Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 23:46:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083612.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_SRR3083612 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083612.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 23:46:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083612.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,936,639
Mapped reads	1,718,599 / 88.74%
Unmapped reads	218,040 / 11.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,904 / 1.08%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	91,995 / 4.75%
Duplication rate	4.49%
Clipped reads	820,731 / 42.38%

2.2. ACGT Content

Number/percentage of A's	30,420,460 / 26.84%
Number/percentage of C's	21,153,213 / 18.67%
Number/percentage of T's	35,677,970 / 31.48%
Number/percentage of G's	26,071,717 / 23.01%
Number/percentage of N's	5,402 / 0%
GC Percentage	41.67%

2.3. Coverage

Mean	0.0366

Standard Deviation	0.3164

2.4. Mapping Quality

Mean Mapping Quality	45.07

2.5. Mismatches and indels

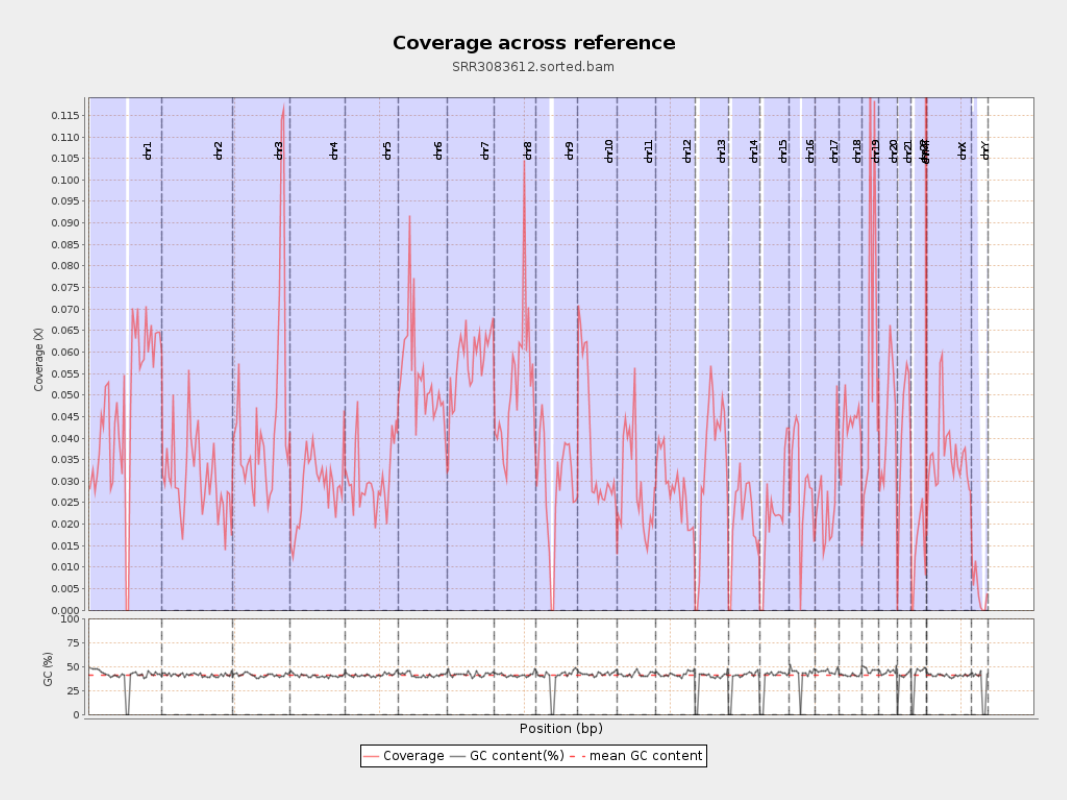
General error rate	0.72%
Mismatches	804,440
Insertions	8,388
Mapped reads with at least one insertion	0.48%
Deletions	25,784
Mapped reads with at least one deletion	1.49%
Homopolymer indels	47.93%

2.6. Chromosome stats

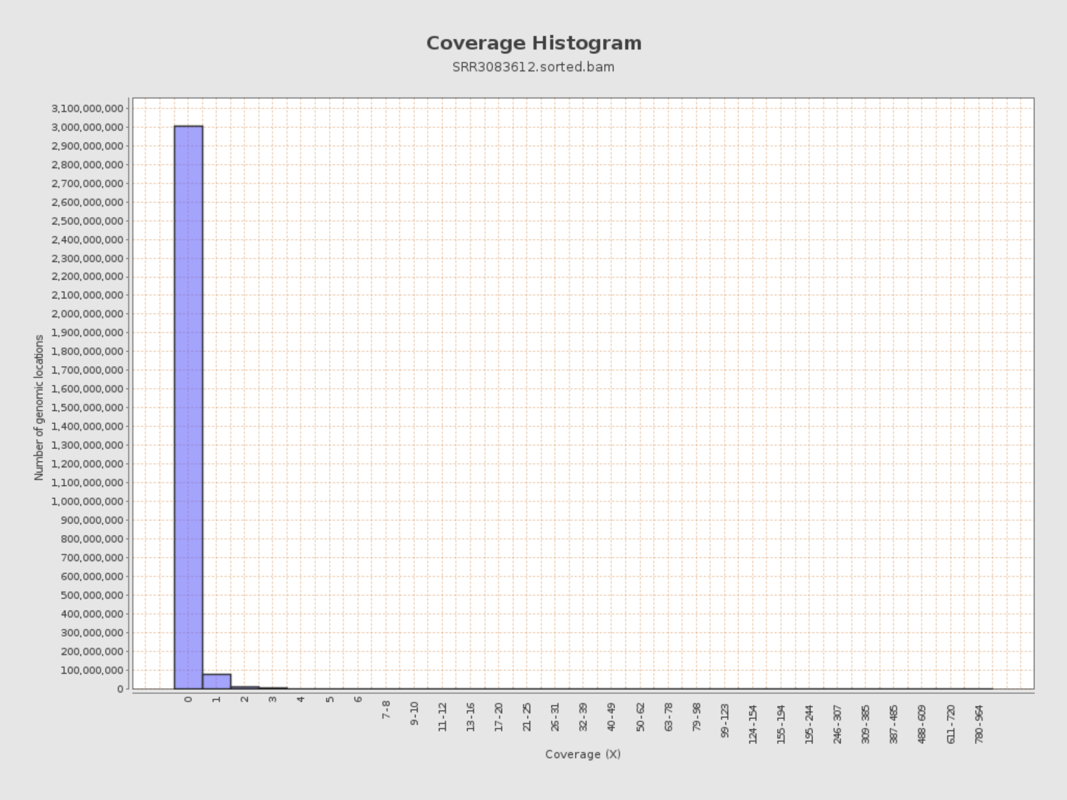
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11646040	0.0467	0.5735
chr2	243199373	7456922	0.0307	0.4555
chr3	198022430	8638103	0.0436	0.2479
chr4	191154276	5488712	0.0287	0.2059
chr5	180915260	5544431	0.0306	0.2059
chr6	171115067	9230491	0.0539	0.3225
chr7	159138663	9212022	0.0579	0.4129

chr8	146364022	7684603	0.0525	0.321
chr9	141213431	4092465	0.029	0.2321
chr10	135534747	5270003	0.0389	0.254
chr11	135006516	3925524	0.0291	0.2292
chr12	133851895	3789804	0.0283	0.1984
chr13	115169878	4040727	0.0351	0.2348
chr14	107349540	2235690	0.0208	0.1712
chr15	102531392	2267524	0.0221	0.1918
chr16	90354753	2613106	0.0289	0.2058
chr17	81195210	2079448	0.0256	0.1956
chr18	78077248	3339965	0.0428	0.3959
chr19	59128983	3478842	0.0588	0.4243
chr20	63025520	2742203	0.0435	0.2571
chr21	48129895	1949309	0.0405	0.2402
chr22	51304566	727161	0.0142	0.1389
chrMT	16571	91189	5.5029	4.0739
chrX	155270560	5582936	0.036	0.2295
chrY	59373566	243272	0.0041	0.0874

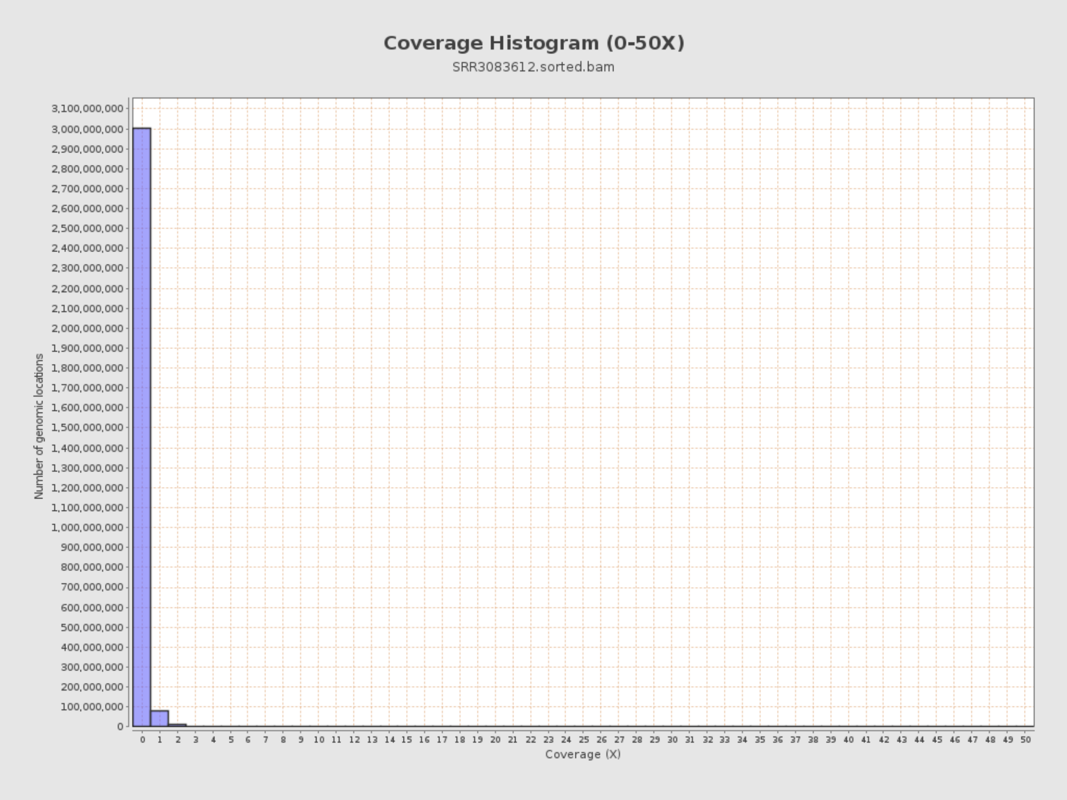
3. Results : Coverage across reference



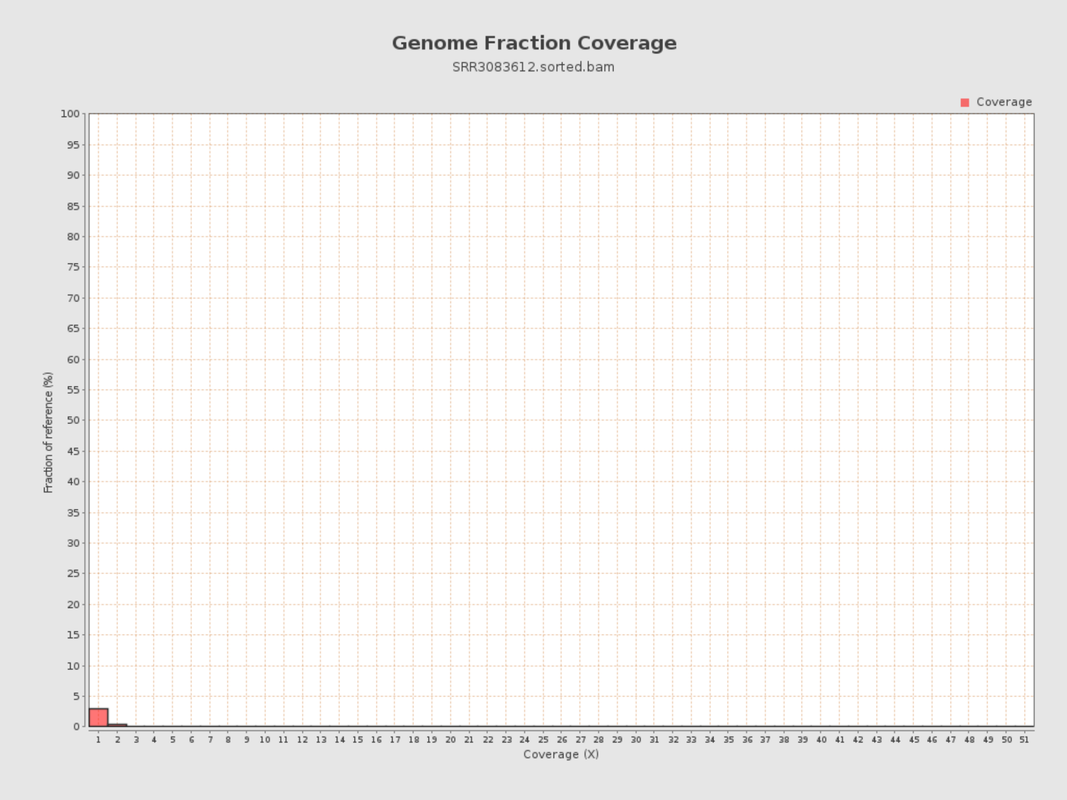
4. Results : Coverage Histogram



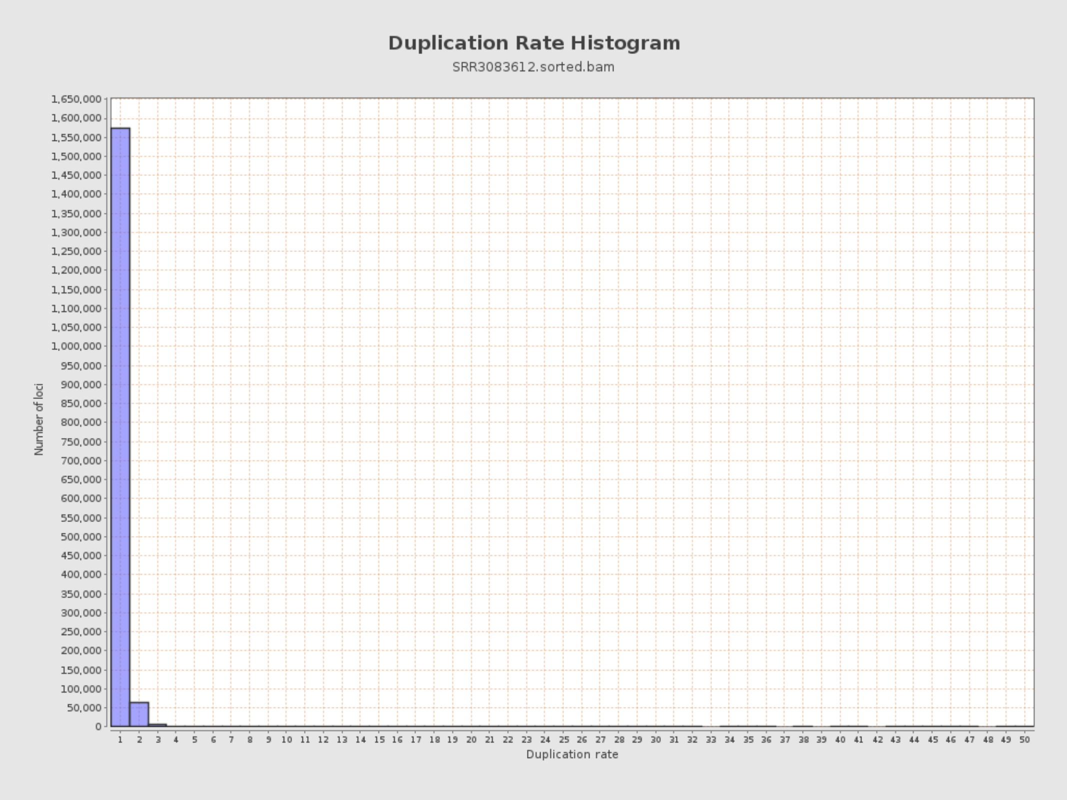
5. Results : Coverage Histogram (0-50X)



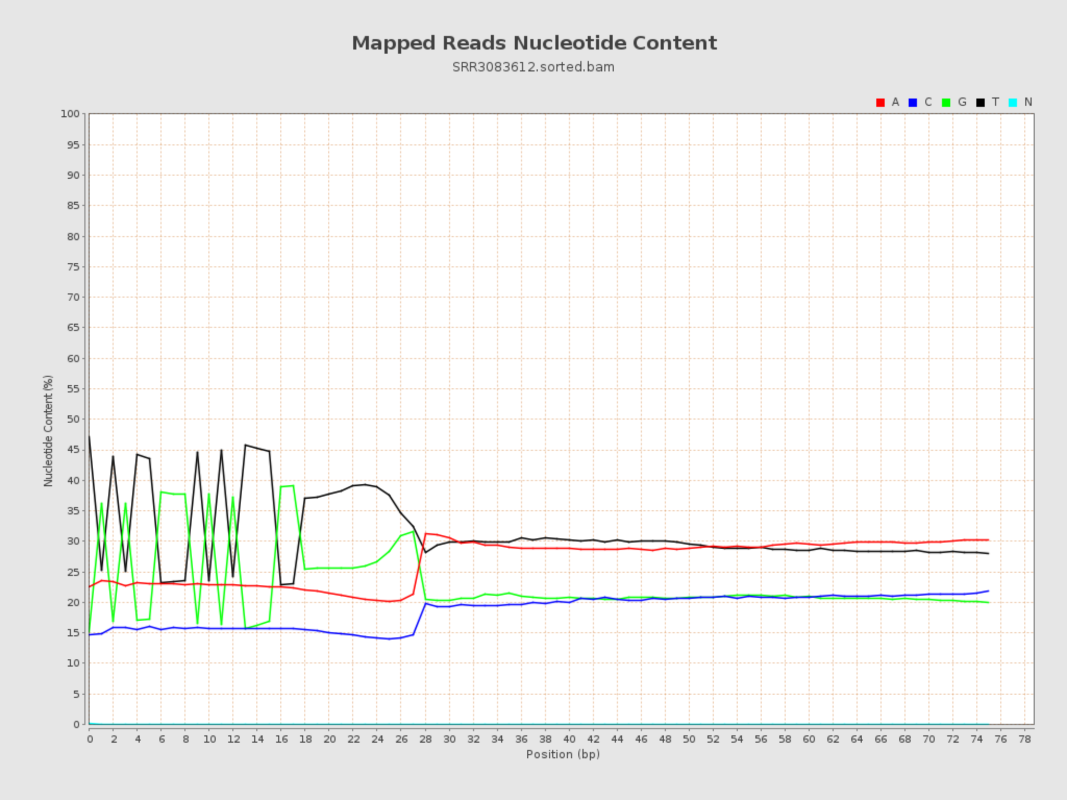
6. Results : Genome Fraction Coverage



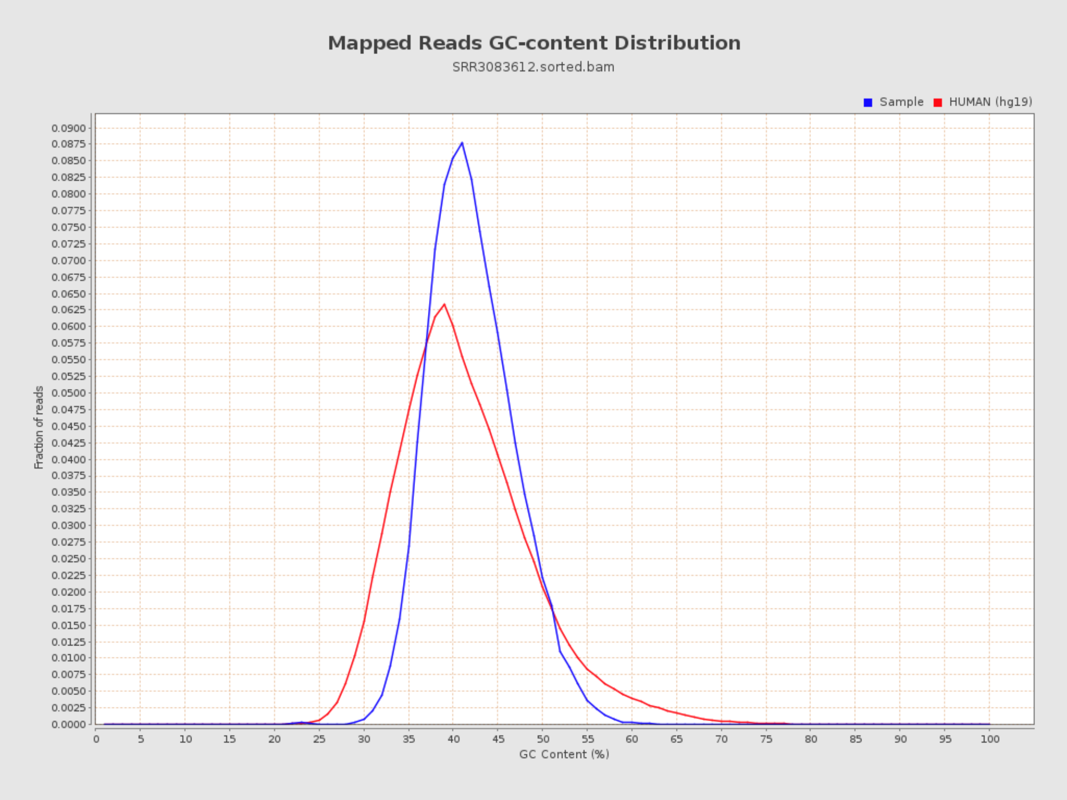
7. Results : Duplication Rate Histogram



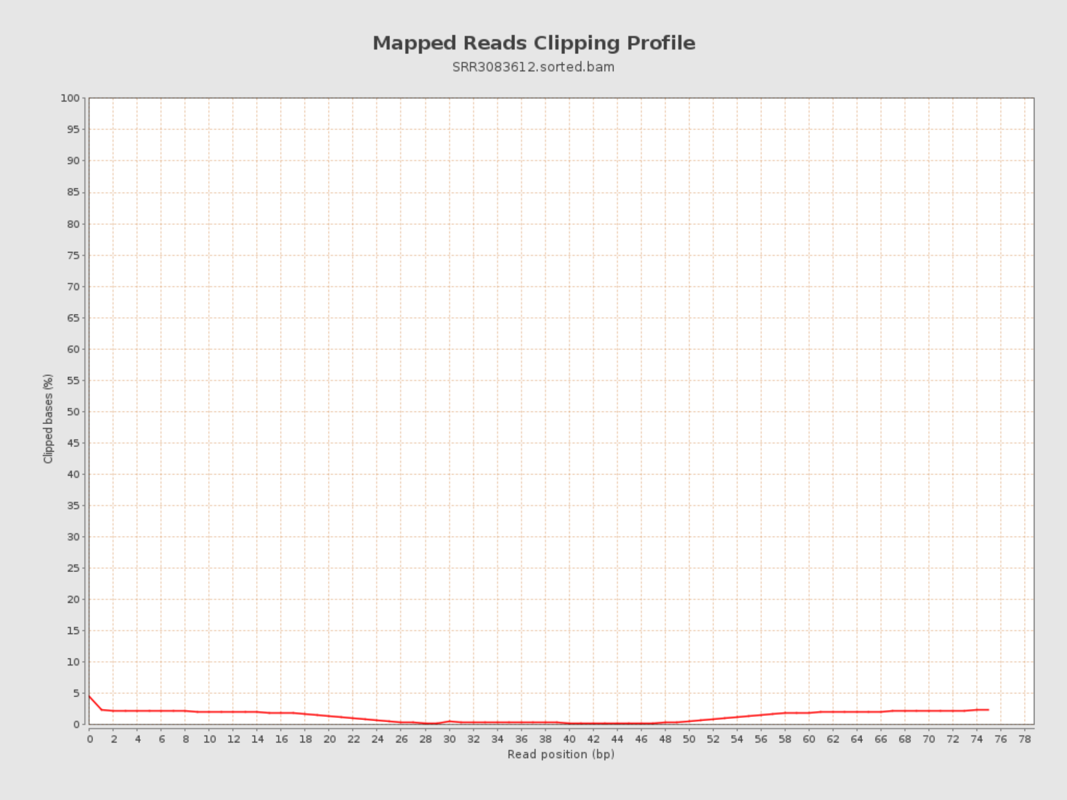
8. Results : Mapped Reads Nucleotide Content



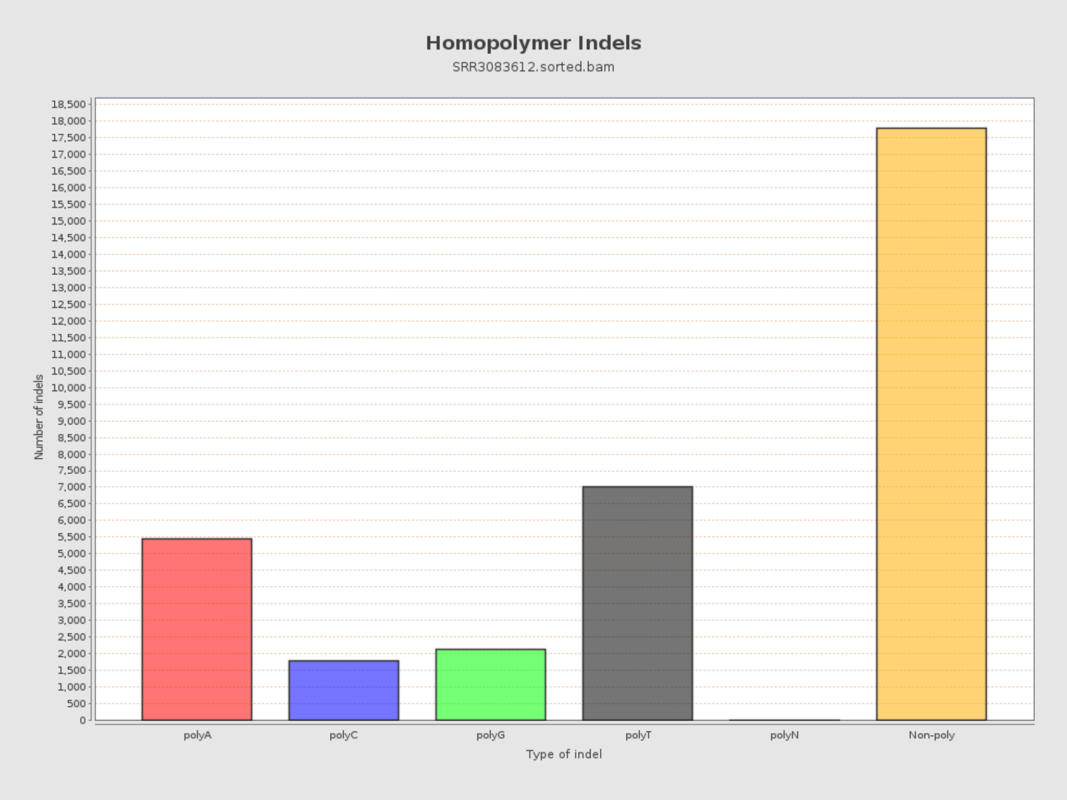
9. Results : Mapped Reads GC-content Distribution



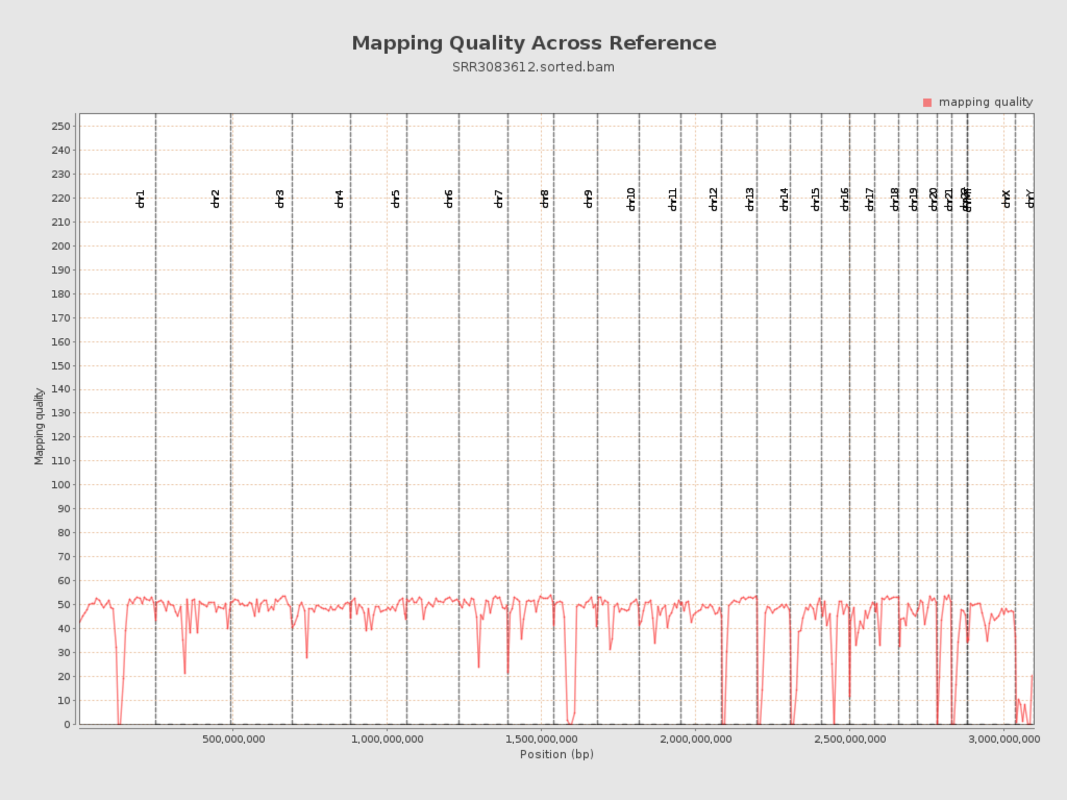
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram