Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 22:25:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524317.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_SRR10524317 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524317.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 22:25:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524317.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,997,777
Mapped reads	2,757,007 / 91.97%
Unmapped reads	240,770 / 8.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,776 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	130,597 / 4.36%
Duplication rate	3.43%
Clipped reads	2,758,560 / 92.02%

2.2. ACGT Content

Number/percentage of A's	40,514,511 / 25.16%
Number/percentage of C's	31,959,389 / 19.85%
Number/percentage of T's	49,988,308 / 31.05%
Number/percentage of G's	38,518,787 / 23.92%
Number/percentage of N's	23,261 / 0.01%
GC Percentage	43.77%

2.3. Coverage

Mean	0.052

Standard Deviation	0.4374

2.4. Mapping Quality

Mean Mapping Quality	44.17

2.5. Mismatches and indels

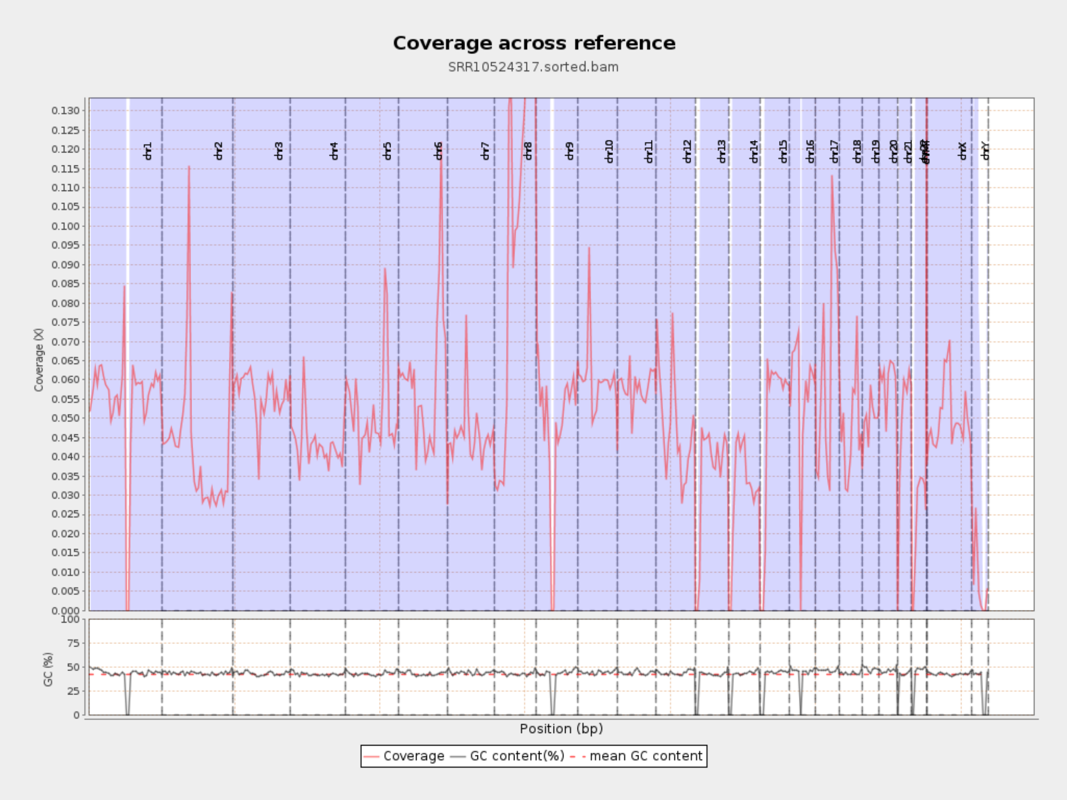
General error rate	0.52%
Mismatches	818,883
Insertions	12,930
Mapped reads with at least one insertion	0.47%
Deletions	28,538
Mapped reads with at least one deletion	1.03%
Homopolymer indels	41.25%

2.6. Chromosome stats

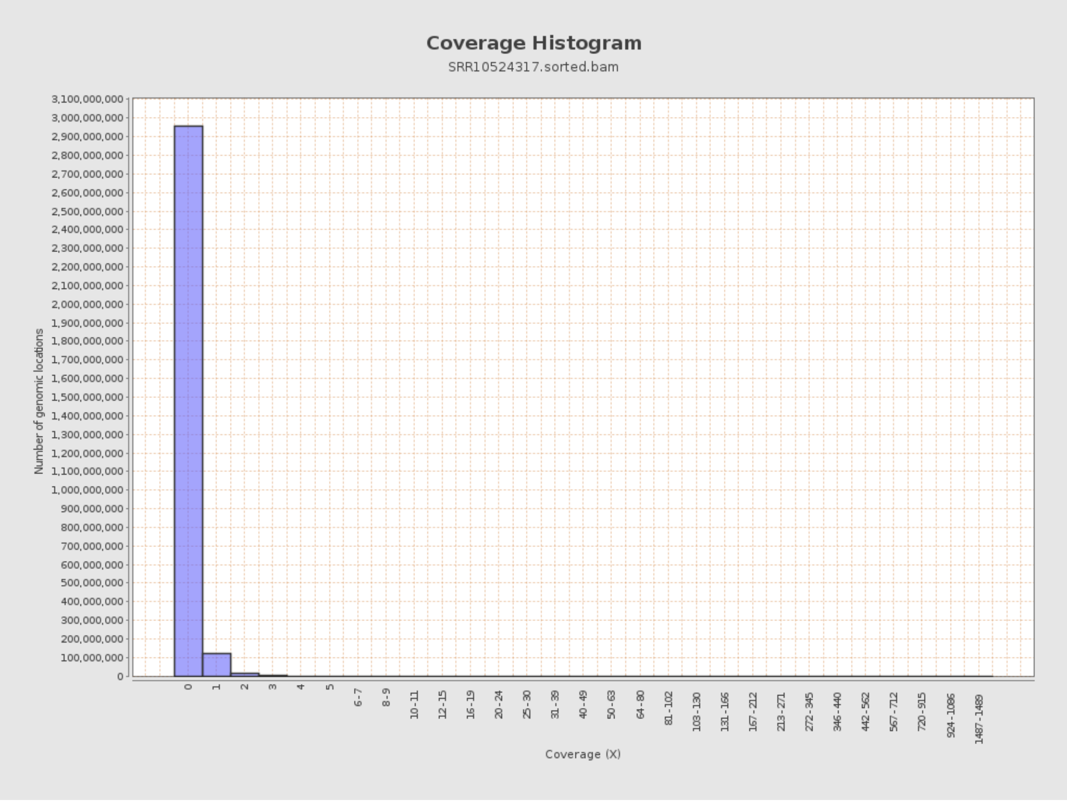
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13595302	0.0545	0.8251
chr2	243199373	10339754	0.0425	0.6445
chr3	198022430	11142507	0.0563	0.2696
chr4	191154276	8267308	0.0432	0.2745
chr5	180915260	9351732	0.0517	0.2602
chr6	171115067	10180721	0.0595	0.3091
chr7	159138663	7315395	0.046	0.5438

chr8	146364022	16886519	0.1154	0.5407
chr9	141213431	6708870	0.0475	0.3312
chr10	135534747	8168103	0.0603	0.411
chr11	135006516	7815206	0.0579	0.3714
chr12	133851895	6381257	0.0477	0.256
chr13	115169878	4064733	0.0353	0.2145
chr14	107349540	3359635	0.0313	0.2153
chr15	102531392	4989896	0.0487	0.2576
chr16	90354753	5103813	0.0565	0.2915
chr17	81195210	5100158	0.0628	0.3257
chr18	78077248	3781961	0.0484	0.622
chr19	59128983	2956601	0.05	0.5432
chr20	63025520	3769456	0.0598	0.2869
chr21	48129895	2330606	0.0484	0.2778
chr22	51304566	1199537	0.0234	0.1745
chrMT	16571	2663	0.1607	0.4194
chrX	155270560	7788195	0.0502	0.2968
chrY	59373566	449191	0.0076	0.1986

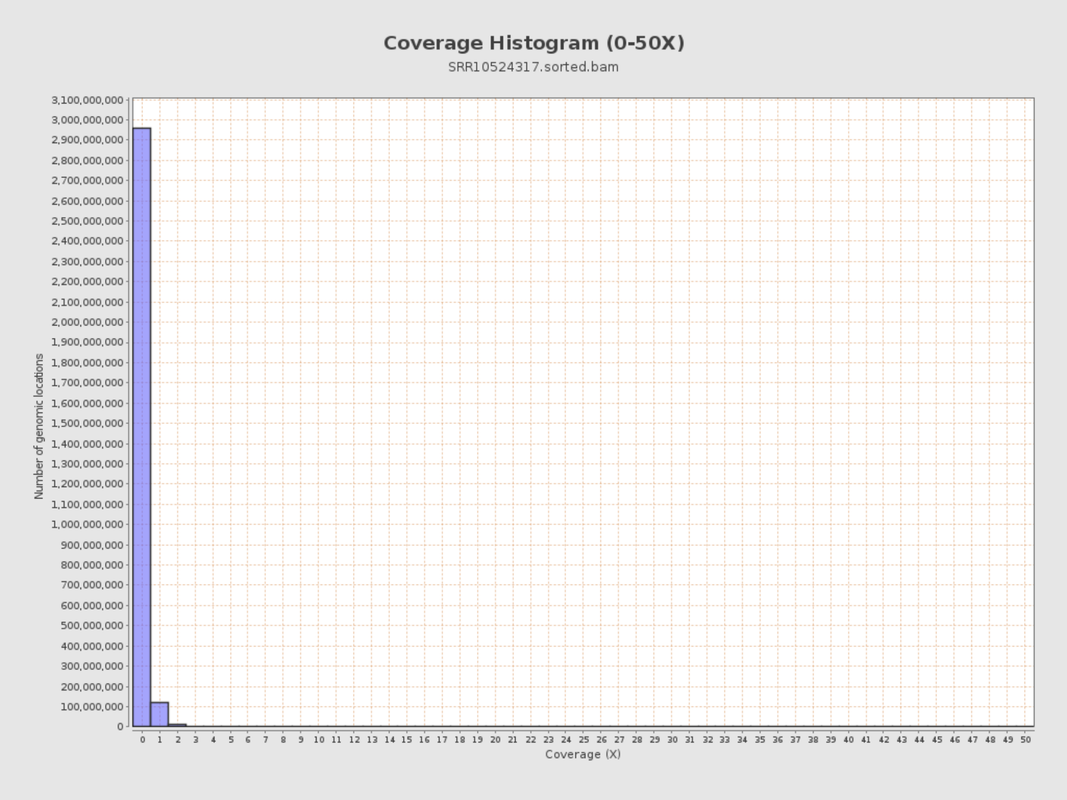
3. Results : Coverage across reference



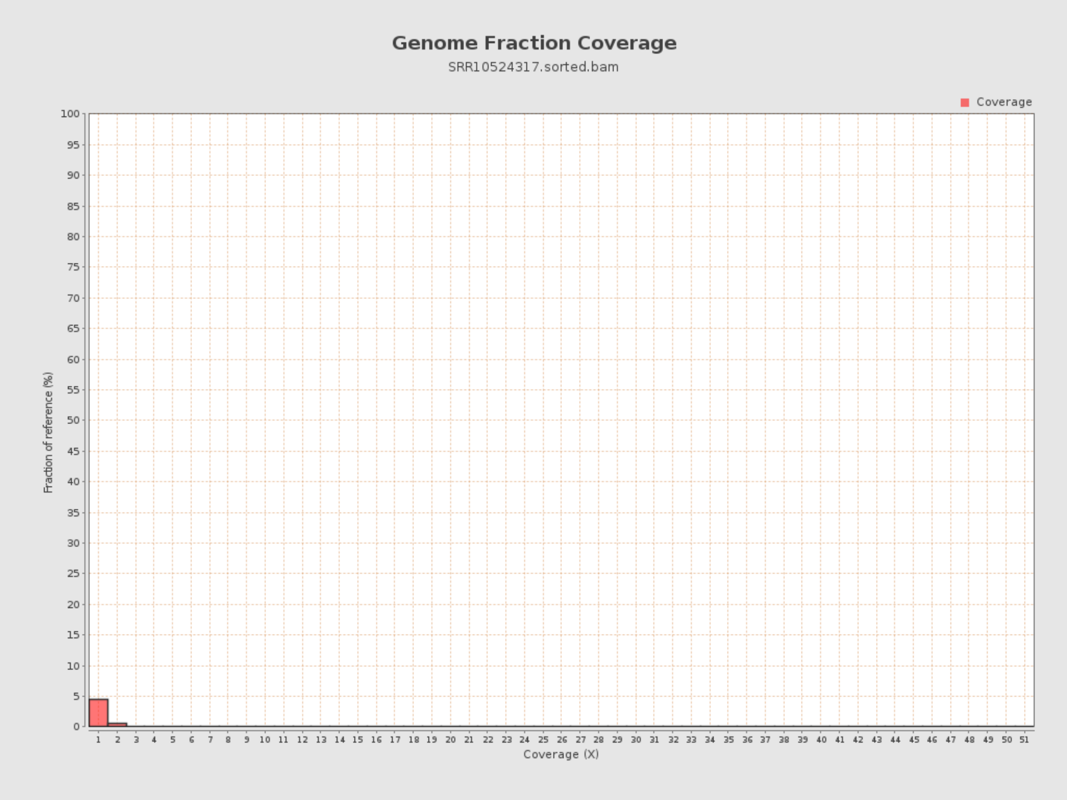
4. Results : Coverage Histogram



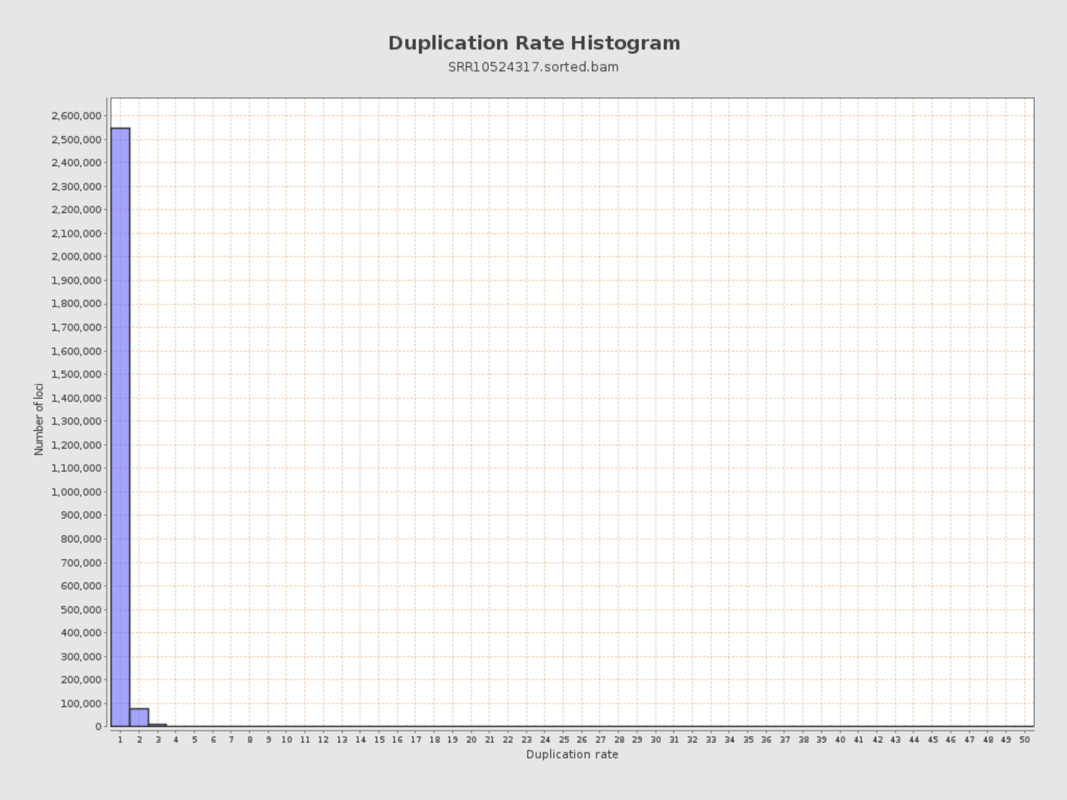
5. Results : Coverage Histogram (0-50X)



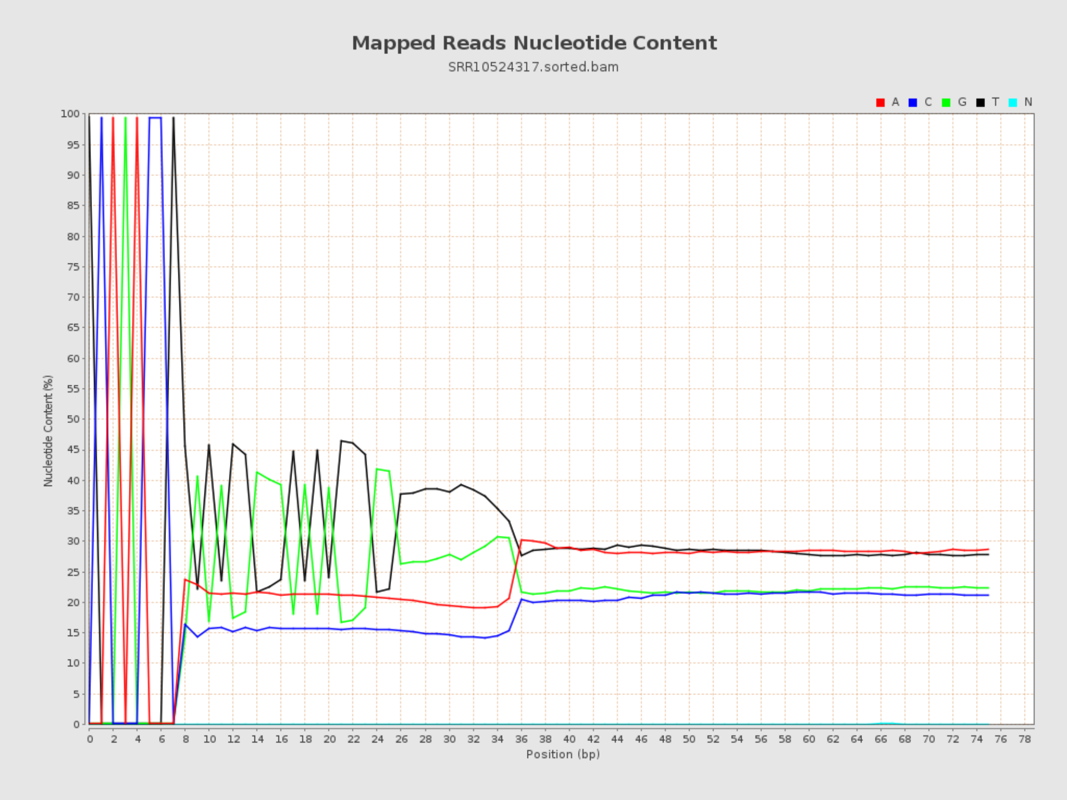
6. Results : Genome Fraction Coverage



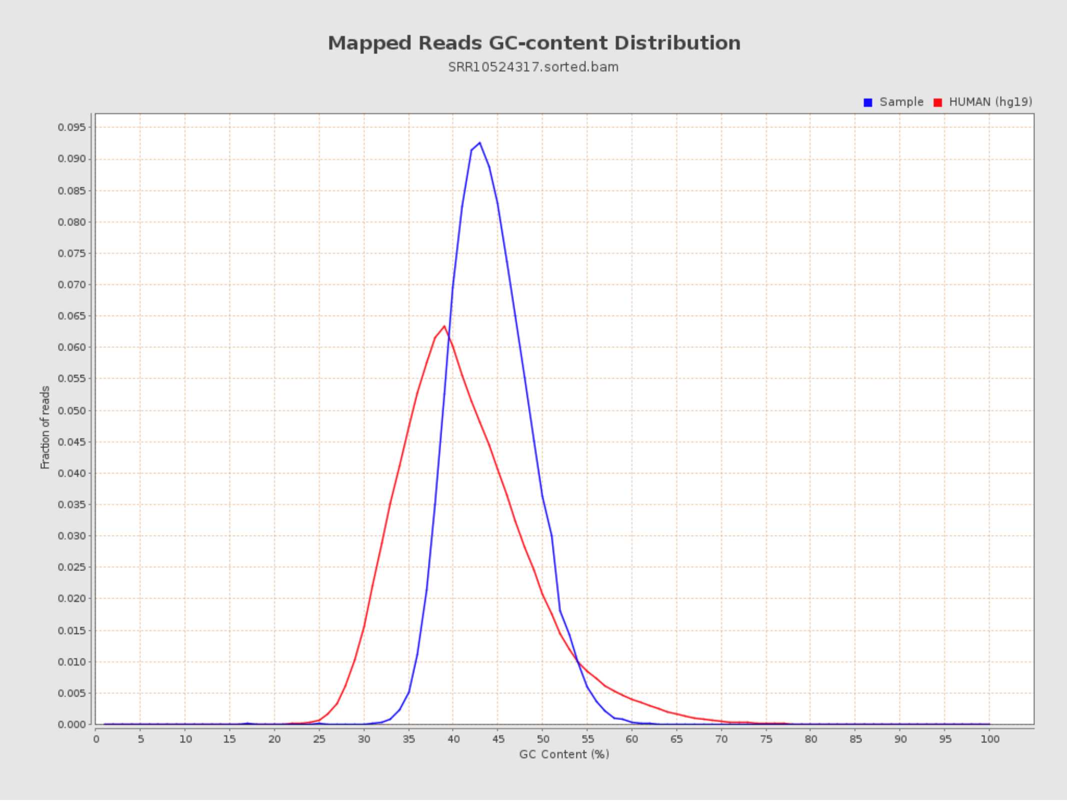
7. Results : Duplication Rate Histogram



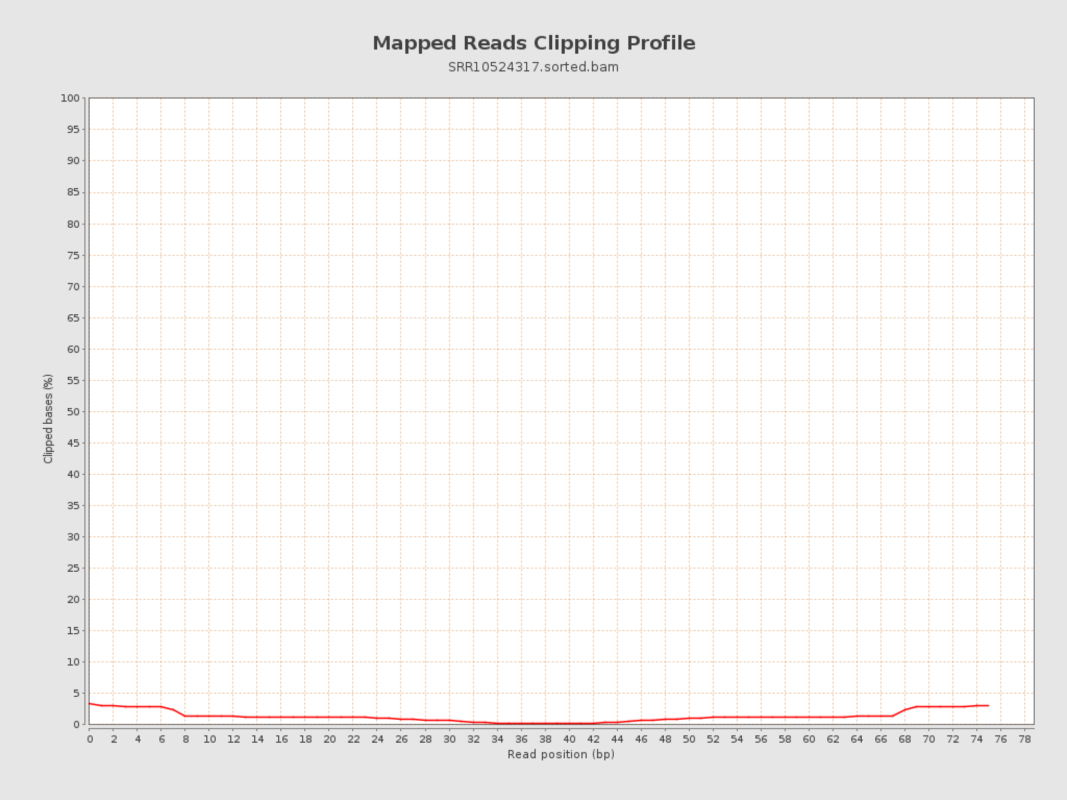
8. Results : Mapped Reads Nucleotide Content



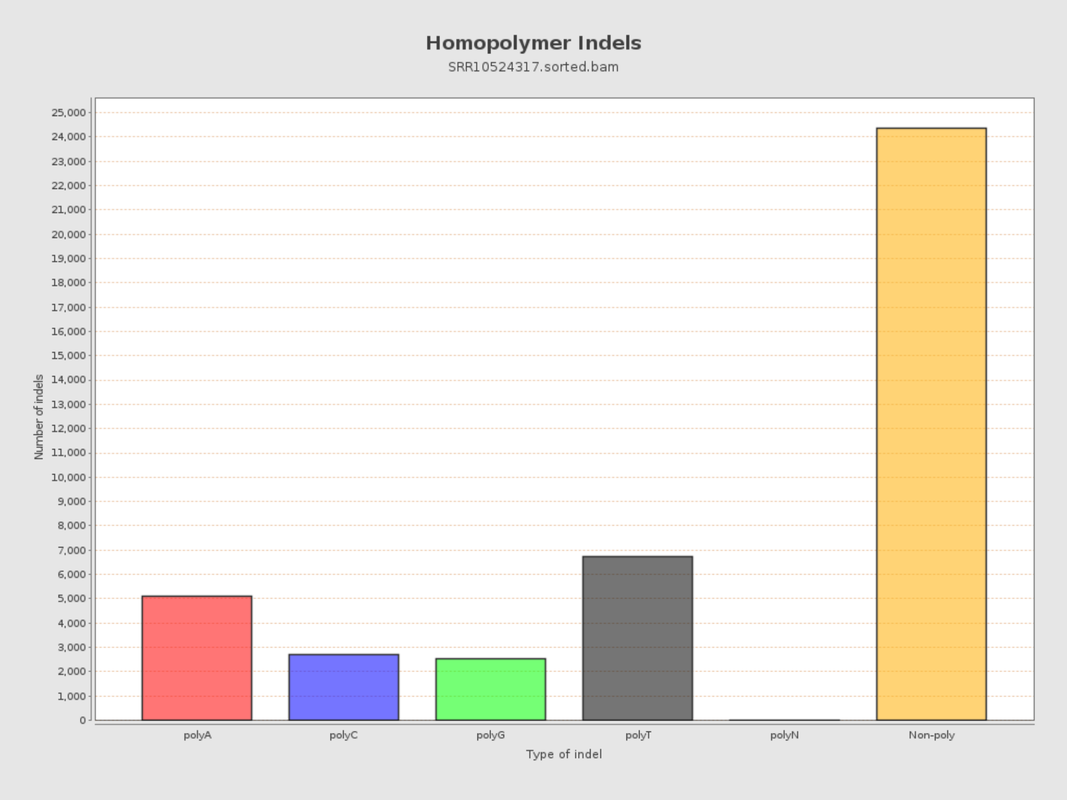
9. Results : Mapped Reads GC-content Distribution



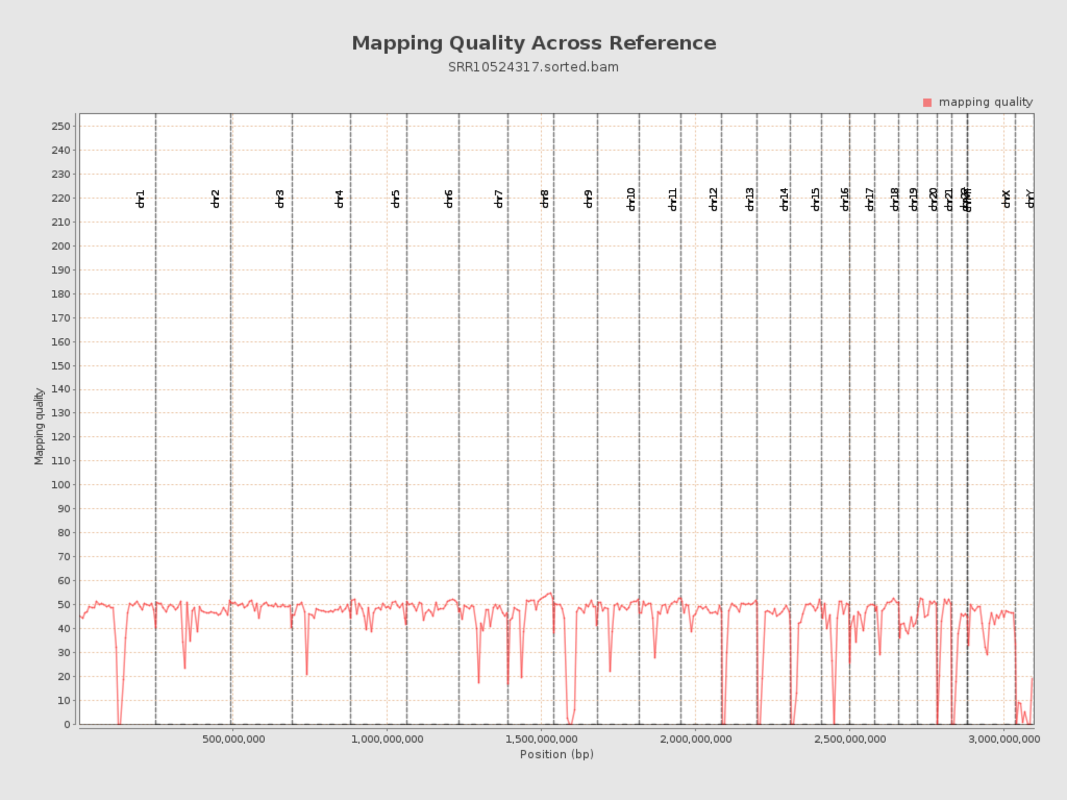
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram