

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:42:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548998.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_SRR1548998 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548998.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:42:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548998.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,534,327
Mapped reads	7,359,742 / 86.24%
Unmapped reads	1,174,585 / 13.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	577,397 / 6.77%
Duplication rate	7.02%
Clipped reads	389,204 / 4.56%

2.2. ACGT Content

Number/percentage of A's	88,306,141 / 30.24%
Number/percentage of C's	57,553,139 / 19.71%
Number/percentage of T's	87,894,393 / 30.1%
Number/percentage of G's	58,289,954 / 19.96%
Number/percentage of N's	2,713 / 0%
GC Percentage	39.67%

2.3. Coverage

Mean	0.0944
Standard Deviation	0.8611

2.4. Mapping Quality

Mean Mapping Quality	44.16
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2.5. Mismatches and indels

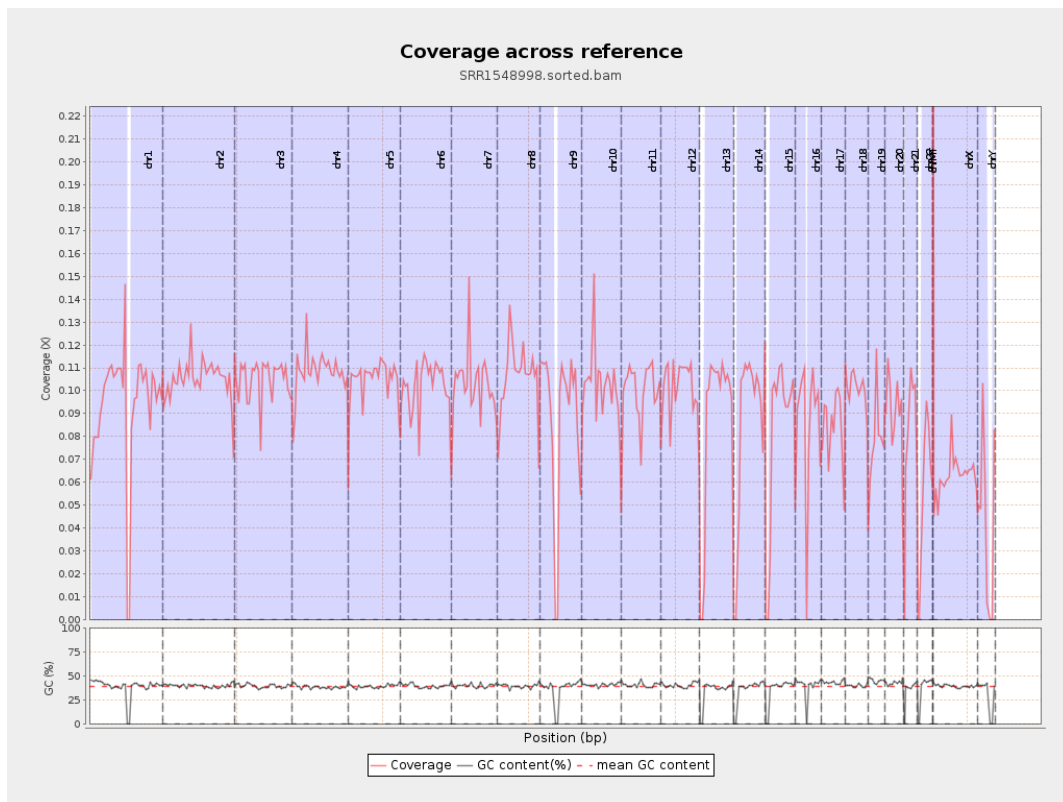
General error rate	0.31%
Mismatches	891,401
Insertions	8,986
Mapped reads with at least one insertion	0.12%
Deletions	25,574
Mapped reads with at least one deletion	0.35%
Homopolymer indels	42.84%

2.6. Chromosome stats

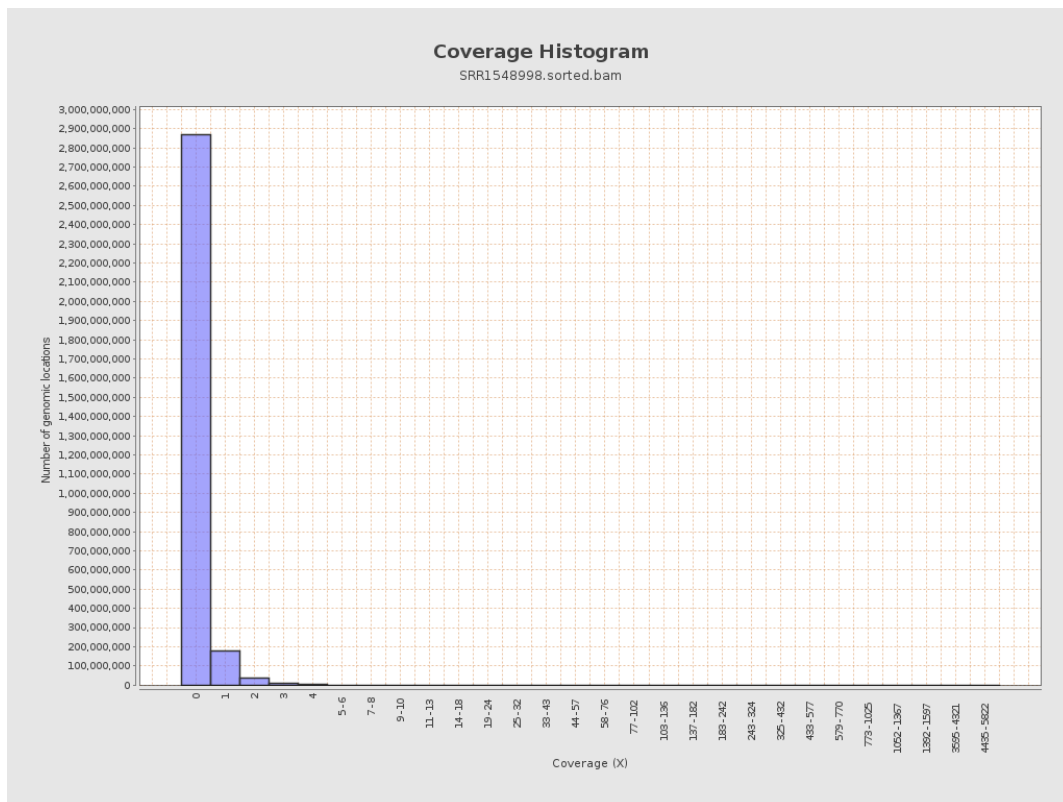
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	23364239	0.0937	1.1847
chr2	243199373	25632050	0.1054	0.5543
chr3	198022430	20795226	0.105	0.3986
chr4	191154276	20738296	0.1085	0.4441
chr5	180915260	18953593	0.1048	0.4046
chr6	171115067	17542299	0.1025	0.4601
chr7	159138663	16354246	0.1028	0.8233
chr8	146364022	15588877	0.1065	2.8736

chr9	141213431	12476274	0.0884	0.514
chr10	135534747	13942049	0.1029	0.5963
chr11	135006516	13505845	0.1	0.5125
chr12	133851895	13613507	0.1017	0.411
chr13	115169878	10011863	0.0869	0.3586
chr14	107349540	9190736	0.0856	0.4414
chr15	102531392	8331775	0.0813	0.3476
chr16	90354753	7593971	0.084	0.3996
chr17	81195210	6893576	0.0849	0.3978
chr18	78077248	7936075	0.1016	1.0702
chr19	59128983	4687293	0.0793	0.9102
chr20	63025520	5808476	0.0922	0.399
chr21	48129895	3865852	0.0803	0.4273
chr22	51304566	2884677	0.0562	0.3101
chrMT	16571	15982	0.9645	1.3866
chrX	155270560	9729627	0.0627	0.3936
chrY	59373566	2623340	0.0442	0.4726

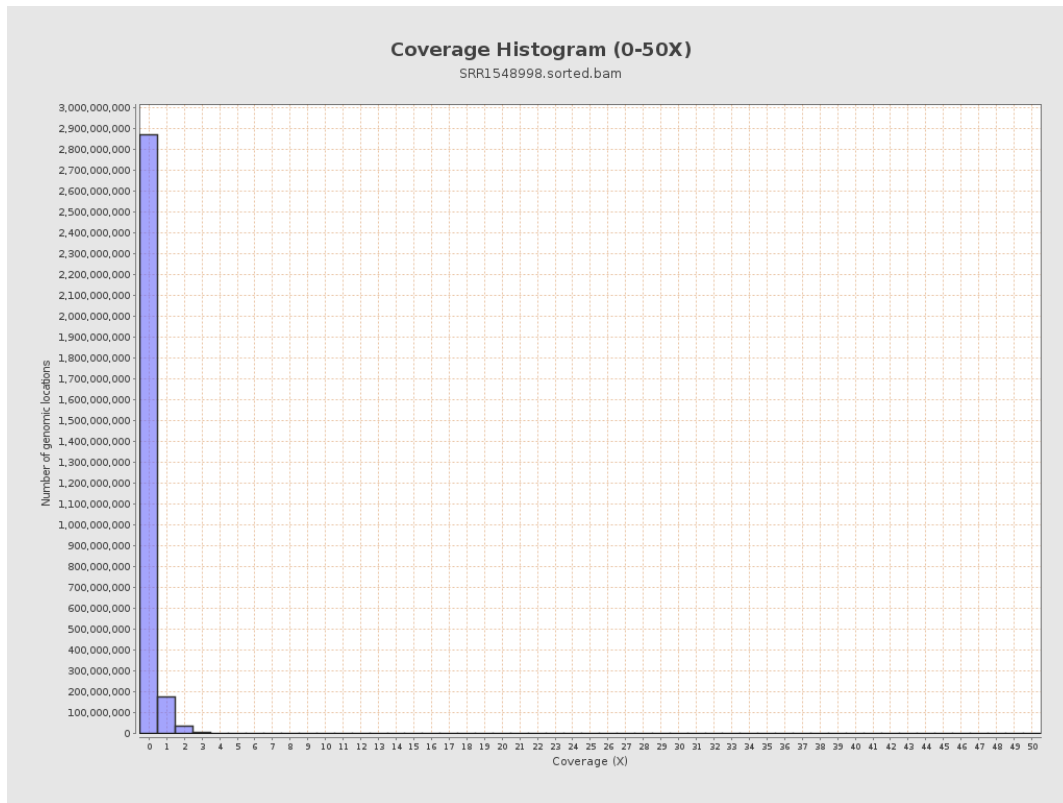
3. Results : Coverage across reference



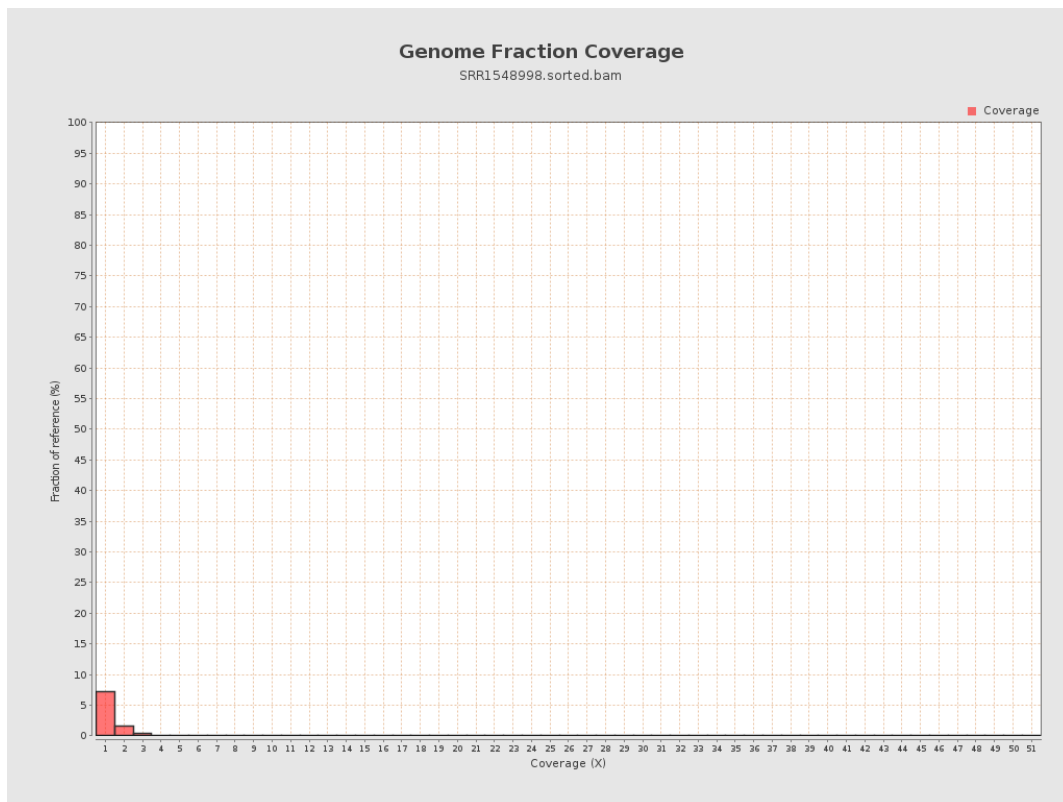
4. Results : Coverage Histogram



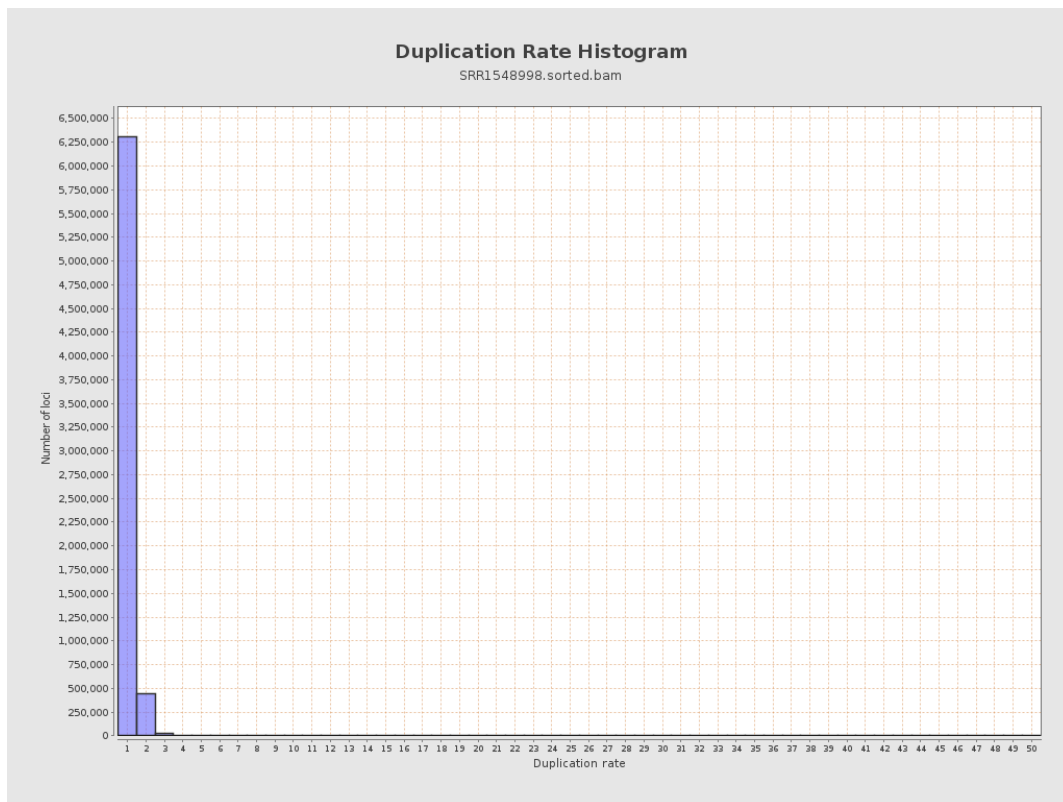
5. Results : Coverage Histogram (0-50X)



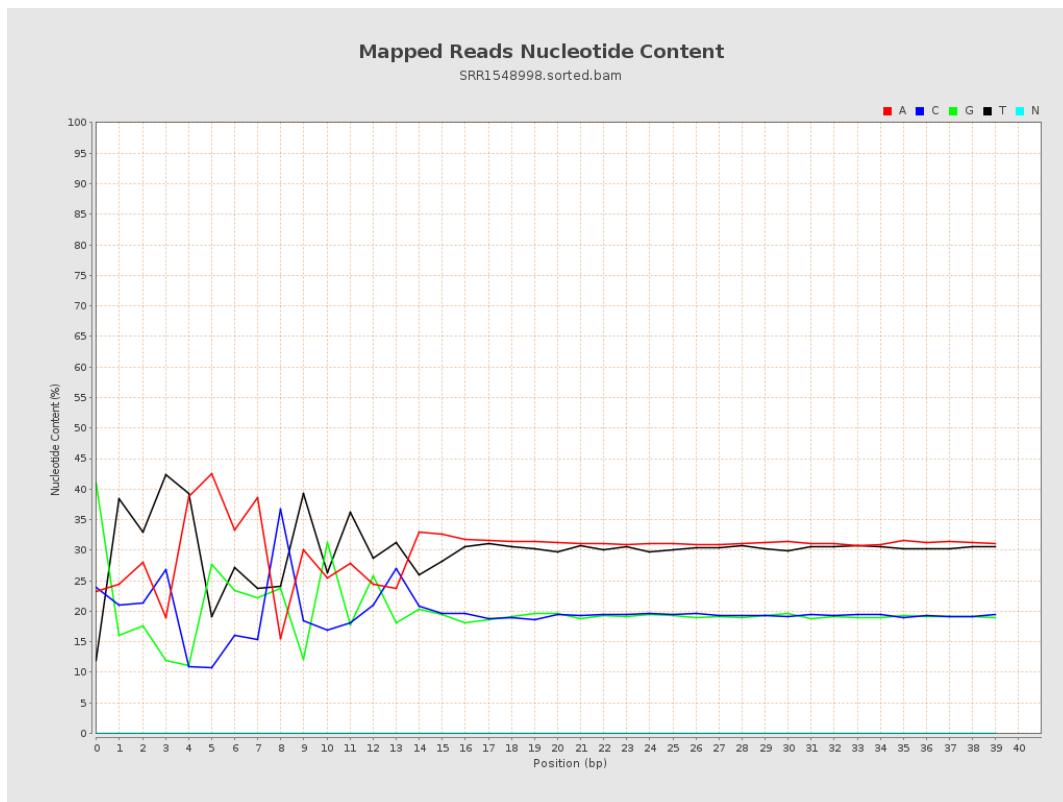
6. Results : Genome Fraction Coverage



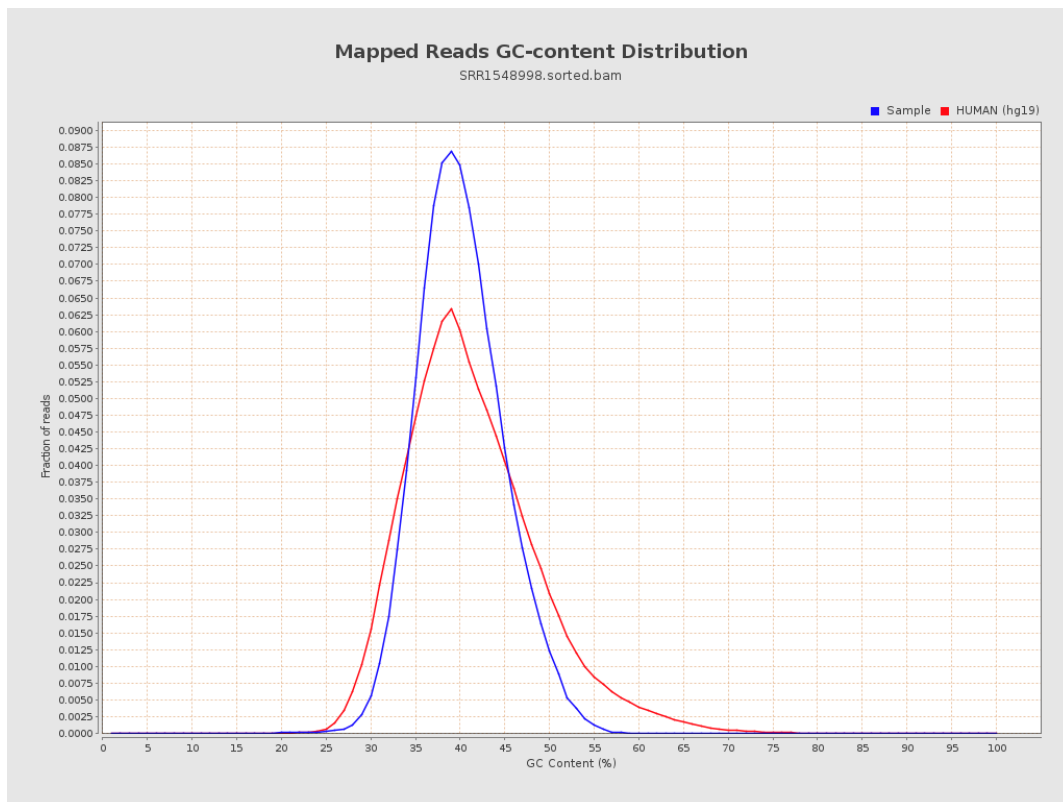
7. Results : Duplication Rate Histogram



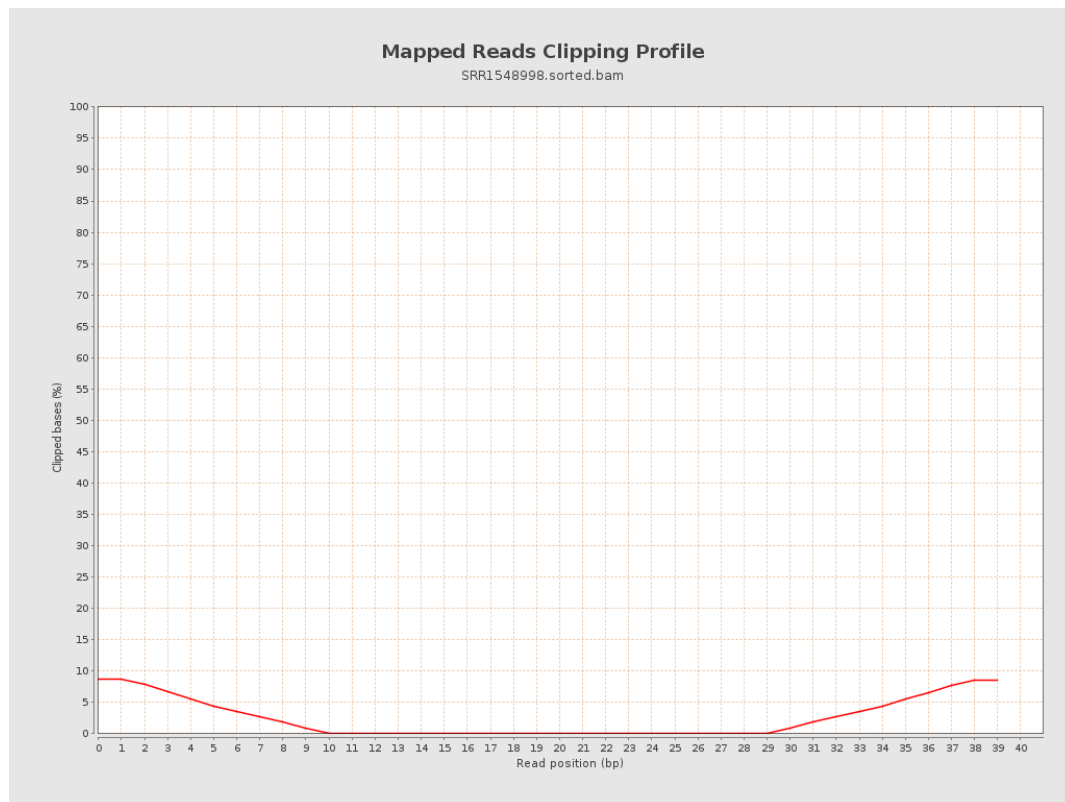
8. Results : Mapped Reads Nucleotide Content



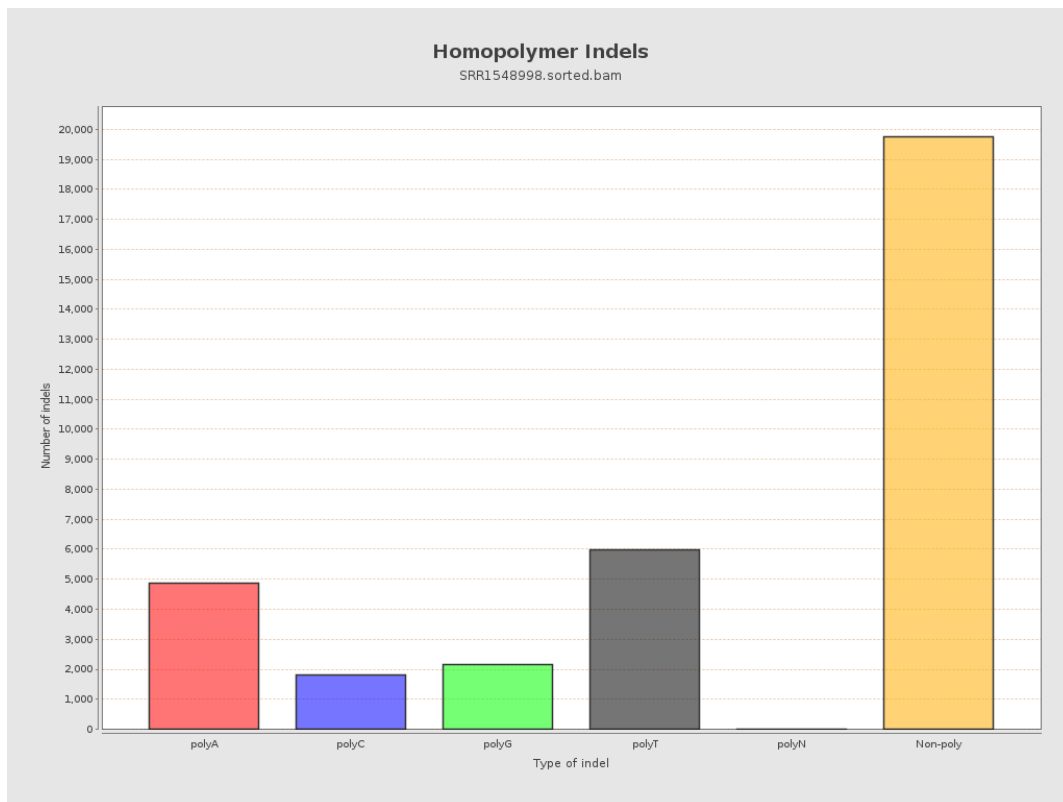
9. Results : Mapped Reads GC-content Distribution



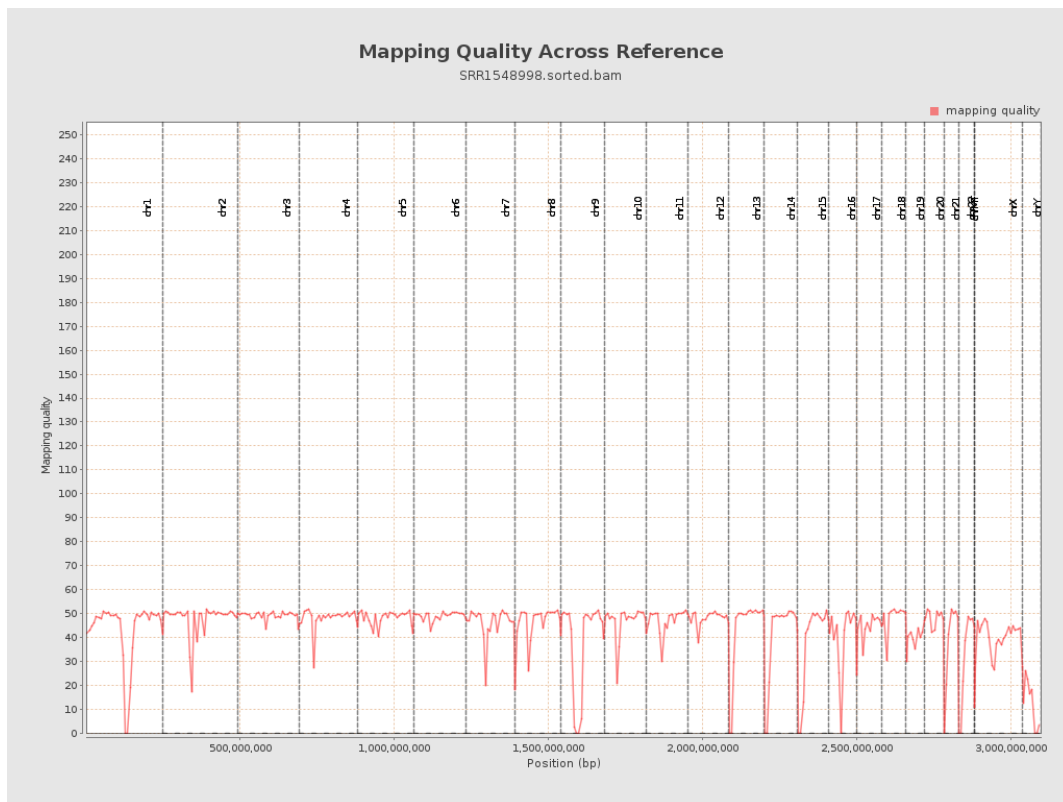
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

