Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 21:45:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524815.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_SRR10524815 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524815.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 21:45:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524815.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,279,040
Mapped reads	1,176,907 / 92.01%
Unmapped reads	102,133 / 7.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,989 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	37,095 / 2.9%
Duplication rate	2.43%
Clipped reads	1,180,574 / 92.3%

2.2. ACGT Content

Number/percentage of A's	16,034,487 / 23.5%
Number/percentage of C's	13,402,605 / 19.64%
Number/percentage of T's	21,243,002 / 31.13%
Number/percentage of G's	17,552,623 / 25.72%
Number/percentage of N's	8,094 / 0.01%
GC Percentage	45.36%

2.3. Coverage

Mean	0.0221

Standard Deviation	0.2029

2.4. Mapping Quality

Mean Mapping Quality	44.94

2.5. Mismatches and indels

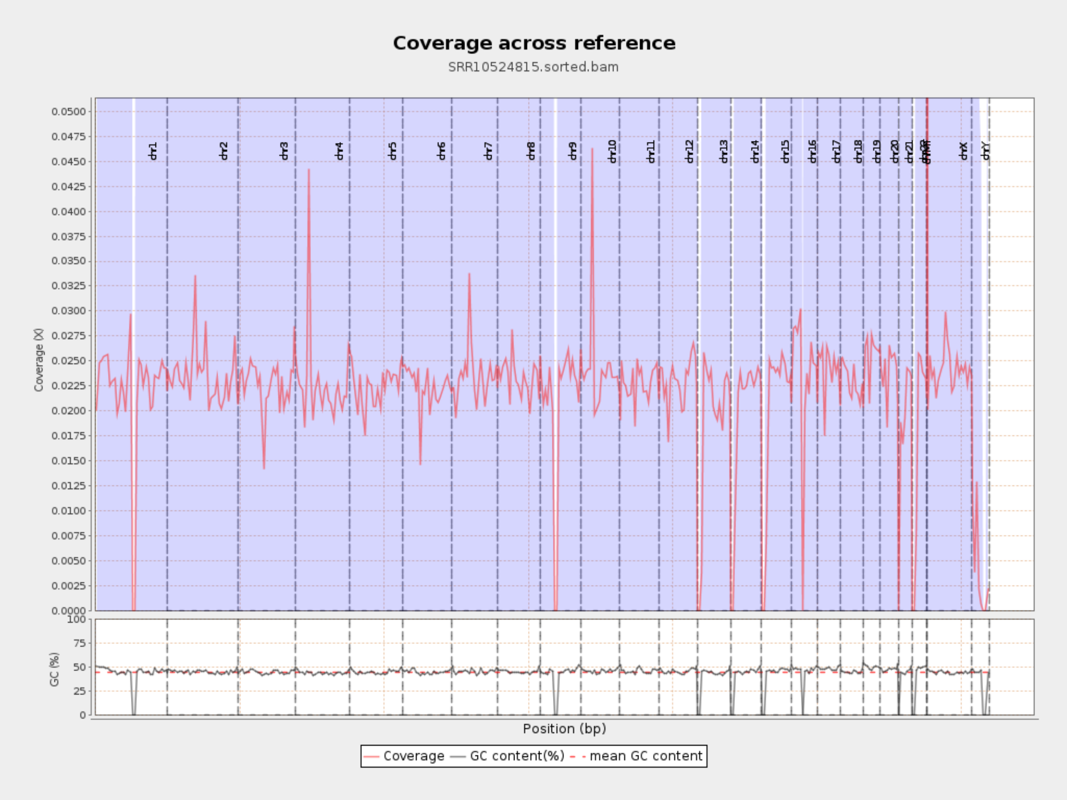
General error rate	0.52%
Mismatches	343,731
Insertions	3,880
Mapped reads with at least one insertion	0.33%
Deletions	13,753
Mapped reads with at least one deletion	1.16%
Homopolymer indels	42.74%

2.6. Chromosome stats

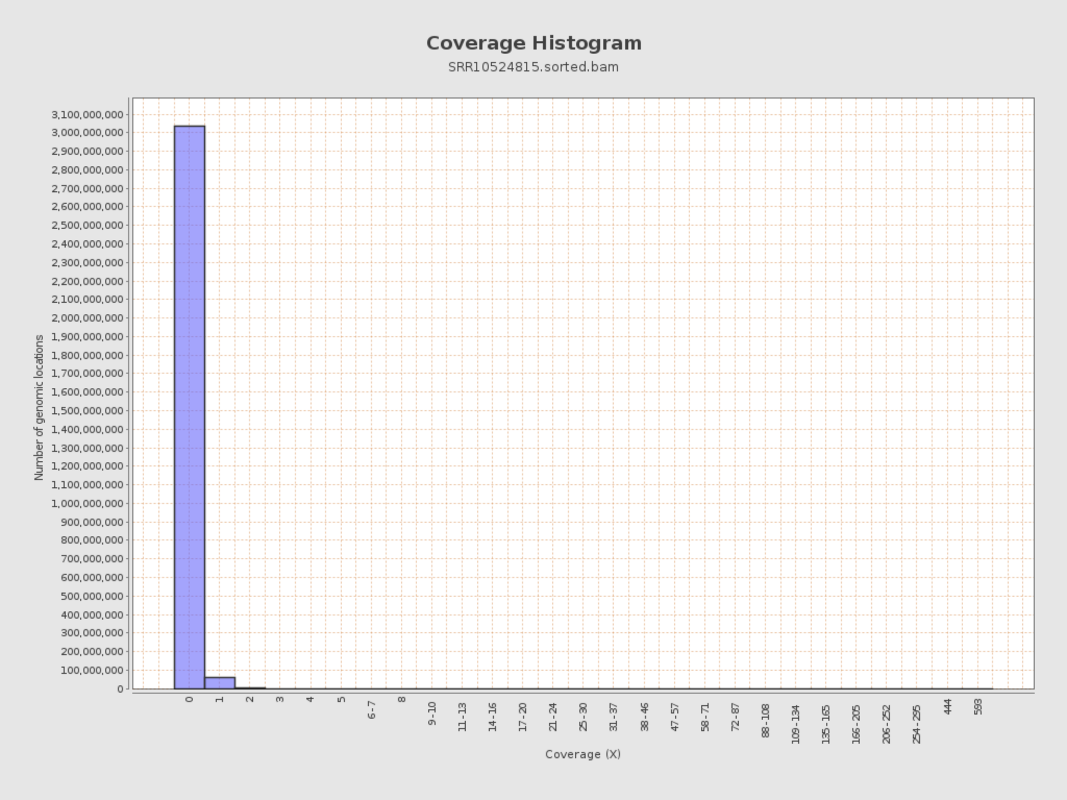
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5450349	0.0219	0.2509
chr2	243199373	5729436	0.0236	0.3065
chr3	198022430	4462250	0.0225	0.163
chr4	191154276	4358717	0.0228	0.1858
chr5	180915260	4057035	0.0224	0.1617
chr6	171115067	3823378	0.0223	0.1721
chr7	159138663	3752026	0.0236	0.2497

chr8	146364022	3410626	0.0233	0.187
chr9	141213431	2909675	0.0206	0.1807
chr10	135534747	3314738	0.0245	0.2471
chr11	135006516	3088400	0.0229	0.189
chr12	133851895	3082382	0.023	0.1648
chr13	115169878	2121433	0.0184	0.1467
chr14	107349540	2065216	0.0192	0.1532
chr15	102531392	1994733	0.0195	0.1512
chr16	90354753	2095988	0.0232	0.1783
chr17	81195210	1967645	0.0242	0.1741
chr18	78077248	1795091	0.023	0.2681
chr19	59128983	1514894	0.0256	0.218
chr20	63025520	1504971	0.0239	0.1719
chr21	48129895	911994	0.0189	0.1659
chr22	51304566	865628	0.0169	0.1407
chrMT	16571	10828	0.6534	0.8822
chrX	155270560	3752076	0.0242	0.1768
chrY	59373566	223683	0.0038	0.1089

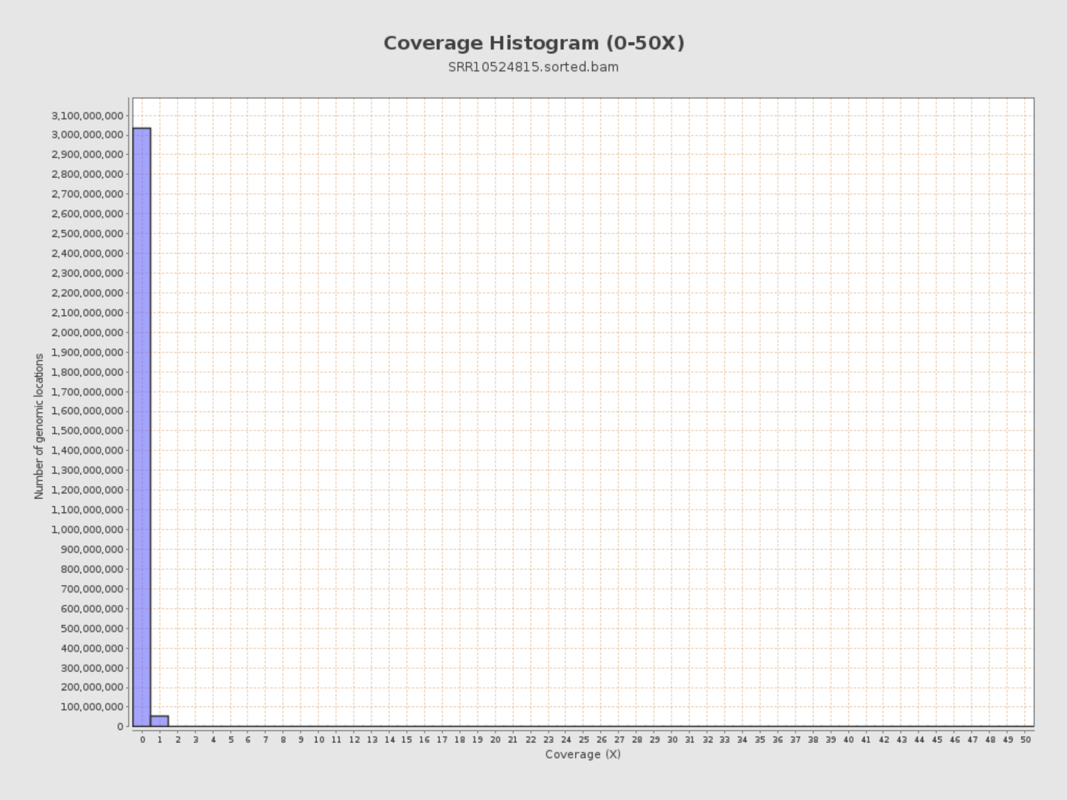
3. Results : Coverage across reference



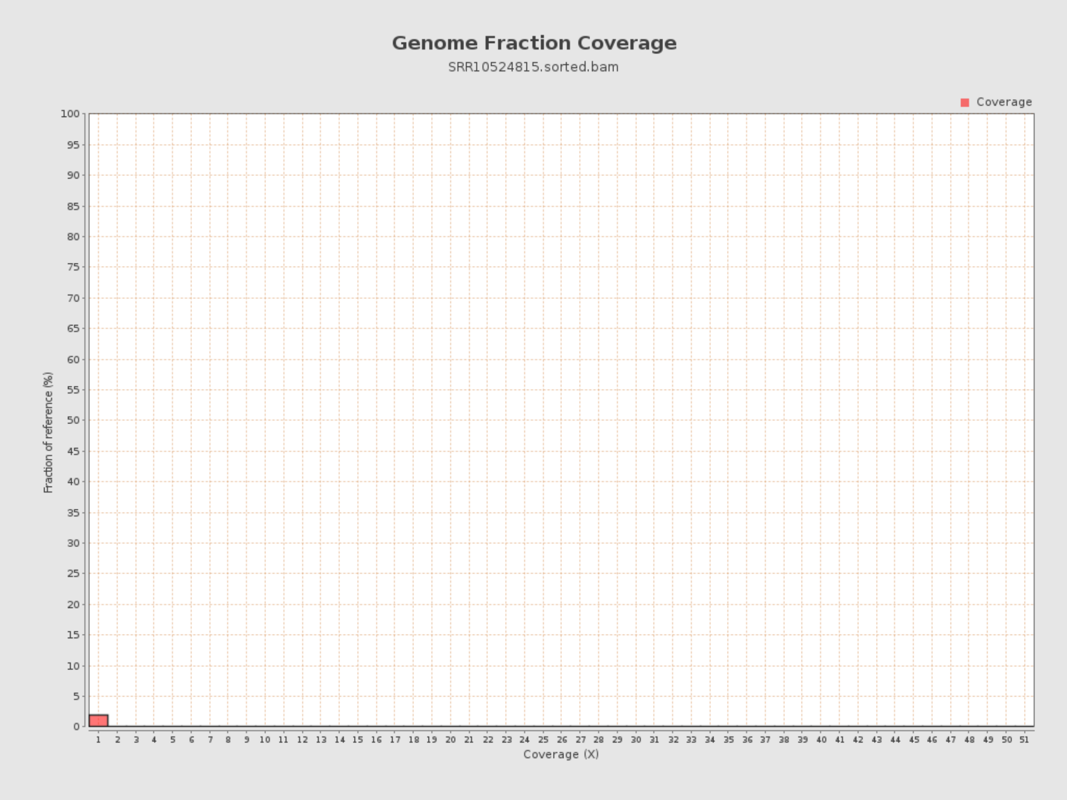
4. Results : Coverage Histogram



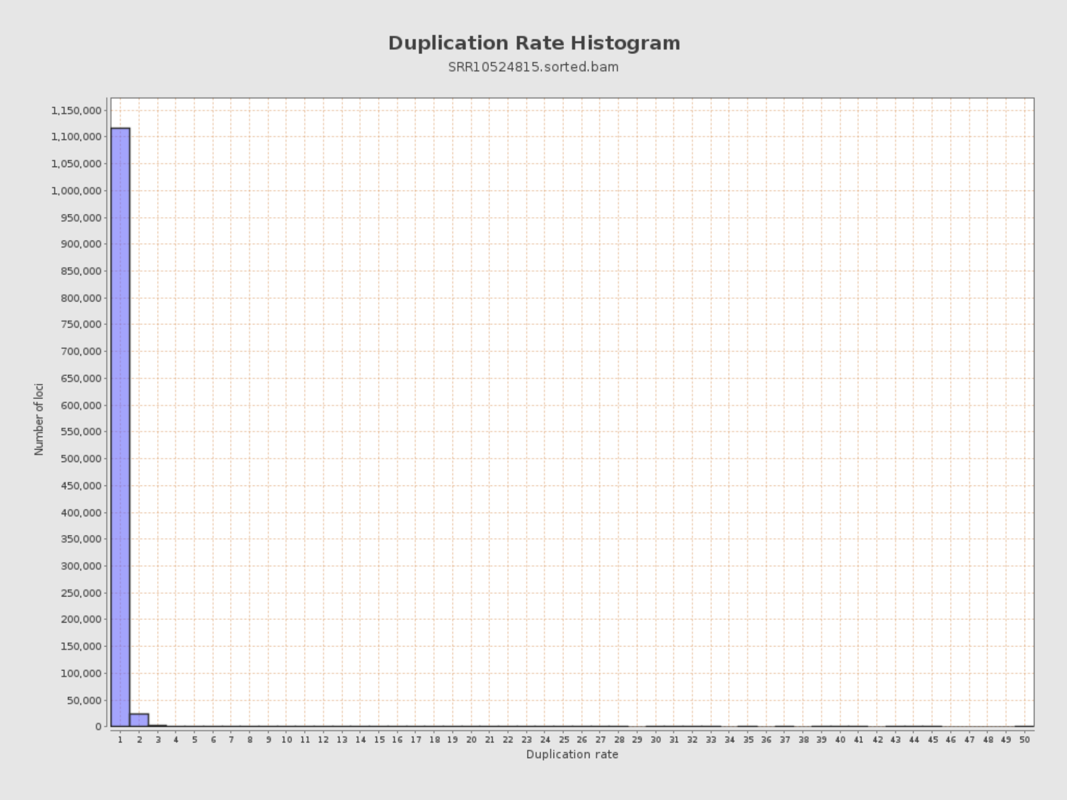
5. Results : Coverage Histogram (0-50X)



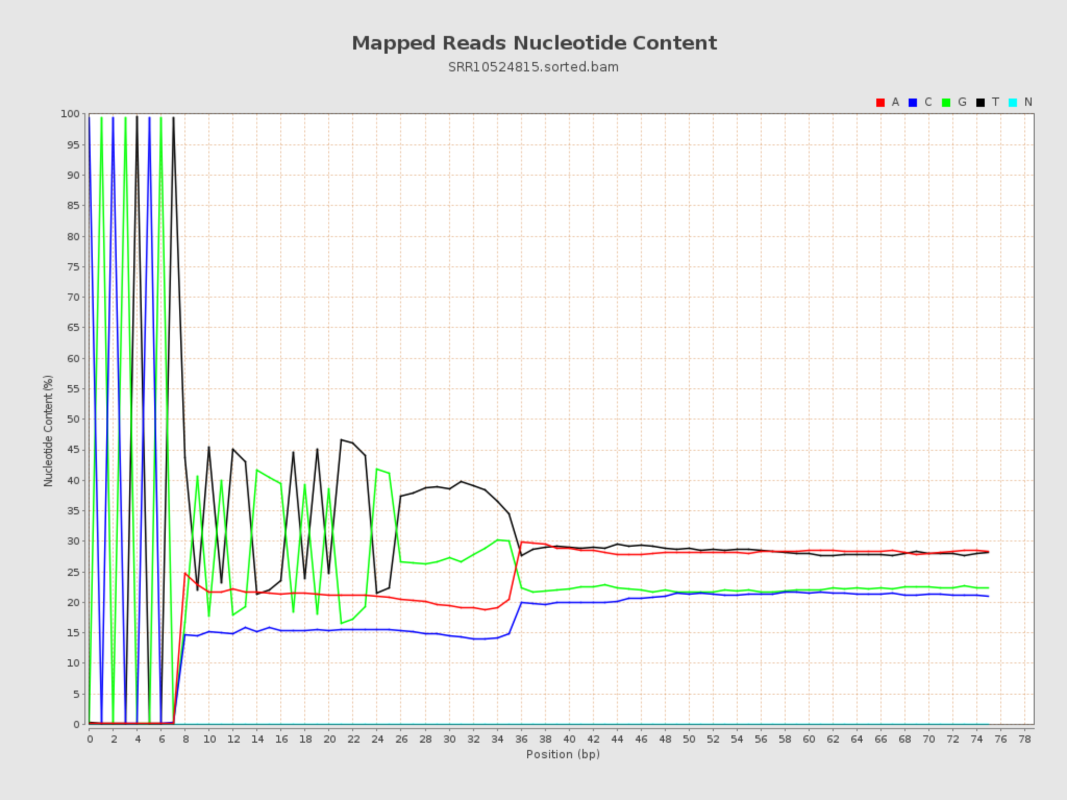
6. Results : Genome Fraction Coverage



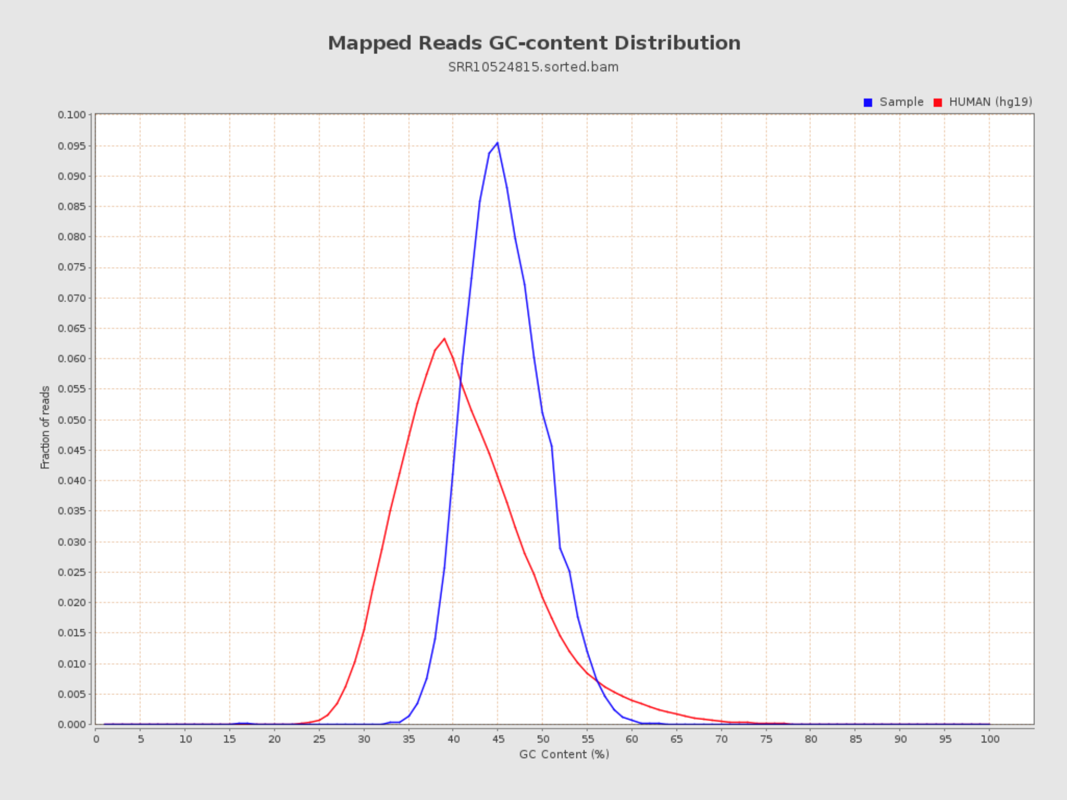
7. Results : Duplication Rate Histogram



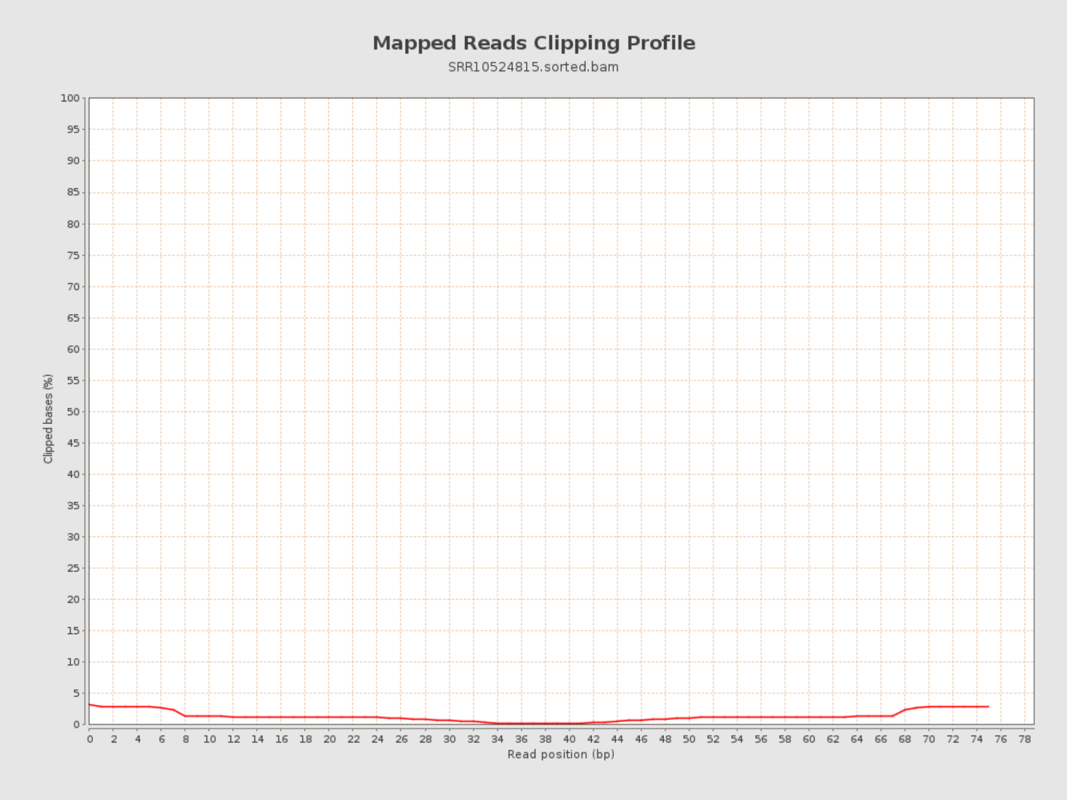
8. Results : Mapped Reads Nucleotide Content



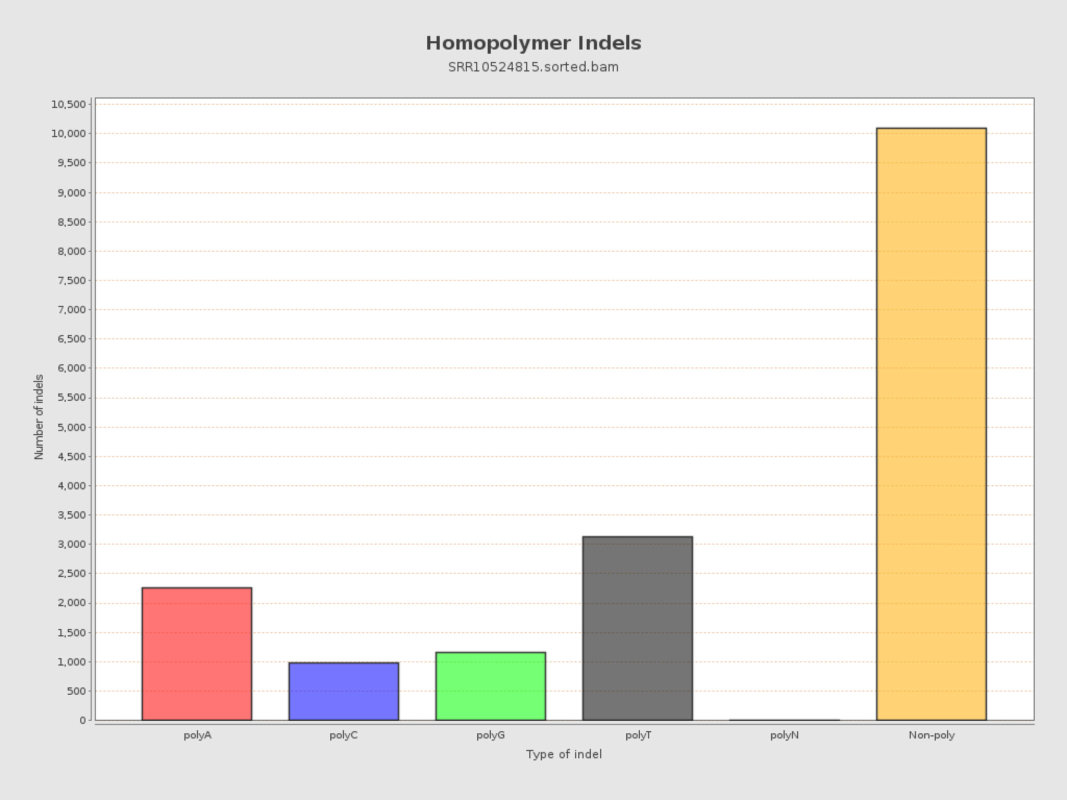
9. Results : Mapped Reads GC-content Distribution



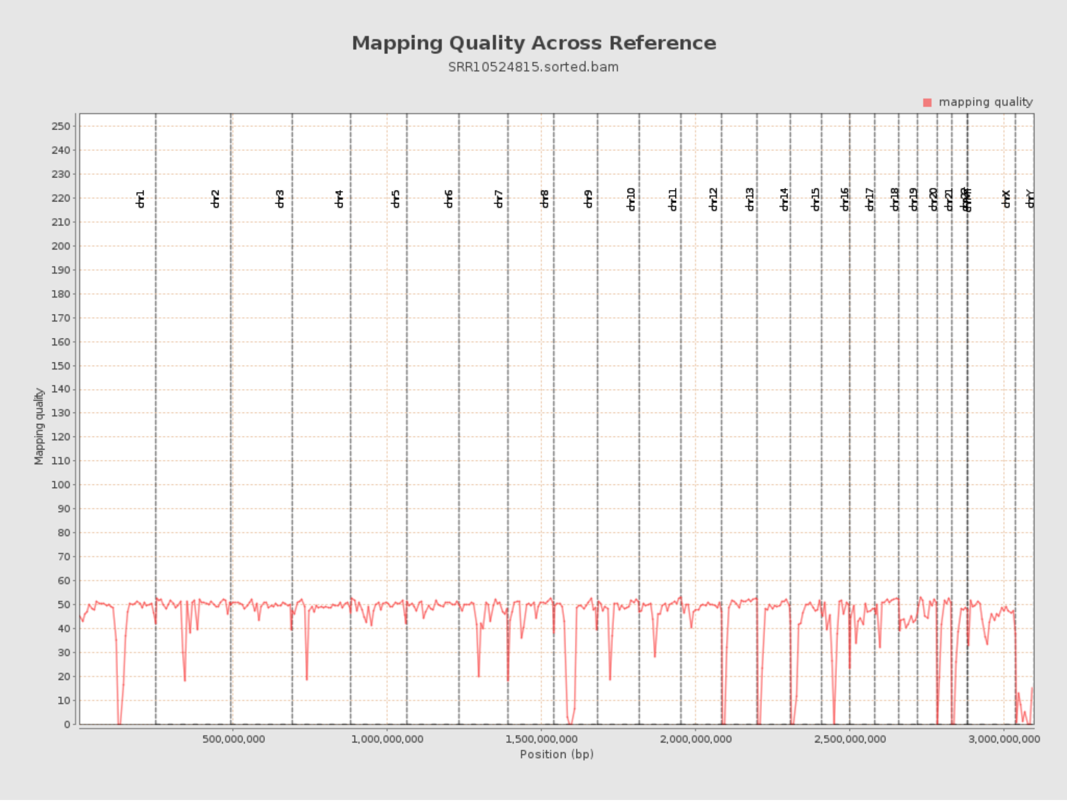
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram