Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 21:38:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013326.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_SRR6013326 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013326.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 21:38:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013326.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,993,155
Mapped reads	1,461,532 / 73.33%
Unmapped reads	531,623 / 26.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,302 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	57,072 / 2.86%
Duplication rate	3.3%
Clipped reads	974,203 / 48.88%

2.2. ACGT Content

Number/percentage of A's	25,552,138 / 28.89%
Number/percentage of C's	14,664,039 / 16.58%
Number/percentage of T's	27,455,839 / 31.04%
Number/percentage of G's	20,756,371 / 23.46%
Number/percentage of N's	30,697 / 0.03%
GC Percentage	40.04%

2.3. Coverage

Mean	0.0286

Standard Deviation	0.2218

2.4. Mapping Quality

Mean Mapping Quality	46.06

2.5. Mismatches and indels

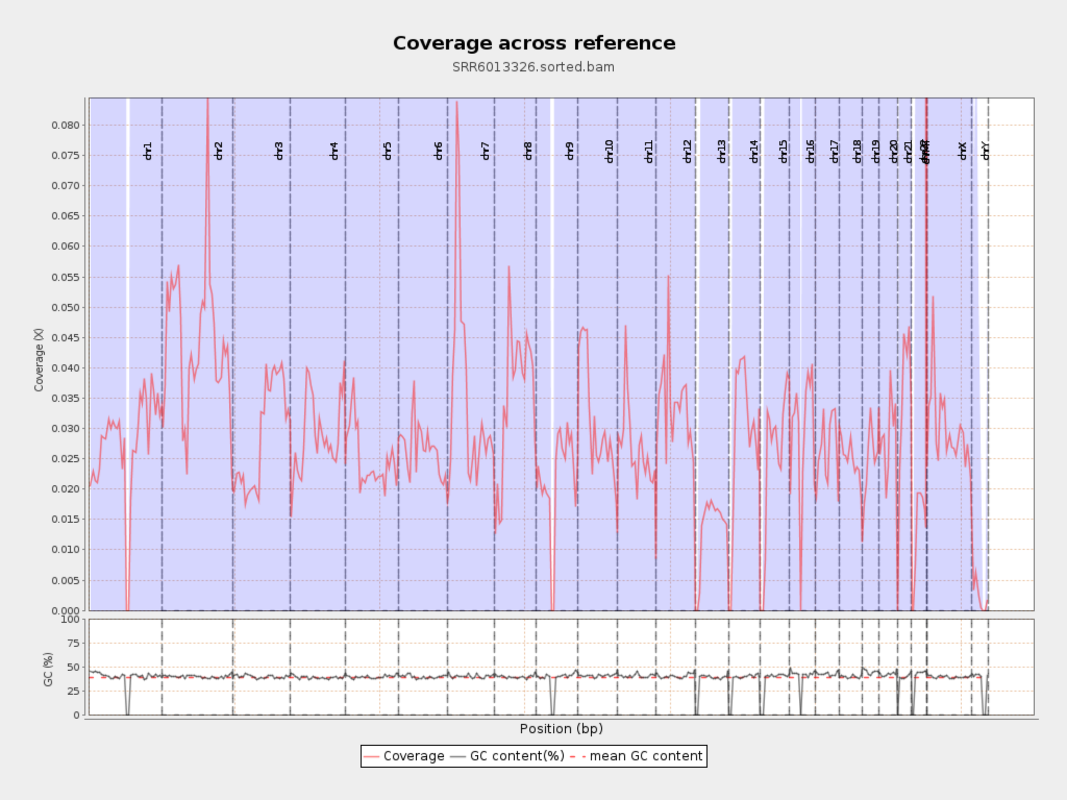
General error rate	1.09%
Mismatches	956,336
Insertions	5,615
Mapped reads with at least one insertion	0.38%
Deletions	23,769
Mapped reads with at least one deletion	1.61%
Homopolymer indels	49.23%

2.6. Chromosome stats

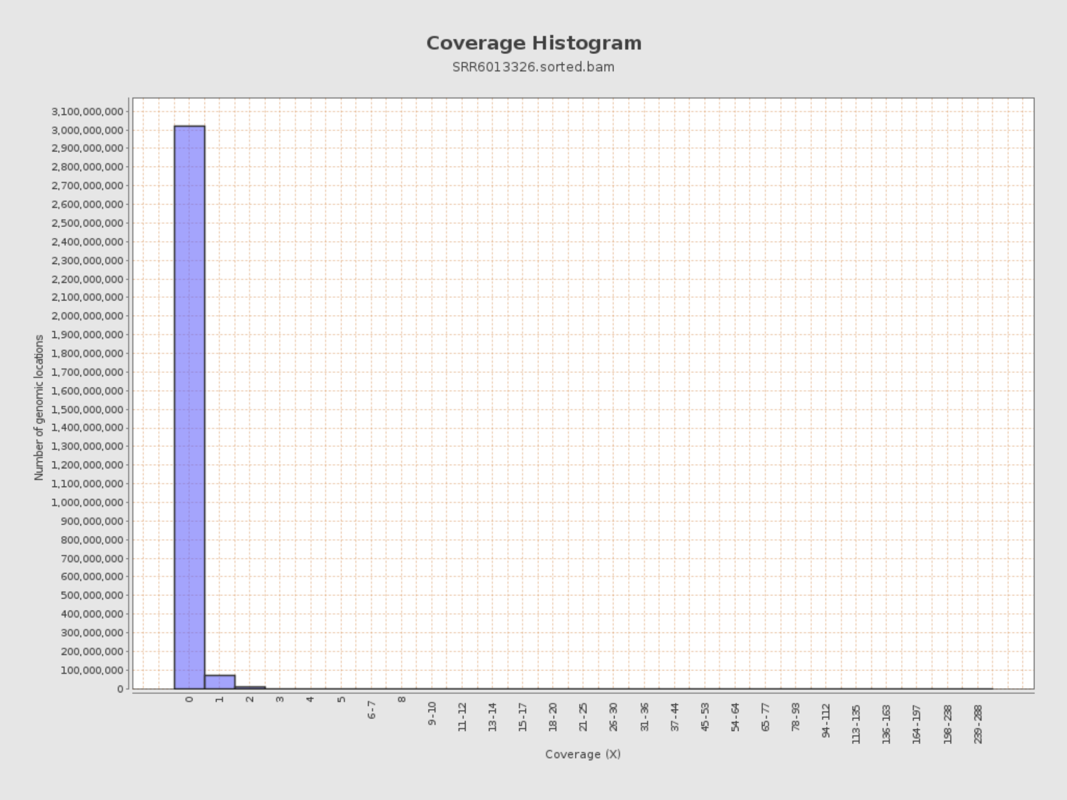
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6837027	0.0274	0.2779
chr2	243199373	10799427	0.0444	0.2707
chr3	198022430	5703579	0.0288	0.19
chr4	191154276	5546963	0.029	0.1945
chr5	180915260	4507753	0.0249	0.178
chr6	171115067	4544037	0.0266	0.209
chr7	159138663	5632675	0.0354	0.3429

chr8	146364022	5204522	0.0356	0.2747
chr9	141213431	3043250	0.0216	0.1862
chr10	135534747	4303090	0.0317	0.2161
chr11	135006516	3610625	0.0267	0.2021
chr12	133851895	4490912	0.0336	0.2069
chr13	115169878	1531594	0.0133	0.1264
chr14	107349540	3070057	0.0286	0.192
chr15	102531392	2553334	0.0249	0.1923
chr16	90354753	2643670	0.0293	0.1956
chr17	81195210	2143167	0.0264	0.1929
chr18	78077248	1961245	0.0251	0.2348
chr19	59128983	1484960	0.0251	0.2188
chr20	63025520	1775026	0.0282	0.1923
chr21	48129895	1638105	0.034	0.2138
chr22	51304566	658298	0.0128	0.1248
chrMT	16571	15414	0.9302	1.3028
chrX	155270560	4640954	0.0299	0.2029
chrY	59373566	158620	0.0027	0.0594

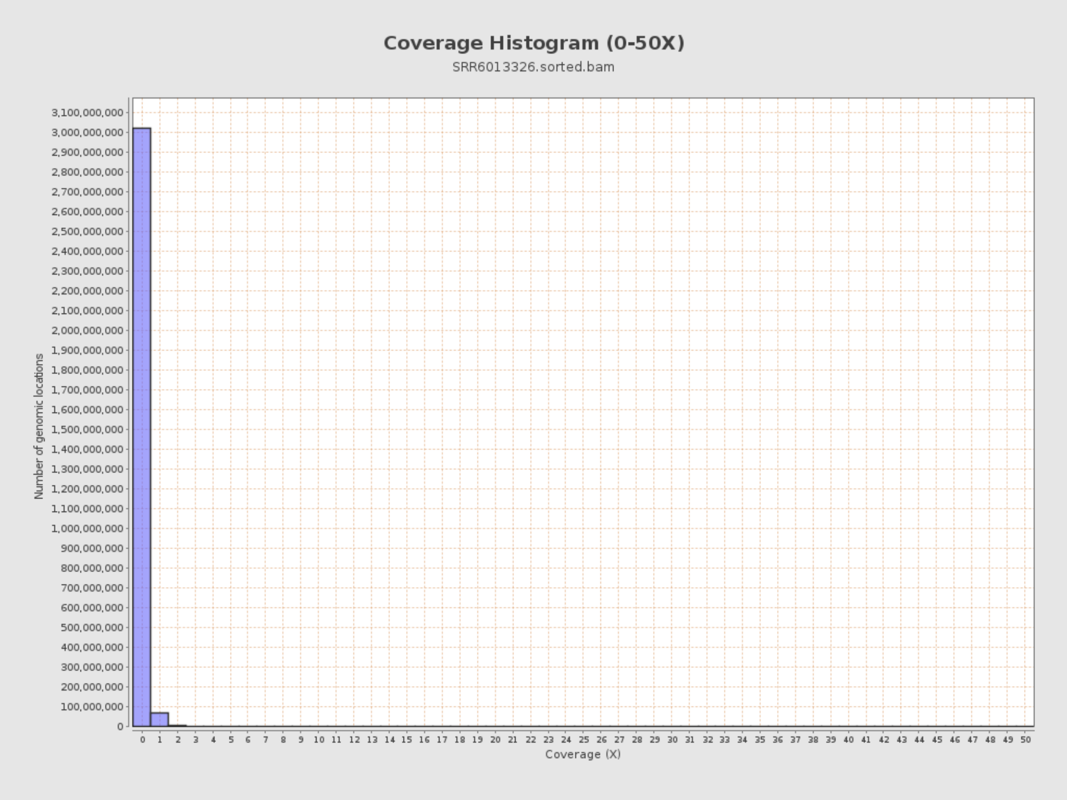
3. Results : Coverage across reference



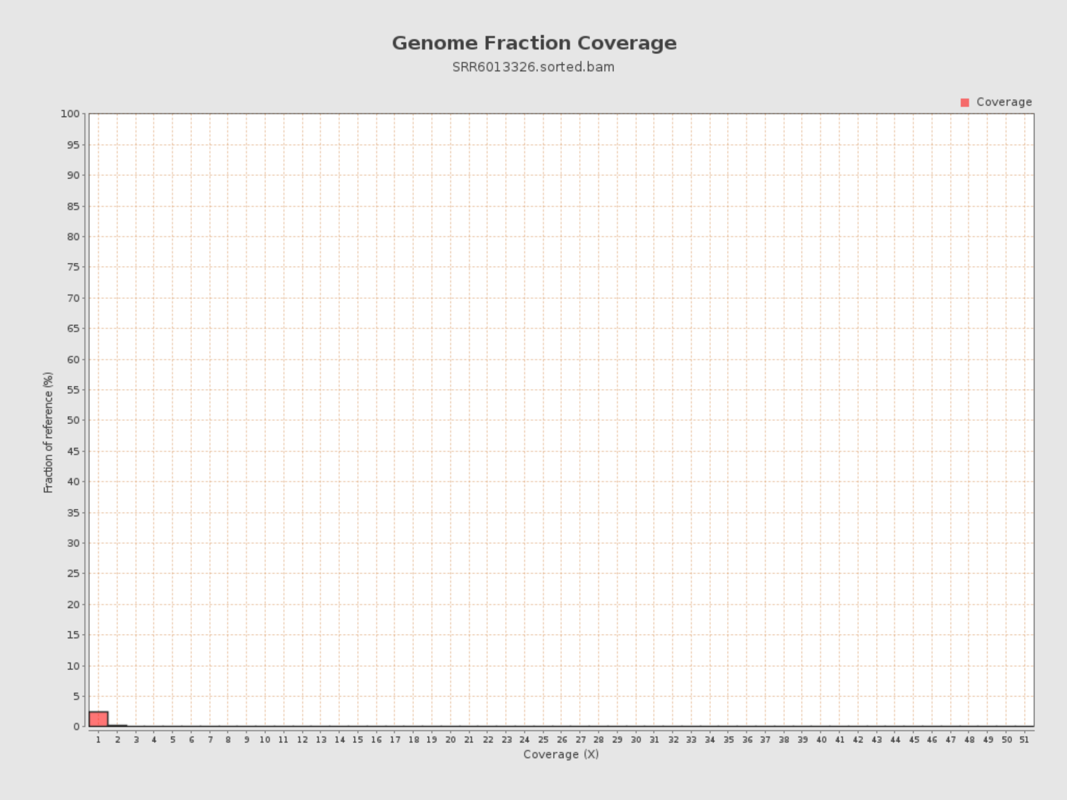
4. Results : Coverage Histogram



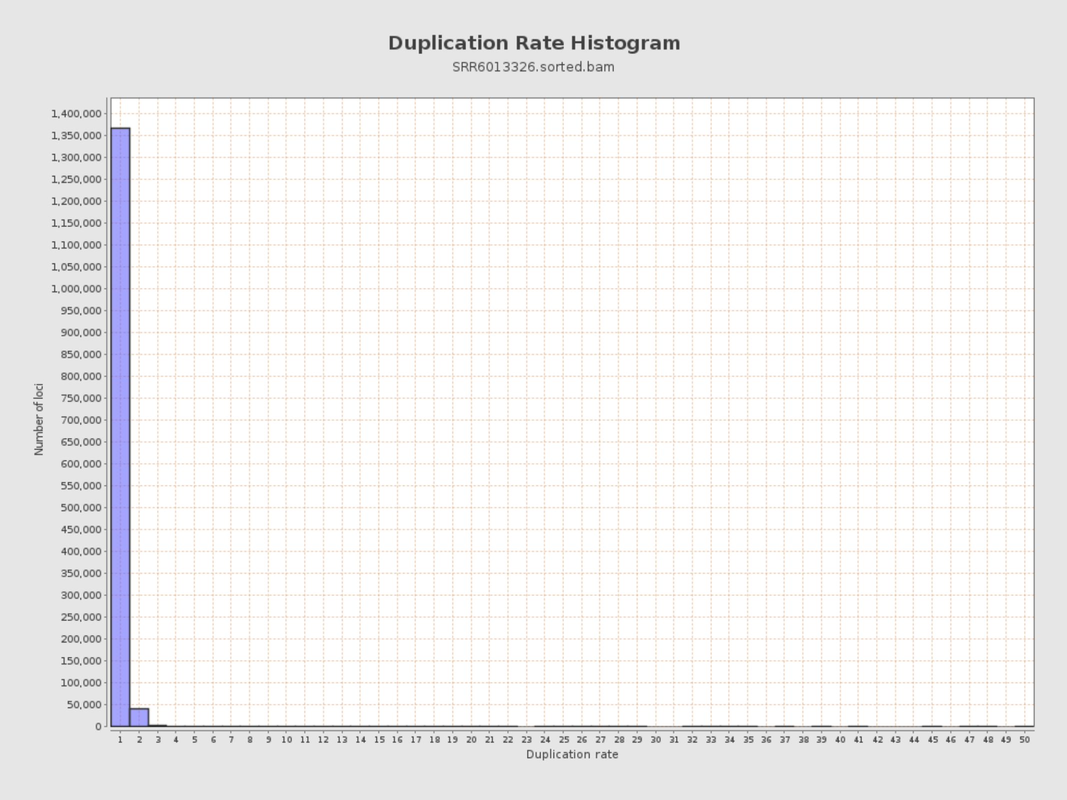
5. Results : Coverage Histogram (0-50X)



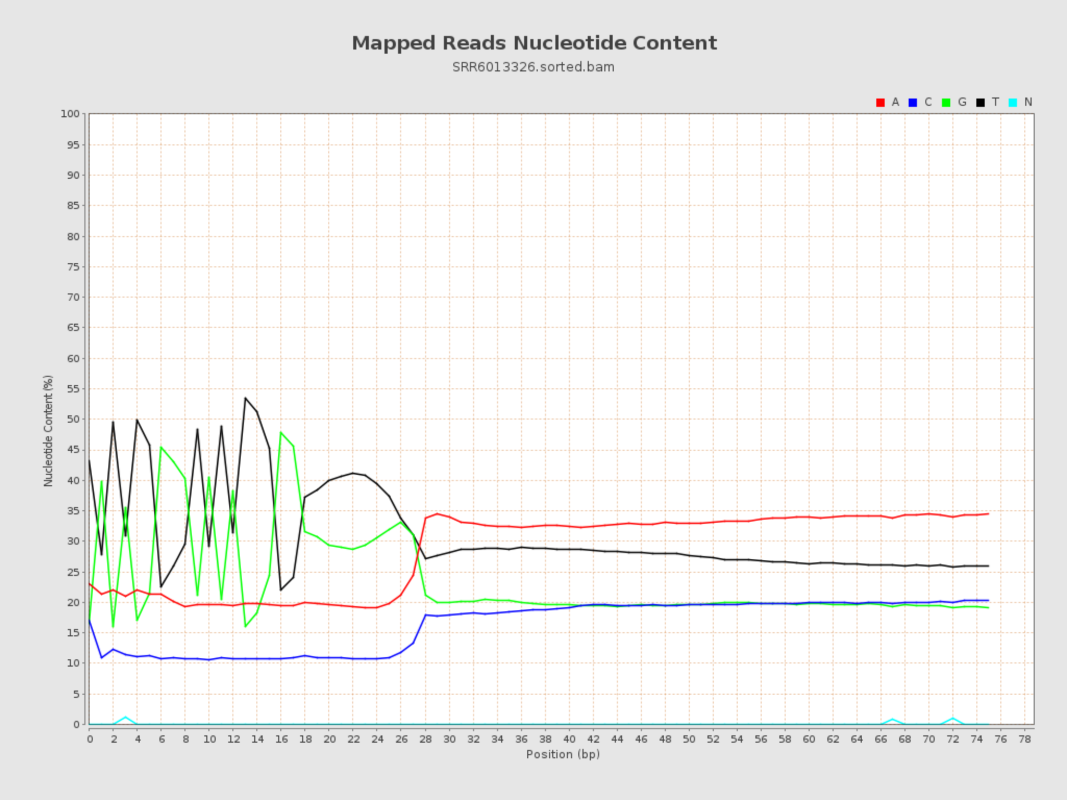
6. Results : Genome Fraction Coverage



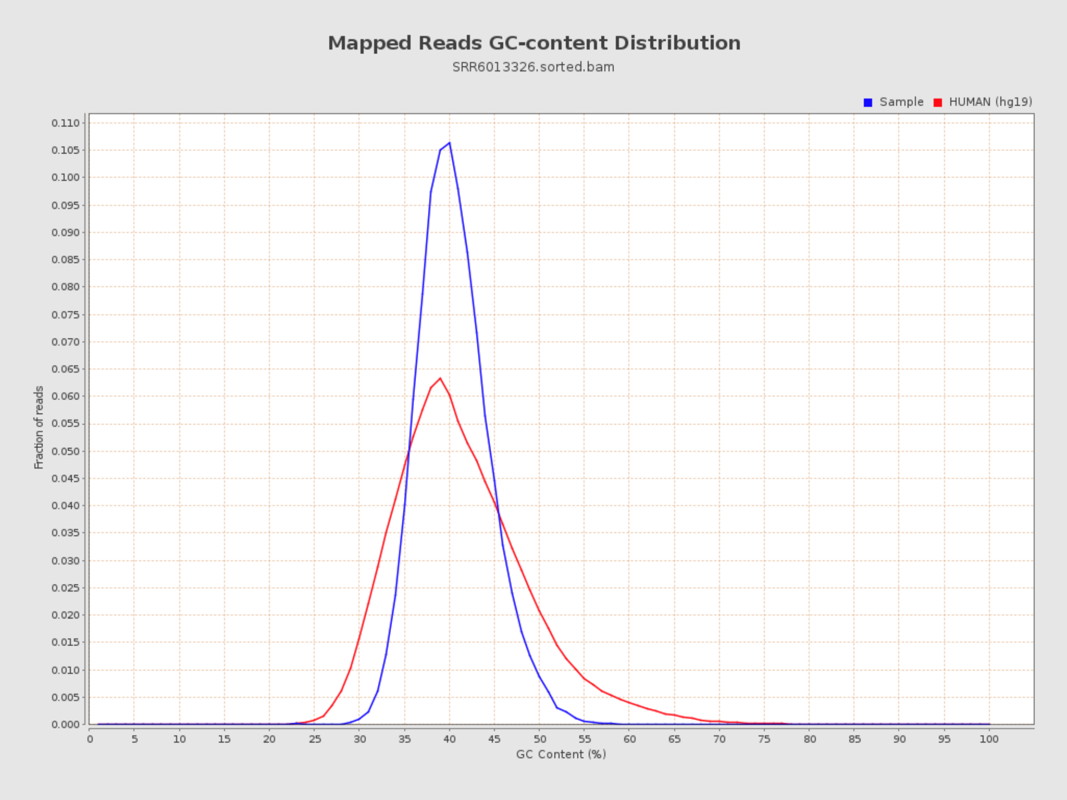
7. Results : Duplication Rate Histogram



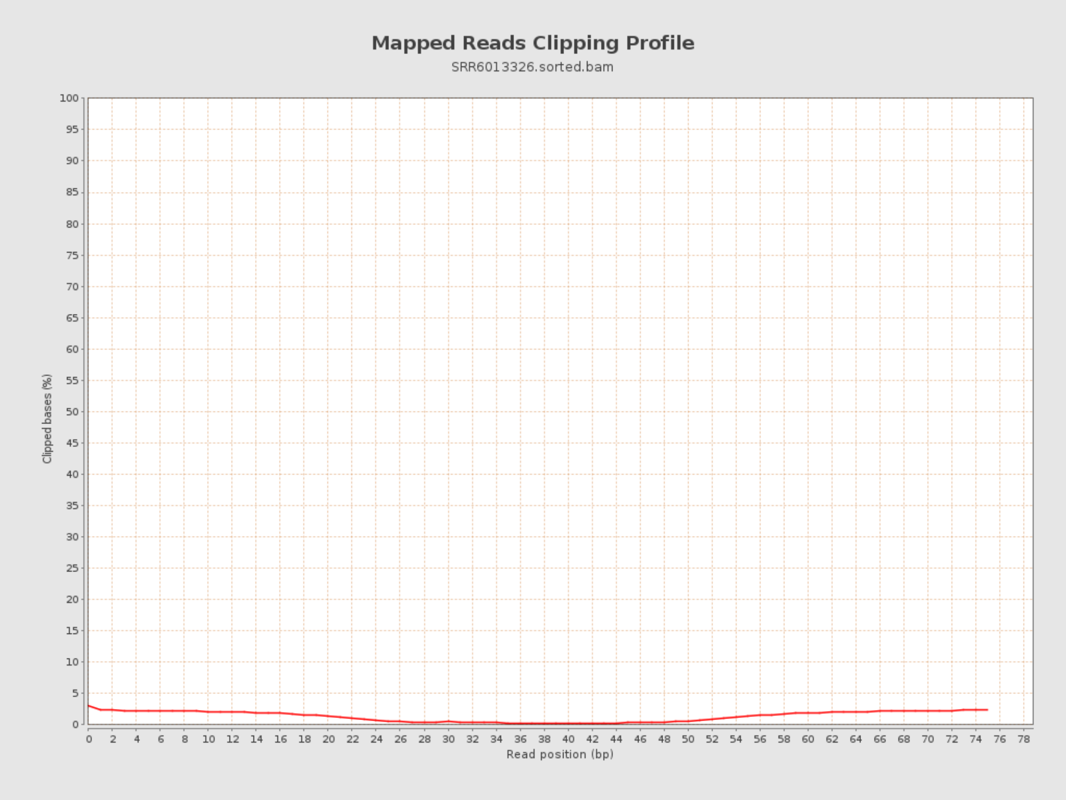
8. Results : Mapped Reads Nucleotide Content



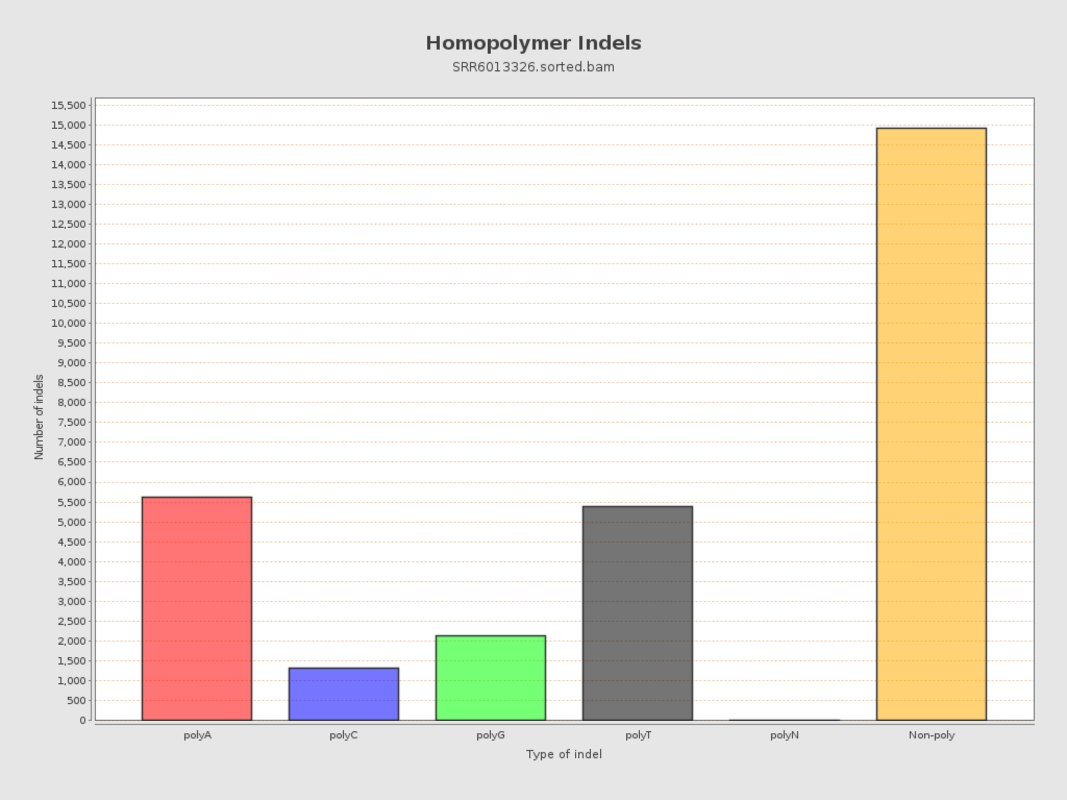
9. Results : Mapped Reads GC-content Distribution



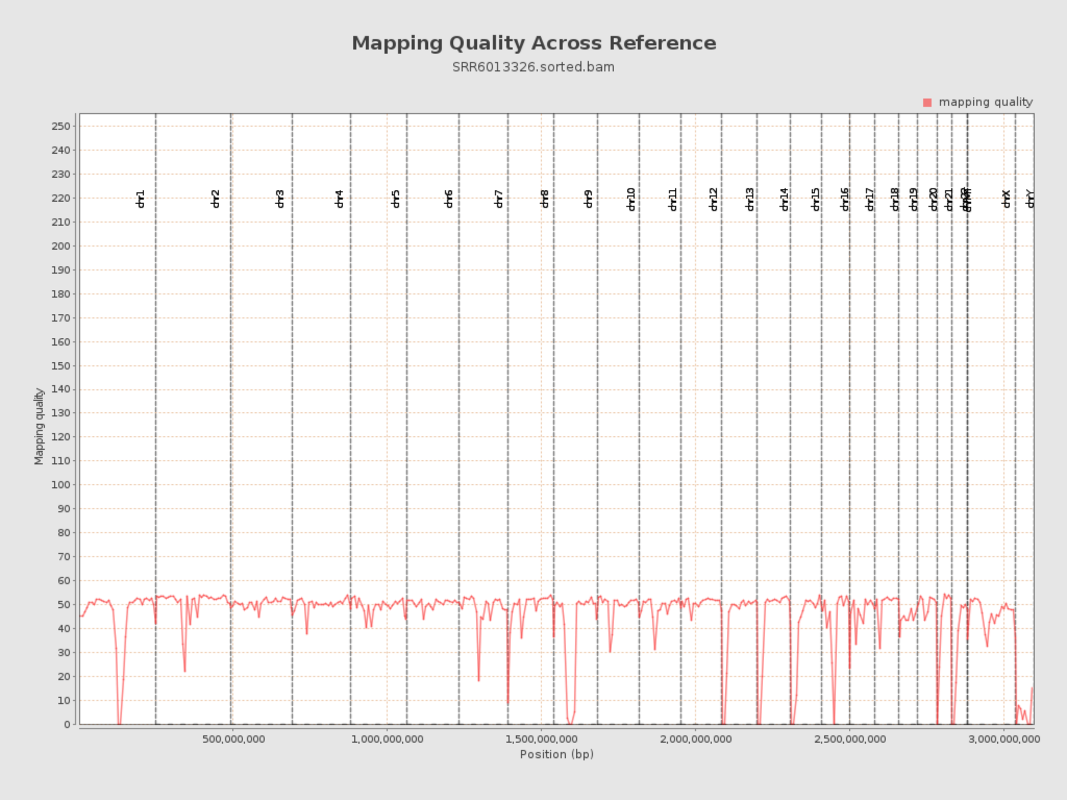
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram