Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 14:48:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818809.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_SRR1818809 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818809.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 14:48:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818809.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,079,036
Mapped reads	1,046,825 / 97.01%
Unmapped reads	32,211 / 2.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,933 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	370,203 / 34.31%
Duplication rate	30.1%
Clipped reads	1,041,482 / 96.52%

2.2. ACGT Content

Number/percentage of A's	19,495,904 / 27.41%
Number/percentage of C's	14,644,152 / 20.59%
Number/percentage of T's	20,914,156 / 29.4%
Number/percentage of G's	16,066,088 / 22.59%
Number/percentage of N's	4,210 / 0.01%
GC Percentage	43.18%

2.3. Coverage

Mean	0.023

Standard Deviation	0.3313

2.4. Mapping Quality

Mean Mapping Quality	47.72

2.5. Mismatches and indels

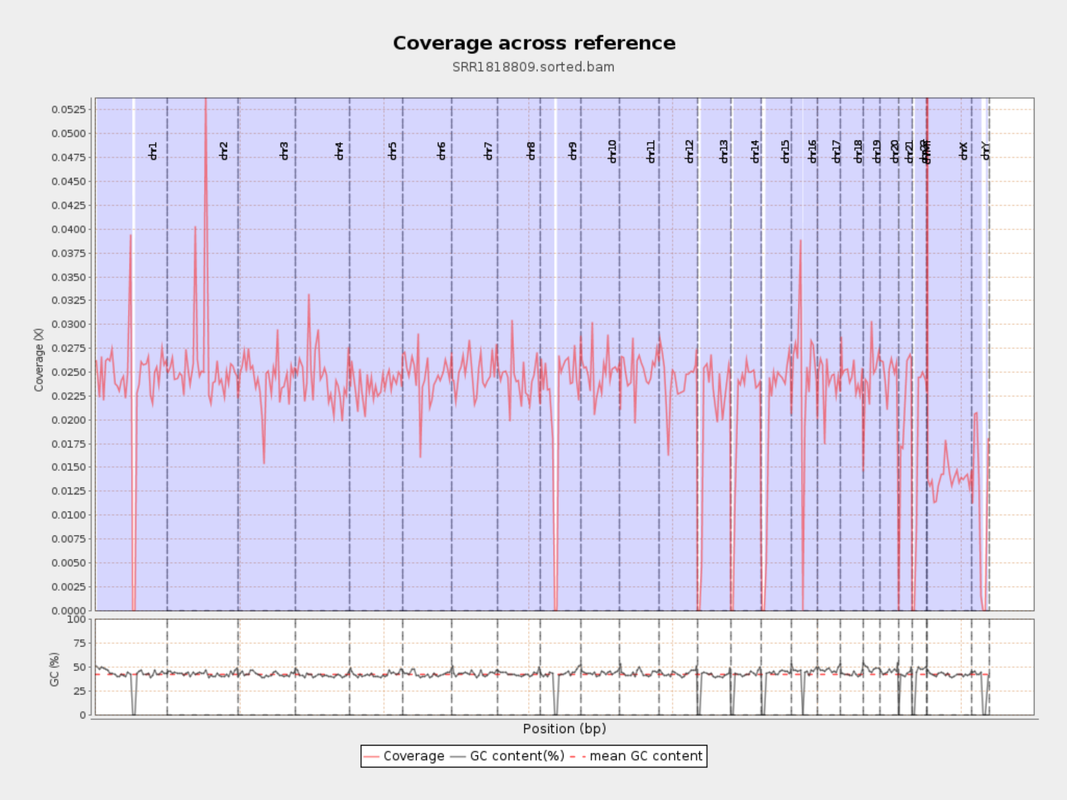
General error rate	0.53%
Mismatches	361,534
Insertions	9,331
Mapped reads with at least one insertion	0.88%
Deletions	18,276
Mapped reads with at least one deletion	1.73%
Homopolymer indels	38.37%

2.6. Chromosome stats

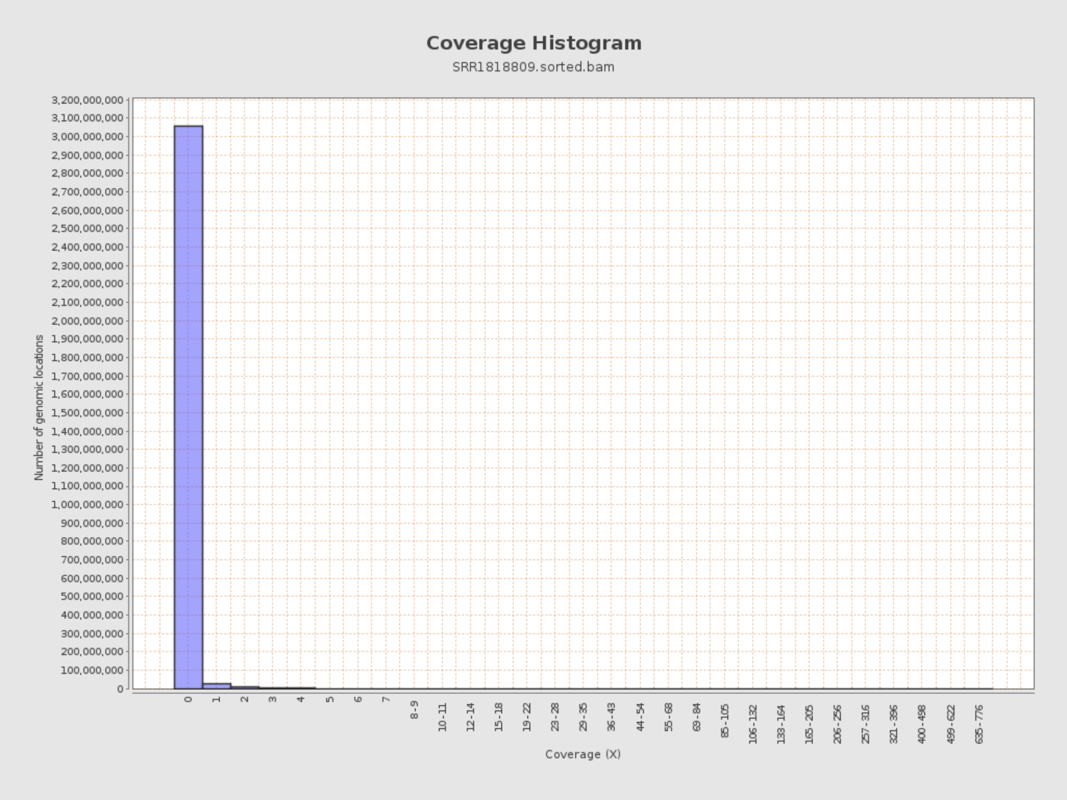
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5906288	0.0237	0.4322
chr2	243199373	6351797	0.0261	0.5778
chr3	198022430	4793154	0.0242	0.2474
chr4	191154276	4680543	0.0245	0.2759
chr5	180915260	4289399	0.0237	0.2578
chr6	171115067	4205204	0.0246	0.2711
chr7	159138663	3979727	0.025	0.2862

chr8	146364022	3546814	0.0242	0.2697
chr9	141213431	3082242	0.0218	0.2709
chr10	135534747	3388916	0.025	0.3392
chr11	135006516	3401272	0.0252	0.2826
chr12	133851895	3225464	0.0241	0.2657
chr13	115169878	2277986	0.0198	0.2235
chr14	107349540	2180153	0.0203	0.2559
chr15	102531392	2024330	0.0197	0.2277
chr16	90354753	2184763	0.0242	0.3978
chr17	81195210	1954685	0.0241	0.2638
chr18	78077248	1920185	0.0246	0.3287
chr19	59128983	1470596	0.0249	0.3599
chr20	63025520	1547891	0.0246	0.2677
chr21	48129895	972313	0.0202	0.2348
chr22	51304566	868736	0.0169	0.2294
chrMT	16571	111511	6.7293	6.9061
chrX	155270560	2153353	0.0139	0.2029
chrY	59373566	637848	0.0107	0.5638

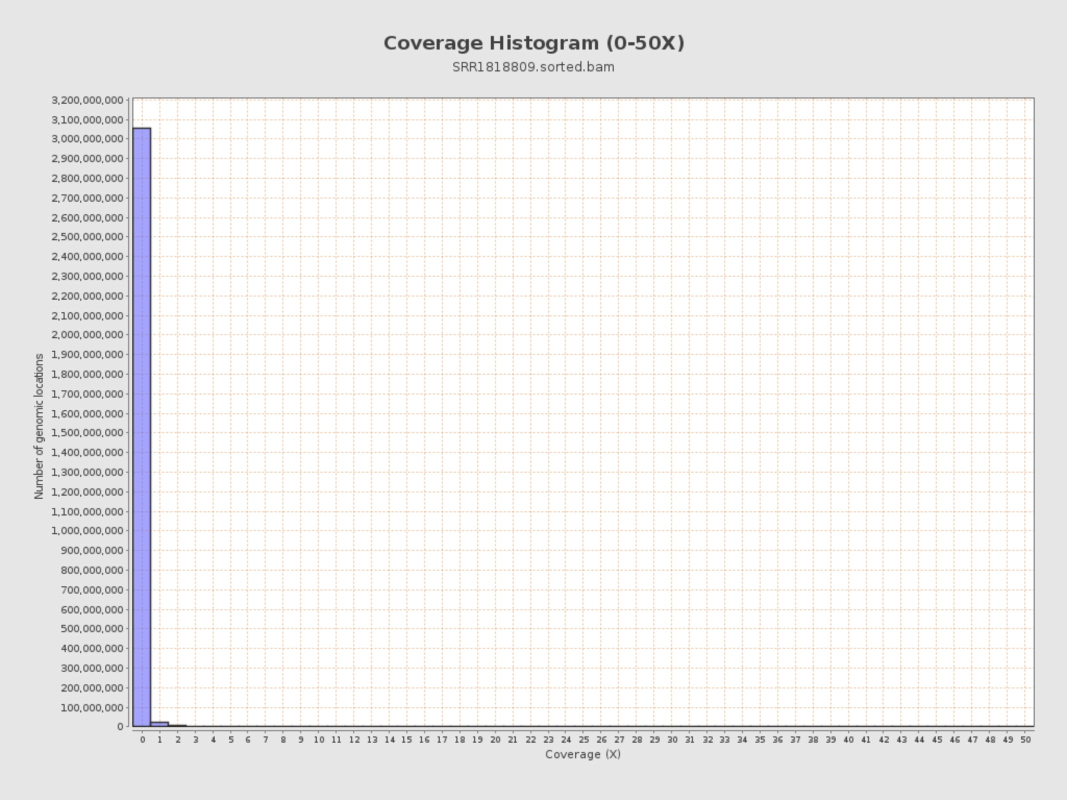
3. Results : Coverage across reference



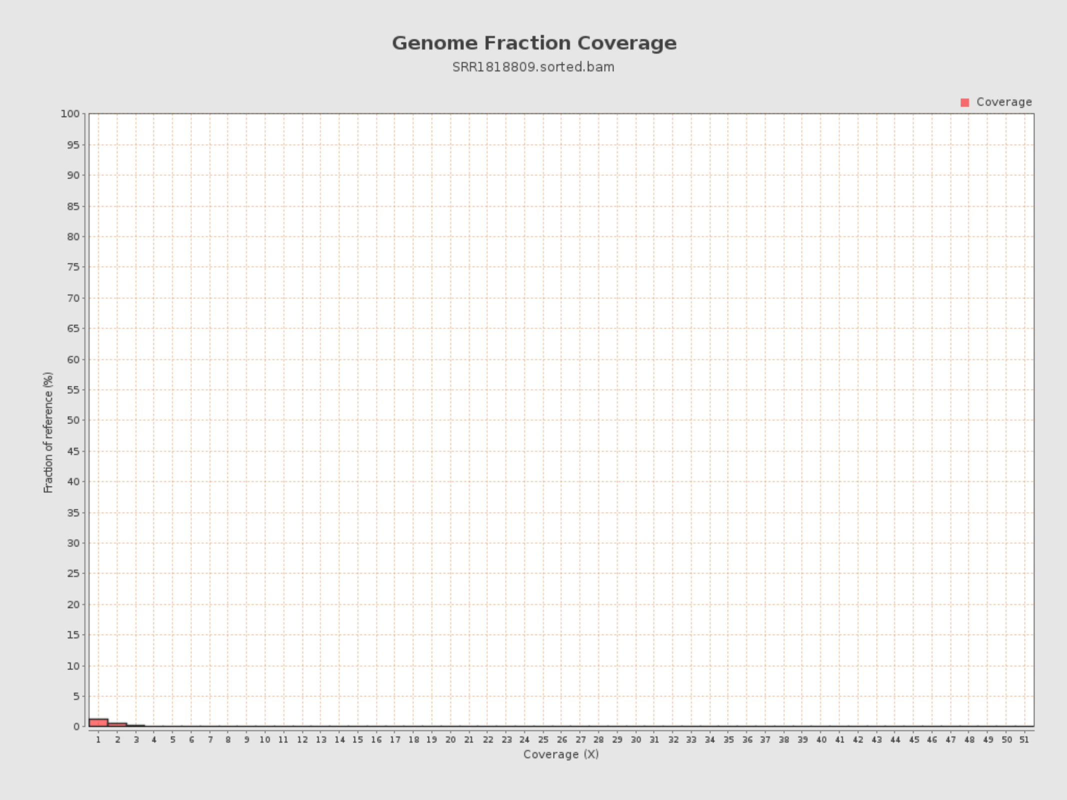
4. Results : Coverage Histogram



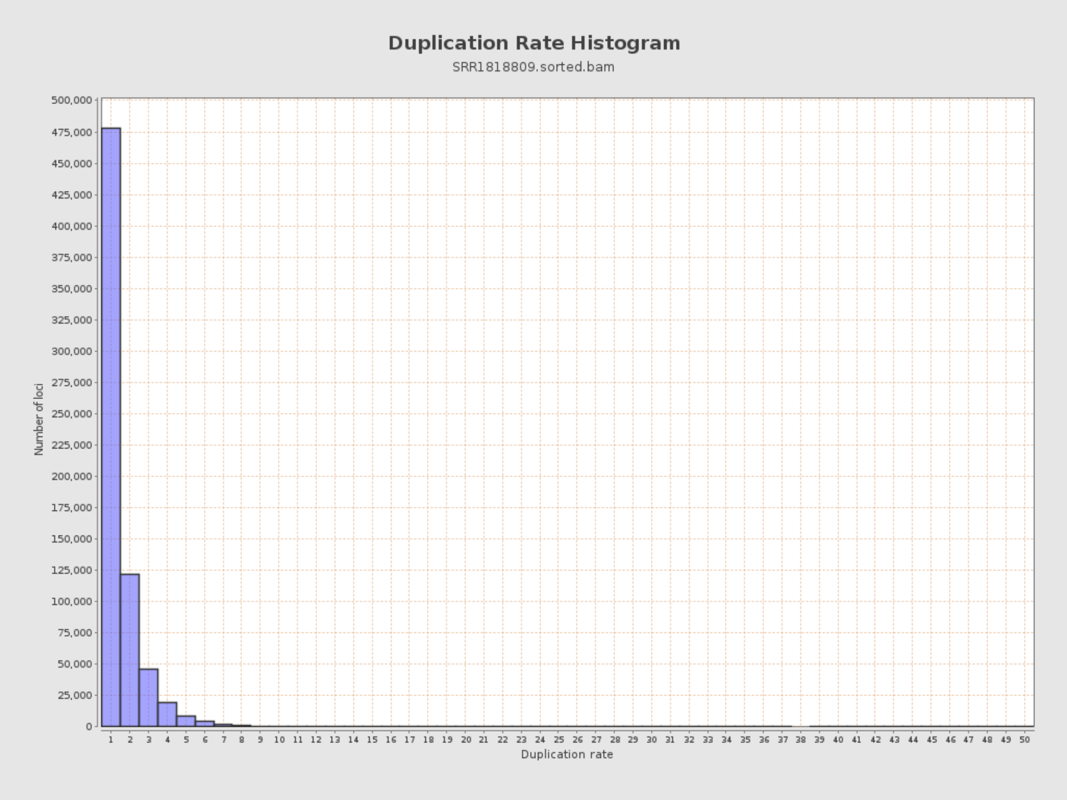
5. Results : Coverage Histogram (0-50X)



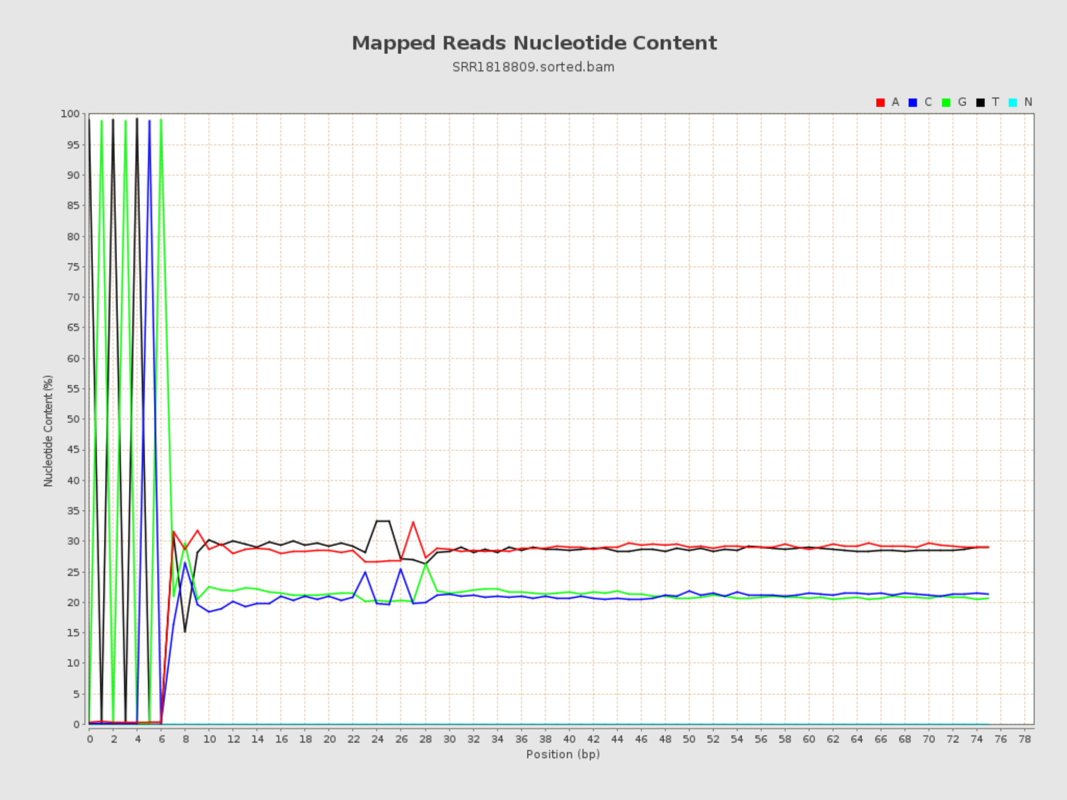
6. Results : Genome Fraction Coverage



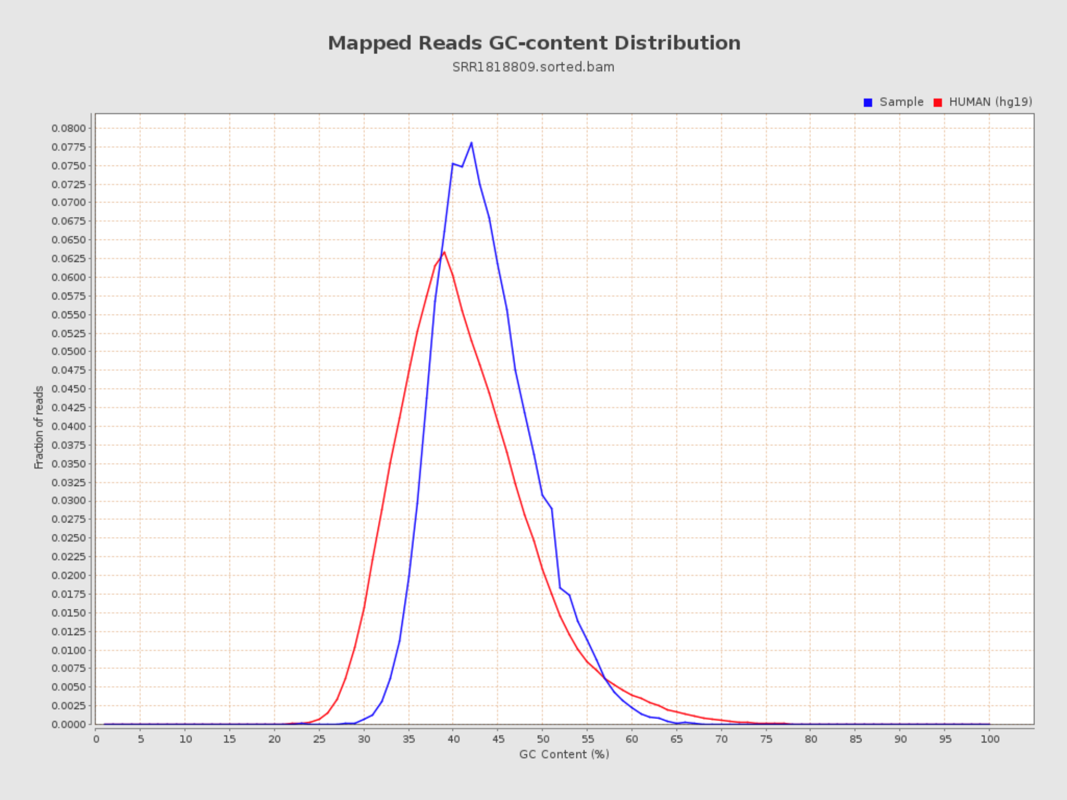
7. Results : Duplication Rate Histogram



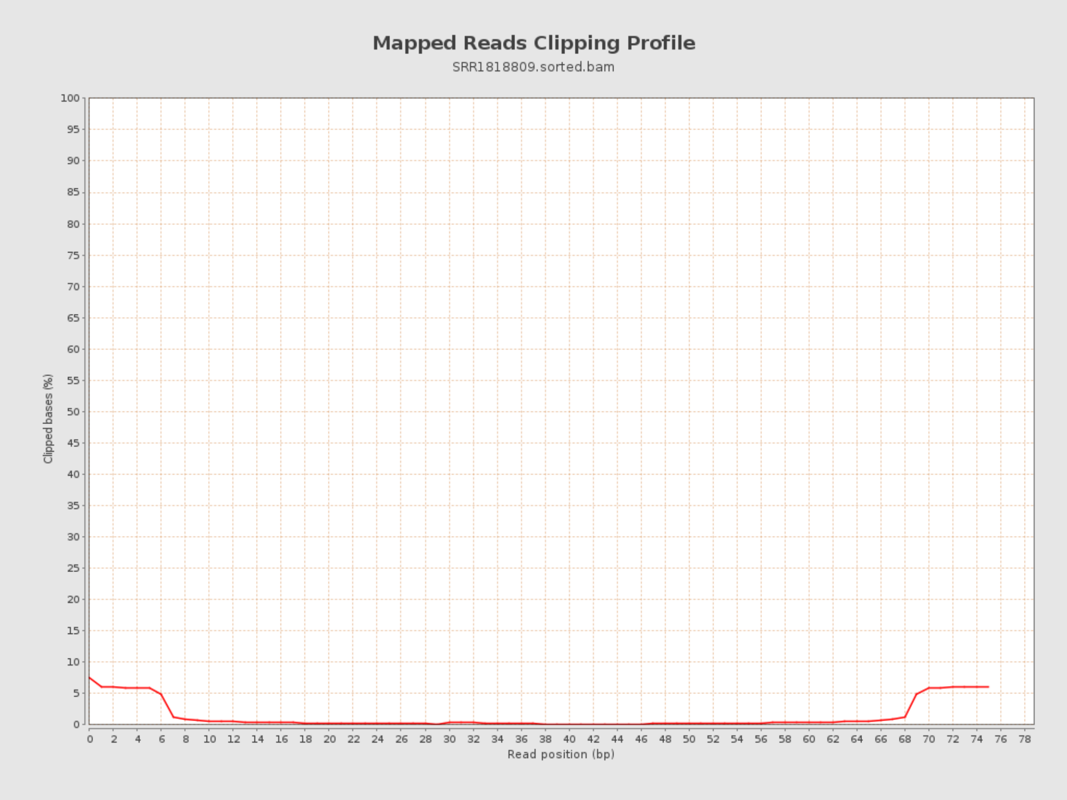
8. Results : Mapped Reads Nucleotide Content



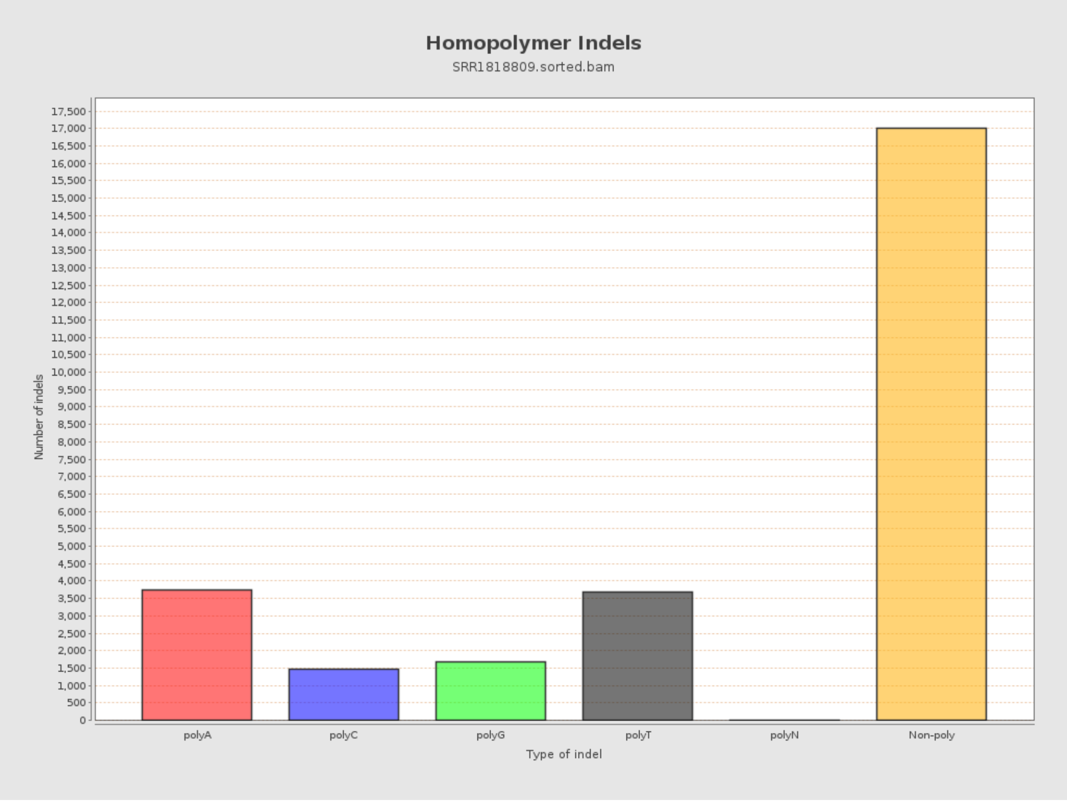
9. Results : Mapped Reads GC-content Distribution



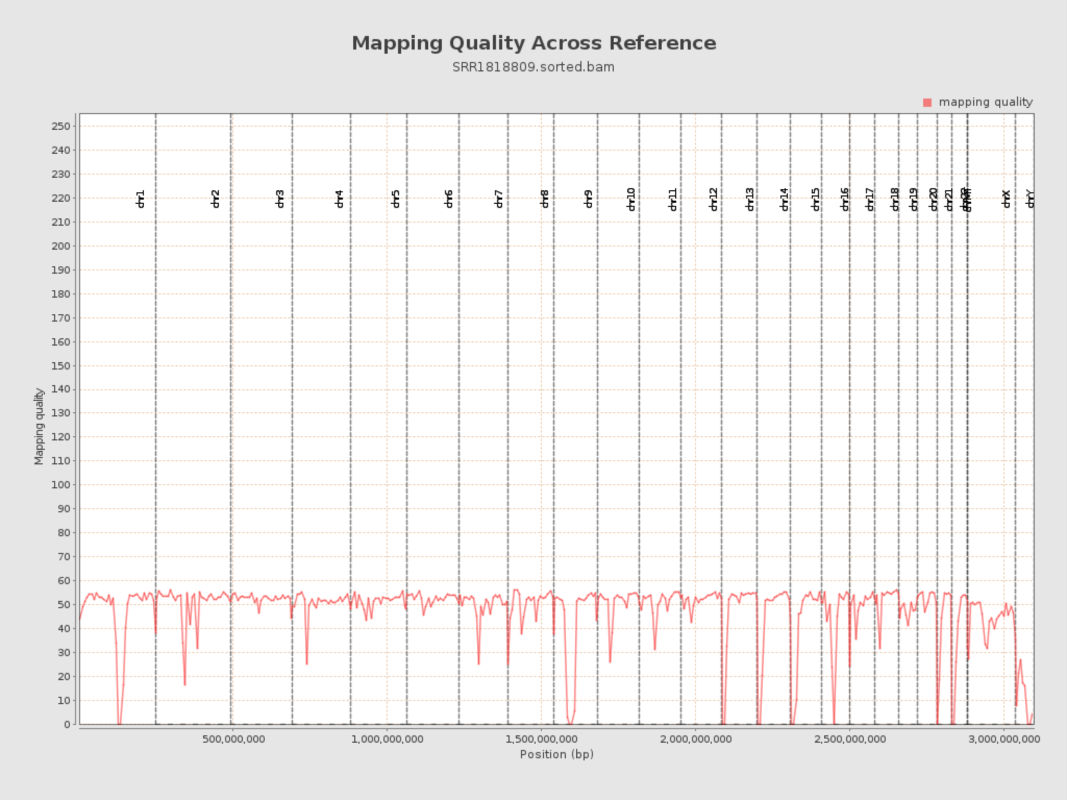
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram