Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 04:00:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063588.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_SRR6063588 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063588.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 04:00:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063588.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,263,413
Mapped reads	3,884,074 / 91.1%
Unmapped reads	379,339 / 8.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	44,363 / 1.04%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	519,198 / 12.18%
Duplication rate	9.89%
Clipped reads	1,805,050 / 42.34%

2.2. ACGT Content

Number/percentage of A's	72,376,282 / 27.96%
Number/percentage of C's	48,511,291 / 18.74%
Number/percentage of T's	81,036,041 / 31.31%
Number/percentage of G's	56,617,588 / 21.88%
Number/percentage of N's	270,345 / 0.1%
GC Percentage	40.62%

2.3. Coverage

Mean	0.0836

Standard Deviation	0.6579

2.4. Mapping Quality

Mean Mapping Quality	44.11

2.5. Mismatches and indels

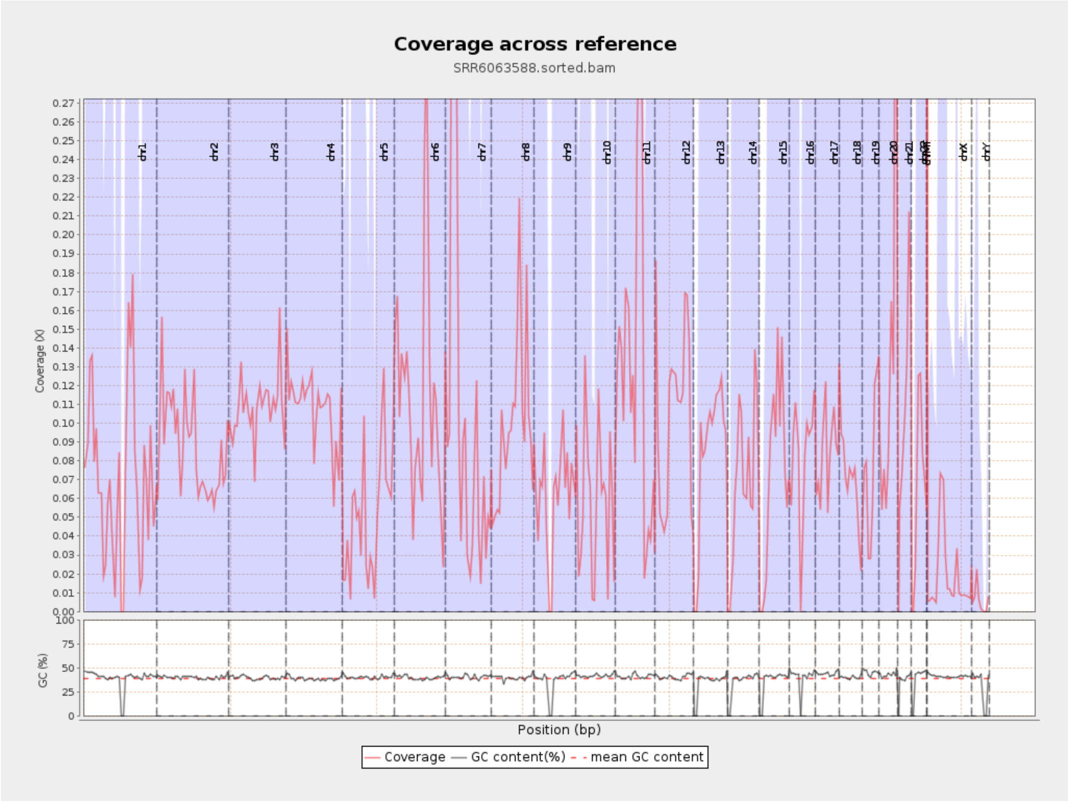
General error rate	0.81%
Mismatches	2,067,679
Insertions	17,919
Mapped reads with at least one insertion	0.46%
Deletions	63,462
Mapped reads with at least one deletion	1.62%
Homopolymer indels	46.46%

2.6. Chromosome stats

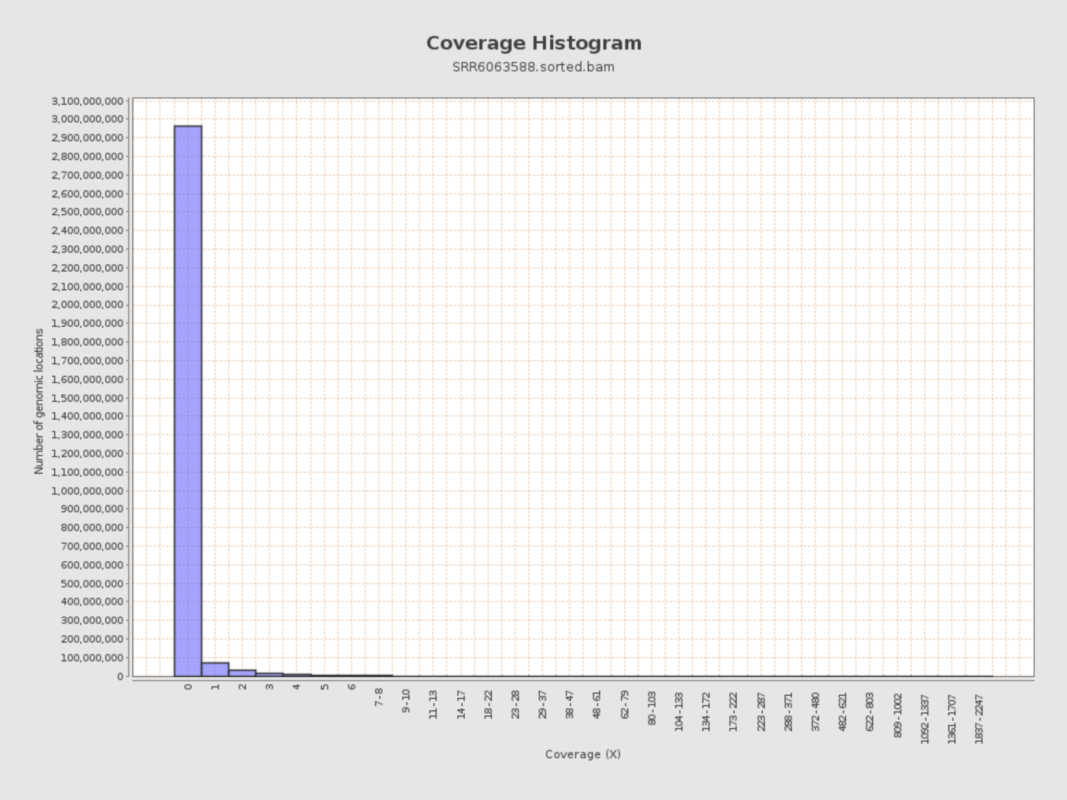
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17404581	0.0698	0.635
chr2	243199373	21272386	0.0875	0.7652
chr3	198022430	21488852	0.1085	0.5594
chr4	191154276	20712127	0.1084	0.5778
chr5	180915260	9596788	0.053	0.3866
chr6	171115067	19367467	0.1132	0.6144
chr7	159138663	16760797	0.1053	0.7719

chr8	146364022	14655127	0.1001	1.4078
chr9	141213431	8628840	0.0611	0.518
chr10	135534747	7928468	0.0585	0.4992
chr11	135006516	17412058	0.129	0.8674
chr12	133851895	14278176	0.1067	0.5629
chr13	115169878	9846995	0.0855	0.5008
chr14	107349540	7630939	0.0711	0.4859
chr15	102531392	7222026	0.0704	0.4504
chr16	90354753	7219564	0.0799	0.4945
chr17	81195210	6730858	0.0829	0.5508
chr18	78077248	5530160	0.0708	0.9334
chr19	59128983	4438927	0.0751	0.581
chr20	63025520	8889736	0.141	0.6787
chr21	48129895	5227707	0.1086	0.5758
chr22	51304566	3420116	0.0667	0.4248
chrMT	16571	33769	2.0378	2.615
chrX	155270560	2847443	0.0183	0.2658
chrY	59373566	378790	0.0064	0.1507

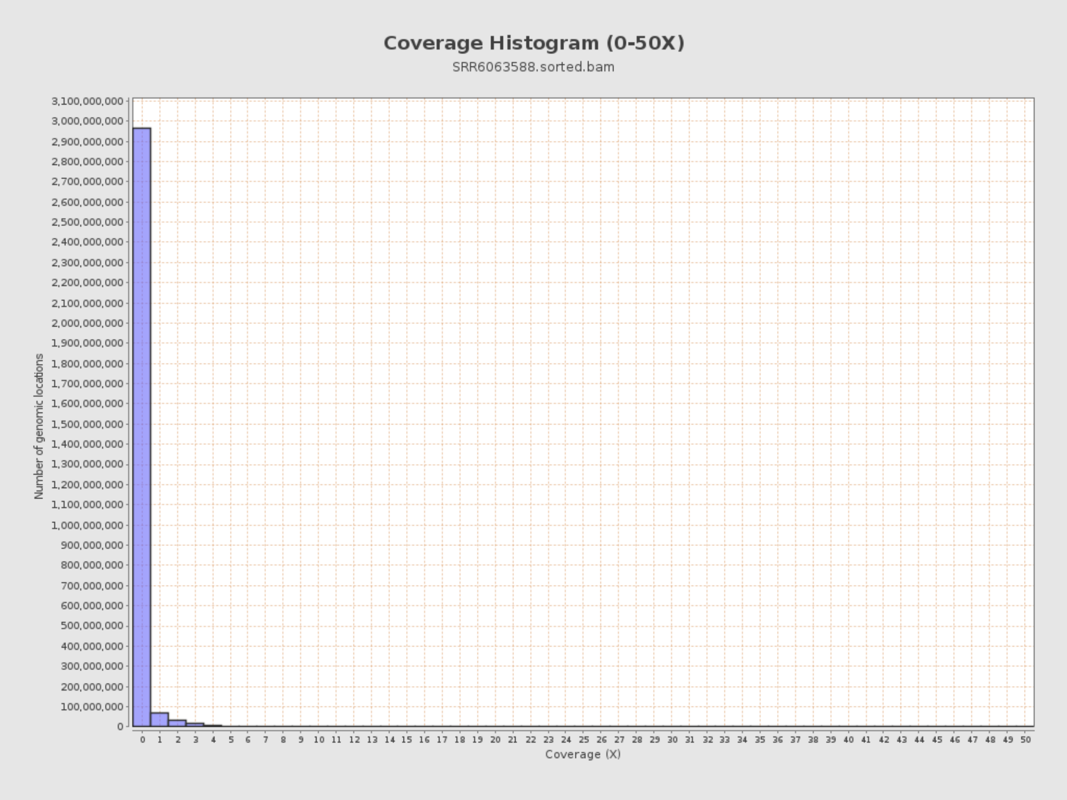
3. Results : Coverage across reference



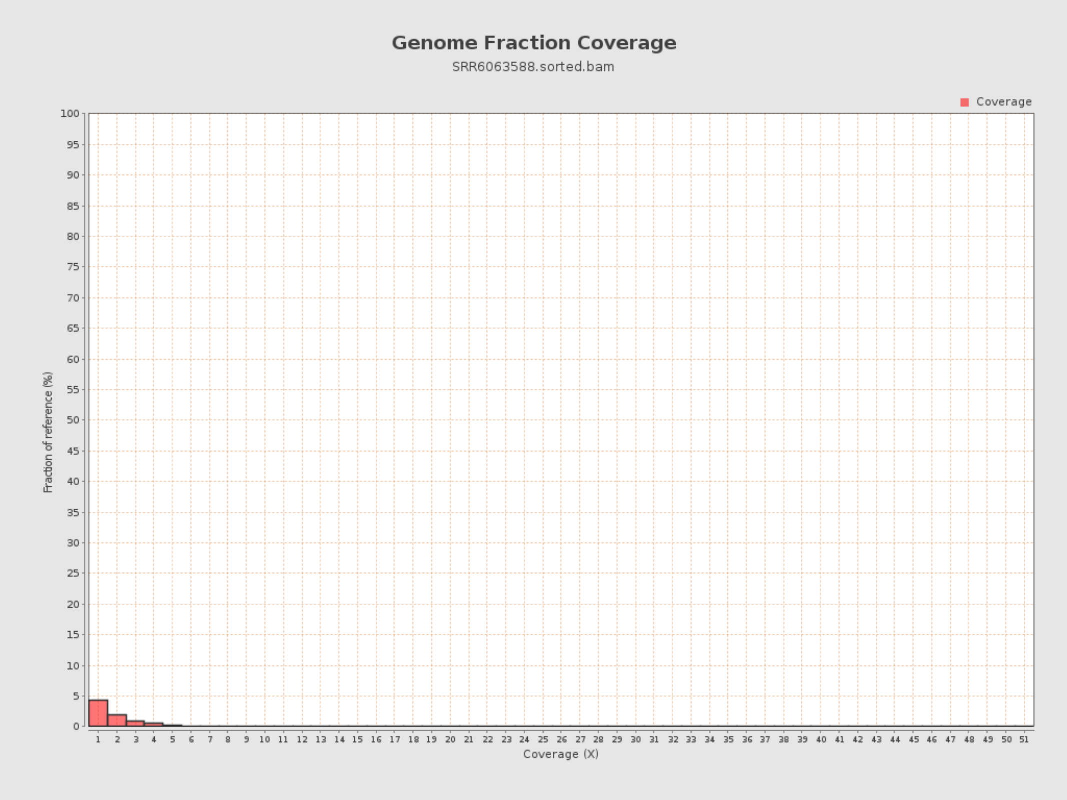
4. Results : Coverage Histogram



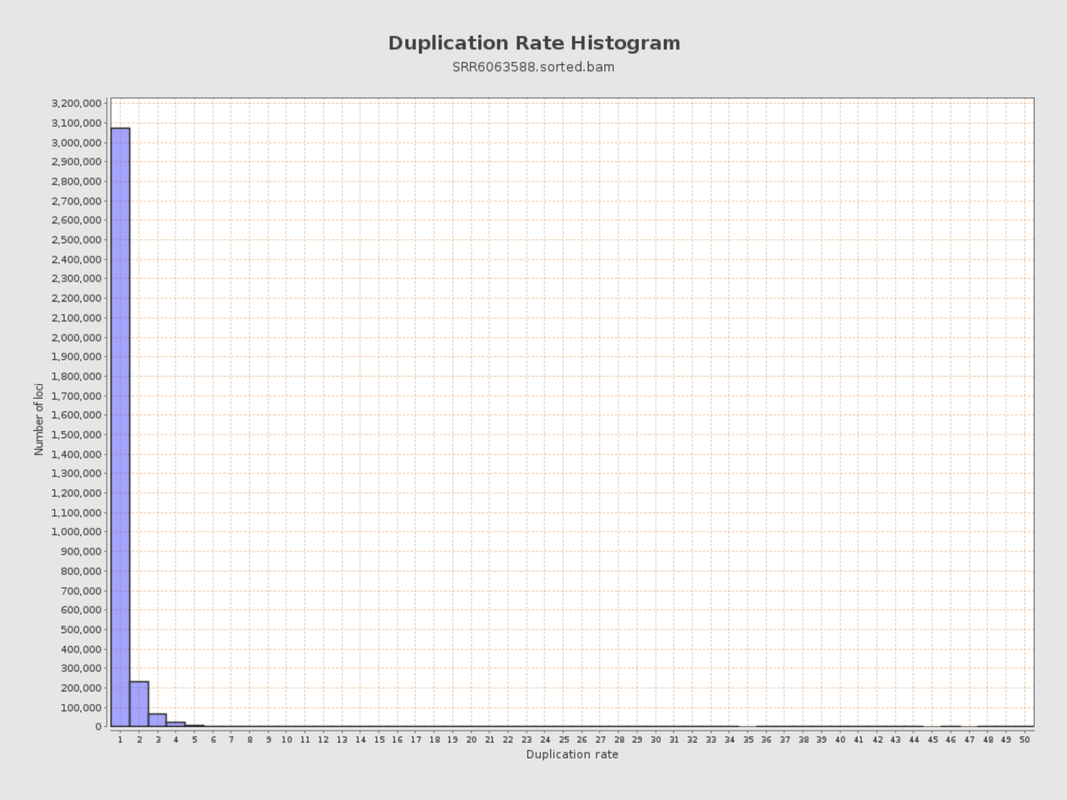
5. Results : Coverage Histogram (0-50X)



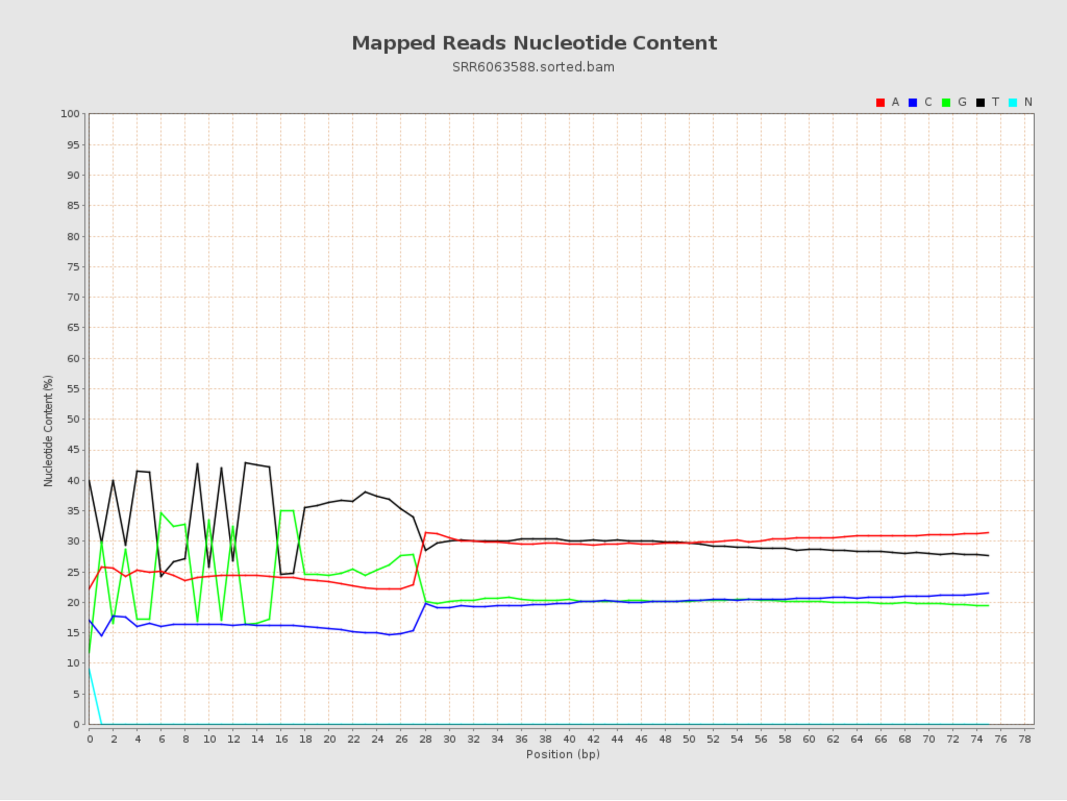
6. Results : Genome Fraction Coverage



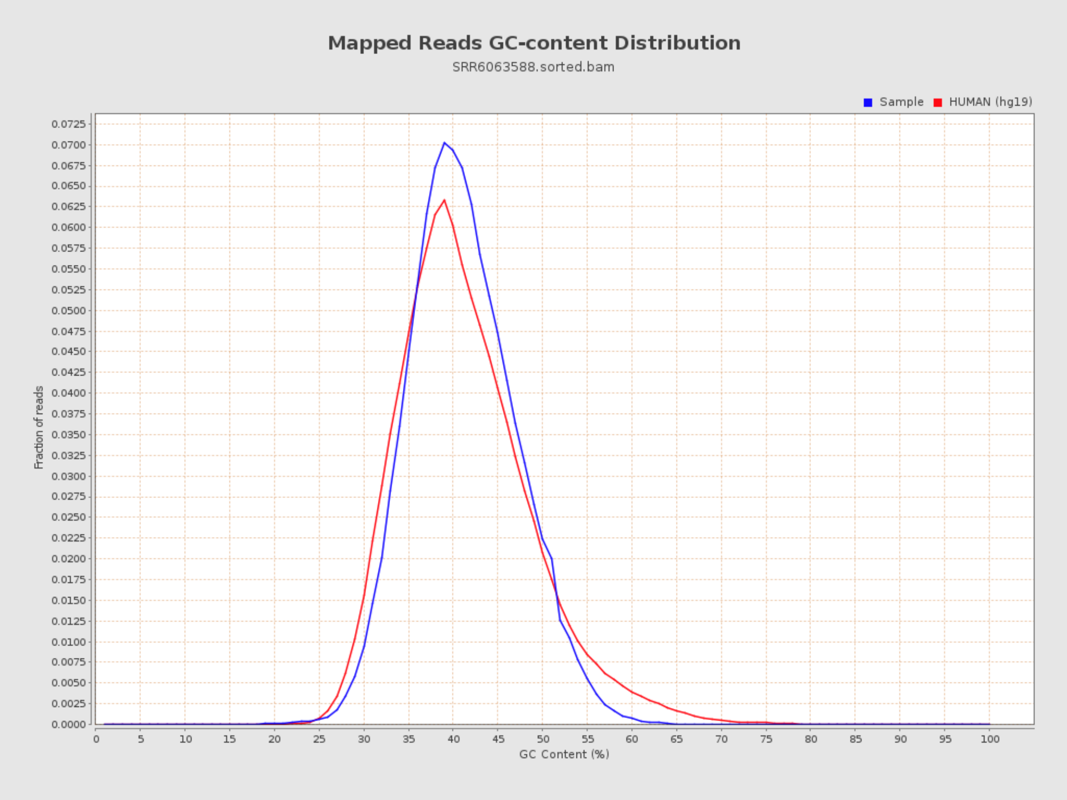
7. Results : Duplication Rate Histogram



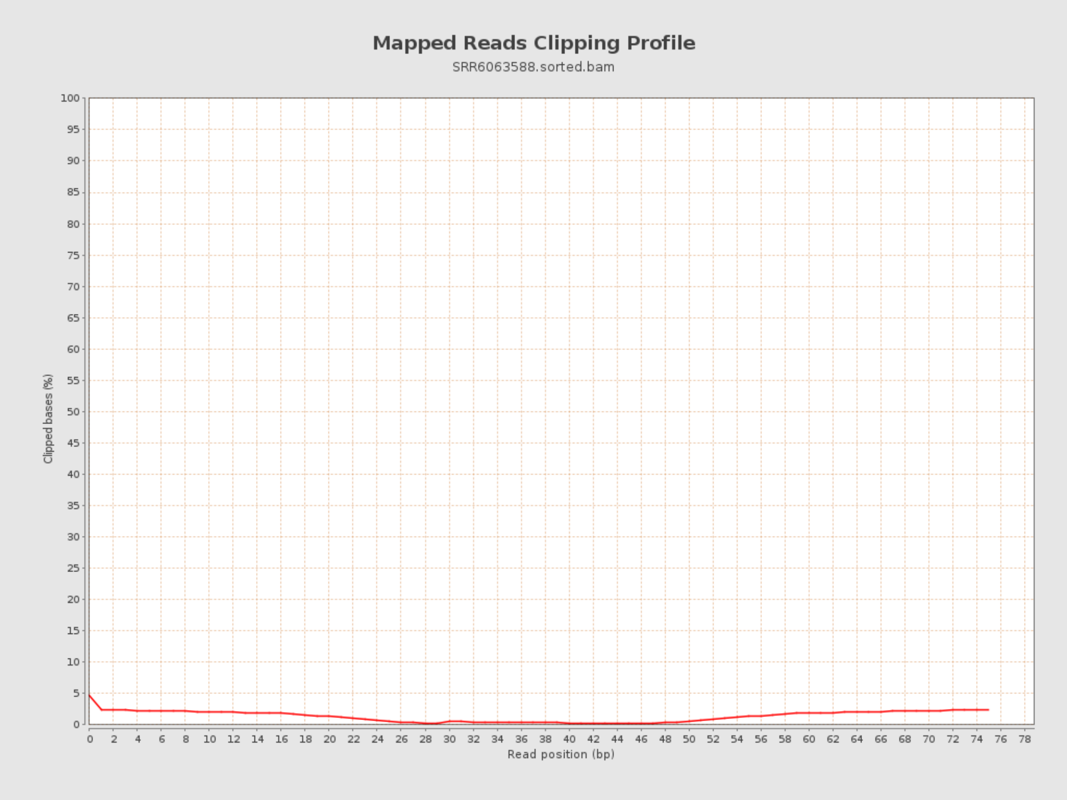
8. Results : Mapped Reads Nucleotide Content



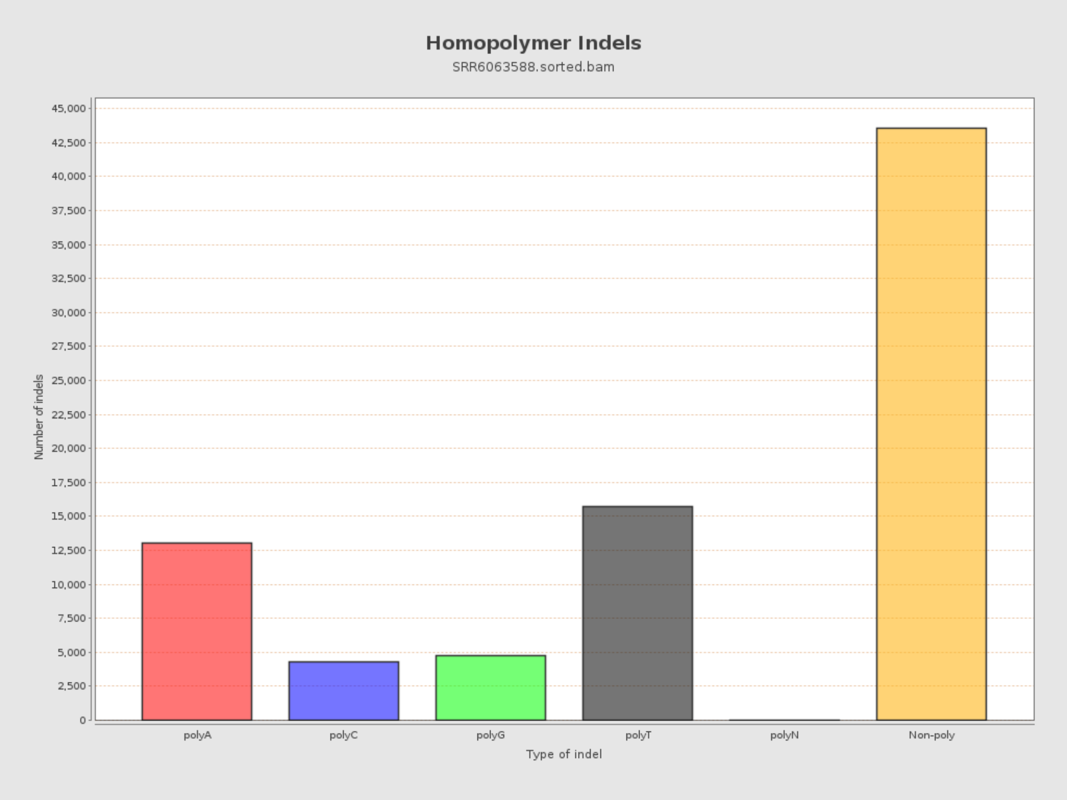
9. Results : Mapped Reads GC-content Distribution



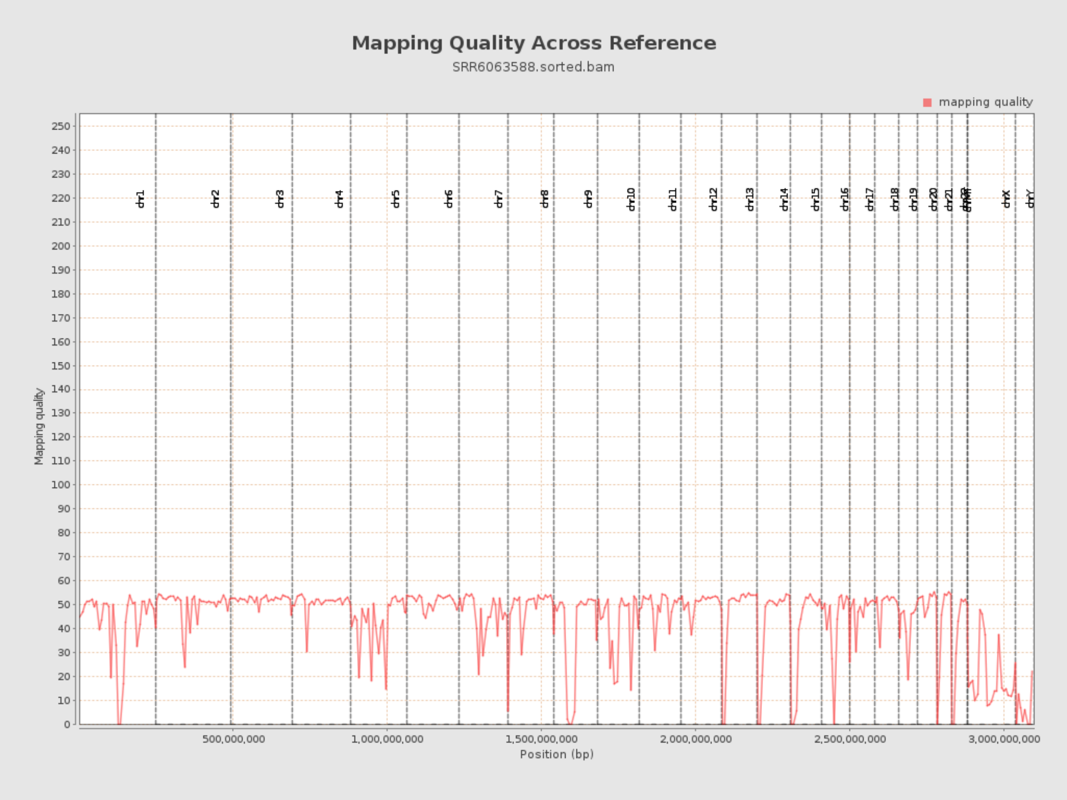
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram