Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 07:44:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3212680.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_SRR3212680 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3212680.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 07:44:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3212680.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,937,917
Mapped reads	2,684,143 / 91.36%
Unmapped reads	253,774 / 8.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,525 / 0.9%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	124,301 / 4.23%
Duplication rate	3.7%
Clipped reads	1,148,459 / 39.09%

2.2. ACGT Content

Number/percentage of A's	50,223,341 / 27.74%
Number/percentage of C's	34,426,385 / 19.02%
Number/percentage of T's	56,210,258 / 31.05%
Number/percentage of G's	40,185,495 / 22.2%
Number/percentage of N's	2,014 / 0%
GC Percentage	41.21%

2.3. Coverage

Mean	0.0585

Standard Deviation	0.4472

2.4. Mapping Quality

Mean Mapping Quality	45.88

2.5. Mismatches and indels

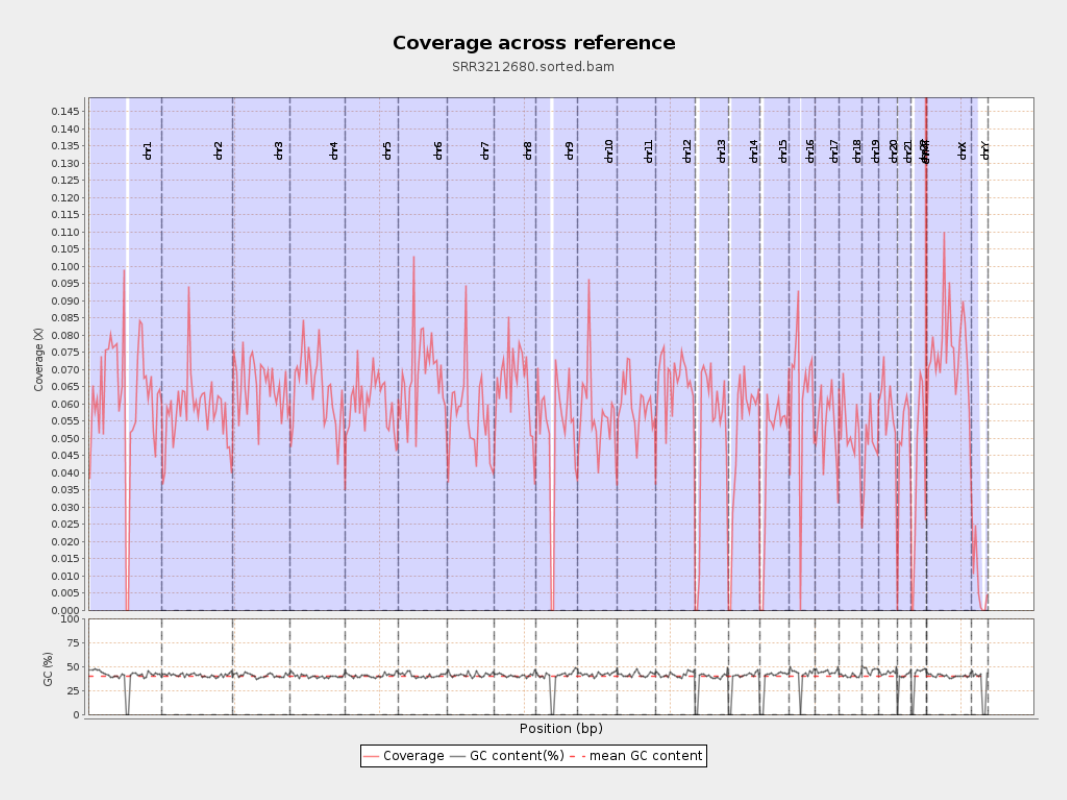
General error rate	0.92%
Mismatches	1,635,629
Insertions	13,870
Mapped reads with at least one insertion	0.51%
Deletions	39,992
Mapped reads with at least one deletion	1.47%
Homopolymer indels	46.96%

2.6. Chromosome stats

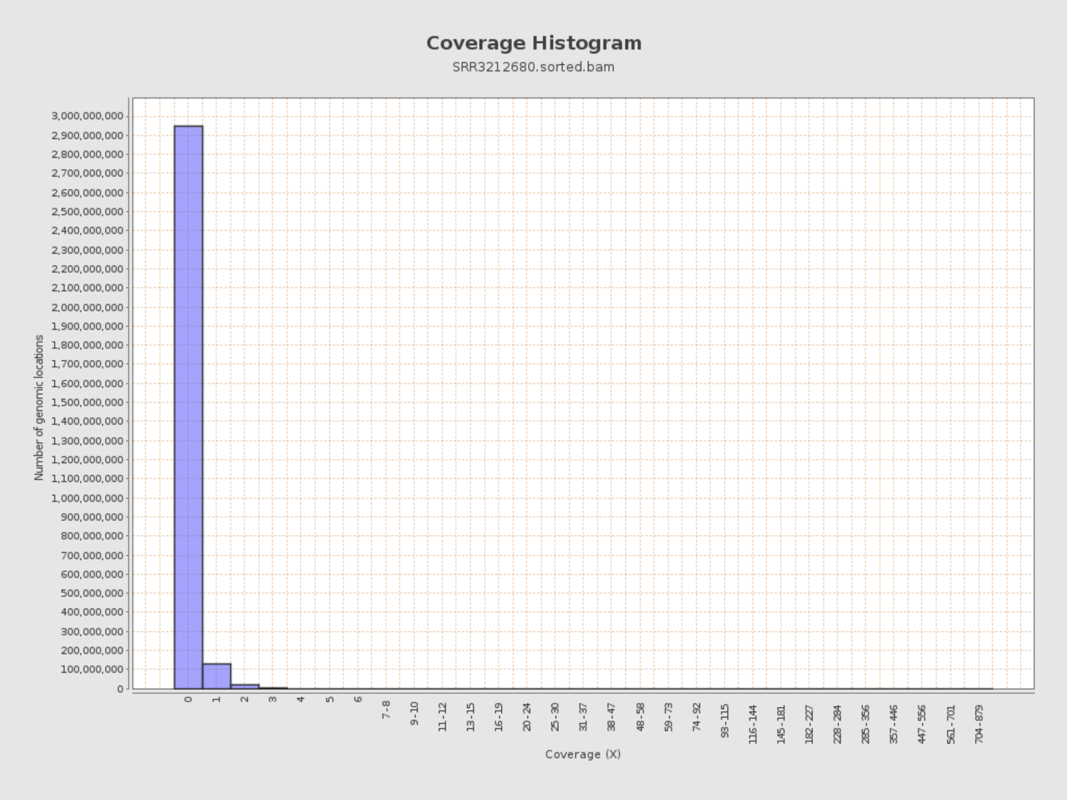
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15366729	0.0617	0.8218
chr2	243199373	14117298	0.058	0.4878
chr3	198022430	12895515	0.0651	0.2976
chr4	191154276	12214391	0.0639	0.3147
chr5	180915260	10927468	0.0604	0.2876
chr6	171115067	11708530	0.0684	0.4294
chr7	159138663	9038131	0.0568	0.5329

chr8	146364022	9522438	0.0651	0.4602
chr9	141213431	7382632	0.0523	0.416
chr10	135534747	7731210	0.057	0.4616
chr11	135006516	8003875	0.0593	0.3947
chr12	133851895	8928145	0.0667	0.306
chr13	115169878	5875185	0.051	0.2625
chr14	107349540	5436642	0.0506	0.2956
chr15	102531392	4761165	0.0464	0.2517
chr16	90354753	5635255	0.0624	0.3417
chr17	81195210	4307594	0.0531	0.321
chr18	78077248	4101603	0.0525	0.7615
chr19	59128983	2837550	0.048	0.6165
chr20	63025520	3668626	0.0582	0.2912
chr21	48129895	2301334	0.0478	0.2941
chr22	51304566	2040510	0.0398	0.2313
chrMT	16571	138527	8.3596	4.7614
chrX	155270560	11692508	0.0753	0.3629
chrY	59373566	479712	0.0081	0.175

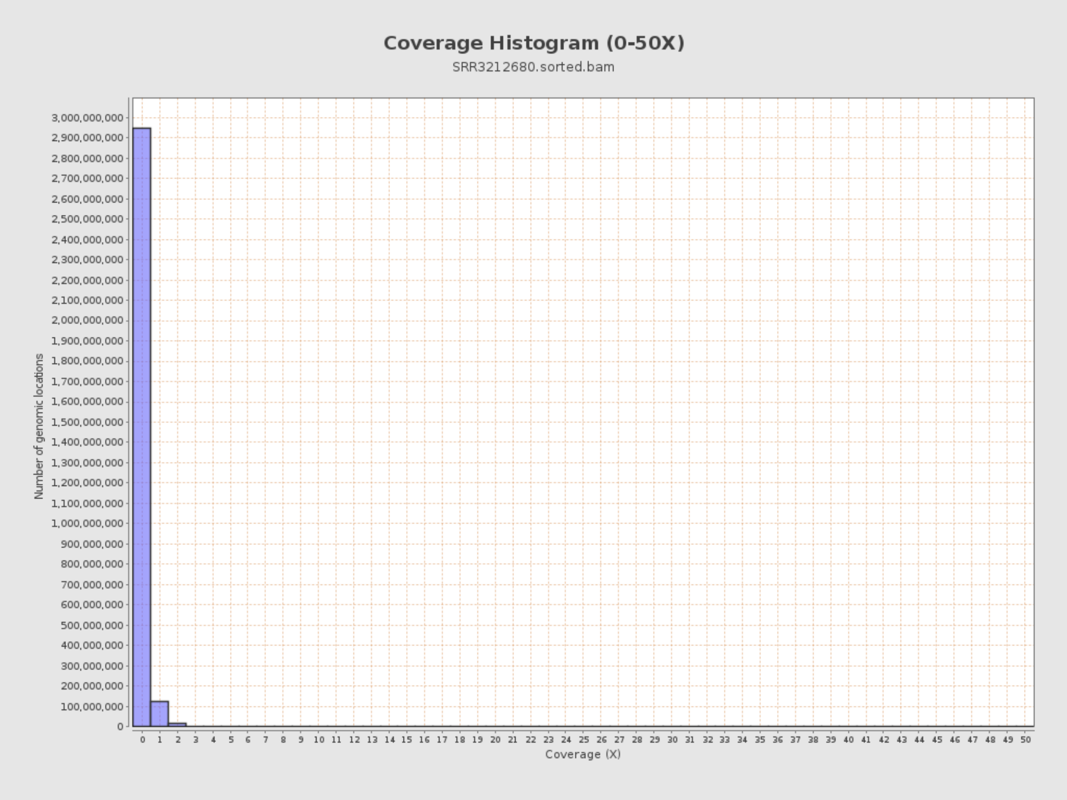
3. Results : Coverage across reference



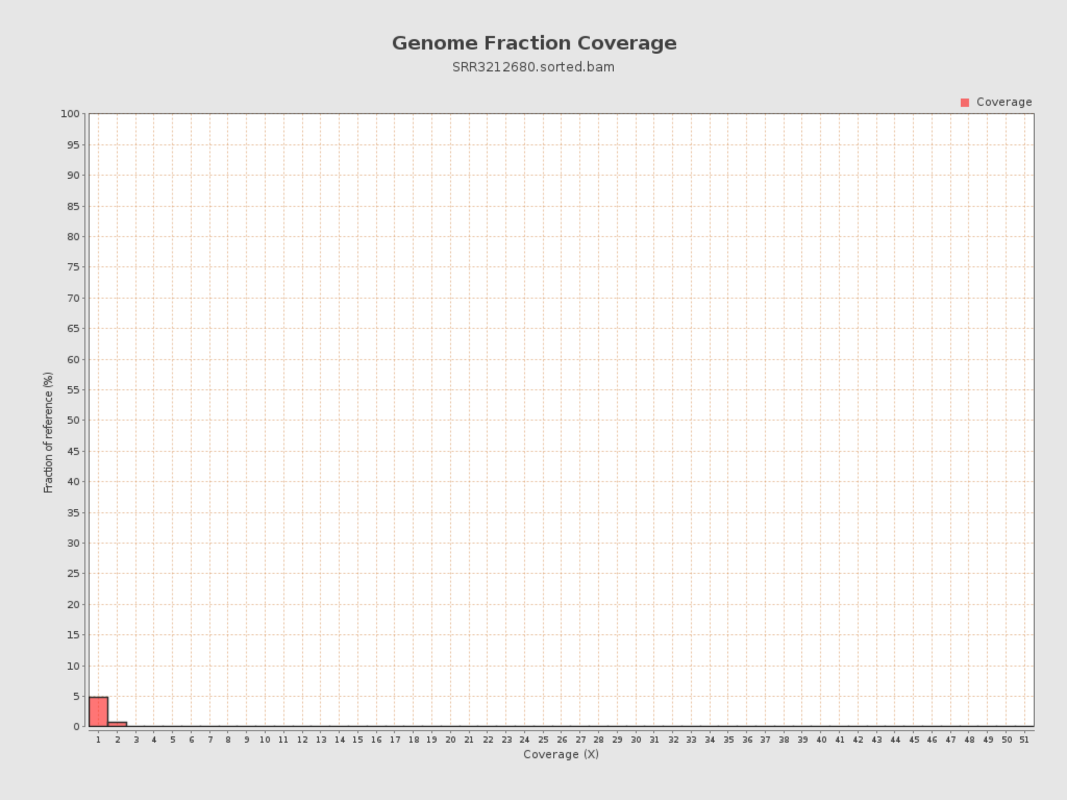
4. Results : Coverage Histogram



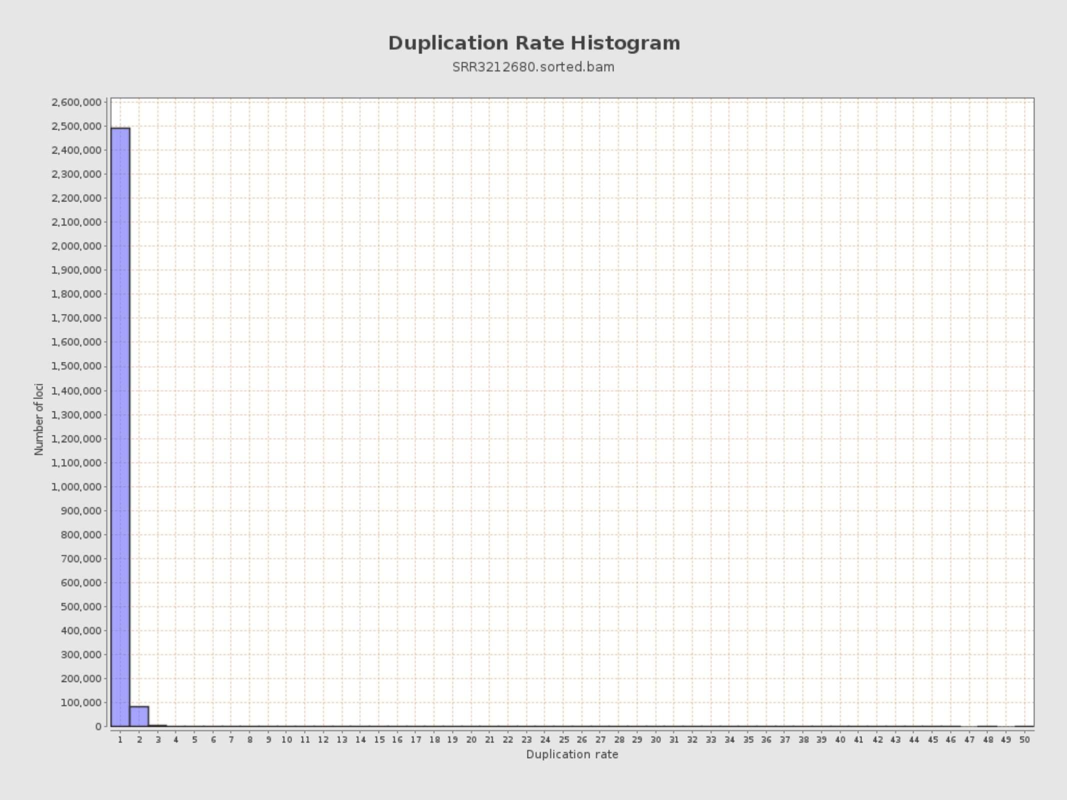
5. Results : Coverage Histogram (0-50X)



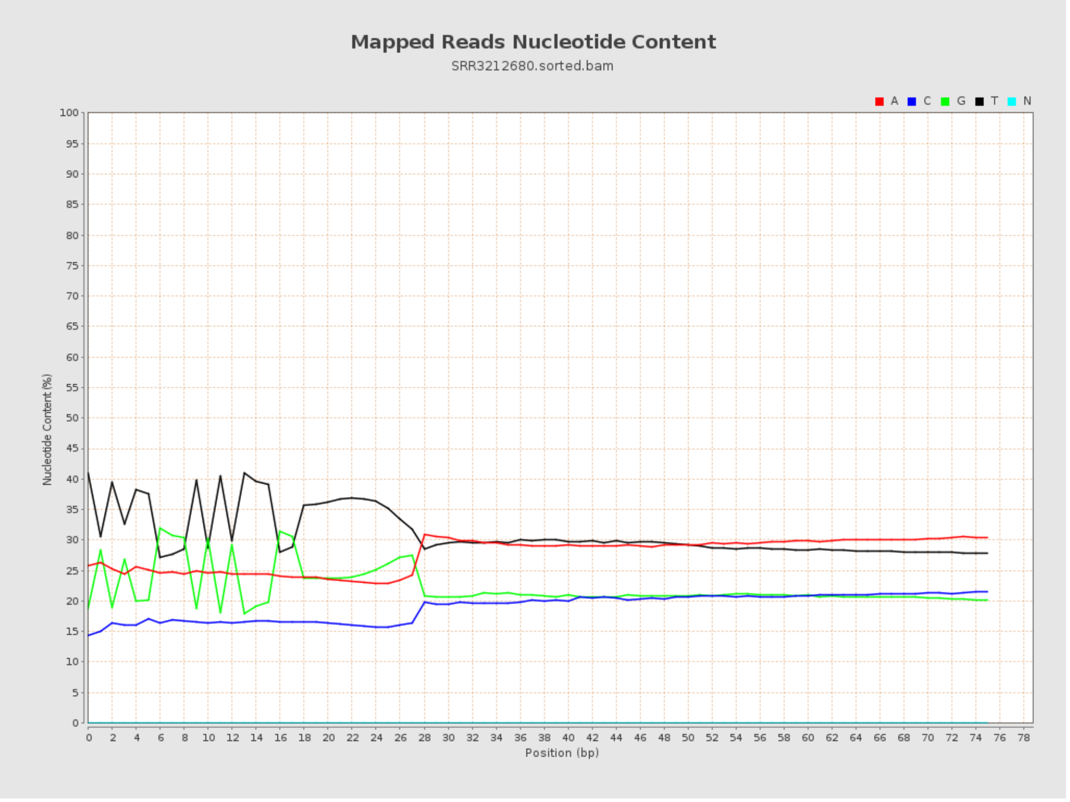
6. Results : Genome Fraction Coverage



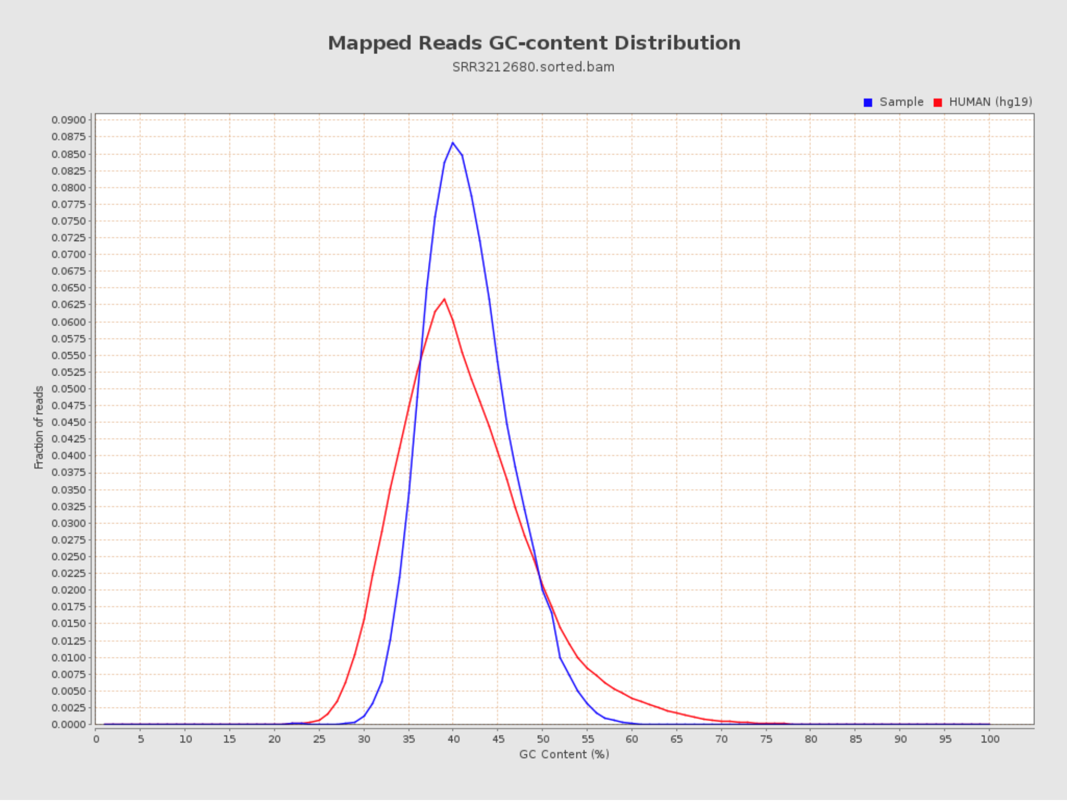
7. Results : Duplication Rate Histogram



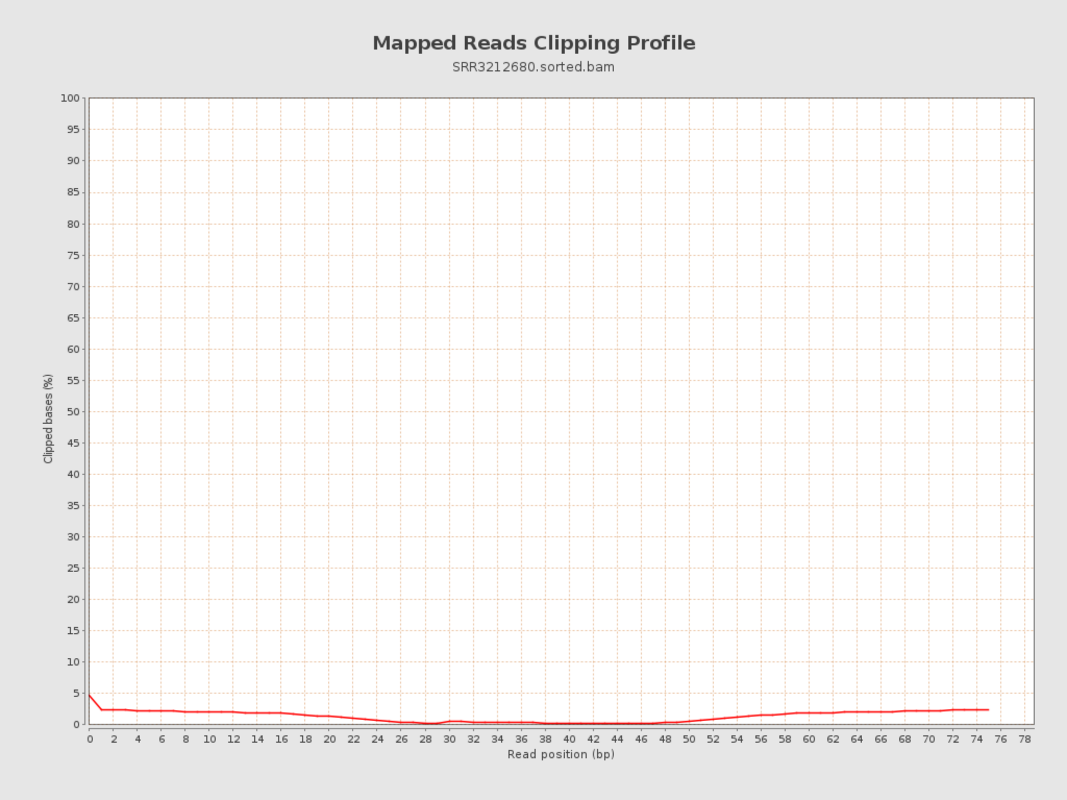
8. Results : Mapped Reads Nucleotide Content



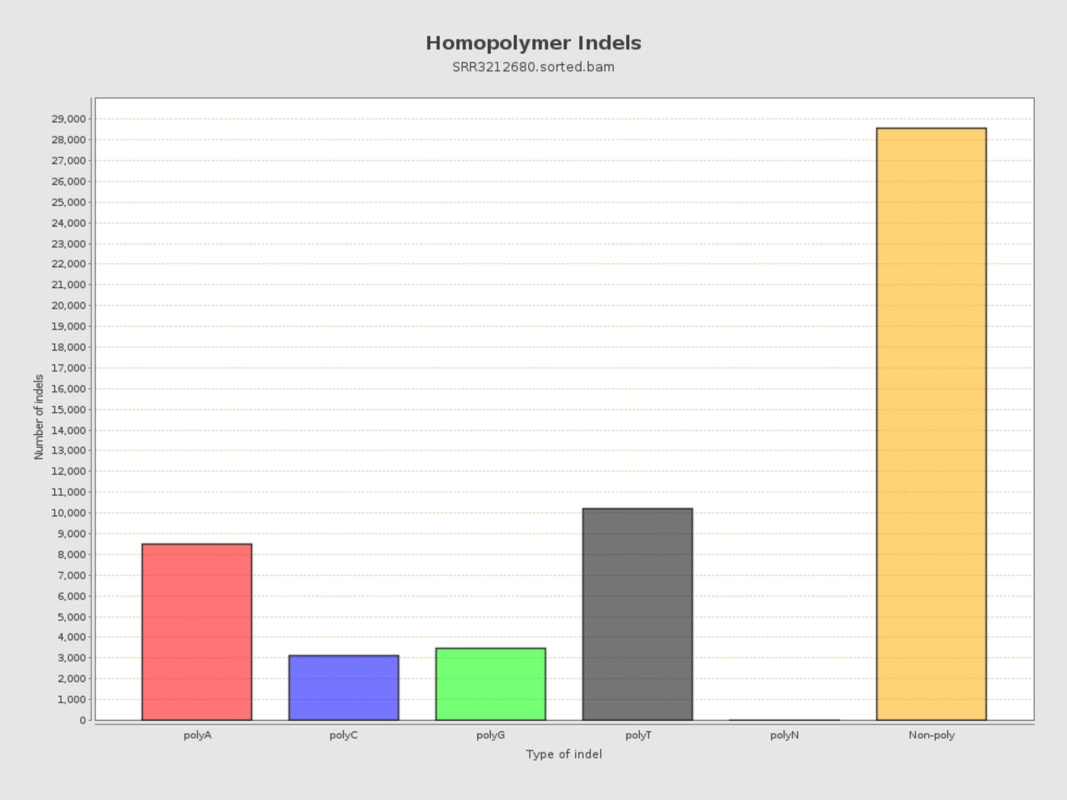
9. Results : Mapped Reads GC-content Distribution



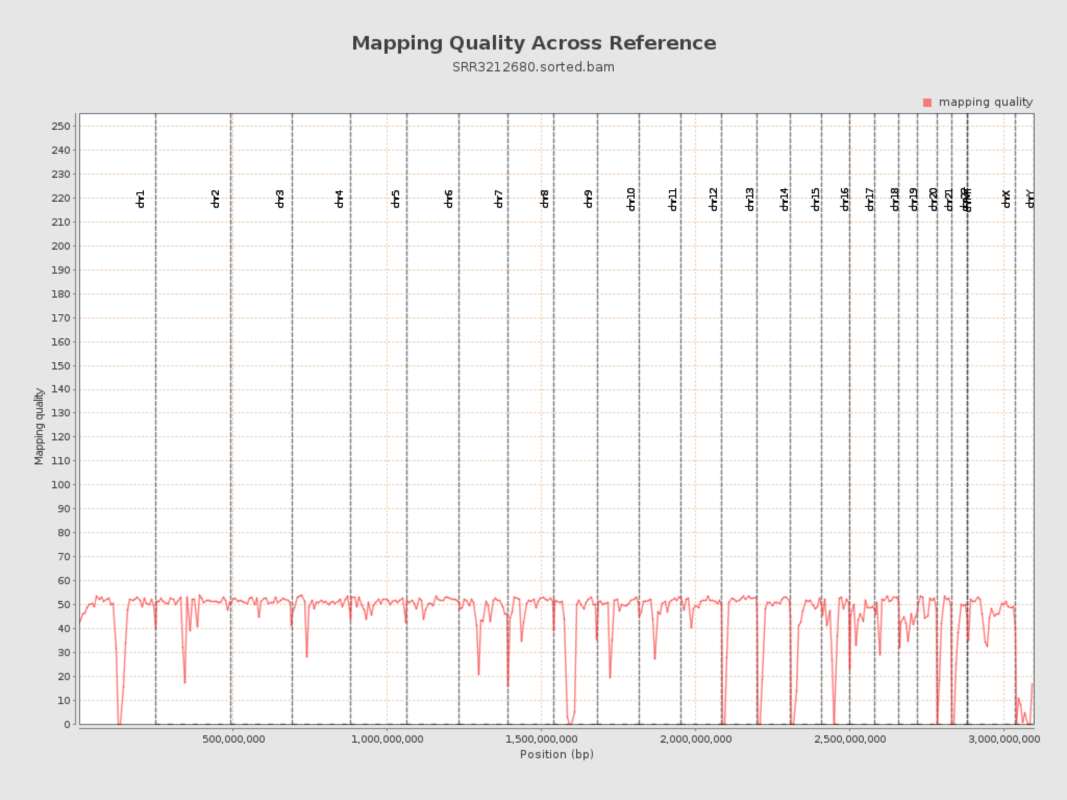
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram