Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 20:16:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524617.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_SRR10524617 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524617.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 20:16:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524617.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,047,276
Mapped reads	3,761,746 / 92.95%
Unmapped reads	285,530 / 7.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,996 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	293,861 / 7.26%
Duplication rate	5.93%
Clipped reads	3,758,489 / 92.86%

2.2. ACGT Content

Number/percentage of A's	55,718,863 / 25.45%
Number/percentage of C's	42,316,765 / 19.33%
Number/percentage of T's	68,727,717 / 31.39%
Number/percentage of G's	52,172,664 / 23.83%
Number/percentage of N's	1,431 / 0%
GC Percentage	43.16%

2.3. Coverage

Mean	0.0707

Standard Deviation	0.5341

2.4. Mapping Quality

Mean Mapping Quality	45.28

2.5. Mismatches and indels

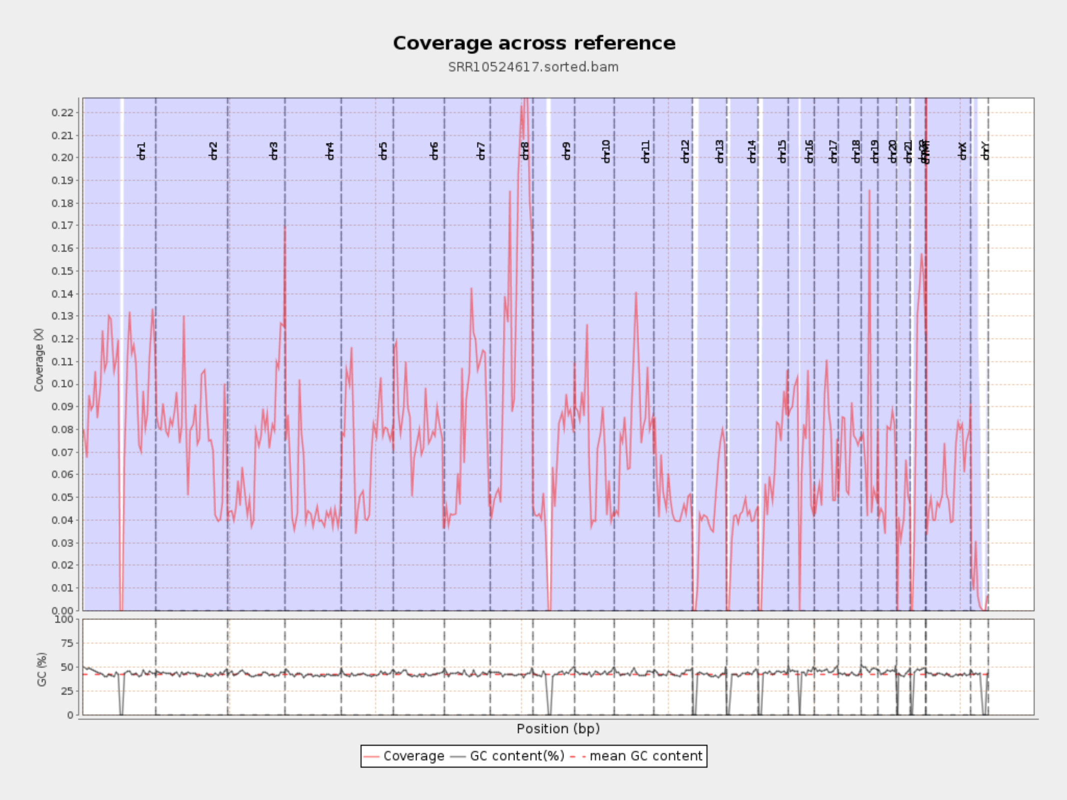
General error rate	0.48%
Mismatches	1,023,255
Insertions	16,150
Mapped reads with at least one insertion	0.43%
Deletions	41,650
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.85%

2.6. Chromosome stats

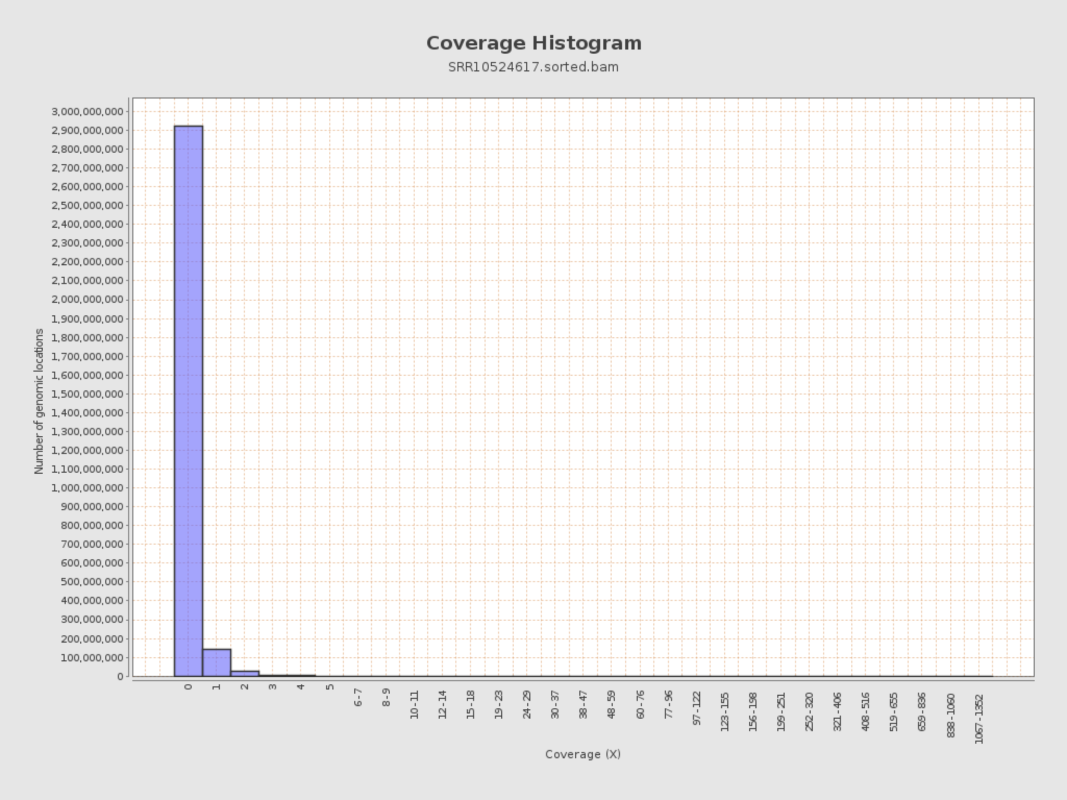
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23924603	0.096	1.0324
chr2	243199373	19223343	0.079	0.6281
chr3	198022430	13924028	0.0703	0.3303
chr4	191154276	9555878	0.05	0.3457
chr5	180915260	13190862	0.0729	0.3359
chr6	171115067	14103873	0.0824	0.3913
chr7	159138663	12894328	0.081	0.7139

chr8	146364022	19515786	0.1333	0.6833
chr9	141213431	8102837	0.0574	0.4664
chr10	135534747	9448435	0.0697	0.5282
chr11	135006516	11139127	0.0825	0.4916
chr12	133851895	6680807	0.0499	0.2901
chr13	115169878	4984820	0.0433	0.2619
chr14	107349540	3917447	0.0365	0.2598
chr15	102531392	5873800	0.0573	0.3232
chr16	90354753	6587387	0.0729	0.3657
chr17	81195210	5466035	0.0673	0.3352
chr18	78077248	5647871	0.0723	0.7862
chr19	59128983	4374712	0.074	0.6863
chr20	63025520	3962370	0.0629	0.3236
chr21	48129895	2016535	0.0419	0.3003
chr22	51304566	4960351	0.0967	0.3905
chrMT	16571	14214	0.8578	1.1463
chrX	155270560	8989525	0.0579	0.376
chrY	59373566	509490	0.0086	0.2288

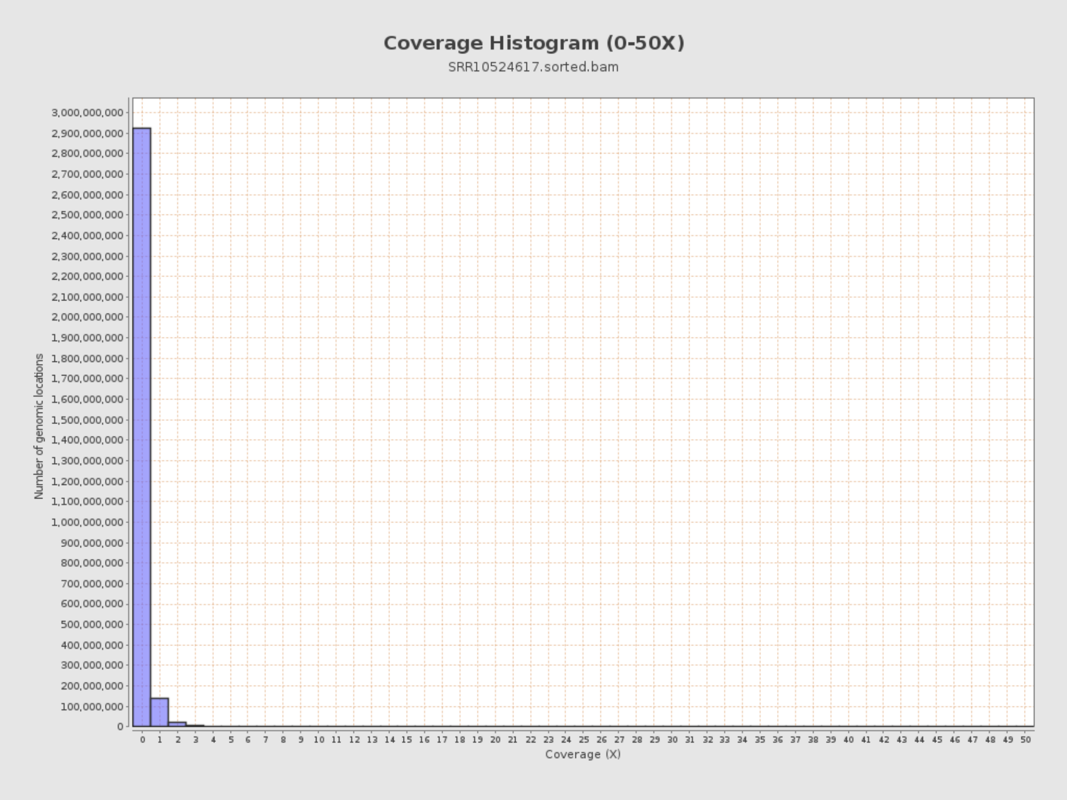
3. Results : Coverage across reference



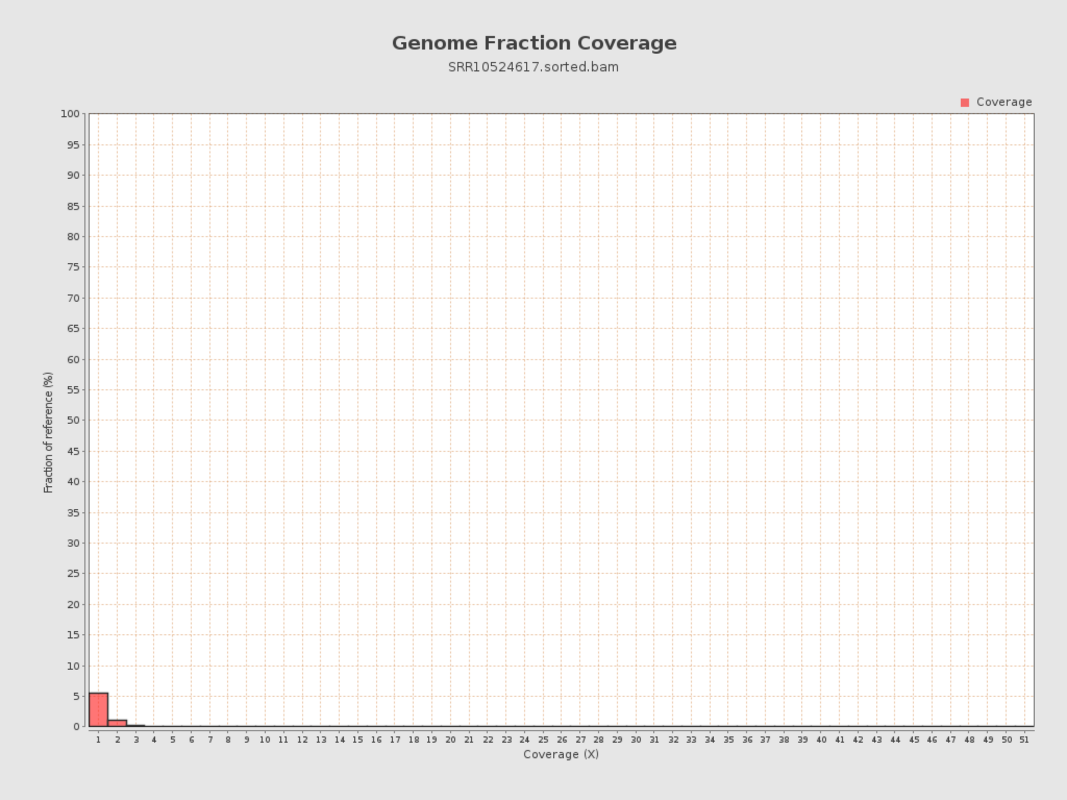
4. Results : Coverage Histogram



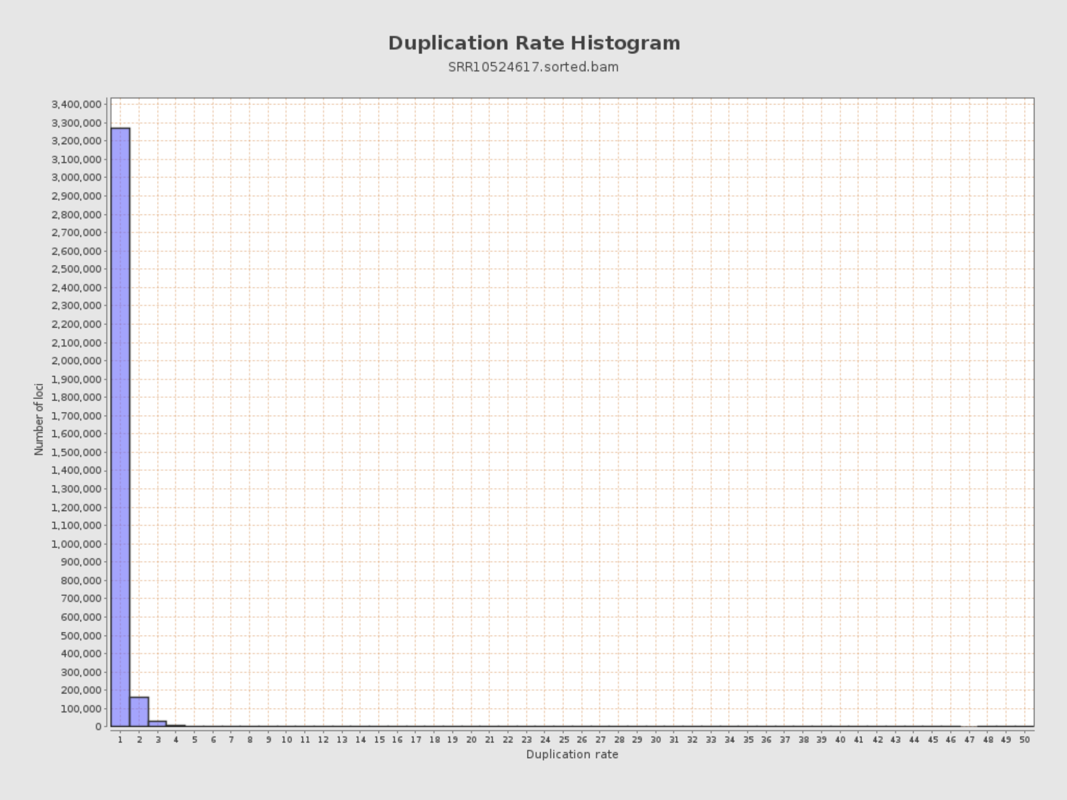
5. Results : Coverage Histogram (0-50X)



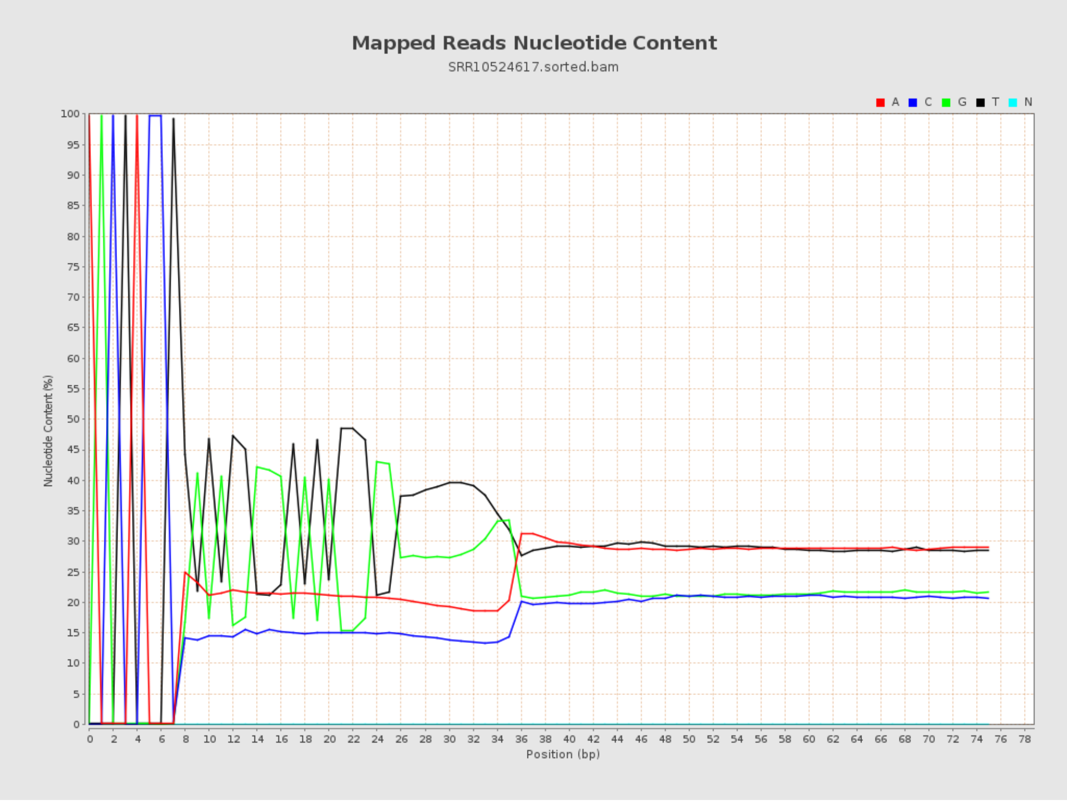
6. Results : Genome Fraction Coverage



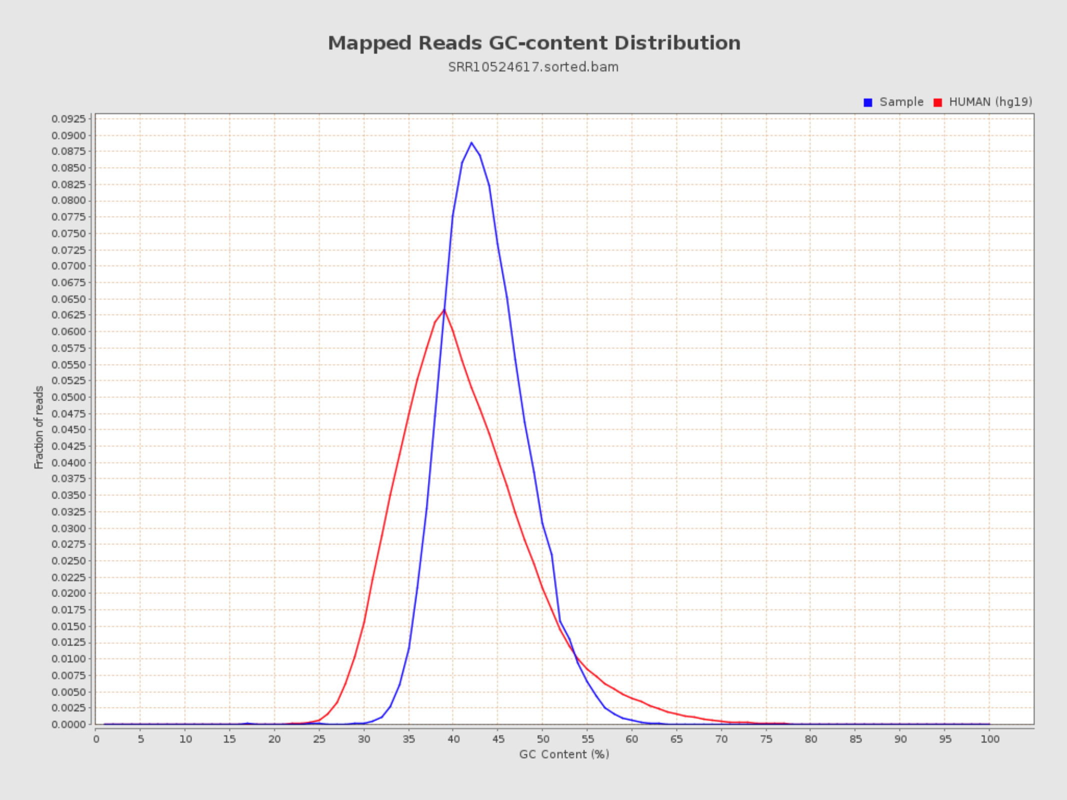
7. Results : Duplication Rate Histogram



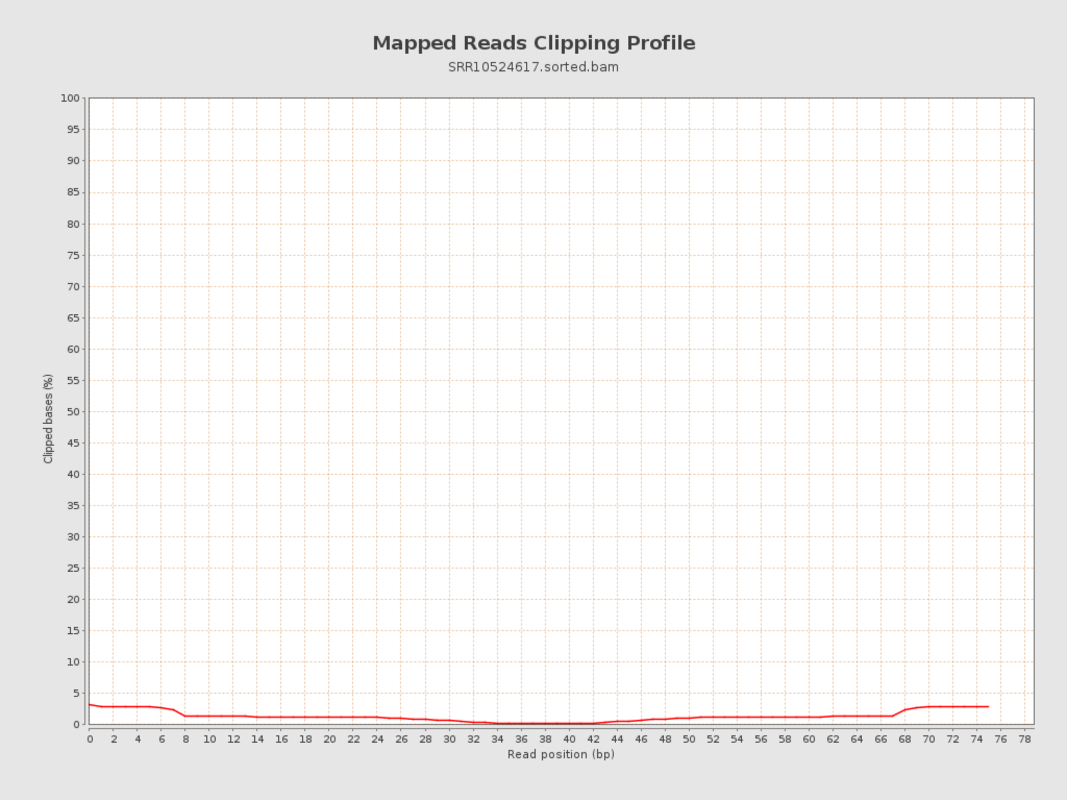
8. Results : Mapped Reads Nucleotide Content



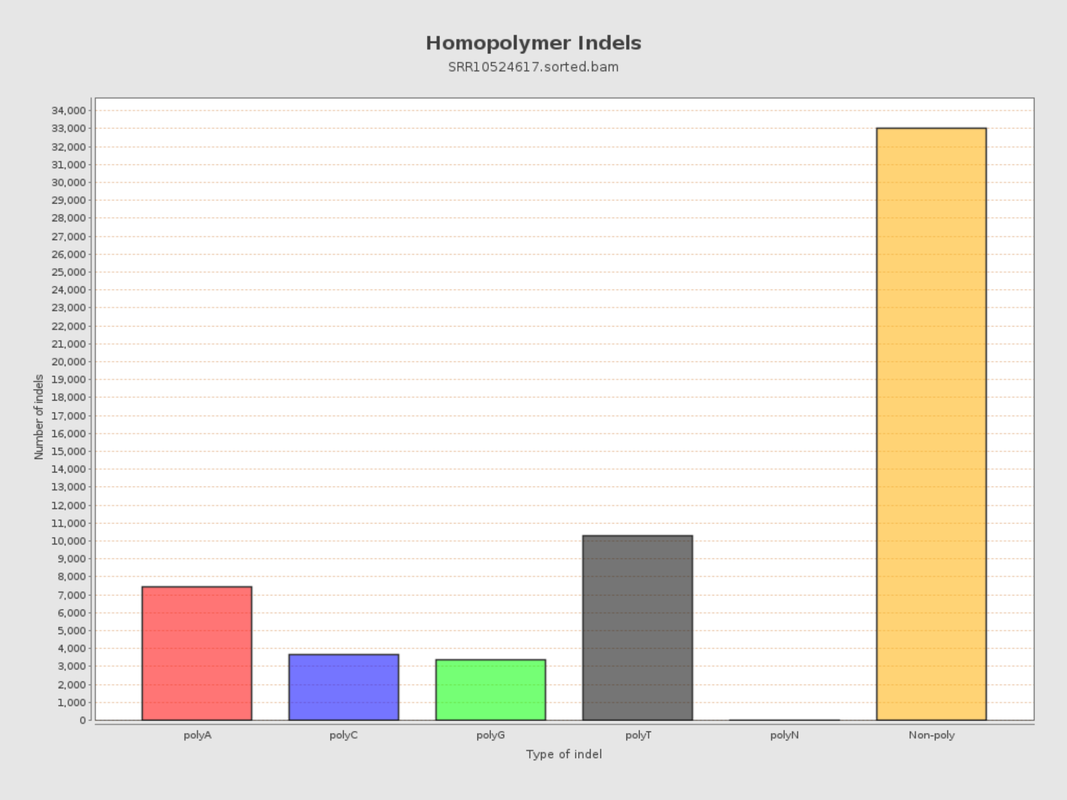
9. Results : Mapped Reads GC-content Distribution



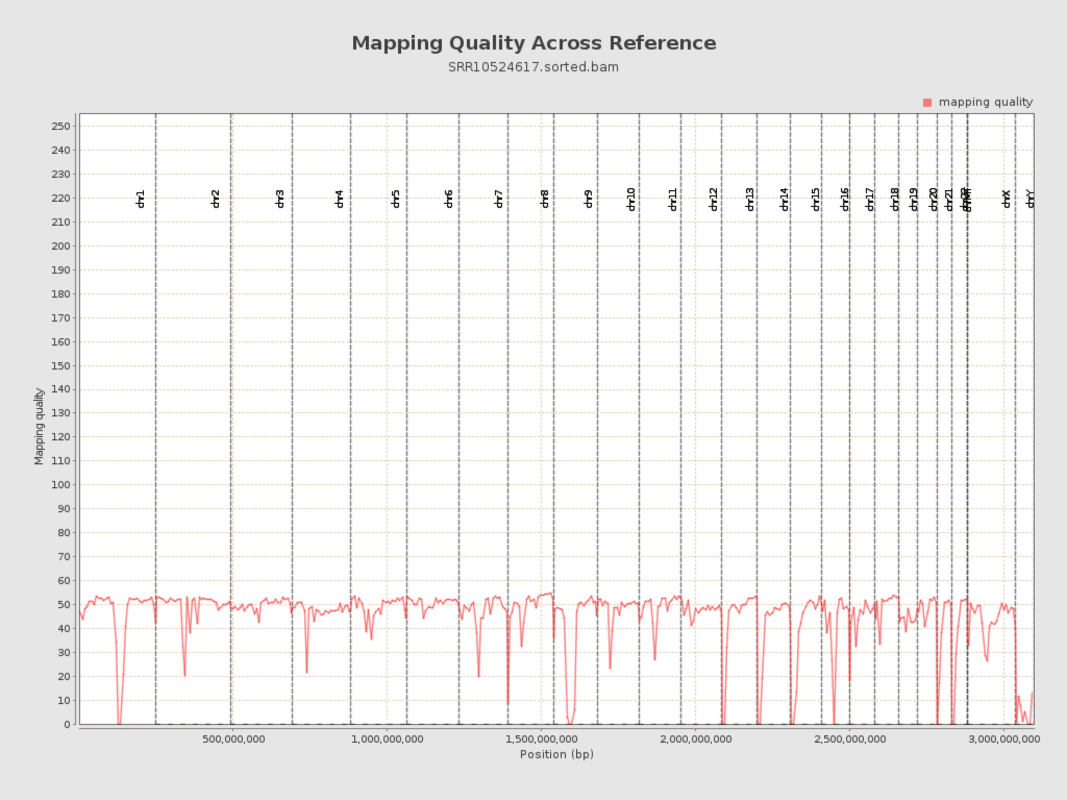
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram