Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 02:25:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080748.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_SRR3080748 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080748.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 02:25:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080748.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,282,842
Mapped reads	8,769,214 / 71.39%
Unmapped reads	3,513,628 / 28.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	48,193 / 0.39%
Read min/max/mean length	30 / 66 / 66.13
Duplicated reads (estimated)	1,221,092 / 9.94%
Duplication rate	10.18%
Clipped reads	1,649,472 / 13.43%

2.2. ACGT Content

Number/percentage of A's	172,631,468 / 31.22%
Number/percentage of C's	111,644,207 / 20.19%
Number/percentage of T's	141,791,458 / 25.65%
Number/percentage of G's	125,569,193 / 22.71%
Number/percentage of N's	1,235,862 / 0.22%
GC Percentage	42.91%

2.3. Coverage

Mean	0.1787

Standard Deviation	1.0385

2.4. Mapping Quality

Mean Mapping Quality	44.37

2.5. Mismatches and indels

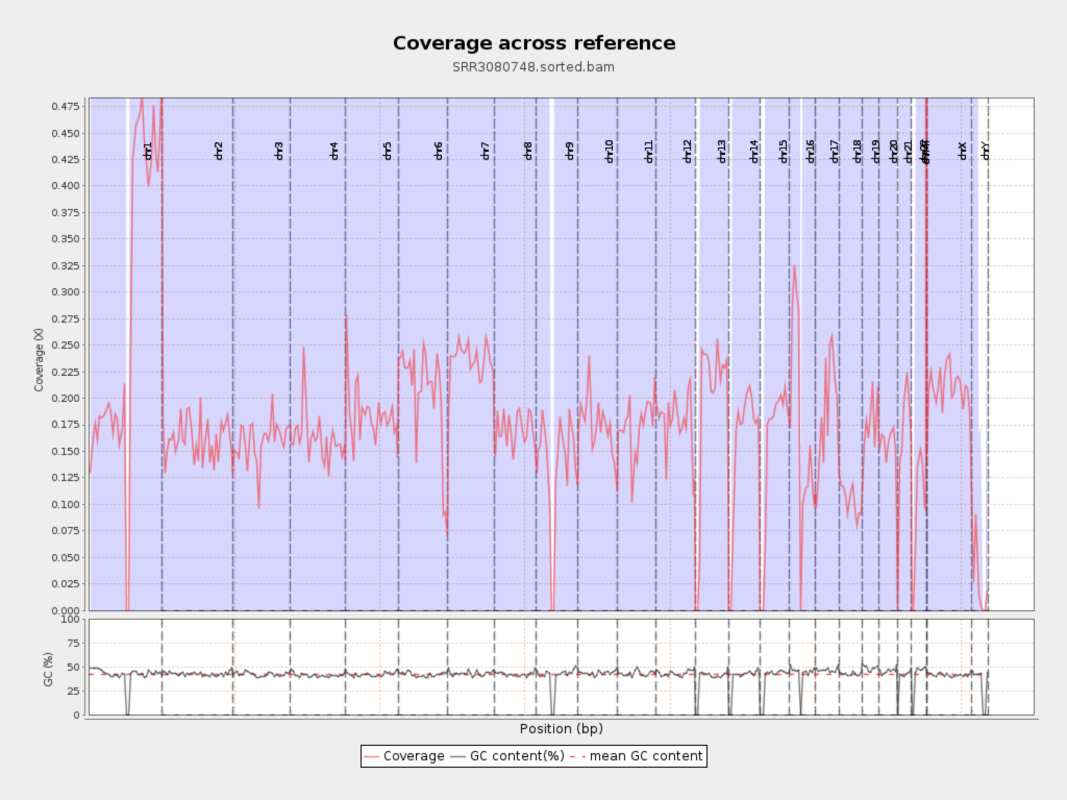
General error rate	1.04%
Mismatches	5,658,653
Insertions	38,730
Mapped reads with at least one insertion	0.44%
Deletions	97,568
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.22%

2.6. Chromosome stats

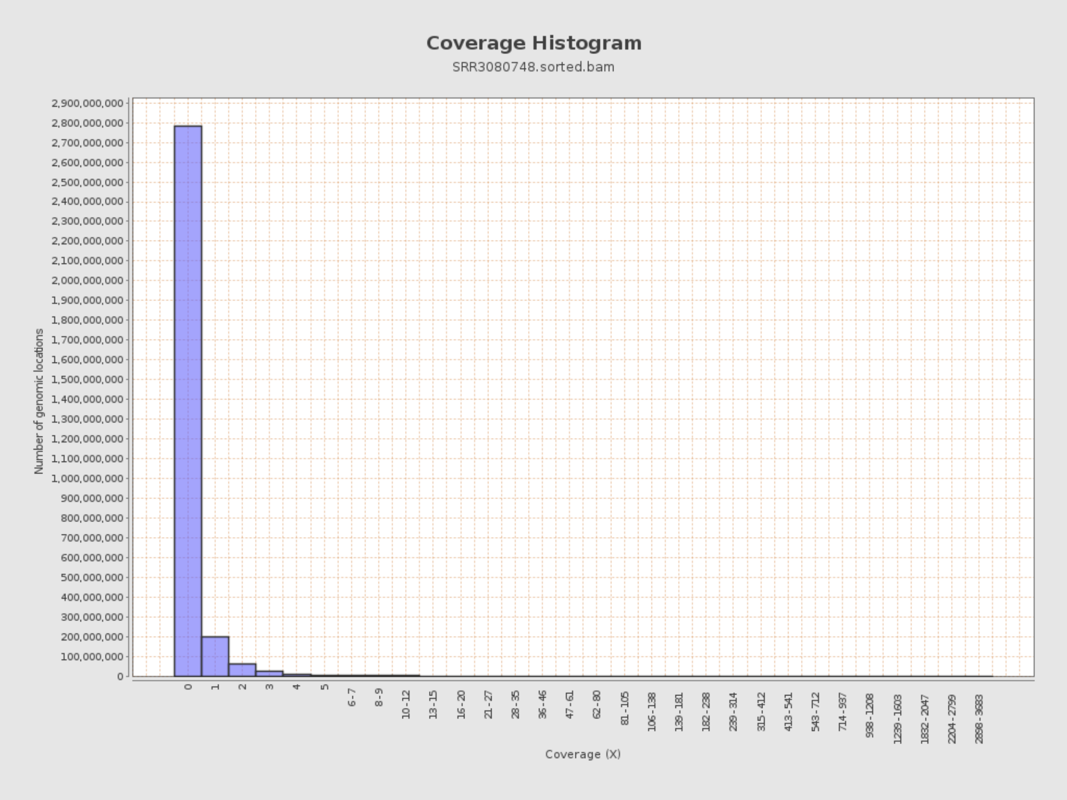
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	69167893	0.2775	1.394
chr2	243199373	39426690	0.1621	0.9152
chr3	198022430	31570249	0.1594	0.663
chr4	191154276	31018374	0.1623	0.7992
chr5	180915260	33455807	0.1849	0.7461
chr6	171115067	35280663	0.2062	1.9835
chr7	159138663	37780140	0.2374	1.3964

chr8	146364022	24924229	0.1703	1.2332
chr9	141213431	19388700	0.1373	0.7309
chr10	135534747	23815889	0.1757	1.1366
chr11	135006516	23382887	0.1732	0.8671
chr12	133851895	23782241	0.1777	0.7578
chr13	115169878	21988080	0.1909	0.754
chr14	107349540	16599098	0.1546	0.7431
chr15	102531392	15762119	0.1537	0.6648
chr16	90354753	15642841	0.1731	0.7655
chr17	81195210	15108201	0.1861	0.7894
chr18	78077248	8136670	0.1042	1.0541
chr19	59128983	10443684	0.1766	1.4923
chr20	63025520	9819616	0.1558	0.6913
chr21	48129895	7814093	0.1624	0.8022
chr22	51304566	4679277	0.0912	0.4896
chrMT	16571	147931	8.9271	8.0161
chrX	155270560	32363411	0.2084	0.8157
chrY	59373566	1556691	0.0262	0.6963

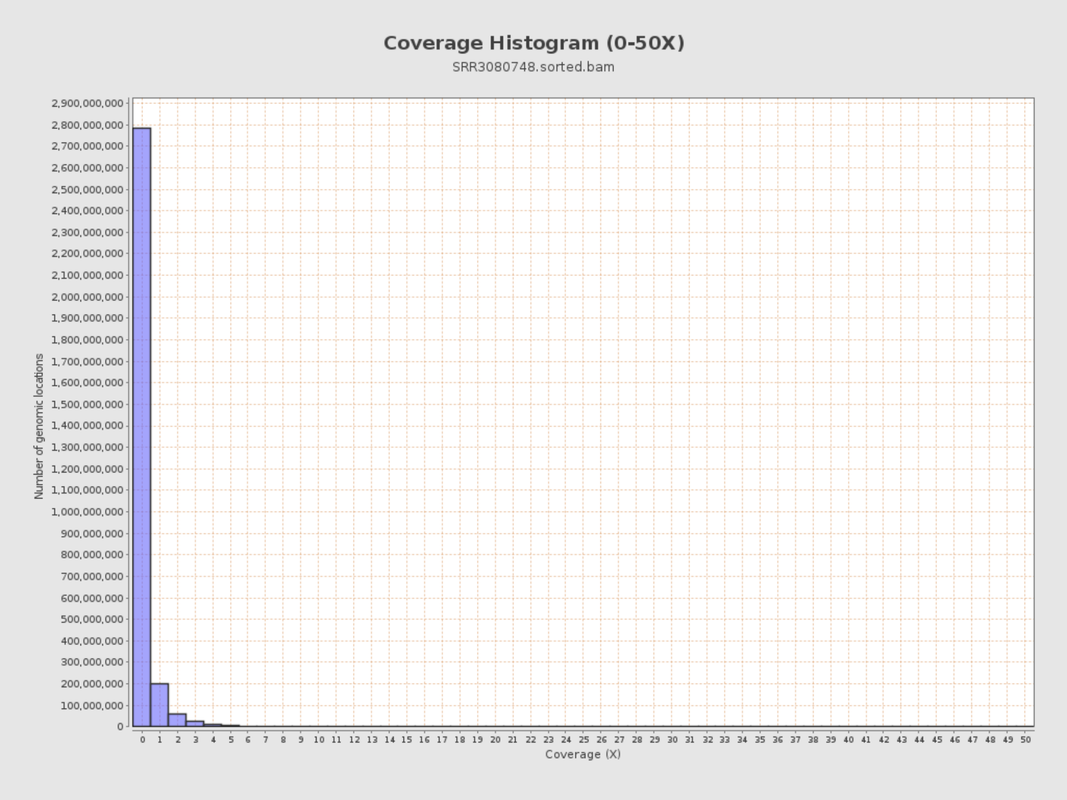
3. Results : Coverage across reference



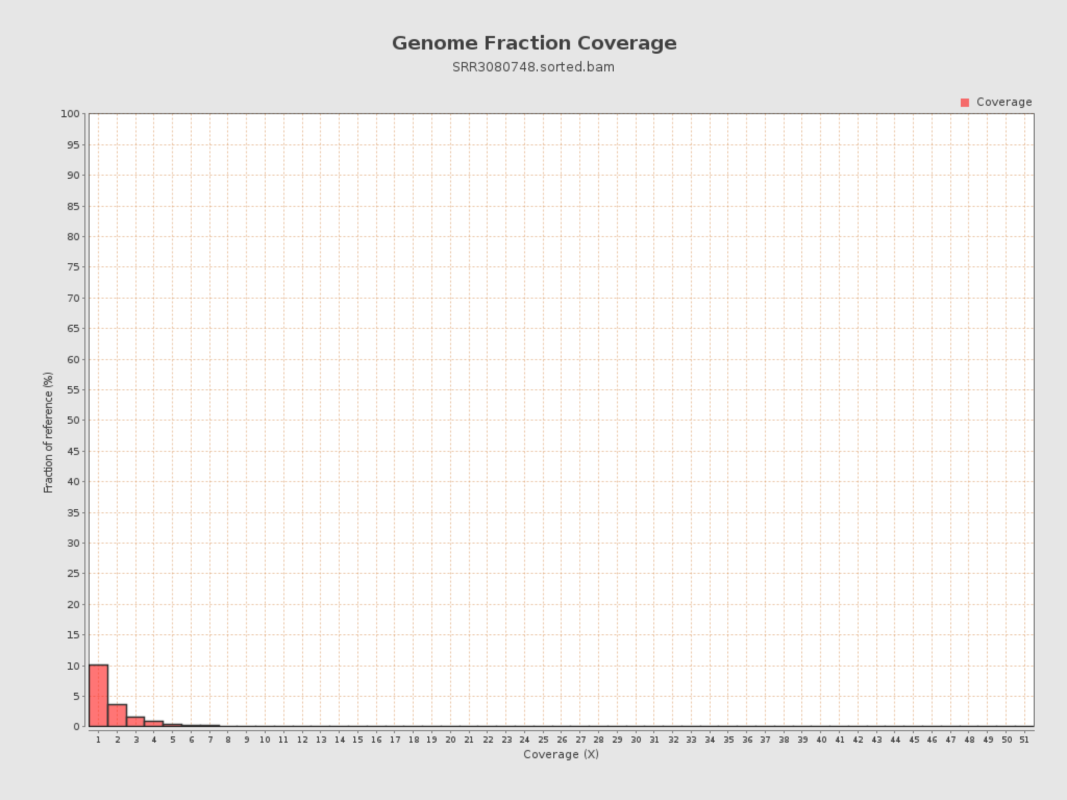
4. Results : Coverage Histogram



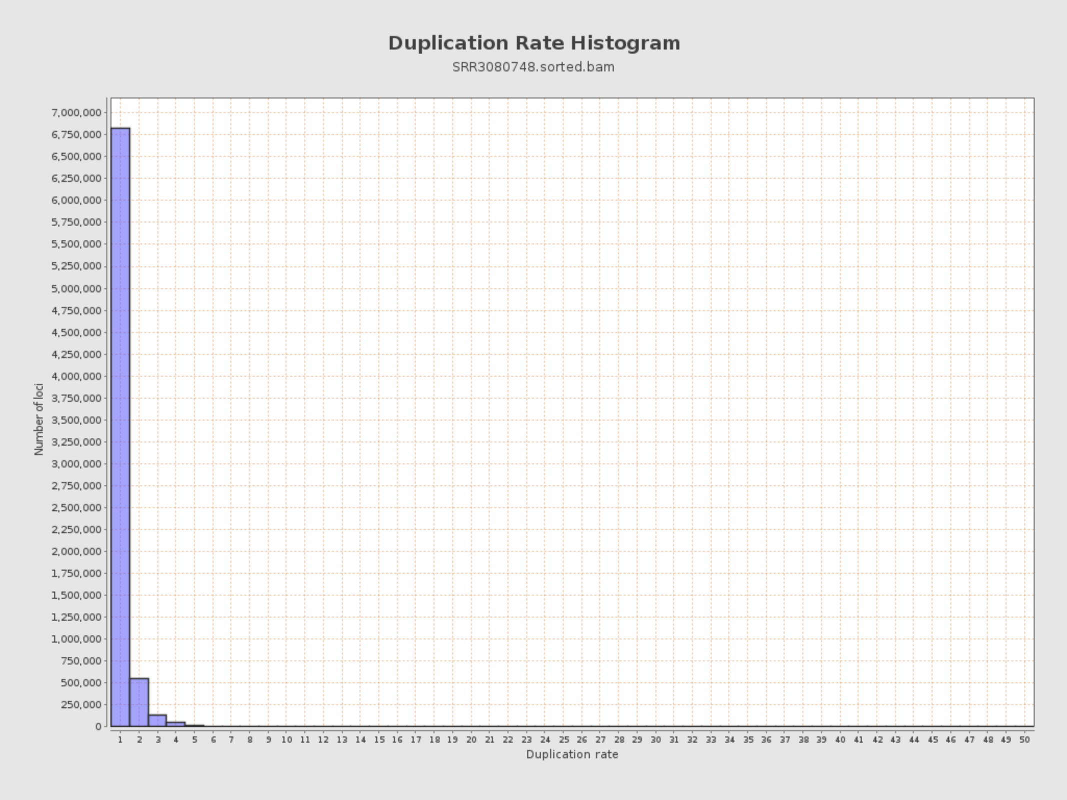
5. Results : Coverage Histogram (0-50X)



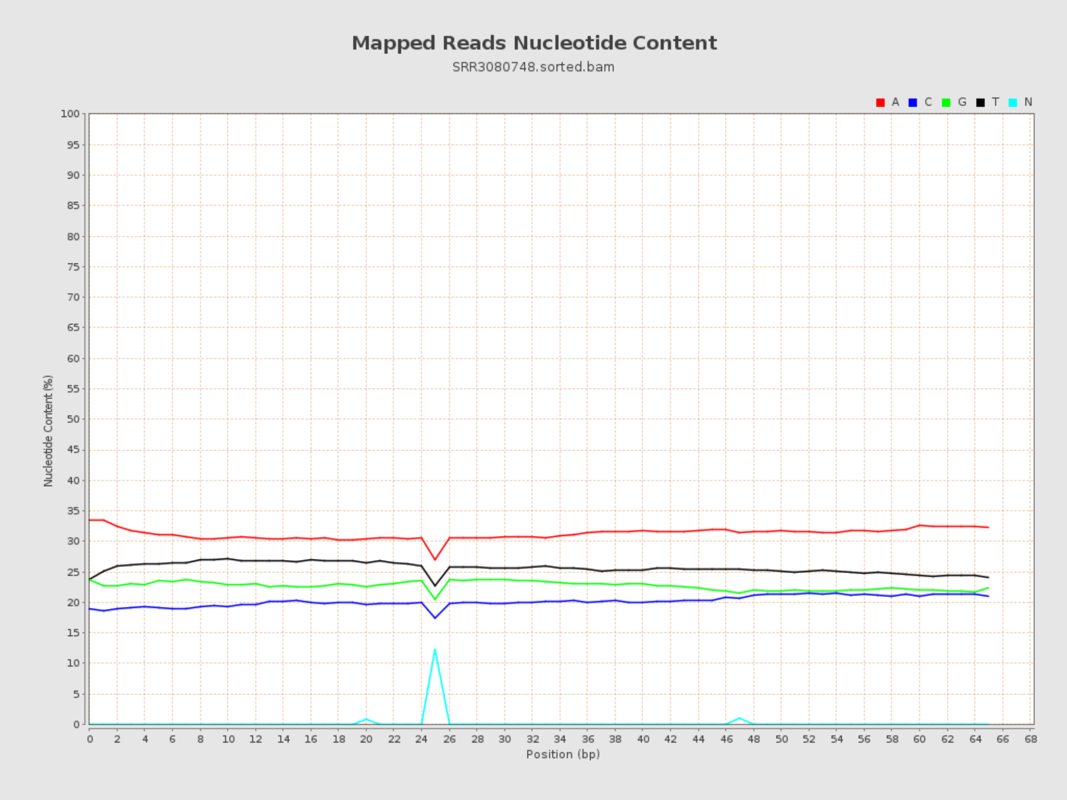
6. Results : Genome Fraction Coverage



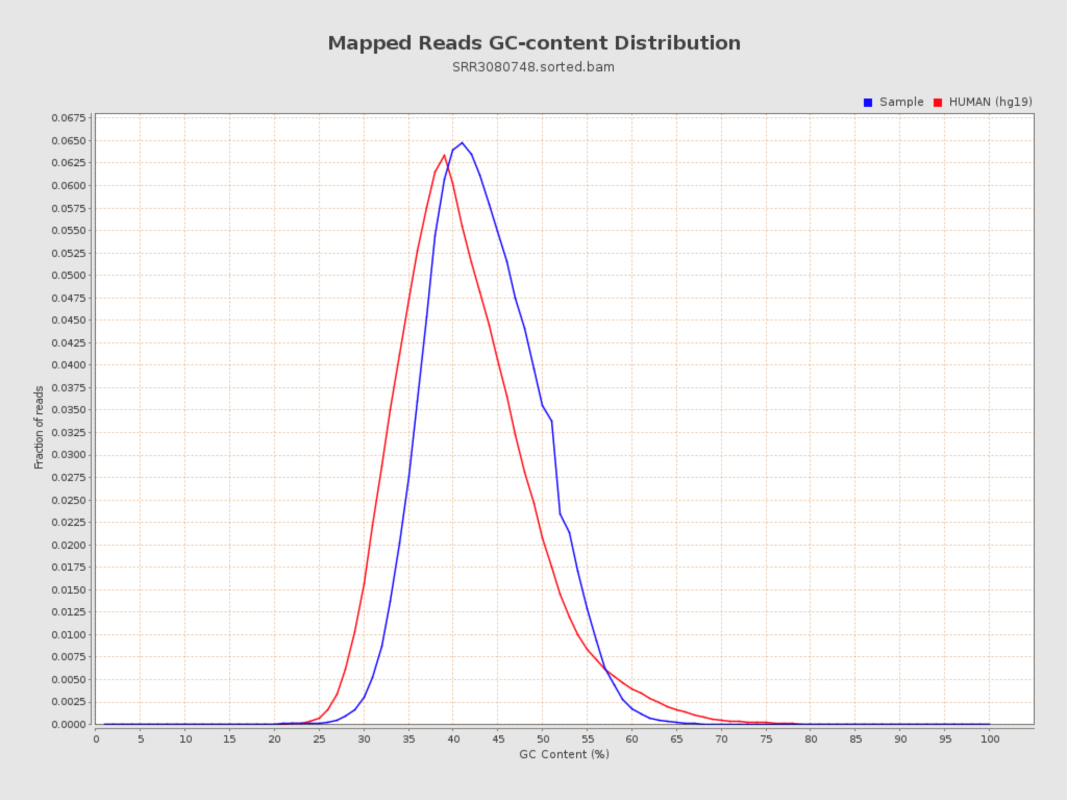
7. Results : Duplication Rate Histogram



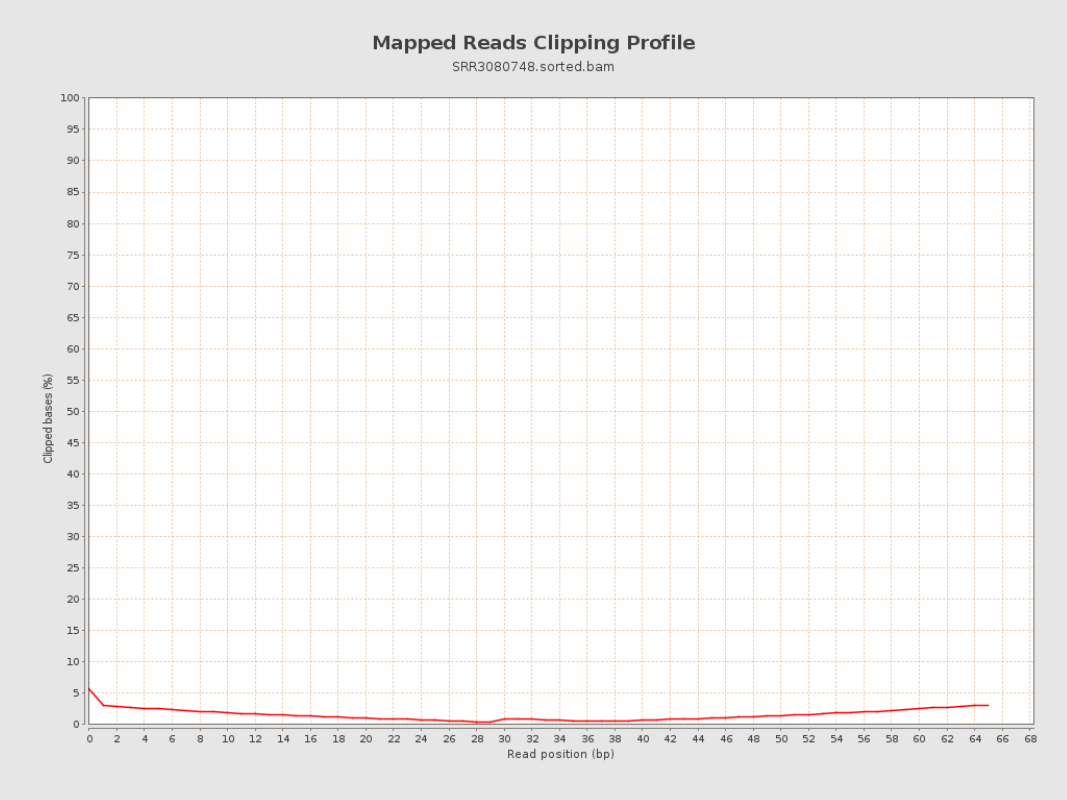
8. Results : Mapped Reads Nucleotide Content



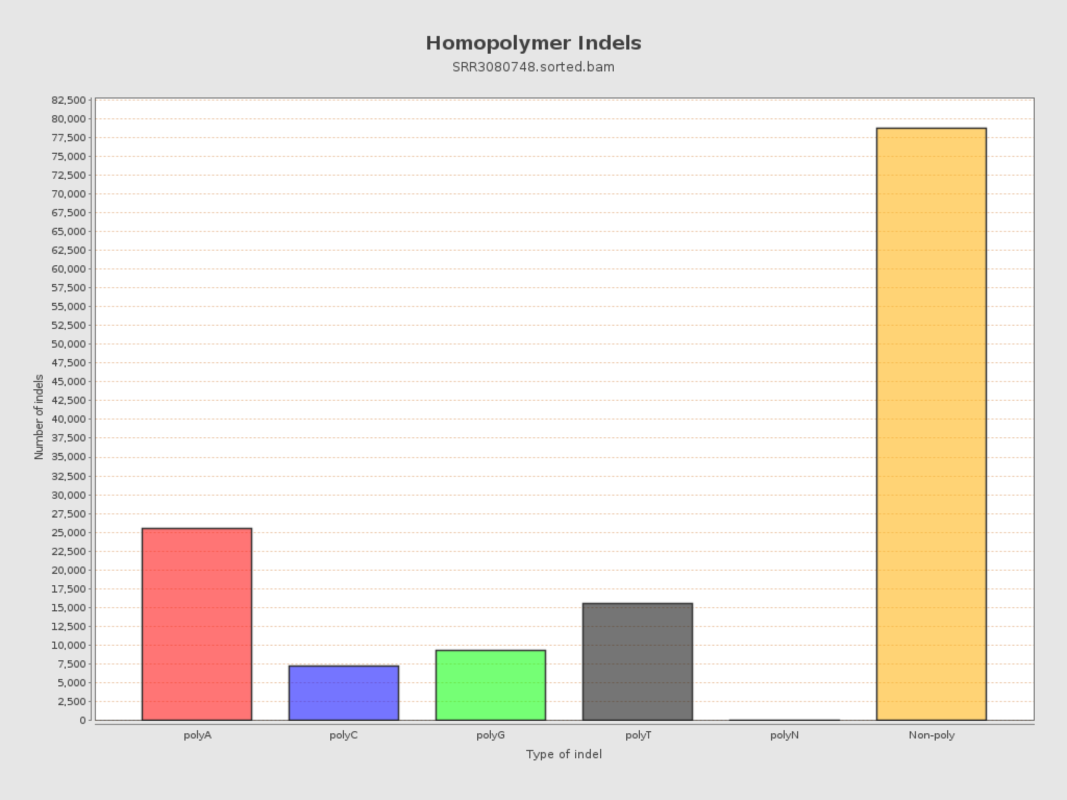
9. Results : Mapped Reads GC-content Distribution



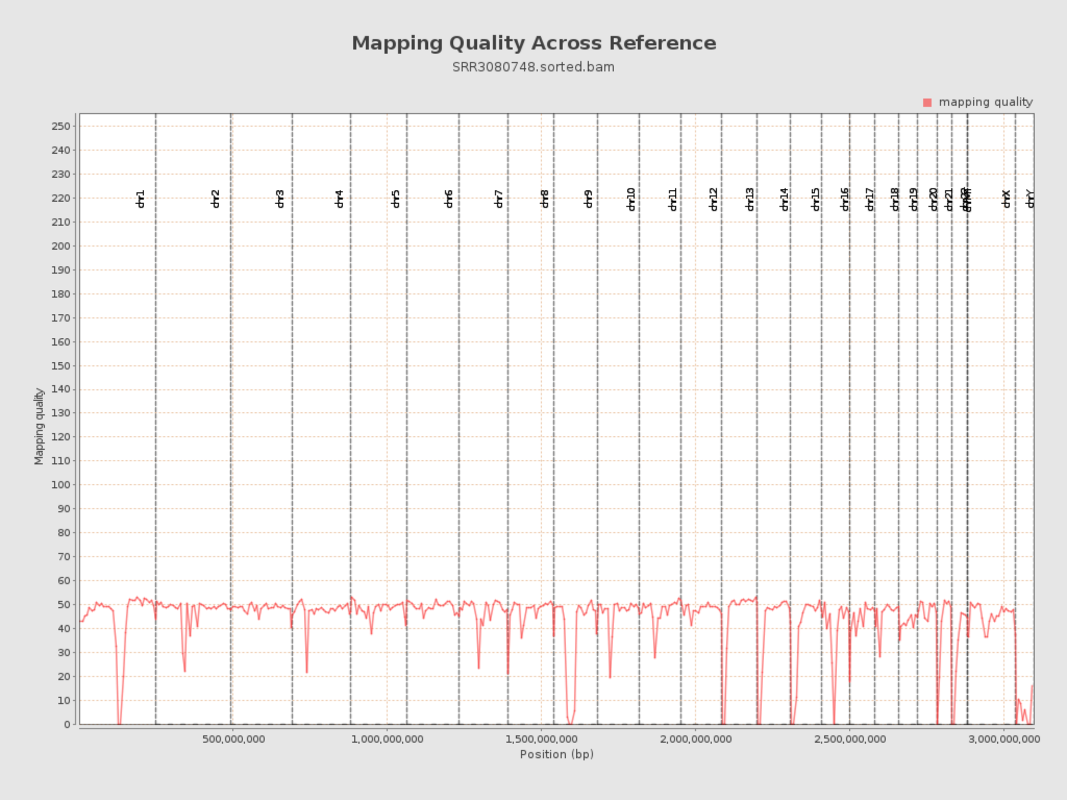
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram