

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 11:50:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524587.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_SRR10524587 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524587.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 11:50:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524587.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,731,928
Mapped reads	2,543,434 / 93.1%
Unmapped reads	188,494 / 6.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,697 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	169,577 / 6.21%
Duplication rate	5.11%
Clipped reads	2,545,890 / 93.19%

2.2. ACGT Content

Number/percentage of A's	38,299,566 / 25.72%
Number/percentage of C's	30,199,322 / 20.28%
Number/percentage of T's	45,289,217 / 30.41%
Number/percentage of G's	35,118,061 / 23.58%
Number/percentage of N's	934 / 0%
GC Percentage	43.86%

2.3. Coverage

Mean	0.0481

Standard Deviation	0.4017
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2.4. Mapping Quality

Mean Mapping Quality	45.47
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2.5. Mismatches and indels

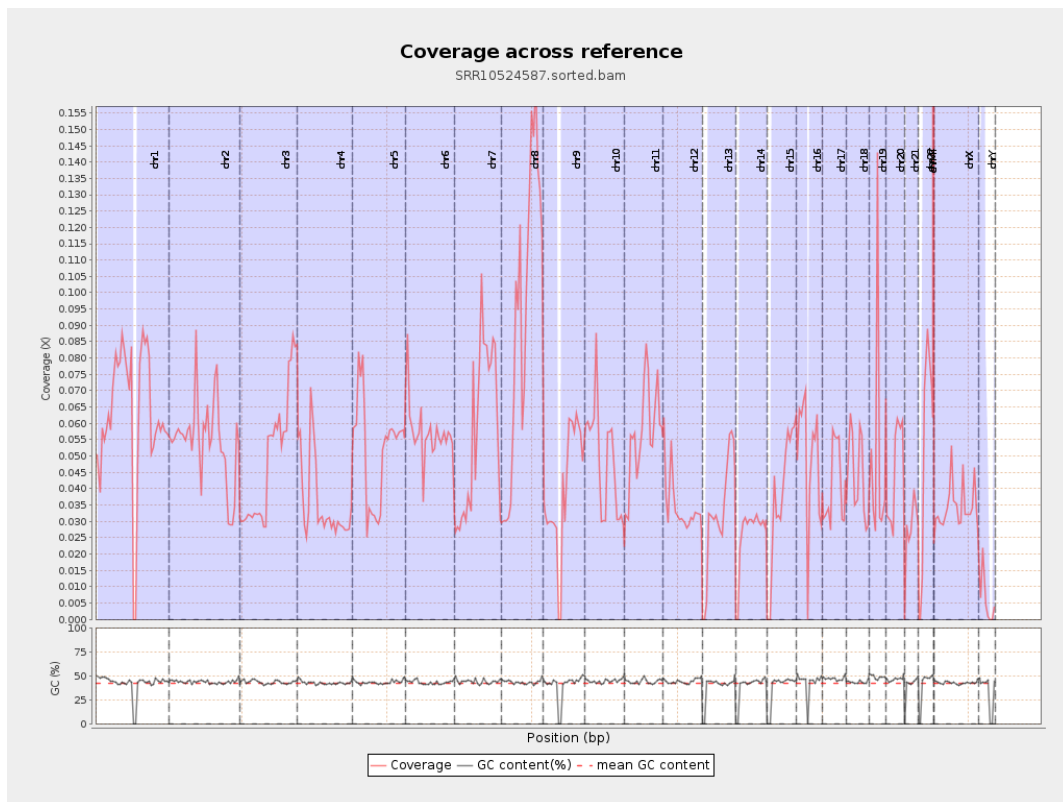
General error rate	0.48%
Mismatches	705,633
Insertions	8,890
Mapped reads with at least one insertion	0.35%
Deletions	28,082
Mapped reads with at least one deletion	1.1%
Homopolymer indels	44.37%

2.6. Chromosome stats

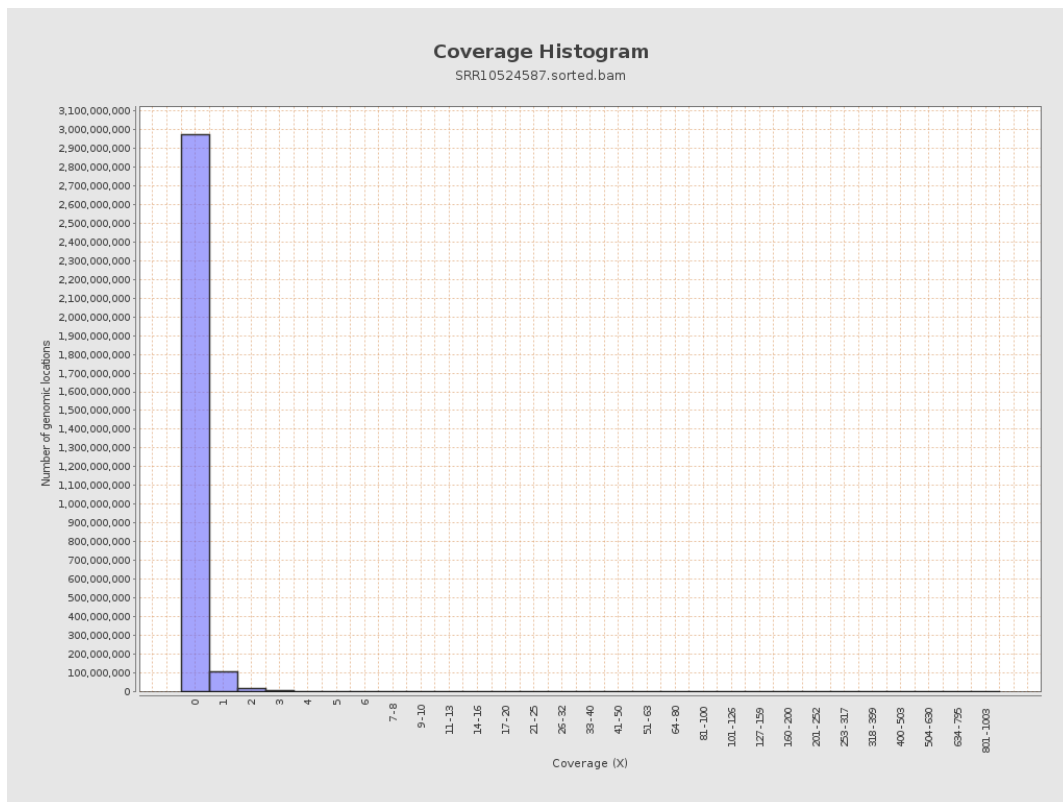
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15662406	0.0628	0.7329
chr2	243199373	13329976	0.0548	0.4628
chr3	198022430	9656154	0.0488	0.2599
chr4	191154276	6762921	0.0354	0.2662
chr5	180915260	9409523	0.052	0.2693
chr6	171115067	9761210	0.057	0.3129
chr7	159138663	9213464	0.0579	0.5579

chr8	146364022	13522608	0.0924	0.5427
chr9	141213431	5573653	0.0395	0.3624
chr10	135534747	6532317	0.0482	0.3954
chr11	135006516	7690932	0.057	0.3929
chr12	133851895	4658215	0.0348	0.2302
chr13	115169878	3720454	0.0323	0.2139
chr14	107349540	2758154	0.0257	0.2058
chr15	102531392	3891202	0.038	0.2426
chr16	90354753	4437581	0.0491	0.2815
chr17	81195210	3346881	0.0412	0.2507
chr18	78077248	3498615	0.0448	0.5886
chr19	59128983	2991316	0.0506	0.5336
chr20	63025520	2822433	0.0448	0.2583
chr21	48129895	1330910	0.0277	0.2265
chr22	51304566	2627841	0.0512	0.2678
chrMT	16571	38781	2.3403	2.0758
chrX	155270560	5361259	0.0345	0.2735
chrY	59373566	356148	0.006	0.1654

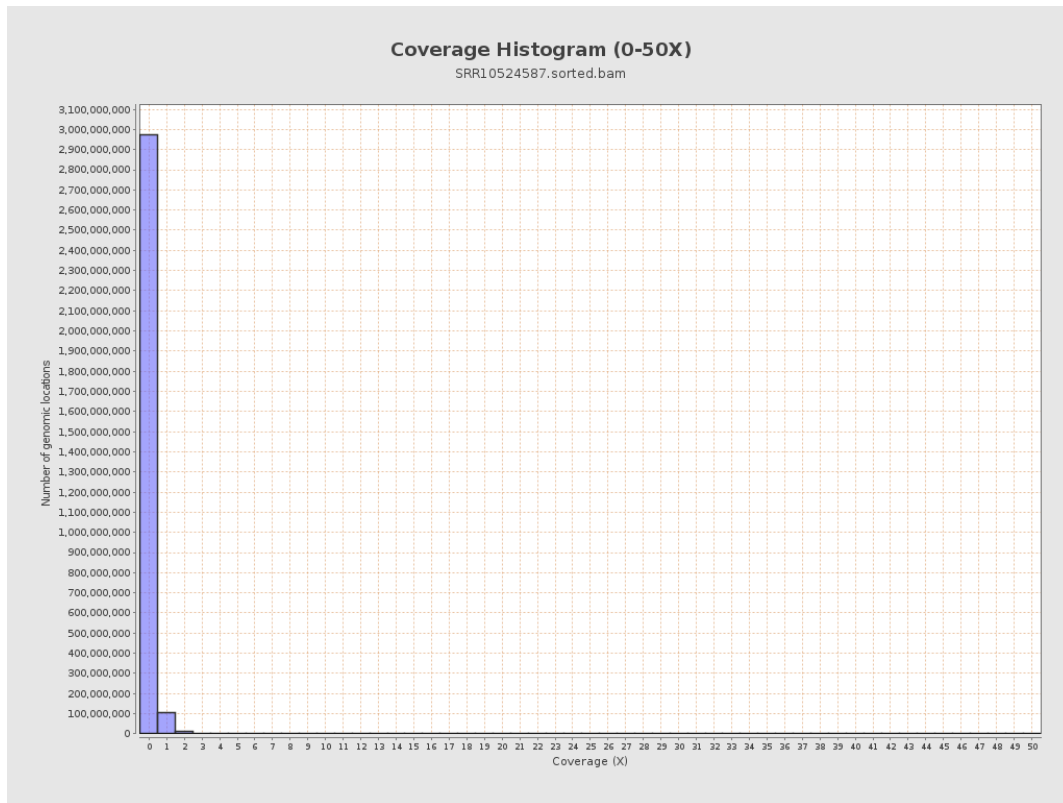
3. Results : Coverage across reference



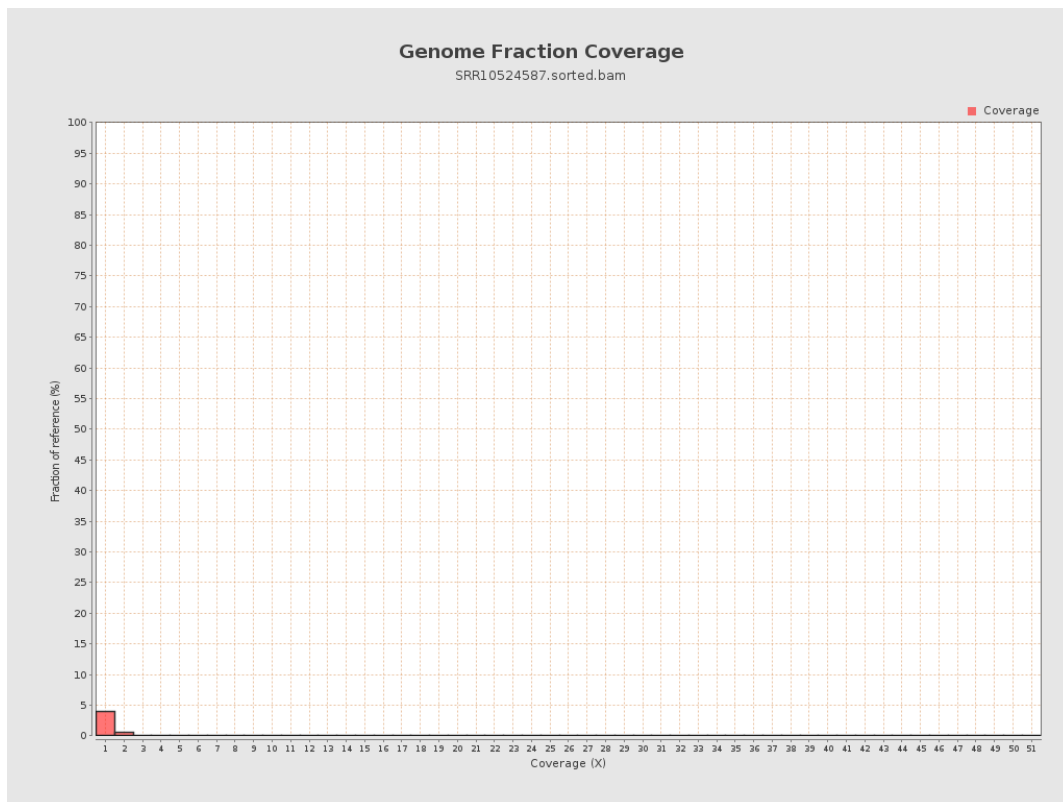
4. Results : Coverage Histogram



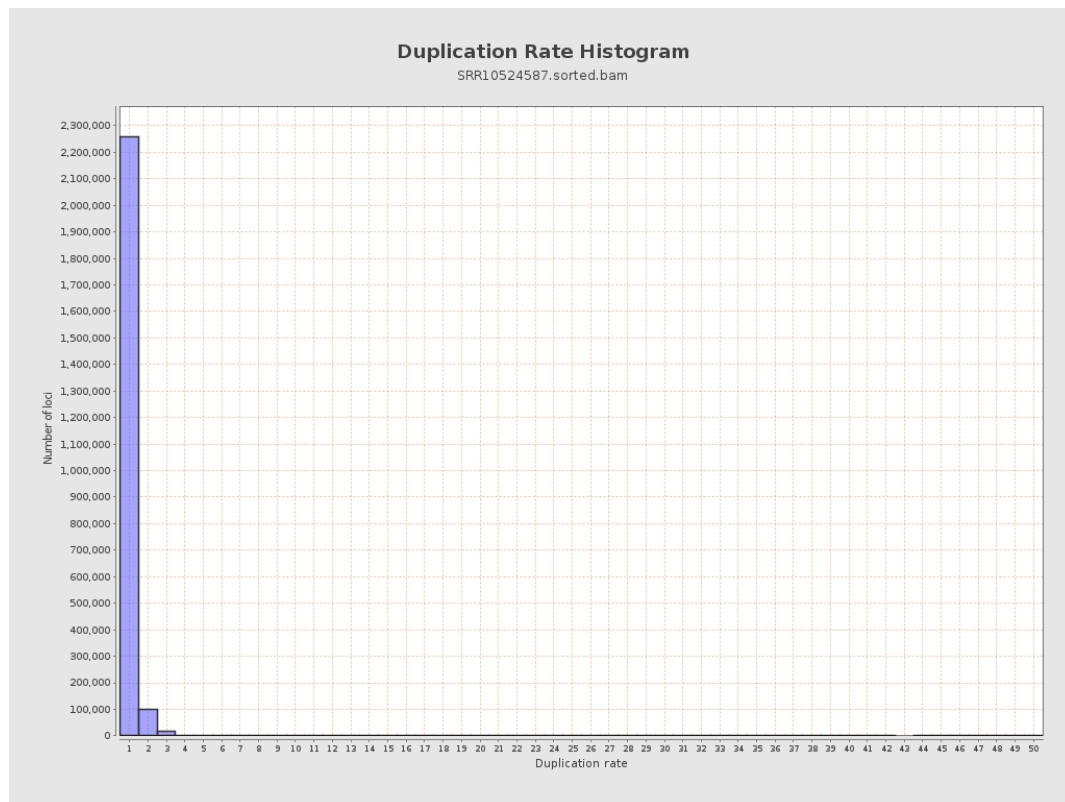
5. Results : Coverage Histogram (0-50X)



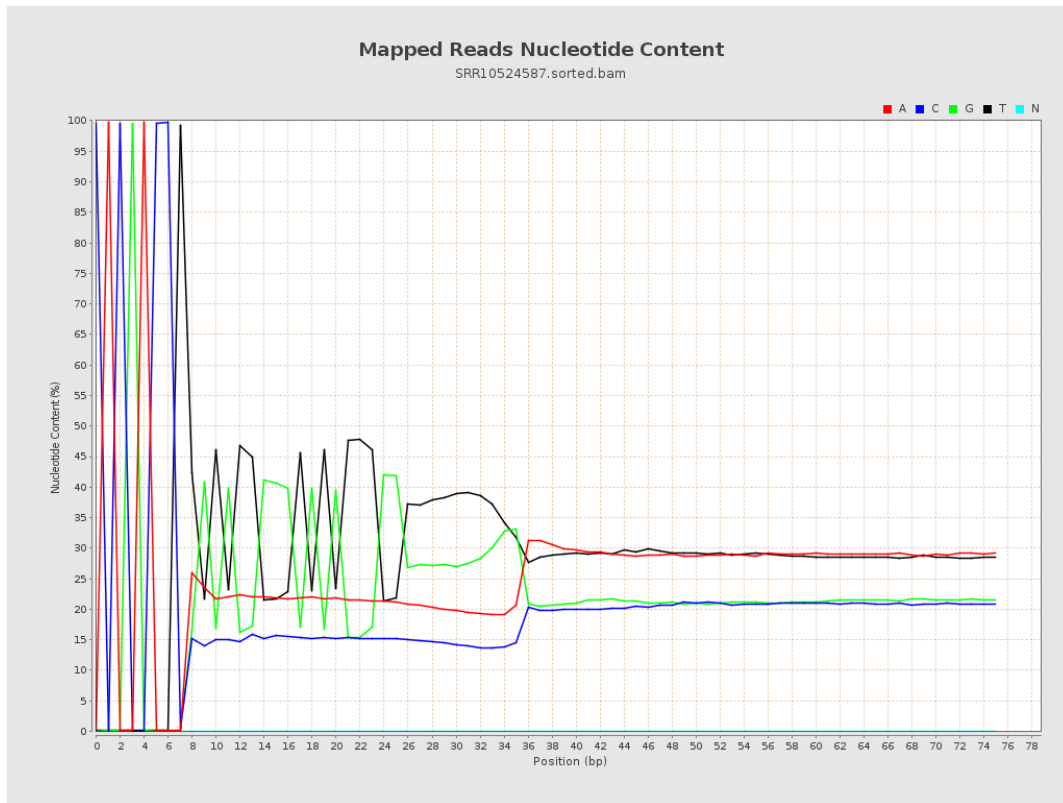
6. Results : Genome Fraction Coverage



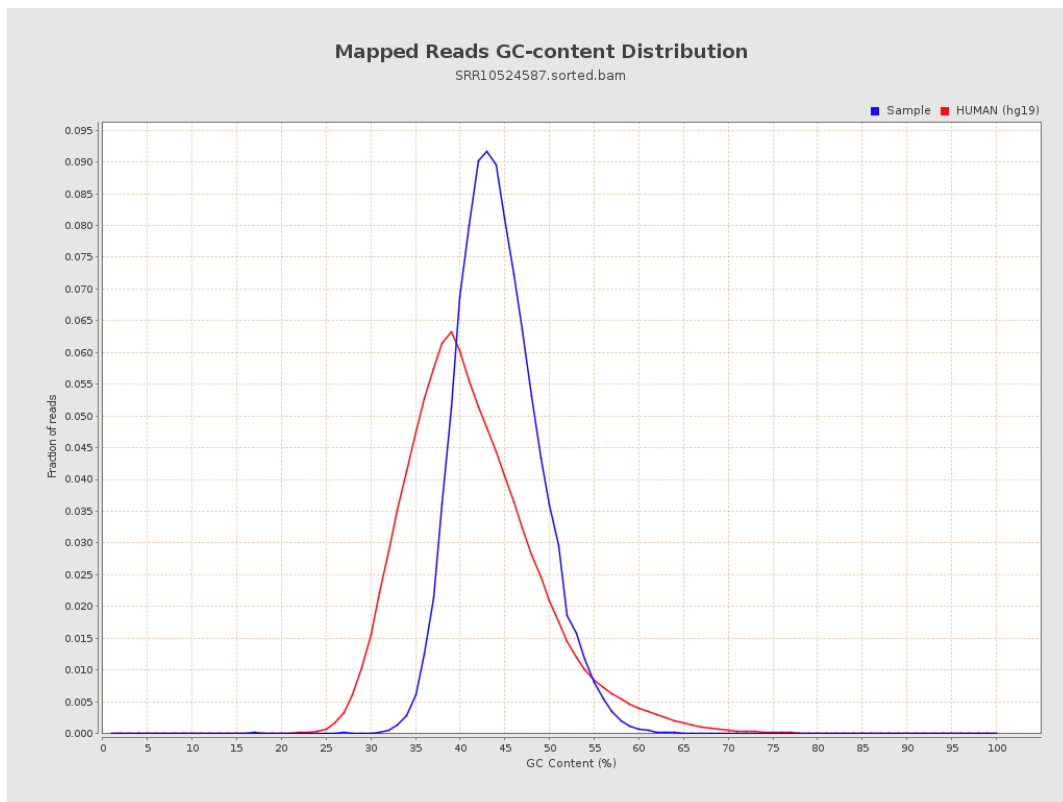
7. Results : Duplication Rate Histogram



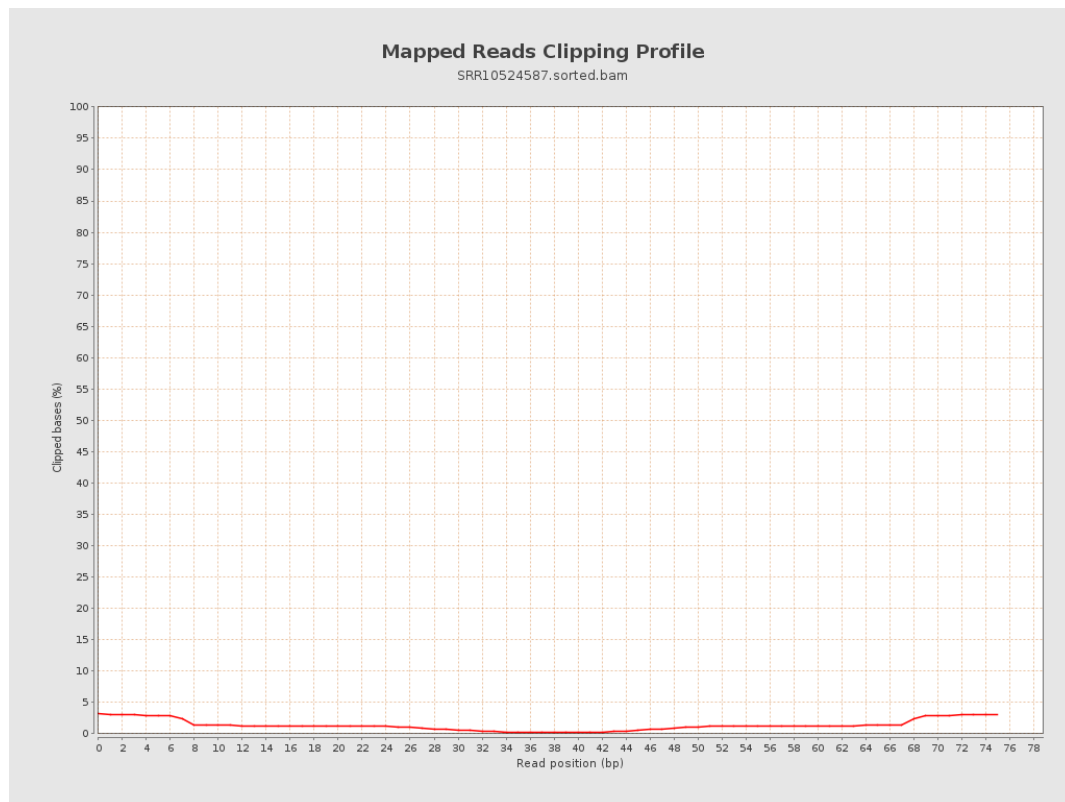
8. Results : Mapped Reads Nucleotide Content



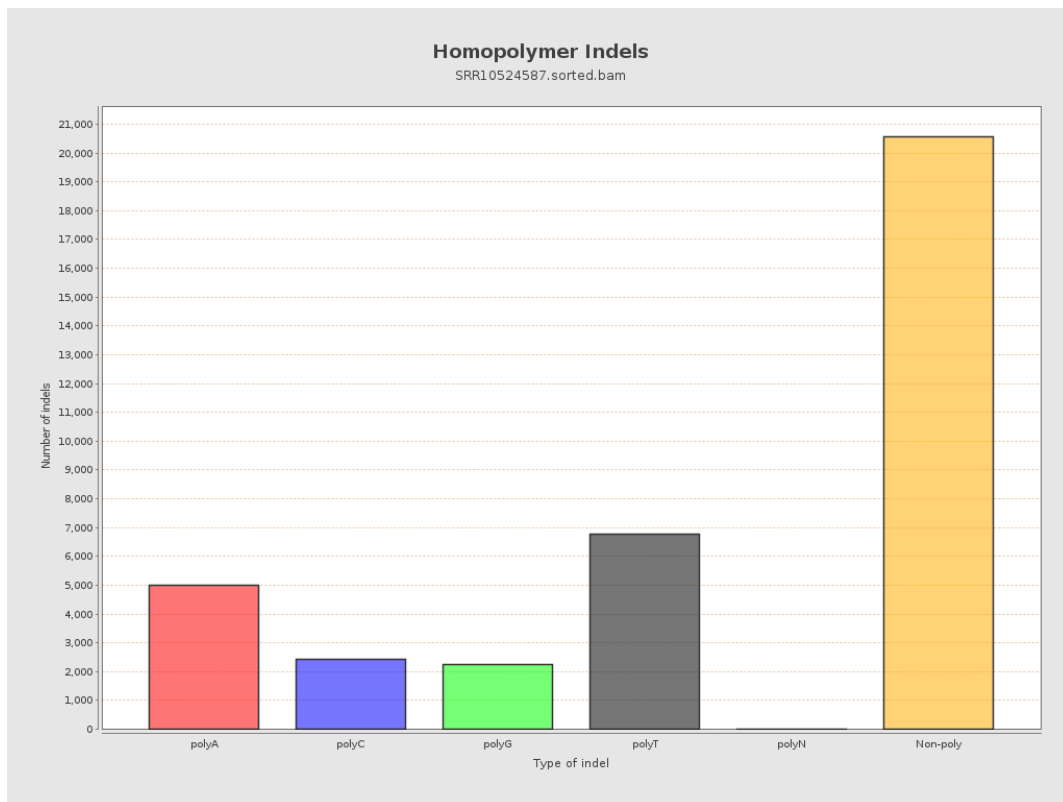
9. Results : Mapped Reads GC-content Distribution



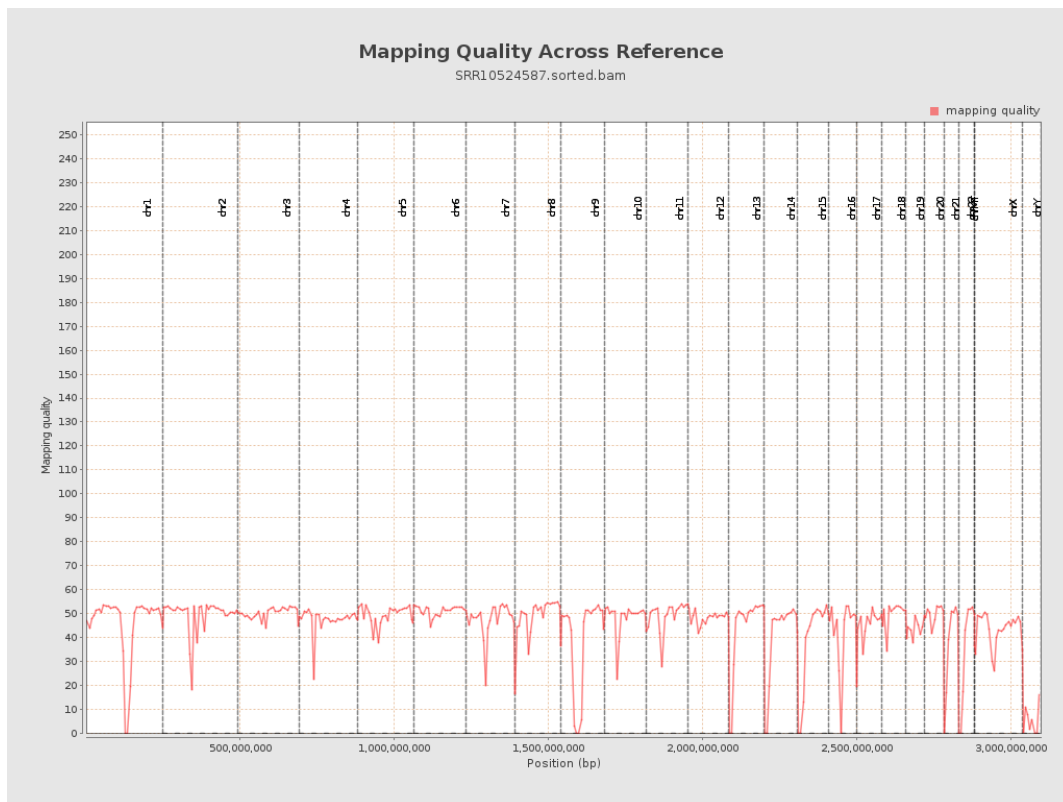
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

