Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 18:23:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082892.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_SRR3082892 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082892.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 18:23:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082892.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,492,483
Mapped reads	3,075,899 / 88.07%
Unmapped reads	416,584 / 11.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,015 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	139,391 / 3.99%
Duplication rate	3.59%
Clipped reads	1,392,659 / 39.88%

2.2. ACGT Content

Number/percentage of A's	56,340,235 / 27.54%
Number/percentage of C's	35,656,916 / 17.43%
Number/percentage of T's	67,681,805 / 33.08%
Number/percentage of G's	44,876,944 / 21.93%
Number/percentage of N's	56,653 / 0.03%
GC Percentage	39.36%

2.3. Coverage

Mean	0.0661

Standard Deviation	0.4703

2.4. Mapping Quality

Mean Mapping Quality	47.17

2.5. Mismatches and indels

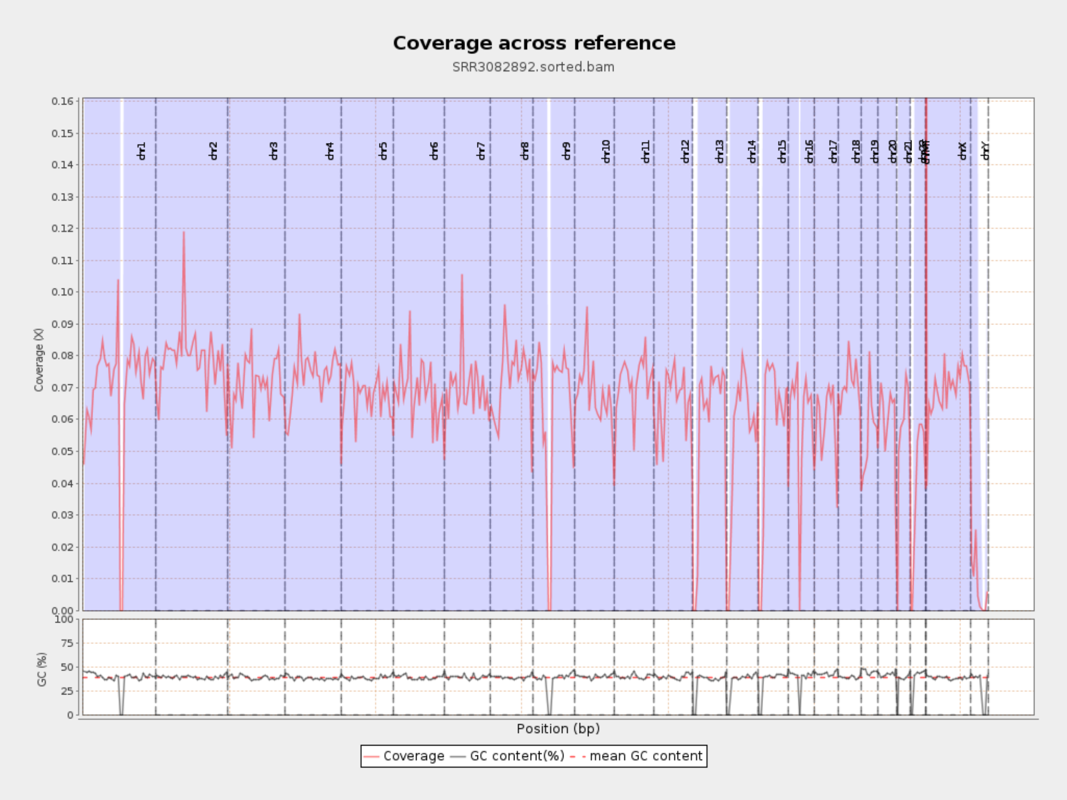
General error rate	0.96%
Mismatches	1,935,145
Insertions	18,691
Mapped reads with at least one insertion	0.6%
Deletions	49,530
Mapped reads with at least one deletion	1.6%
Homopolymer indels	49.35%

2.6. Chromosome stats

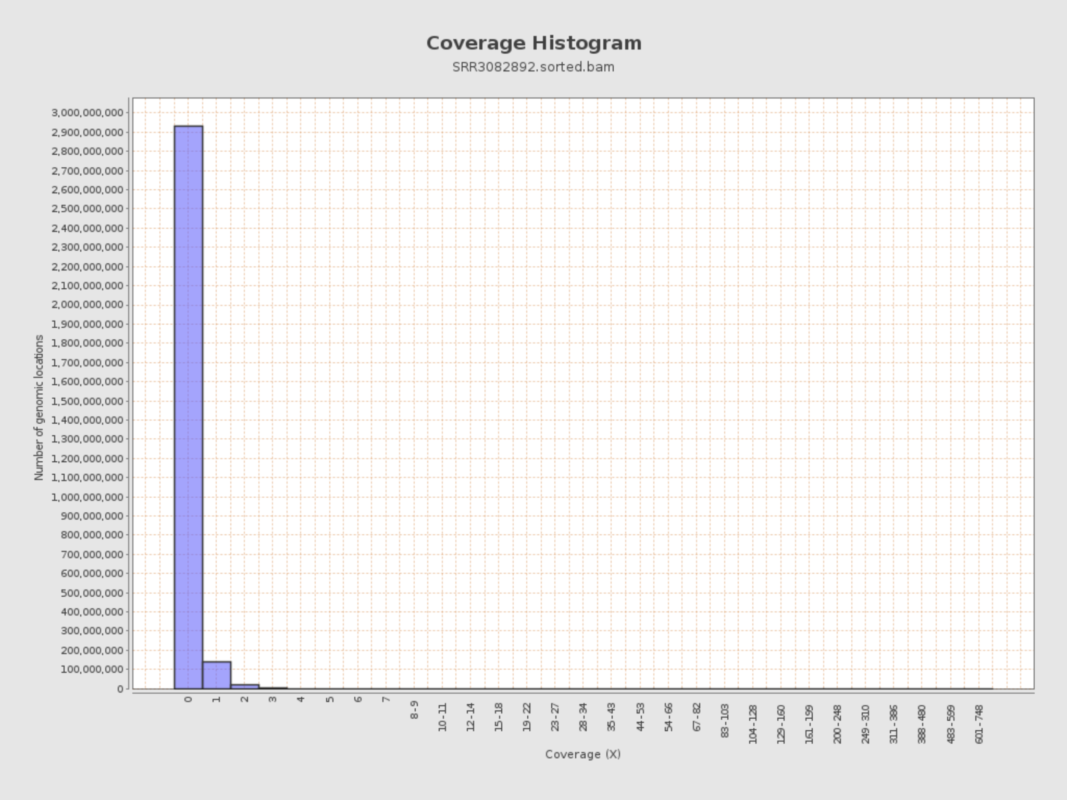
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17478933	0.0701	0.7291
chr2	243199373	19300755	0.0794	0.5721
chr3	198022430	14177473	0.0716	0.3186
chr4	191154276	14129220	0.0739	0.3463
chr5	180915260	12240417	0.0677	0.3074
chr6	171115067	11836630	0.0692	0.4569
chr7	159138663	11101727	0.0698	0.7425

chr8	146364022	10600003	0.0724	0.516
chr9	141213431	8970327	0.0635	0.5222
chr10	135534747	9290784	0.0685	0.4281
chr11	135006516	9683694	0.0717	0.4401
chr12	133851895	8769636	0.0655	0.3099
chr13	115169878	6679455	0.058	0.2858
chr14	107349540	5843843	0.0544	0.3058
chr15	102531392	5799683	0.0566	0.2802
chr16	90354753	5272411	0.0584	0.3387
chr17	81195210	4872976	0.06	0.3597
chr18	78077248	5562082	0.0712	0.7813
chr19	59128983	3298797	0.0558	0.5368
chr20	63025520	3874789	0.0615	0.3053
chr21	48129895	2663276	0.0553	0.3092
chr22	51304566	1999105	0.039	0.2312
chrMT	16571	19120	1.1538	1.4163
chrX	155270560	10781264	0.0694	0.3484
chrY	59373566	446570	0.0075	0.1915

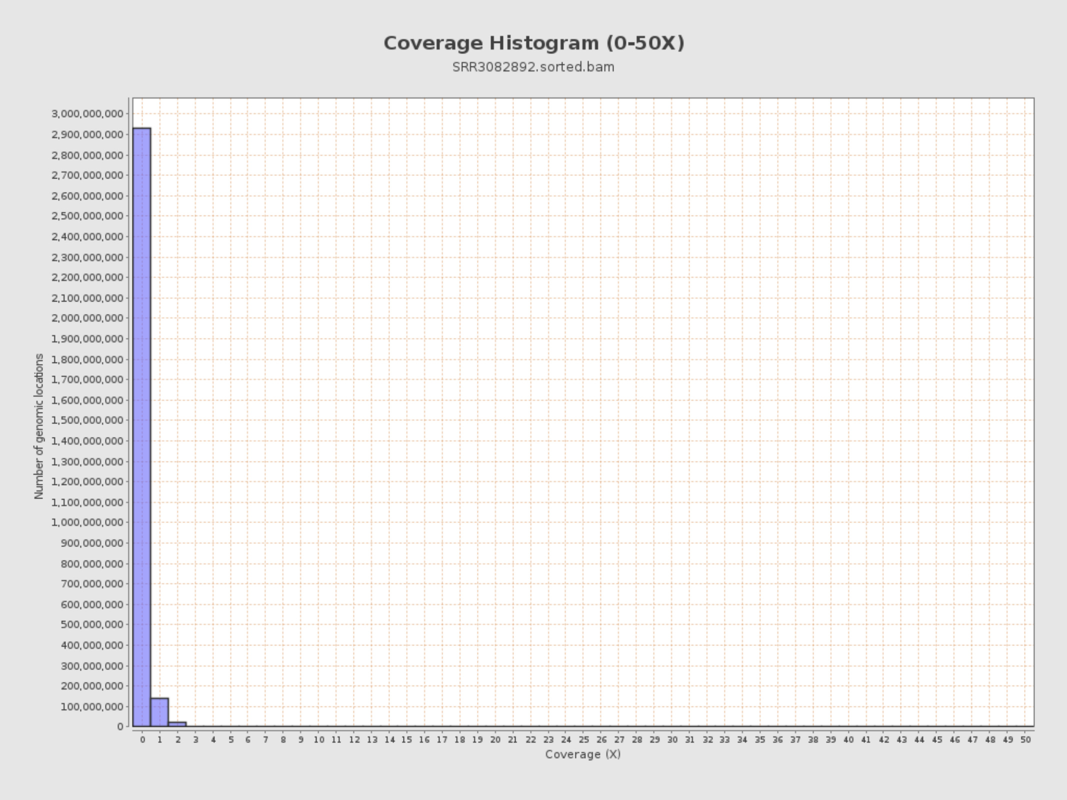
3. Results : Coverage across reference



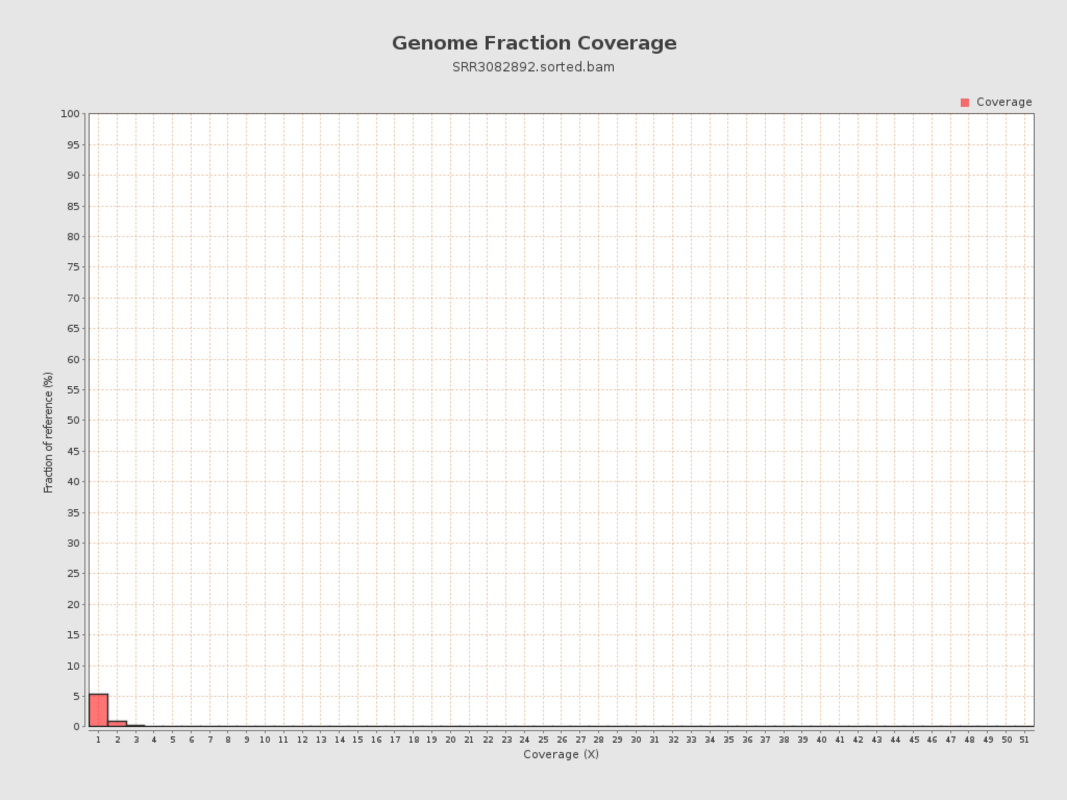
4. Results : Coverage Histogram



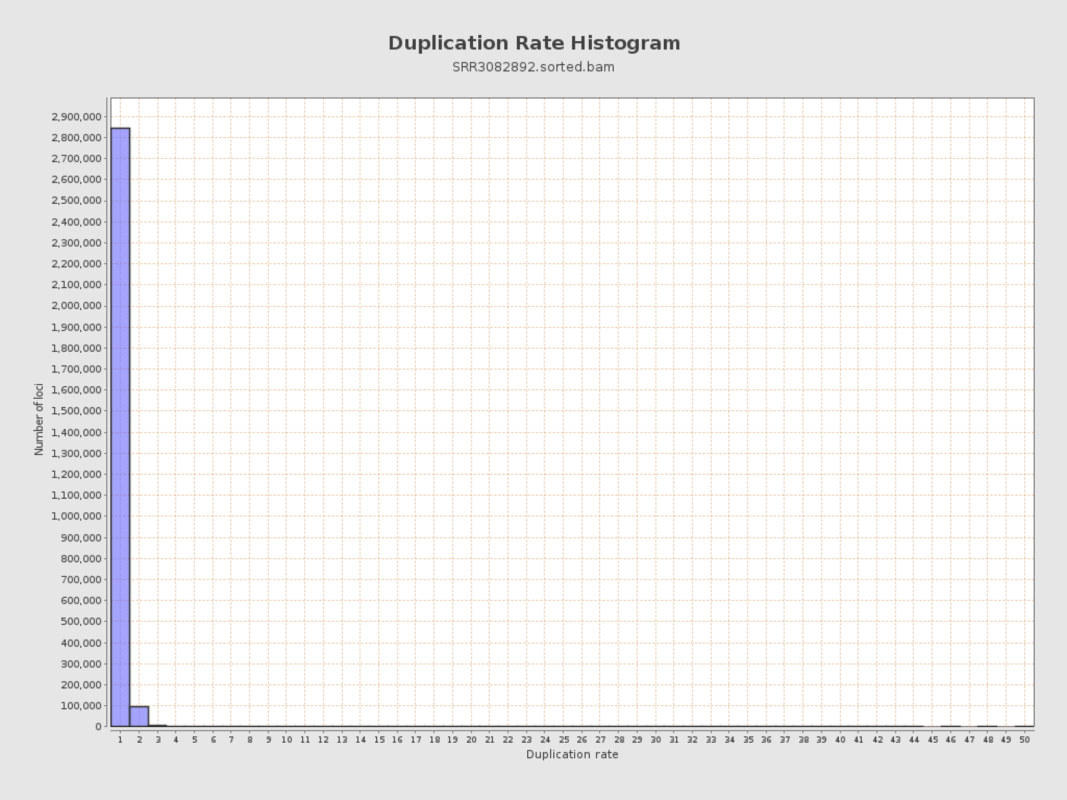
5. Results : Coverage Histogram (0-50X)



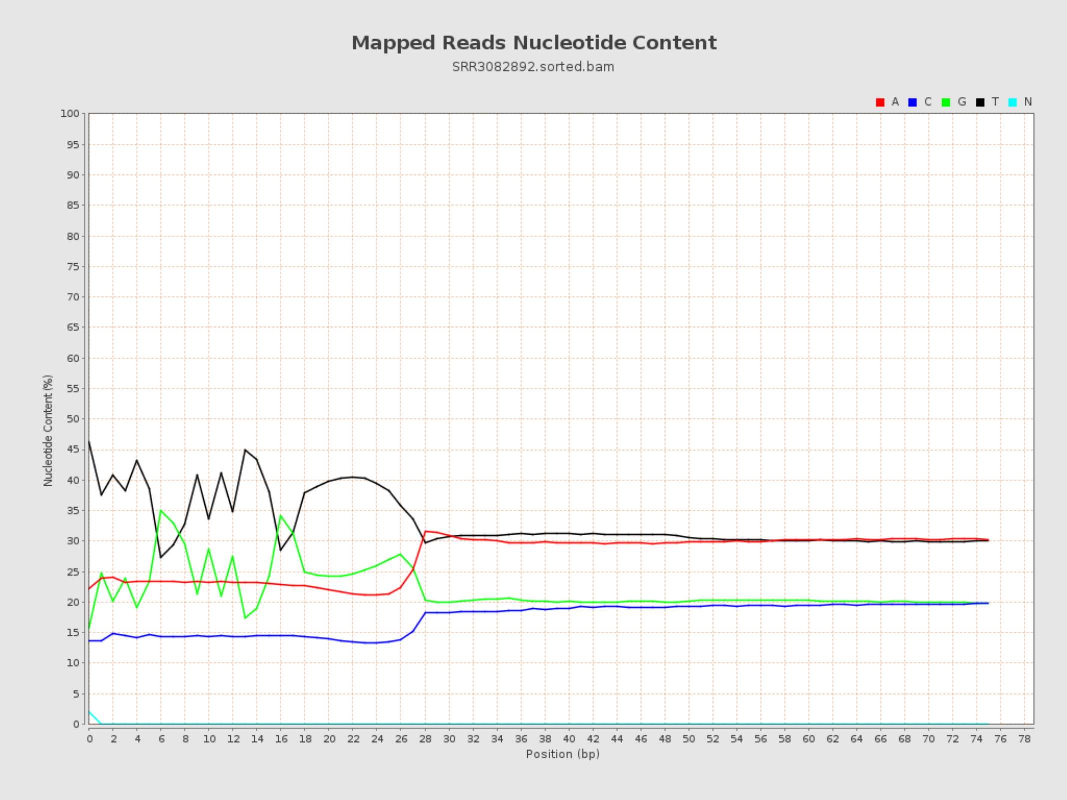
6. Results : Genome Fraction Coverage



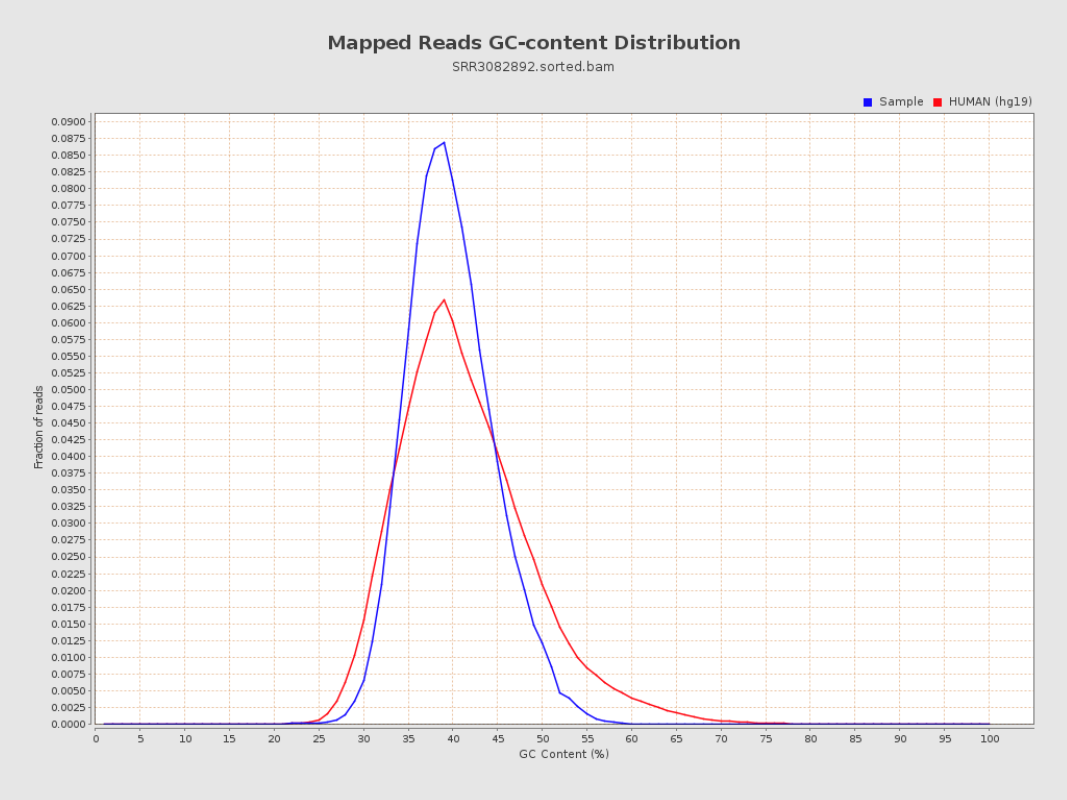
7. Results : Duplication Rate Histogram



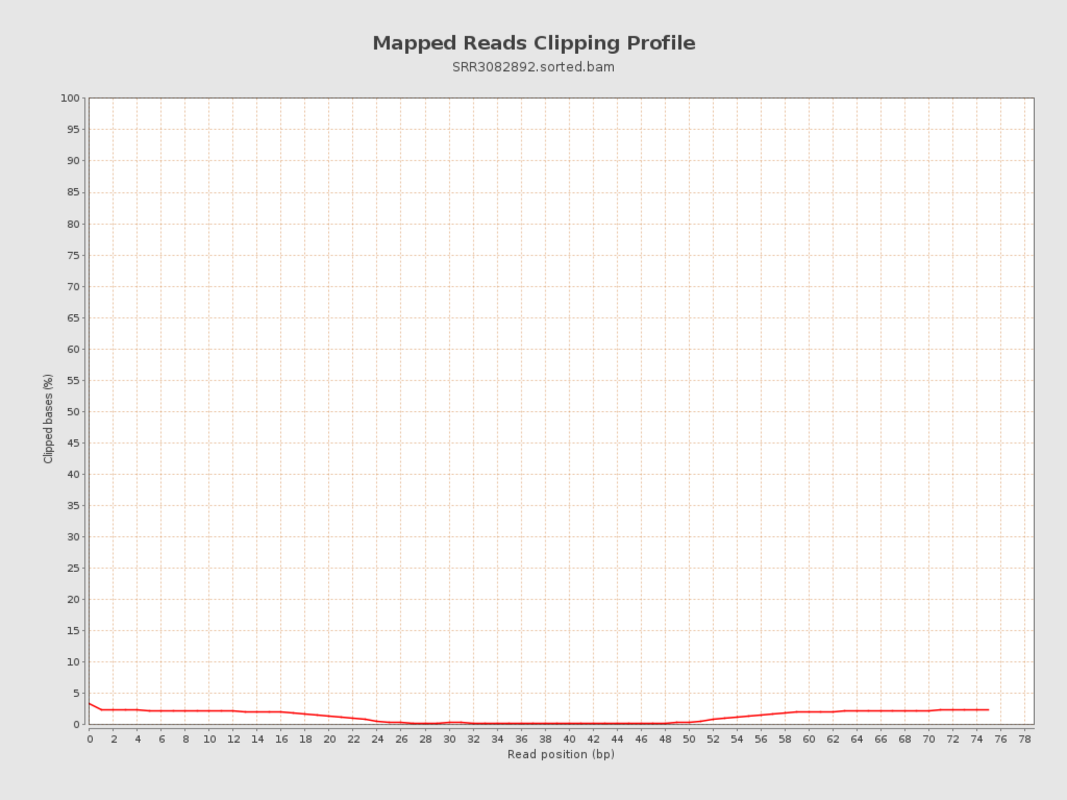
8. Results : Mapped Reads Nucleotide Content



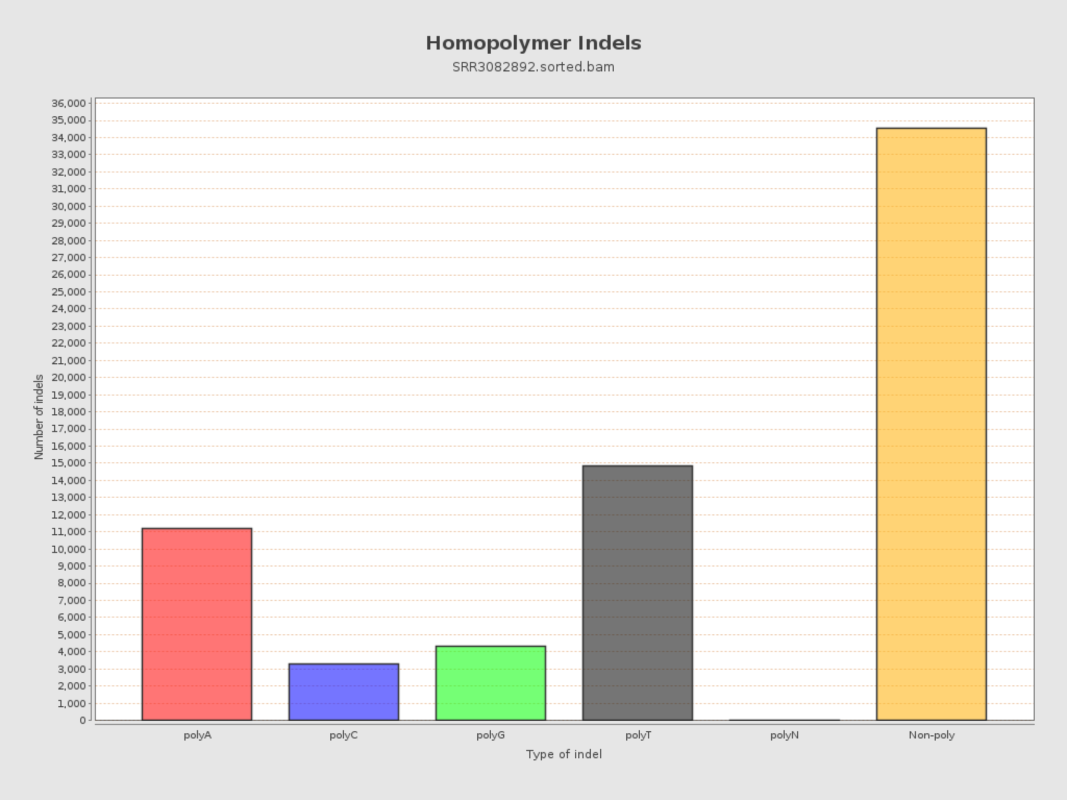
9. Results : Mapped Reads GC-content Distribution



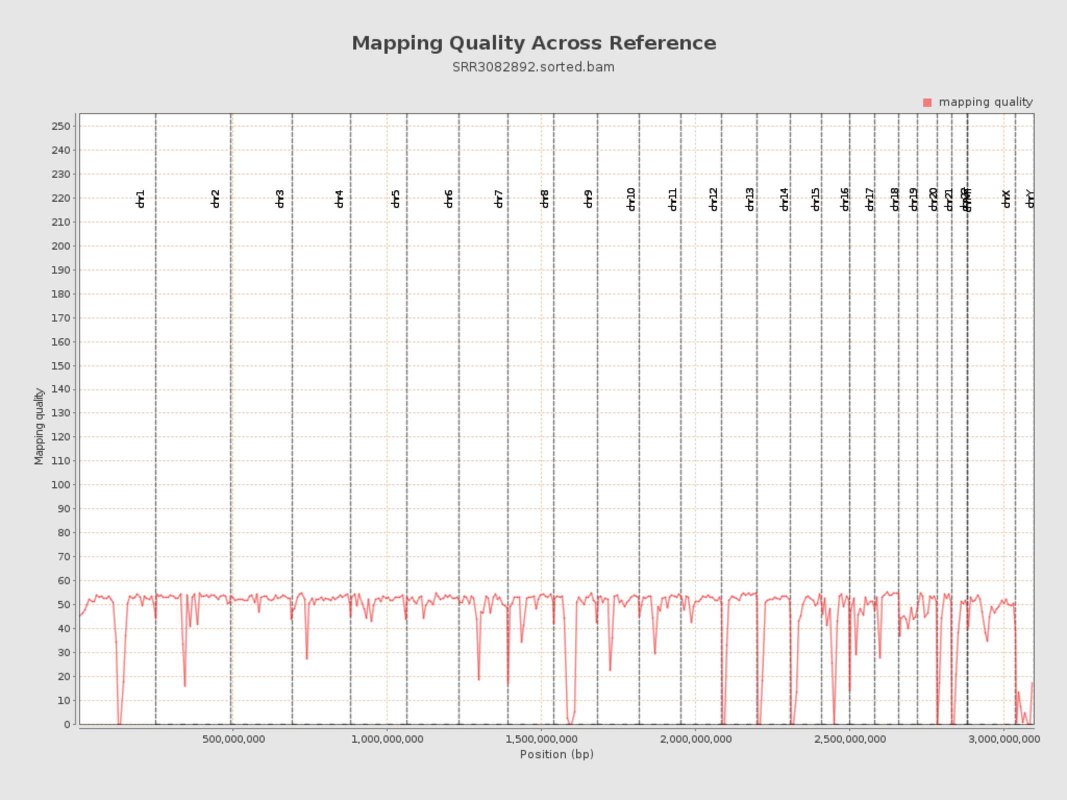
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram