Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 16:22:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068939.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_SRR6068939 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068939.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 16:22:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068939.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,927,458
Mapped reads	1,487,805 / 77.19%
Unmapped reads	439,653 / 22.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,323 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	63,500 / 3.29%
Duplication rate	3.04%
Clipped reads	939,210 / 48.73%

2.2. ACGT Content

Number/percentage of A's	23,499,563 / 25.24%
Number/percentage of C's	15,922,863 / 17.1%
Number/percentage of T's	30,588,455 / 32.85%
Number/percentage of G's	22,890,581 / 24.58%
Number/percentage of N's	209,525 / 0.23%
GC Percentage	41.69%

2.3. Coverage

Mean	0.0301

Standard Deviation	0.3439

2.4. Mapping Quality

Mean Mapping Quality	44.69

2.5. Mismatches and indels

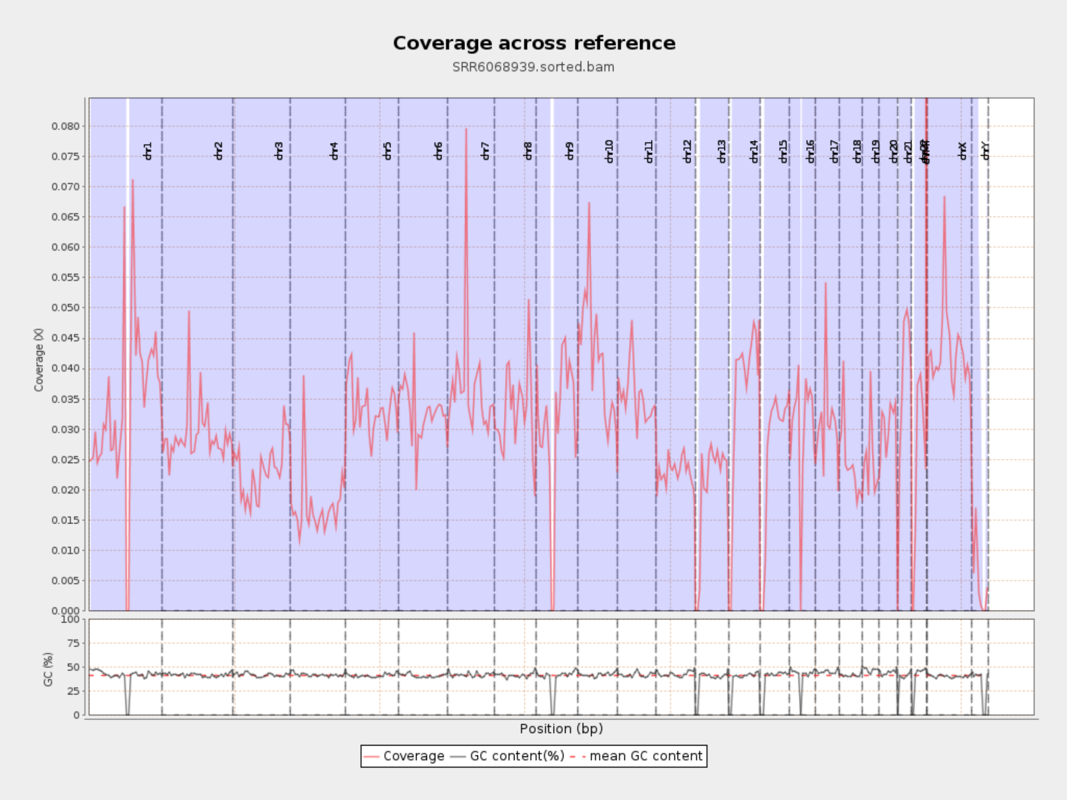
General error rate	0.98%
Mismatches	901,988
Insertions	8,116
Mapped reads with at least one insertion	0.54%
Deletions	26,840
Mapped reads with at least one deletion	1.79%
Homopolymer indels	47.26%

2.6. Chromosome stats

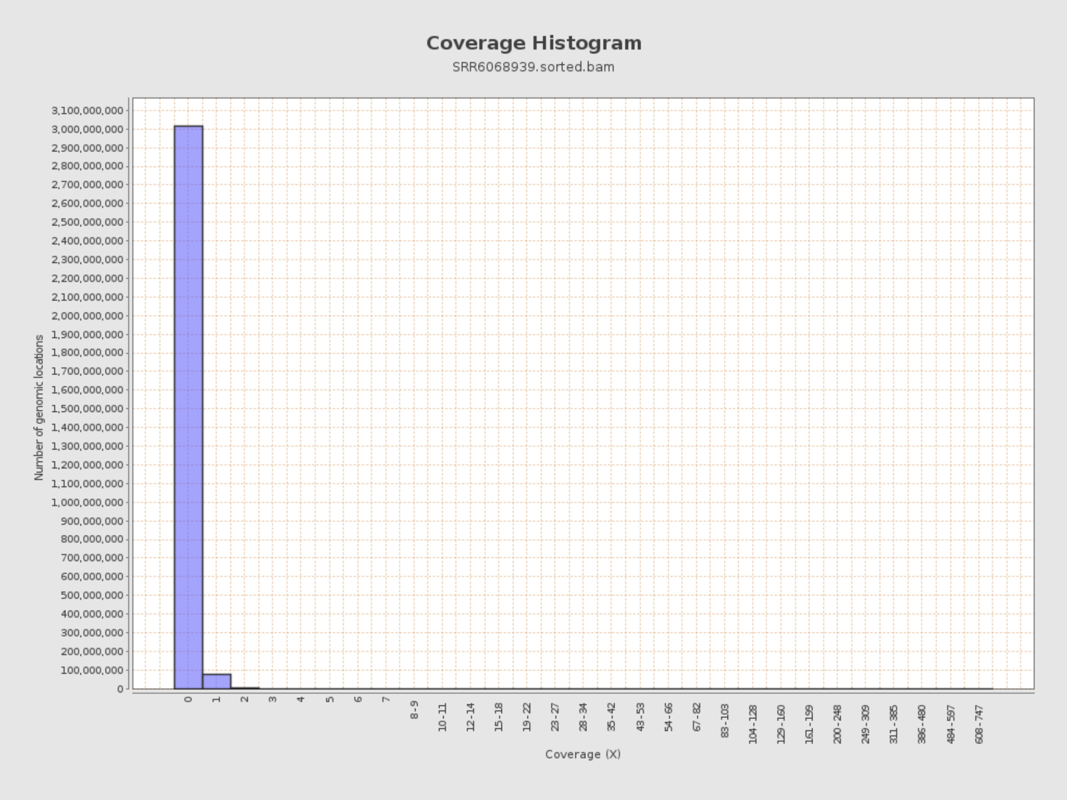
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8522789	0.0342	0.5932
chr2	243199373	7056117	0.029	0.3078
chr3	198022430	4615284	0.0233	0.1668
chr4	191154276	3255079	0.017	0.1789
chr5	180915260	6033767	0.0334	0.2015
chr6	171115067	5640640	0.033	0.2535
chr7	159138663	5913541	0.0372	0.6459

chr8	146364022	4824794	0.033	0.449
chr9	141213431	4283616	0.0303	0.2823
chr10	135534747	5737307	0.0423	0.3187
chr11	135006516	4756341	0.0352	0.4085
chr12	133851895	3077578	0.023	0.1698
chr13	115169878	2341707	0.0203	0.1556
chr14	107349540	3792570	0.0353	0.2124
chr15	102531392	2659743	0.0259	0.1756
chr16	90354753	2737407	0.0303	0.2097
chr17	81195210	2542267	0.0313	0.2303
chr18	78077248	1934912	0.0248	0.5578
chr19	59128983	1472181	0.0249	0.4572
chr20	63025520	1903970	0.0302	0.201
chr21	48129895	1774504	0.0369	0.2245
chr22	51304566	1213333	0.0236	0.1653
chrMT	16571	150438	9.0784	5.4516
chrX	155270560	6612574	0.0426	0.2878
chrY	59373566	302015	0.0051	0.1347

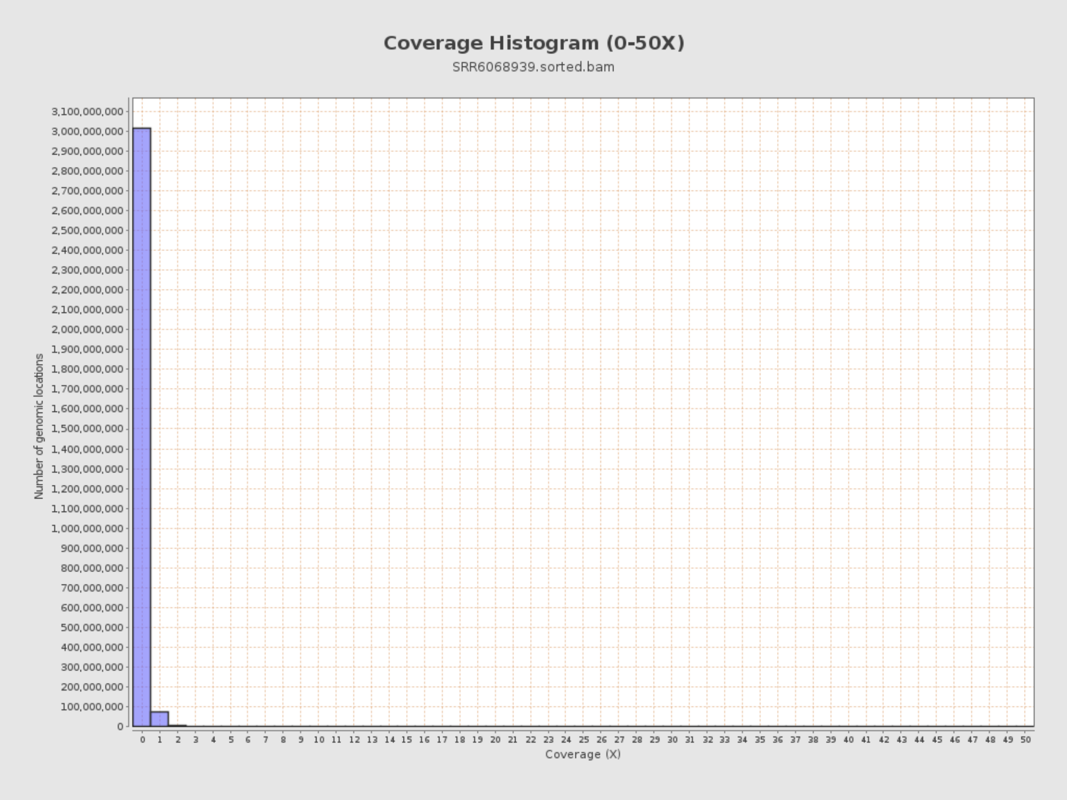
3. Results : Coverage across reference



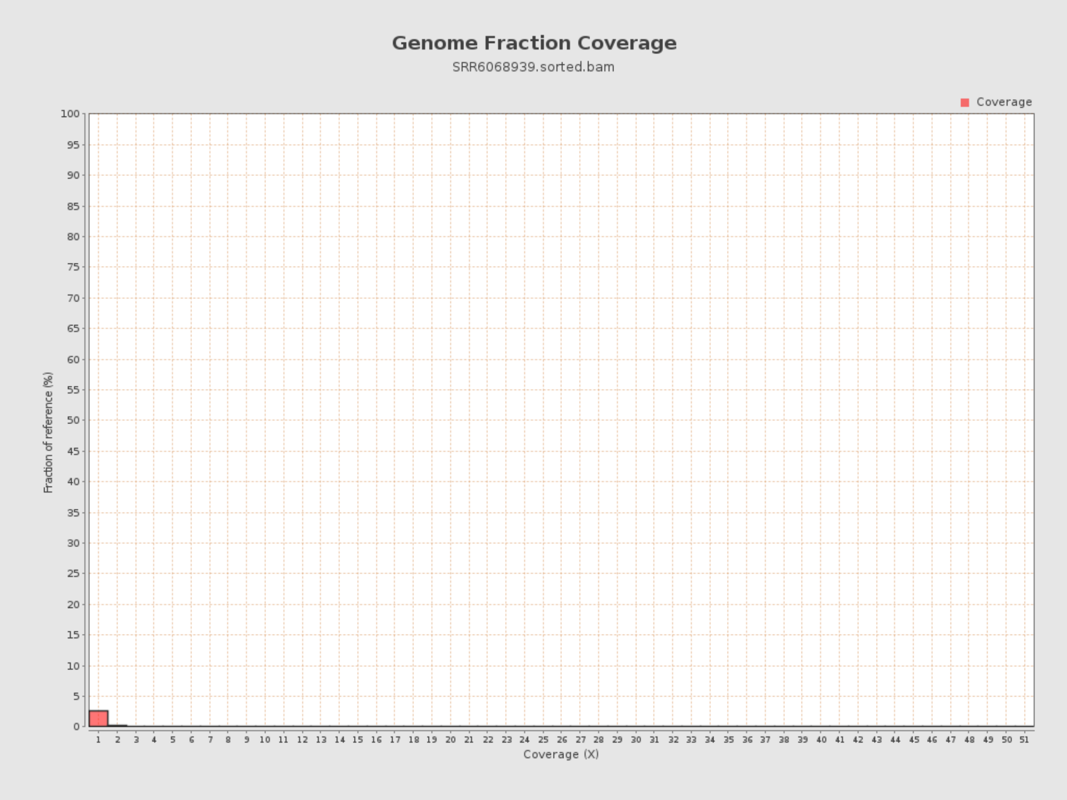
4. Results : Coverage Histogram



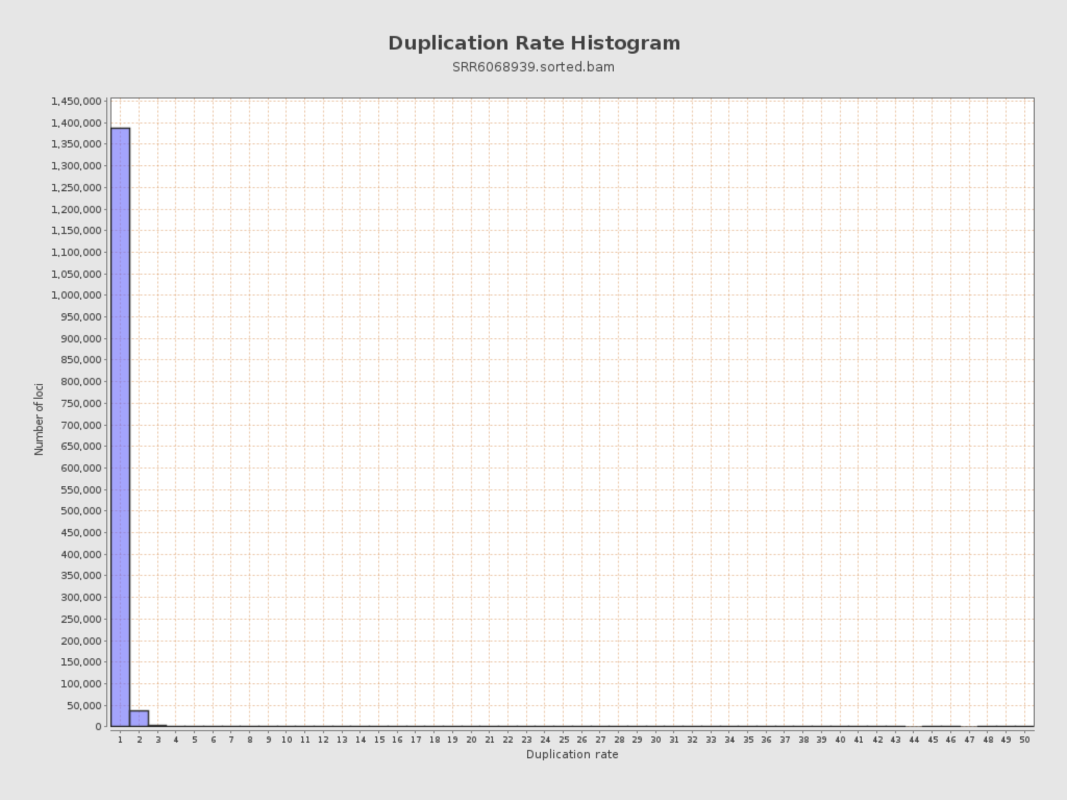
5. Results : Coverage Histogram (0-50X)



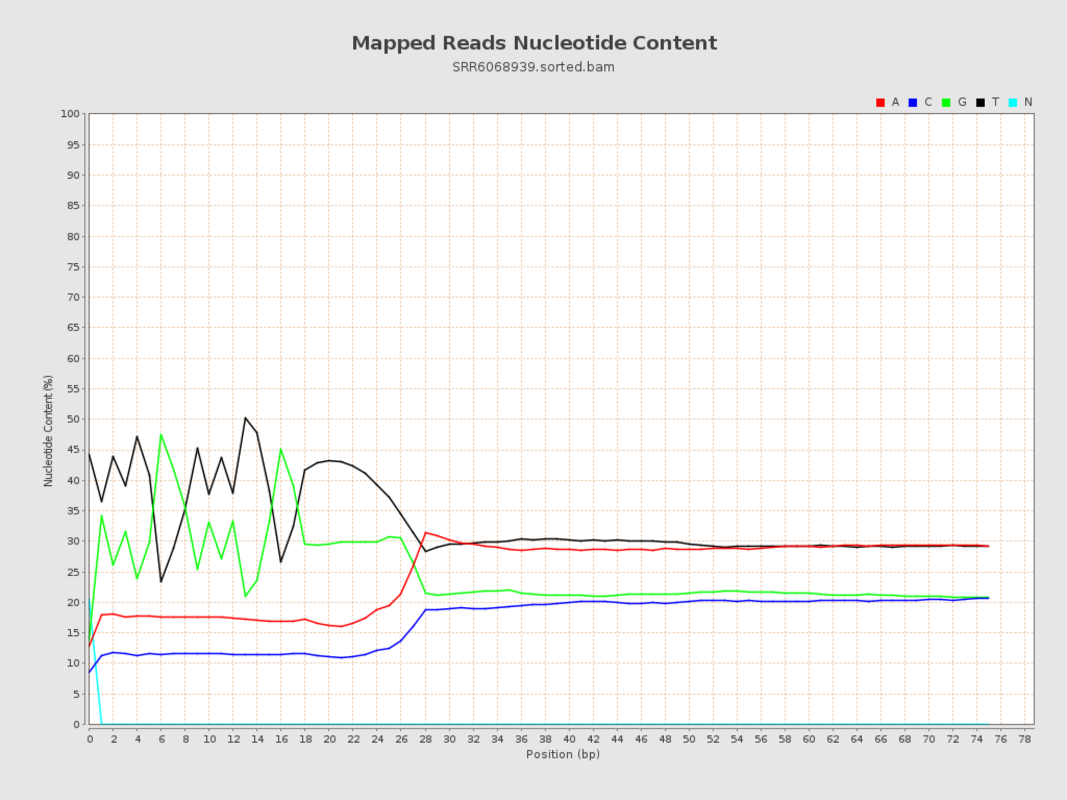
6. Results : Genome Fraction Coverage



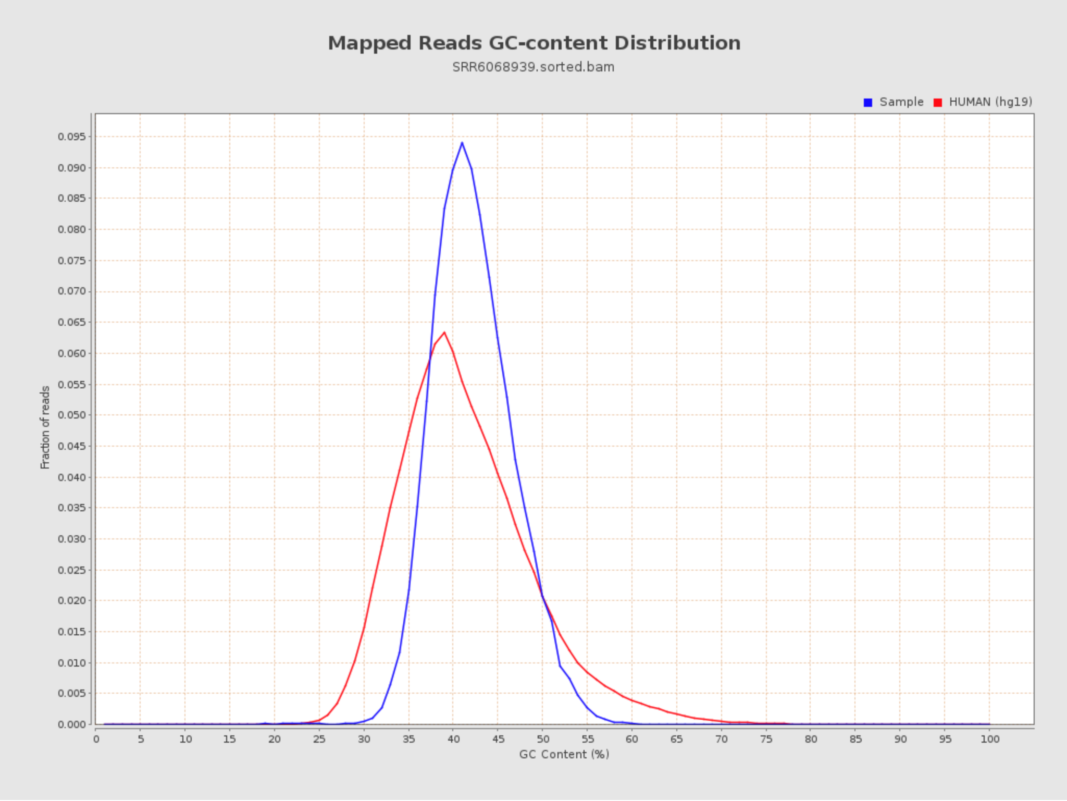
7. Results : Duplication Rate Histogram



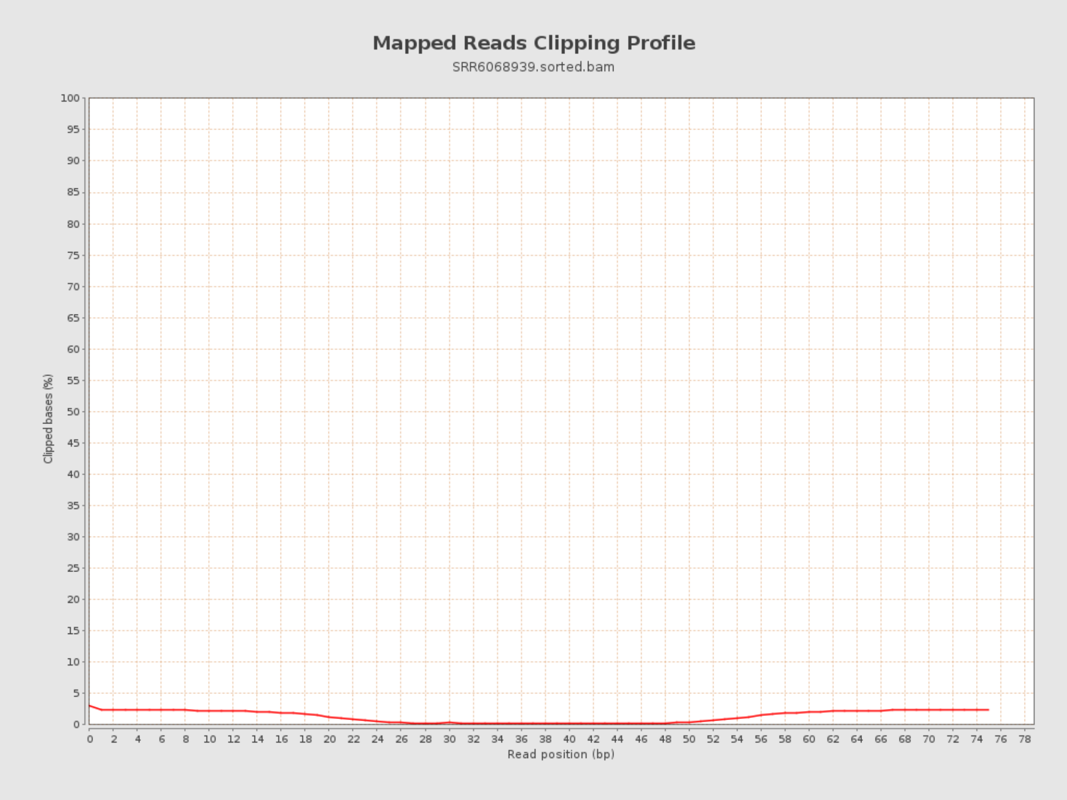
8. Results : Mapped Reads Nucleotide Content



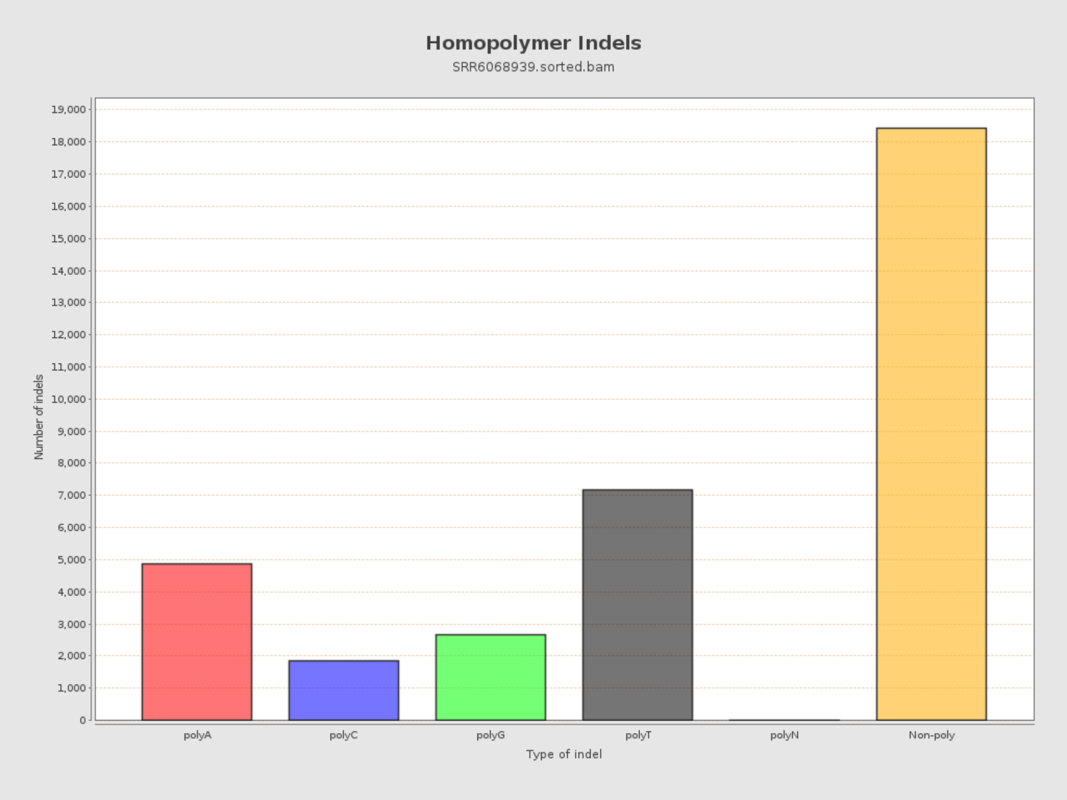
9. Results : Mapped Reads GC-content Distribution



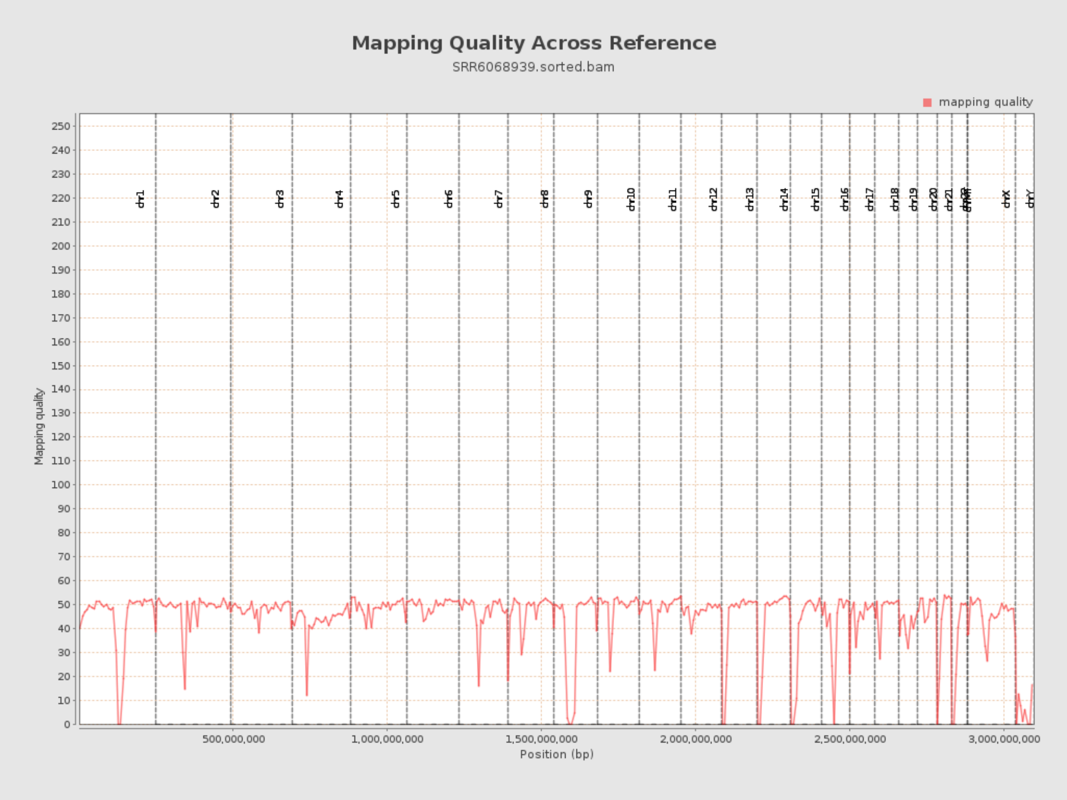
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram