

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 21:22:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548958.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_SRR1548958 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548958.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 21:22:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548958.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,291,488
Mapped reads	5,488,074 / 87.23%
Unmapped reads	803,414 / 12.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	246,523 / 3.92%
Duplication rate	2.64%
Clipped reads	433,116 / 6.88%

2.2. ACGT Content

Number/percentage of A's	62,040,428 / 28.59%
Number/percentage of C's	45,712,361 / 21.06%
Number/percentage of T's	63,370,461 / 29.2%
Number/percentage of G's	45,910,792 / 21.15%
Number/percentage of N's	305 / 0%
GC Percentage	42.22%

2.3. Coverage

Mean	0.0701
Standard Deviation	0.7358

2.4. Mapping Quality

Mean Mapping Quality	37.35
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2.5. Mismatches and indels

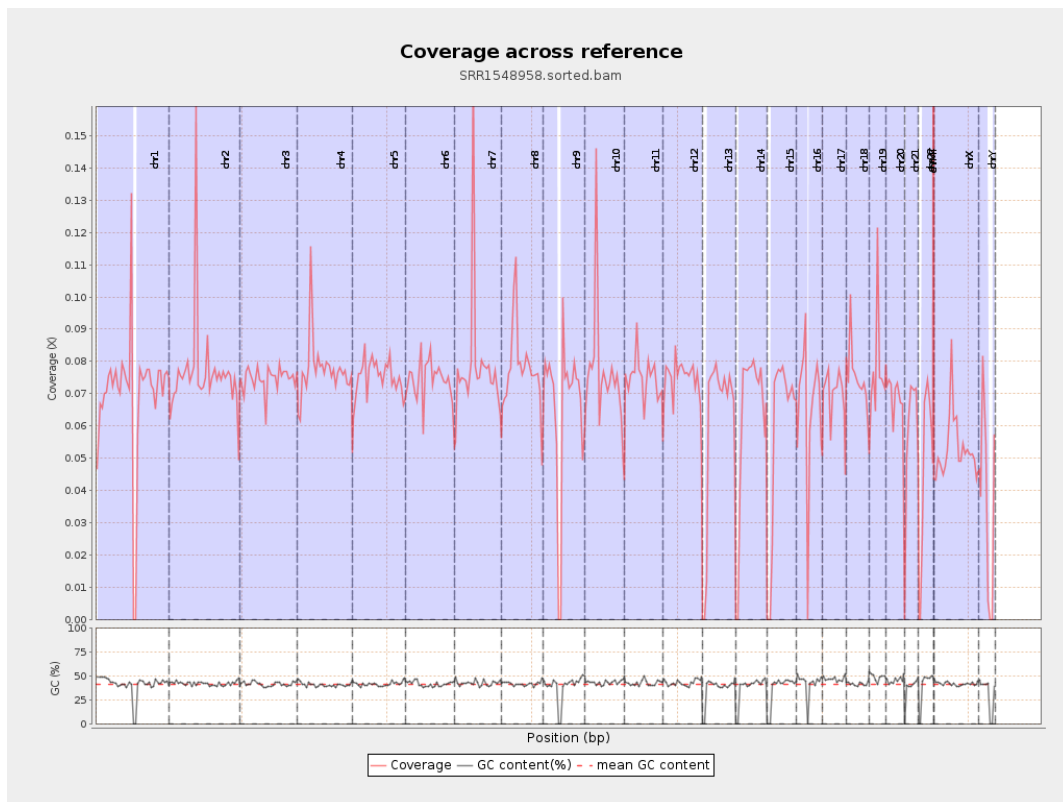
General error rate	0.31%
Mismatches	673,215
Insertions	7,275
Mapped reads with at least one insertion	0.13%
Deletions	16,643
Mapped reads with at least one deletion	0.3%
Homopolymer indels	39.67%

2.6. Chromosome stats

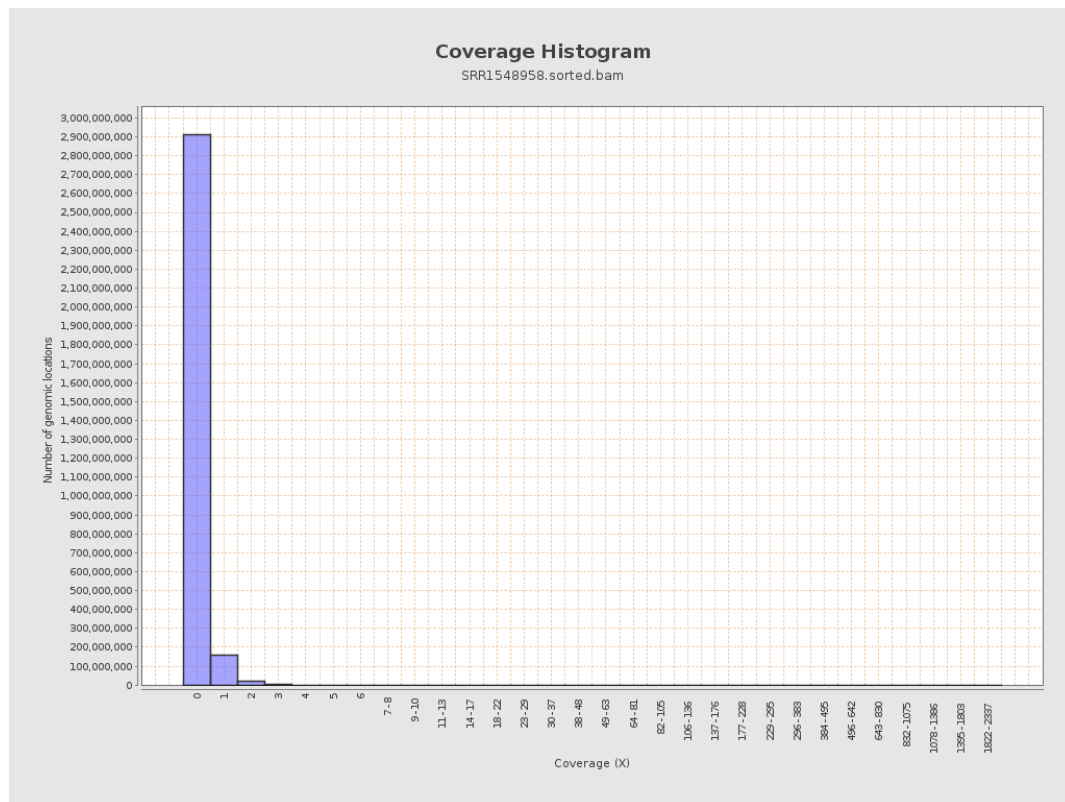
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17342815	0.0696	1.3305
chr2	243199373	18627561	0.0766	0.74
chr3	198022430	14772199	0.0746	0.3151
chr4	191154276	14768147	0.0773	0.3694
chr5	180915260	13607270	0.0752	0.3342
chr6	171115067	12683924	0.0741	0.3431
chr7	159138663	12627304	0.0793	1.1087
chr8	146364022	11346109	0.0775	1.2366

chr9	141213431	9266132	0.0656	0.7743
chr10	135534747	10336177	0.0763	0.6248
chr11	135006516	10035896	0.0743	0.5291
chr12	133851895	10007043	0.0748	0.344
chr13	115169878	7012270	0.0609	0.2743
chr14	107349540	6723728	0.0626	0.4204
chr15	102531392	6060124	0.0591	0.2812
chr16	90354753	5963483	0.066	0.3981
chr17	81195210	5635918	0.0694	0.3267
chr18	78077248	5904727	0.0756	1.54
chr19	59128983	4601976	0.0778	1.3137
chr20	63025520	4281036	0.0679	0.3375
chr21	48129895	2783553	0.0578	0.4266
chr22	51304566	2371531	0.0462	0.3325
chrMT	16571	6729	0.4061	0.739
chrX	155270560	8214334	0.0529	0.4357
chrY	59373566	2075991	0.035	0.3603

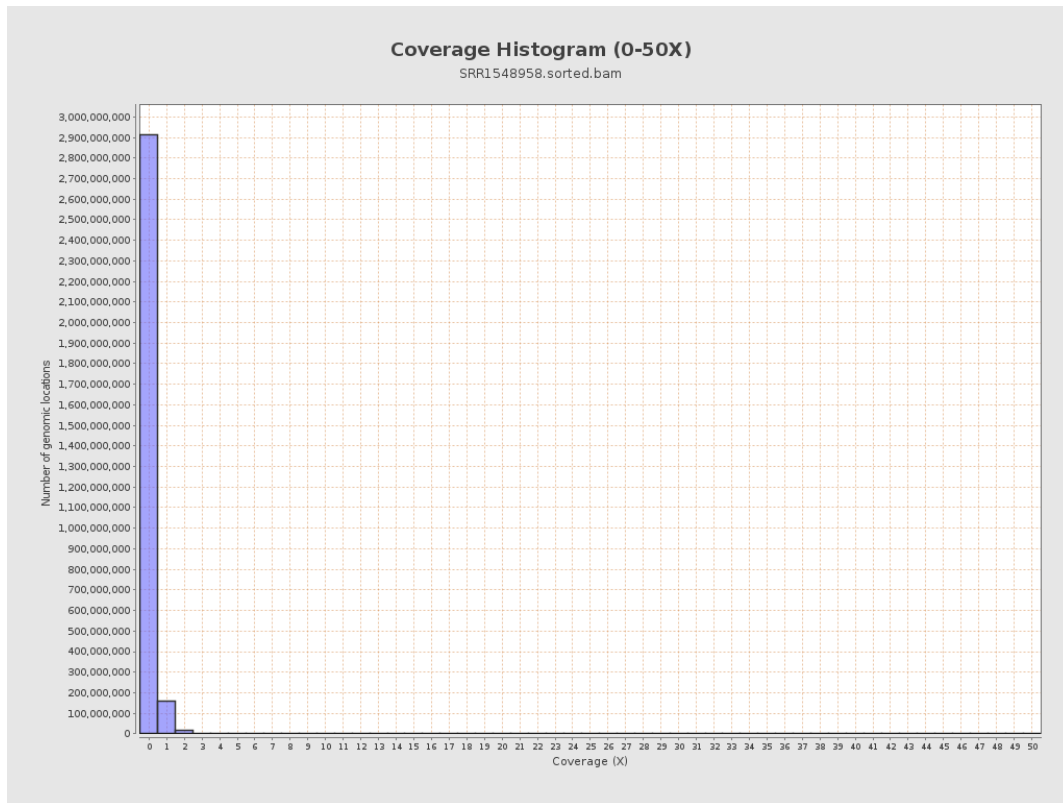
3. Results : Coverage across reference



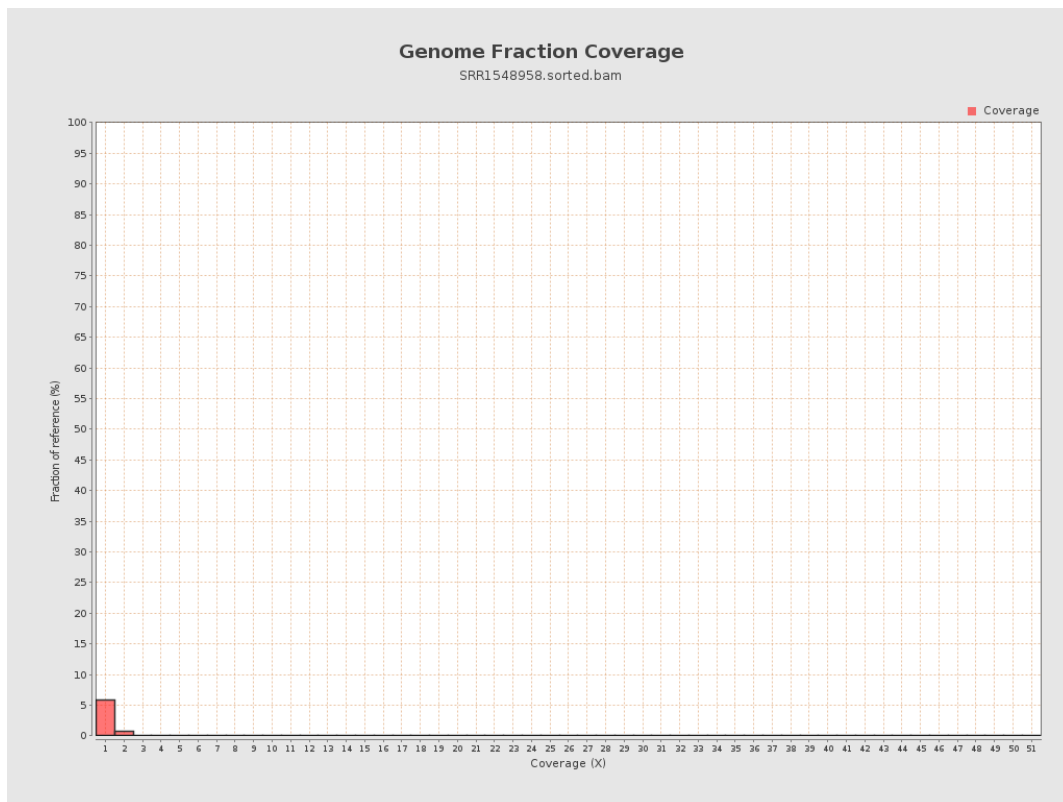
4. Results : Coverage Histogram



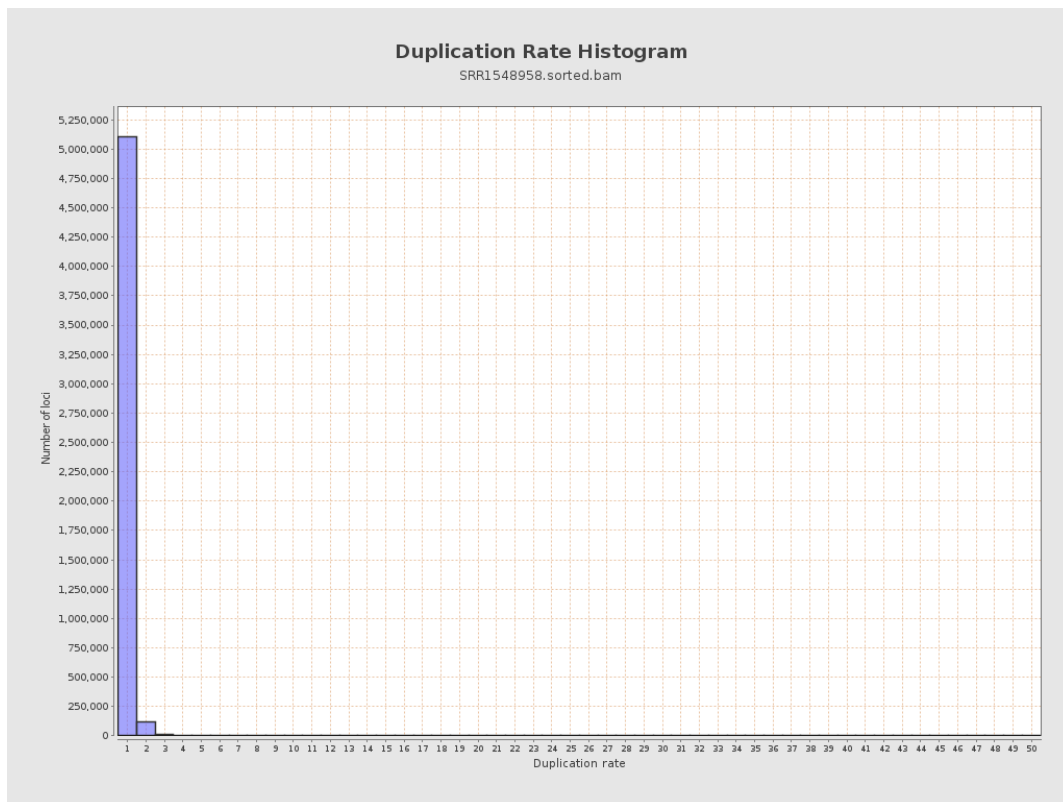
5. Results : Coverage Histogram (0-50X)



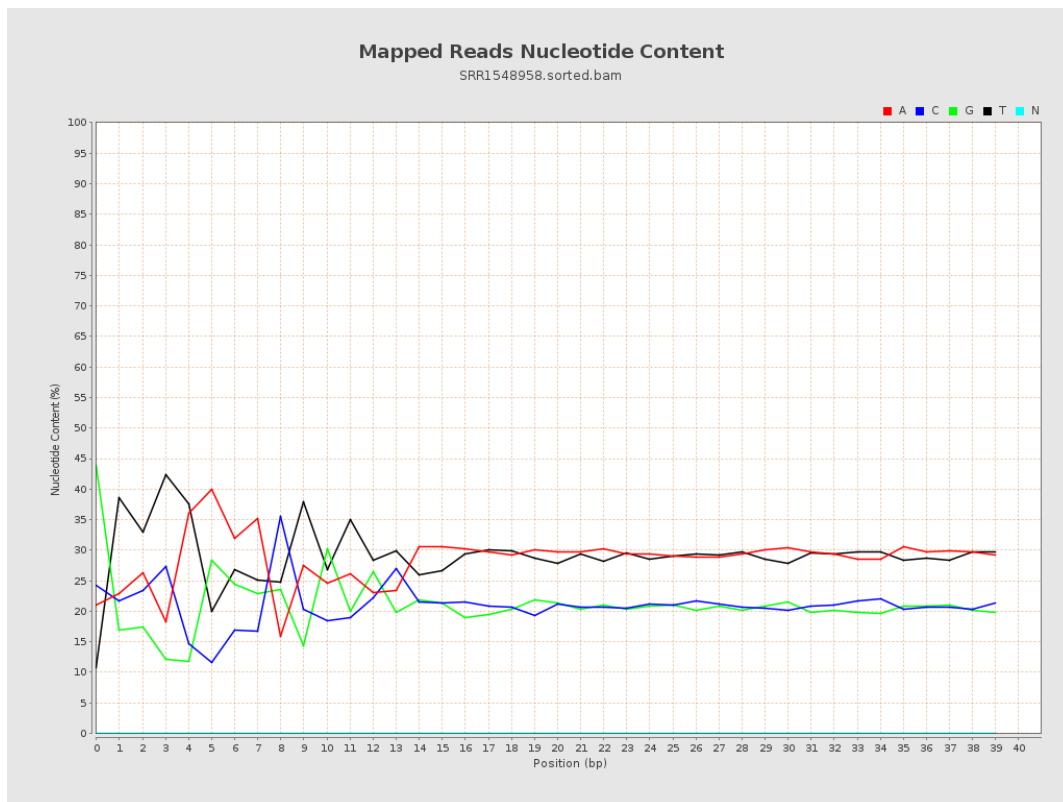
6. Results : Genome Fraction Coverage



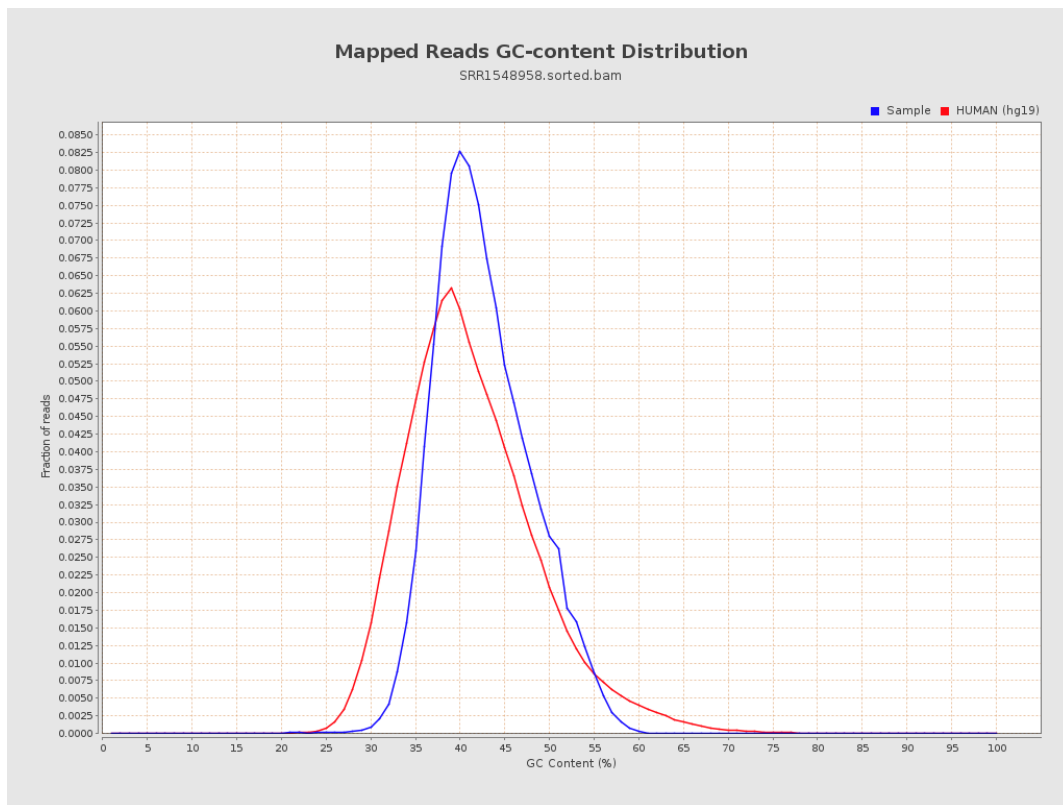
7. Results : Duplication Rate Histogram



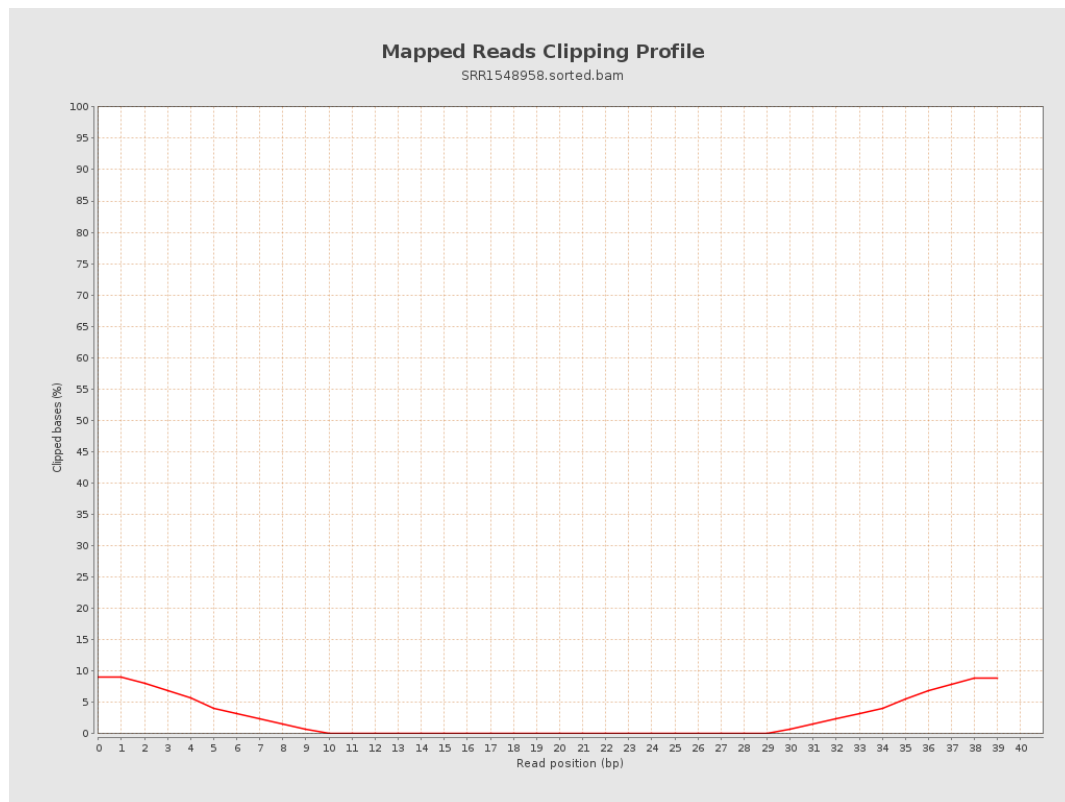
8. Results : Mapped Reads Nucleotide Content



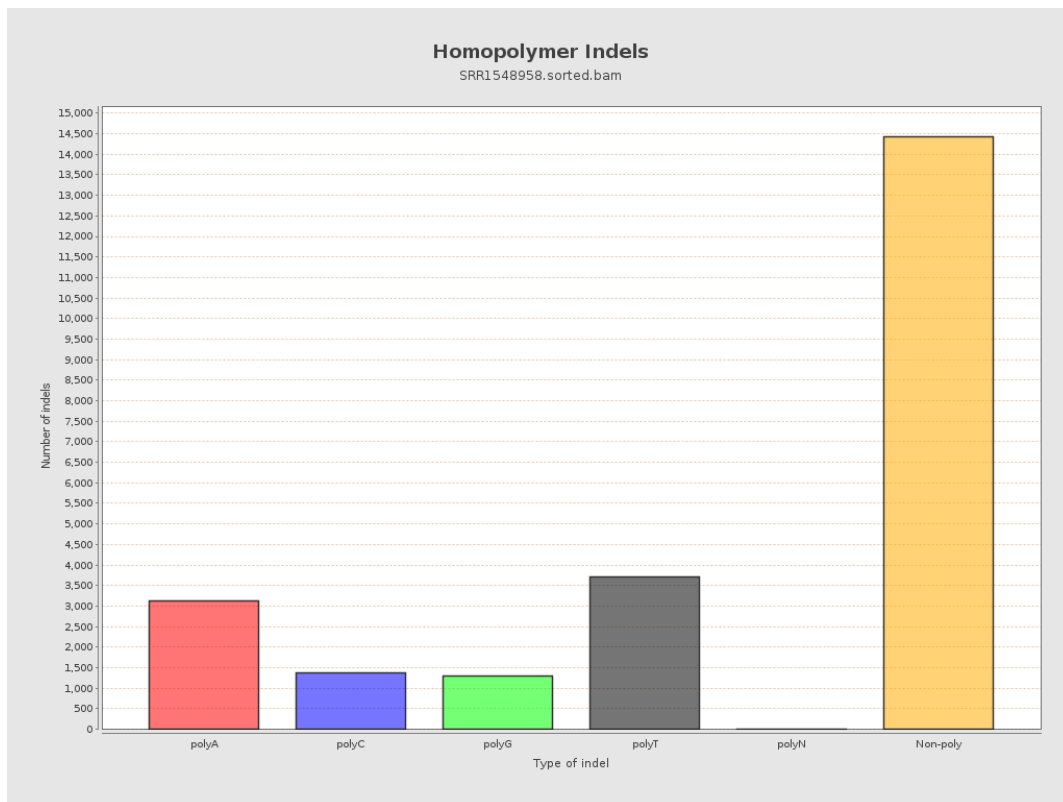
9. Results : Mapped Reads GC-content Distribution



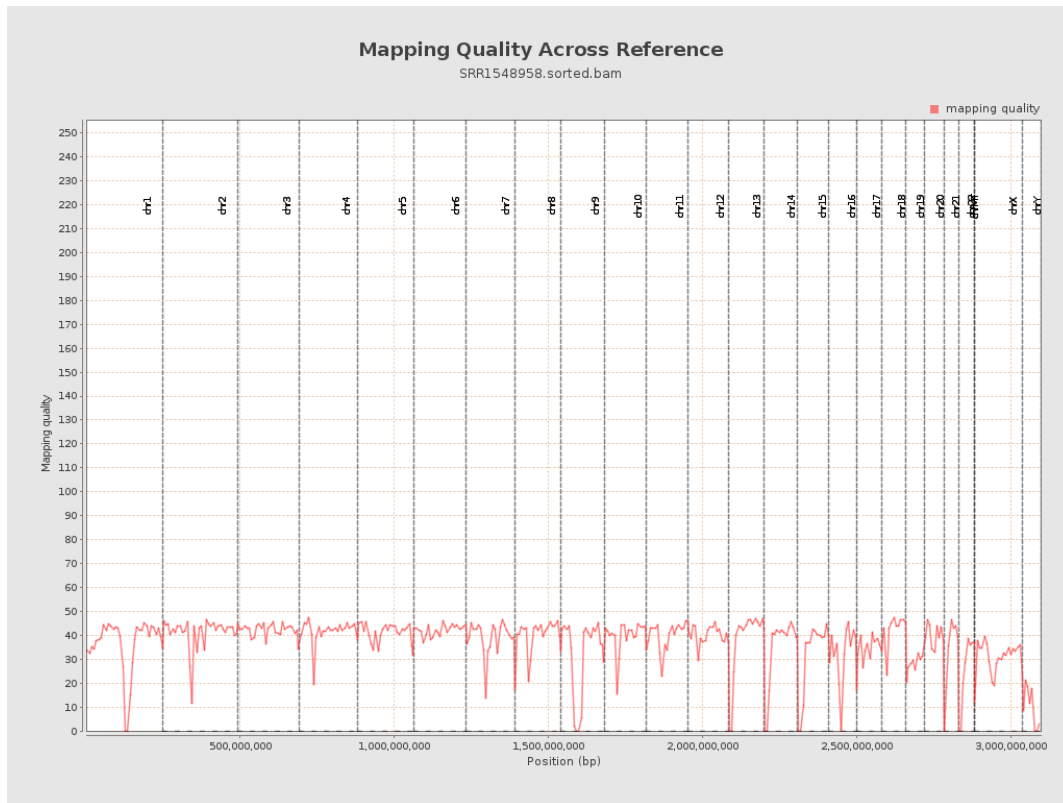
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

