Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 06:47:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063603.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_SRR6063603 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063603.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 06:47:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063603.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,762,100
Mapped reads	4,506,185 / 94.63%
Unmapped reads	255,915 / 5.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,353 / 0.68%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	633,818 / 13.31%
Duplication rate	11.58%
Clipped reads	2,404,610 / 50.49%

2.2. ACGT Content

Number/percentage of A's	73,615,582 / 25.49%
Number/percentage of C's	52,641,568 / 18.23%
Number/percentage of T's	93,577,133 / 32.41%
Number/percentage of G's	68,904,761 / 23.86%
Number/percentage of N's	32,342 / 0.01%
GC Percentage	42.09%

2.3. Coverage

Mean	0.0933

Standard Deviation	0.9845

2.4. Mapping Quality

Mean Mapping Quality	45.54

2.5. Mismatches and indels

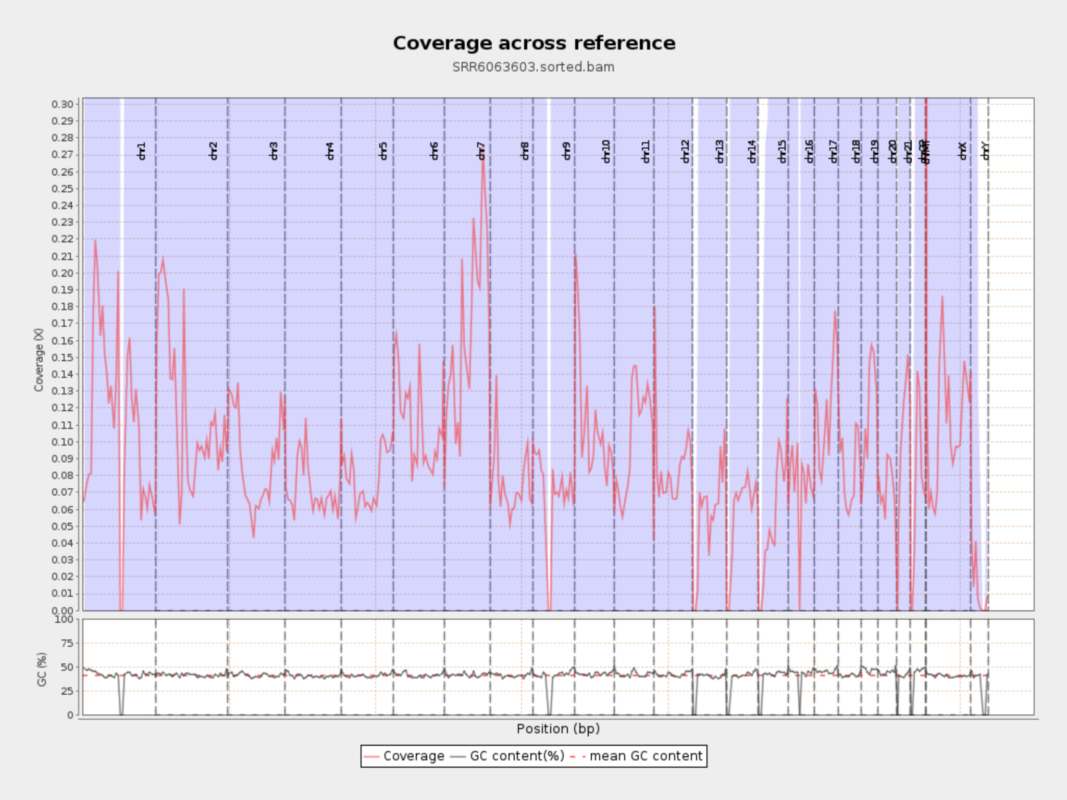
General error rate	0.53%
Mismatches	1,494,594
Insertions	17,957
Mapped reads with at least one insertion	0.4%
Deletions	64,640
Mapped reads with at least one deletion	1.42%
Homopolymer indels	44.6%

2.6. Chromosome stats

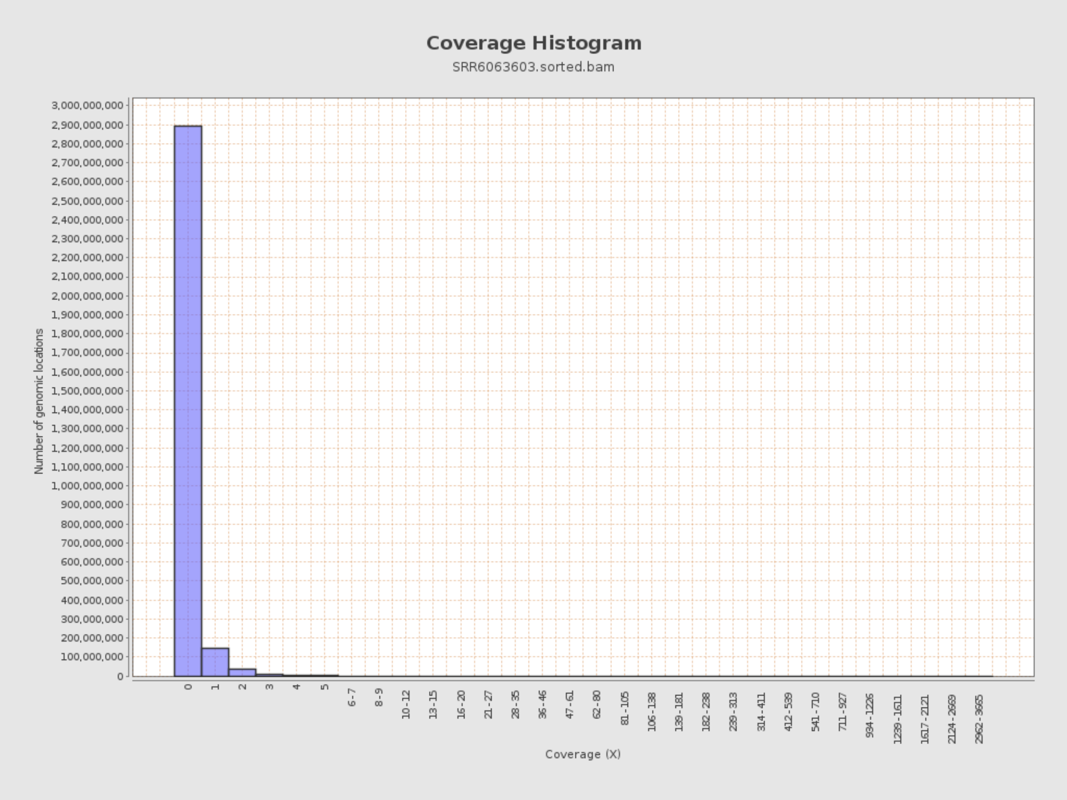
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27711534	0.1112	2.0858
chr2	243199373	28933756	0.119	1.7364
chr3	198022430	17401874	0.0879	0.4012
chr4	191154276	13761944	0.072	0.4004
chr5	180915260	14348636	0.0793	0.3839
chr6	171115067	19058901	0.1114	0.6602
chr7	159138663	26732087	0.168	1.415

chr8	146364022	11046103	0.0755	0.8751
chr9	141213431	9510337	0.0673	0.65
chr10	135534747	15126659	0.1116	0.6523
chr11	135006516	13898577	0.1029	0.5522
chr12	133851895	11557429	0.0863	0.4319
chr13	115169878	6579336	0.0571	0.3749
chr14	107349540	6293171	0.0586	0.3835
chr15	102531392	5451467	0.0532	0.3572
chr16	90354753	6612272	0.0732	0.408
chr17	81195210	9805323	0.1208	0.5083
chr18	78077248	6583433	0.0843	1.2491
chr19	59128983	7013480	0.1186	1.3158
chr20	63025520	4588800	0.0728	0.3963
chr21	48129895	4974851	0.1034	0.4576
chr22	51304566	3672472	0.0716	0.3575
chrMT	16571	397833	24.0078	13.1489
chrX	155270560	17035286	0.1097	0.5574
chrY	59373566	789306	0.0133	0.4137

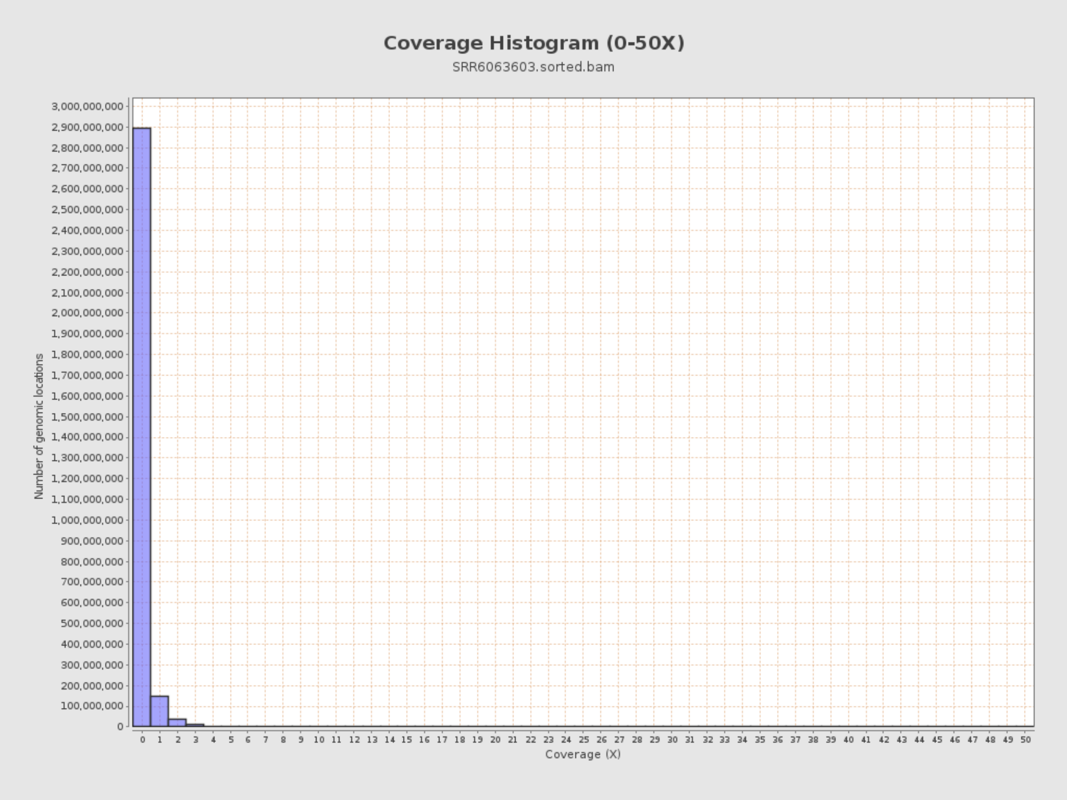
3. Results : Coverage across reference



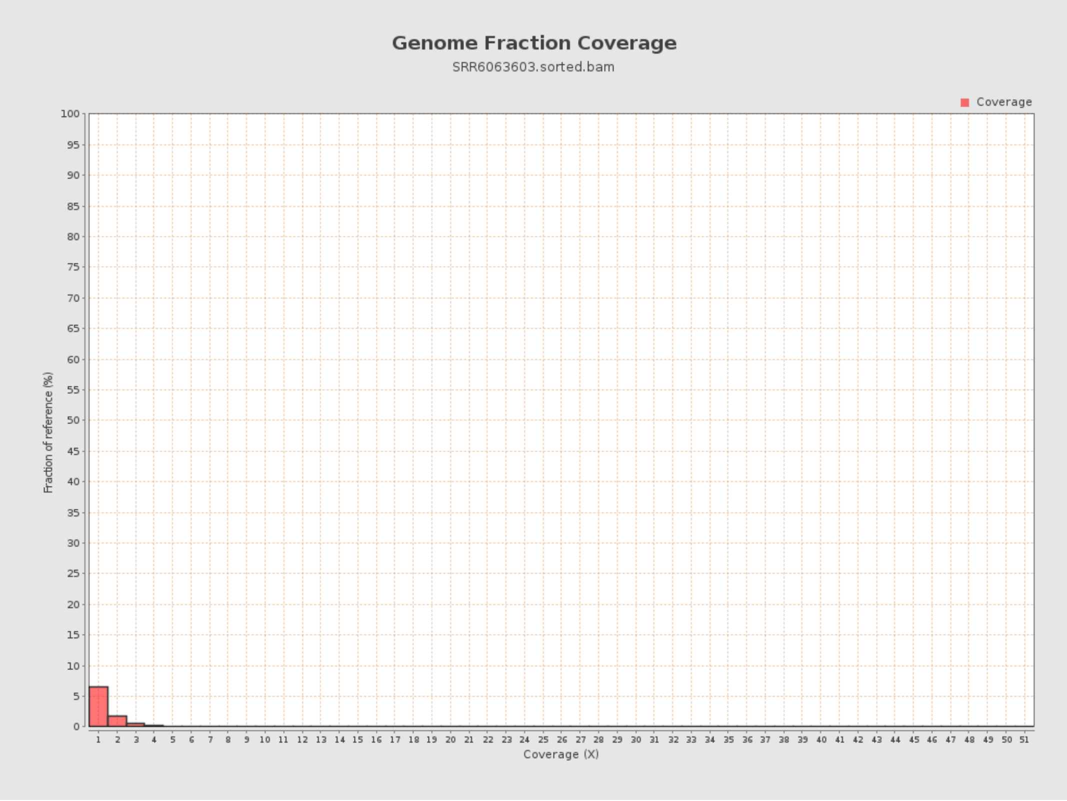
4. Results : Coverage Histogram



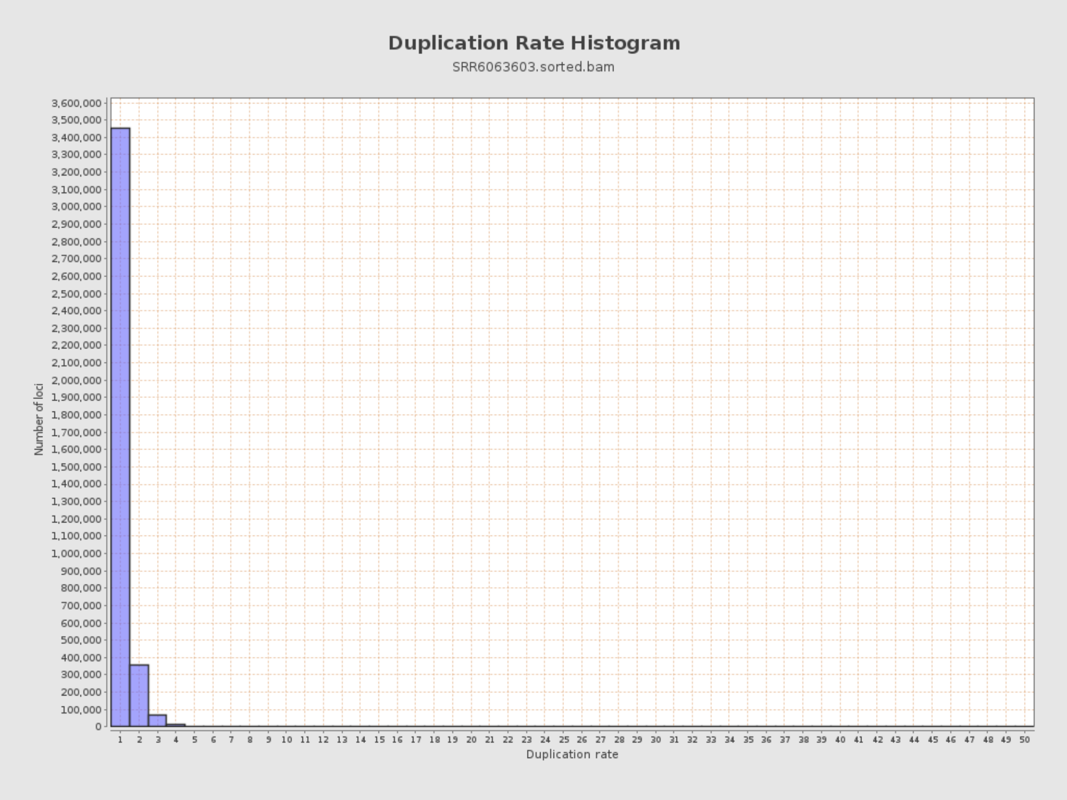
5. Results : Coverage Histogram (0-50X)



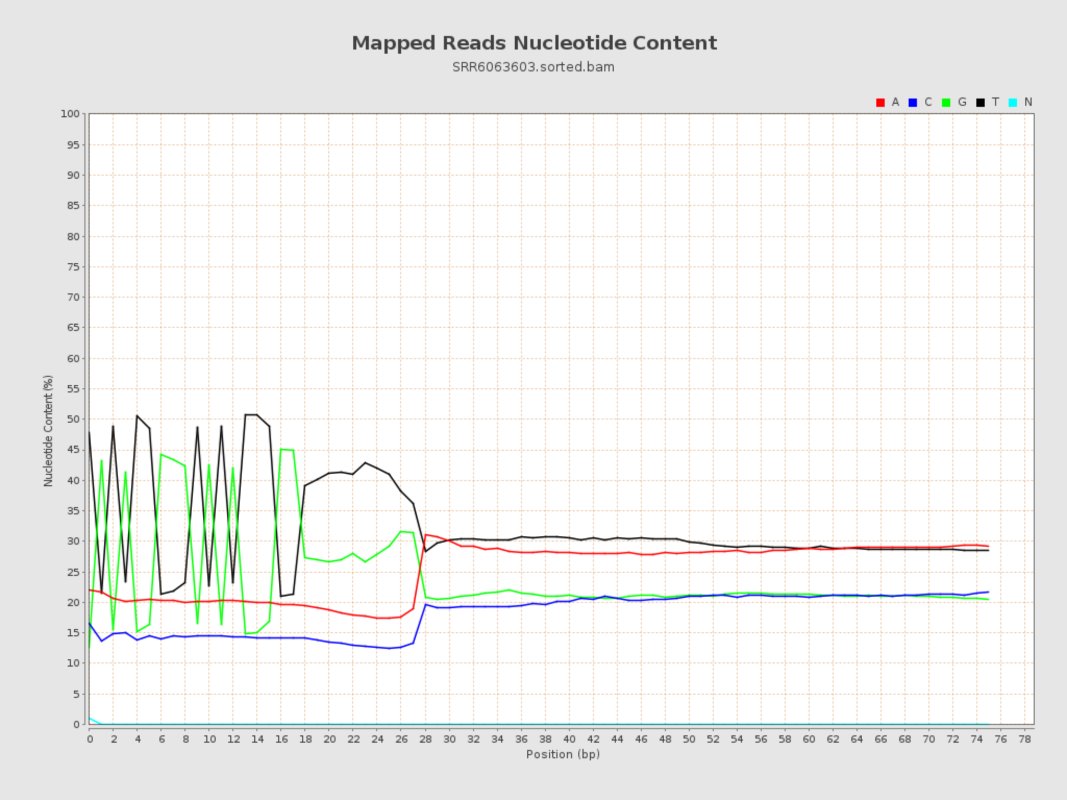
6. Results : Genome Fraction Coverage



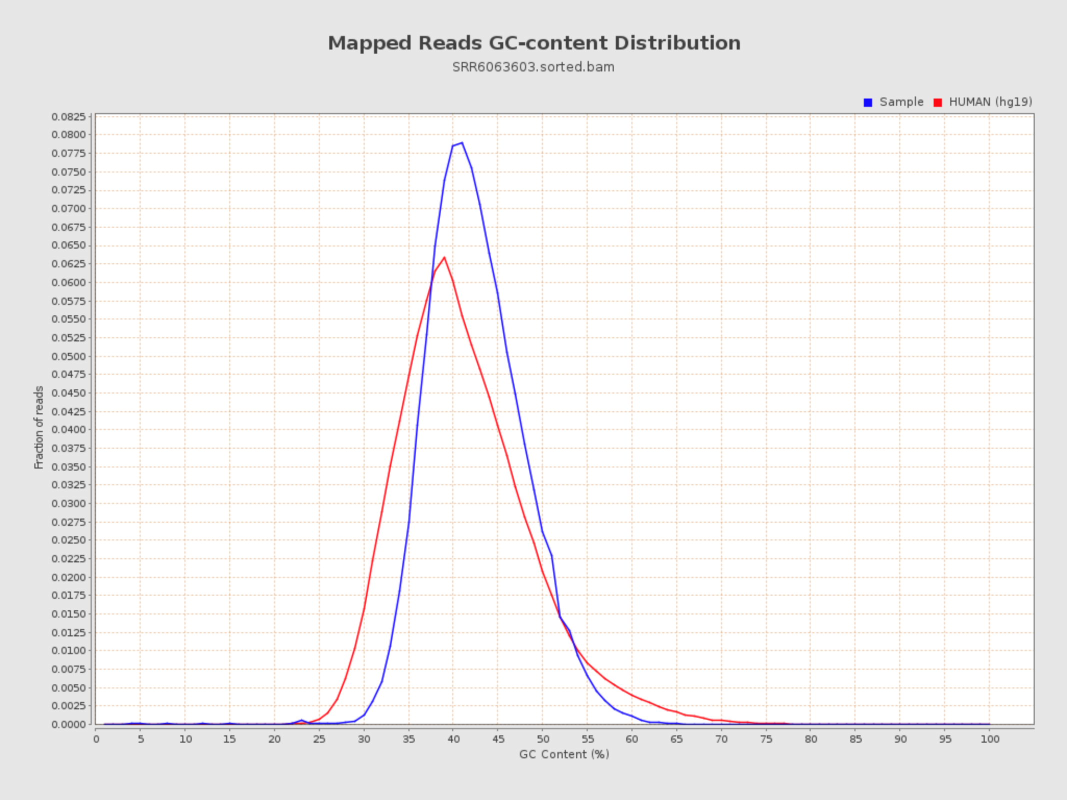
7. Results : Duplication Rate Histogram



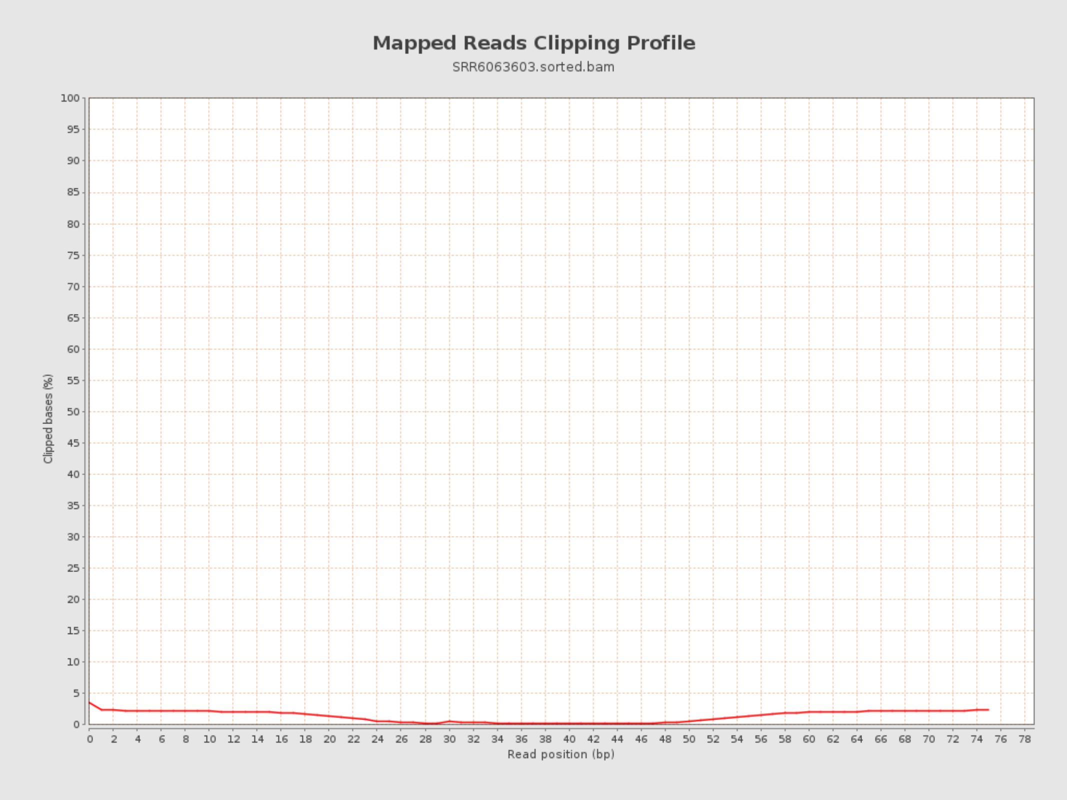
8. Results : Mapped Reads Nucleotide Content



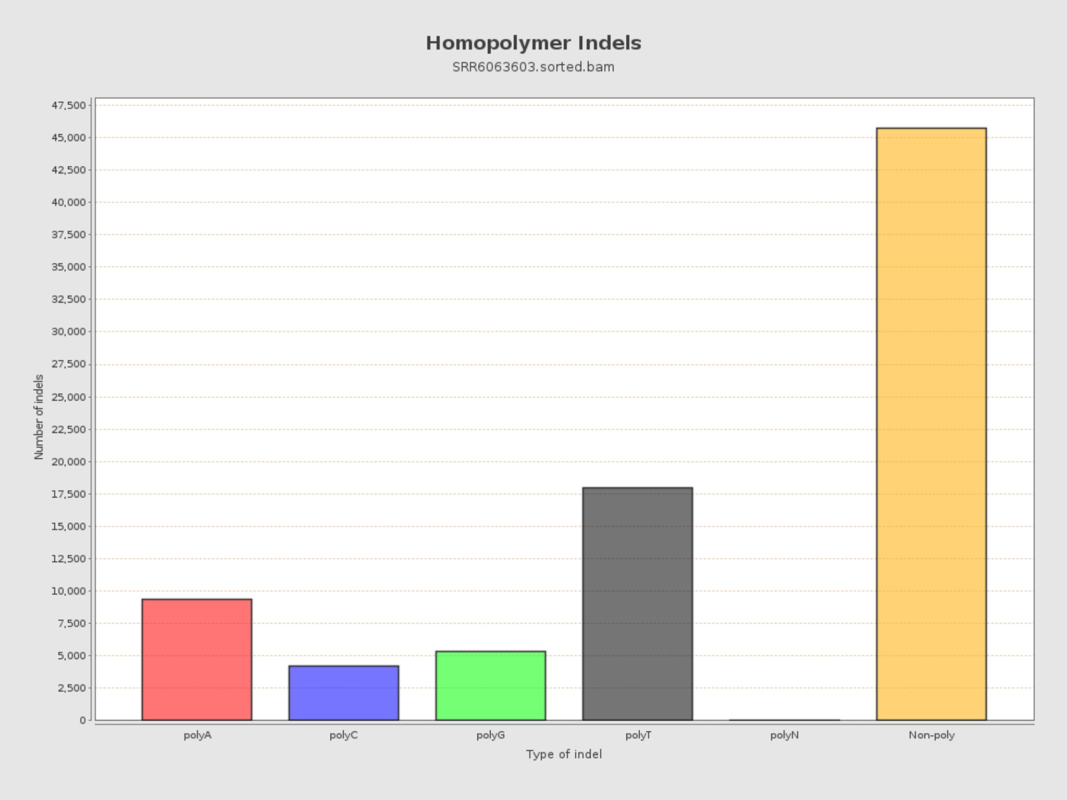
9. Results : Mapped Reads GC-content Distribution



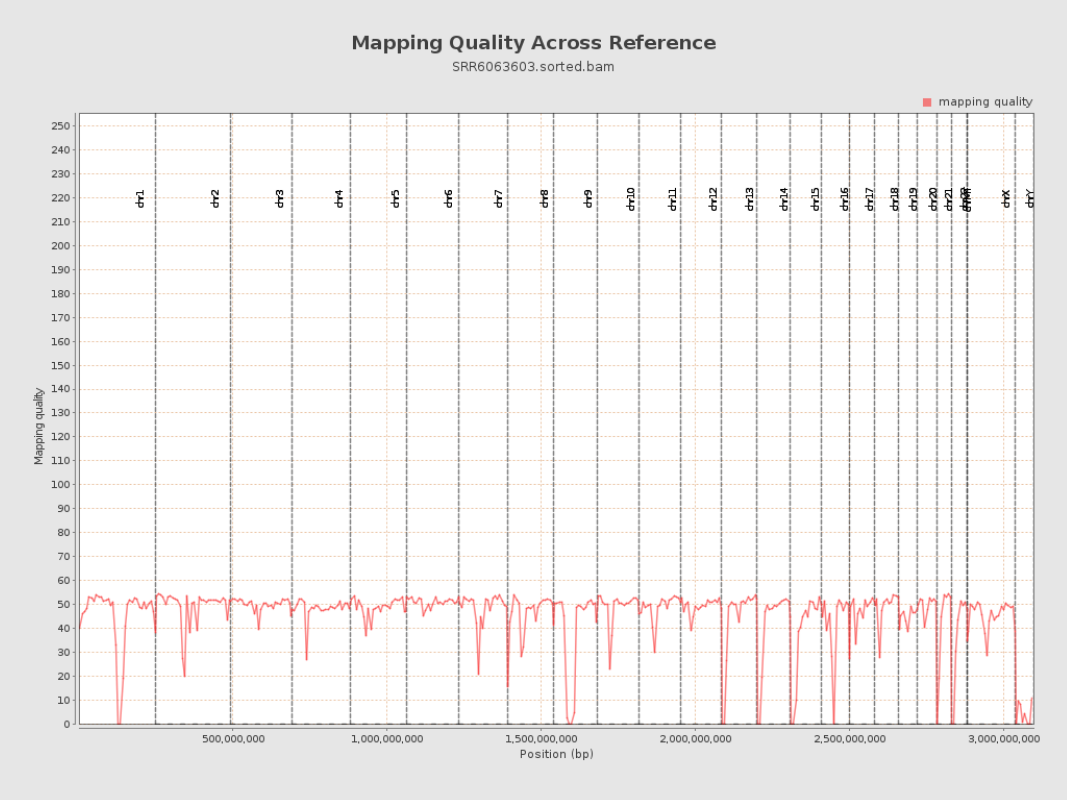
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram