

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 06:27:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063598.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_SRR6063598 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063598.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 06:27:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063598.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,415,807
Mapped reads	780,359 / 55.12%
Unmapped reads	635,448 / 44.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,731 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	154,659 / 10.92%
Duplication rate	13.01%
Clipped reads	424,482 / 29.98%

2.2. ACGT Content

Number/percentage of A's	13,738,773 / 27.52%
Number/percentage of C's	9,338,161 / 18.71%
Number/percentage of T's	15,713,565 / 31.48%
Number/percentage of G's	11,127,801 / 22.29%
Number/percentage of N's	1,379 / 0%
GC Percentage	41%

2.3. Coverage

Mean	0.0161

Standard Deviation	0.3563
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2.4. Mapping Quality

Mean Mapping Quality	45.04
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2.5. Mismatches and indels

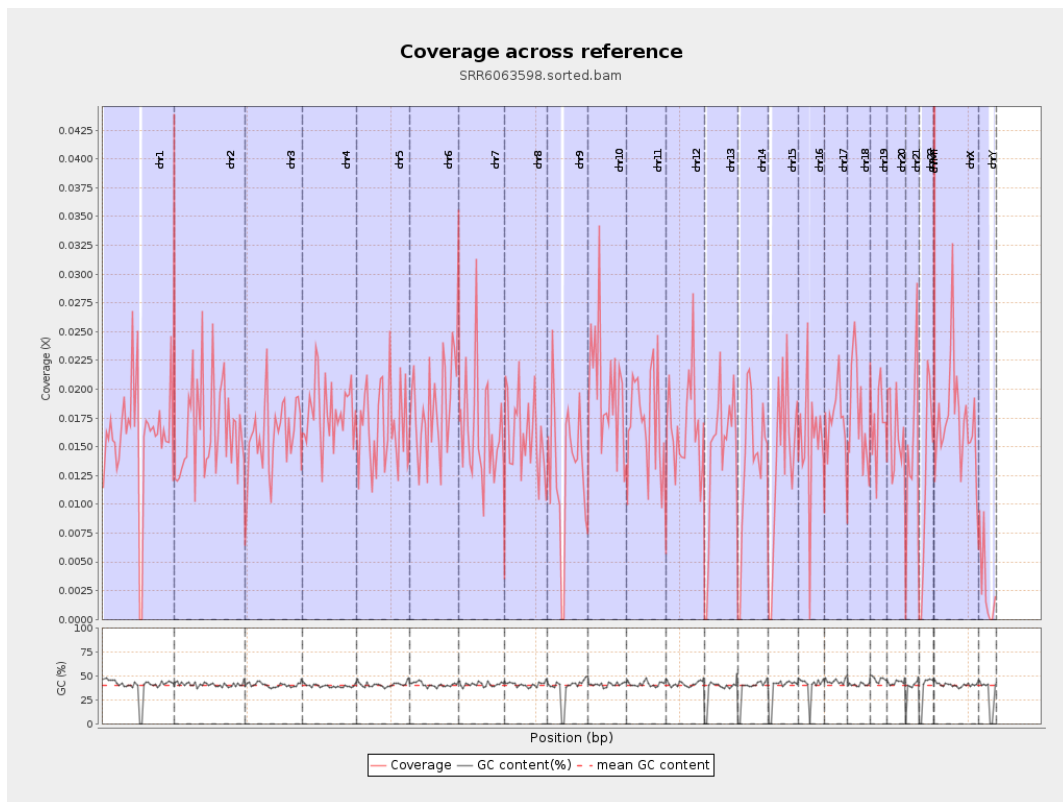
General error rate	0.8%
Mismatches	390,543
Insertions	3,942
Mapped reads with at least one insertion	0.5%
Deletions	11,848
Mapped reads with at least one deletion	1.5%
Homopolymer indels	45.57%

2.6. Chromosome stats

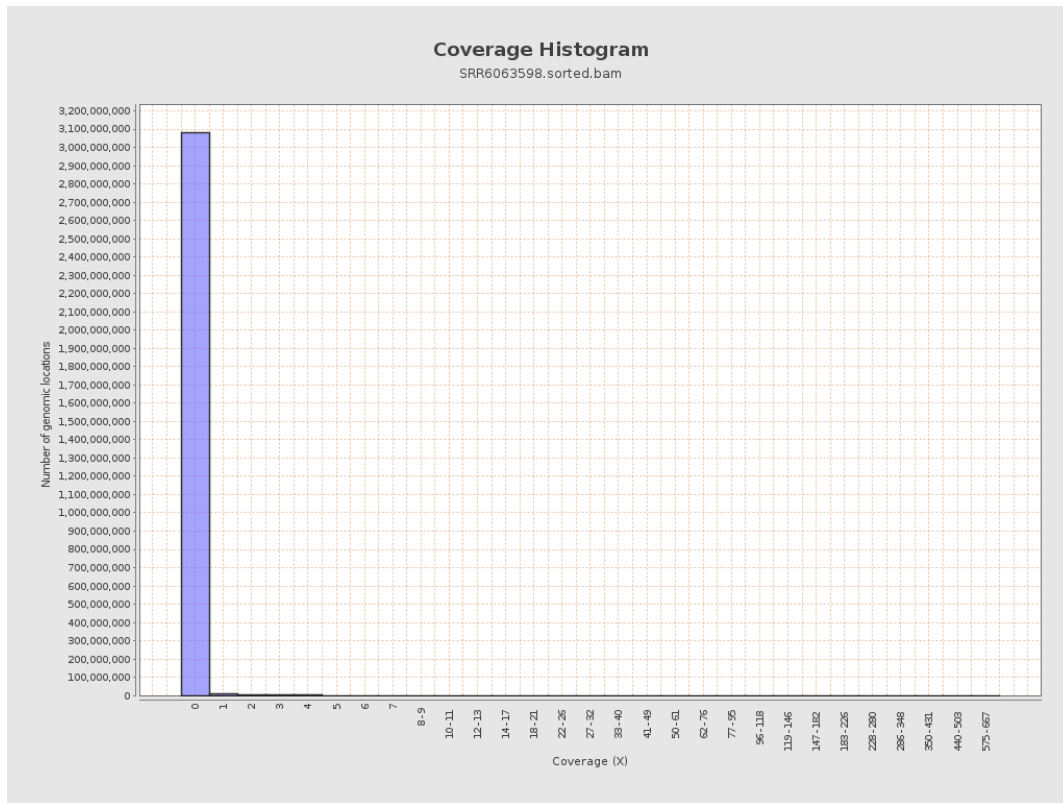
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3990212	0.016	0.38
chr2	243199373	4015161	0.0165	0.3961
chr3	198022430	3186865	0.0161	0.3071
chr4	191154276	3450504	0.0181	0.4204
chr5	180915260	3039581	0.0168	0.3175
chr6	171115067	3193951	0.0187	0.3627
chr7	159138663	2607398	0.0164	0.3411

chr8	146364022	2351920	0.0161	0.3689
chr9	141213431	1863584	0.0132	0.3007
chr10	135534747	2702192	0.0199	0.3567
chr11	135006516	2335186	0.0173	0.3096
chr12	133851895	2250389	0.0168	0.308
chr13	115169878	1660540	0.0144	0.3182
chr14	107349540	1476914	0.0138	0.4338
chr15	102531392	1422335	0.0139	0.5544
chr16	90354753	1383785	0.0153	0.2856
chr17	81195210	1401909	0.0173	0.3114
chr18	78077248	1379106	0.0177	0.3895
chr19	59128983	1012794	0.0171	0.3229
chr20	63025520	1016359	0.0161	0.3106
chr21	48129895	706335	0.0147	0.2817
chr22	51304566	620337	0.0121	0.3068
chrMT	16571	6740	0.4067	1.0922
chrX	155270560	2695900	0.0174	0.3485
chrY	59373566	169296	0.0029	0.1497

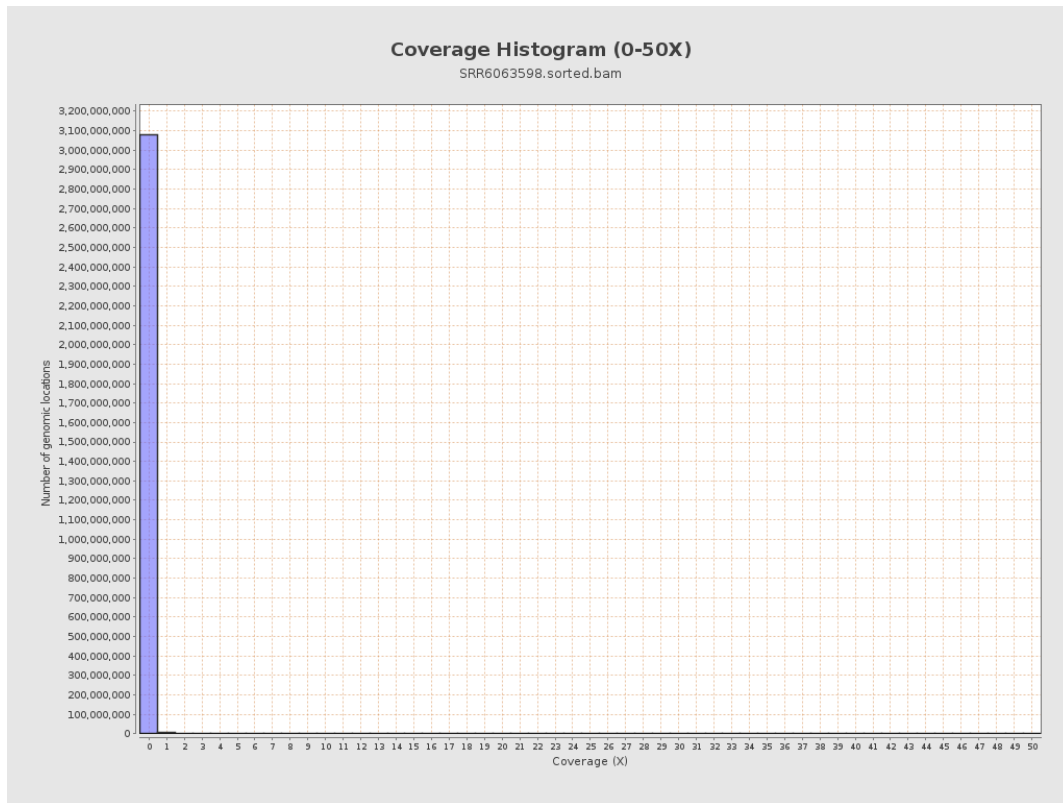
3. Results : Coverage across reference



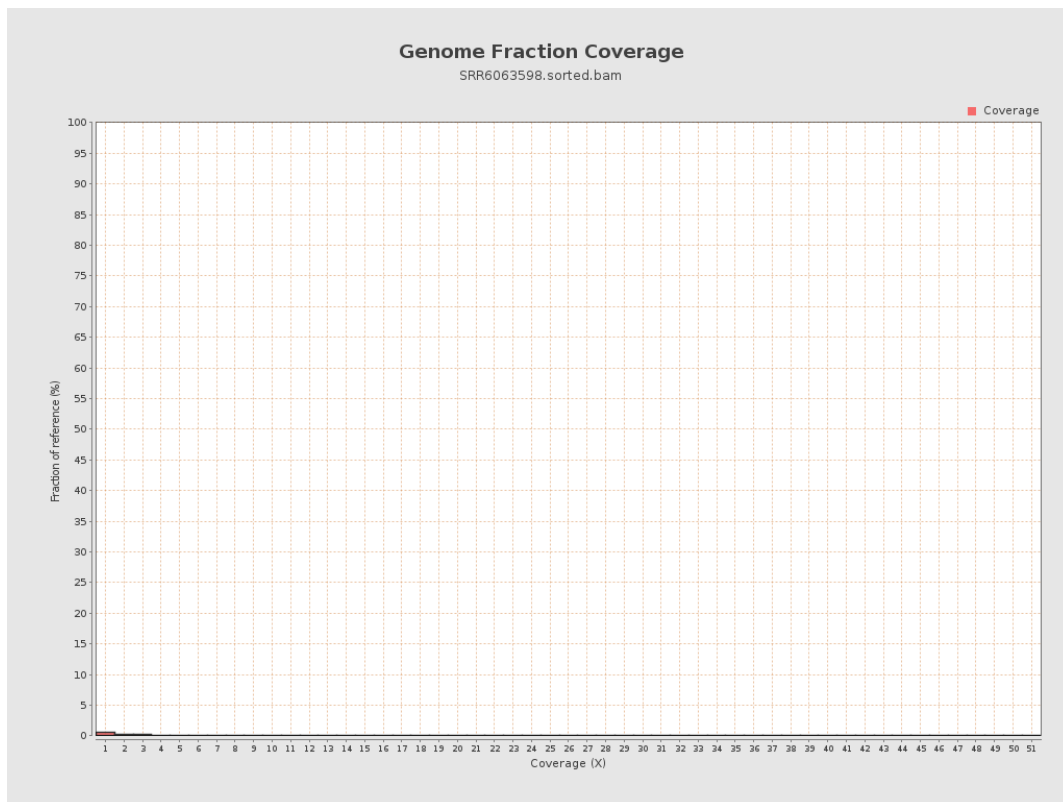
4. Results : Coverage Histogram



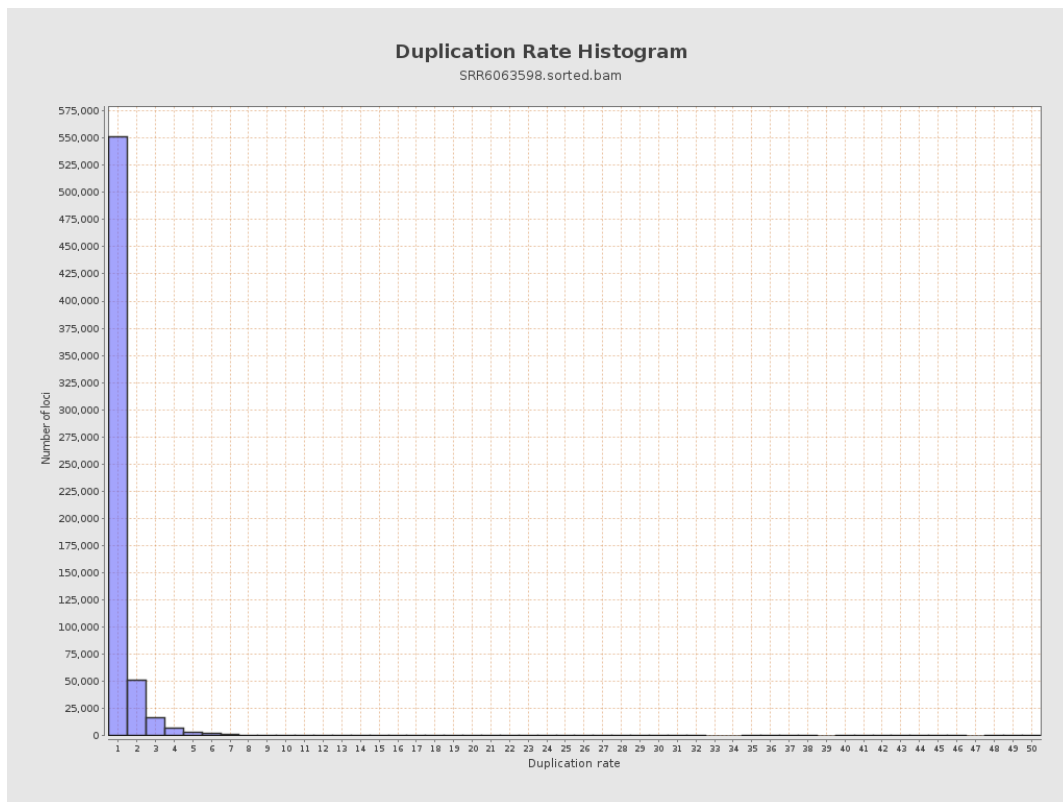
5. Results : Coverage Histogram (0-50X)



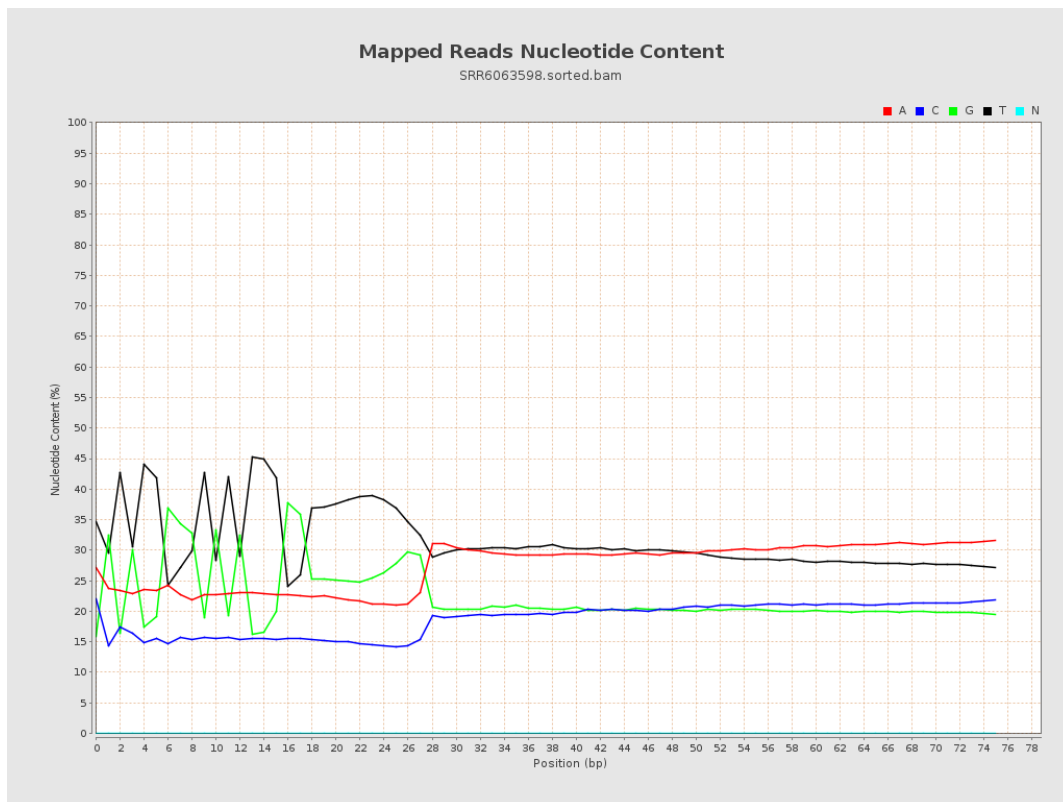
6. Results : Genome Fraction Coverage



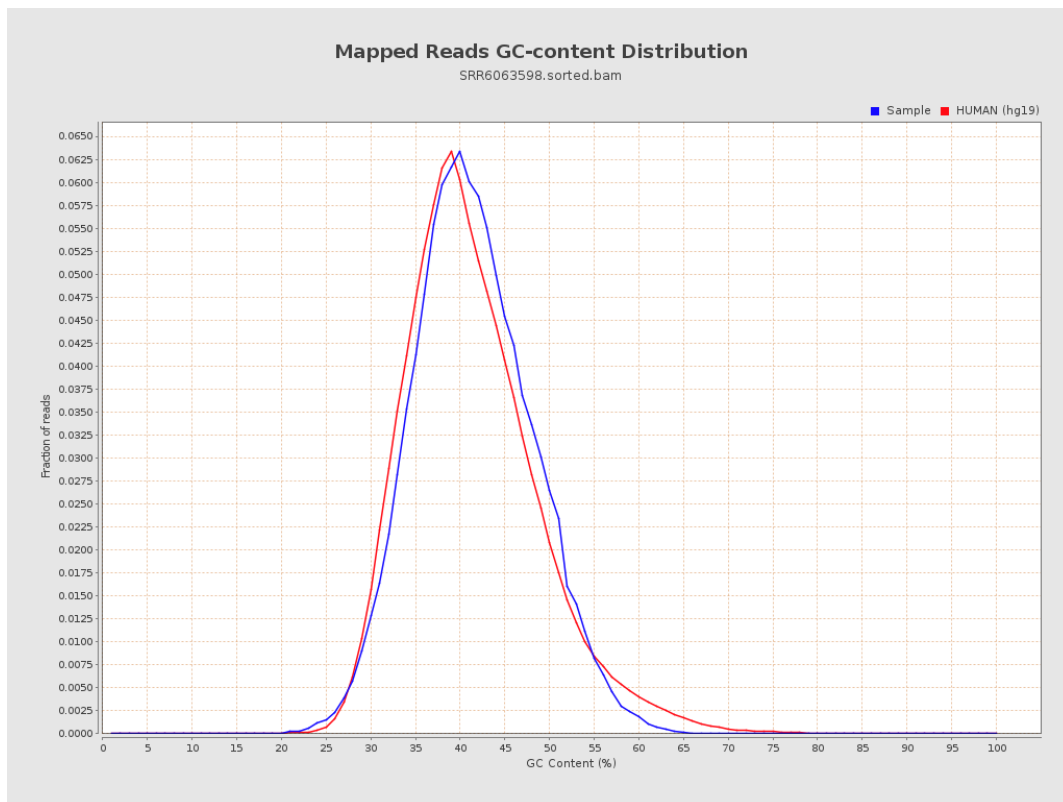
7. Results : Duplication Rate Histogram



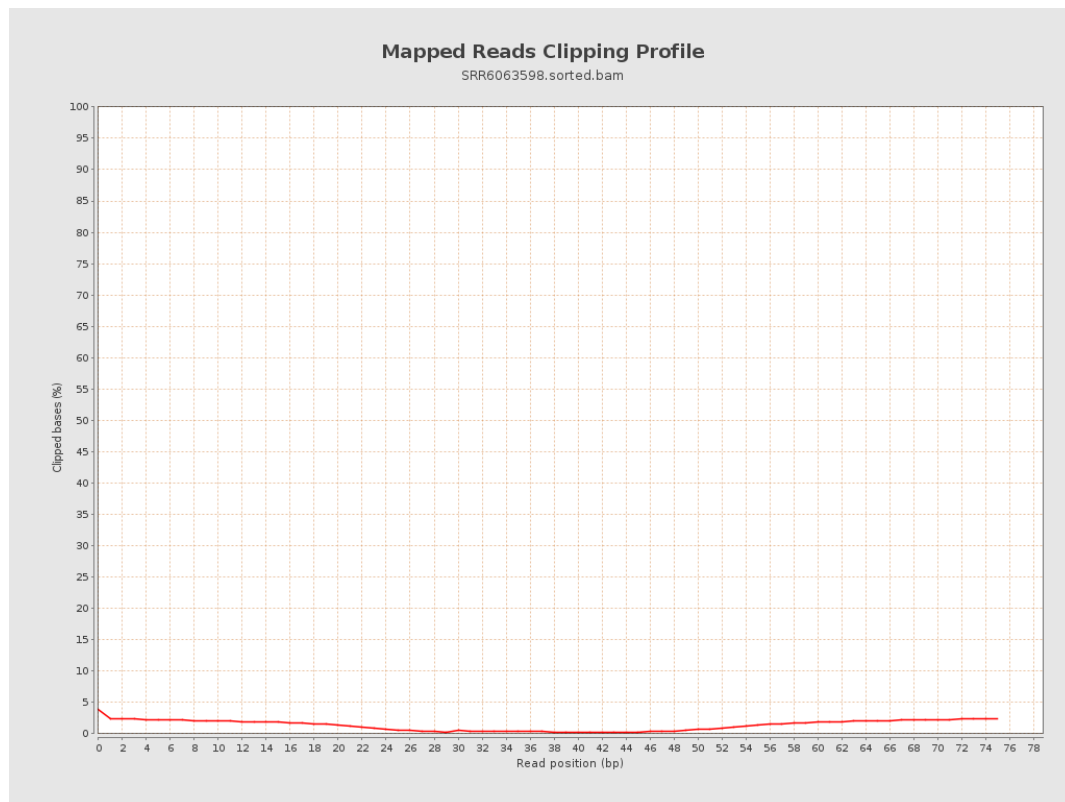
8. Results : Mapped Reads Nucleotide Content



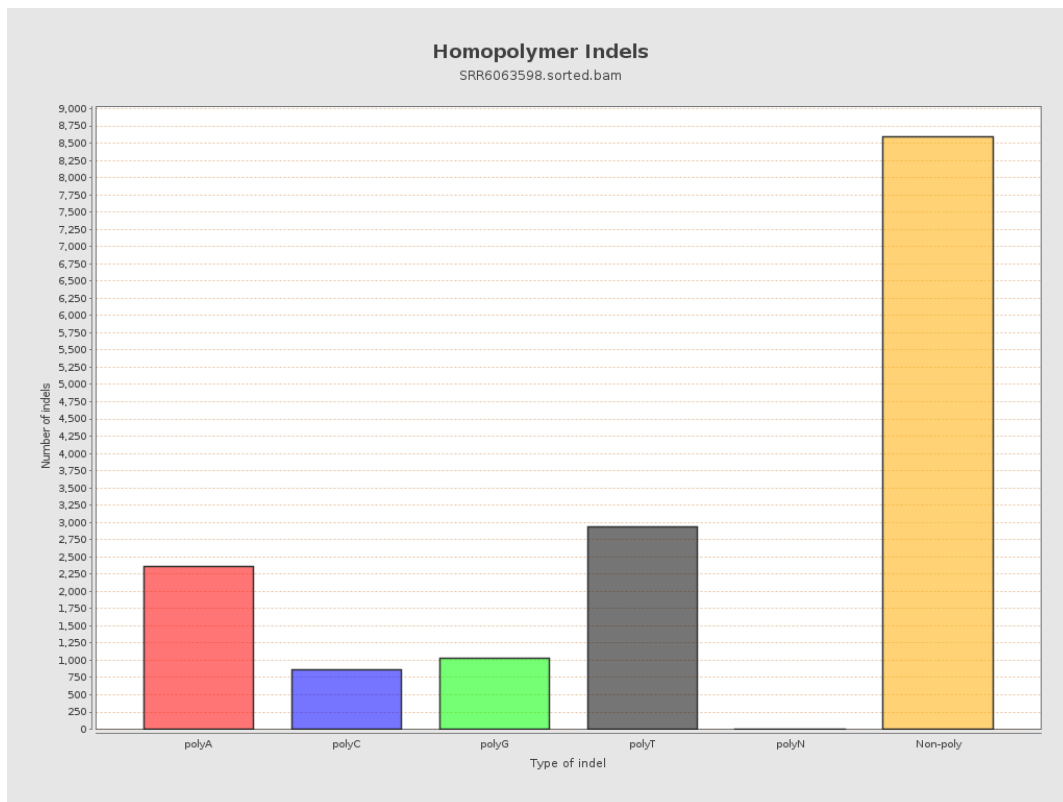
9. Results : Mapped Reads GC-content Distribution



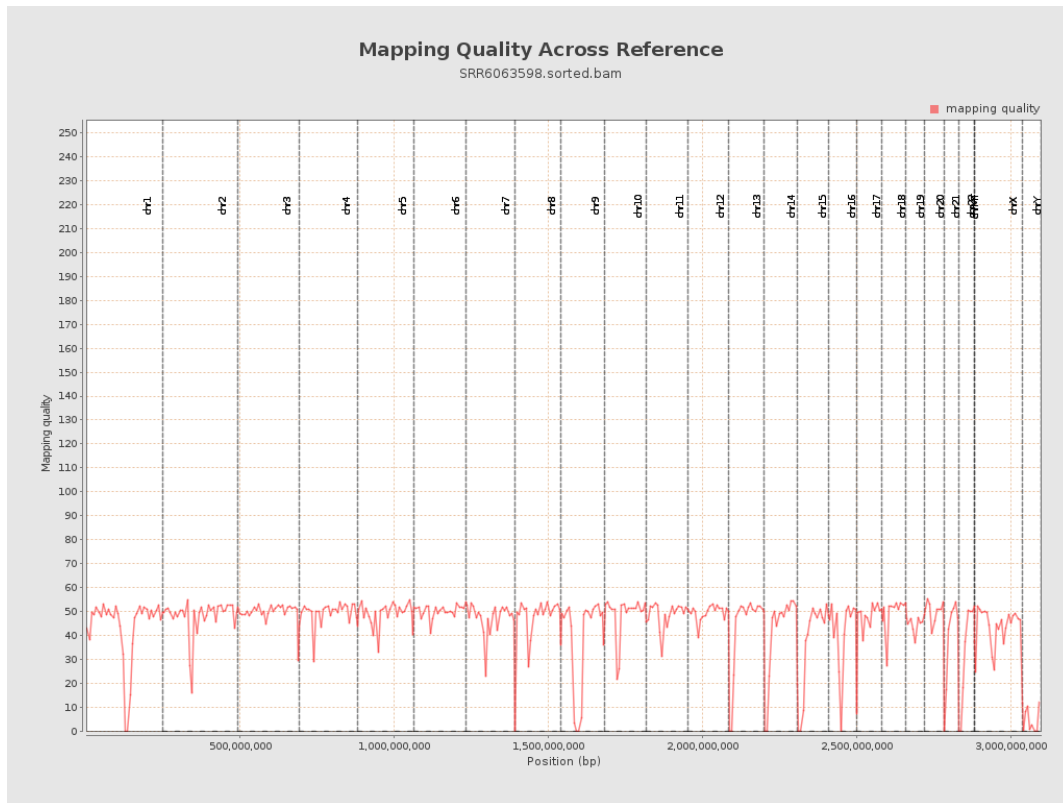
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

