Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 06:32:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063600.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_SRR6063600 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063600.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 06:32:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063600.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,050,177
Mapped reads	1,066,106 / 52%
Unmapped reads	984,071 / 48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,570 / 0.56%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	225,677 / 11.01%
Duplication rate	14.34%
Clipped reads	583,795 / 28.48%

2.2. ACGT Content

Number/percentage of A's	18,725,767 / 27.42%
Number/percentage of C's	12,256,366 / 17.95%
Number/percentage of T's	22,107,659 / 32.37%
Number/percentage of G's	15,200,913 / 22.26%
Number/percentage of N's	1,687 / 0%
GC Percentage	40.21%

2.3. Coverage

Mean	0.0221

Standard Deviation	0.3821

2.4. Mapping Quality

Mean Mapping Quality	45.63

2.5. Mismatches and indels

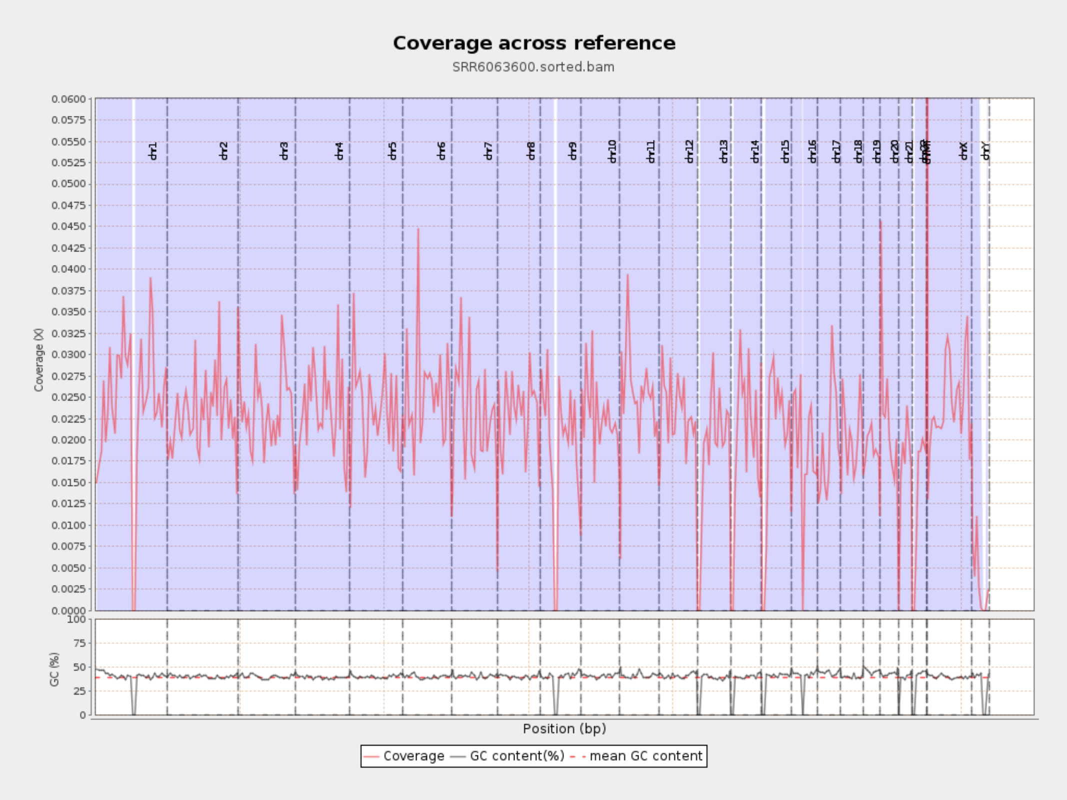
General error rate	0.83%
Mismatches	555,500
Insertions	5,690
Mapped reads with at least one insertion	0.53%
Deletions	19,357
Mapped reads with at least one deletion	1.8%
Homopolymer indels	46.87%

2.6. Chromosome stats

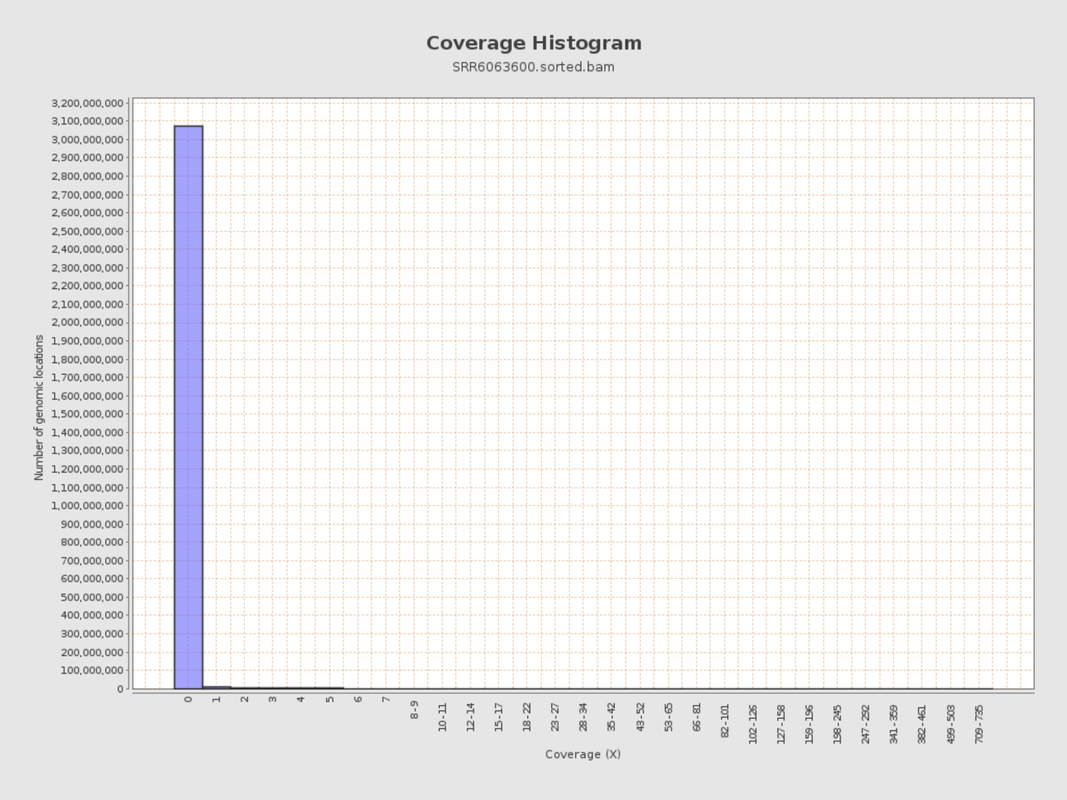
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6094828	0.0245	0.4361
chr2	243199373	5626917	0.0231	0.4293
chr3	198022430	4695708	0.0237	0.3537
chr4	191154276	4497786	0.0235	0.4757
chr5	180915260	4289356	0.0237	0.3586
chr6	171115067	4310810	0.0252	0.4036
chr7	159138663	3703252	0.0233	0.3835

chr8	146364022	3406778	0.0233	0.3814
chr9	141213431	2762401	0.0196	0.339
chr10	135534747	3119298	0.023	0.371
chr11	135006516	3438971	0.0255	0.3924
chr12	133851895	3113166	0.0233	0.3607
chr13	115169878	2151338	0.0187	0.336
chr14	107349540	2091903	0.0195	0.3599
chr15	102531392	2034856	0.0198	0.4574
chr16	90354753	1664186	0.0184	0.3006
chr17	81195210	1597401	0.0197	0.3349
chr18	78077248	1611734	0.0206	0.401
chr19	59128983	1121076	0.019	0.3269
chr20	63025520	1423895	0.0226	0.3552
chr21	48129895	817971	0.017	0.2881
chr22	51304566	742371	0.0145	0.2861
chrMT	16571	19463	1.1745	2.1146
chrX	155270560	3788385	0.0244	0.3675
chrY	59373566	200715	0.0034	0.1329

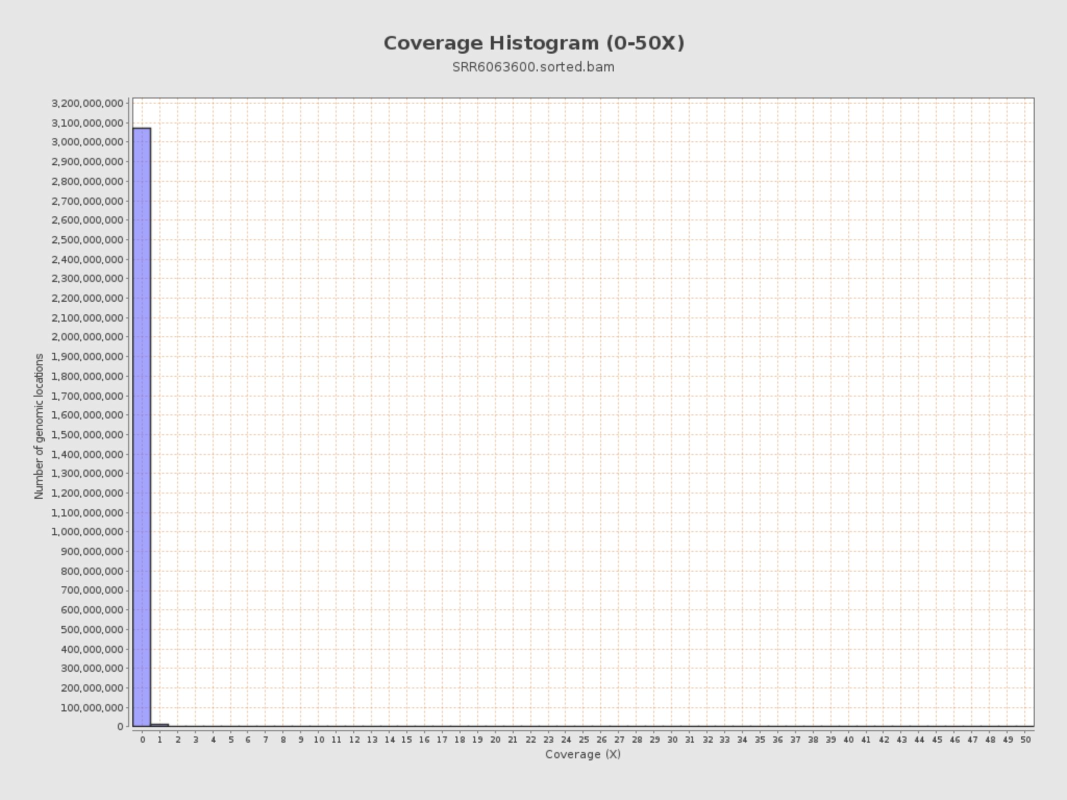
3. Results : Coverage across reference



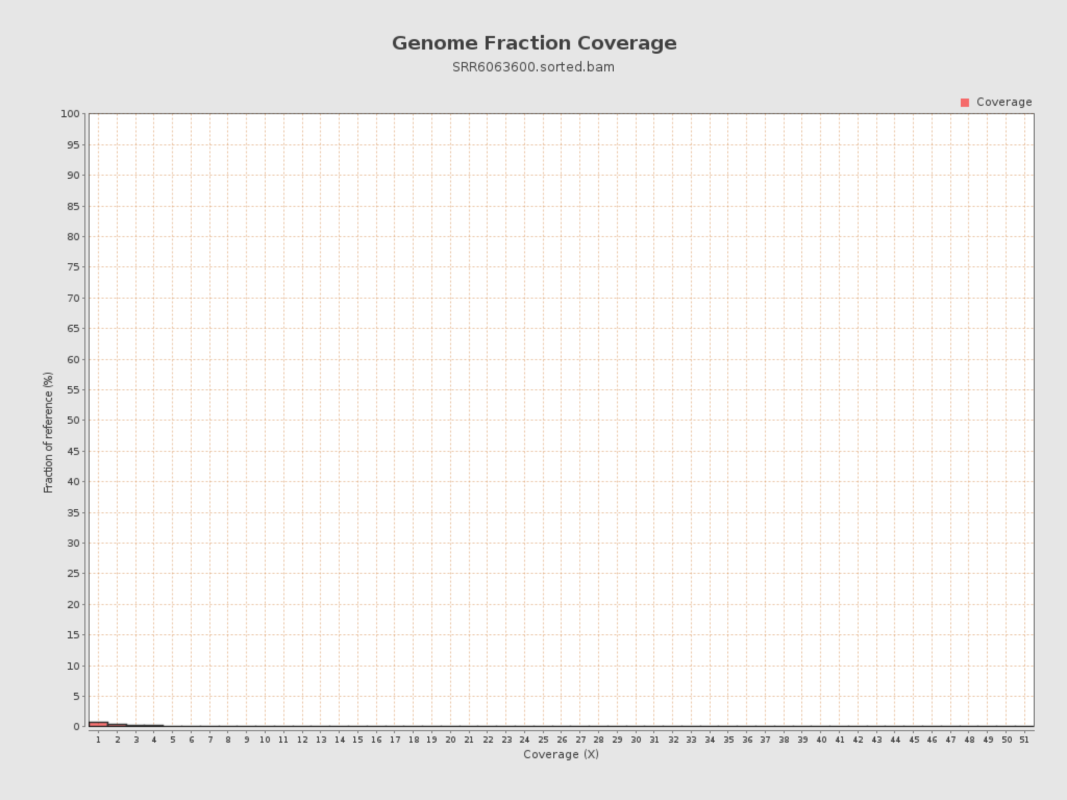
4. Results : Coverage Histogram



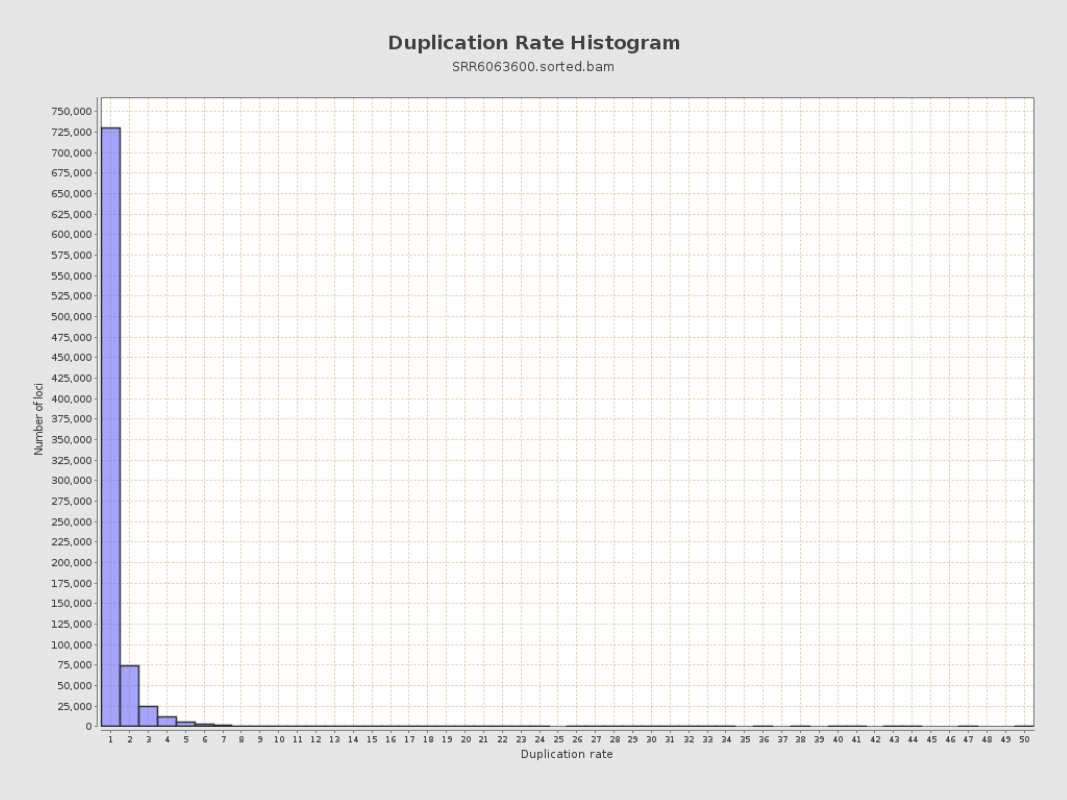
5. Results : Coverage Histogram (0-50X)



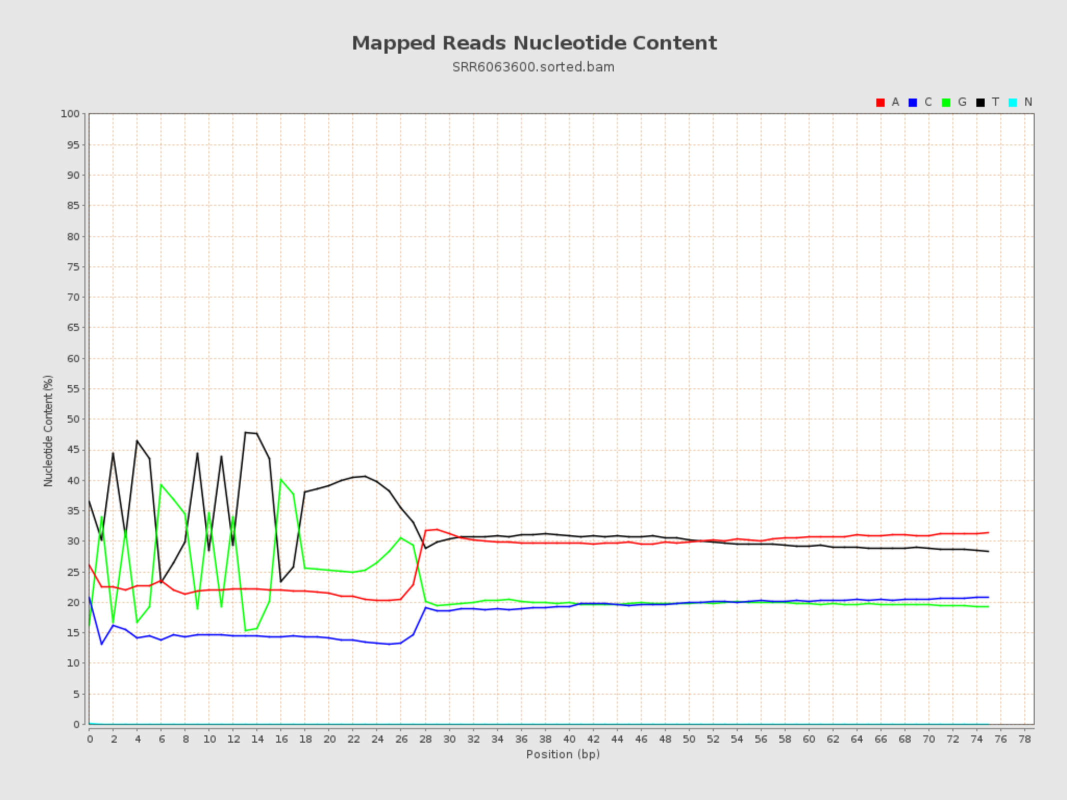
6. Results : Genome Fraction Coverage



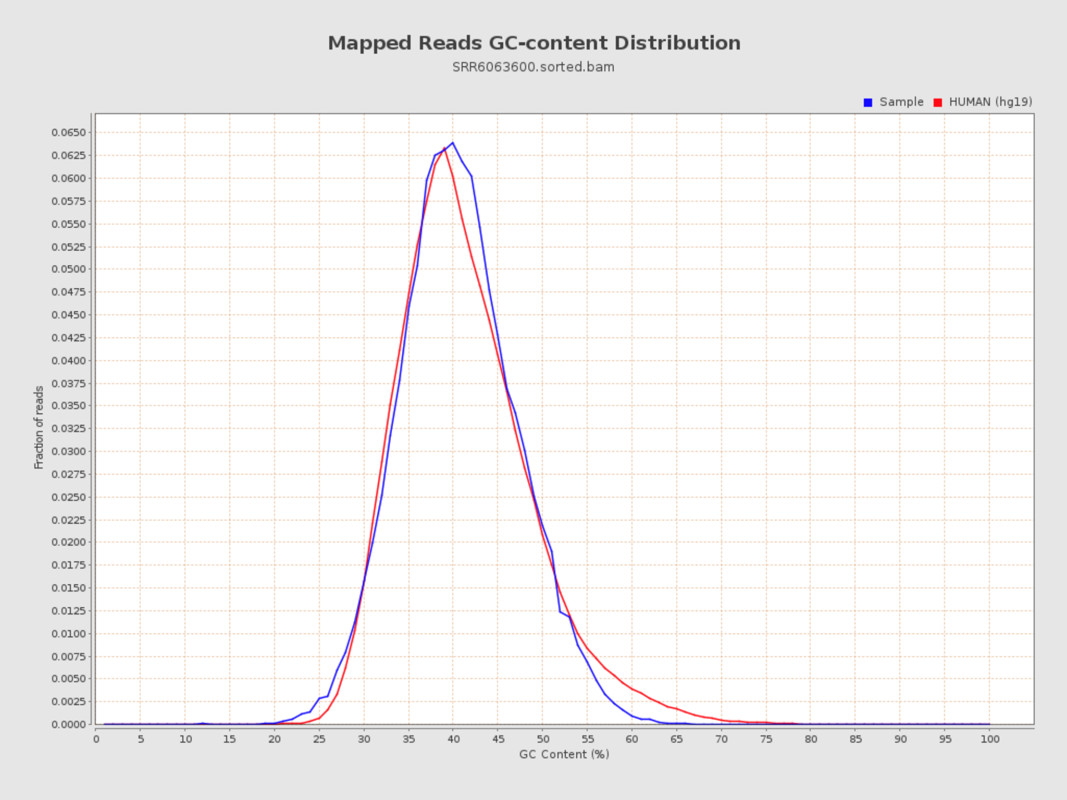
7. Results : Duplication Rate Histogram



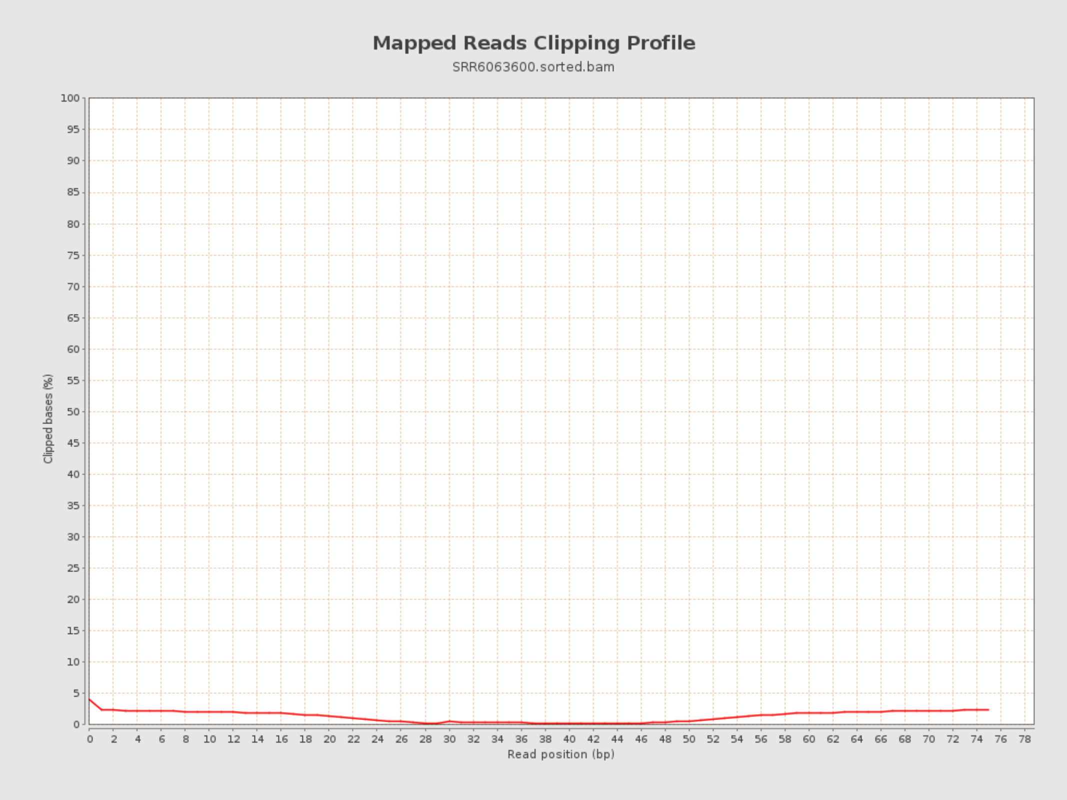
8. Results : Mapped Reads Nucleotide Content



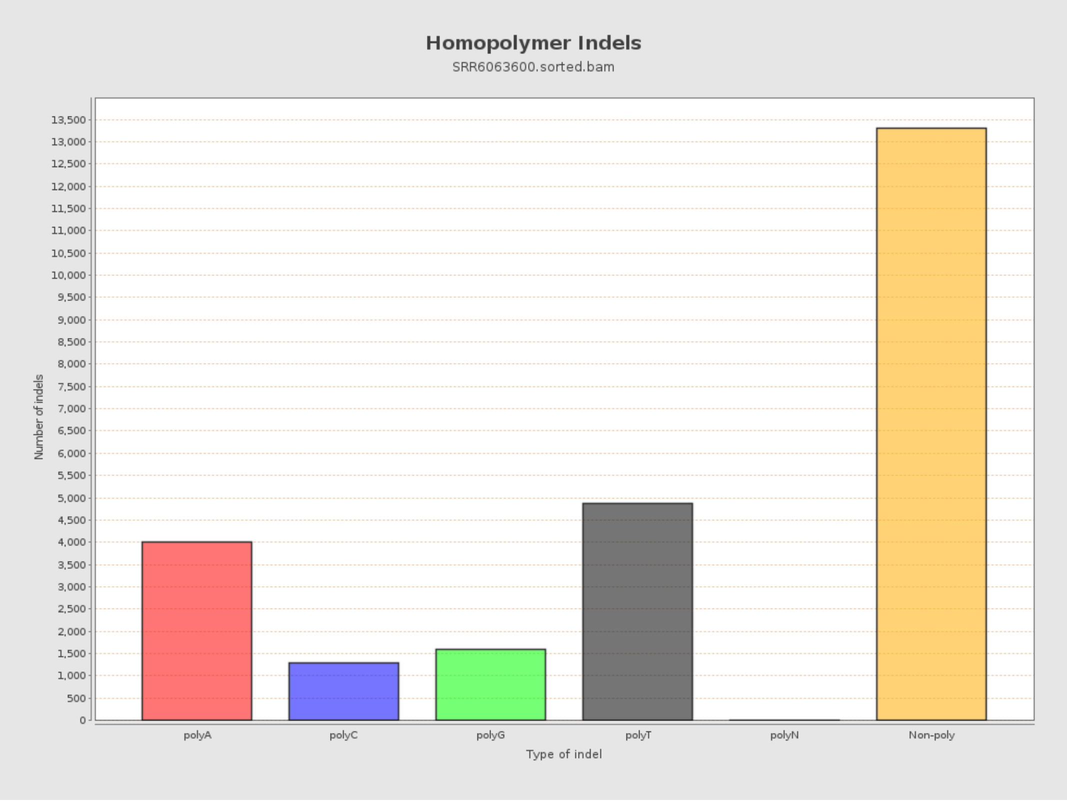
9. Results : Mapped Reads GC-content Distribution



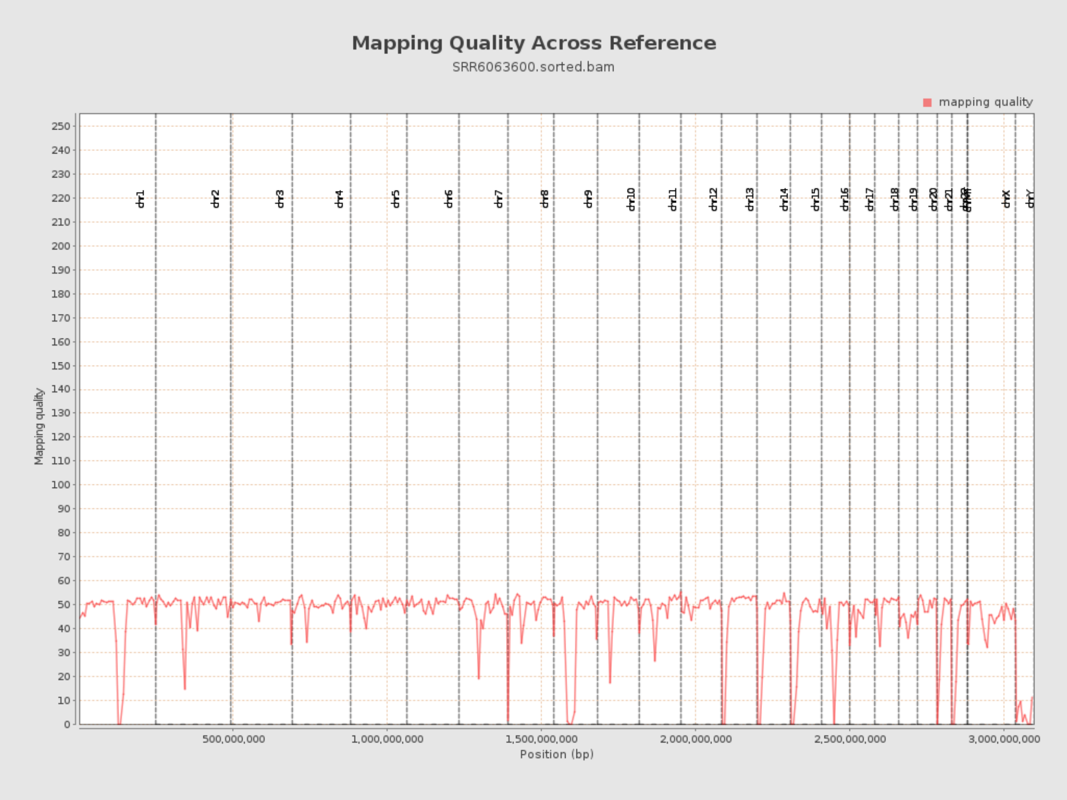
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram