

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 21:51:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524303.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_SRR10524303 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524303.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 21:51:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524303.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,448,877
Mapped reads	2,241,756 / 91.54%
Unmapped reads	207,121 / 8.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,339 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	88,927 / 3.63%
Duplication rate	2.81%
Clipped reads	2,244,501 / 91.65%

2.2. ACGT Content

Number/percentage of A's	32,030,751 / 24.49%
Number/percentage of C's	22,702,705 / 17.36%
Number/percentage of T's	41,703,920 / 31.89%
Number/percentage of G's	34,334,365 / 26.25%
Number/percentage of N's	18,684 / 0.01%
GC Percentage	43.61%

2.3. Coverage

Mean	0.0423

Standard Deviation	0.3777
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2.4. Mapping Quality

Mean Mapping Quality	44.37
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2.5. Mismatches and indels

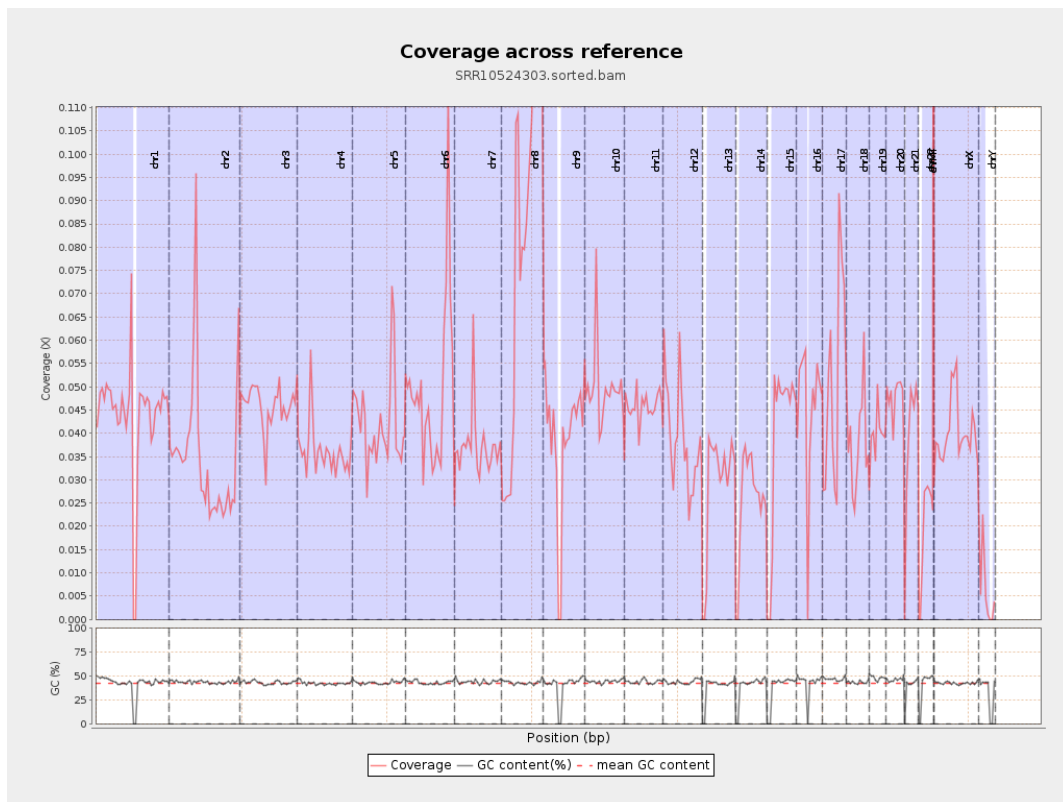
General error rate	0.52%
Mismatches	668,955
Insertions	9,068
Mapped reads with at least one insertion	0.4%
Deletions	23,481
Mapped reads with at least one deletion	1.04%
Homopolymer indels	43.5%

2.6. Chromosome stats

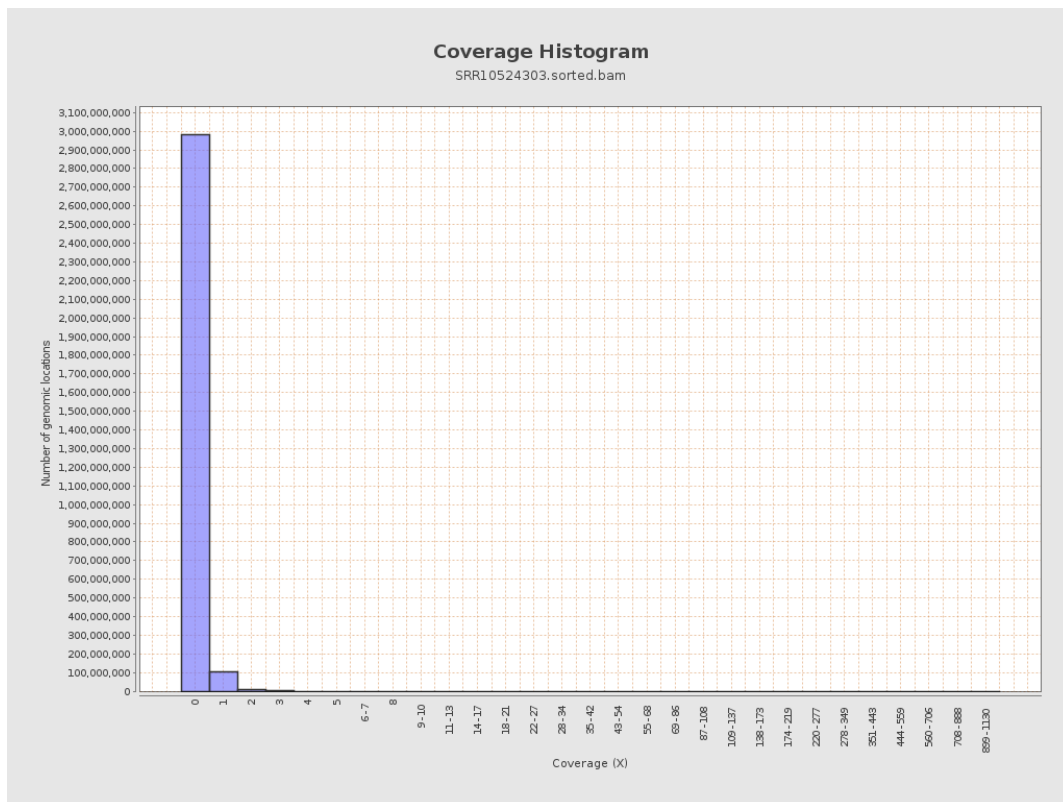
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10912107	0.0438	0.7535
chr2	243199373	8512329	0.035	0.5084
chr3	198022430	9061044	0.0458	0.237
chr4	191154276	6869901	0.0359	0.2453
chr5	180915260	7633368	0.0422	0.2283
chr6	171115067	8412703	0.0492	0.2745
chr7	159138663	5960087	0.0375	0.4696

chr8	146364022	13701081	0.0936	0.4607
chr9	141213431	5405248	0.0383	0.2789
chr10	135534747	6698034	0.0494	0.3612
chr11	135006516	6181541	0.0458	0.2998
chr12	133851895	5186714	0.0387	0.2224
chr13	115169878	3334721	0.029	0.1901
chr14	107349540	2764041	0.0257	0.1904
chr15	102531392	4054479	0.0395	0.222
chr16	90354753	4153048	0.046	0.2617
chr17	81195210	4116153	0.0507	0.2799
chr18	78077248	3026005	0.0388	0.5101
chr19	59128983	2368263	0.0401	0.457
chr20	63025520	3001607	0.0476	0.2493
chr21	48129895	1877923	0.039	0.2456
chr22	51304566	993473	0.0194	0.1544
chrMT	16571	5455	0.3292	0.6529
chrX	155270560	6233402	0.0401	0.2548
chrY	59373566	364745	0.0061	0.171

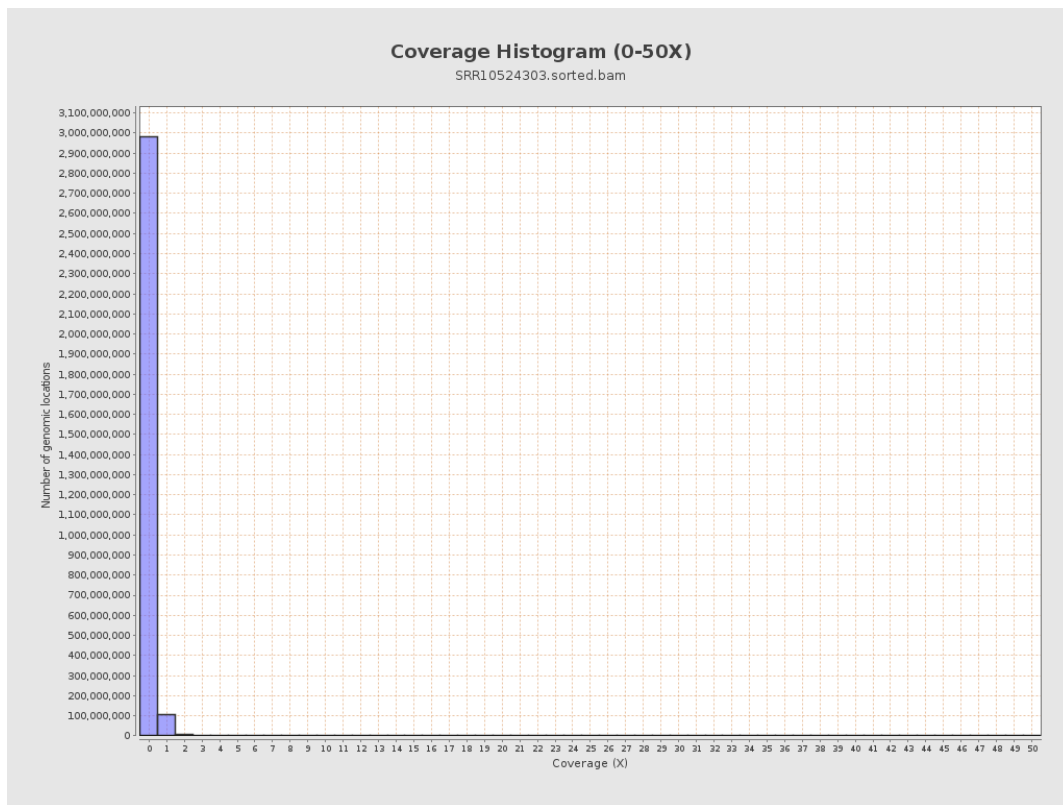
3. Results : Coverage across reference



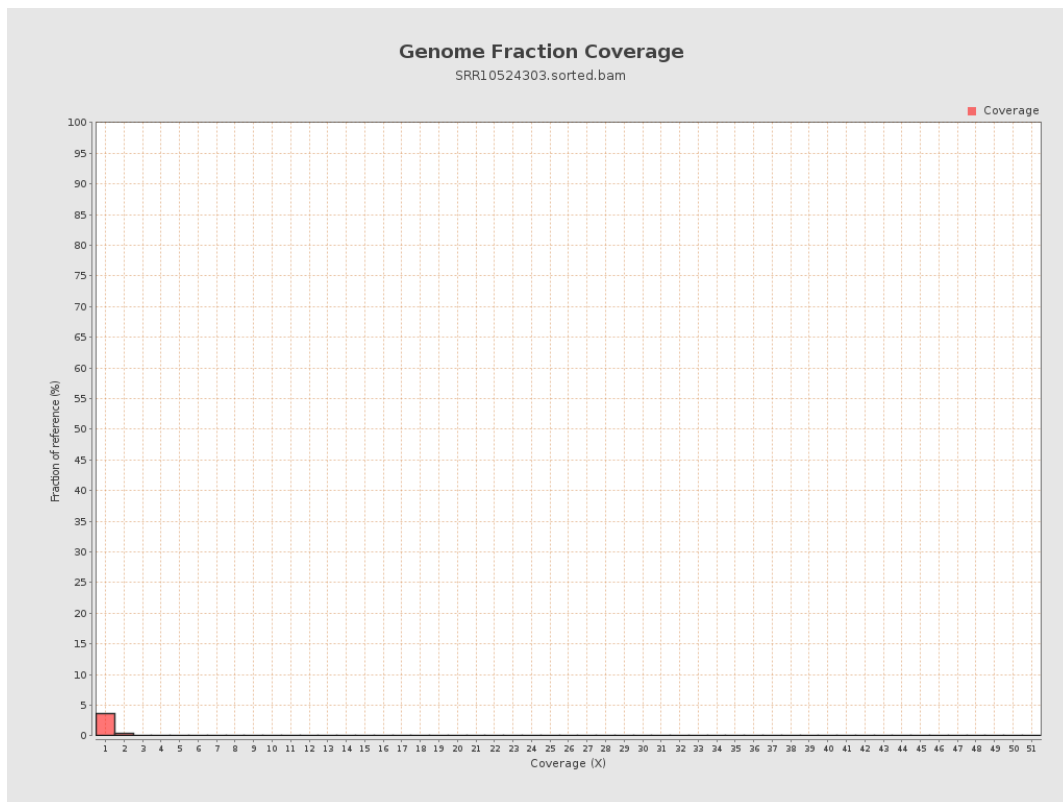
4. Results : Coverage Histogram



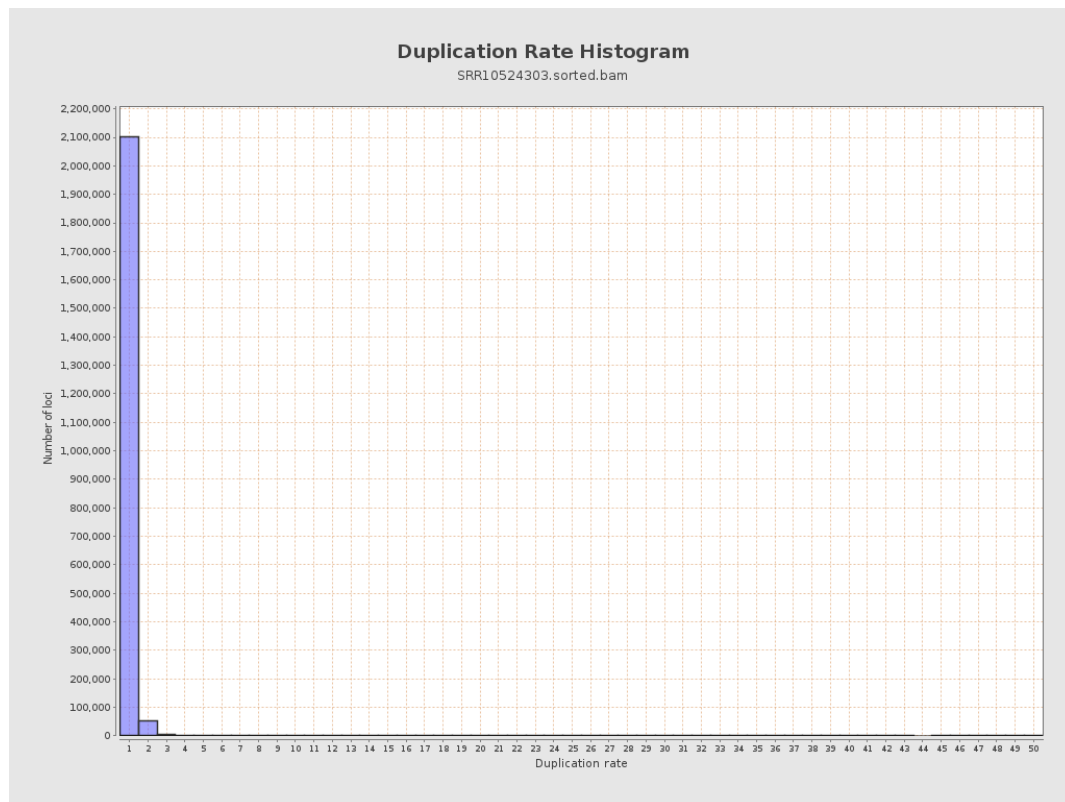
5. Results : Coverage Histogram (0-50X)



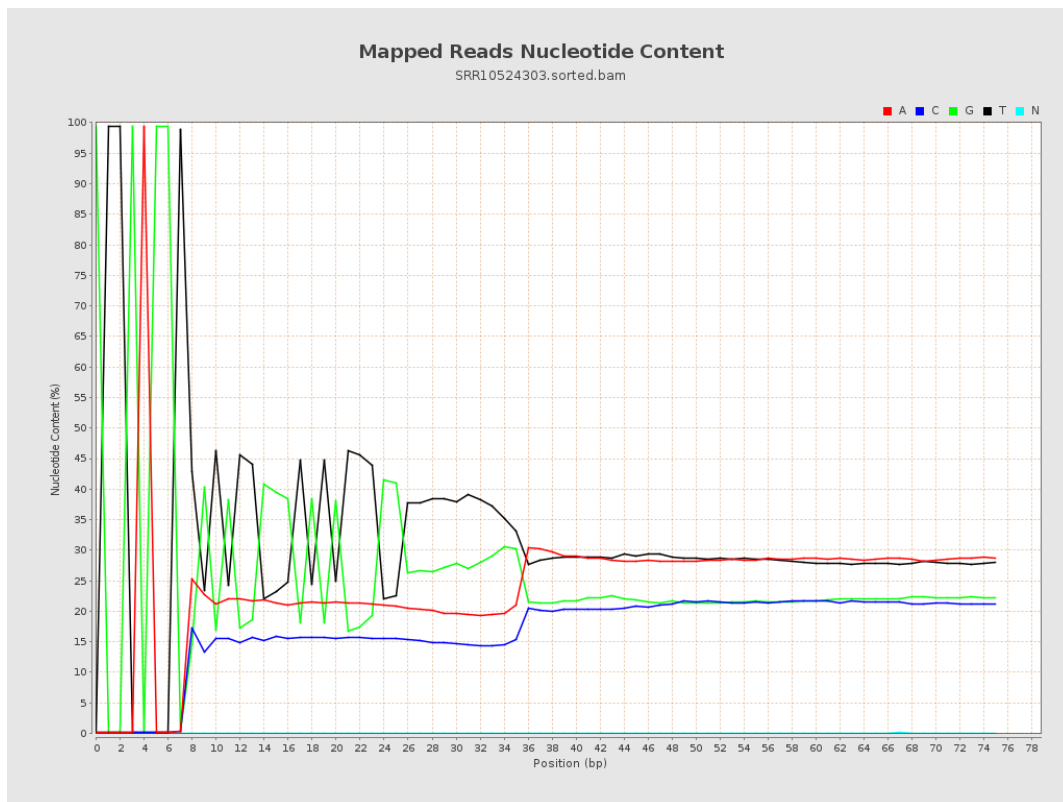
6. Results : Genome Fraction Coverage



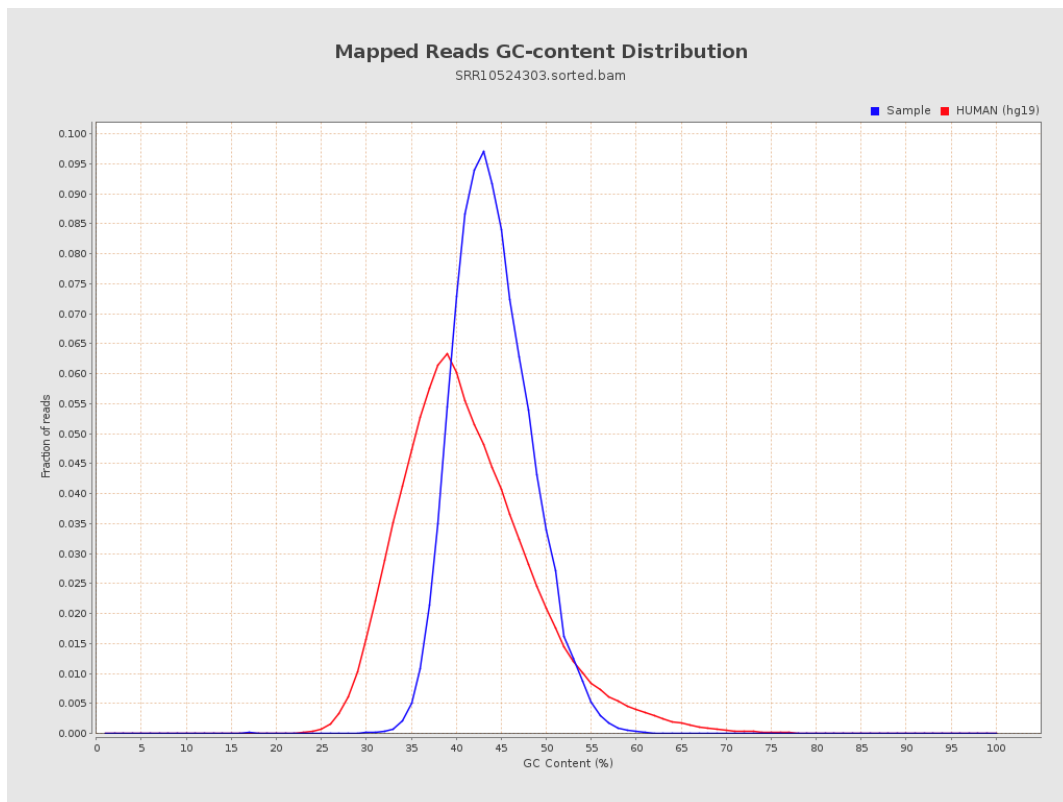
7. Results : Duplication Rate Histogram



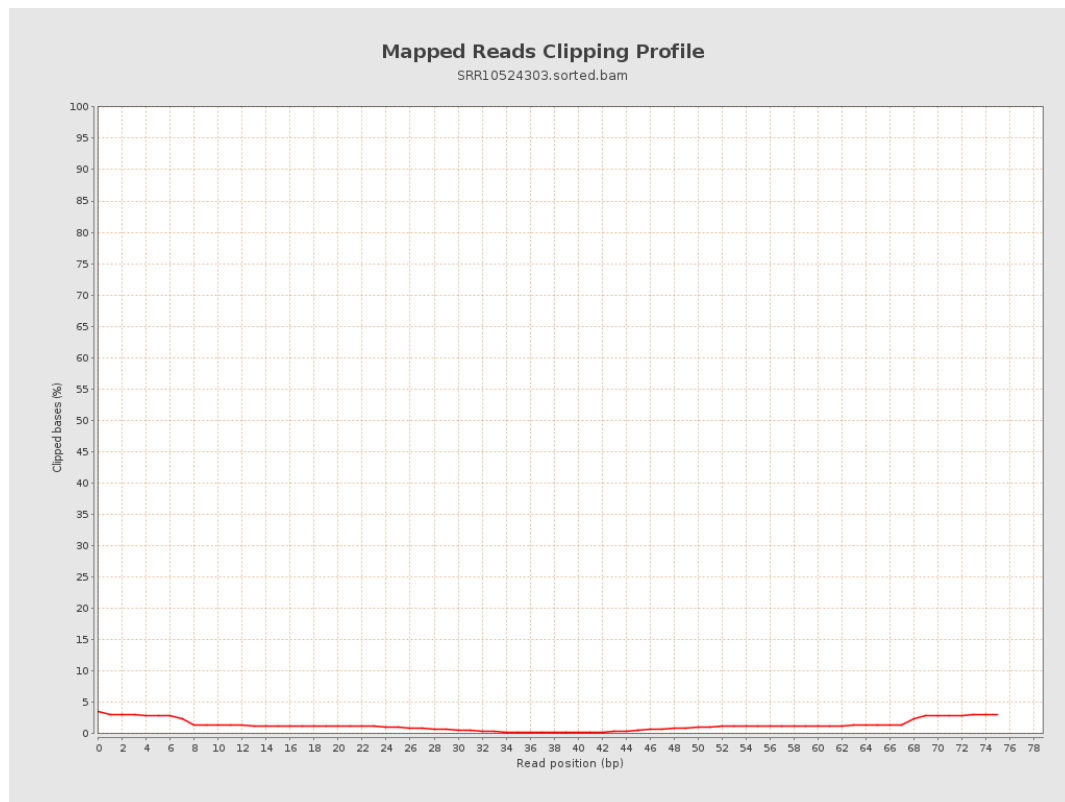
8. Results : Mapped Reads Nucleotide Content



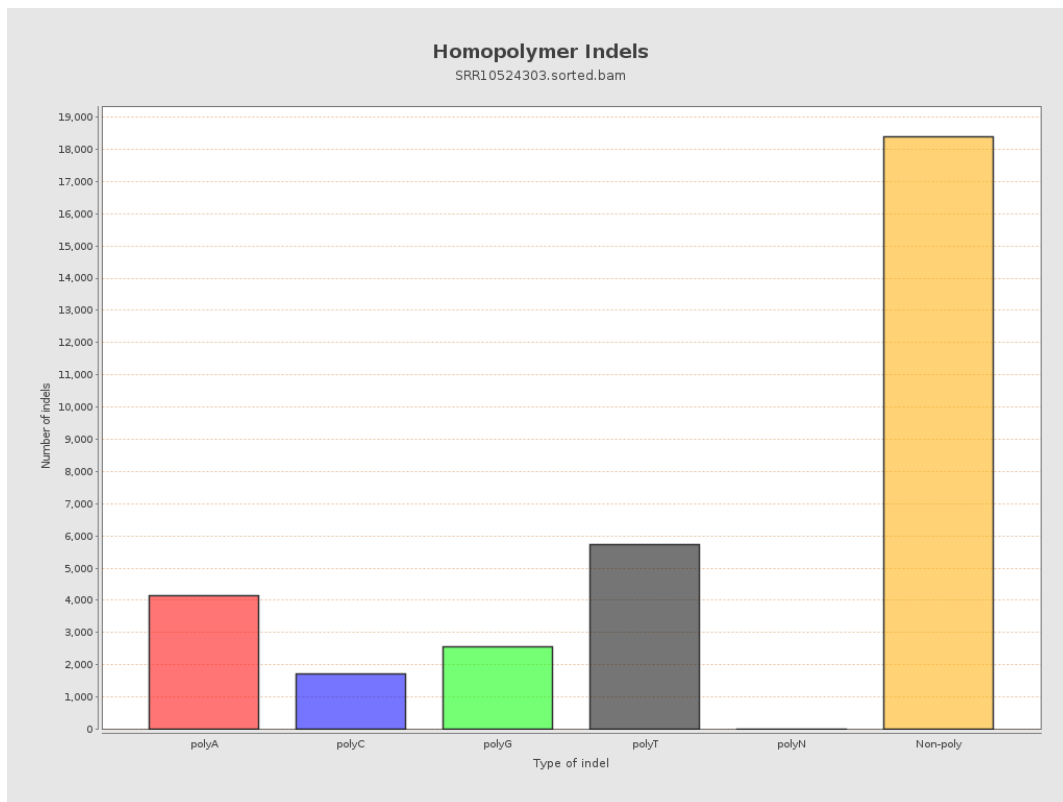
9. Results : Mapped Reads GC-content Distribution



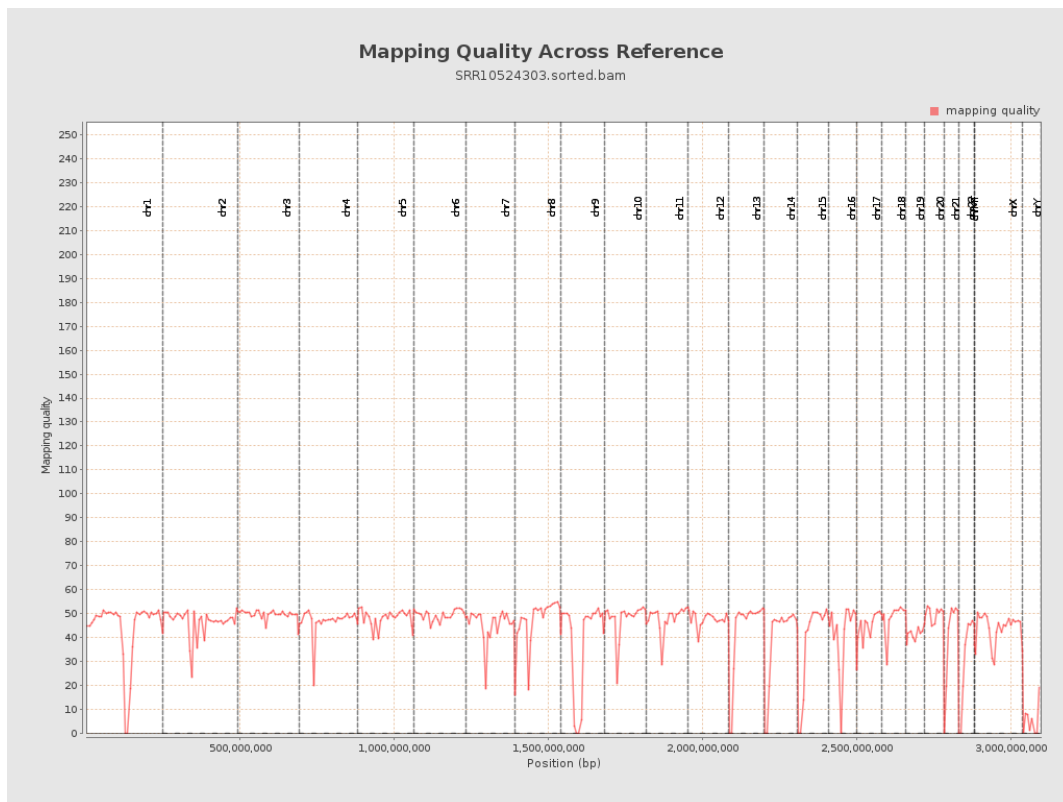
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

