Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 20:21:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548956.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_SRR1548956 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548956.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 20:21:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548956.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,409,934
Mapped reads	7,195,995 / 85.57%
Unmapped reads	1,213,939 / 14.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	360,039 / 4.28%
Duplication rate	3.03%
Clipped reads	586,132 / 6.97%

2.2. ACGT Content

Number/percentage of A's	80,180,718 / 28.19%
Number/percentage of C's	61,219,694 / 21.53%
Number/percentage of T's	81,801,694 / 28.76%
Number/percentage of G's	61,204,846 / 21.52%
Number/percentage of N's	398 / 0%
GC Percentage	43.05%

2.3. Coverage

Mean	0.0919
Standard Deviation	0.9046

2.4. Mapping Quality

Mean Mapping Quality	36.93

2.5. Mismatches and indels

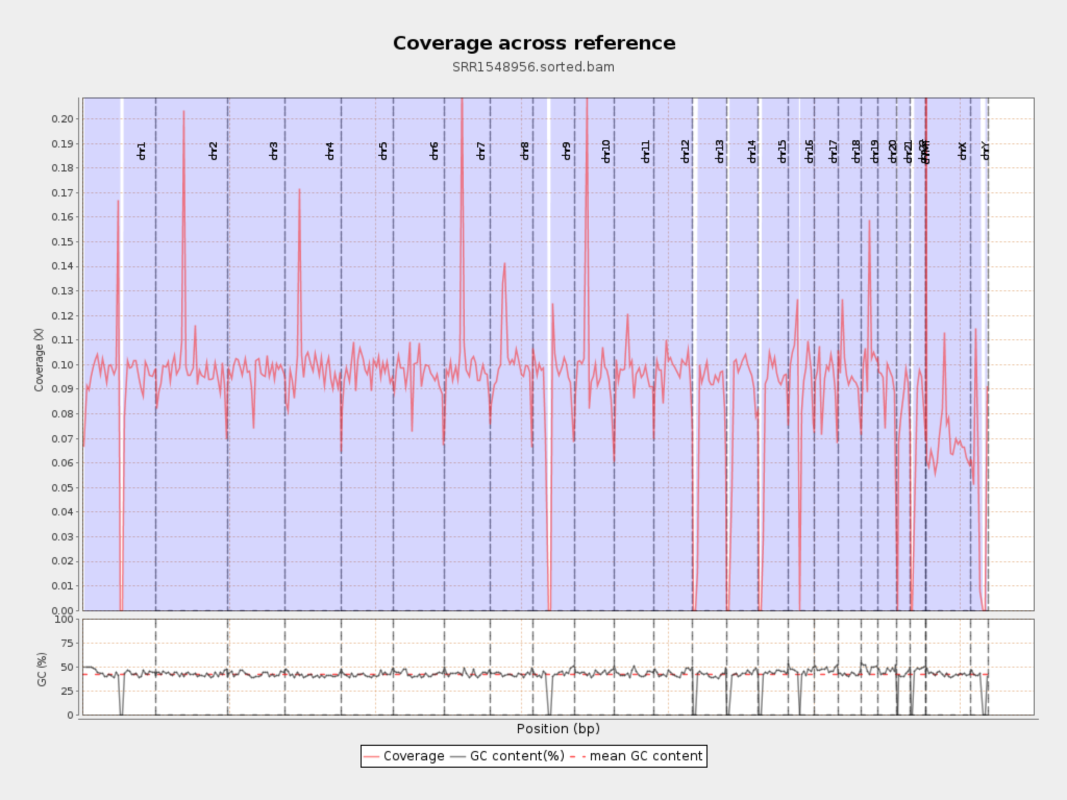
General error rate	0.31%
Mismatches	880,376
Insertions	9,285
Mapped reads with at least one insertion	0.13%
Deletions	20,384
Mapped reads with at least one deletion	0.28%
Homopolymer indels	39.65%

2.6. Chromosome stats

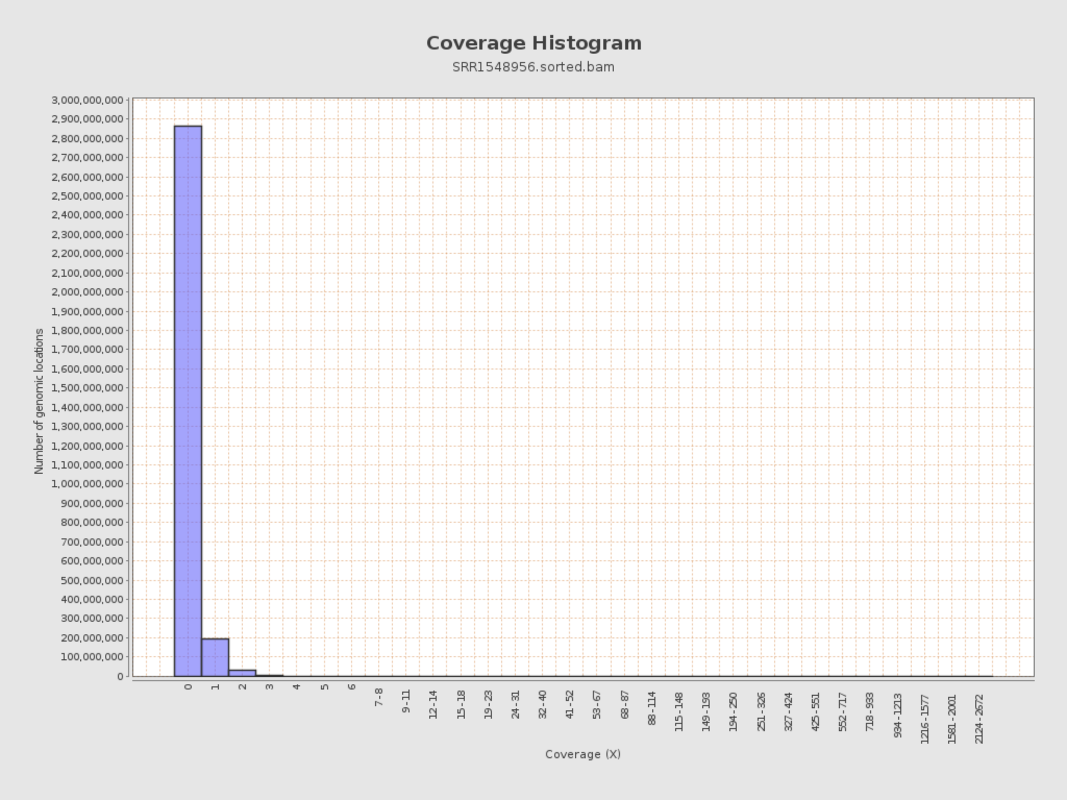
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22918629	0.092	1.6885
chr2	243199373	24285594	0.0999	0.9183
chr3	198022430	19256705	0.0972	0.3723
chr4	191154276	19060457	0.0997	0.4819
chr5	180915260	17659184	0.0976	0.39
chr6	171115067	16393320	0.0958	0.4085
chr7	159138663	16409240	0.1031	1.3917
chr8	146364022	14738001	0.1007	1.4342

chr9	141213431	12148583	0.086	0.8926
chr10	135534747	13763422	0.1015	0.8258
chr11	135006516	13052649	0.0967	0.6219
chr12	133851895	13152117	0.0983	0.4161
chr13	115169878	9011675	0.0782	0.3219
chr14	107349540	8732746	0.0813	0.5377
chr15	102531392	7957444	0.0776	0.3385
chr16	90354753	8106193	0.0897	0.4899
chr17	81195210	7639194	0.0941	0.4052
chr18	78077248	7605779	0.0974	1.7577
chr19	59128983	6333378	0.1071	1.7004
chr20	63025520	5726226	0.0909	0.4126
chr21	48129895	3659878	0.076	0.554
chr22	51304566	3252566	0.0634	0.414
chrMT	16571	11750	0.7091	1.1499
chrX	155270560	10642987	0.0685	0.5458
chrY	59373566	2915853	0.0491	0.5391

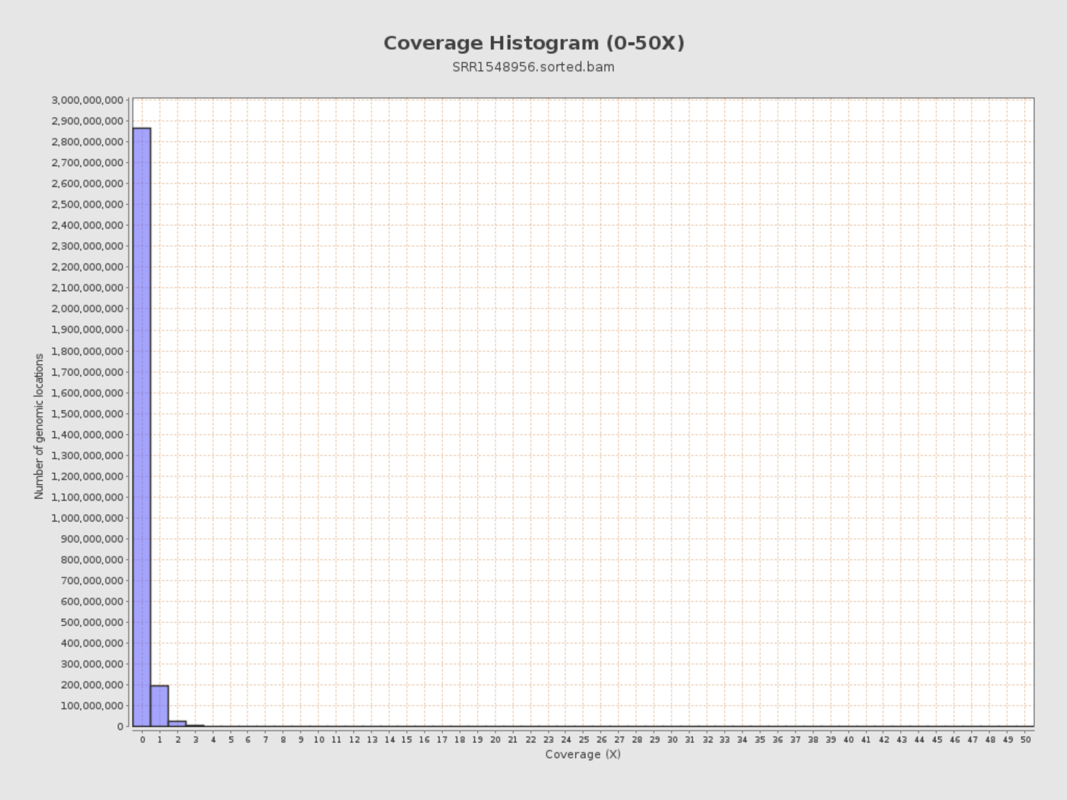
3. Results : Coverage across reference



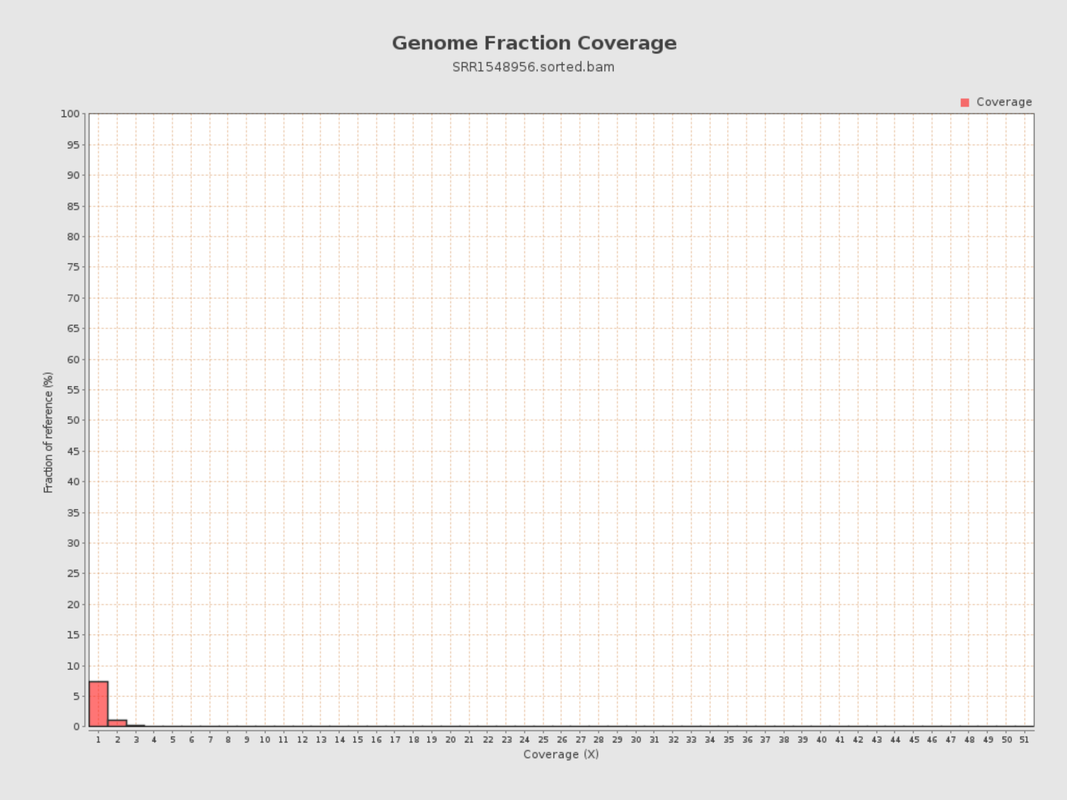
4. Results : Coverage Histogram



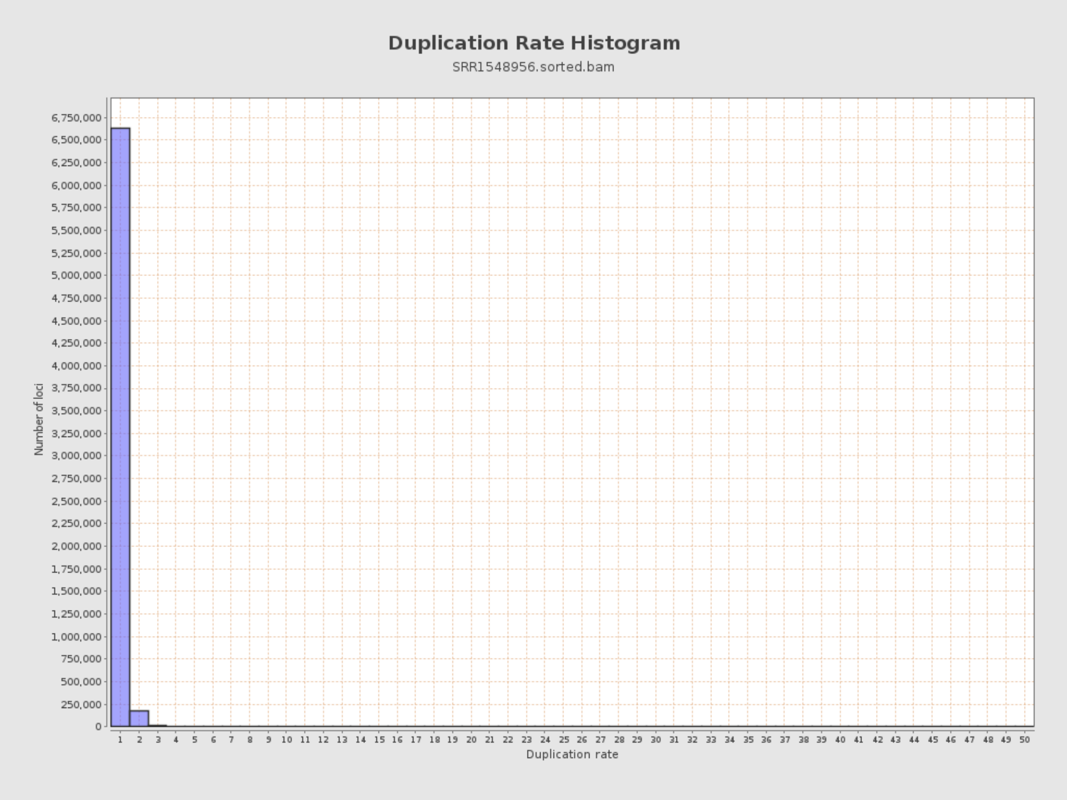
5. Results : Coverage Histogram (0-50X)



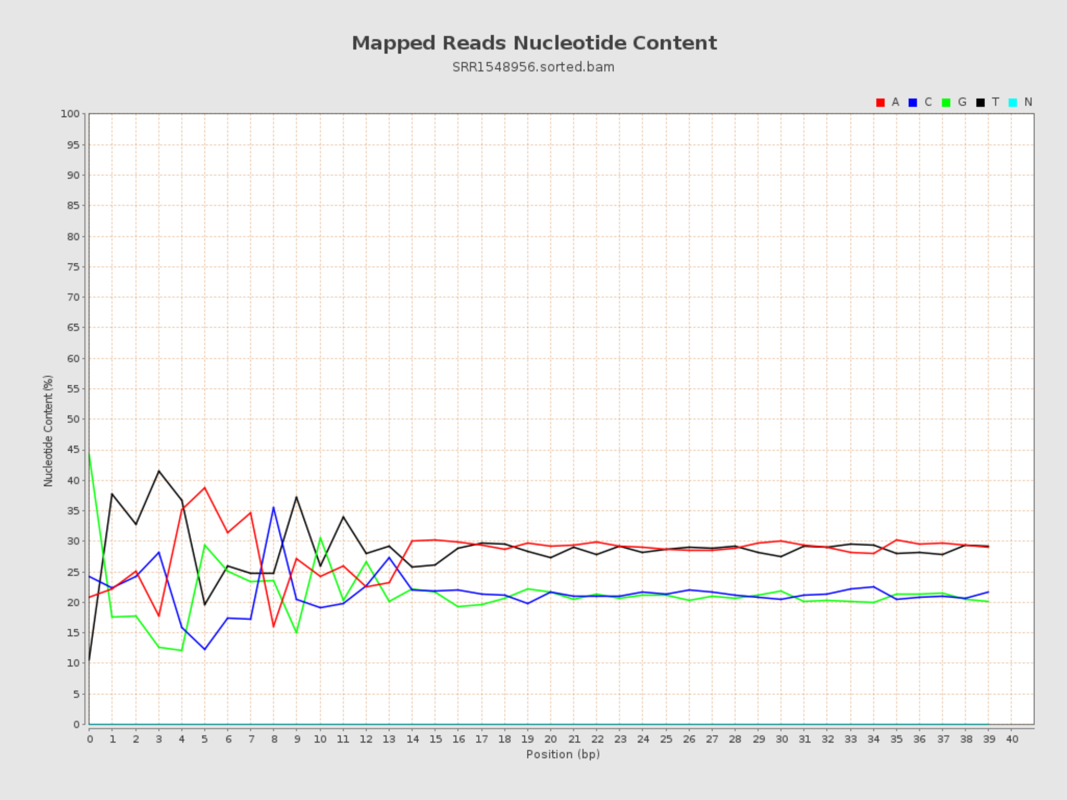
6. Results : Genome Fraction Coverage



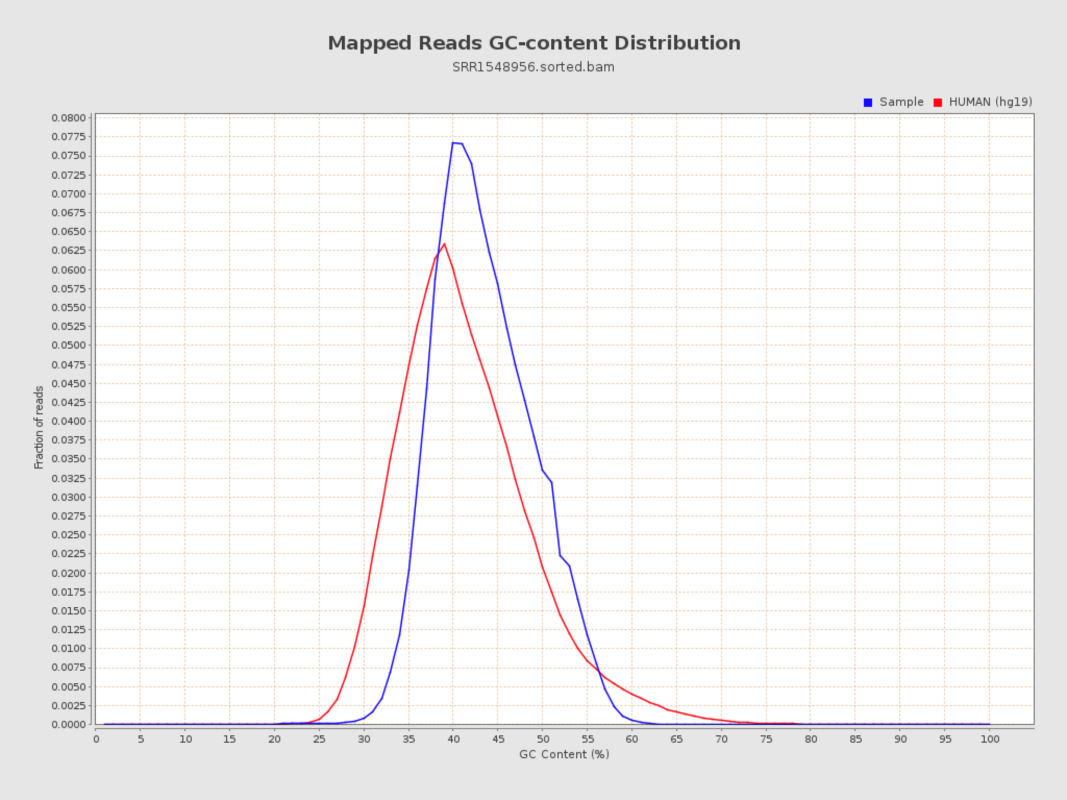
7. Results : Duplication Rate Histogram



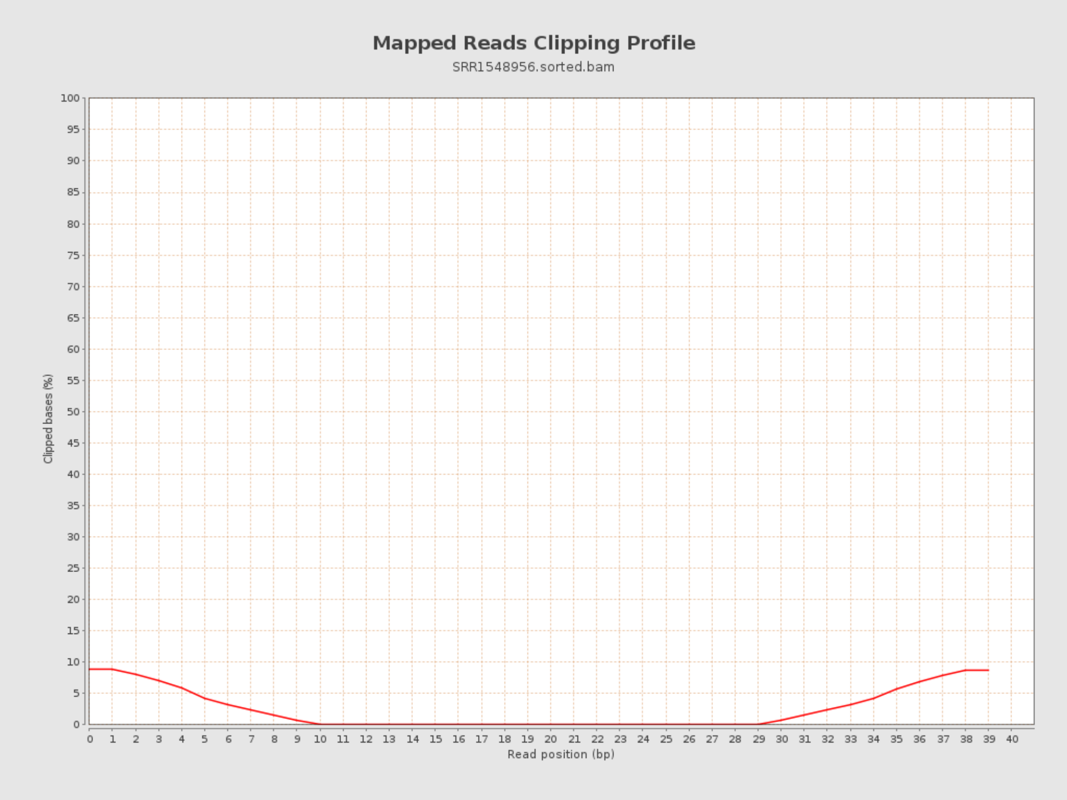
8. Results : Mapped Reads Nucleotide Content



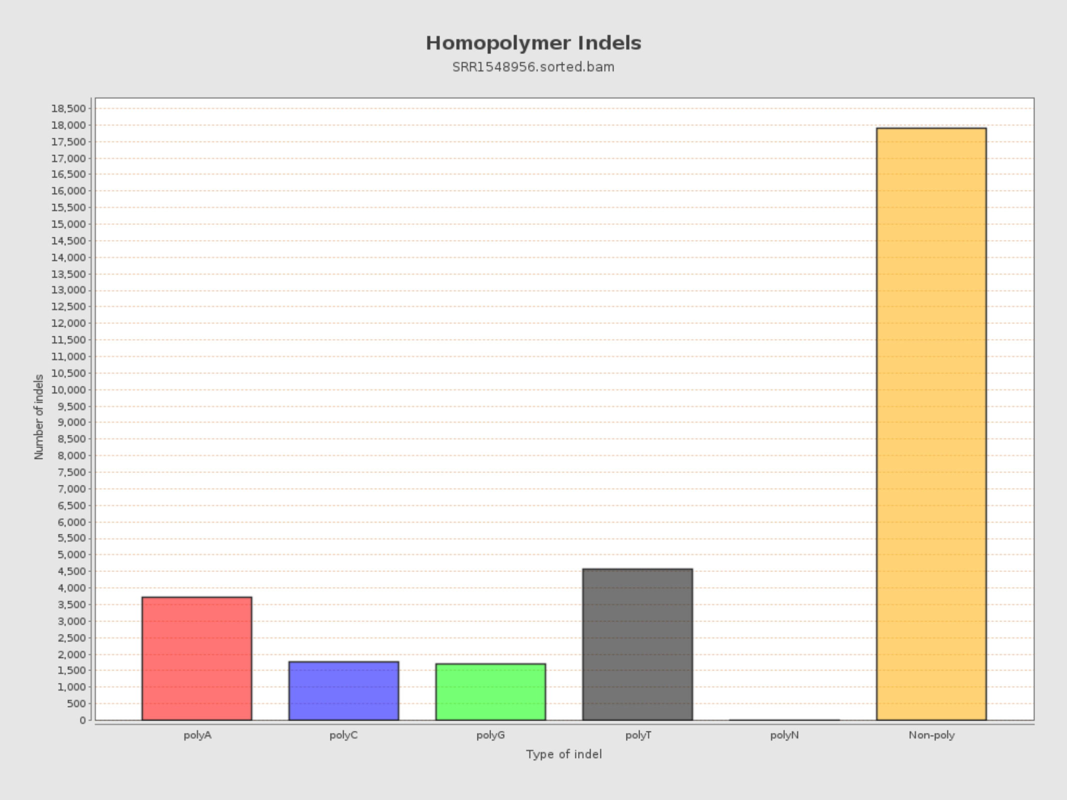
9. Results : Mapped Reads GC-content Distribution



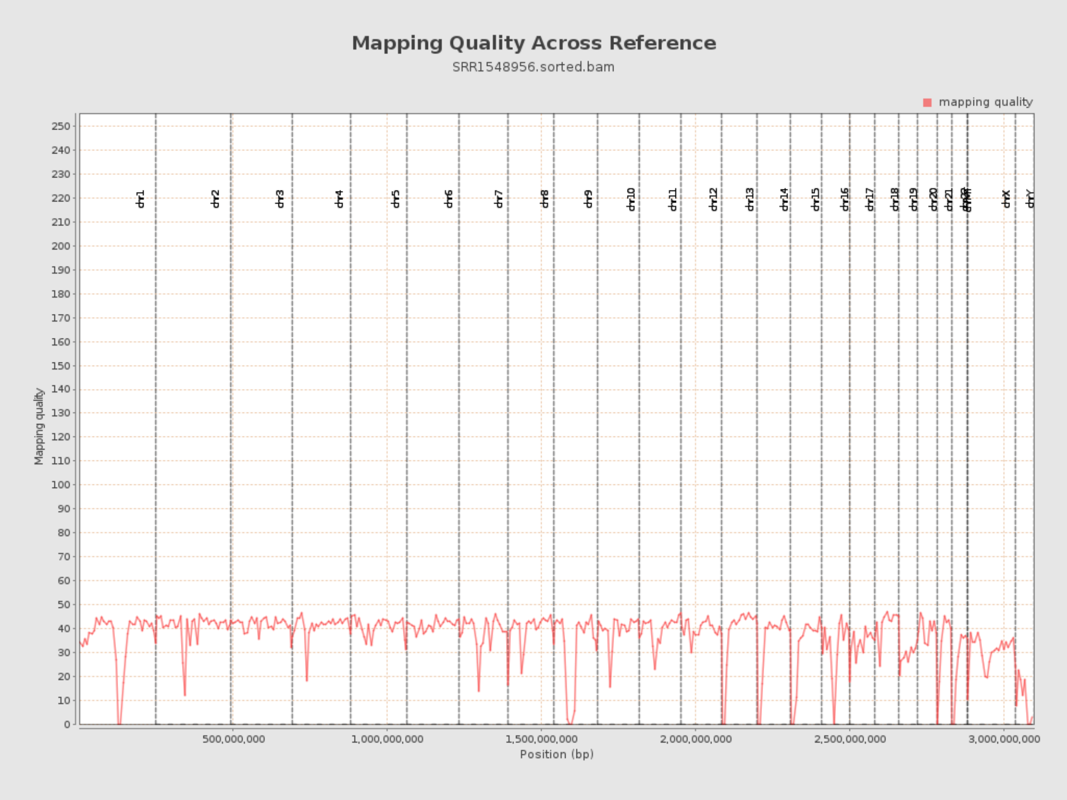
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram