Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 11:49:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068128.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_SRR6068128 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068128.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 11:49:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068128.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,159,833
Mapped reads	4,855,110 / 94.09%
Unmapped reads	304,723 / 5.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,990 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	1,750,352 / 33.92%
Duplication rate	21.41%
Clipped reads	2,943,365 / 57.04%

2.2. ACGT Content

Number/percentage of A's	80,201,970 / 26.27%
Number/percentage of C's	53,712,507 / 17.6%
Number/percentage of T's	100,517,416 / 32.93%
Number/percentage of G's	70,788,743 / 23.19%
Number/percentage of N's	33,318 / 0.01%
GC Percentage	40.79%

2.3. Coverage

Mean	0.0987

Standard Deviation	0.9911

2.4. Mapping Quality

Mean Mapping Quality	46.1

2.5. Mismatches and indels

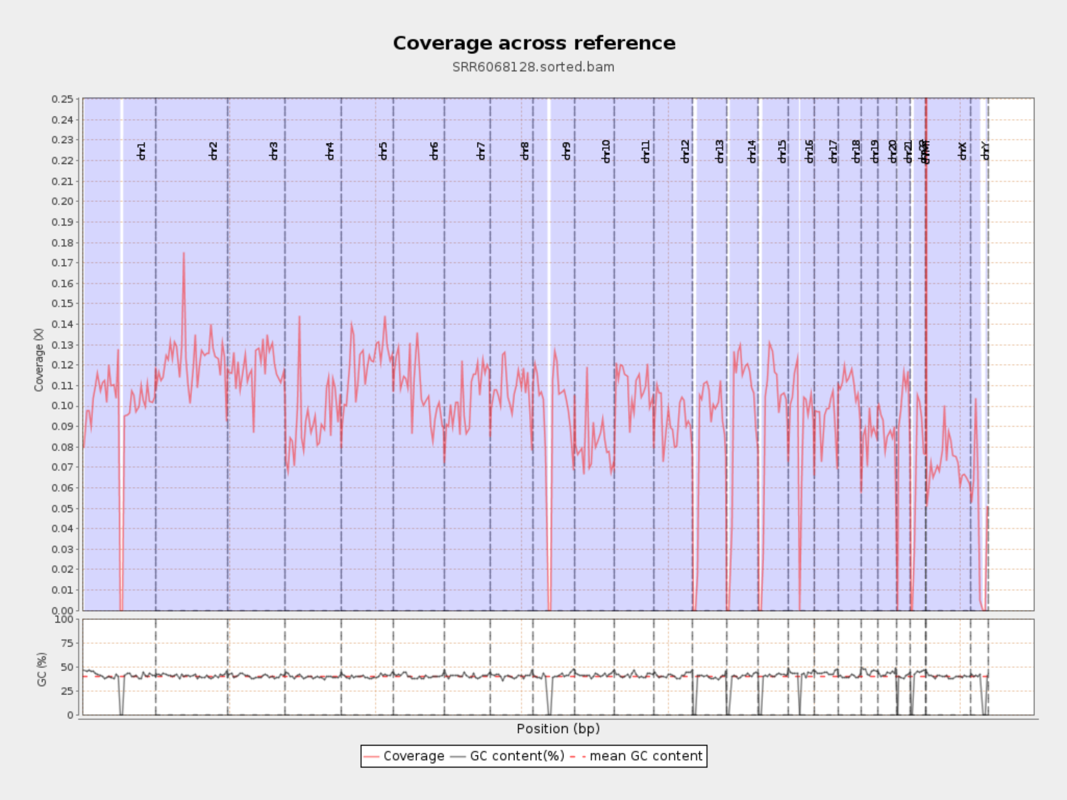
General error rate	0.64%
Mismatches	1,925,218
Insertions	20,831
Mapped reads with at least one insertion	0.43%
Deletions	83,308
Mapped reads with at least one deletion	1.7%
Homopolymer indels	47.86%

2.6. Chromosome stats

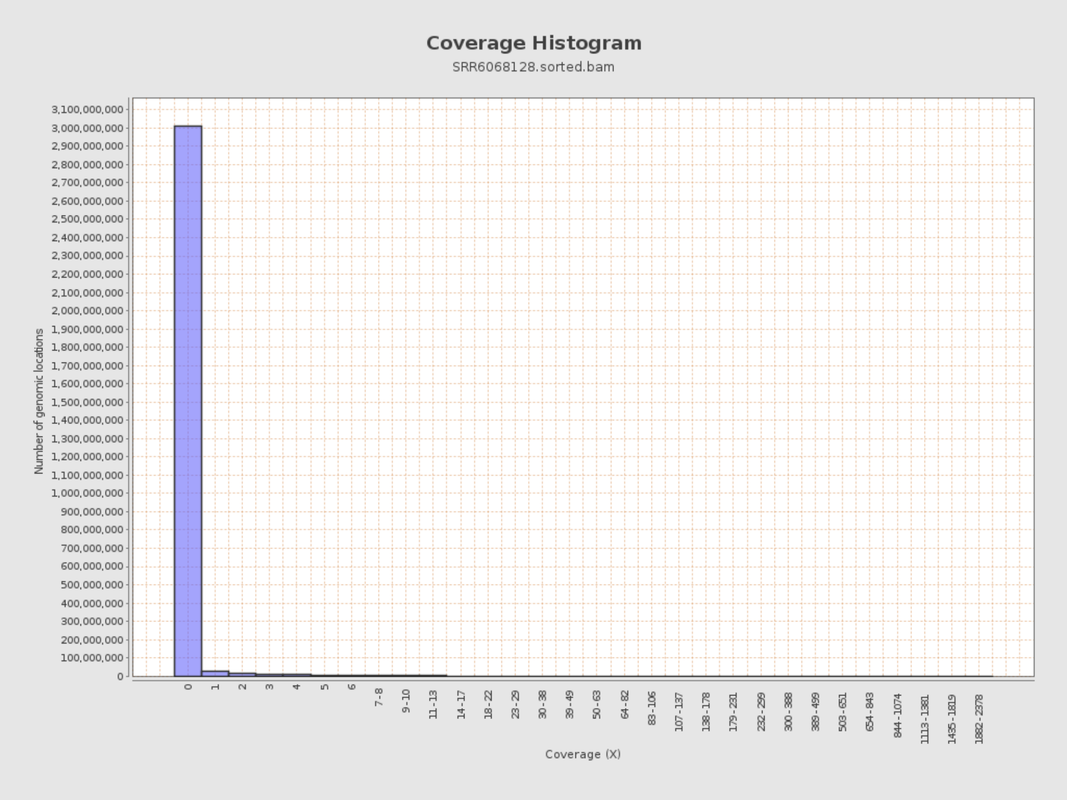
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24403660	0.0979	1.2156
chr2	243199373	29997988	0.1233	1.2815
chr3	198022430	23457088	0.1185	0.8842
chr4	191154276	17770386	0.093	0.8266
chr5	180915260	21845661	0.1208	0.8936
chr6	171115067	18364458	0.1073	0.9046
chr7	159138663	16556555	0.104	1.0311

chr8	146364022	15680235	0.1071	1.614
chr9	141213431	13147828	0.0931	0.8935
chr10	135534747	10974115	0.081	0.8679
chr11	135006516	14668167	0.1086	0.9827
chr12	133851895	12526720	0.0936	0.7894
chr13	115169878	9762446	0.0848	0.7603
chr14	107349540	10264264	0.0956	0.8138
chr15	102531392	9136697	0.0891	0.7798
chr16	90354753	8184857	0.0906	0.7789
chr17	81195210	7673542	0.0945	0.8177
chr18	78077248	8609481	0.1103	1.4046
chr19	59128983	5048840	0.0854	0.9748
chr20	63025520	5525115	0.0877	0.7746
chr21	48129895	4476249	0.093	0.8182
chr22	51304566	3304828	0.0644	0.6584
chrMT	16571	440492	26.5821	19.0997
chrX	155270560	11054407	0.0712	0.7045
chrY	59373566	2529924	0.0426	0.534

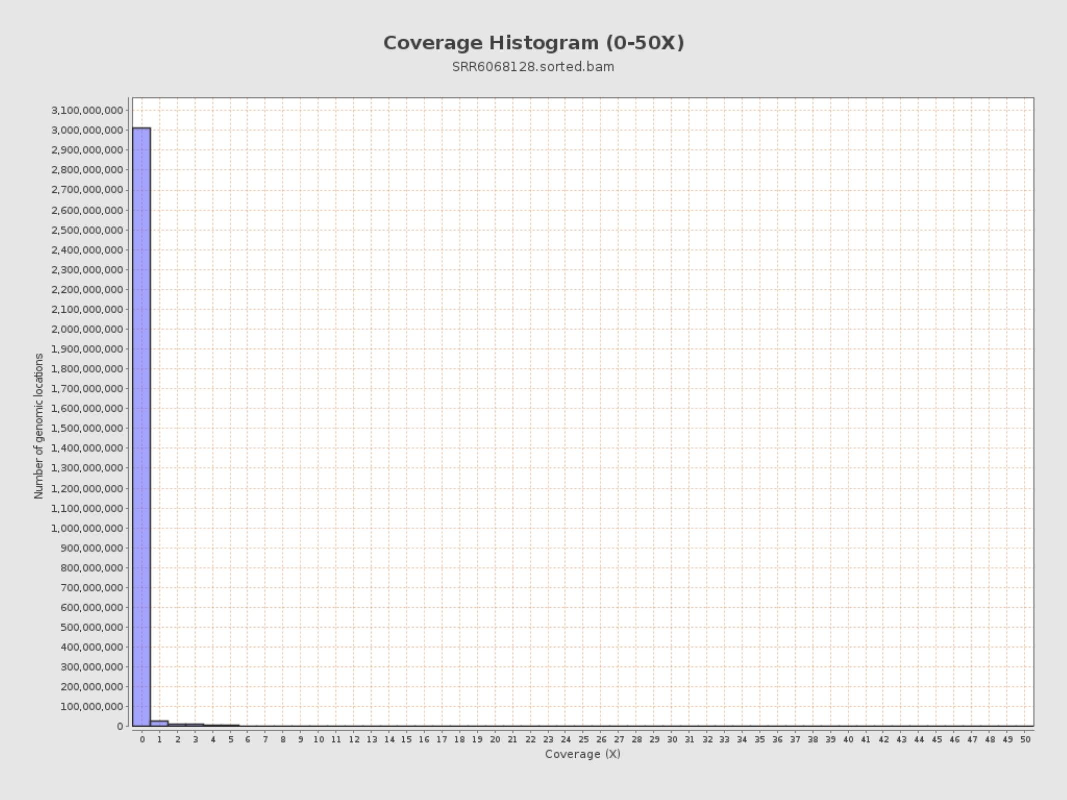
3. Results : Coverage across reference



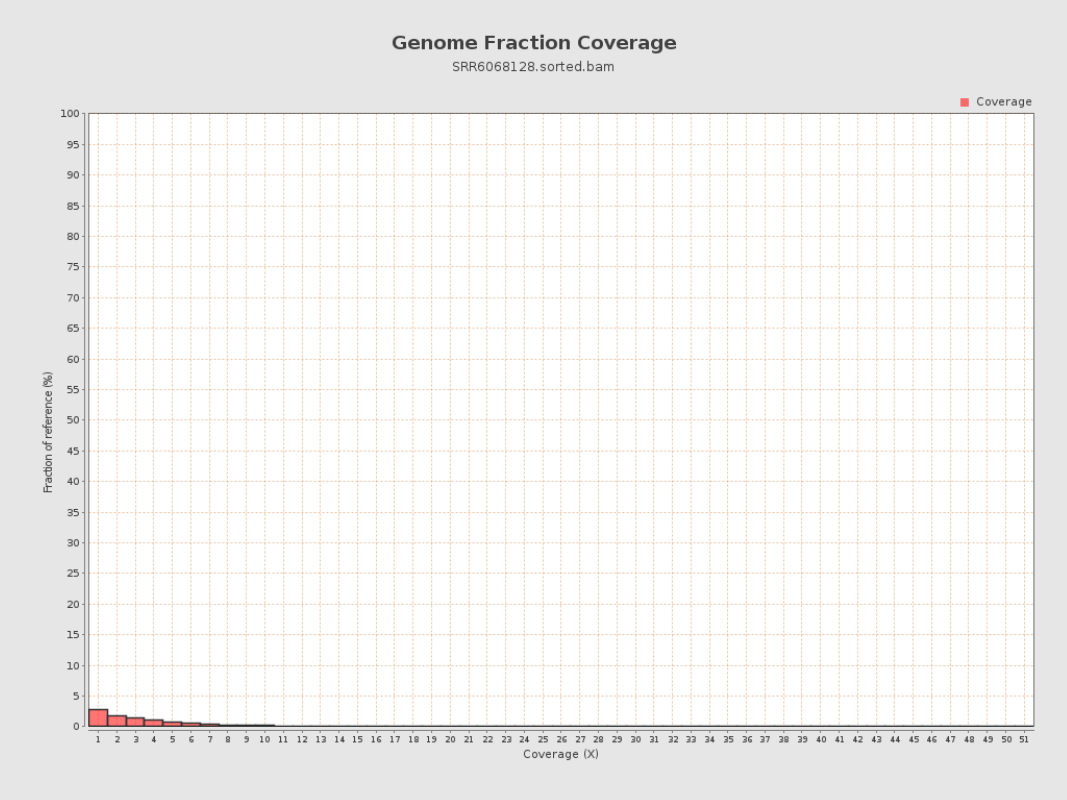
4. Results : Coverage Histogram



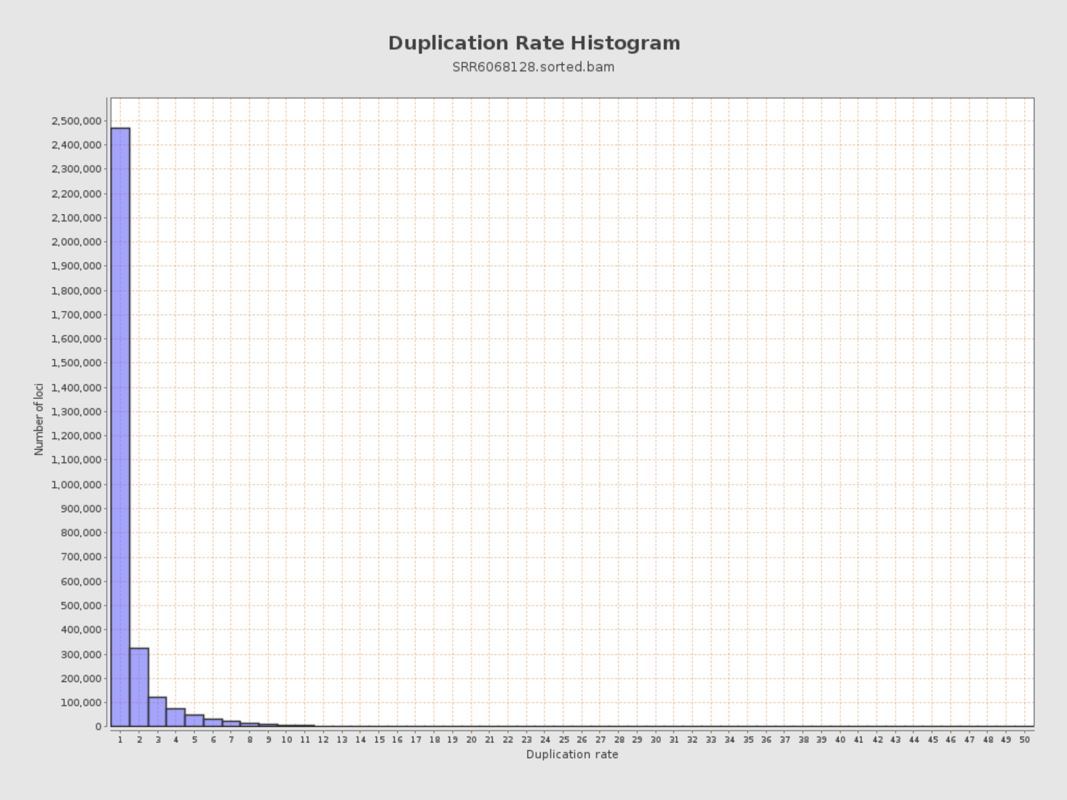
5. Results : Coverage Histogram (0-50X)



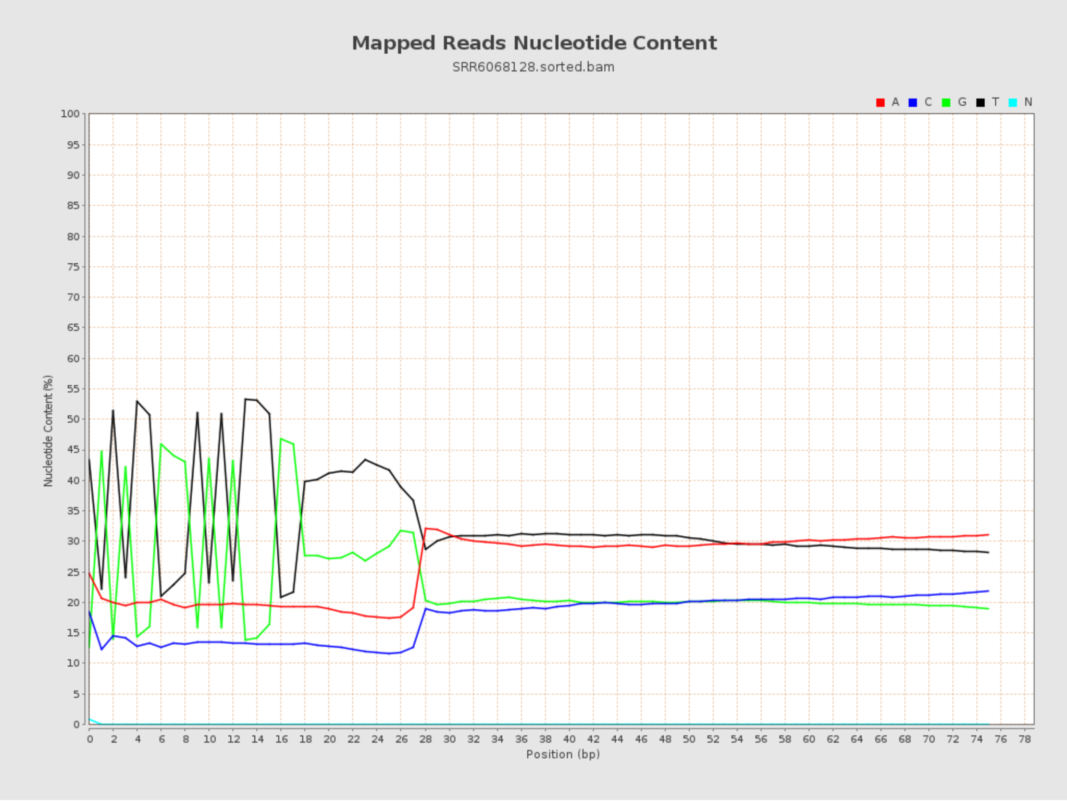
6. Results : Genome Fraction Coverage



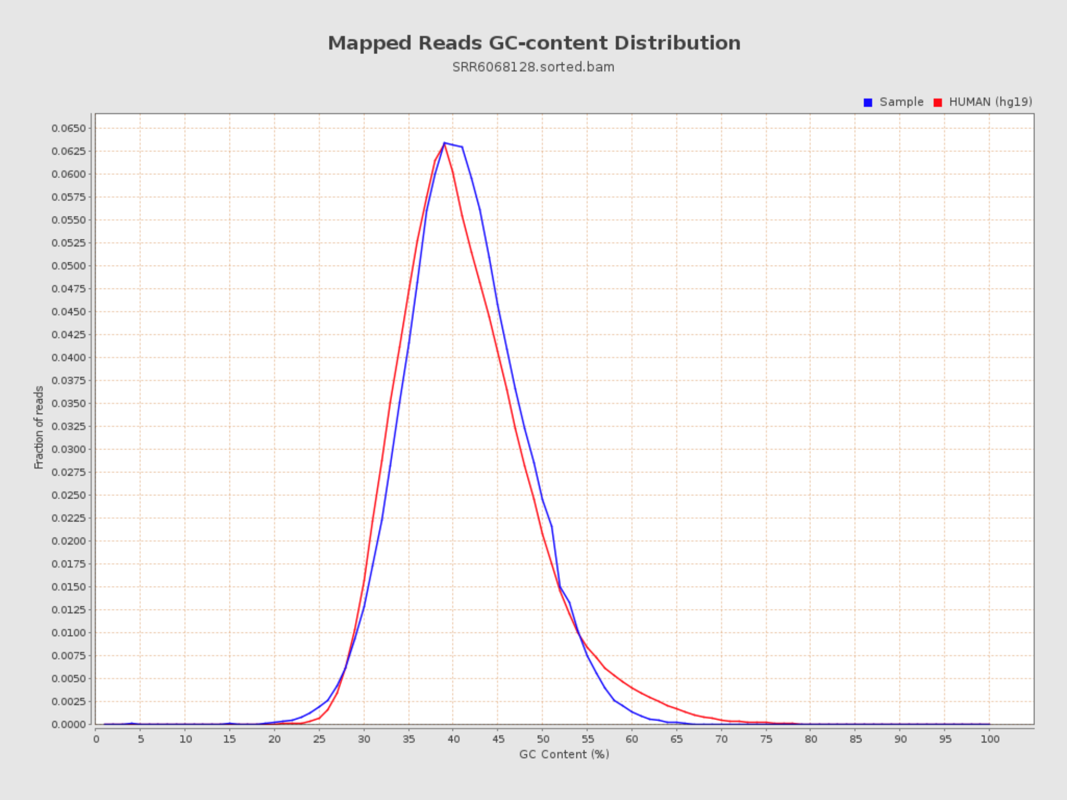
7. Results : Duplication Rate Histogram



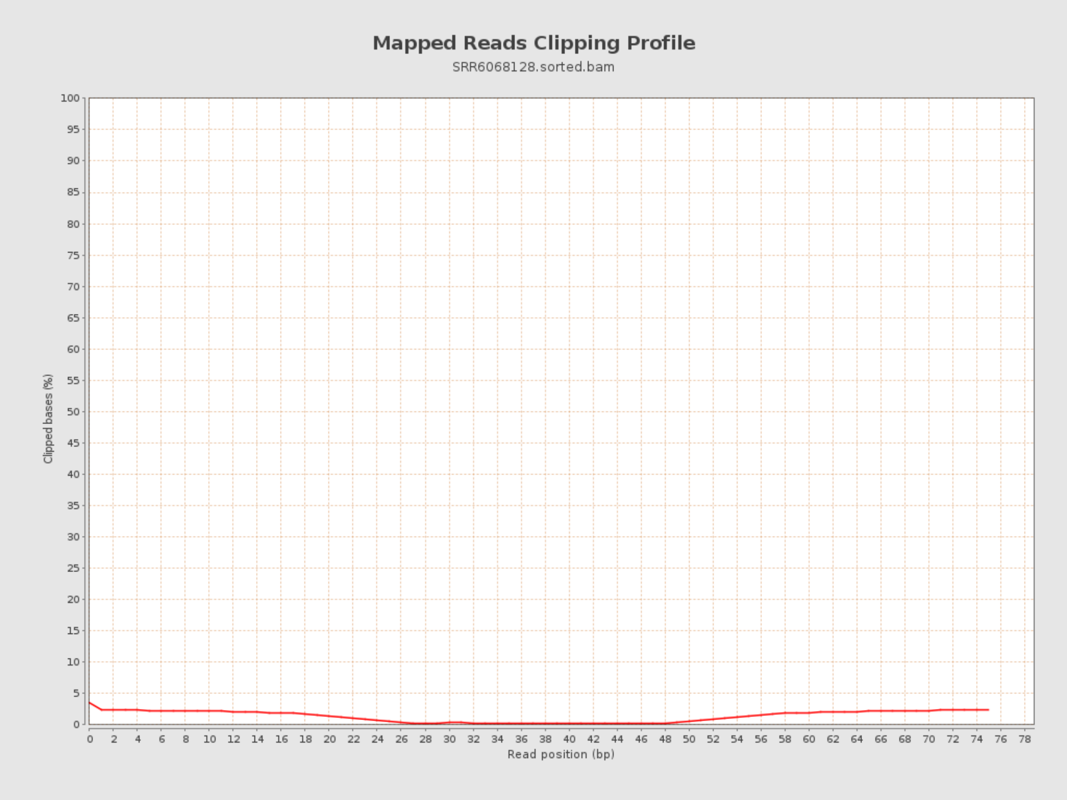
8. Results : Mapped Reads Nucleotide Content



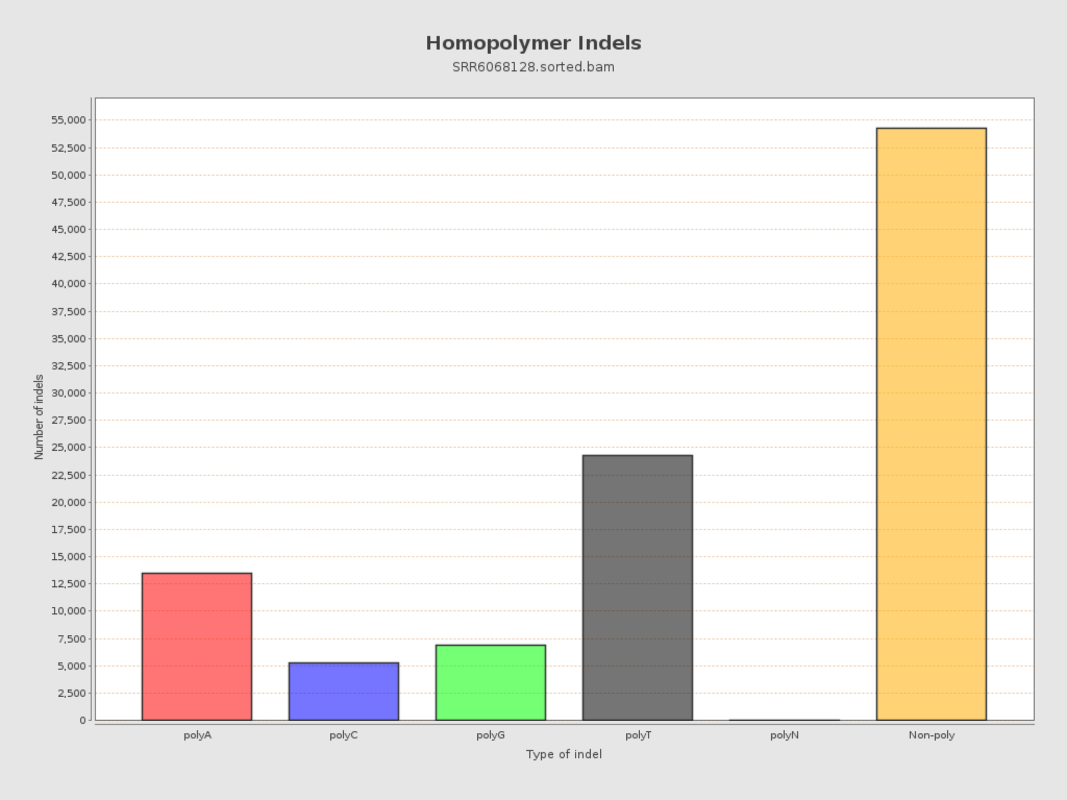
9. Results : Mapped Reads GC-content Distribution



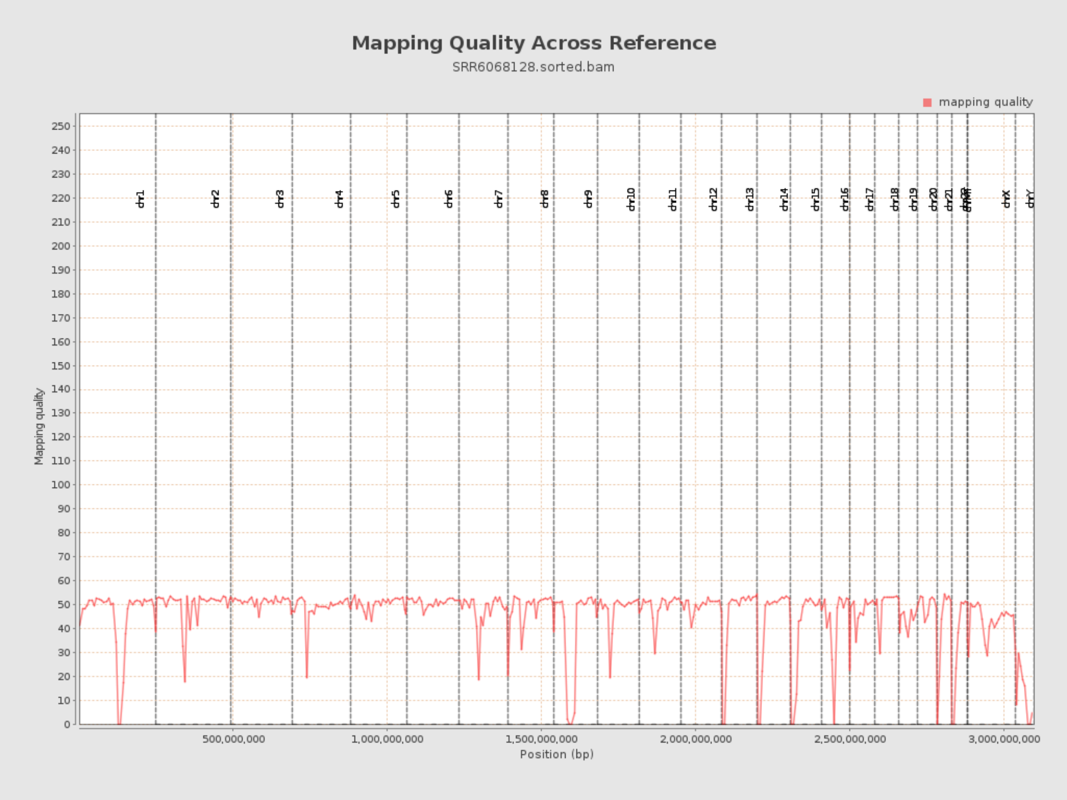
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram