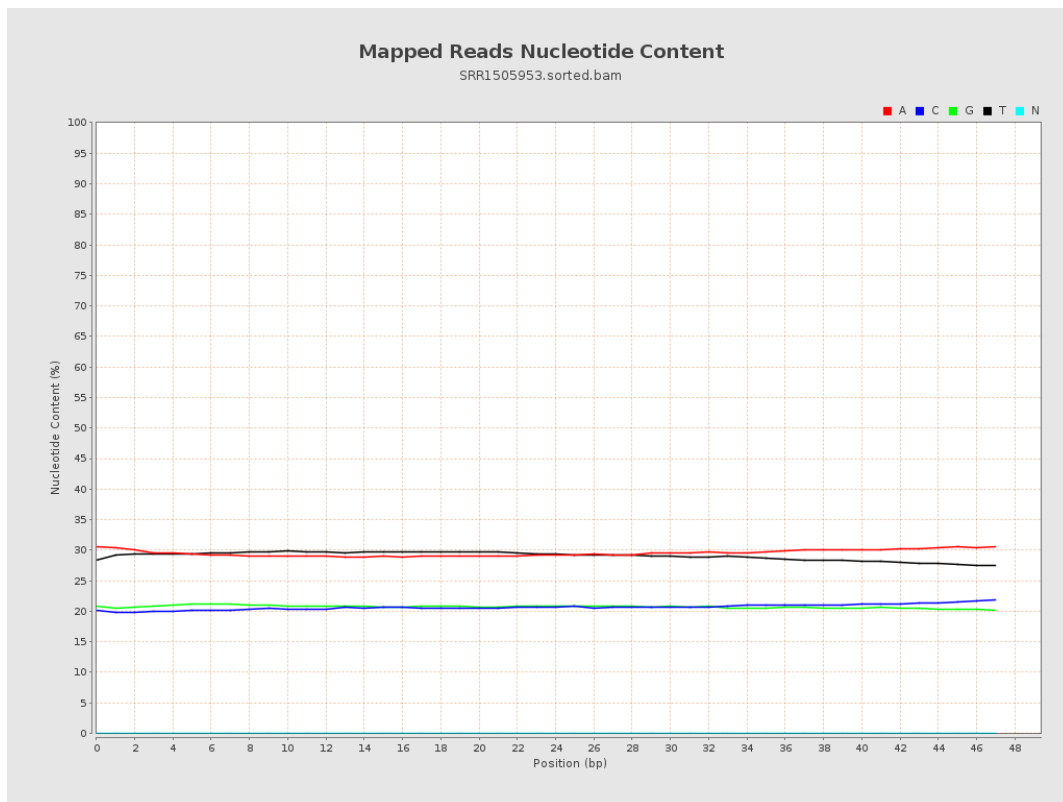
6. Results : Genome Fraction Coverage



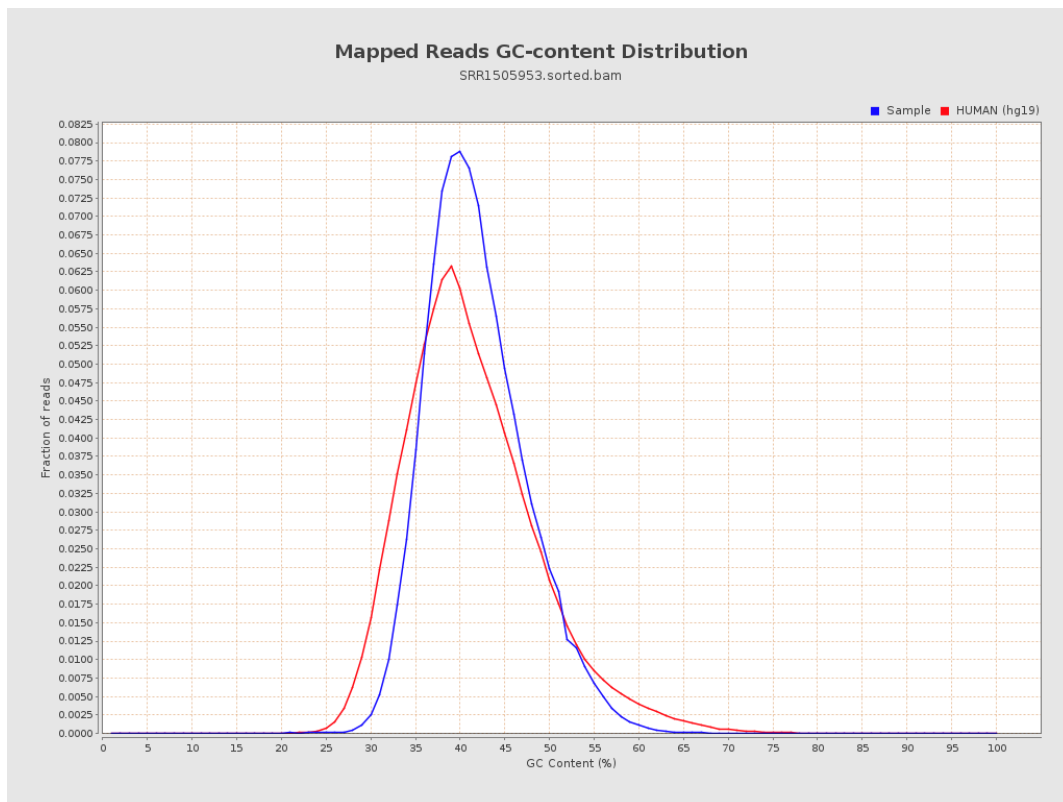
7. Results : Duplication Rate Histogram



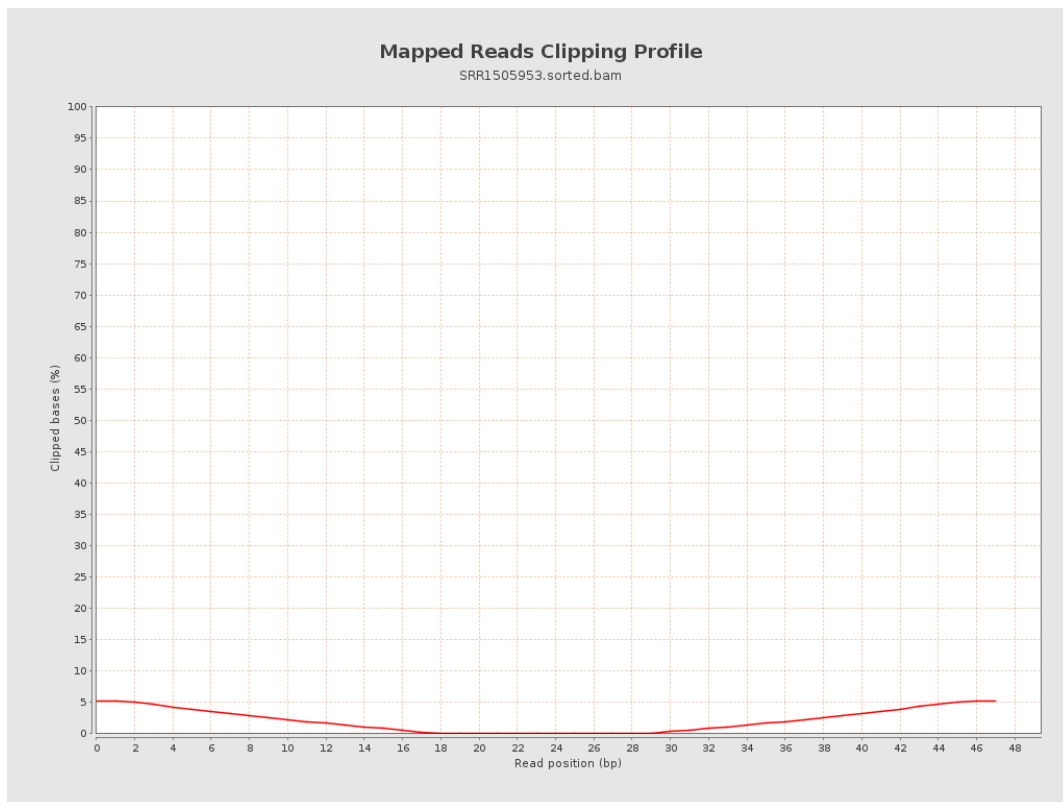
8. Results : Mapped Reads Nucleotide Content



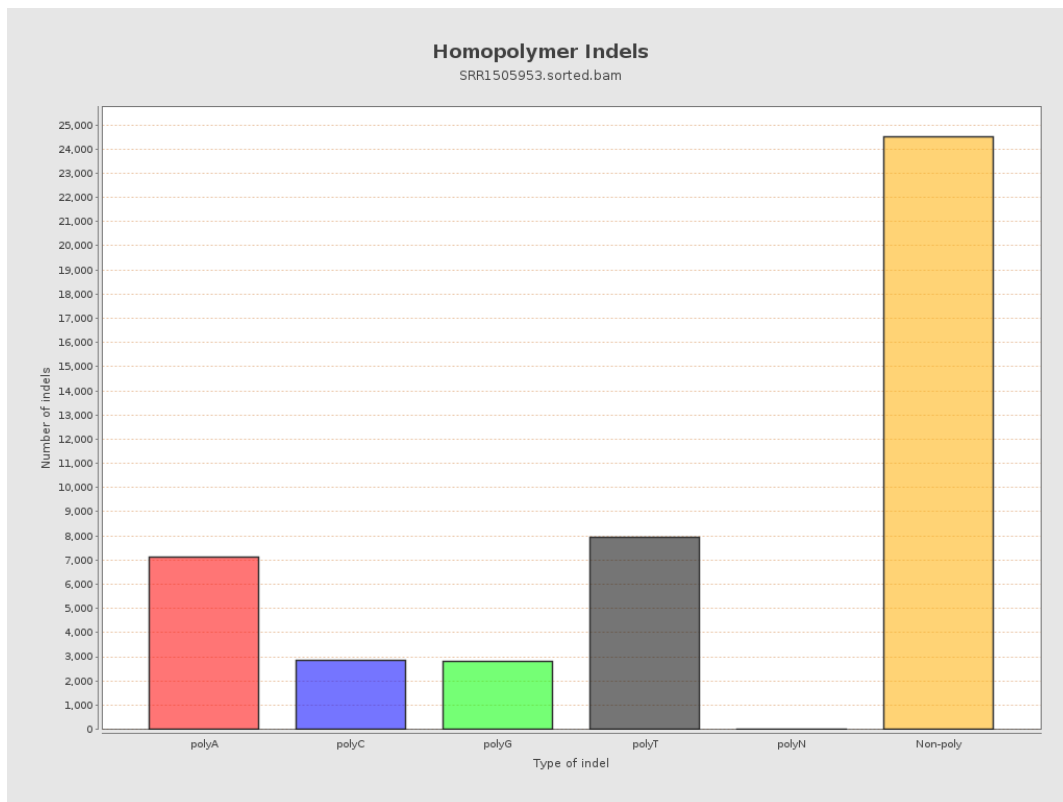
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

