

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 15:40:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548948.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_SRR1548948 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548948.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 15:40:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548948.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,400,695
Mapped reads	3,770,516 / 85.68%
Unmapped reads	630,179 / 14.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	132,939 / 3.02%
Duplication rate	2.67%
Clipped reads	221,584 / 5.04%

2.2. ACGT Content

Number/percentage of A's	42,376,133 / 28.34%
Number/percentage of C's	31,870,365 / 21.31%
Number/percentage of T's	43,178,073 / 28.87%
Number/percentage of G's	32,113,908 / 21.48%
Number/percentage of N's	1,320 / 0%
GC Percentage	42.79%

2.3. Coverage

Mean	0.0483
Standard Deviation	0.4939

2.4. Mapping Quality

Mean Mapping Quality	43.99
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2.5. Mismatches and indels

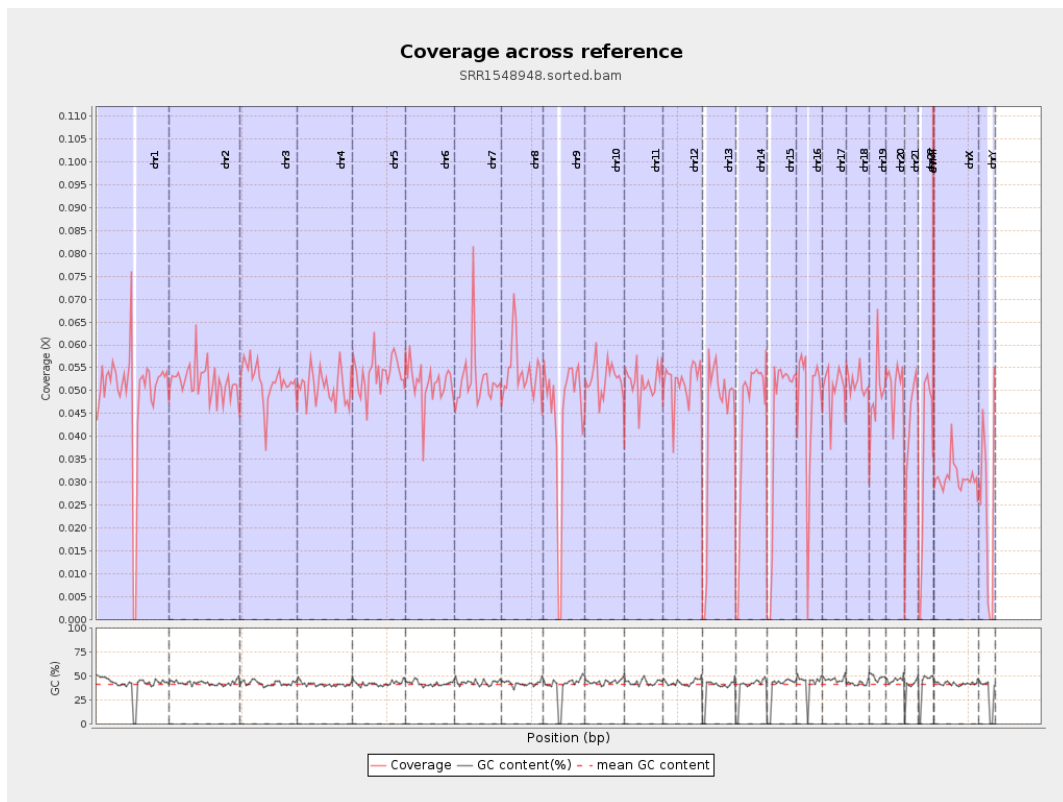
General error rate	0.22%
Mismatches	327,668
Insertions	3,793
Mapped reads with at least one insertion	0.1%
Deletions	10,538
Mapped reads with at least one deletion	0.28%
Homopolymer indels	43.12%

2.6. Chromosome stats

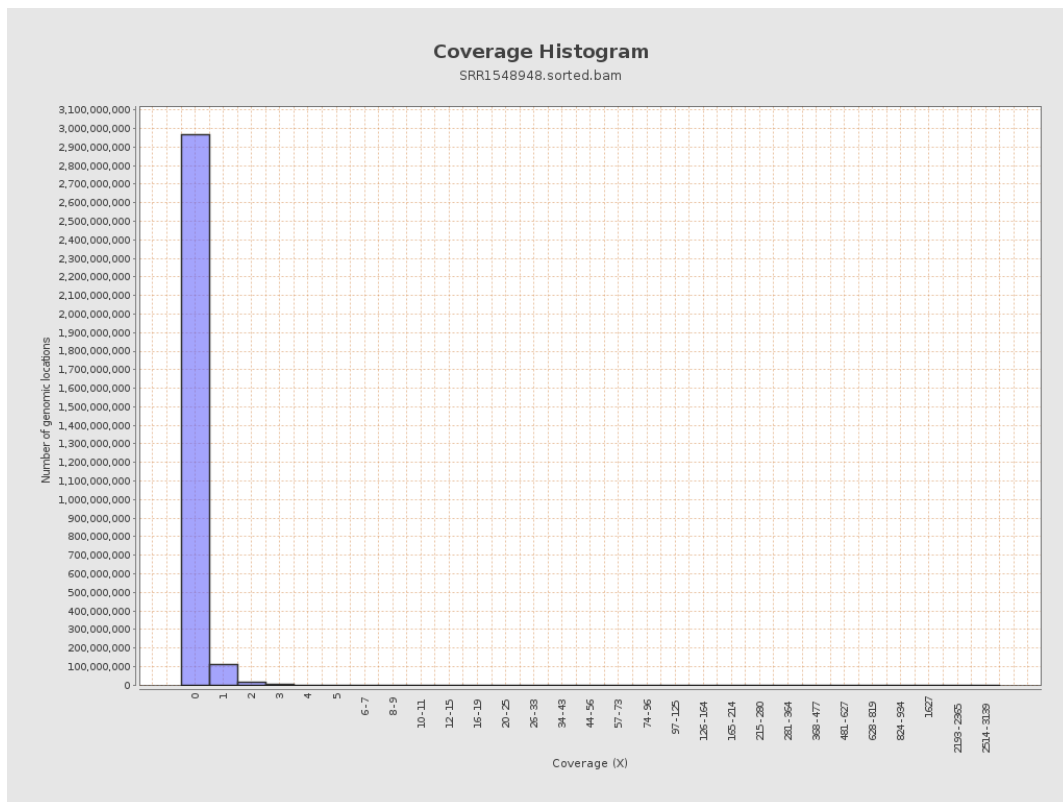
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12269468	0.0492	0.7329
chr2	243199373	12647519	0.052	0.3244
chr3	198022430	10283051	0.0519	0.2584
chr4	191154276	9711457	0.0508	0.2622
chr5	180915260	9723749	0.0537	0.2637
chr6	171115067	8841271	0.0517	0.2705
chr7	159138663	8357584	0.0525	0.55
chr8	146364022	7876825	0.0538	1.5438

chr9	141213431	6260132	0.0443	0.302
chr10	135534747	7136182	0.0527	0.3138
chr11	135006516	6977958	0.0517	0.3364
chr12	133851895	6926844	0.0518	0.2611
chr13	115169878	4938999	0.0429	0.232
chr14	107349540	4660017	0.0434	0.2544
chr15	102531392	4367874	0.0426	0.2321
chr16	90354753	4262014	0.0472	0.2557
chr17	81195210	4088804	0.0504	0.2624
chr18	78077248	4045572	0.0518	0.5103
chr19	59128983	2948171	0.0499	0.5834
chr20	63025520	3227189	0.0512	0.2618
chr21	48129895	1968638	0.0409	0.2576
chr22	51304566	1778629	0.0347	0.2978
chrMT	16571	9034	0.5452	0.986
chrX	155270560	4826805	0.0311	0.2375
chrY	59373566	1420095	0.0239	0.2919

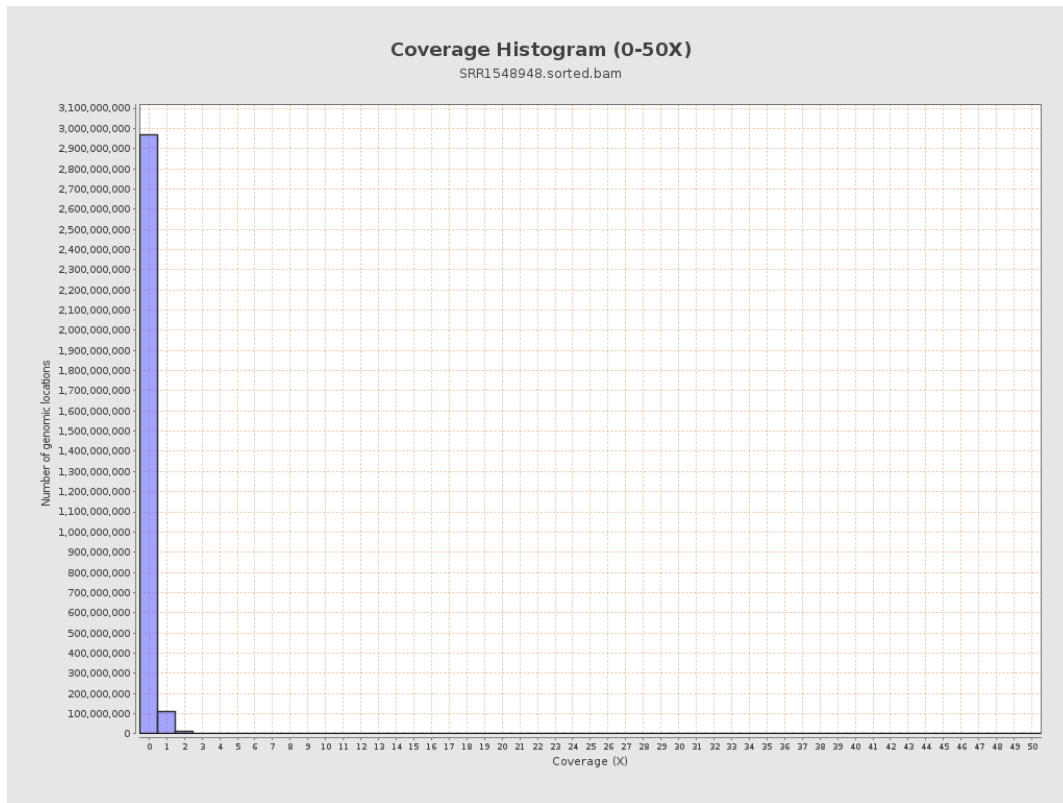
3. Results : Coverage across reference



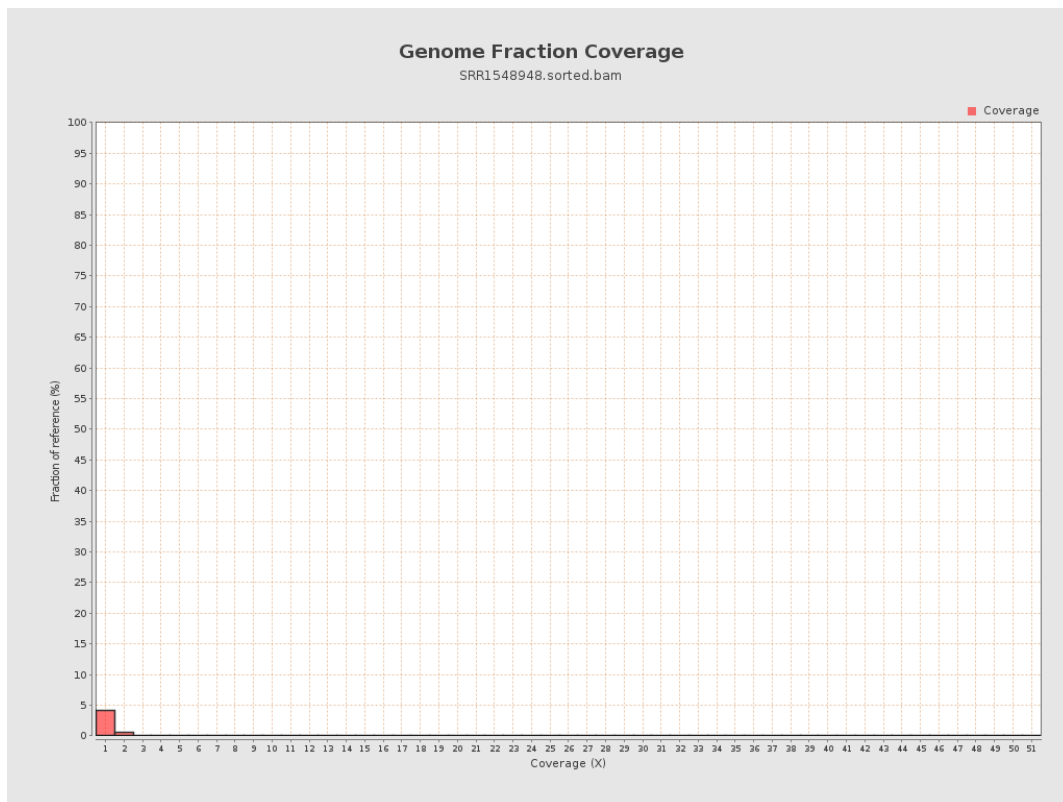
4. Results : Coverage Histogram



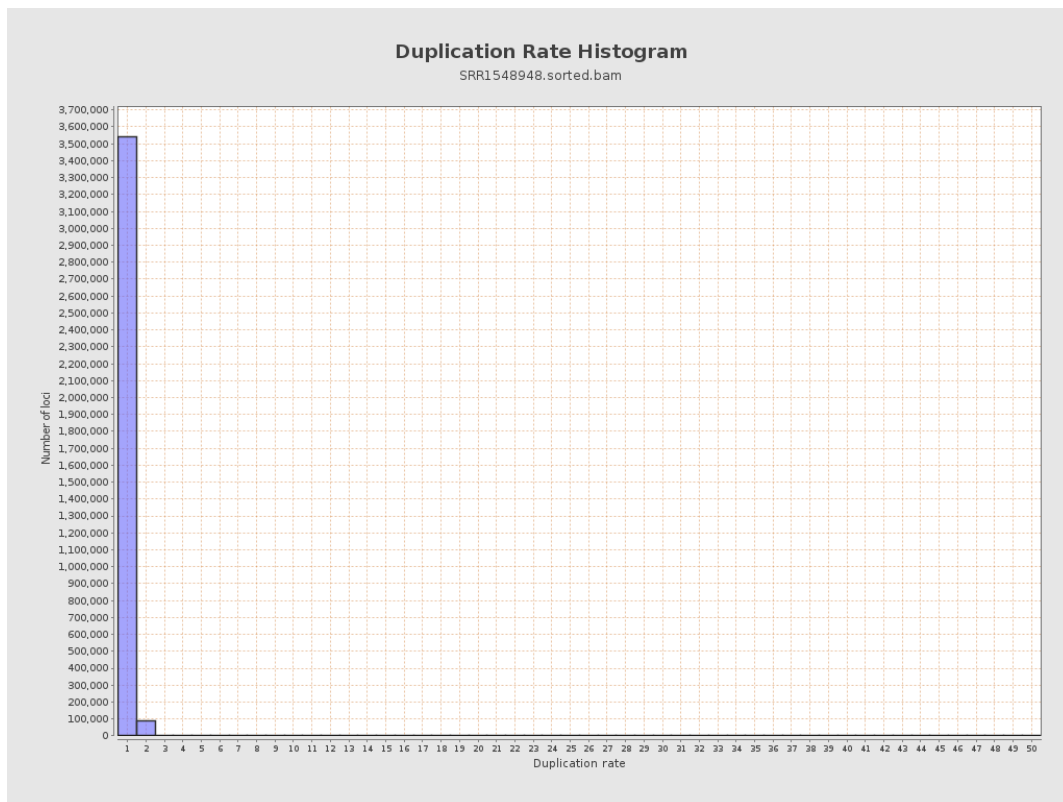
5. Results : Coverage Histogram (0-50X)



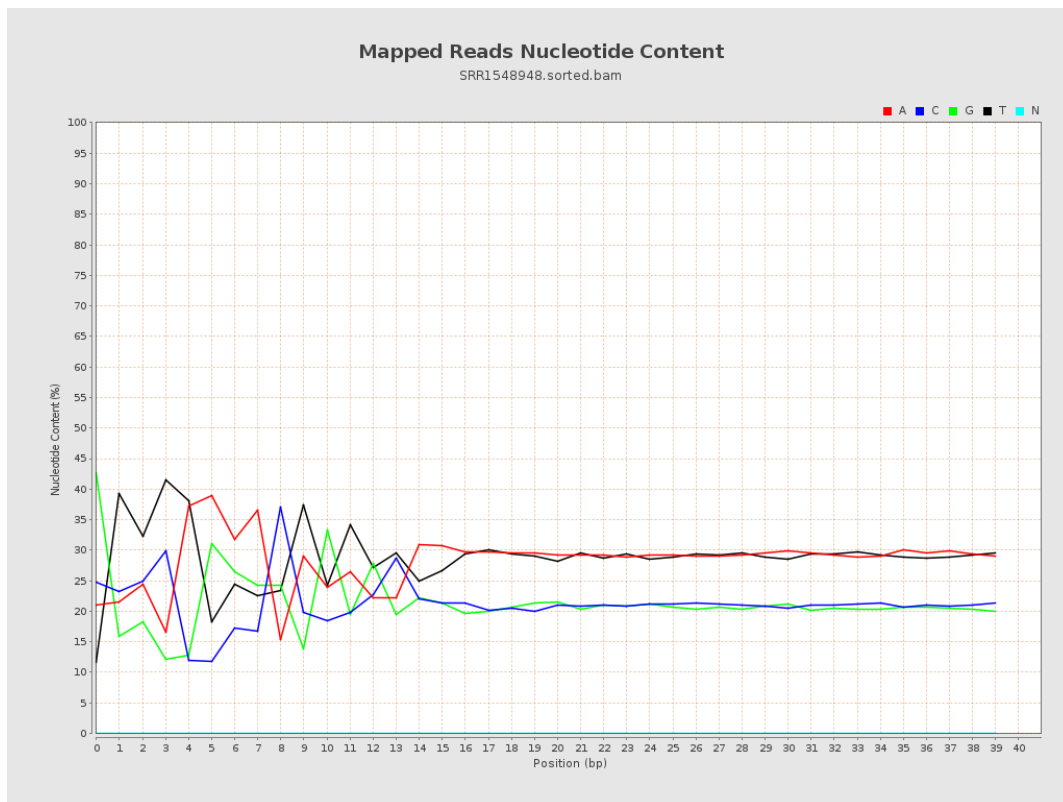
6. Results : Genome Fraction Coverage



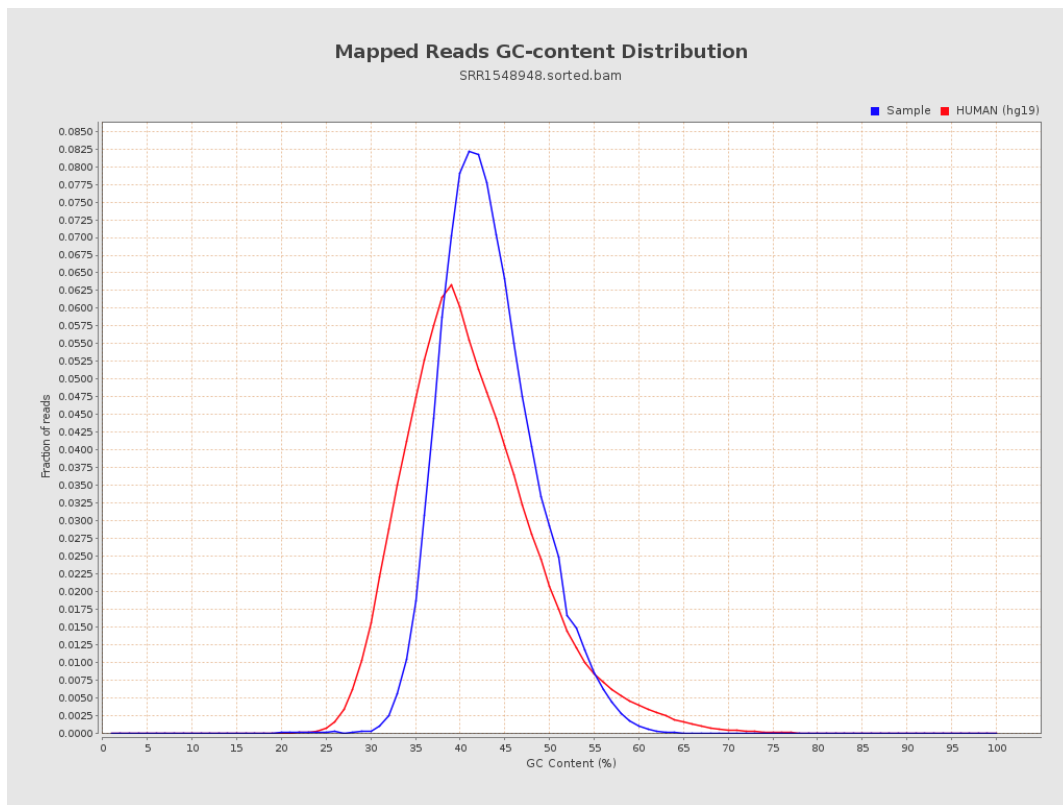
7. Results : Duplication Rate Histogram



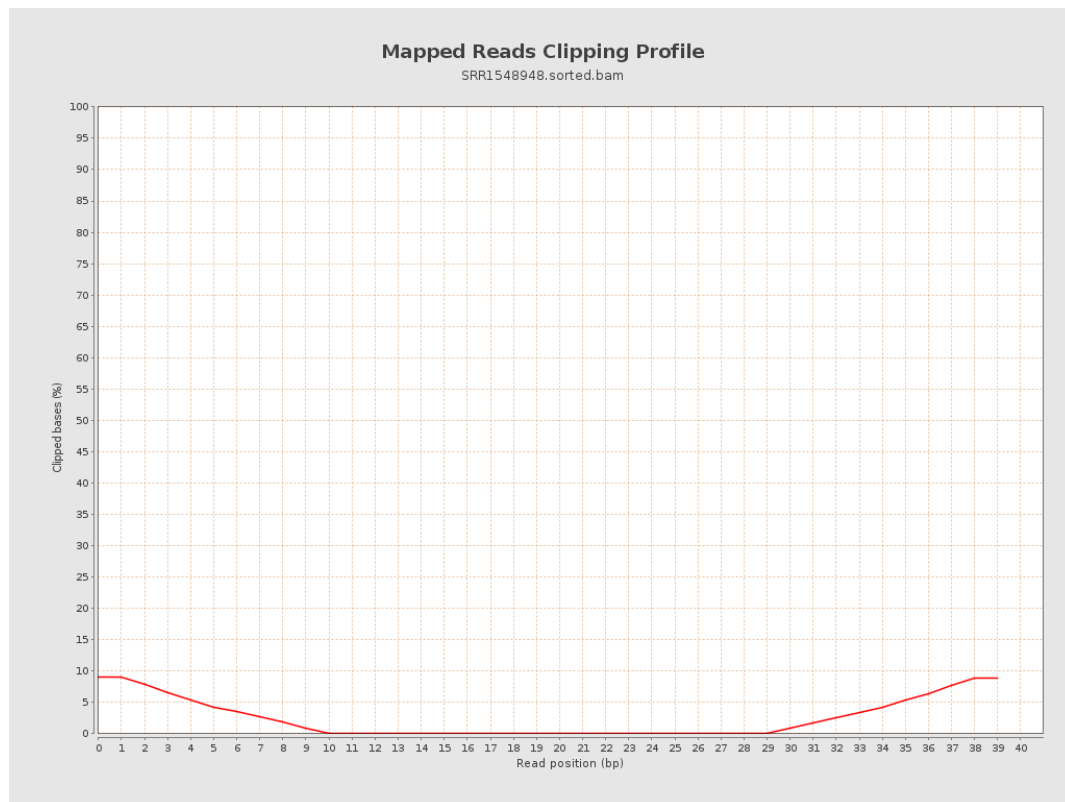
8. Results : Mapped Reads Nucleotide Content



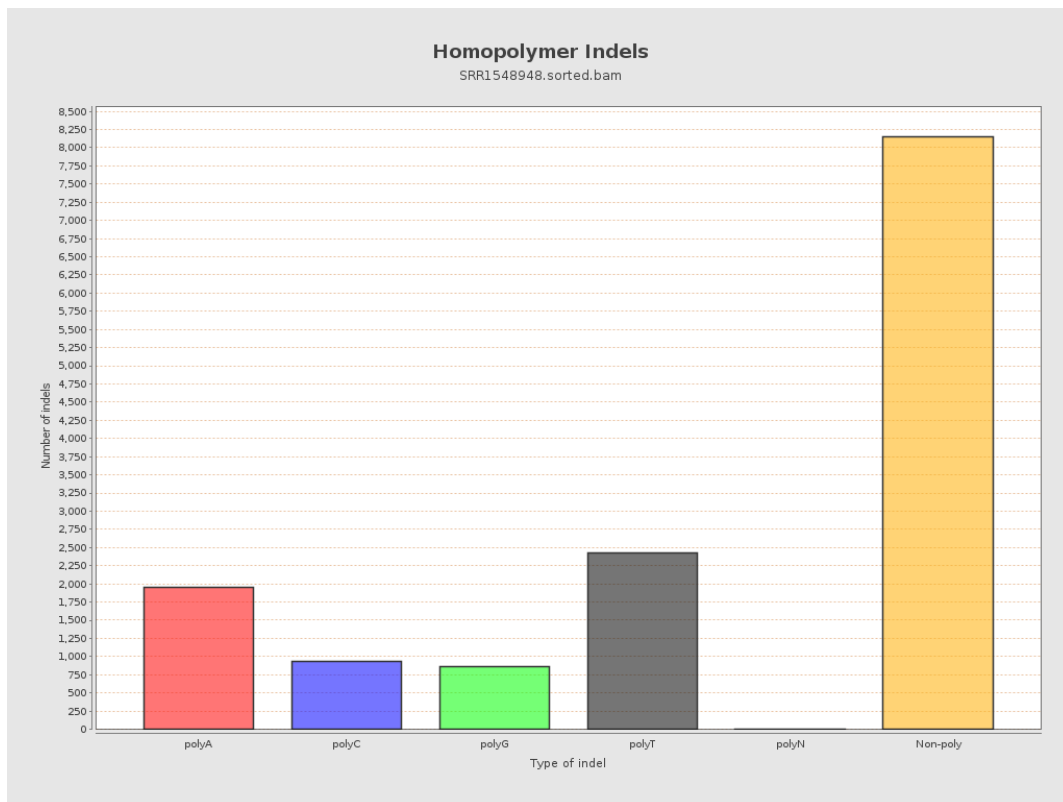
9. Results : Mapped Reads GC-content Distribution



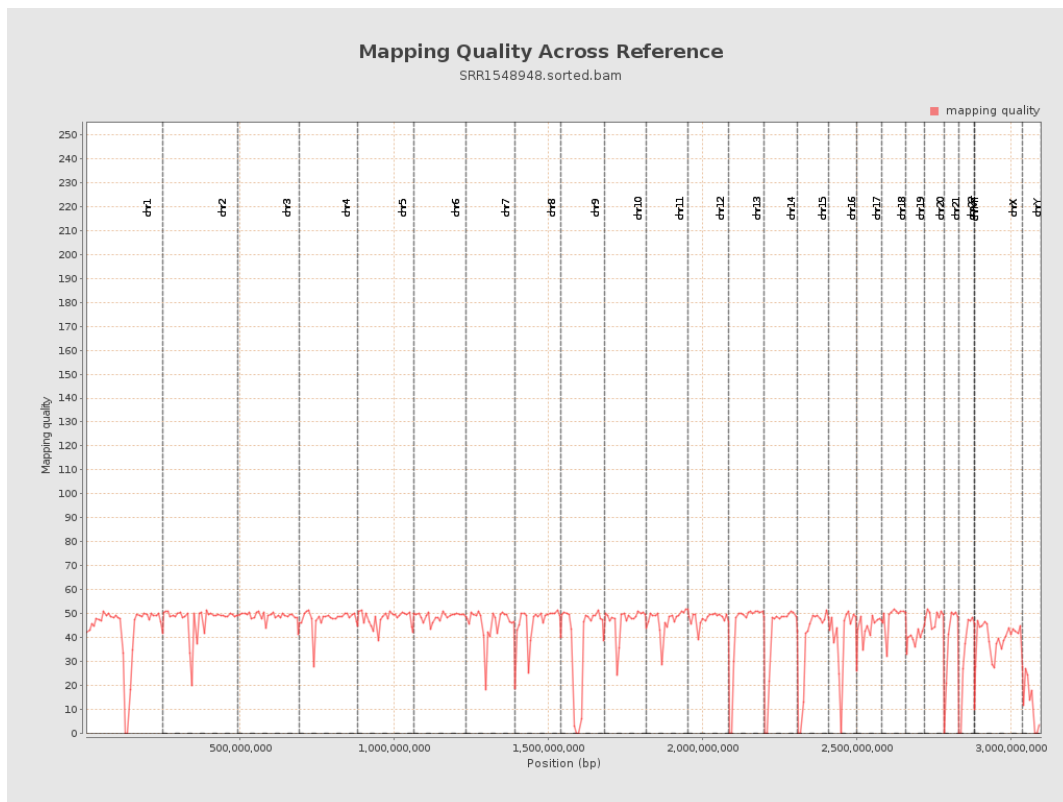
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

