Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 04:01:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524916.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_SRR10524916 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524916.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 04:01:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524916.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,031,746
Mapped reads	1,881,541 / 92.61%
Unmapped reads	150,205 / 7.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,200 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	133,451 / 6.57%
Duplication rate	5.52%
Clipped reads	1,884,235 / 92.74%

2.2. ACGT Content

Number/percentage of A's	28,224,521 / 25.57%
Number/percentage of C's	22,739,655 / 20.6%
Number/percentage of T's	33,395,315 / 30.26%
Number/percentage of G's	26,006,740 / 23.56%
Number/percentage of N's	838 / 0%
GC Percentage	44.17%

2.3. Coverage

Mean	0.0357

Standard Deviation	0.3239

2.4. Mapping Quality

Mean Mapping Quality	45.12

2.5. Mismatches and indels

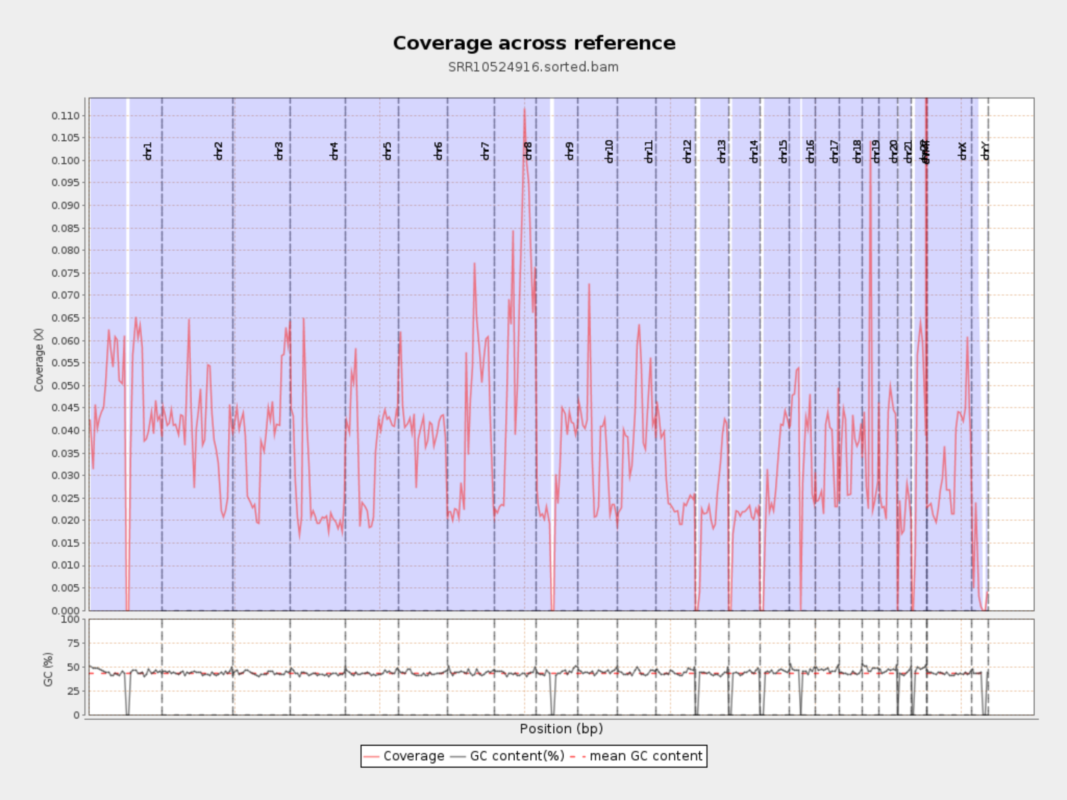
General error rate	0.52%
Mismatches	560,935
Insertions	8,247
Mapped reads with at least one insertion	0.44%
Deletions	20,826
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.16%

2.6. Chromosome stats

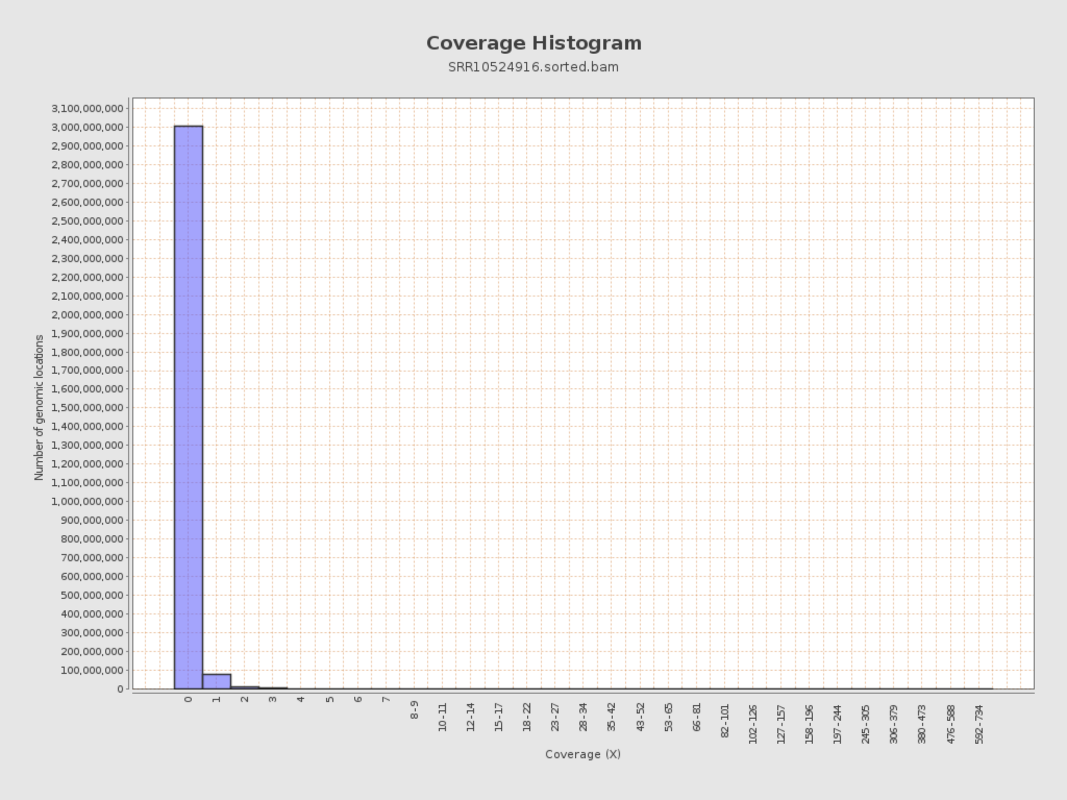
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11460012	0.046	0.5831
chr2	243199373	9830994	0.0404	0.3967
chr3	198022430	7876100	0.0398	0.2327
chr4	191154276	4854411	0.0254	0.248
chr5	180915260	6674917	0.0369	0.2248
chr6	171115067	7060727	0.0413	0.2495
chr7	159138663	6638690	0.0417	0.3883

chr8	146364022	8870637	0.0606	0.4494
chr9	141213431	4005974	0.0284	0.2493
chr10	135534747	4772041	0.0352	0.3711
chr11	135006516	5520804	0.0409	0.2798
chr12	133851895	3695577	0.0276	0.2005
chr13	115169878	2650761	0.023	0.1786
chr14	107349540	2009728	0.0187	0.1676
chr15	102531392	2818080	0.0275	0.1958
chr16	90354753	3405432	0.0377	0.2425
chr17	81195210	2591195	0.0319	0.2214
chr18	78077248	2854279	0.0366	0.4109
chr19	59128983	2312092	0.0391	0.4062
chr20	63025520	2188423	0.0347	0.2277
chr21	48129895	968433	0.0201	0.2135
chr22	51304566	1937535	0.0378	0.2311
chrMT	16571	22306	1.3461	1.5309
chrX	155270560	5027759	0.0324	0.2289
chrY	59373566	355278	0.006	0.2247

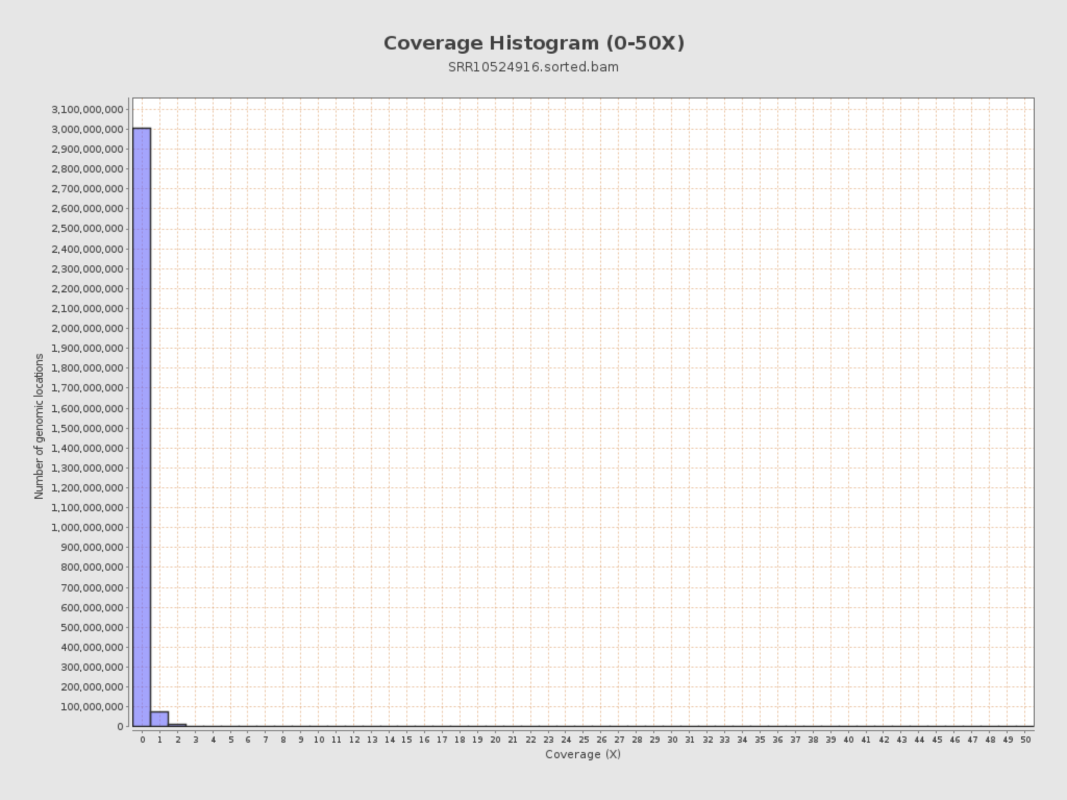
3. Results : Coverage across reference



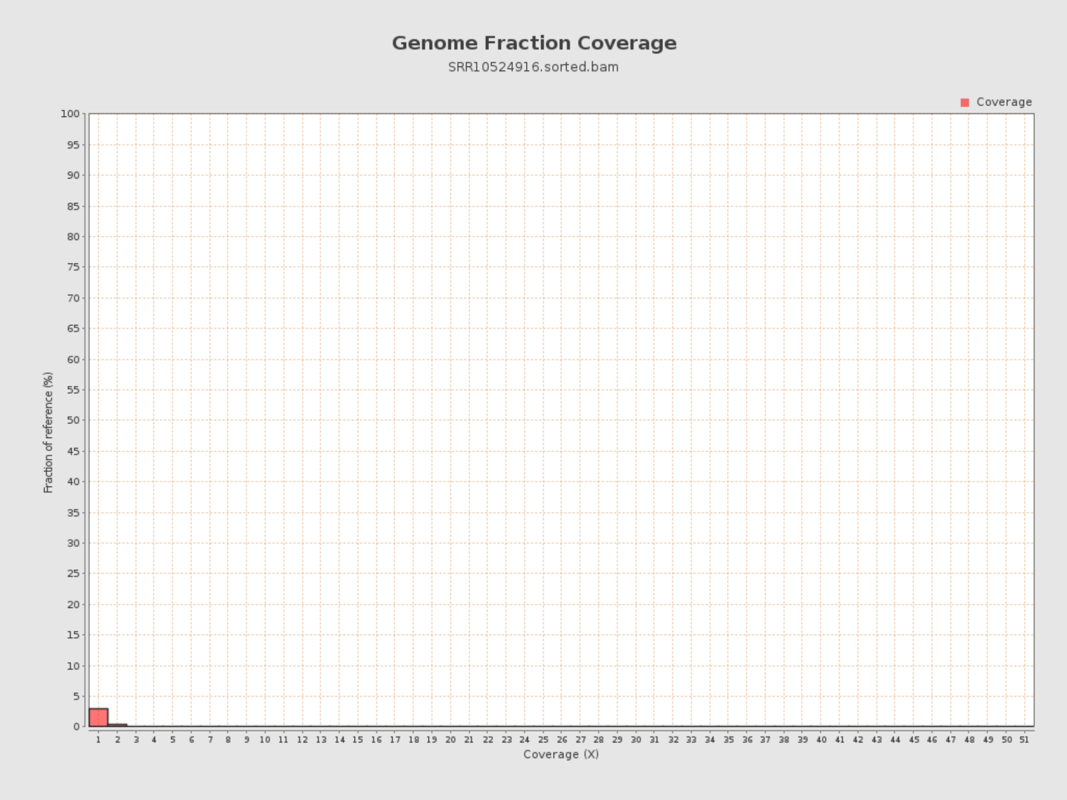
4. Results : Coverage Histogram



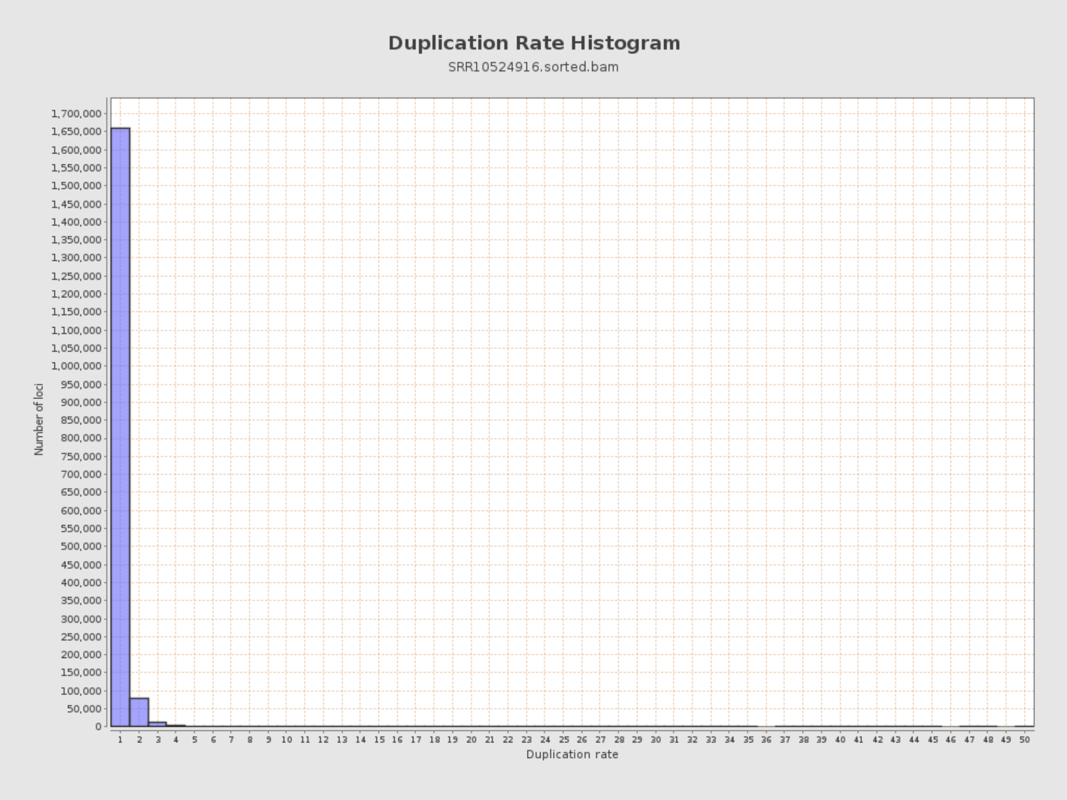
5. Results : Coverage Histogram (0-50X)



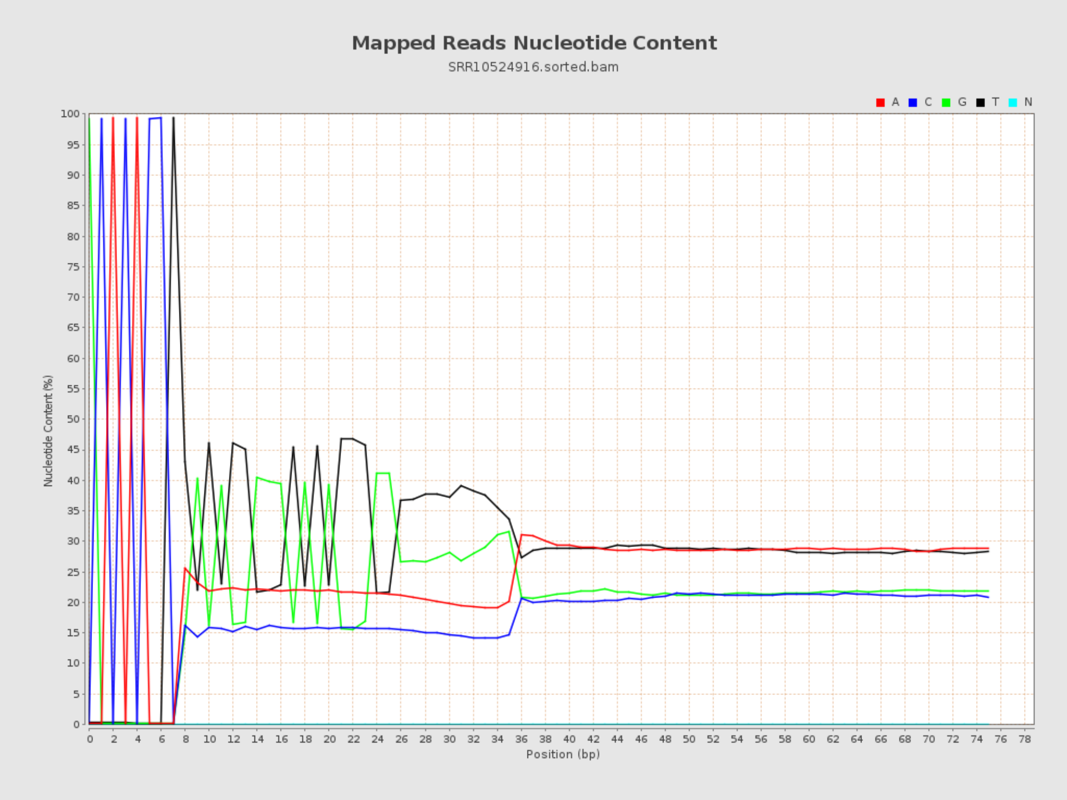
6. Results : Genome Fraction Coverage



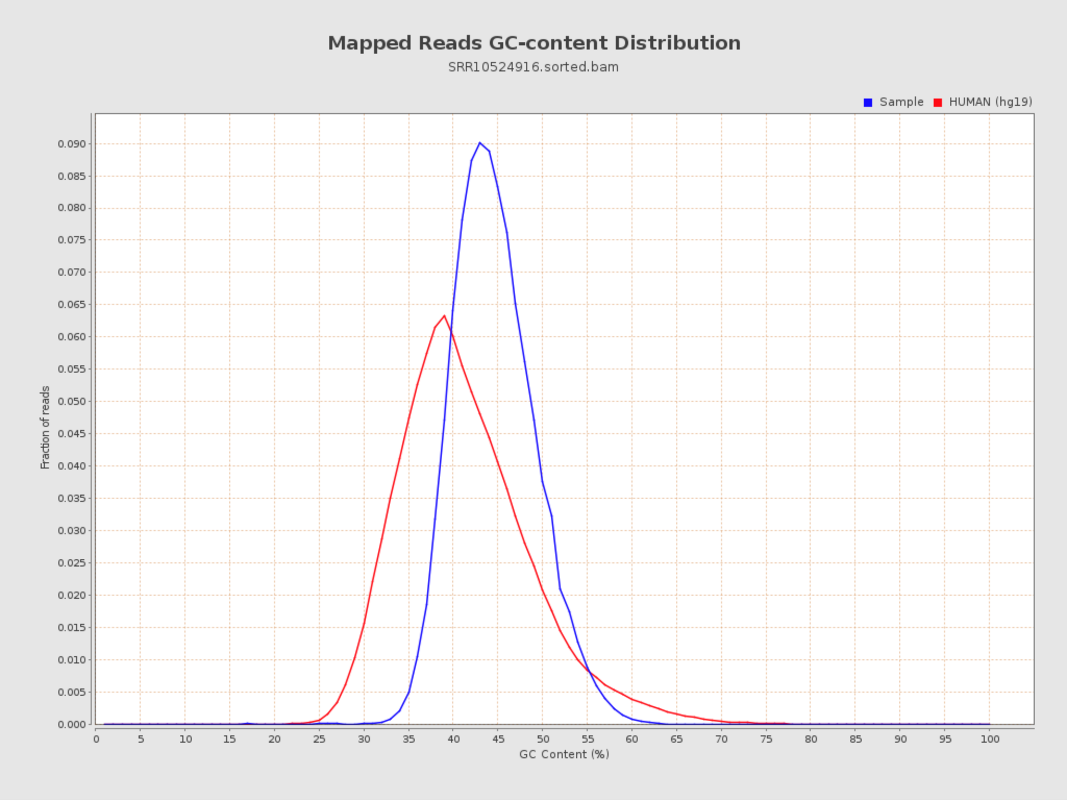
7. Results : Duplication Rate Histogram



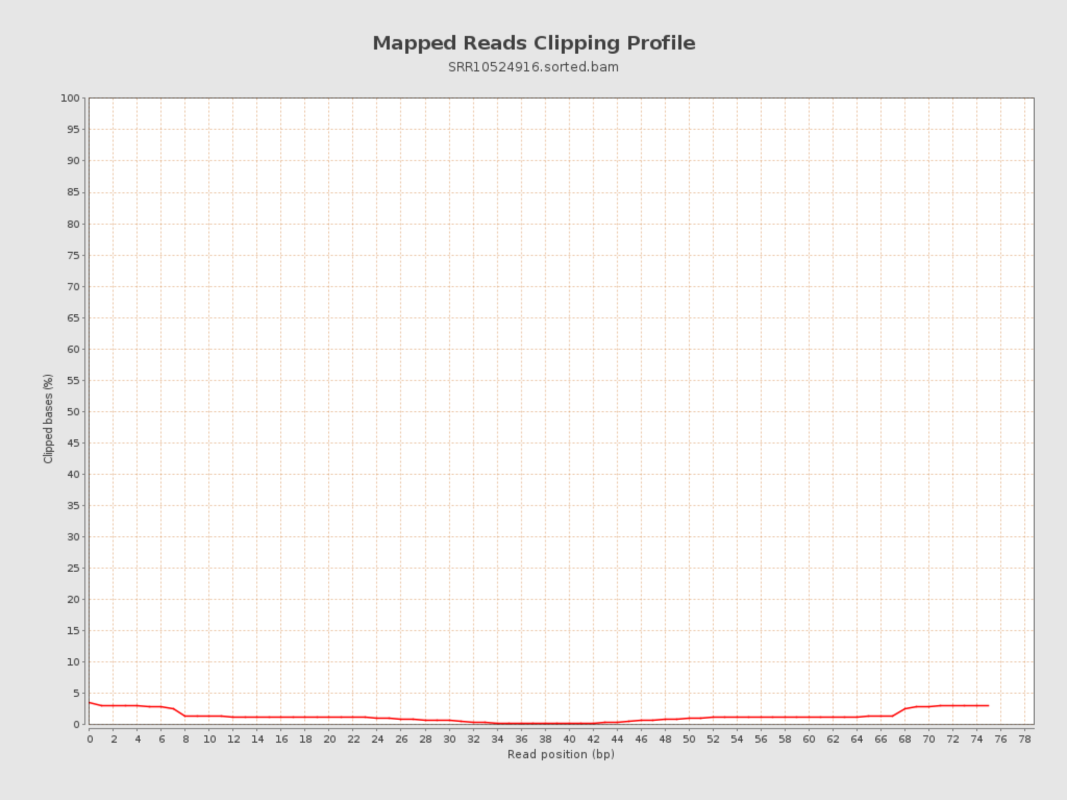
8. Results : Mapped Reads Nucleotide Content



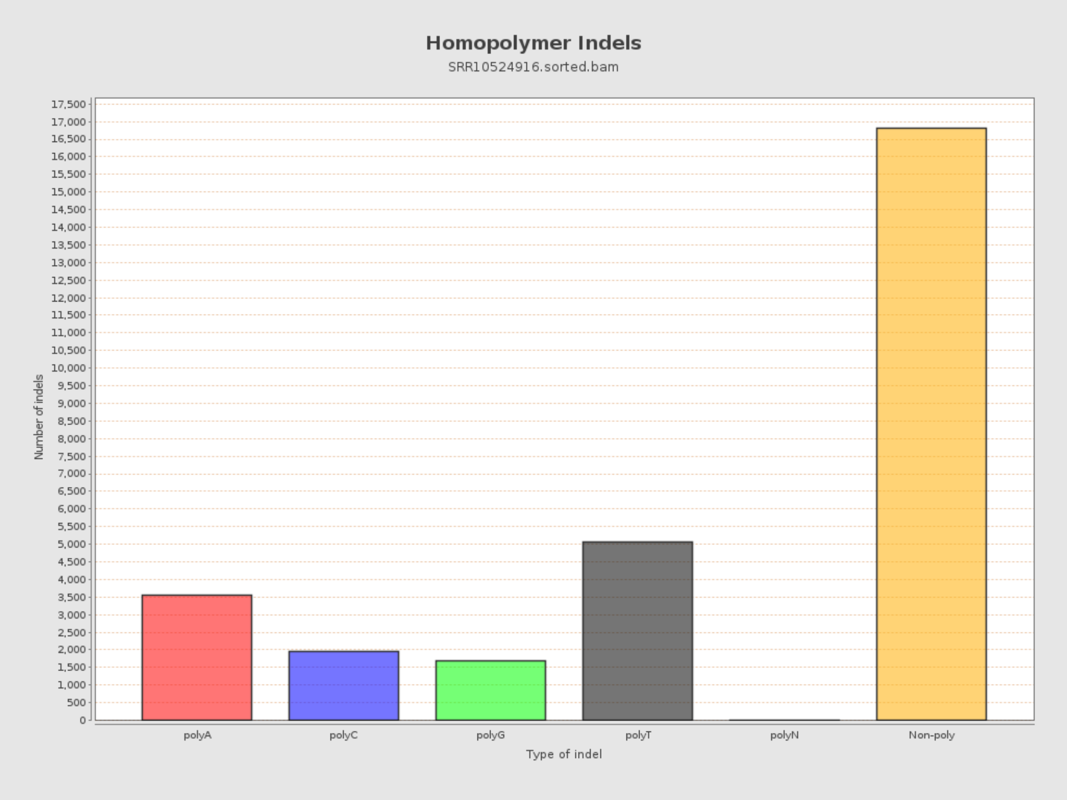
9. Results : Mapped Reads GC-content Distribution



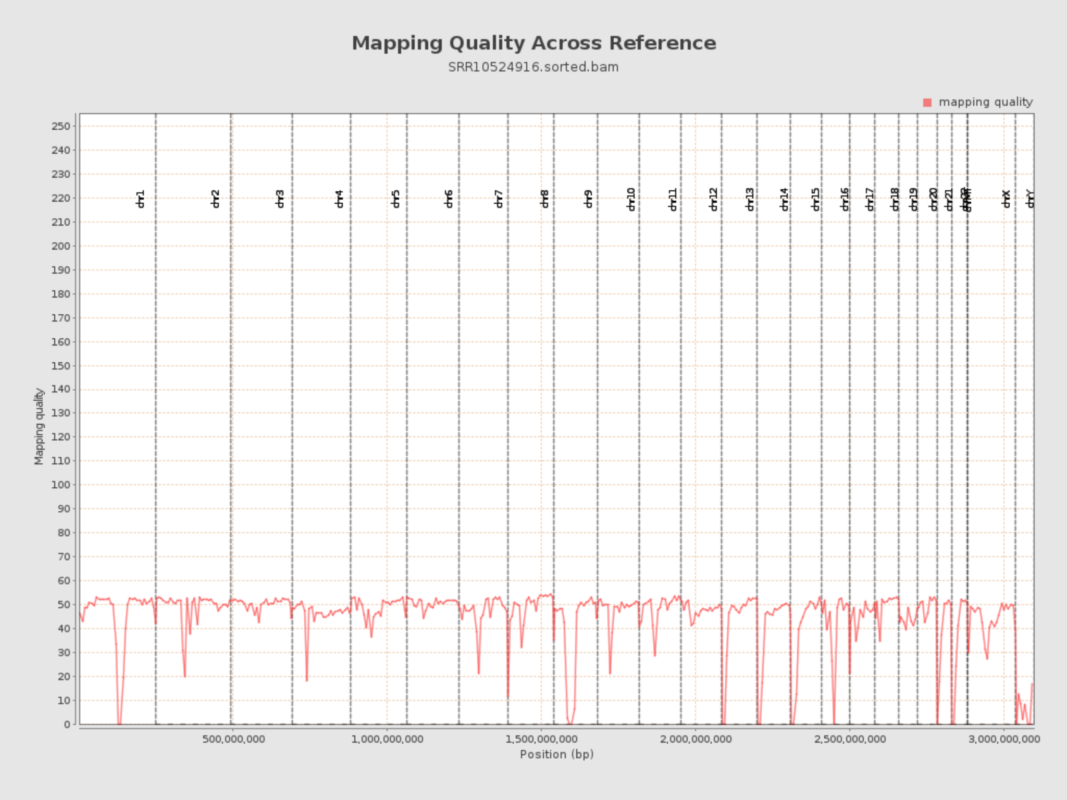
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram