Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 00:45:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063532.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_SRR6063532 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063532.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 00:45:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063532.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,581,855
Mapped reads	4,341,343 / 94.75%
Unmapped reads	240,512 / 5.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	42,665 / 0.93%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	803,625 / 17.54%
Duplication rate	14.51%
Clipped reads	2,387,025 / 52.1%

2.2. ACGT Content

Number/percentage of A's	72,628,752 / 26.07%
Number/percentage of C's	50,587,324 / 18.16%
Number/percentage of T's	90,078,844 / 32.33%
Number/percentage of G's	65,293,881 / 23.43%
Number/percentage of N's	31,668 / 0.01%
GC Percentage	41.59%

2.3. Coverage

Mean	0.09

Standard Deviation	0.8608

2.4. Mapping Quality

Mean Mapping Quality	45.22

2.5. Mismatches and indels

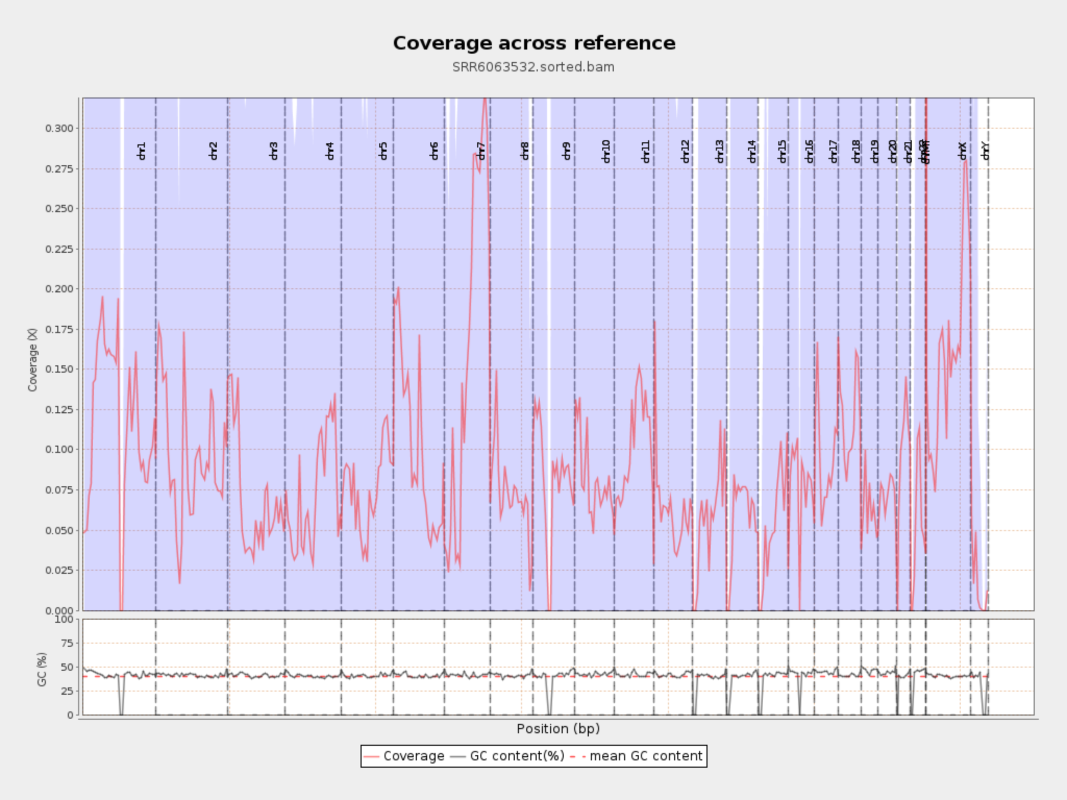
General error rate	0.54%
Mismatches	1,480,307
Insertions	17,972
Mapped reads with at least one insertion	0.41%
Deletions	60,116
Mapped reads with at least one deletion	1.37%
Homopolymer indels	44.12%

2.6. Chromosome stats

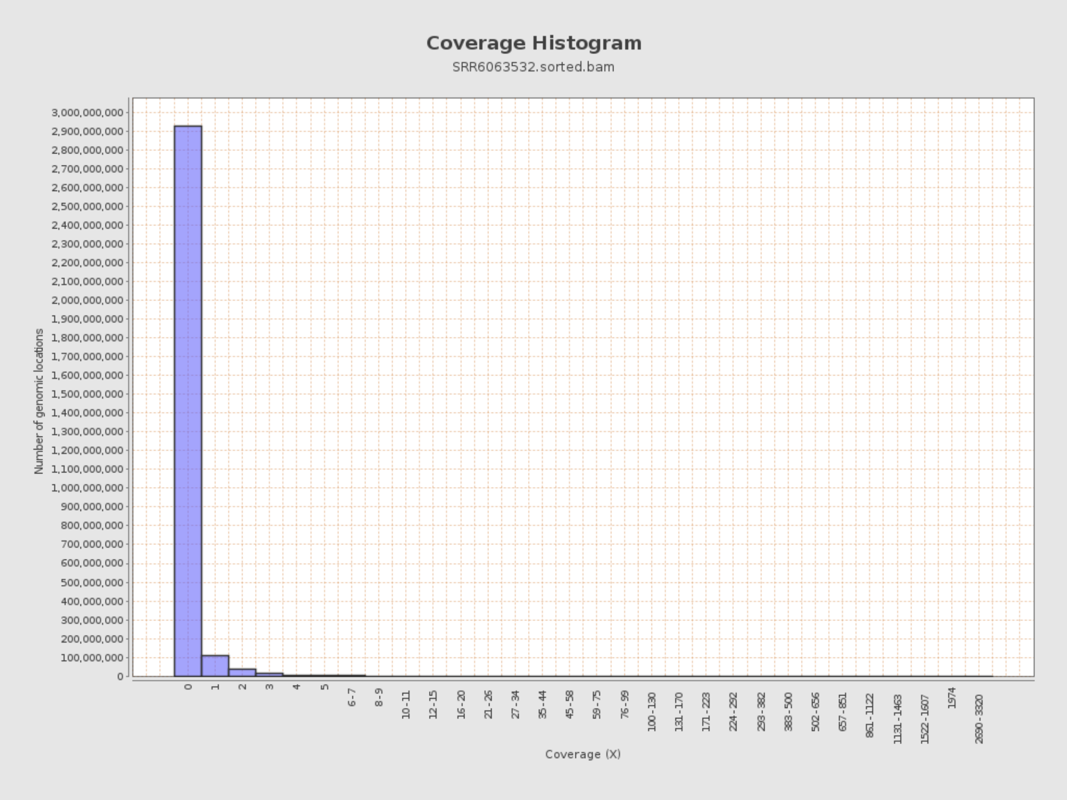
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29127128	0.1169	1.4417
chr2	243199373	23756936	0.0977	1.6601
chr3	198022430	13877064	0.0701	0.4029
chr4	191154276	13997548	0.0732	0.5099
chr5	180915260	13831544	0.0765	0.4251
chr6	171115067	17728542	0.1036	0.6633
chr7	159138663	26199367	0.1646	1.1086

chr8	146364022	10569037	0.0722	0.8397
chr9	141213431	11670769	0.0826	0.664
chr10	135534747	11189943	0.0826	0.6206
chr11	135006516	13823195	0.1024	0.6597
chr12	133851895	8653997	0.0647	0.4164
chr13	115169878	6689595	0.0581	0.4087
chr14	107349540	6252048	0.0582	0.391
chr15	102531392	5330944	0.052	0.3783
chr16	90354753	6823926	0.0755	0.455
chr17	81195210	7770312	0.0957	0.5522
chr18	78077248	9445057	0.121	1.2274
chr19	59128983	3731014	0.0631	1.0465
chr20	63025520	4587063	0.0728	0.4455
chr21	48129895	4683119	0.0973	0.5205
chr22	51304566	2700171	0.0526	0.3401
chrMT	16571	456662	27.5579	17.735
chrX	155270560	24872636	0.1602	0.6997
chrY	59373566	958377	0.0161	0.5206

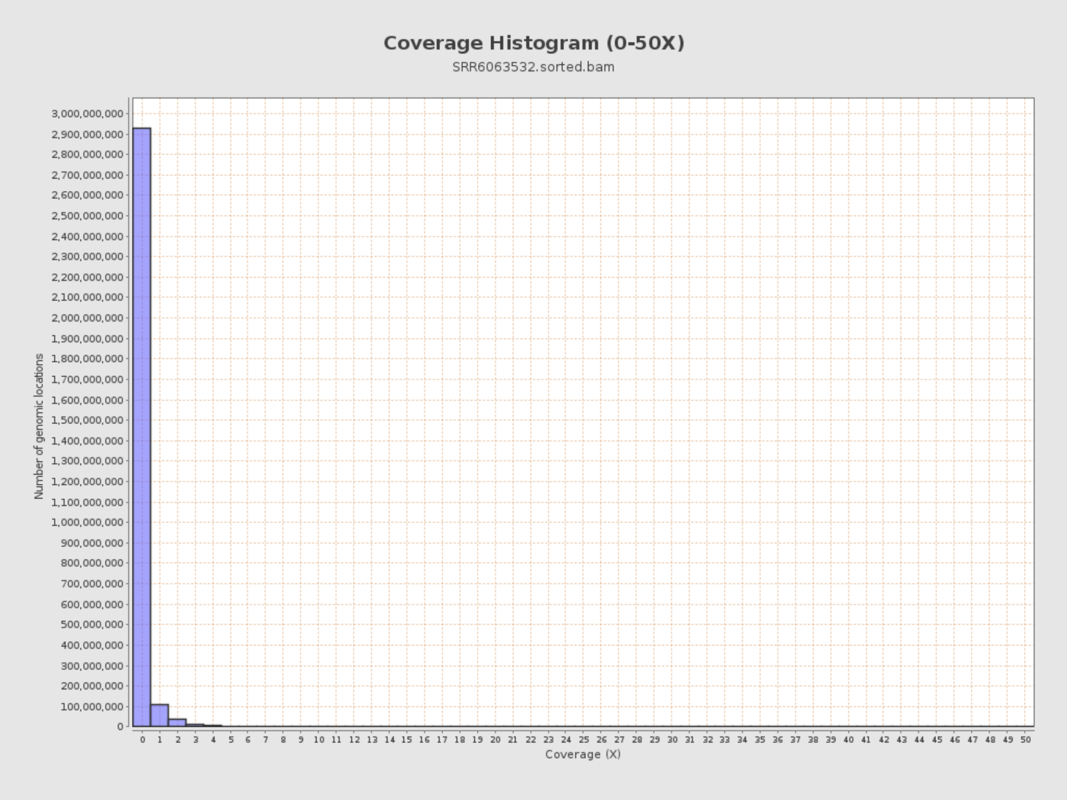
3. Results : Coverage across reference



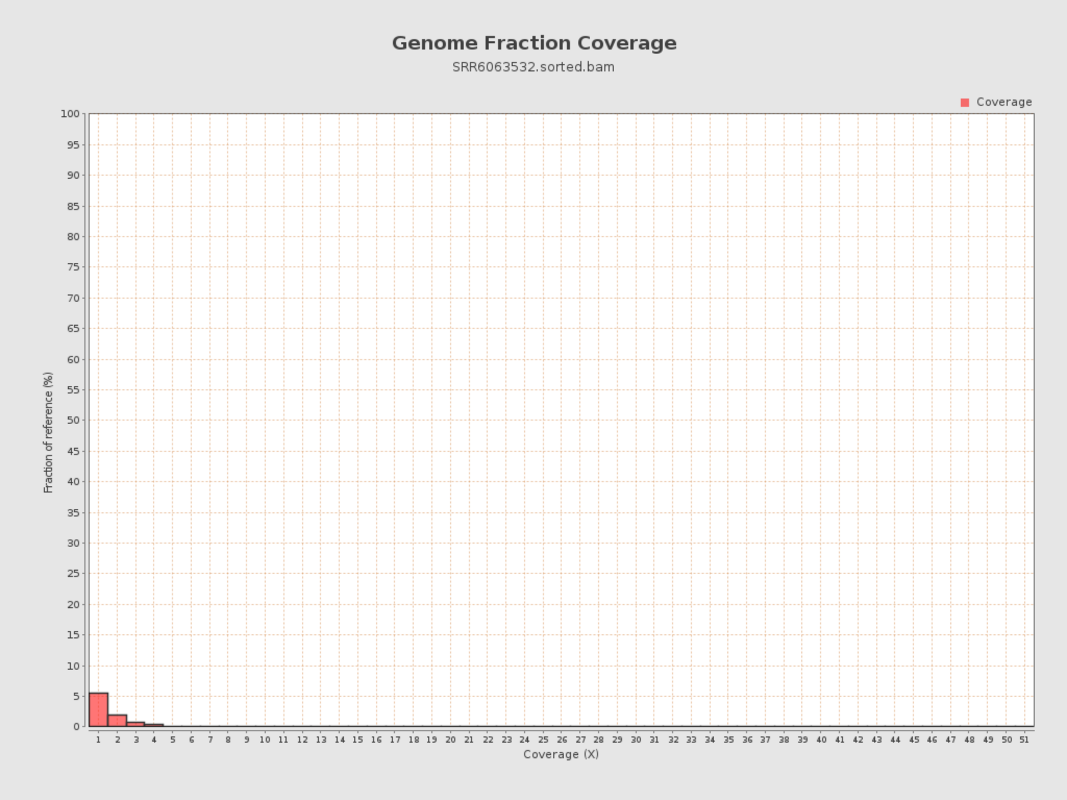
4. Results : Coverage Histogram



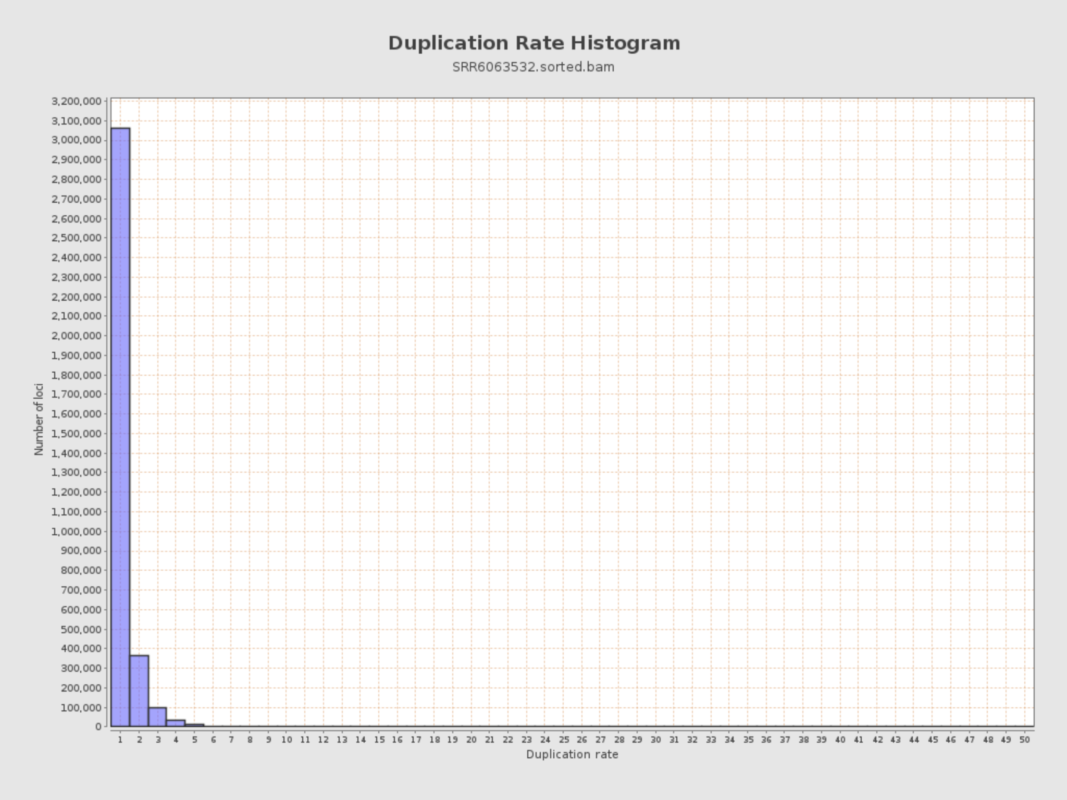
5. Results : Coverage Histogram (0-50X)



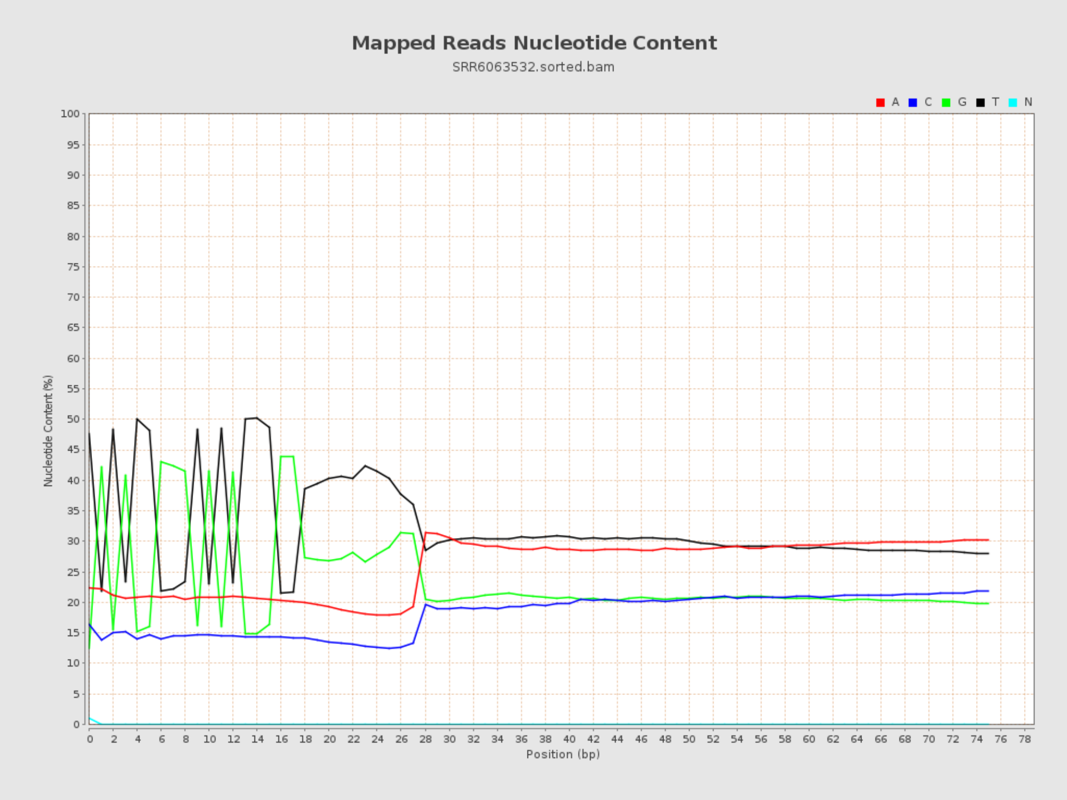
6. Results : Genome Fraction Coverage



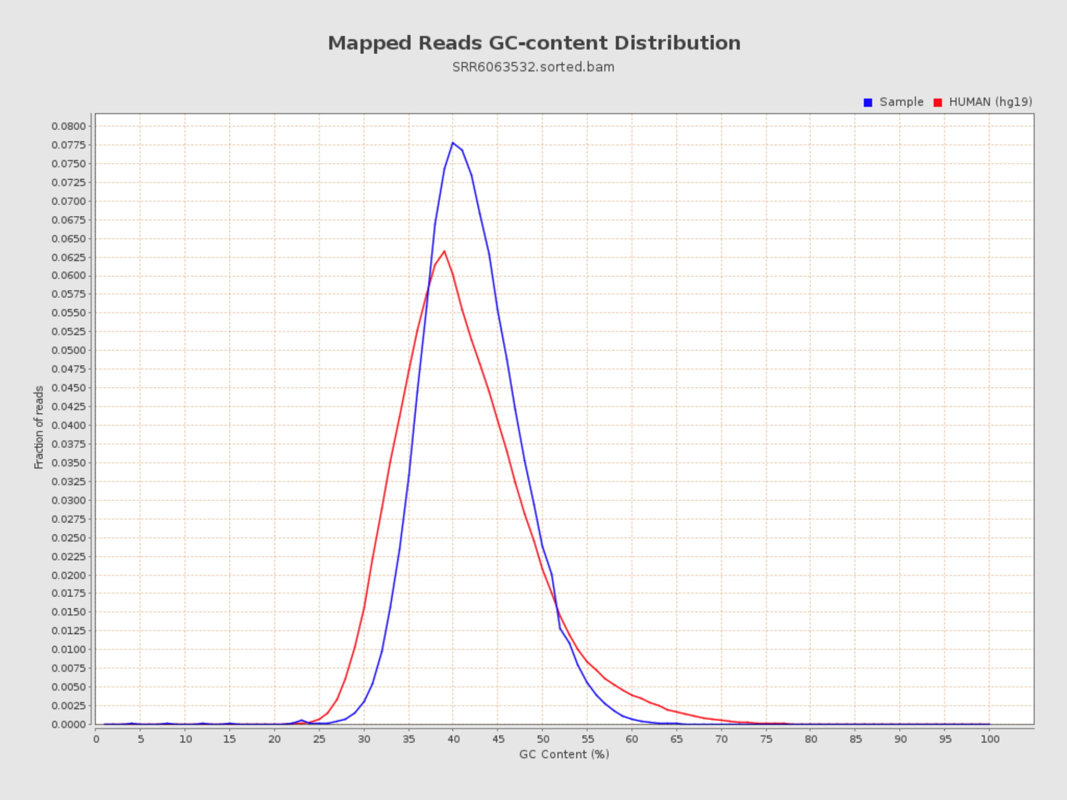
7. Results : Duplication Rate Histogram



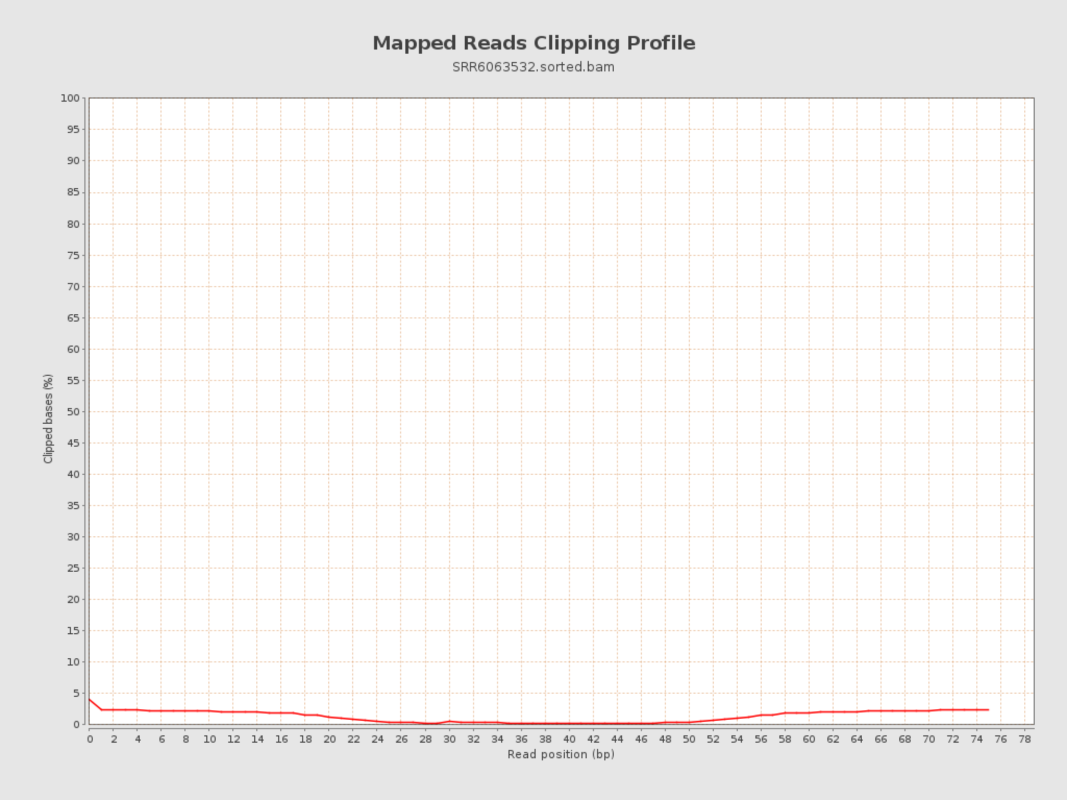
8. Results : Mapped Reads Nucleotide Content



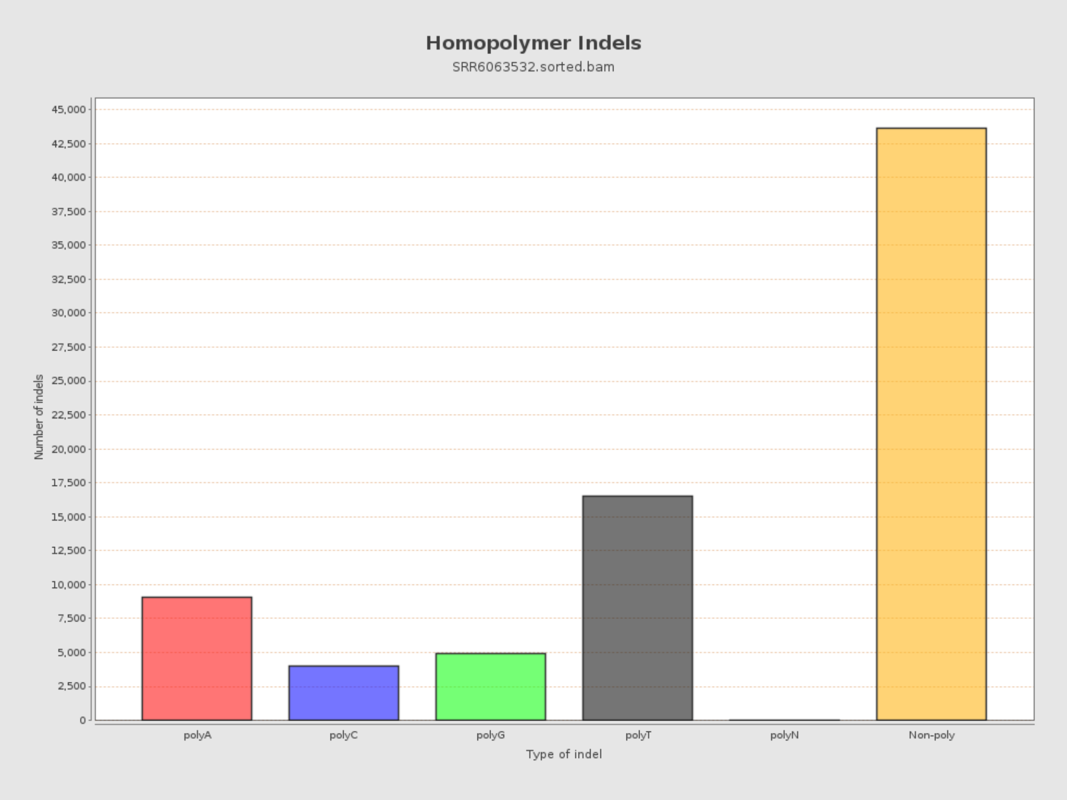
9. Results : Mapped Reads GC-content Distribution



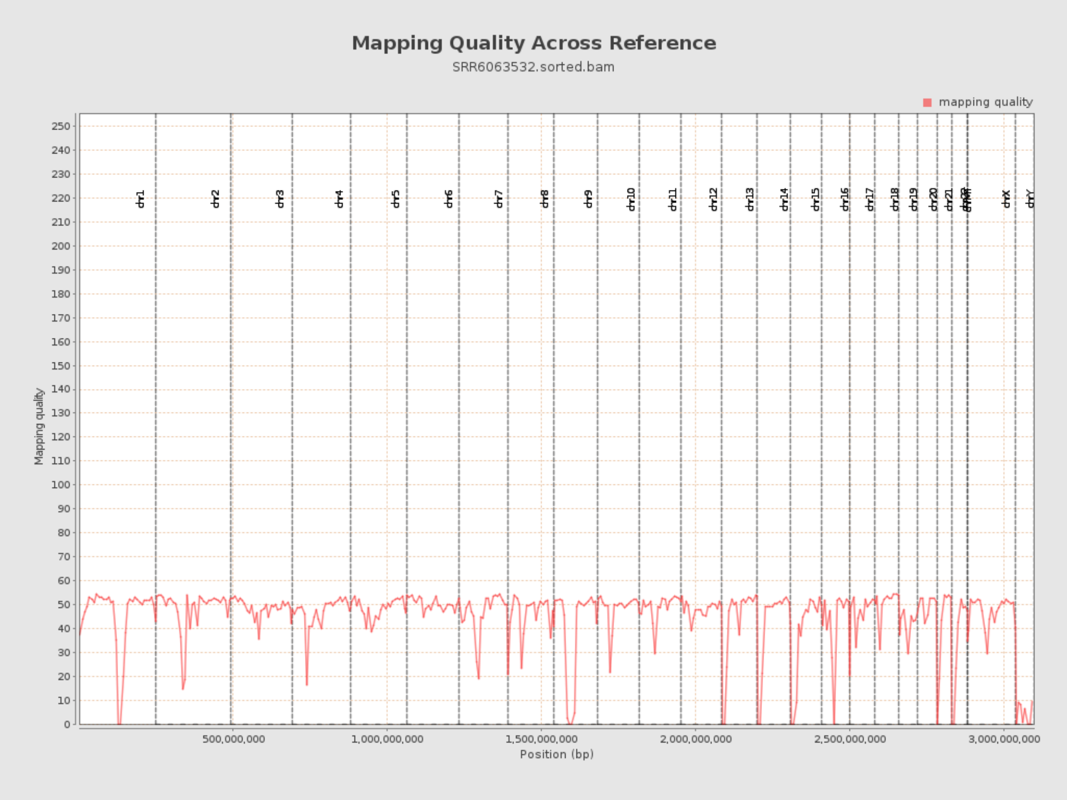
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram