Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 11:53:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524588.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_SRR10524588 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524588.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 11:53:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524588.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,226,624
Mapped reads	1,112,115 / 90.66%
Unmapped reads	114,509 / 9.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,598 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	25,450 / 2.07%
Duplication rate	1.53%
Clipped reads	1,112,038 / 90.66%

2.2. ACGT Content

Number/percentage of A's	16,715,177 / 26.1%
Number/percentage of C's	11,940,564 / 18.65%
Number/percentage of T's	20,544,551 / 32.08%
Number/percentage of G's	14,830,397 / 23.16%
Number/percentage of N's	1,876 / 0%
GC Percentage	41.81%

2.3. Coverage

Mean	0.0207

Standard Deviation	0.2088

2.4. Mapping Quality

Mean Mapping Quality	45.12

2.5. Mismatches and indels

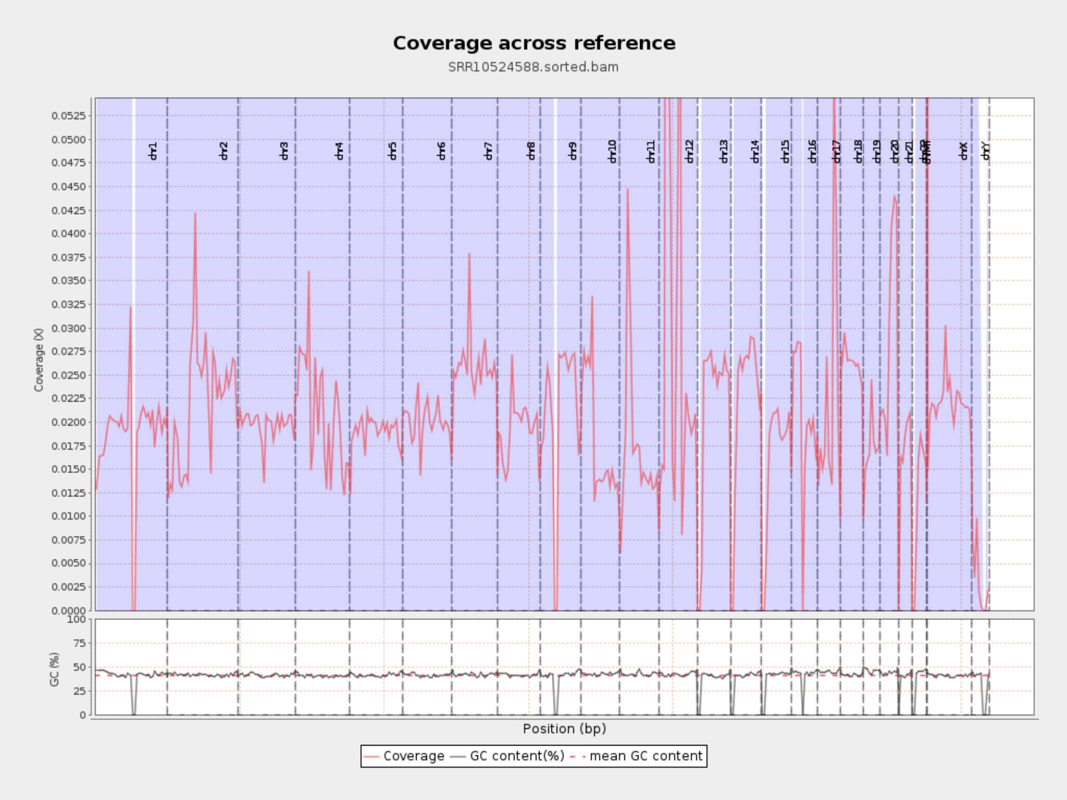
General error rate	0.49%
Mismatches	306,698
Insertions	4,444
Mapped reads with at least one insertion	0.4%
Deletions	10,354
Mapped reads with at least one deletion	0.92%
Homopolymer indels	42.32%

2.6. Chromosome stats

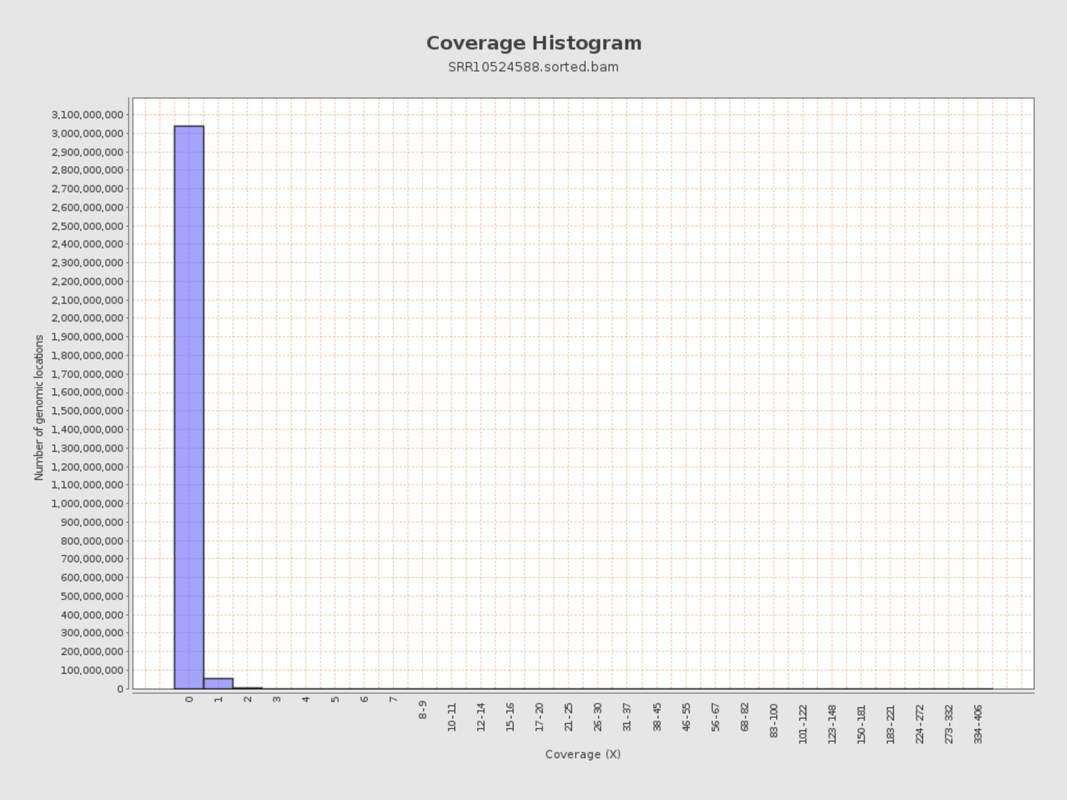
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4618423	0.0185	0.3368
chr2	243199373	5392205	0.0222	0.2256
chr3	198022430	3906523	0.0197	0.1476
chr4	191154276	4010606	0.021	0.1658
chr5	180915260	3472041	0.0192	0.147
chr6	171115067	3442321	0.0201	0.1603
chr7	159138663	4155240	0.0261	0.2823

chr8	146364022	2829204	0.0193	0.1938
chr9	141213431	2976248	0.0211	0.2184
chr10	135534747	2464839	0.0182	0.1984
chr11	135006516	2302799	0.0171	0.1743
chr12	133851895	4376059	0.0327	0.2102
chr13	115169878	2467889	0.0214	0.1542
chr14	107349540	2348309	0.0219	0.1651
chr15	102531392	1633897	0.0159	0.133
chr16	90354753	1799484	0.0199	0.1568
chr17	81195210	1878726	0.0231	0.1654
chr18	78077248	2065181	0.0265	0.3776
chr19	59128983	1030949	0.0174	0.2514
chr20	63025520	1871890	0.0297	0.1864
chr21	48129895	782060	0.0162	0.1465
chr22	51304566	604457	0.0118	0.1139
chrMT	16571	7789	0.47	0.7142
chrX	155270560	3432803	0.0221	0.1791
chrY	59373566	179792	0.003	0.0815

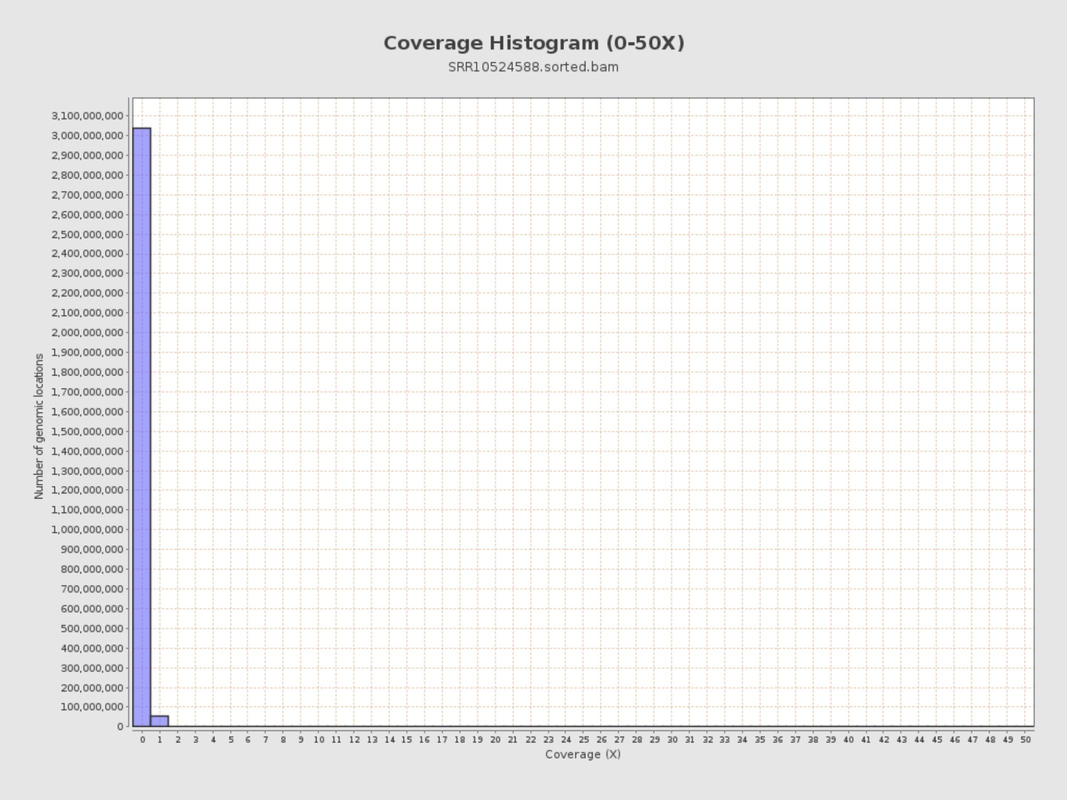
3. Results : Coverage across reference



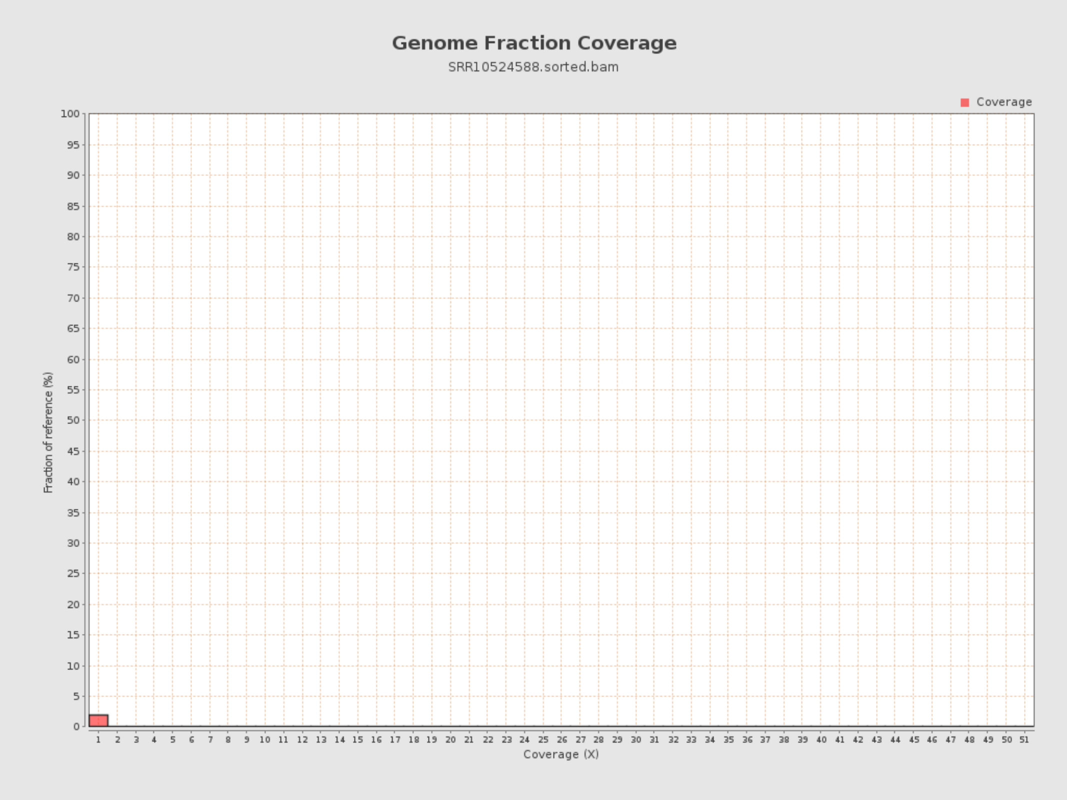
4. Results : Coverage Histogram



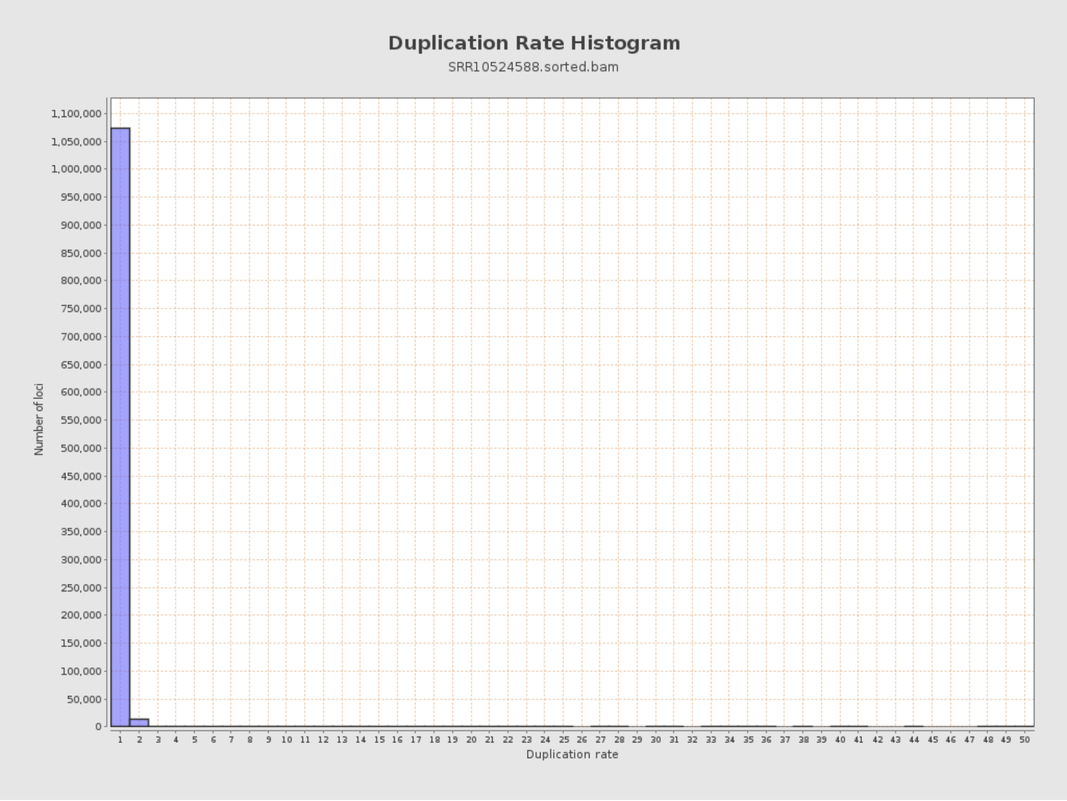
5. Results : Coverage Histogram (0-50X)



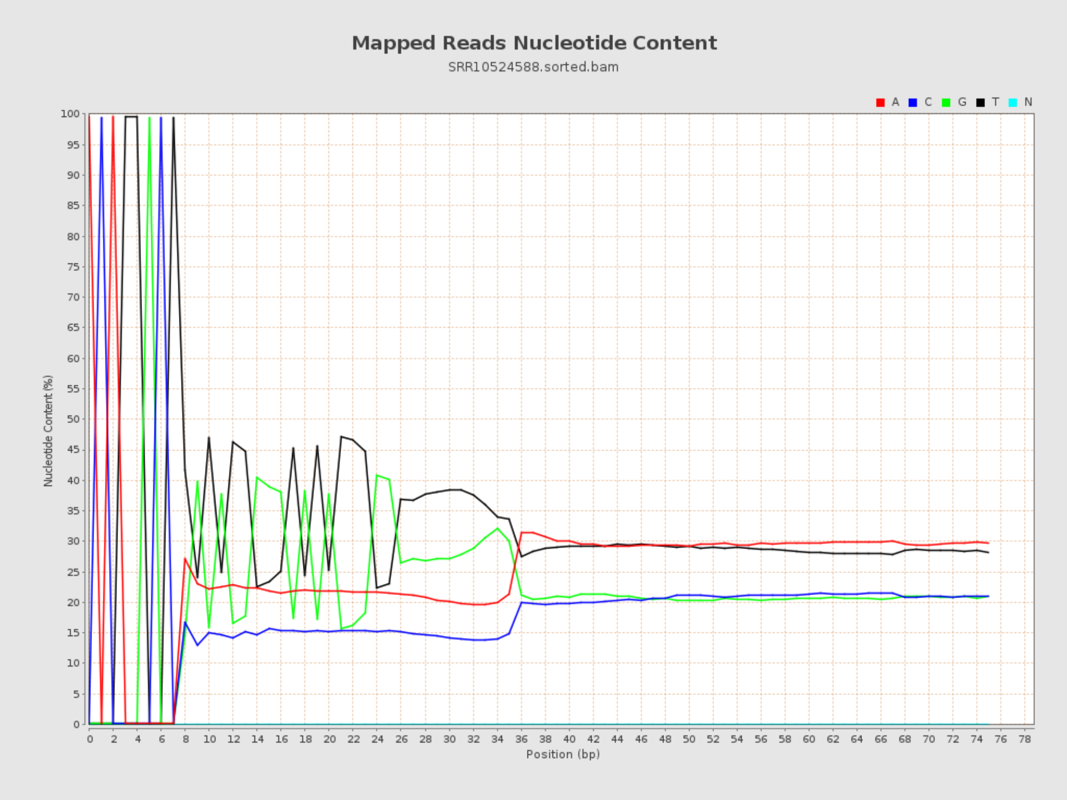
6. Results : Genome Fraction Coverage



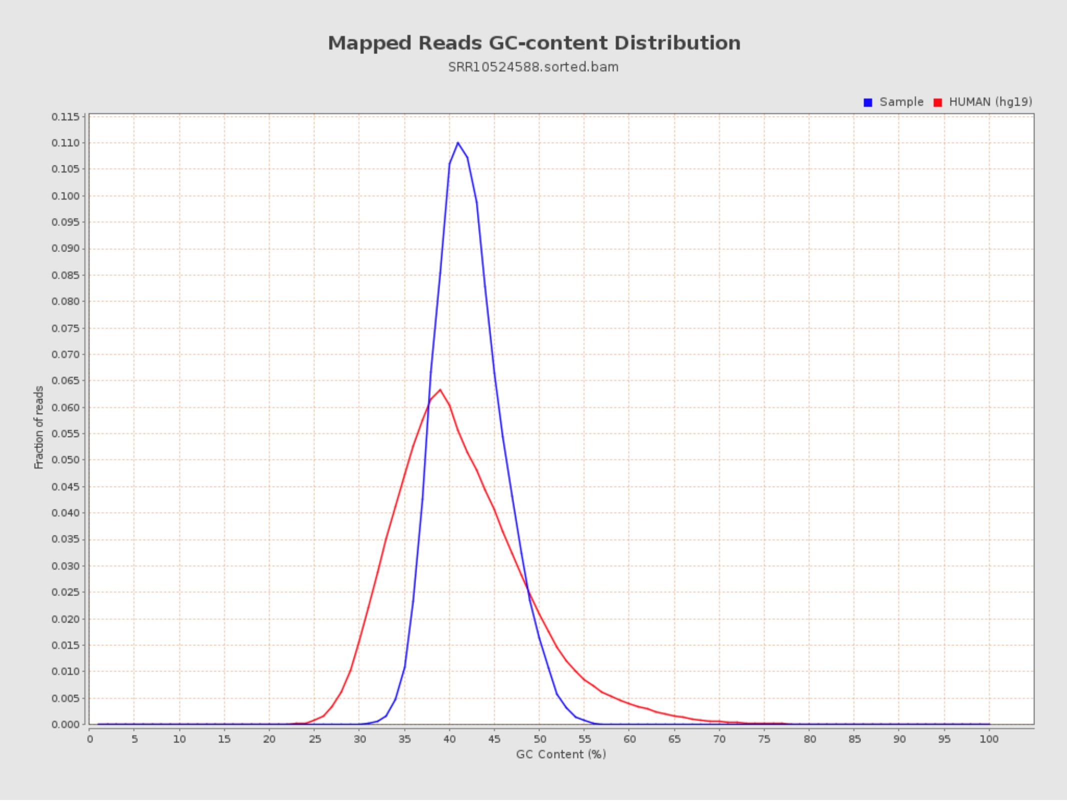
7. Results : Duplication Rate Histogram



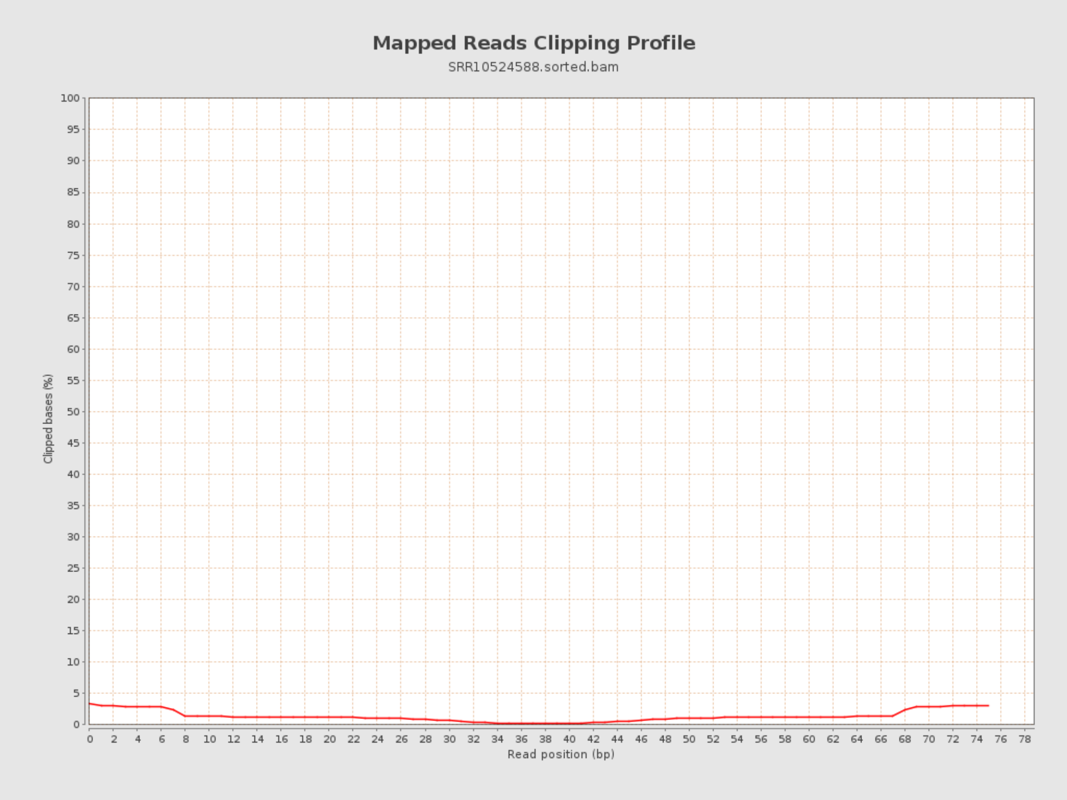
8. Results : Mapped Reads Nucleotide Content



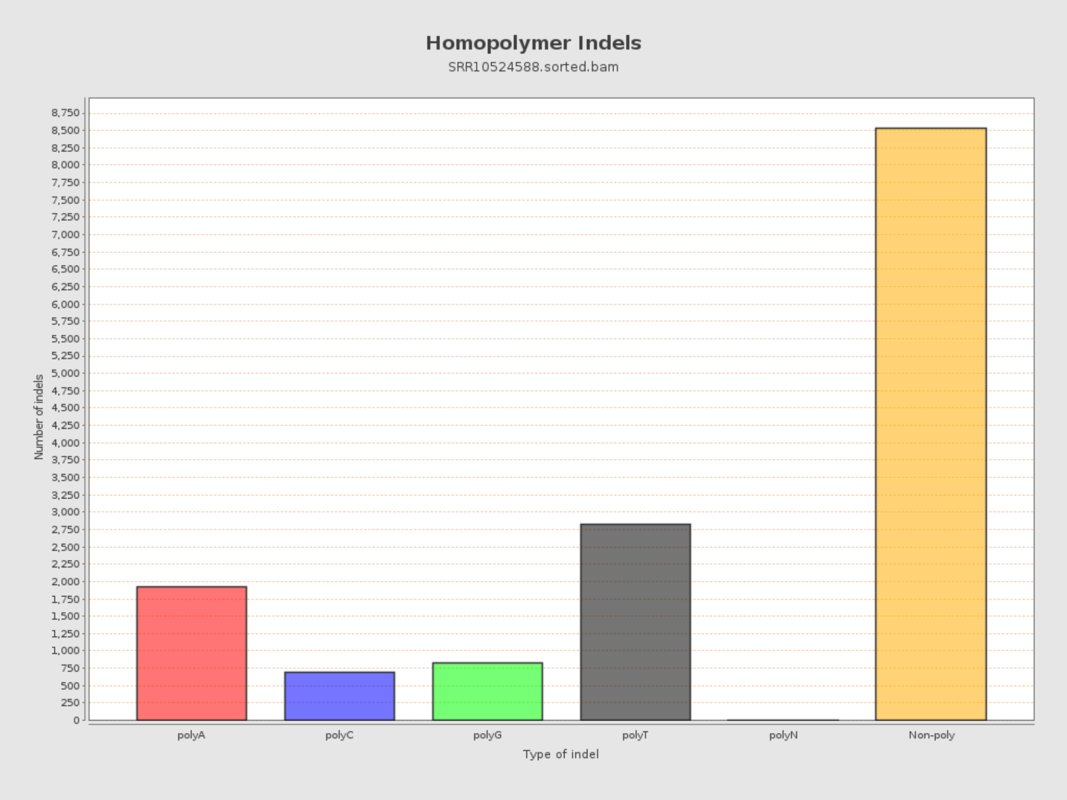
9. Results : Mapped Reads GC-content Distribution



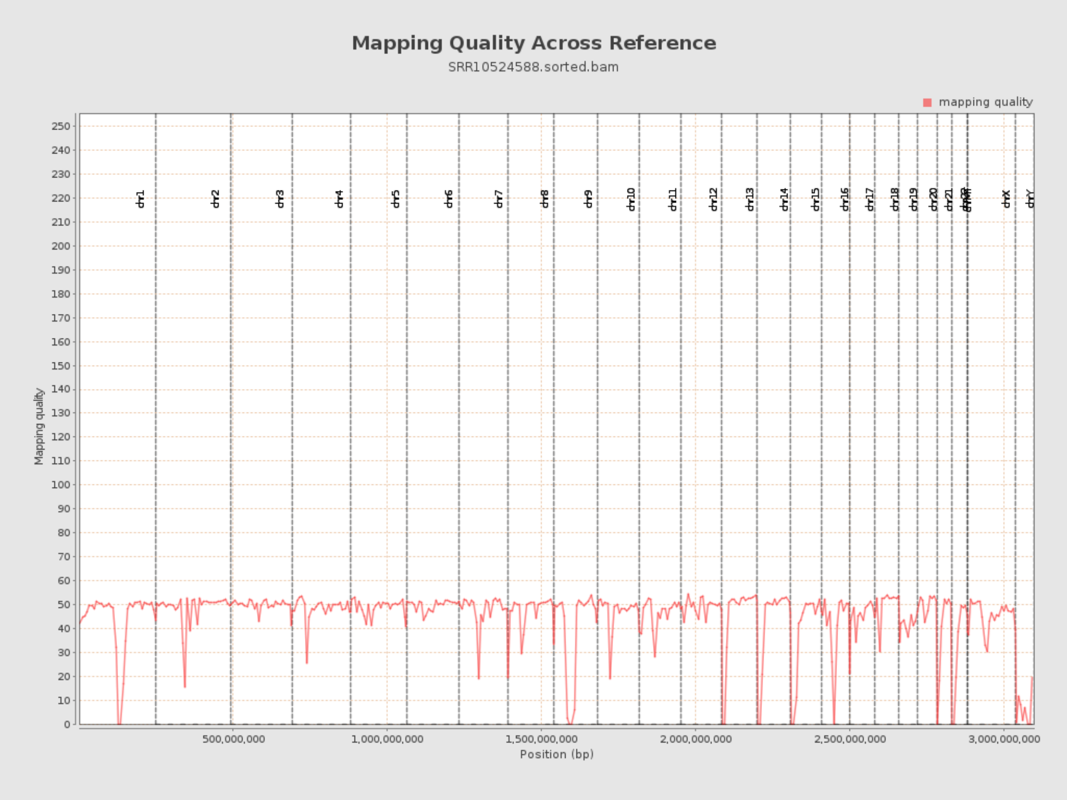
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram