Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 08:00:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068069.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_SRR6068069 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068069.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 08:00:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068069.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,681,421
Mapped reads	4,357,668 / 93.08%
Unmapped reads	323,753 / 6.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,969 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	915,712 / 19.56%
Duplication rate	15.66%
Clipped reads	2,279,273 / 48.69%

2.2. ACGT Content

Number/percentage of A's	72,515,710 / 25.75%
Number/percentage of C's	51,159,233 / 18.17%
Number/percentage of T's	91,251,956 / 32.4%
Number/percentage of G's	66,647,085 / 23.67%
Number/percentage of N's	31,998 / 0.01%
GC Percentage	41.83%

2.3. Coverage

Mean	0.091

Standard Deviation	1.0044

2.4. Mapping Quality

Mean Mapping Quality	45.78

2.5. Mismatches and indels

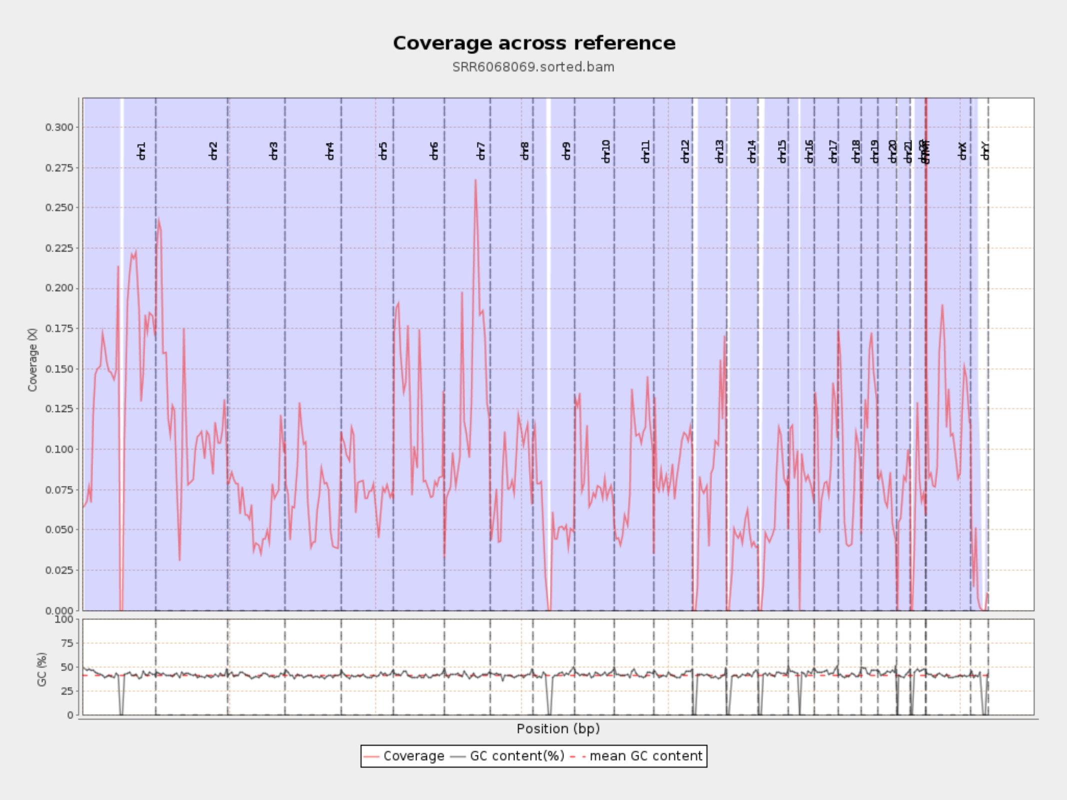
General error rate	0.55%
Mismatches	1,508,412
Insertions	18,947
Mapped reads with at least one insertion	0.43%
Deletions	61,571
Mapped reads with at least one deletion	1.4%
Homopolymer indels	44.47%

2.6. Chromosome stats

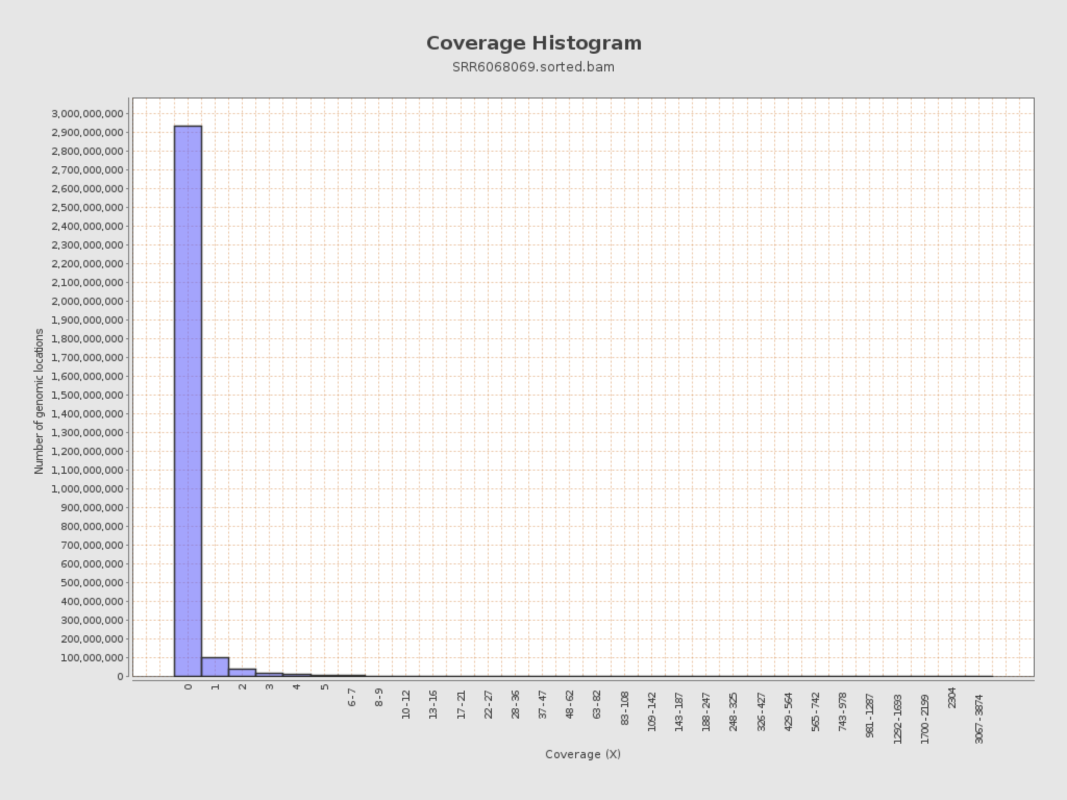
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	36426380	0.1461	1.9587
chr2	243199373	28954229	0.1191	1.8358
chr3	198022430	13030391	0.0658	0.408
chr4	191154276	13376879	0.07	0.4805
chr5	180915260	14368839	0.0794	0.4461
chr6	171115067	19923165	0.1164	0.7225
chr7	159138663	21194457	0.1332	1.4489

chr8	146364022	12163486	0.0831	1.2048
chr9	141213431	7288111	0.0516	0.5655
chr10	135534747	11515996	0.085	0.605
chr11	135006516	12003081	0.0889	0.5712
chr12	133851895	12319227	0.092	0.4936
chr13	115169878	9471671	0.0822	0.5176
chr14	107349540	4275209	0.0398	0.3456
chr15	102531392	5813699	0.0567	0.4102
chr16	90354753	7272337	0.0805	0.4708
chr17	81195210	7881015	0.0971	0.5178
chr18	78077248	6754532	0.0865	1.197
chr19	59128983	7649309	0.1294	1.2773
chr20	63025520	4338842	0.0688	0.4447
chr21	48129895	3338260	0.0694	0.4552
chr22	51304566	3123496	0.0609	0.3857
chrMT	16571	138895	8.3818	6.8567
chrX	155270560	18158167	0.1169	0.6429
chrY	59373566	933946	0.0157	0.5292

3. Results : Coverage across reference



4. Results : Coverage Histogram



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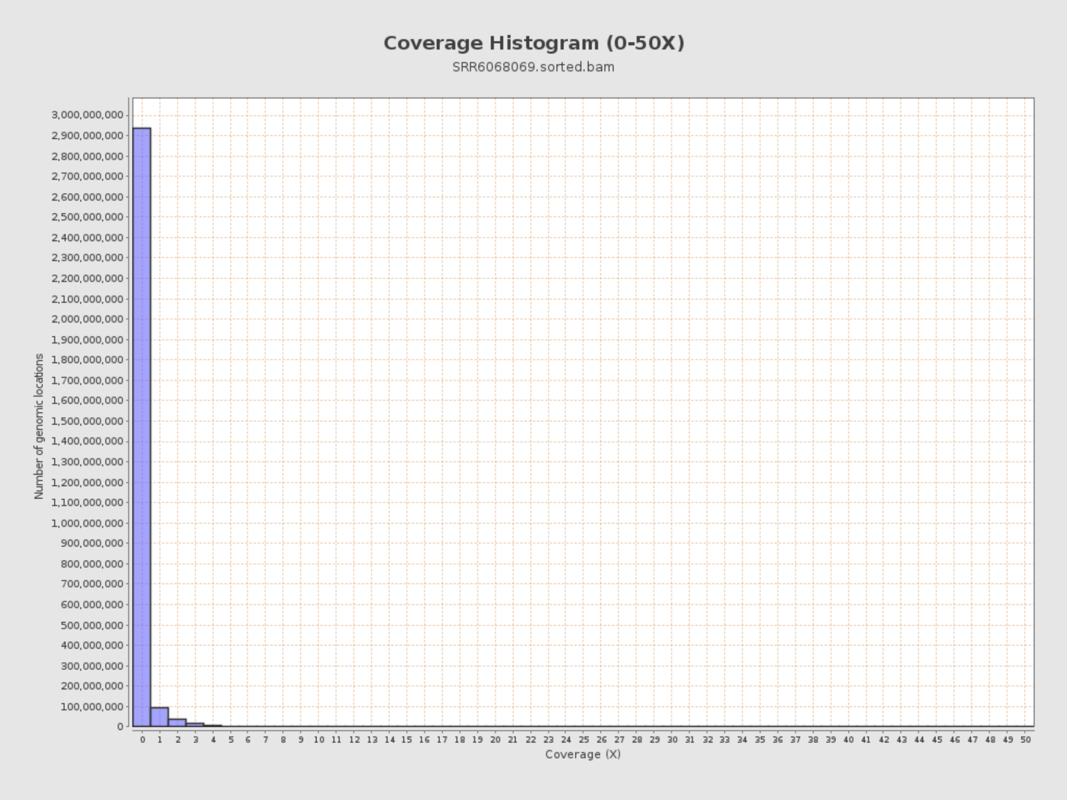
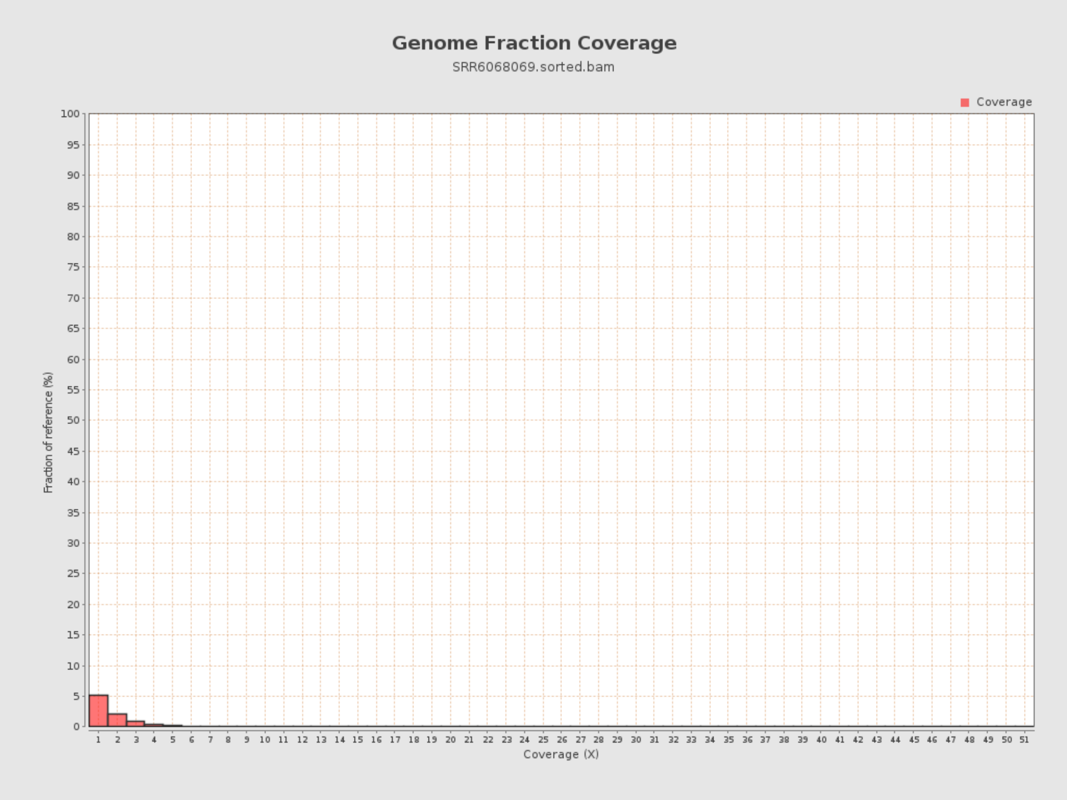
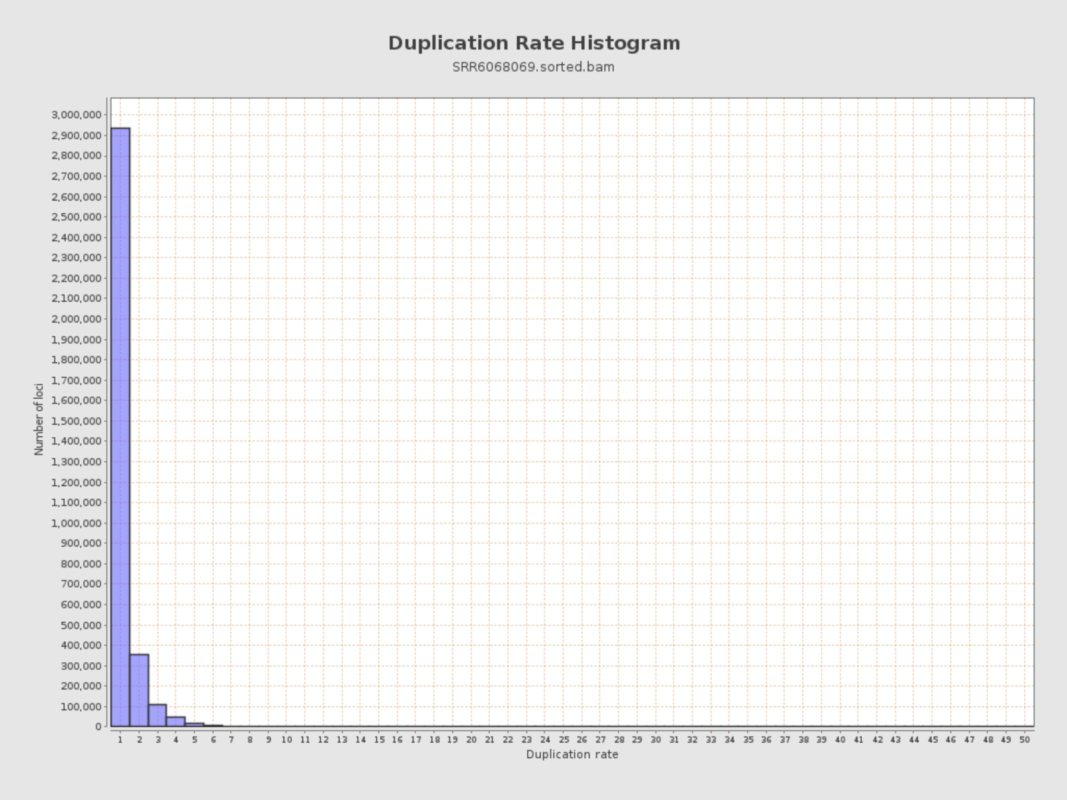
5. Results : Coverage Histogram (0-50X)



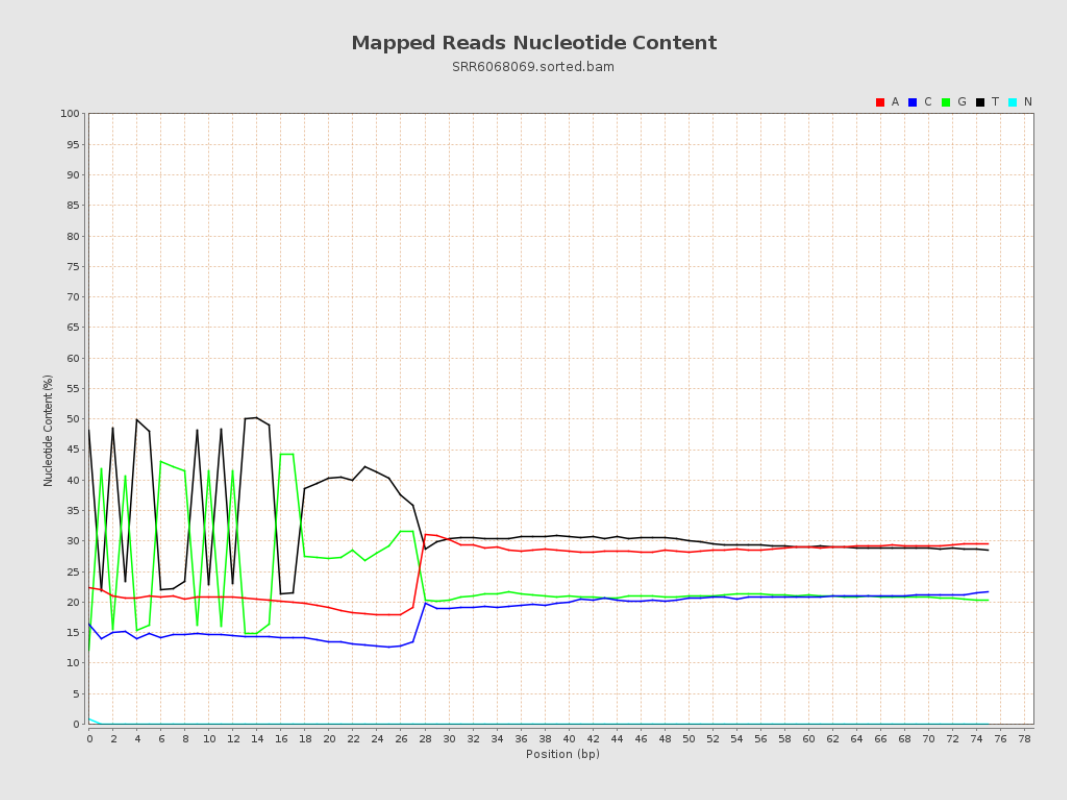
6. Results : Genome Fraction Coverage



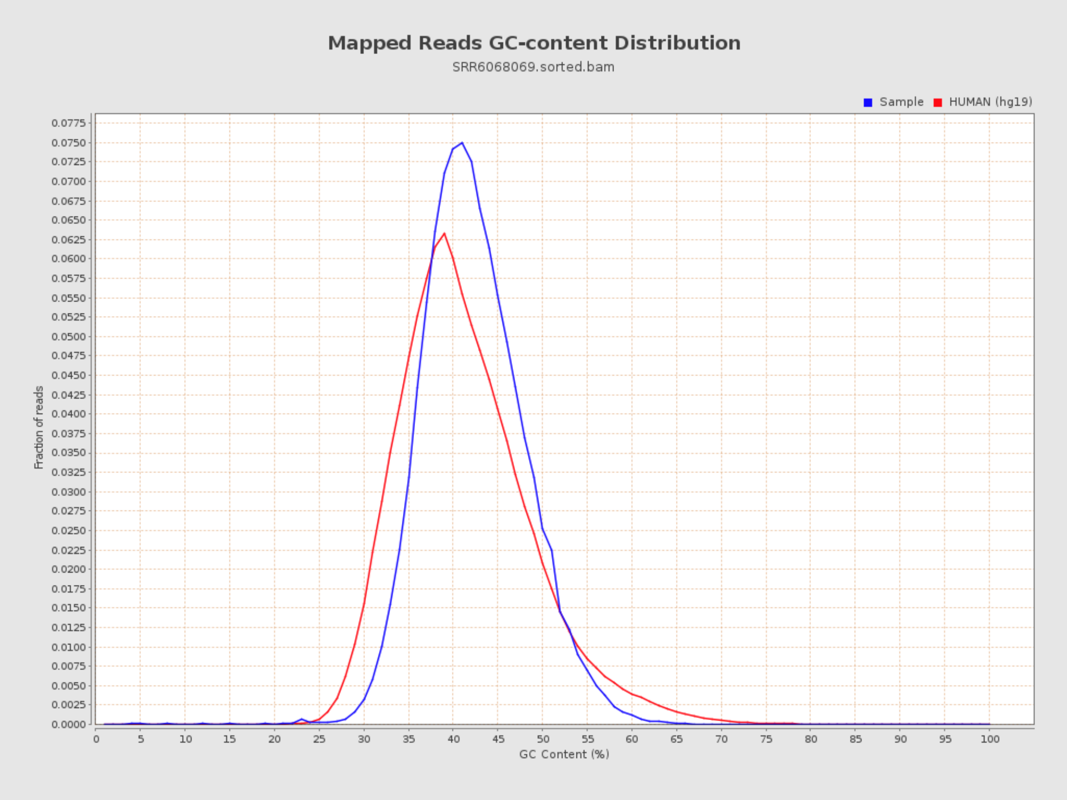
7. Results : Duplication Rate Histogram



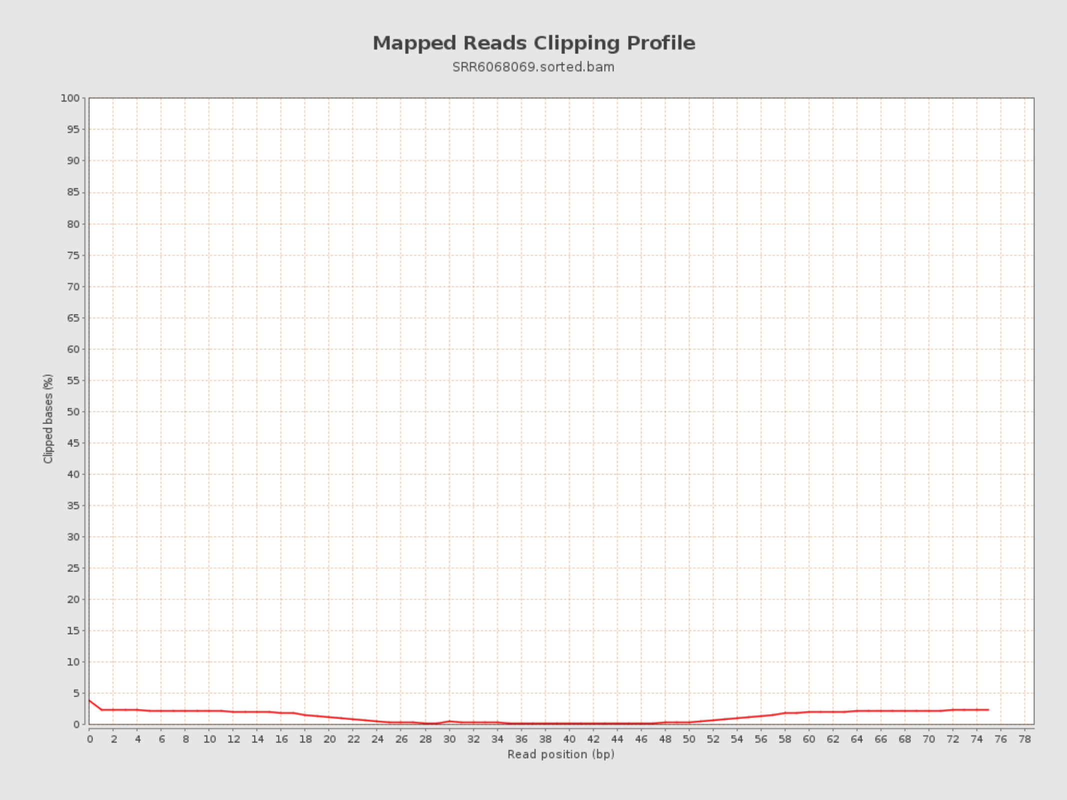
8. Results : Mapped Reads Nucleotide Content



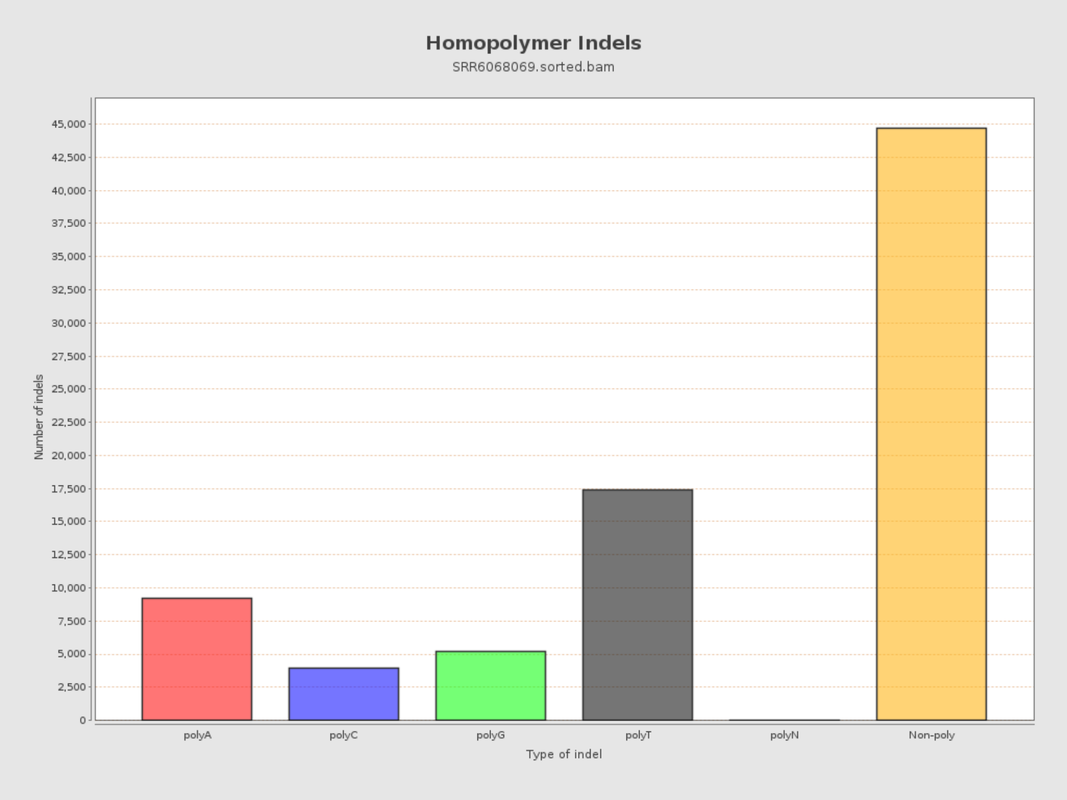
9. Results : Mapped Reads GC-content Distribution



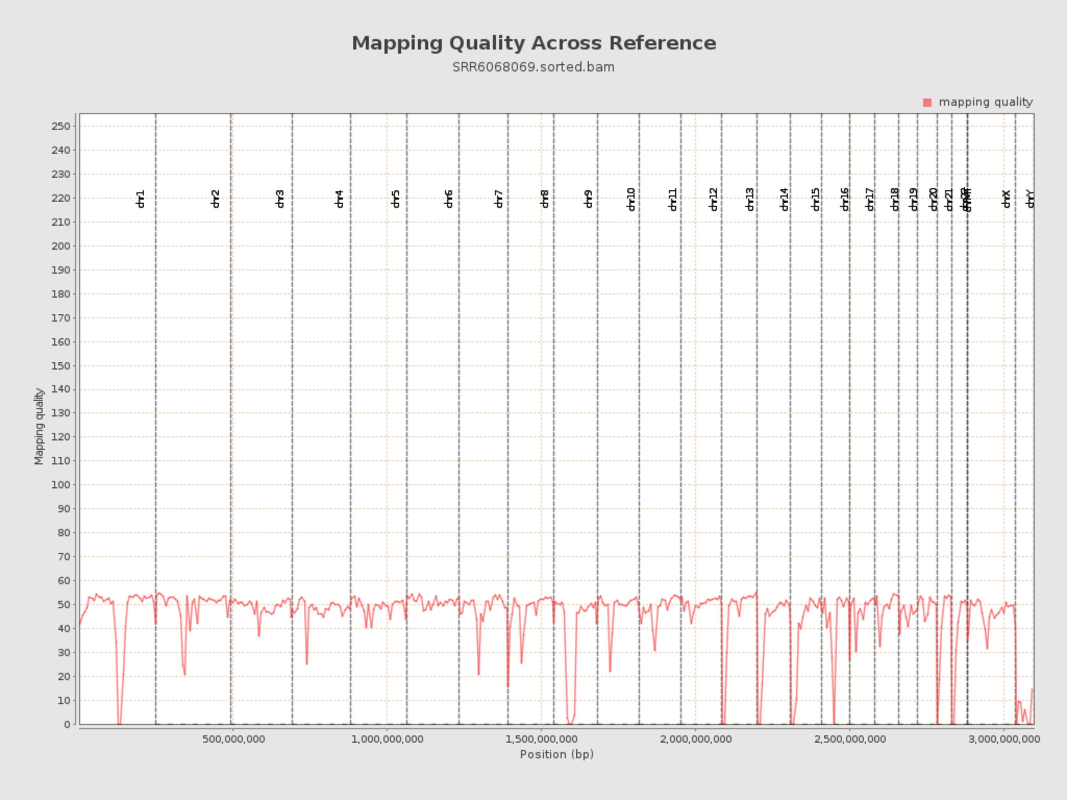
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram