Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 23:26:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053609.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_SRR053609 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053609.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 23:26:25 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053609.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,687,962
Mapped reads	5,498,803 / 63.29%
Unmapped reads	3,189,159 / 36.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	136 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,451,512 / 16.71%
Duplication rate	20.05%
Clipped reads	640,213 / 7.37%

2.2. ACGT Content

Number/percentage of A's	77,585,047 / 30.06%
Number/percentage of C's	49,168,729 / 19.05%
Number/percentage of T's	77,824,855 / 30.15%
Number/percentage of G's	53,369,801 / 20.68%
Number/percentage of N's	159,814 / 0.06%
GC Percentage	39.73%

2.3. Coverage

Mean	0.0834

Standard Deviation	0.8525

2.4. Mapping Quality

Mean Mapping Quality	45.24

2.5. Mismatches and indels

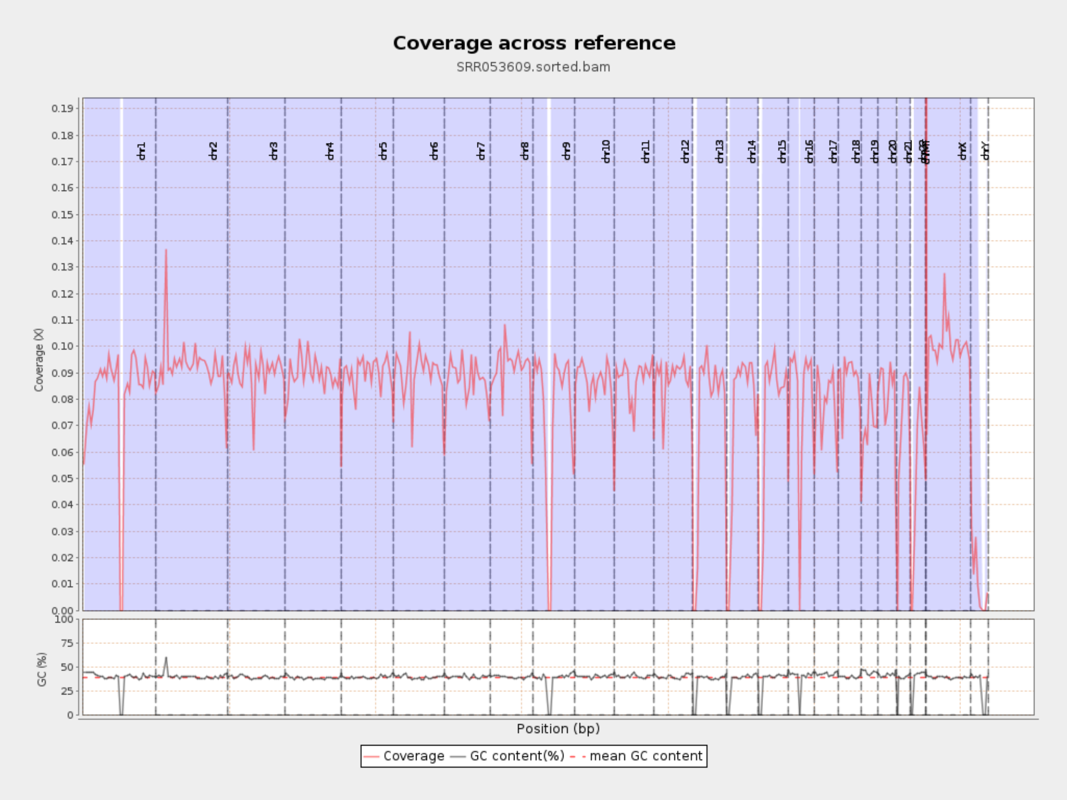
General error rate	0.89%
Mismatches	2,284,673
Insertions	13,743
Mapped reads with at least one insertion	0.25%
Deletions	36,198
Mapped reads with at least one deletion	0.66%
Homopolymer indels	46.53%

2.6. Chromosome stats

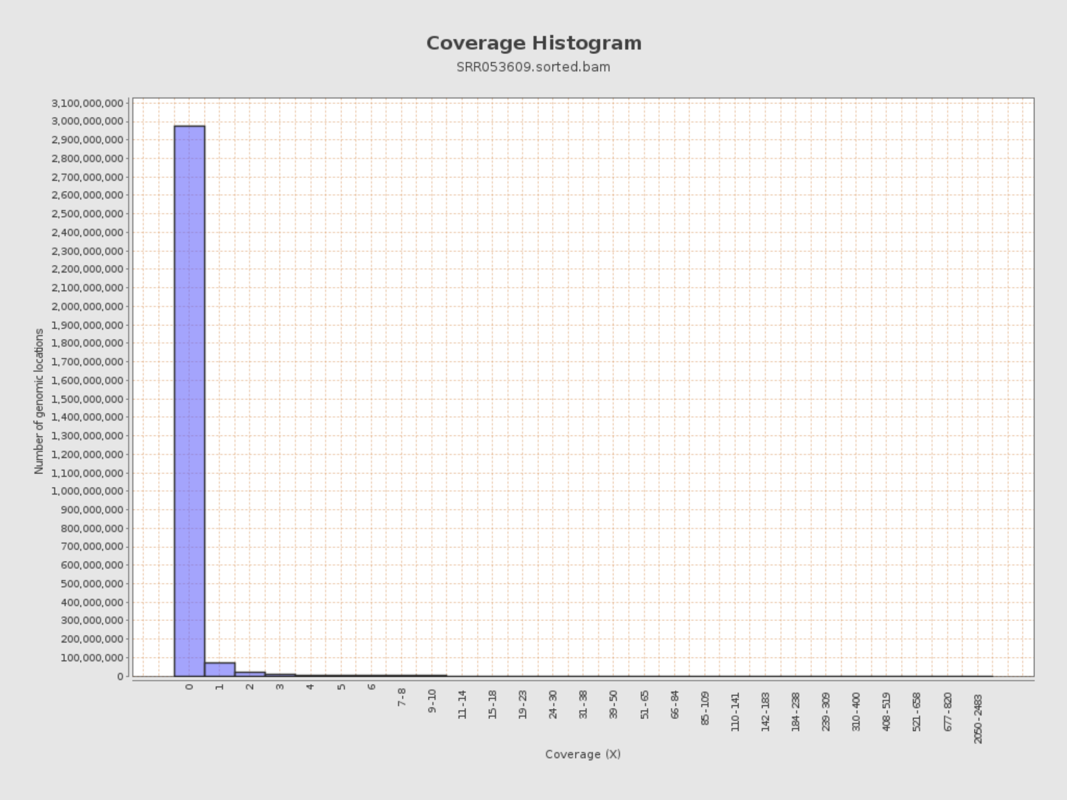
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20265745	0.0813	0.7388
chr2	243199373	22570694	0.0928	1.9397
chr3	198022430	17853118	0.0902	0.655
chr4	191154276	17225486	0.0901	0.6787
chr5	180915260	16182929	0.0895	0.6523
chr6	171115067	15454985	0.0903	0.7315
chr7	159138663	13872585	0.0872	0.9039

chr8	146364022	13393514	0.0915	0.6997
chr9	141213431	10593222	0.075	0.6303
chr10	135534747	11792126	0.087	0.6741
chr11	135006516	11734382	0.0869	0.729
chr12	133851895	11793573	0.0881	0.661
chr13	115169878	8465259	0.0735	0.5986
chr14	107349540	7867270	0.0733	0.6225
chr15	102531392	7364995	0.0718	0.5858
chr16	90354753	7004430	0.0775	0.6234
chr17	81195210	6420448	0.0791	0.6167
chr18	78077248	6875785	0.0881	0.7546
chr19	59128983	4195494	0.071	0.7033
chr20	63025520	5268534	0.0836	0.6368
chr21	48129895	3221481	0.0669	0.6012
chr22	51304566	2544037	0.0496	0.4576
chrMT	16571	36798	2.2206	4.2947
chrX	155270560	15540671	0.1001	0.7707
chrY	59373566	622393	0.0105	0.2207

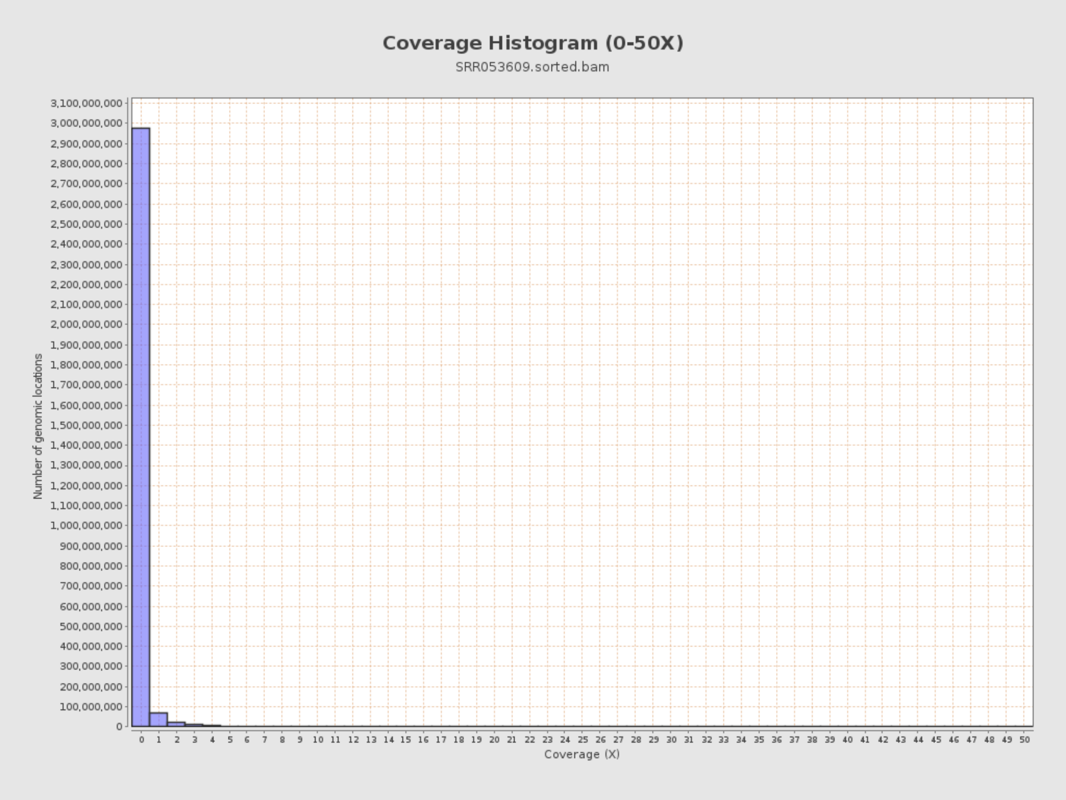
3. Results : Coverage across reference



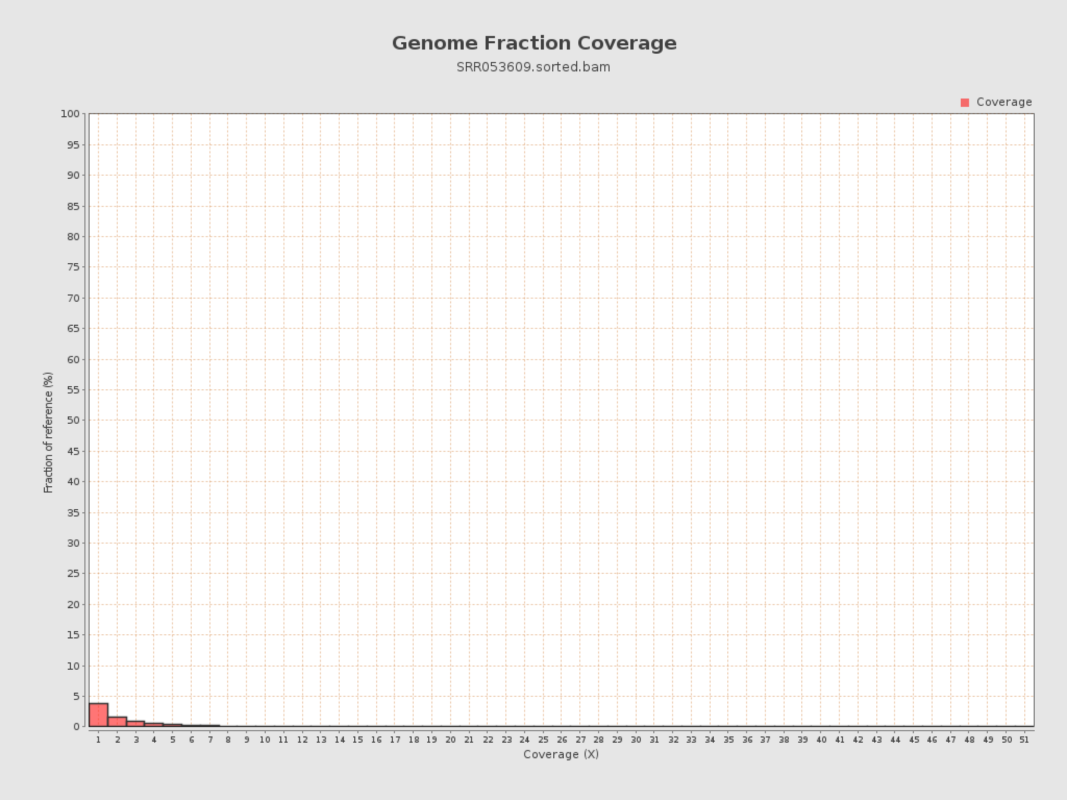
4. Results : Coverage Histogram



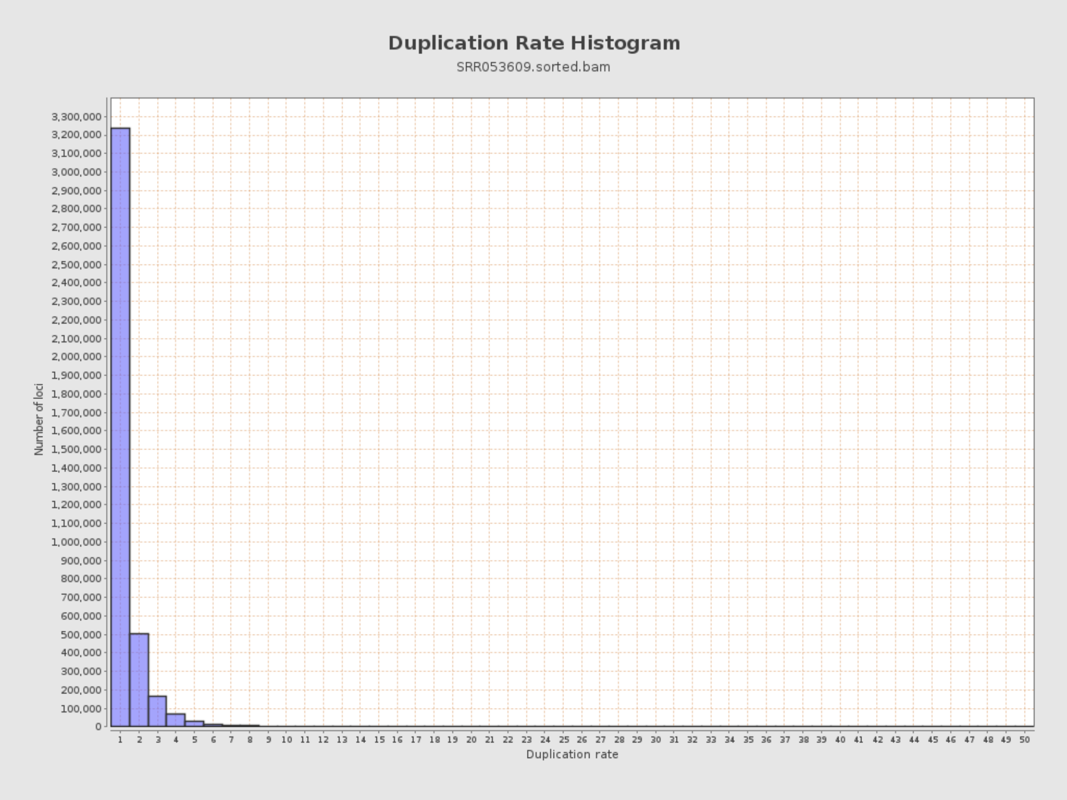
5. Results : Coverage Histogram (0-50X)



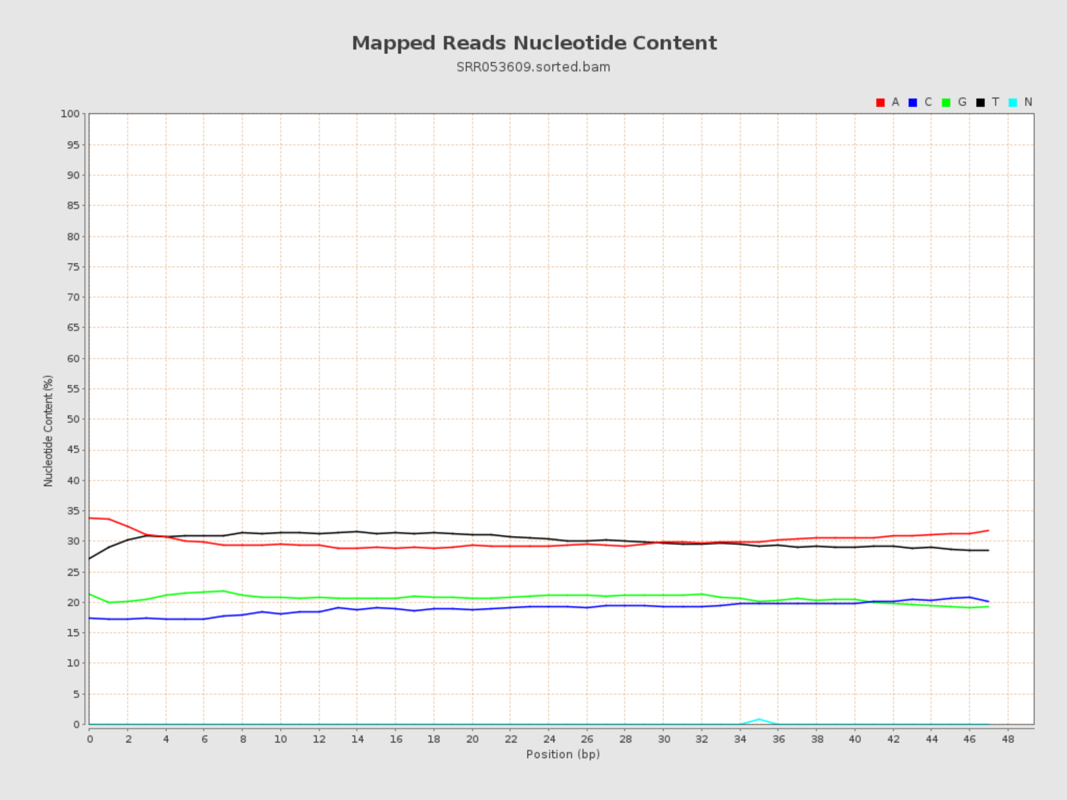
6. Results : Genome Fraction Coverage



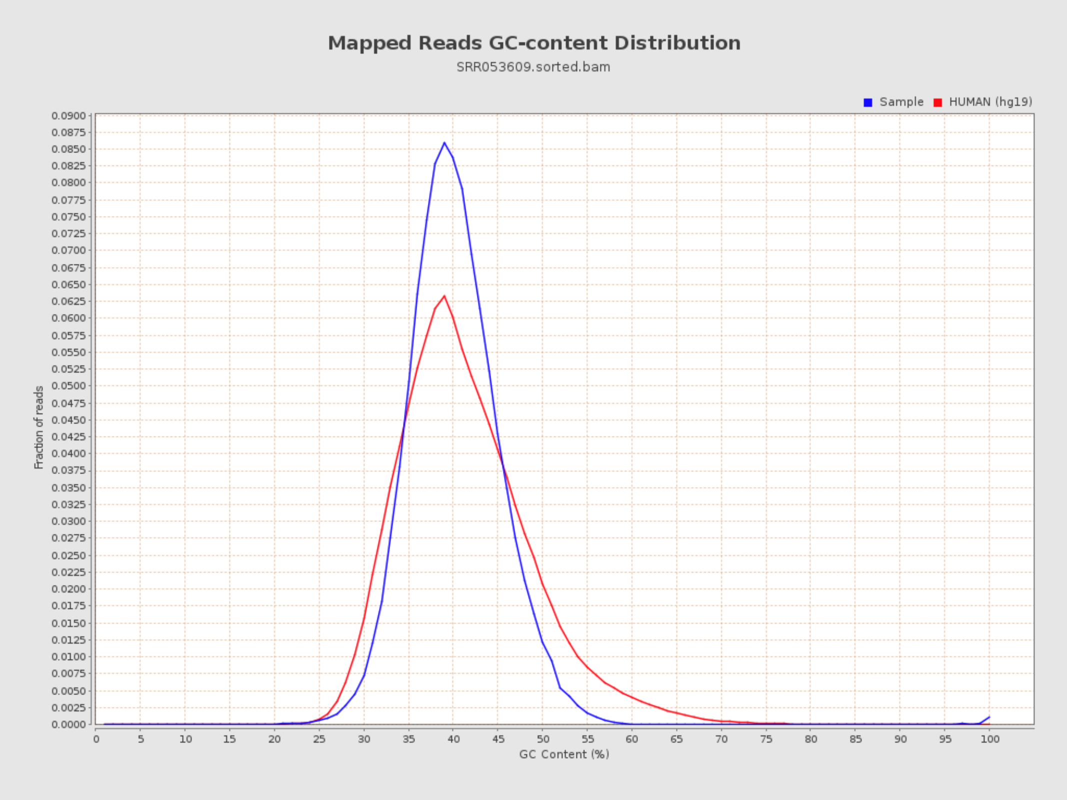
7. Results : Duplication Rate Histogram



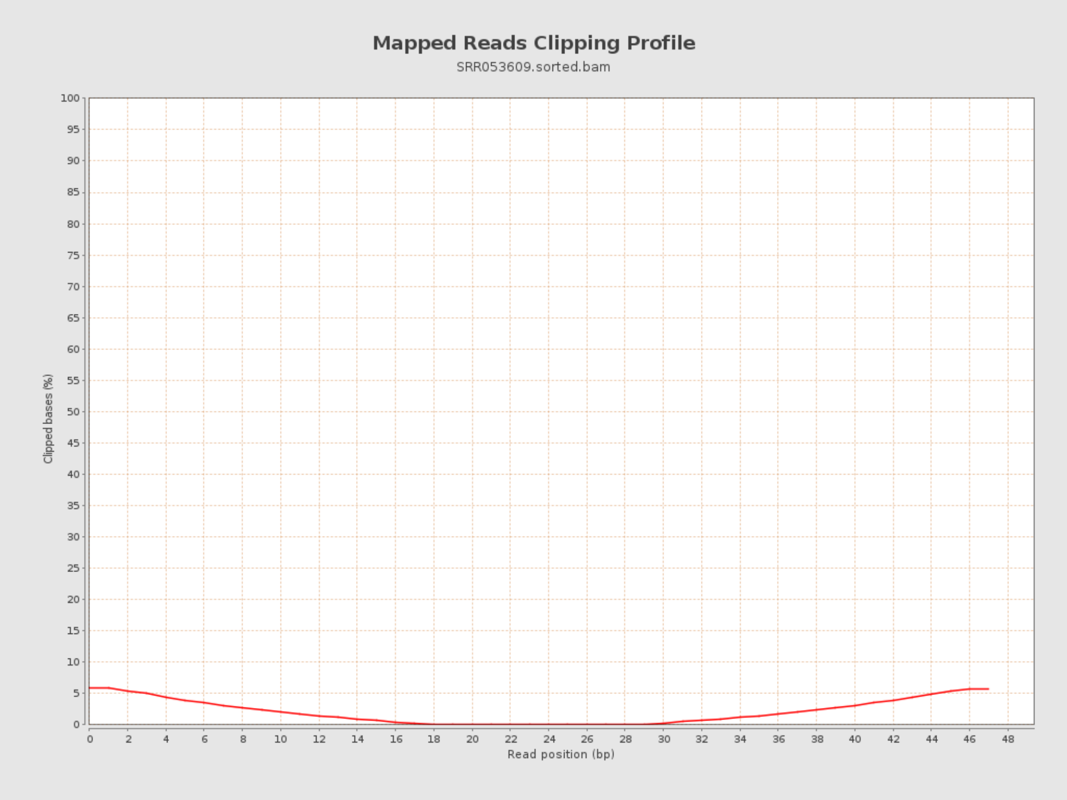
8. Results : Mapped Reads Nucleotide Content



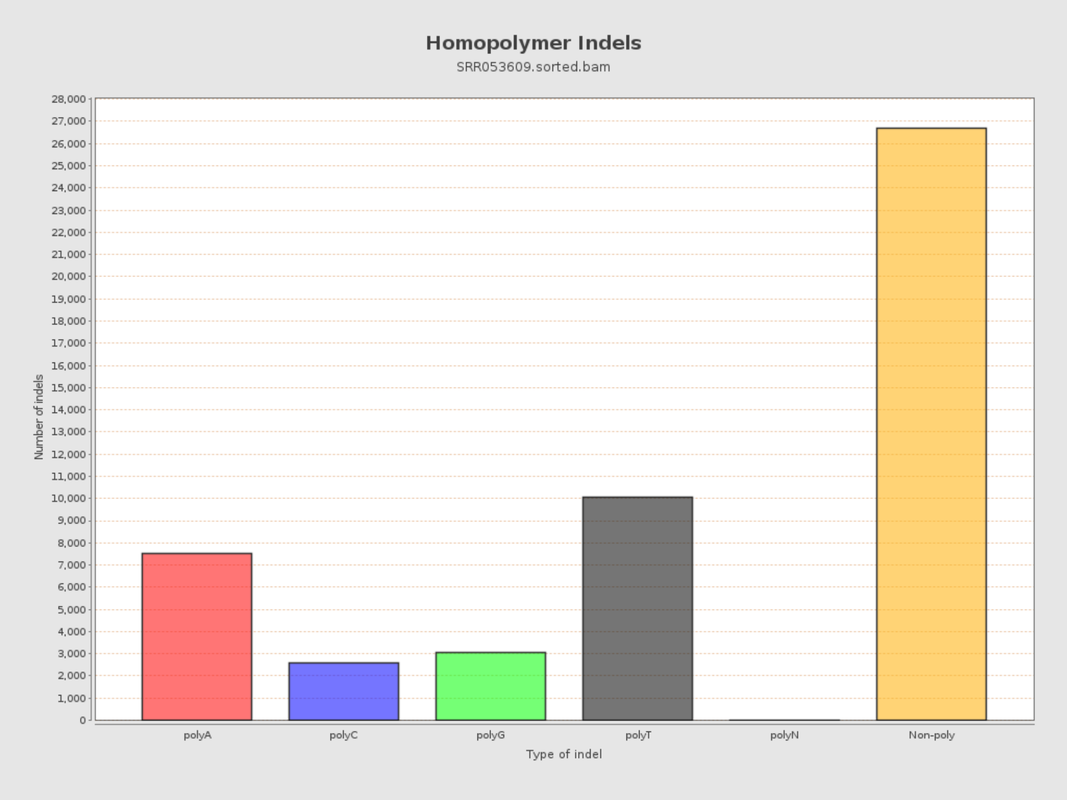
9. Results : Mapped Reads GC-content Distribution



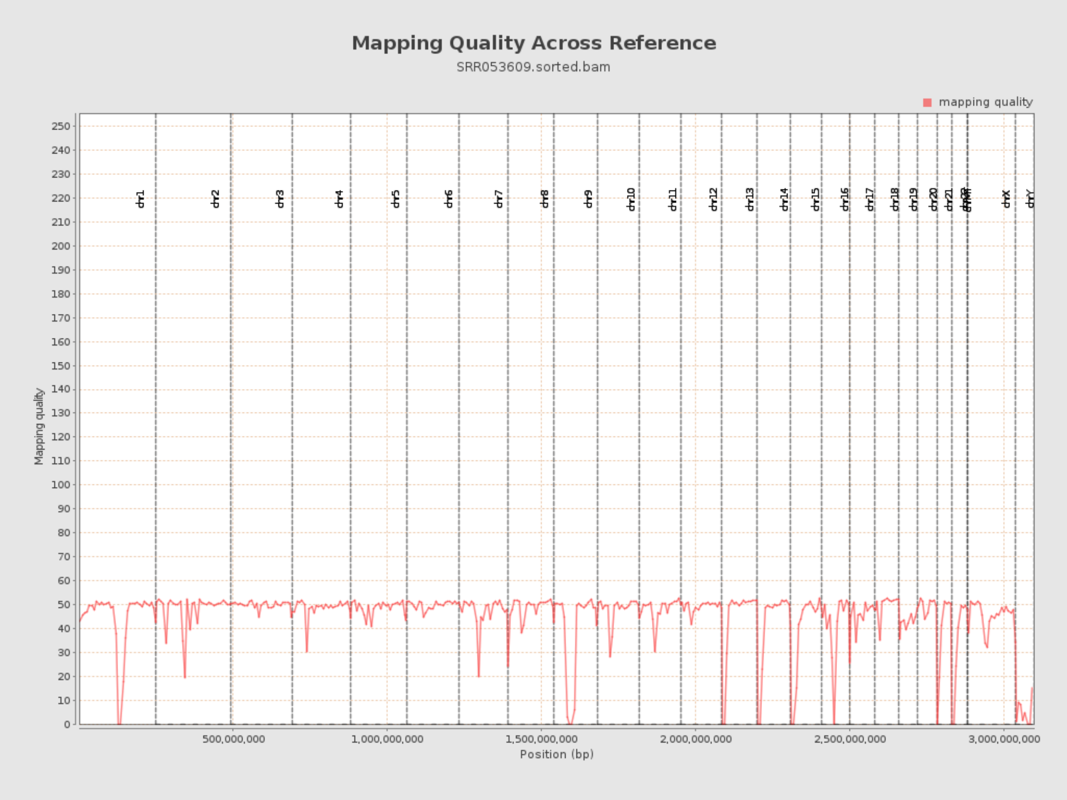
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram