Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 00:50:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063533.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_SRR6063533 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063533.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 00:50:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063533.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,971,613
Mapped reads	2,544,827 / 85.64%
Unmapped reads	426,786 / 14.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,246 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	189,530 / 6.38%
Duplication rate	6.01%
Clipped reads	1,554,245 / 52.3%

2.2. ACGT Content

Number/percentage of A's	42,074,908 / 26.31%
Number/percentage of C's	28,683,992 / 17.94%
Number/percentage of T's	51,437,480 / 32.16%
Number/percentage of G's	37,733,585 / 23.59%
Number/percentage of N's	2,766 / 0%
GC Percentage	41.53%

2.3. Coverage

Mean	0.0517

Standard Deviation	0.4624

2.4. Mapping Quality

Mean Mapping Quality	43.93

2.5. Mismatches and indels

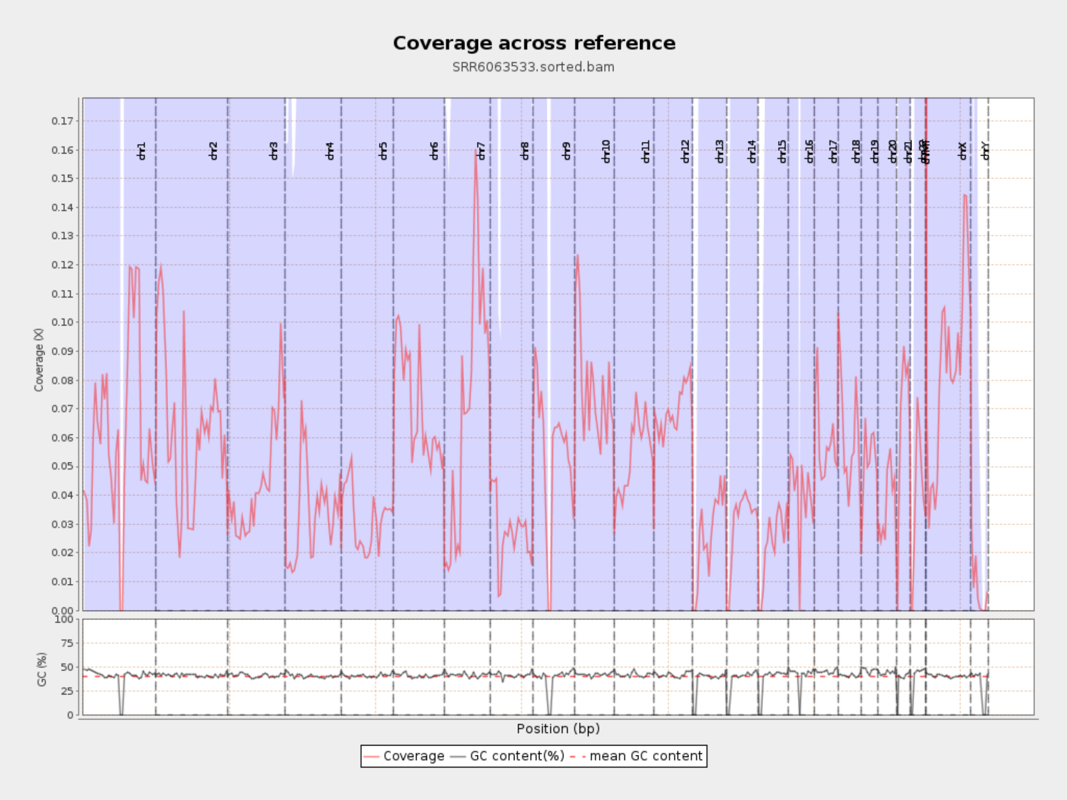
General error rate	0.84%
Mismatches	1,330,306
Insertions	11,738
Mapped reads with at least one insertion	0.46%
Deletions	45,924
Mapped reads with at least one deletion	1.78%
Homopolymer indels	45.38%

2.6. Chromosome stats

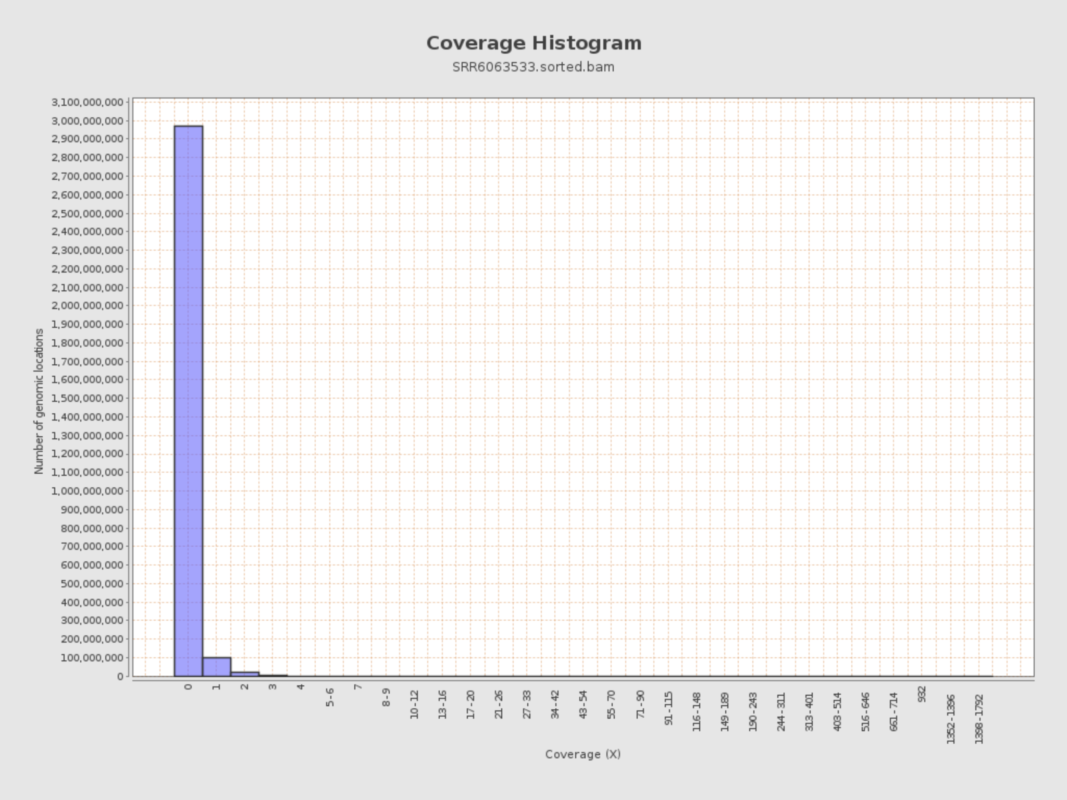
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15052999	0.0604	0.6521
chr2	243199373	15559842	0.064	0.8759
chr3	198022430	8827676	0.0446	0.2612
chr4	191154276	6479666	0.0339	0.2494
chr5	180915260	5757013	0.0318	0.2218
chr6	171115067	12200196	0.0713	0.4121
chr7	159138663	11381190	0.0715	0.6326

chr8	146364022	3919945	0.0268	0.4675
chr9	141213431	7769085	0.055	0.4538
chr10	135534747	10626747	0.0784	0.4444
chr11	135006516	7295119	0.054	0.3701
chr12	133851895	9341187	0.0698	0.338
chr13	115169878	3096459	0.0269	0.2065
chr14	107349540	3289363	0.0306	0.2524
chr15	102531392	2352383	0.0229	0.2118
chr16	90354753	3528673	0.0391	0.2595
chr17	81195210	4827551	0.0595	0.3227
chr18	78077248	4808013	0.0616	0.6381
chr19	59128983	3053448	0.0516	0.5234
chr20	63025520	2364870	0.0375	0.2524
chr21	48129895	3099014	0.0644	0.3298
chr22	51304566	1986468	0.0387	0.2394
chrMT	16571	32013	1.9319	2.126
chrX	155270560	12914678	0.0832	0.4169
chrY	59373566	443202	0.0075	0.1504

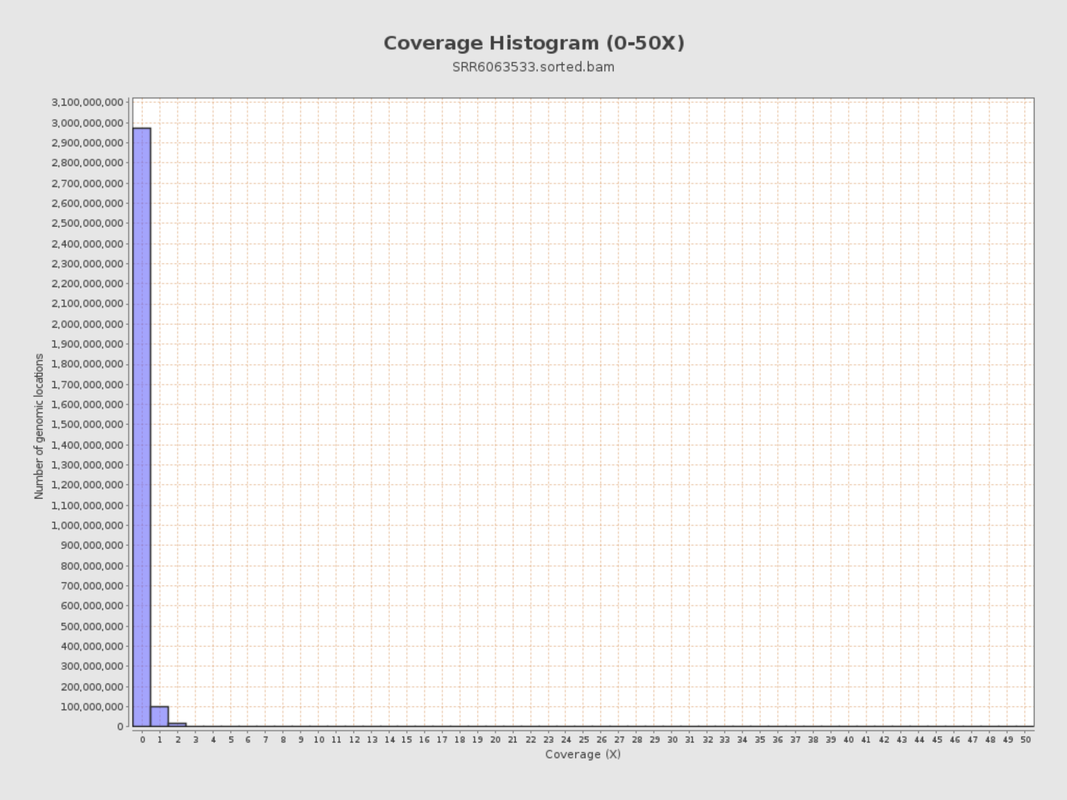
3. Results : Coverage across reference



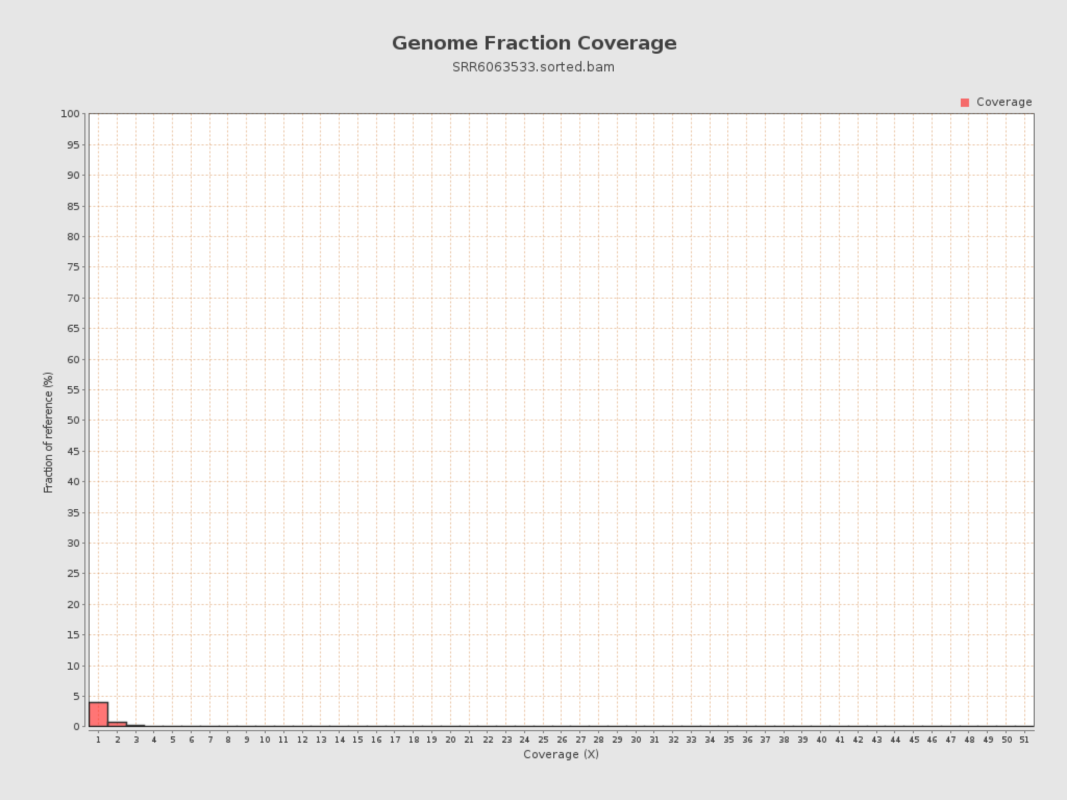
4. Results : Coverage Histogram



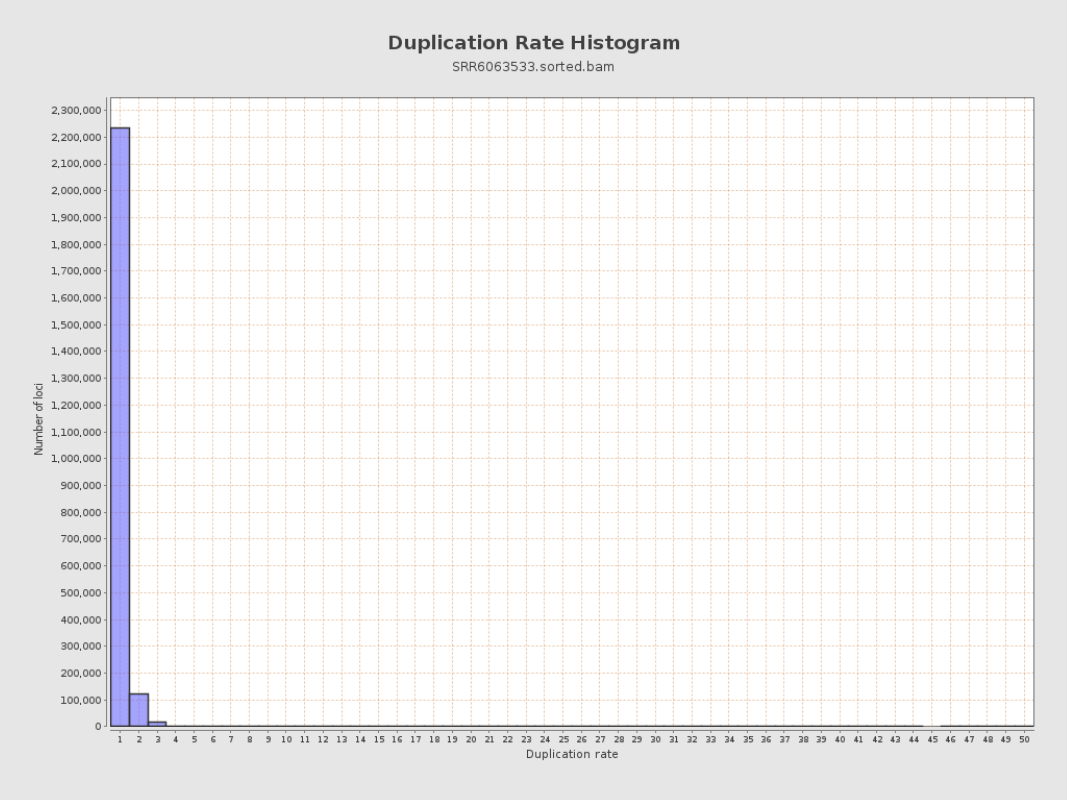
5. Results : Coverage Histogram (0-50X)



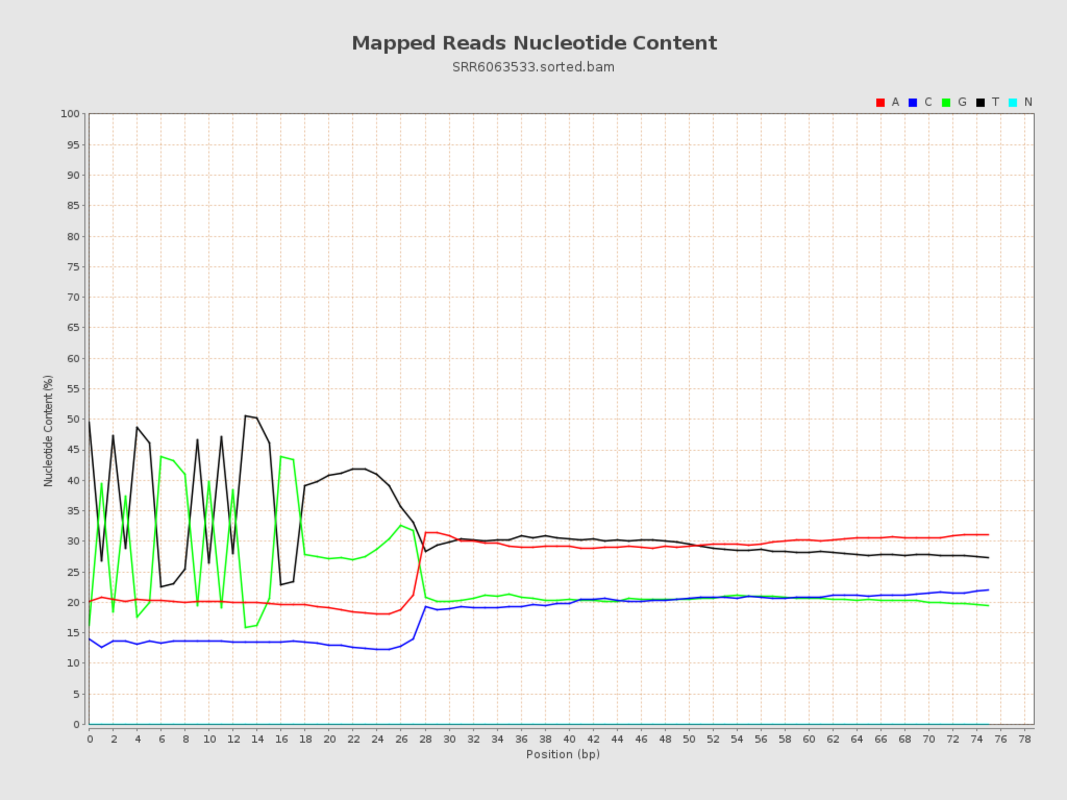
6. Results : Genome Fraction Coverage



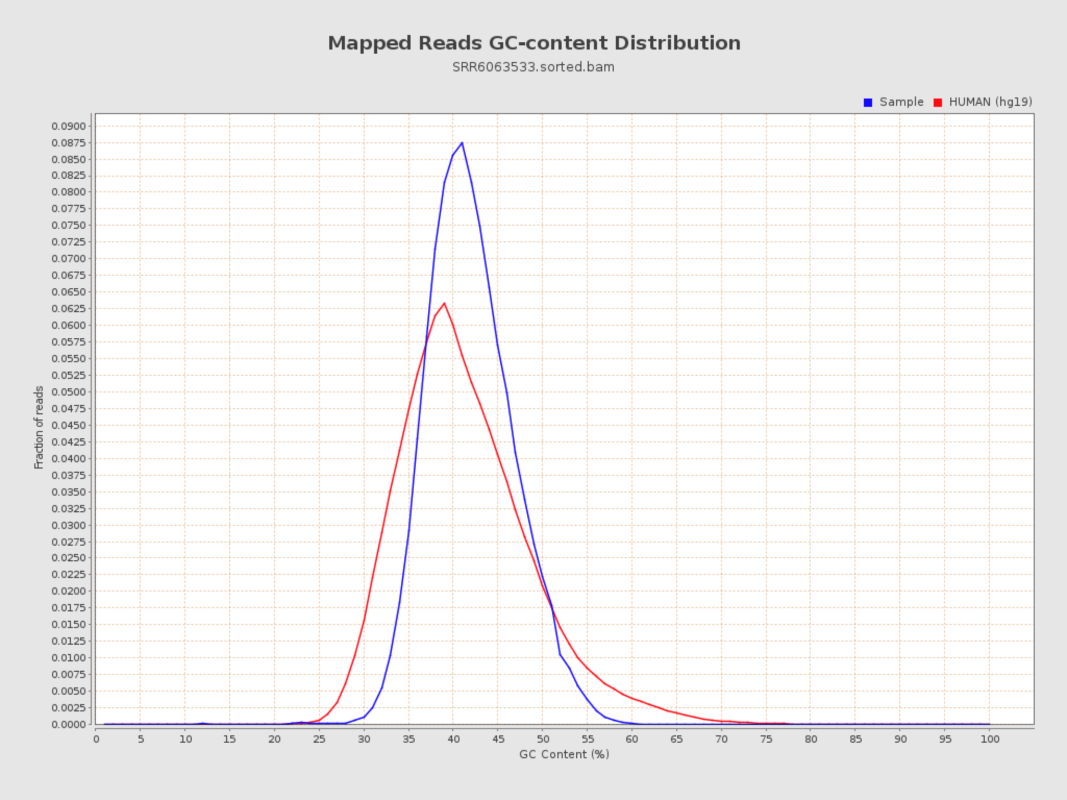
7. Results : Duplication Rate Histogram



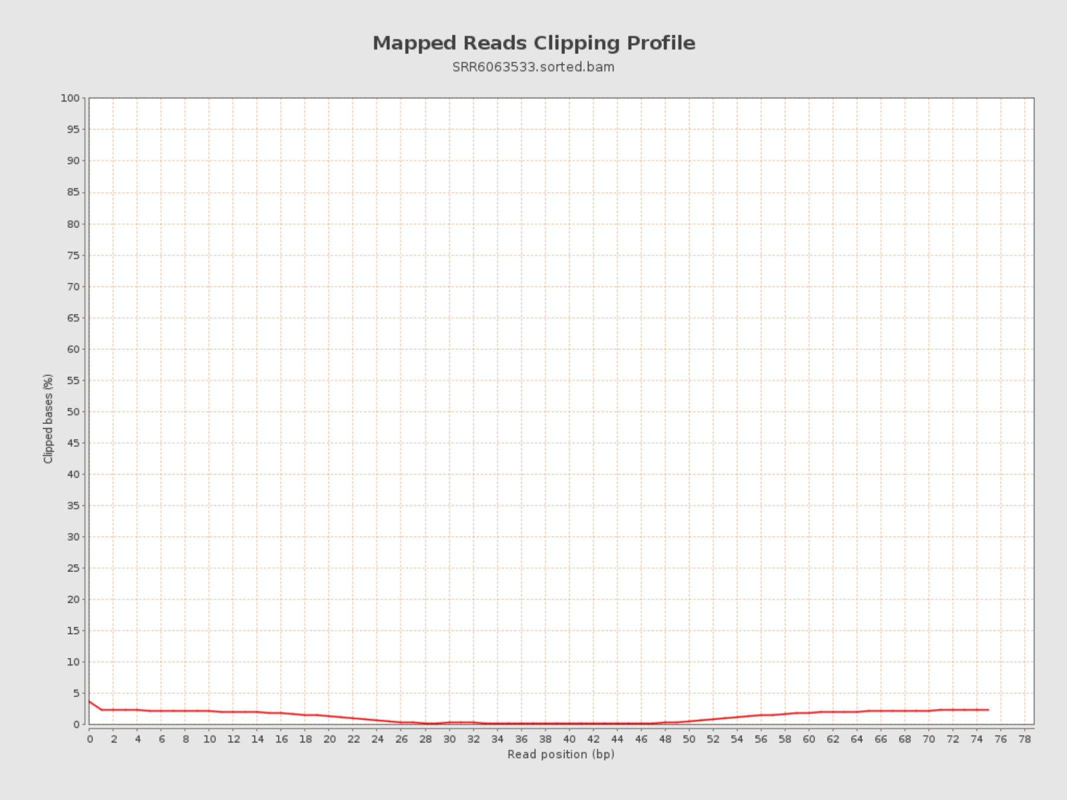
8. Results : Mapped Reads Nucleotide Content



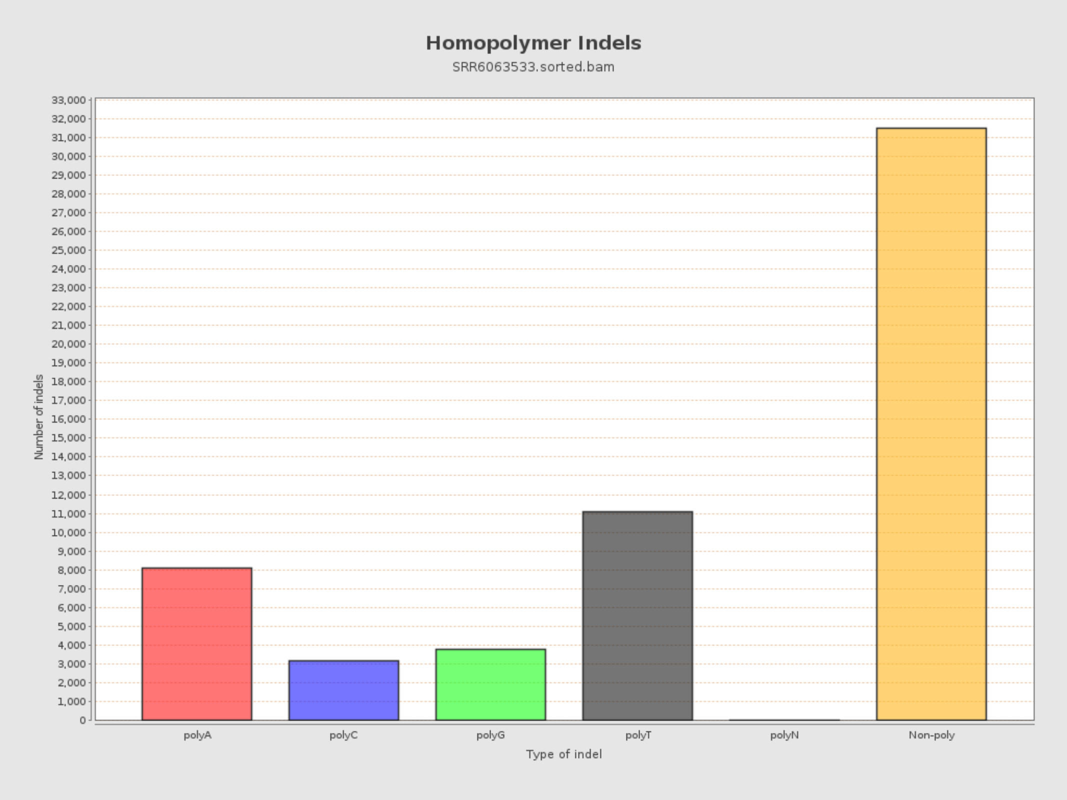
9. Results : Mapped Reads GC-content Distribution



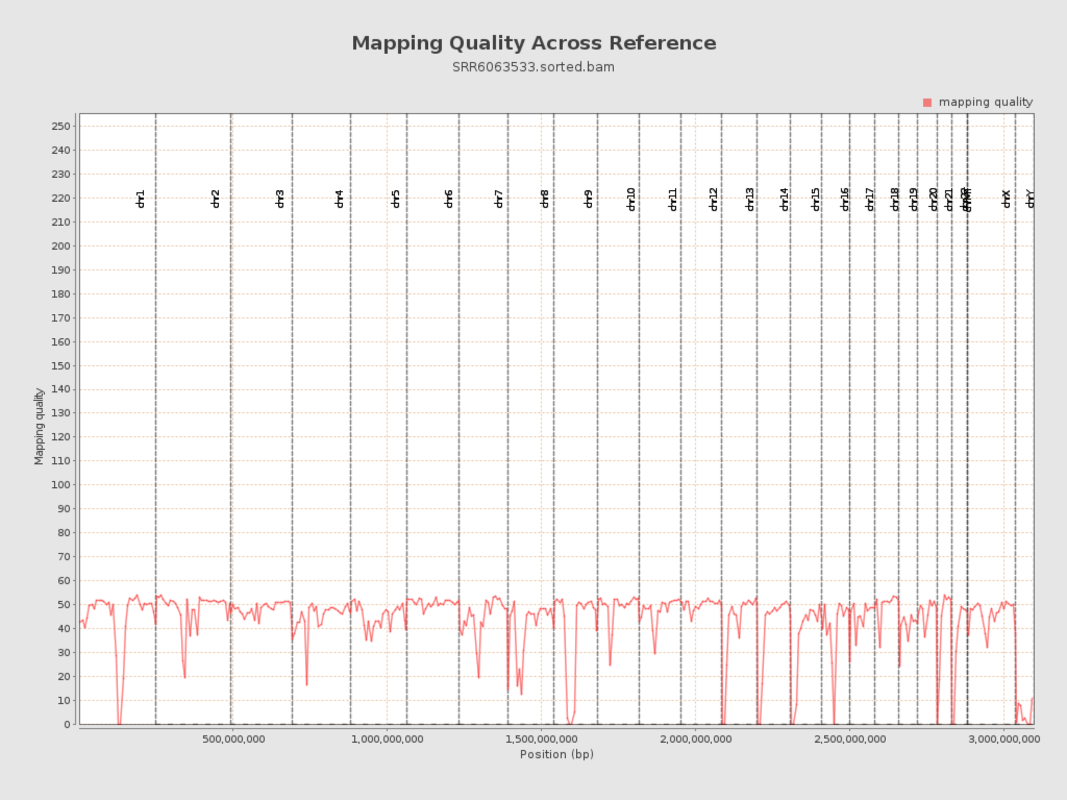
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram