Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 02:33:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506323.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_SRR1506323 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506323.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 02:33:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506323.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,160,676
Mapped reads	6,880,216 / 84.31%
Unmapped reads	1,280,460 / 15.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	75,340 / 0.92%
Read min/max/mean length	30 / 94 / 94.33
Duplicated reads (estimated)	1,051,632 / 12.89%
Duplication rate	11.08%
Clipped reads	4,057,484 / 49.72%

2.2. ACGT Content

Number/percentage of A's	148,734,728 / 27.18%
Number/percentage of C's	104,584,969 / 19.11%
Number/percentage of T's	156,128,409 / 28.53%
Number/percentage of G's	137,709,792 / 25.16%
Number/percentage of N's	132,340 / 0.02%
GC Percentage	44.27%

2.3. Coverage

Mean	0.1769

Standard Deviation	1.1517

2.4. Mapping Quality

Mean Mapping Quality	47.91

2.5. Mismatches and indels

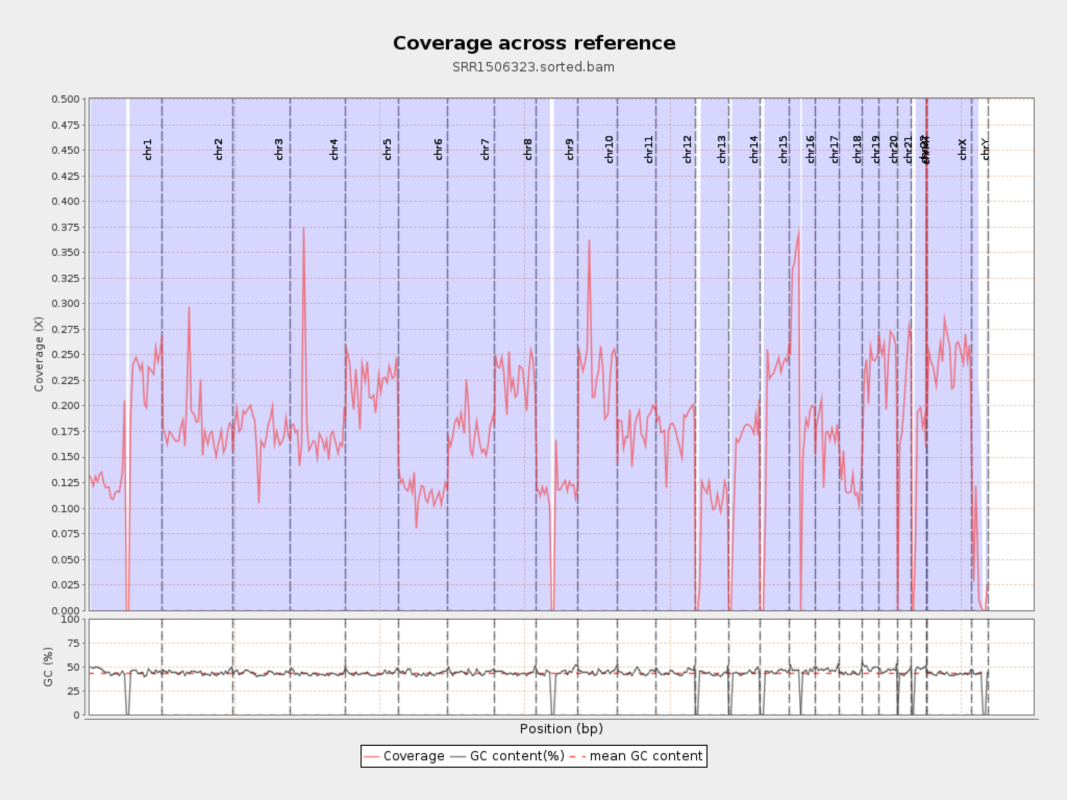
General error rate	0.7%
Mismatches	3,734,803
Insertions	43,238
Mapped reads with at least one insertion	0.61%
Deletions	111,235
Mapped reads with at least one deletion	1.59%
Homopolymer indels	43.1%

2.6. Chromosome stats

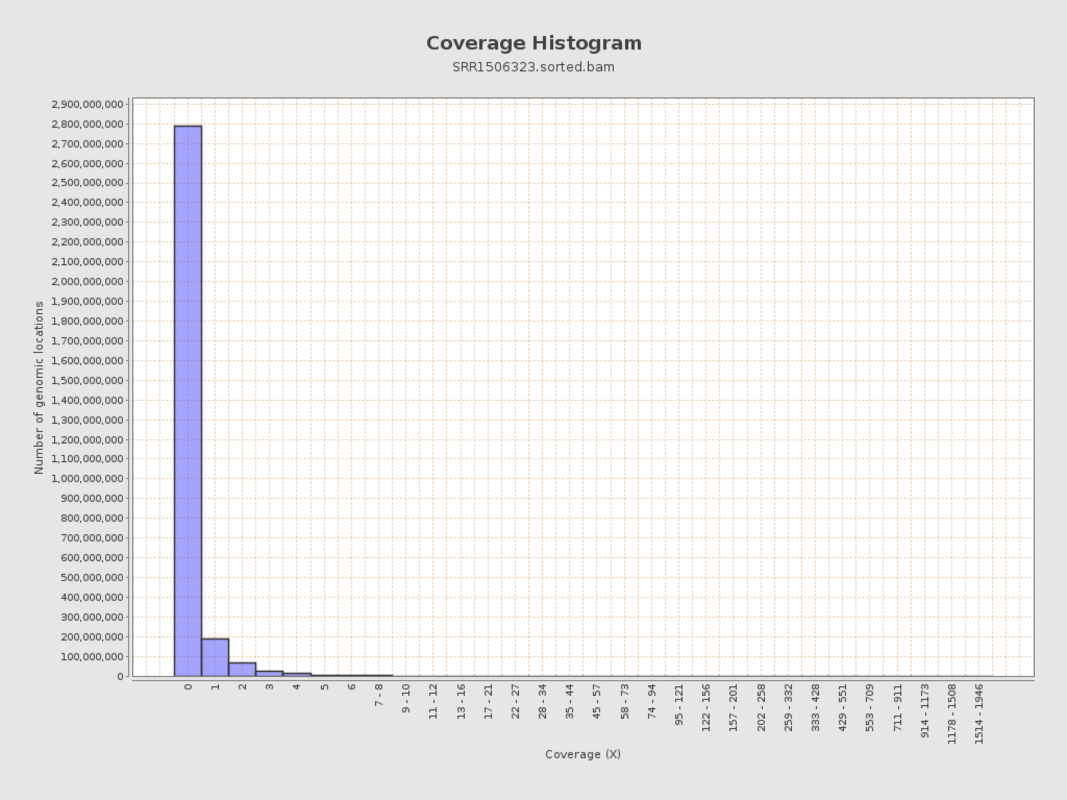
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	41505764	0.1665	1.7915
chr2	243199373	43473477	0.1788	1.4041
chr3	198022430	34815750	0.1758	0.6778
chr4	191154276	33398875	0.1747	1.0668
chr5	180915260	40276153	0.2226	0.7831
chr6	171115067	19848902	0.116	0.6071
chr7	159138663	27826642	0.1749	1.5111

chr8	146364022	33504059	0.2289	1.3884
chr9	141213431	15212877	0.1077	1.1604
chr10	135534747	32532863	0.24	1.462
chr11	135006516	24167277	0.179	1.1399
chr12	133851895	23738871	0.1774	0.7111
chr13	115169878	10837637	0.0941	0.4841
chr14	107349540	15745529	0.1467	0.7599
chr15	102531392	19979820	0.1949	0.7413
chr16	90354753	20698621	0.2291	0.9949
chr17	81195210	14069957	0.1733	0.8397
chr18	78077248	9667357	0.1238	1.6799
chr19	59128983	13976244	0.2364	1.4022
chr20	63025520	15742757	0.2498	0.9227
chr21	48129895	9501811	0.1974	0.9809
chr22	51304566	6675760	0.1301	0.6382
chrMT	16571	17487	1.0553	2.2007
chrX	155270560	38386964	0.2472	0.9849
chrY	59373566	1914162	0.0322	1.0761

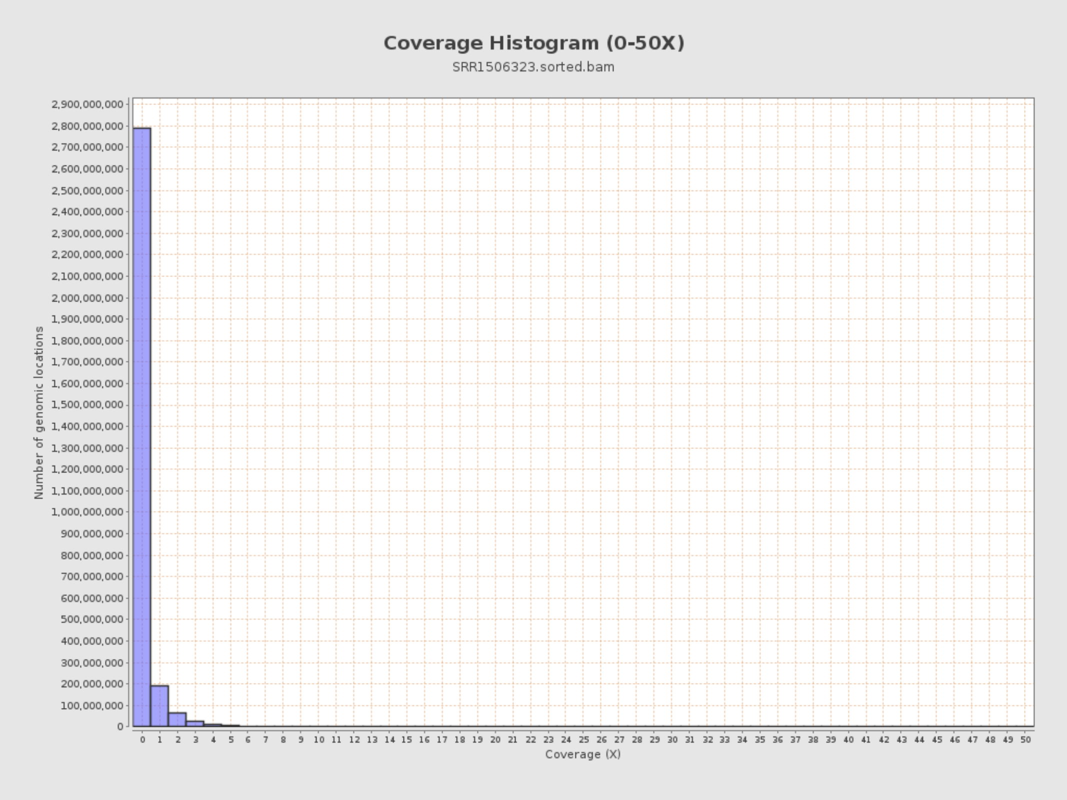
3. Results : Coverage across reference



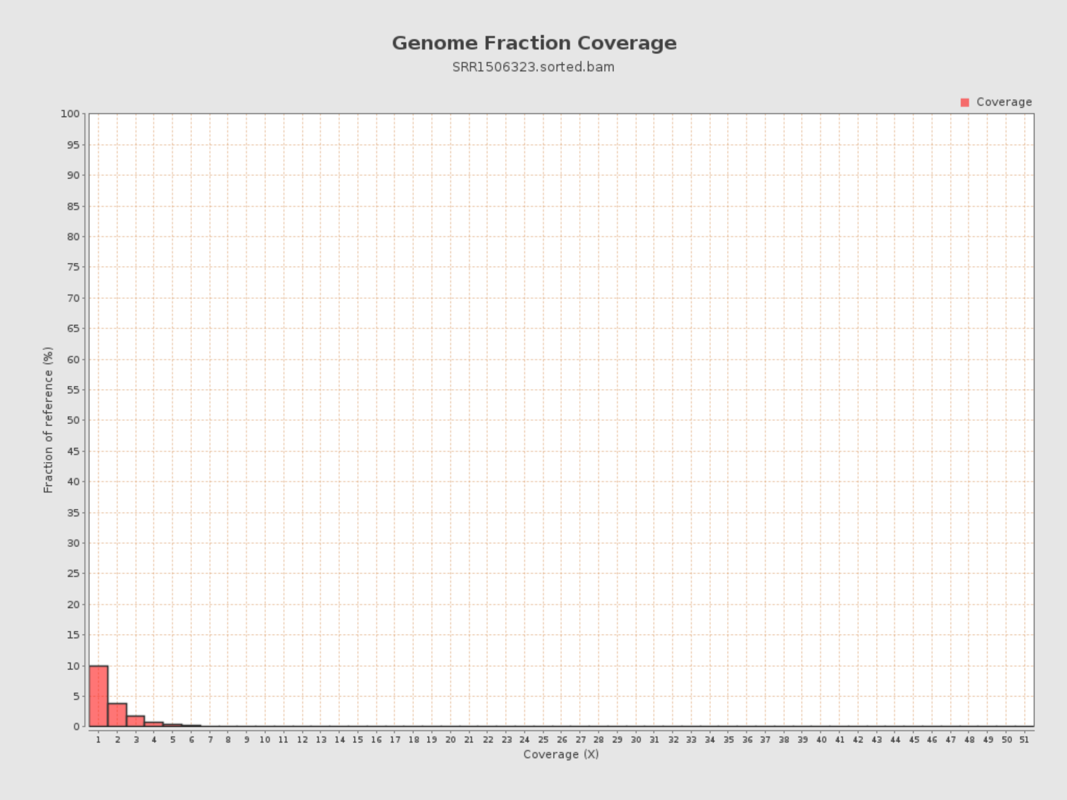
4. Results : Coverage Histogram



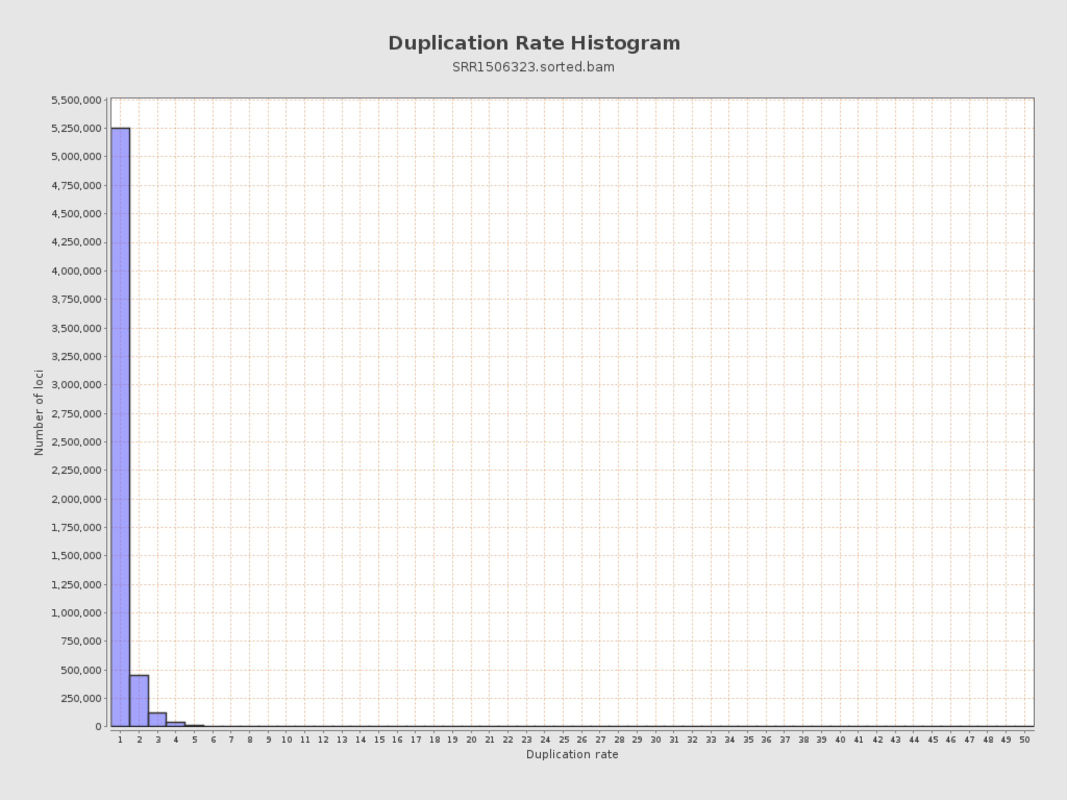
5. Results : Coverage Histogram (0-50X)



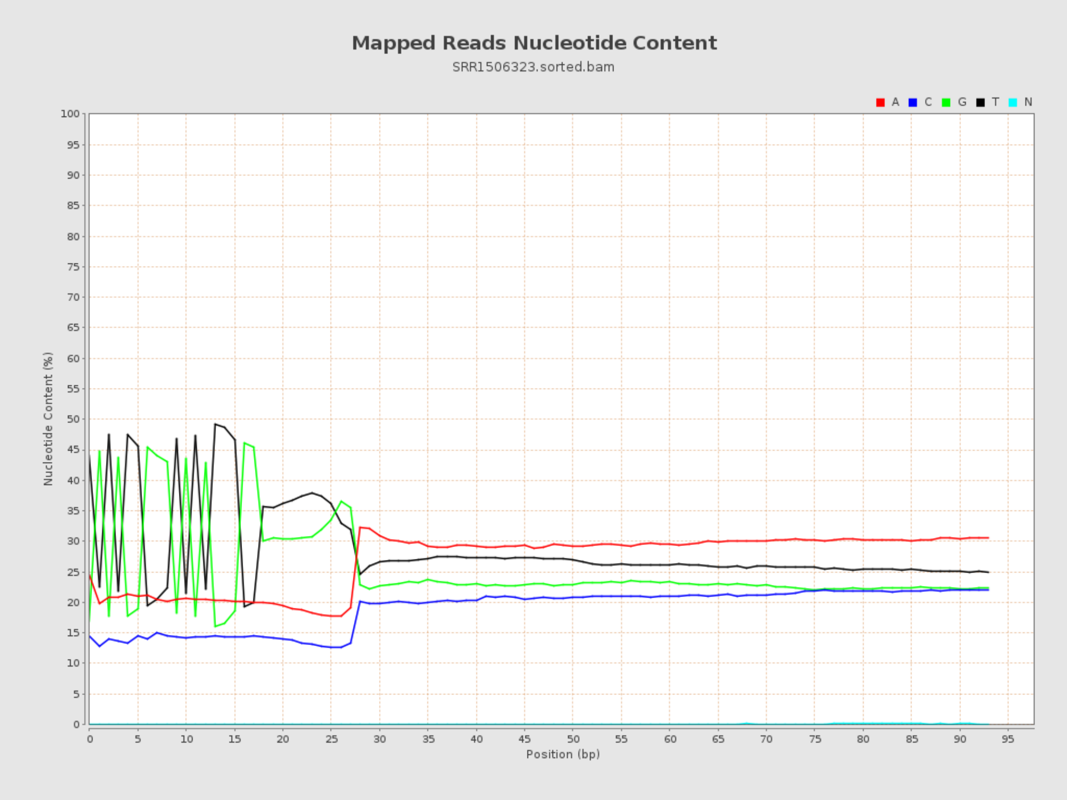
6. Results : Genome Fraction Coverage



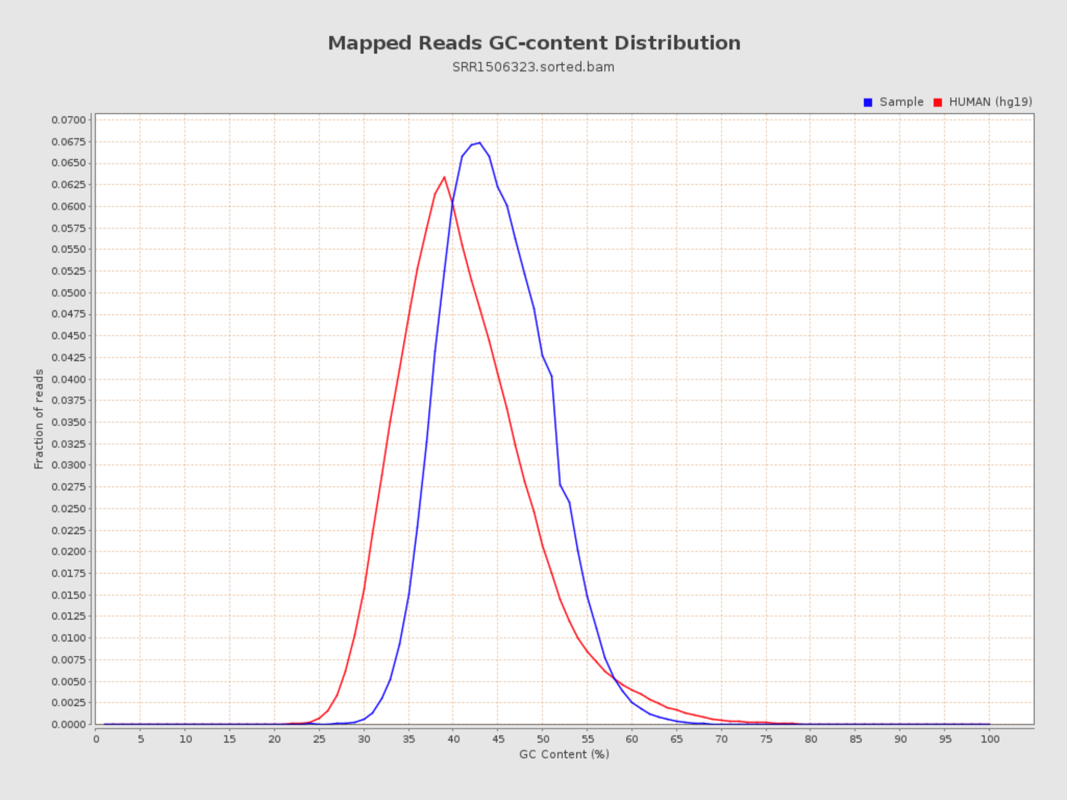
7. Results : Duplication Rate Histogram



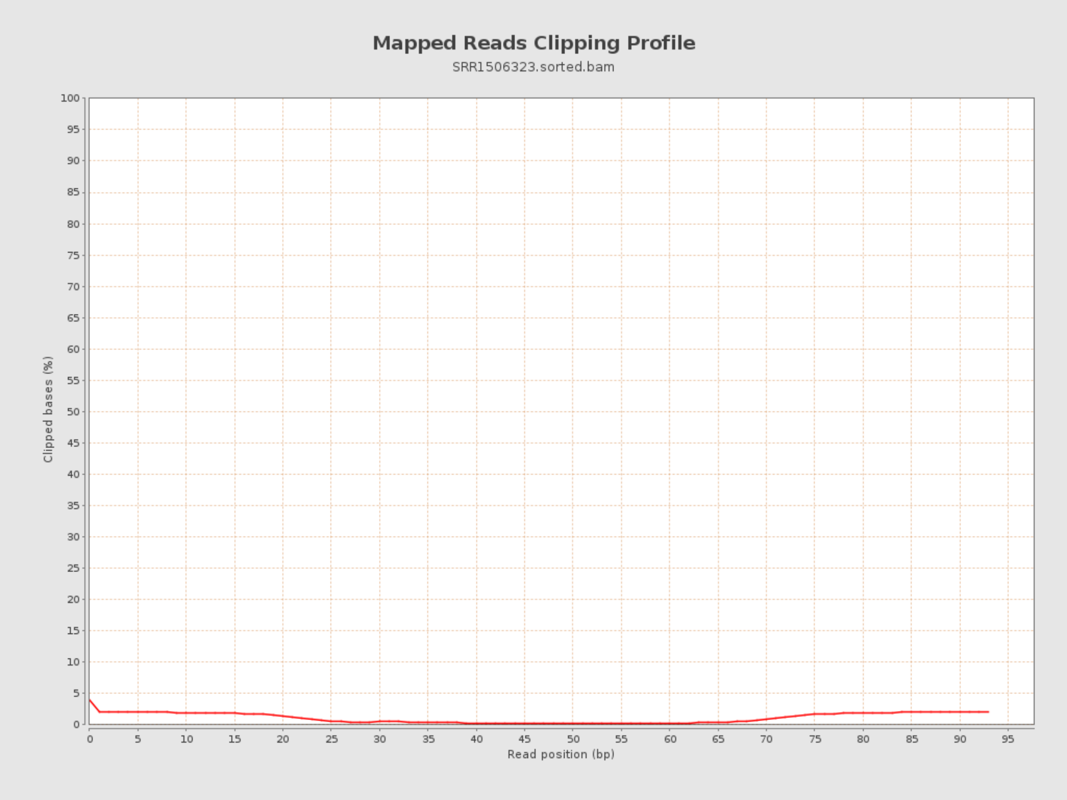
8. Results : Mapped Reads Nucleotide Content



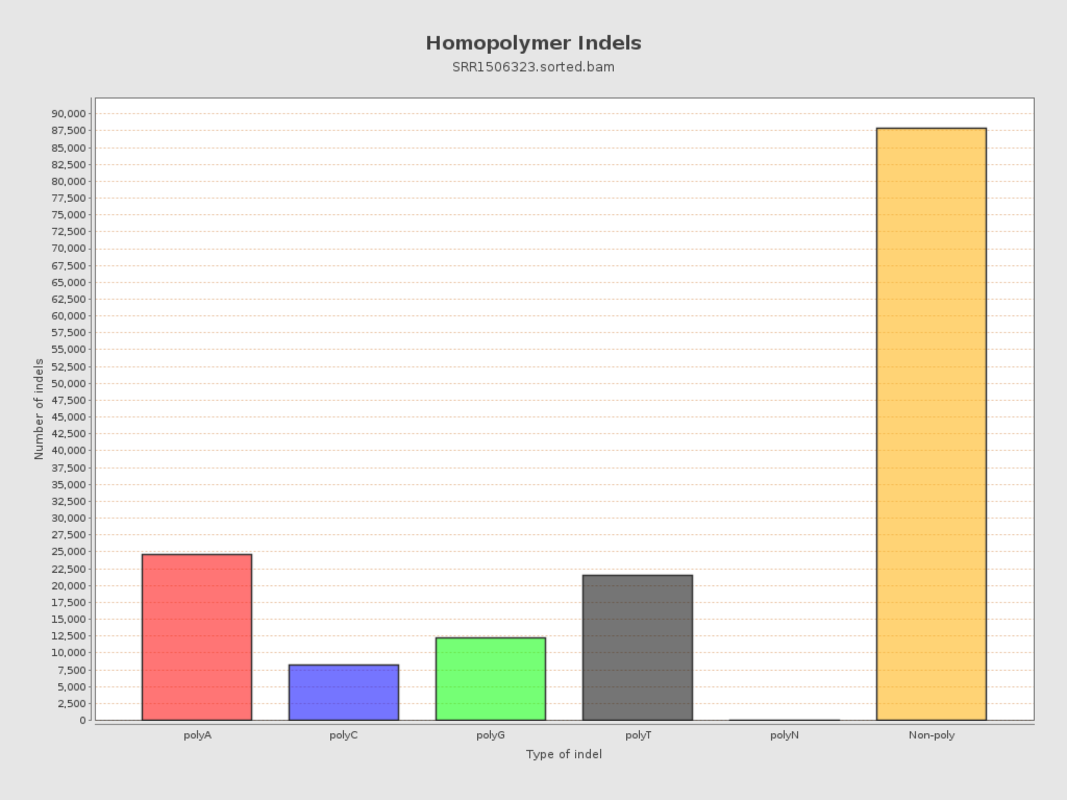
9. Results : Mapped Reads GC-content Distribution



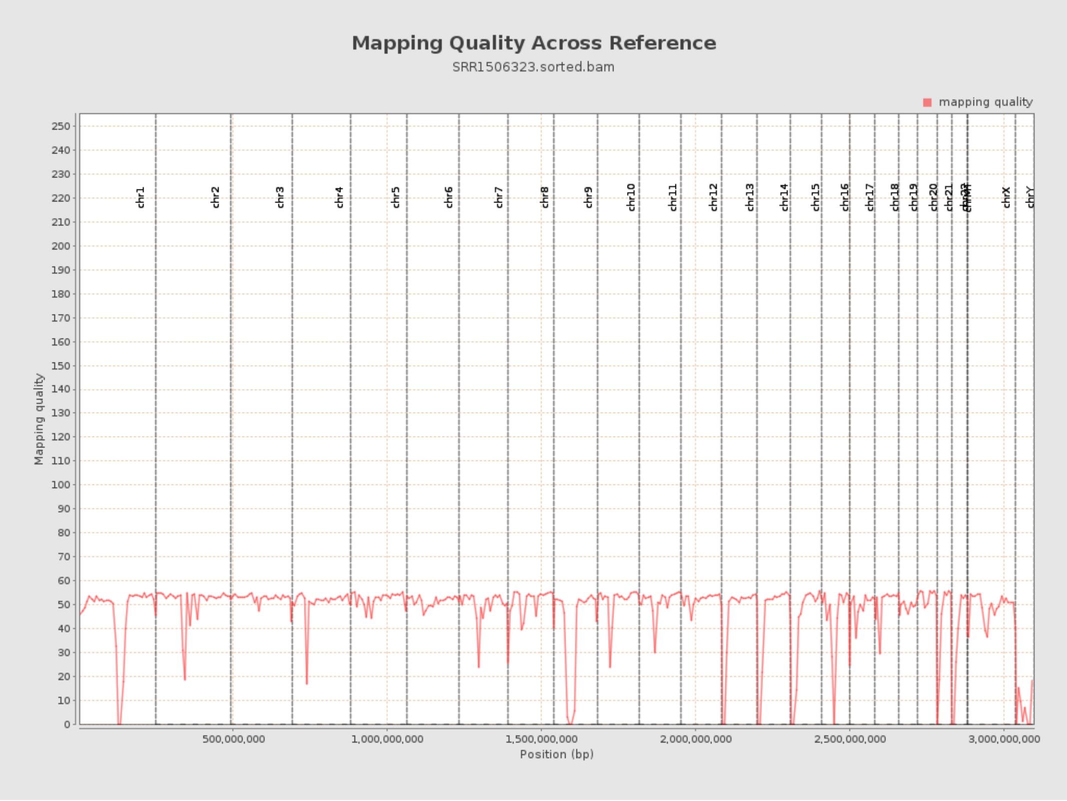
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram