Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 03:01:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524419.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_SRR10524419 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524419.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 03:01:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524419.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,299,908
Mapped reads	4,875,988 / 92%
Unmapped reads	423,920 / 8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,970 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	498,834 / 9.41%
Duplication rate	7.15%
Clipped reads	4,885,497 / 92.18%

2.2. ACGT Content

Number/percentage of A's	71,123,812 / 24.92%
Number/percentage of C's	55,110,043 / 19.31%
Number/percentage of T's	90,389,794 / 31.67%
Number/percentage of G's	68,752,553 / 24.09%
Number/percentage of N's	29,866 / 0.01%
GC Percentage	43.4%

2.3. Coverage

Mean	0.0922

Standard Deviation	0.8362

2.4. Mapping Quality

Mean Mapping Quality	44.87

2.5. Mismatches and indels

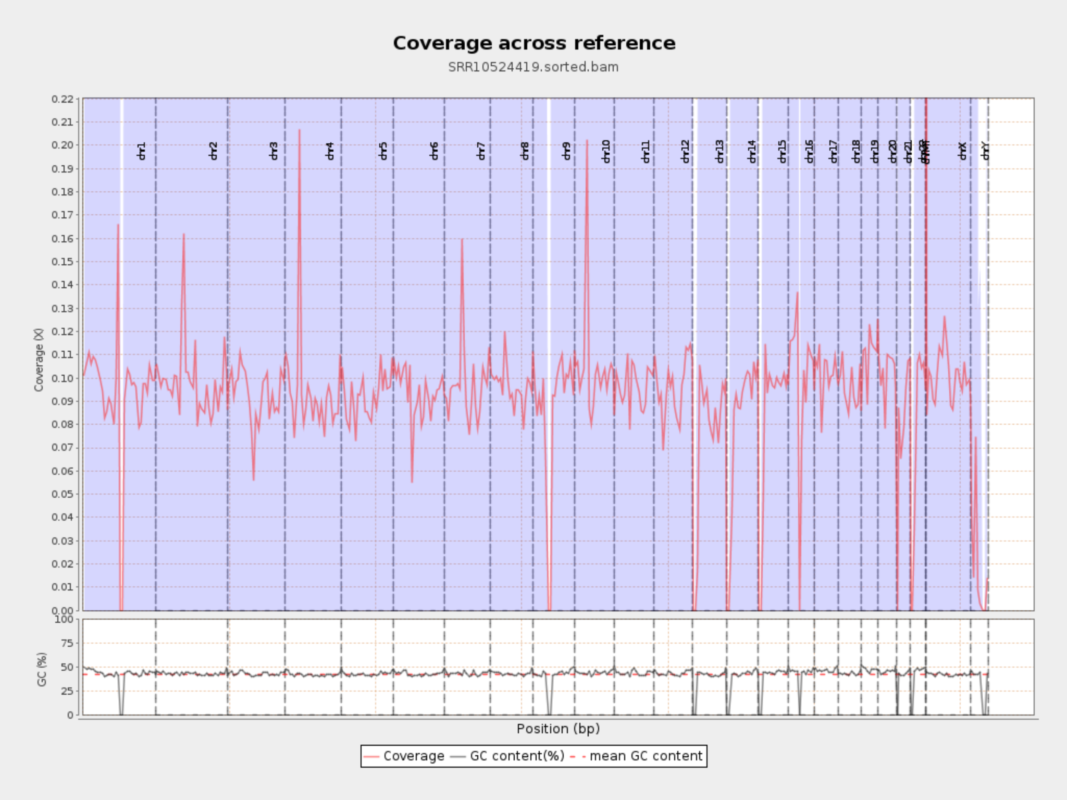
General error rate	0.52%
Mismatches	1,441,711
Insertions	23,007
Mapped reads with at least one insertion	0.47%
Deletions	47,089
Mapped reads with at least one deletion	0.96%
Homopolymer indels	40.15%

2.6. Chromosome stats

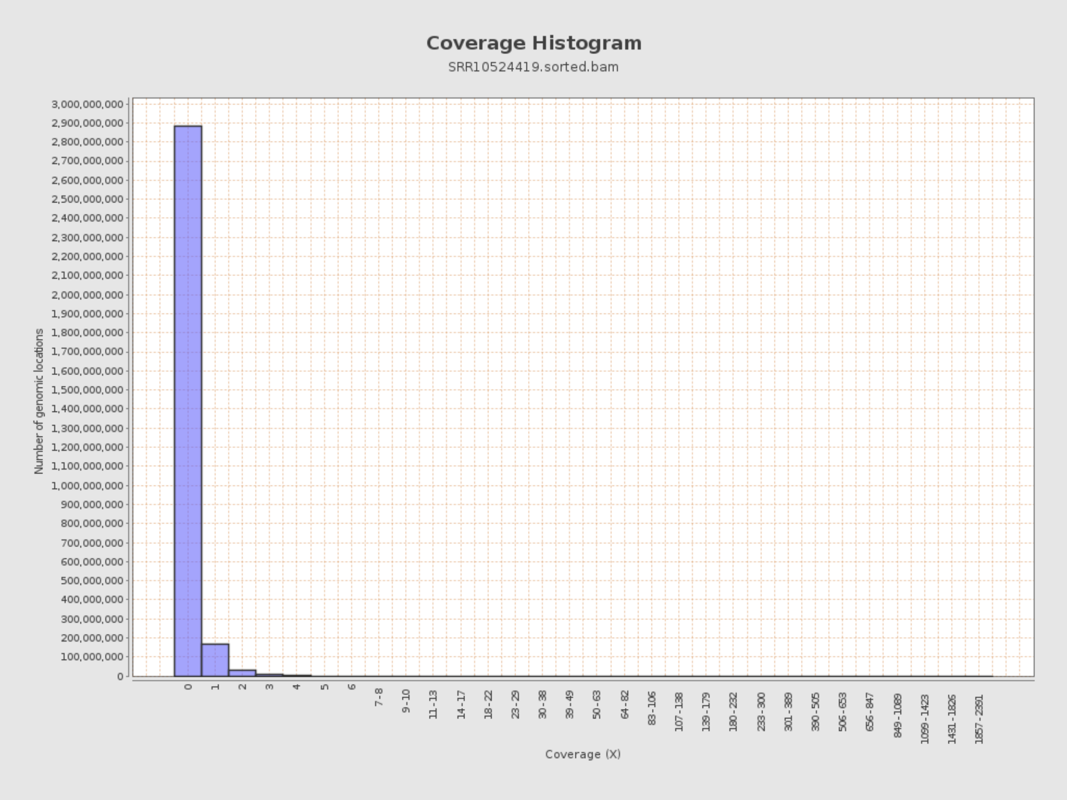
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23190628	0.093	1.7338
chr2	243199373	24026483	0.0988	1.2064
chr3	198022430	18356987	0.0927	0.4006
chr4	191154276	18102987	0.0947	0.7003
chr5	180915260	16737598	0.0925	0.3974
chr6	171115067	15925525	0.0931	0.4816
chr7	159138663	15501270	0.0974	1.0808

chr8	146364022	14052777	0.096	0.5557
chr9	141213431	11963319	0.0847	0.572
chr10	135534747	14167305	0.1045	0.9901
chr11	135006516	12988910	0.0962	0.641
chr12	133851895	12936068	0.0966	0.4278
chr13	115169878	8512611	0.0739	0.3566
chr14	107349540	8556434	0.0797	0.4044
chr15	102531392	8355617	0.0815	0.3743
chr16	90354753	8909068	0.0986	0.4901
chr17	81195210	8323900	0.1025	0.5019
chr18	78077248	7458479	0.0955	1.2202
chr19	59128983	6512701	0.1101	1.0845
chr20	63025520	6434235	0.1021	0.4728
chr21	48129895	3903497	0.0811	0.6343
chr22	51304566	3765706	0.0734	0.3618
chrMT	16571	20764	1.253	1.5563
chrX	155270560	15684638	0.101	0.4922
chrY	59373566	1097138	0.0185	0.6404

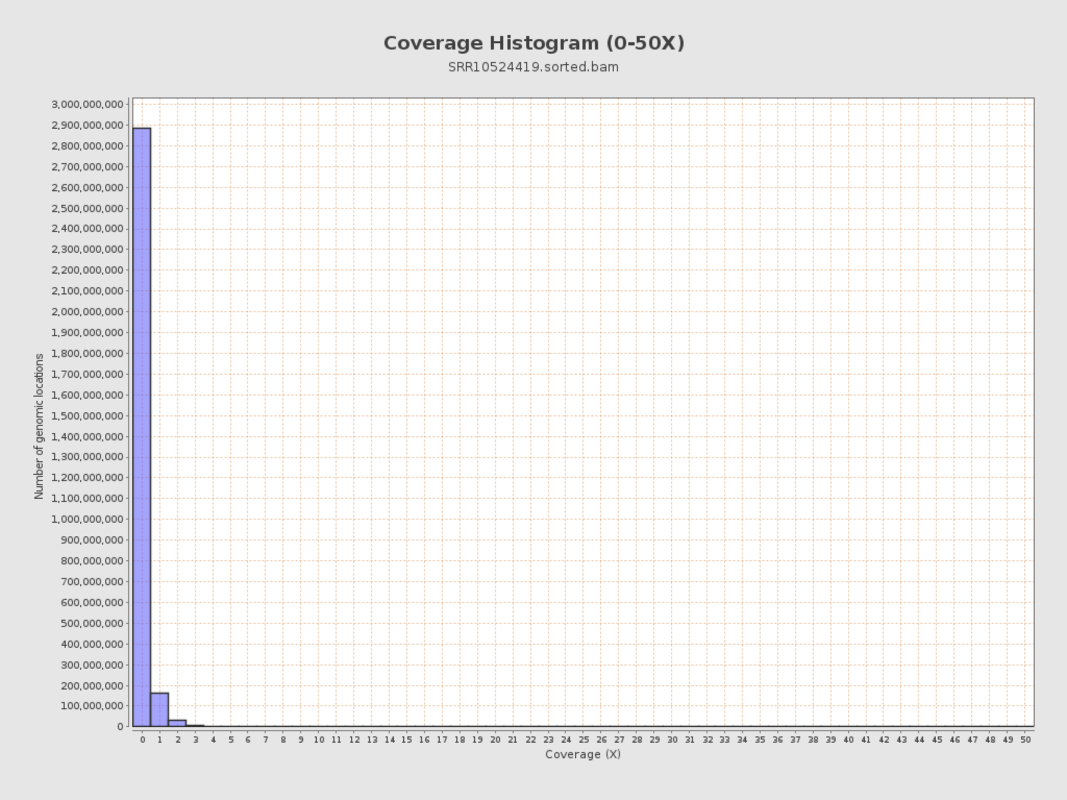
3. Results : Coverage across reference



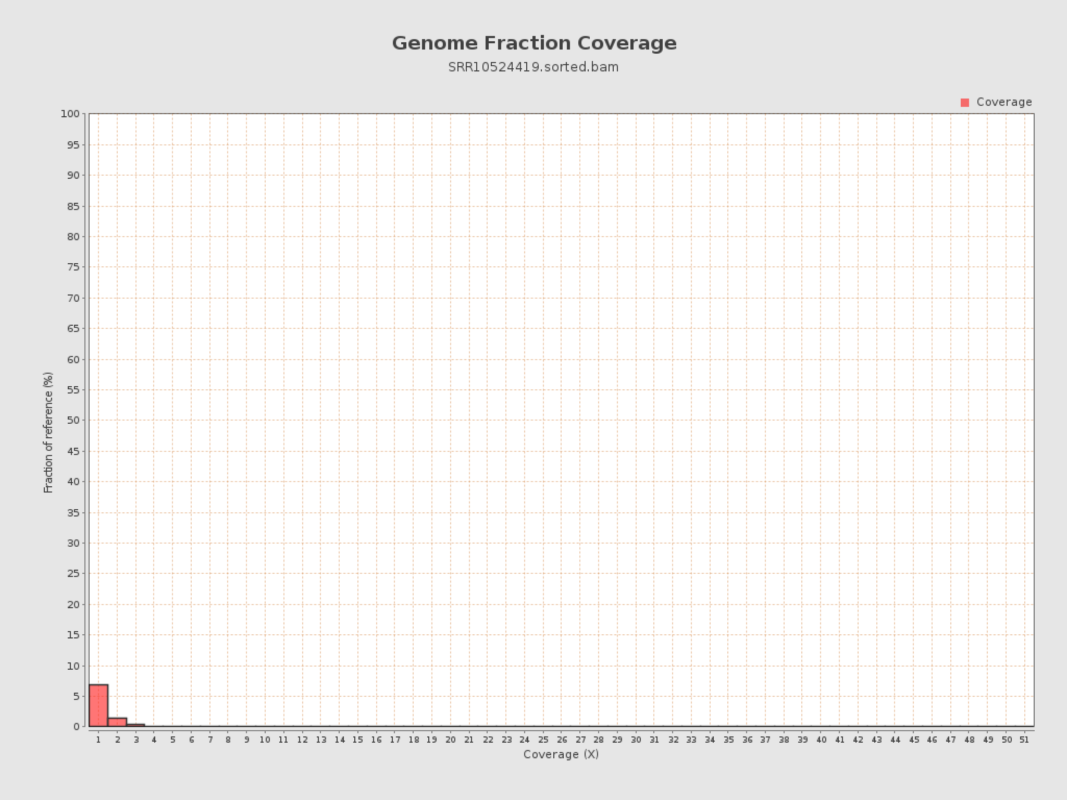
4. Results : Coverage Histogram



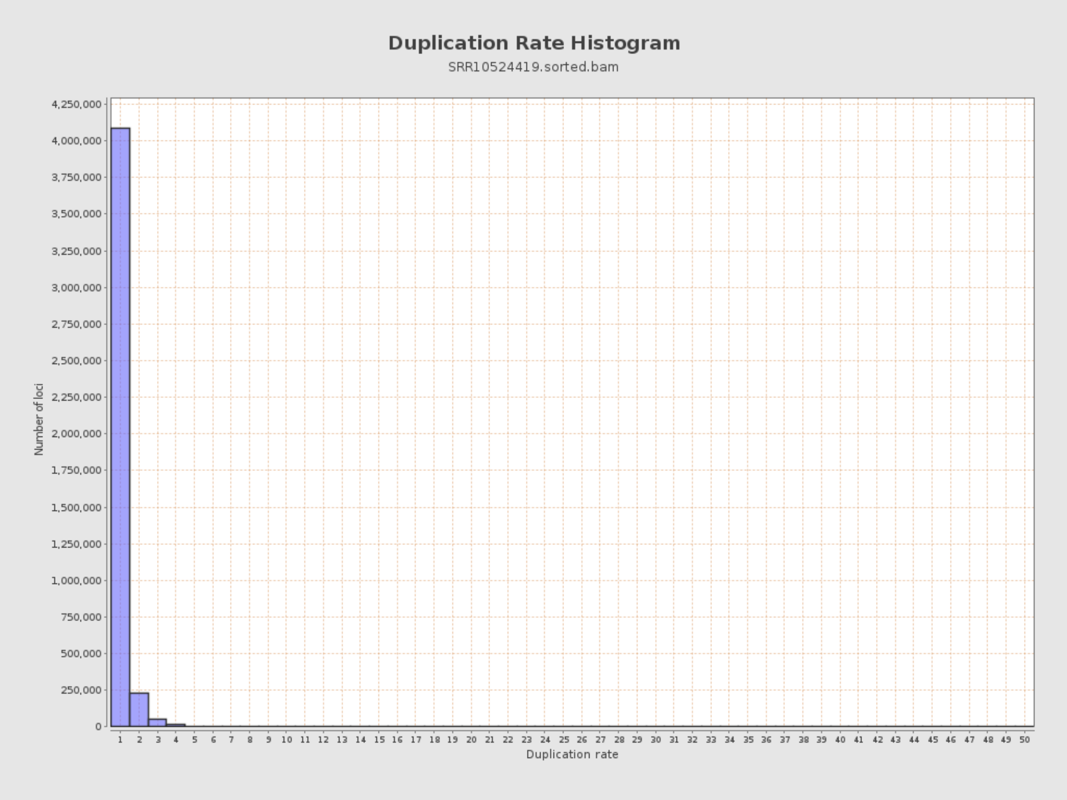
5. Results : Coverage Histogram (0-50X)



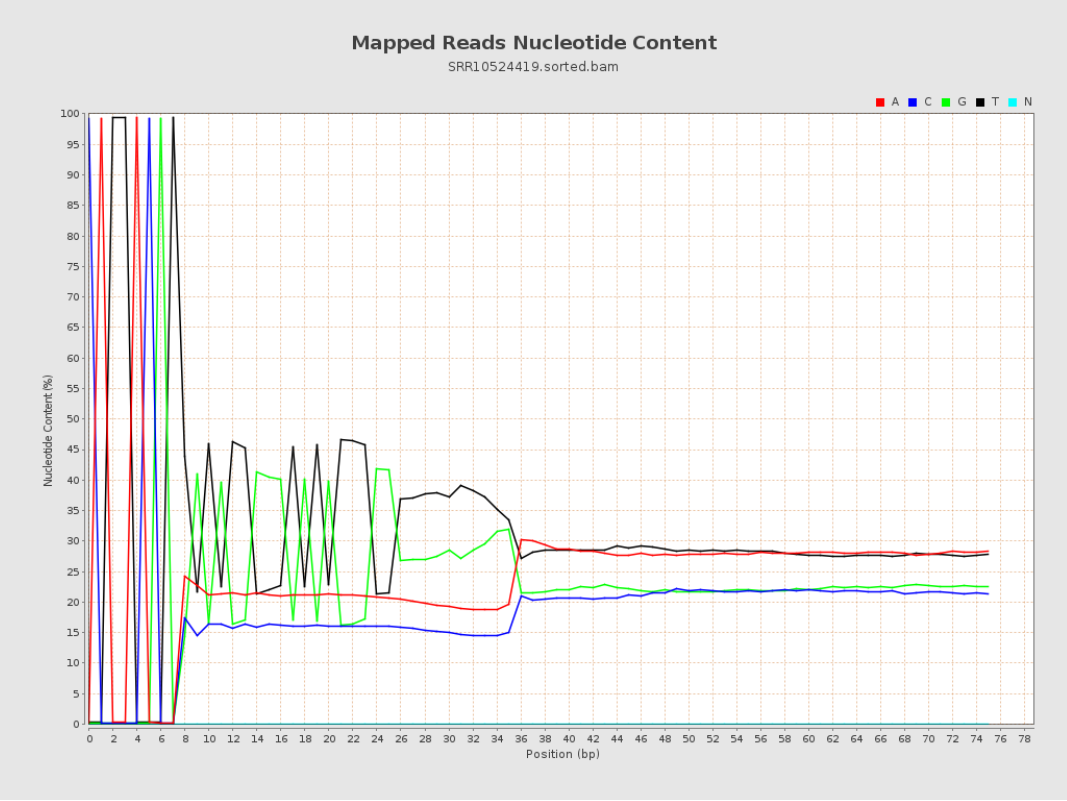
6. Results : Genome Fraction Coverage



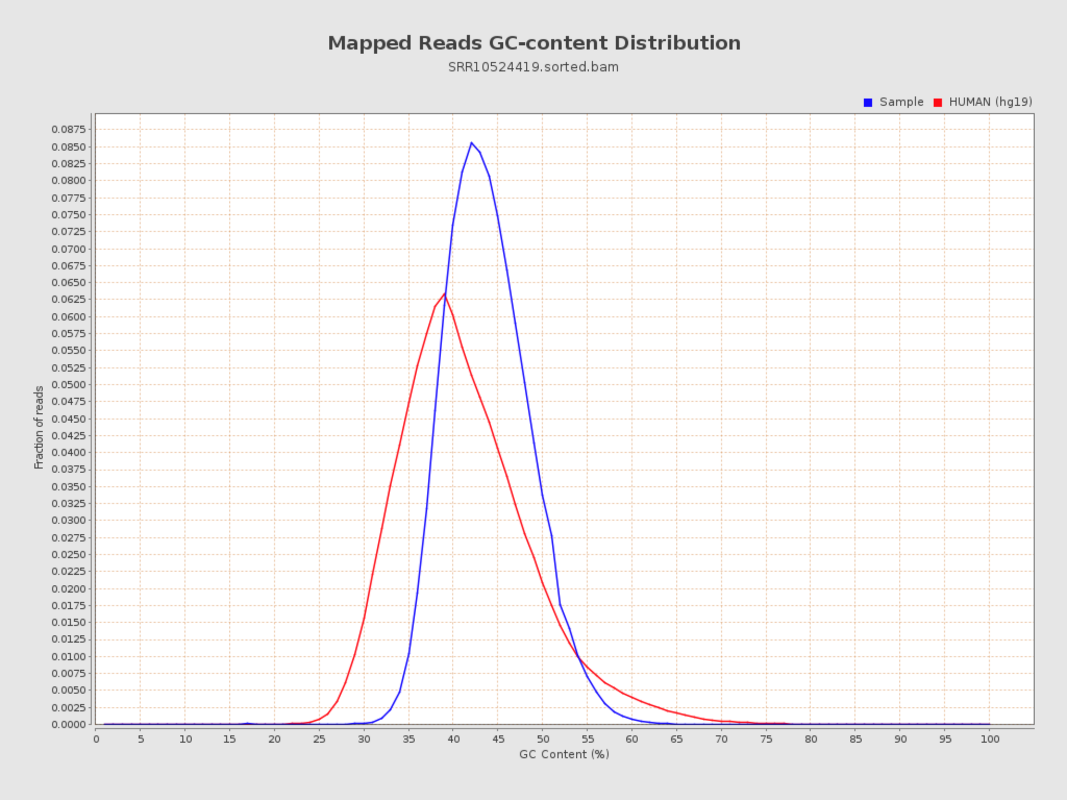
7. Results : Duplication Rate Histogram



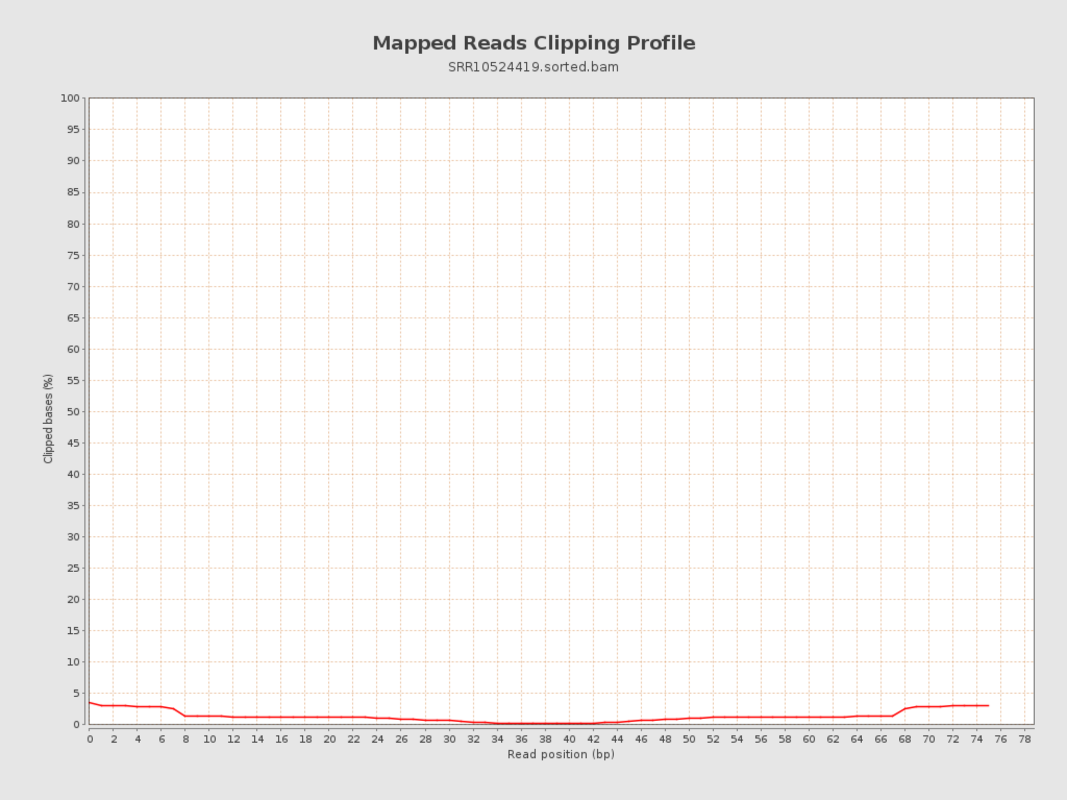
8. Results : Mapped Reads Nucleotide Content



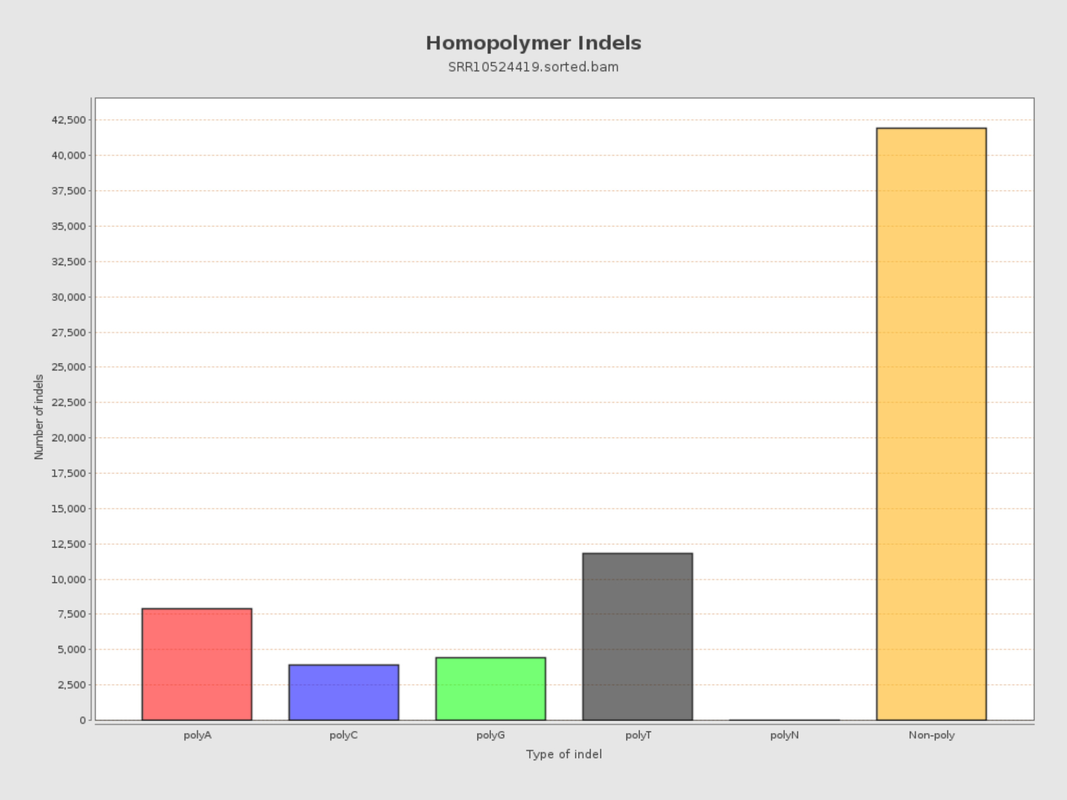
9. Results : Mapped Reads GC-content Distribution



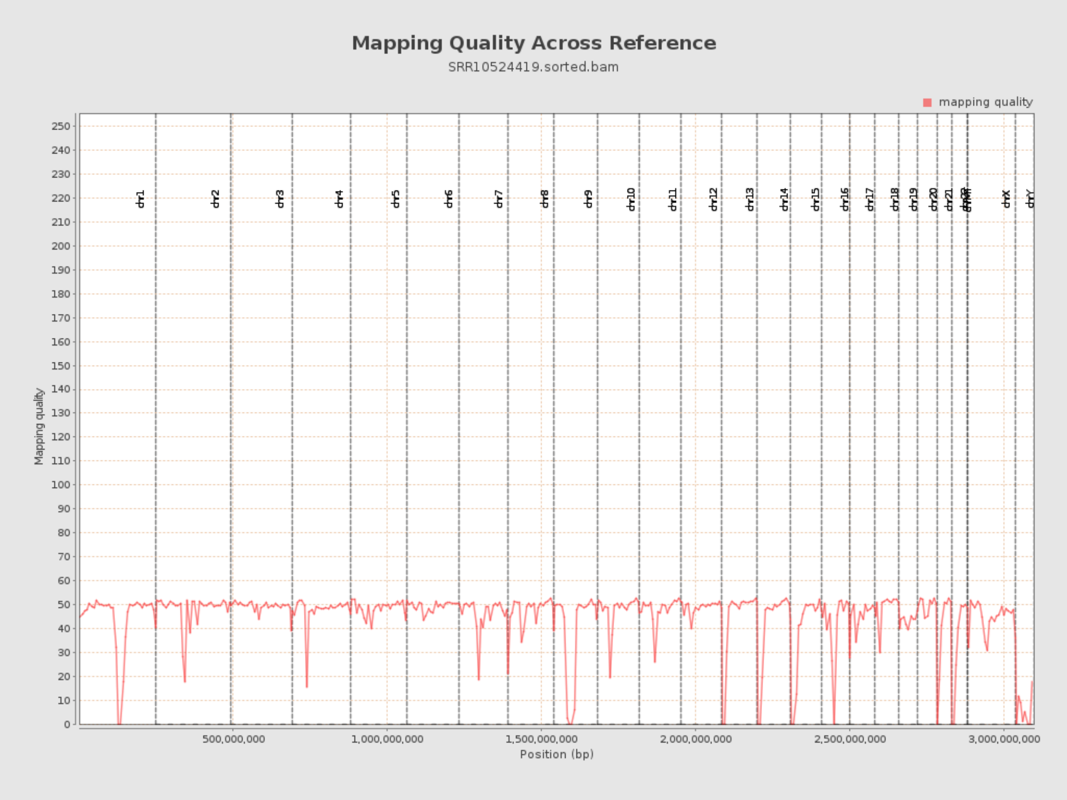
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram