Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 19:52:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013289.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_SRR6013289 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013289.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 19:52:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013289.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,872,769
Mapped reads	1,376,885 / 73.52%
Unmapped reads	495,884 / 26.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,225 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	141,913 / 7.58%
Duplication rate	8.37%
Clipped reads	745,793 / 39.82%

2.2. ACGT Content

Number/percentage of A's	23,355,060 / 26.31%
Number/percentage of C's	16,543,614 / 18.64%
Number/percentage of T's	28,001,297 / 31.55%
Number/percentage of G's	20,859,392 / 23.5%
Number/percentage of N's	998 / 0%
GC Percentage	42.14%

2.3. Coverage

Mean	0.0287

Standard Deviation	0.3245

2.4. Mapping Quality

Mean Mapping Quality	44.84

2.5. Mismatches and indels

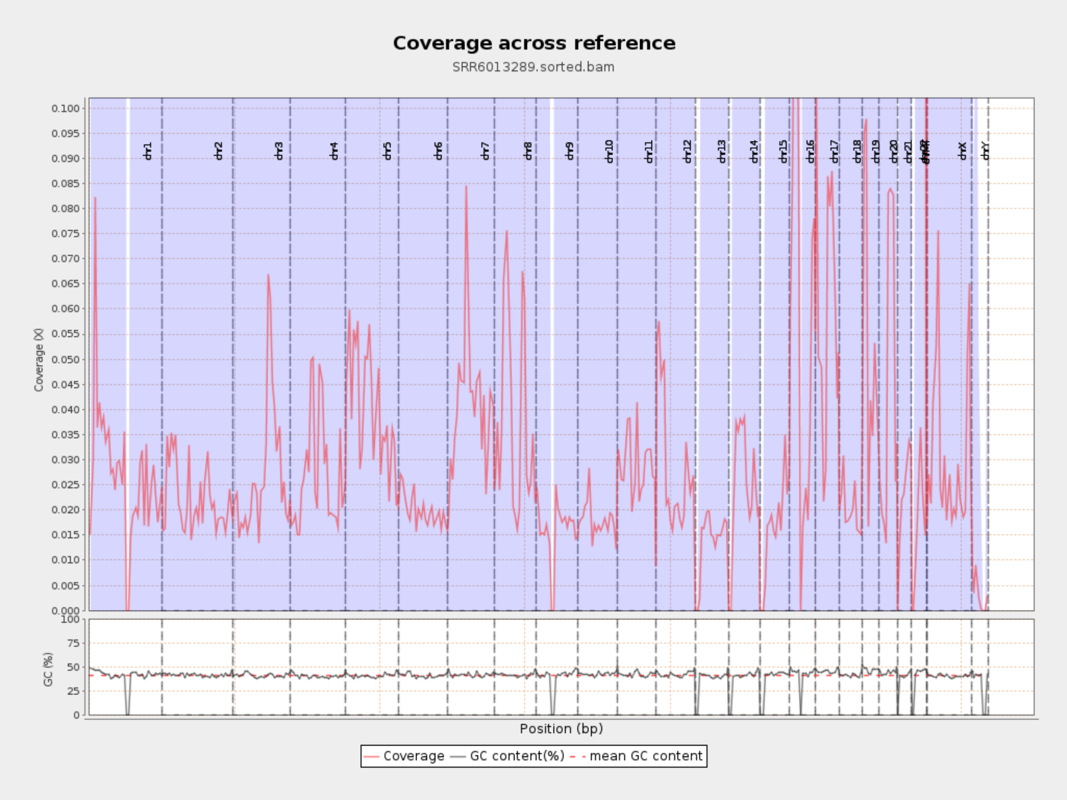
General error rate	0.77%
Mismatches	668,613
Insertions	5,864
Mapped reads with at least one insertion	0.42%
Deletions	23,042
Mapped reads with at least one deletion	1.66%
Homopolymer indels	46.6%

2.6. Chromosome stats

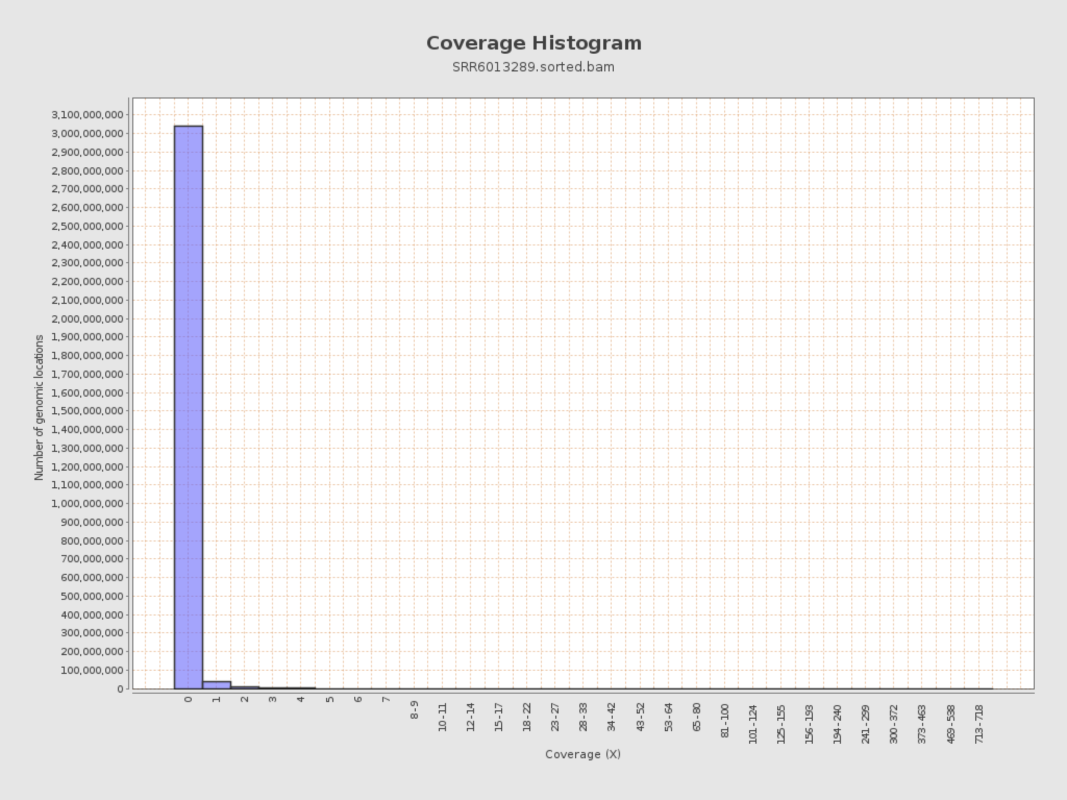
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6746048	0.0271	0.4367
chr2	243199373	5394490	0.0222	0.3731
chr3	198022430	5371808	0.0271	0.2374
chr4	191154276	5119340	0.0268	0.2392
chr5	180915260	7305514	0.0404	0.2945
chr6	171115067	3418502	0.02	0.2298
chr7	159138663	6658247	0.0418	0.6706

chr8	146364022	5495767	0.0375	0.3452
chr9	141213431	2230030	0.0158	0.2138
chr10	135534747	2442294	0.018	0.2213
chr11	135006516	3944492	0.0292	0.2696
chr12	133851895	3808088	0.0285	0.2455
chr13	115169878	1558590	0.0135	0.1701
chr14	107349540	2668680	0.0249	0.2326
chr15	102531392	1696809	0.0165	0.1892
chr16	90354753	5641078	0.0624	0.3677
chr17	81195210	4925783	0.0607	0.3699
chr18	78077248	1583770	0.0203	0.3227
chr19	59128983	3063689	0.0518	0.4501
chr20	63025520	2768668	0.0439	0.3082
chr21	48129895	1104006	0.0229	0.2204
chr22	51304566	826002	0.0161	0.1808
chrMT	16571	21332	1.2873	1.7259
chrX	155270560	4826359	0.0311	0.2616
chrY	59373566	180201	0.003	0.0777

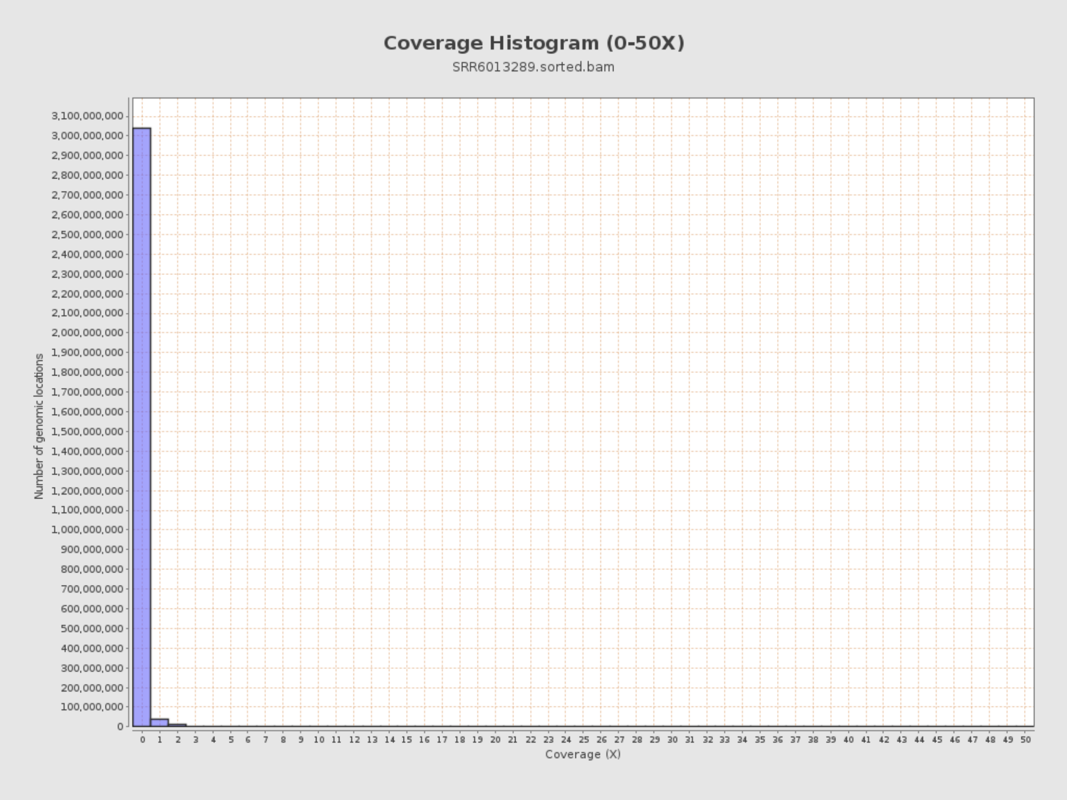
3. Results : Coverage across reference



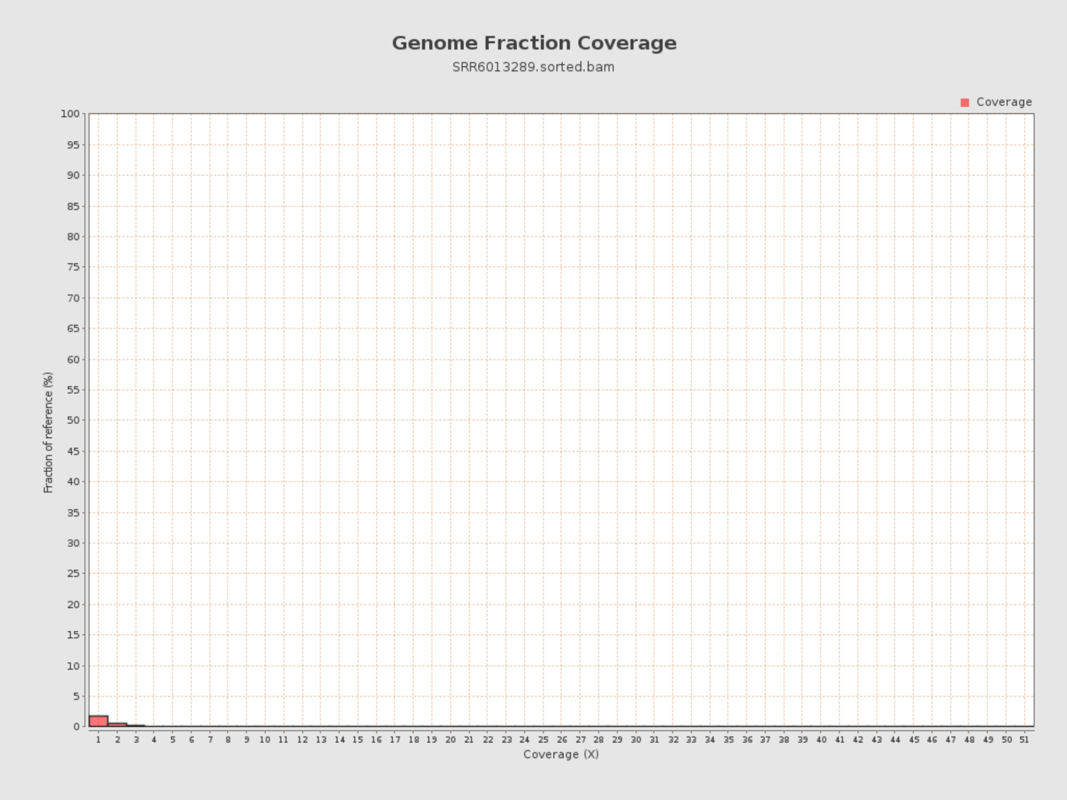
4. Results : Coverage Histogram



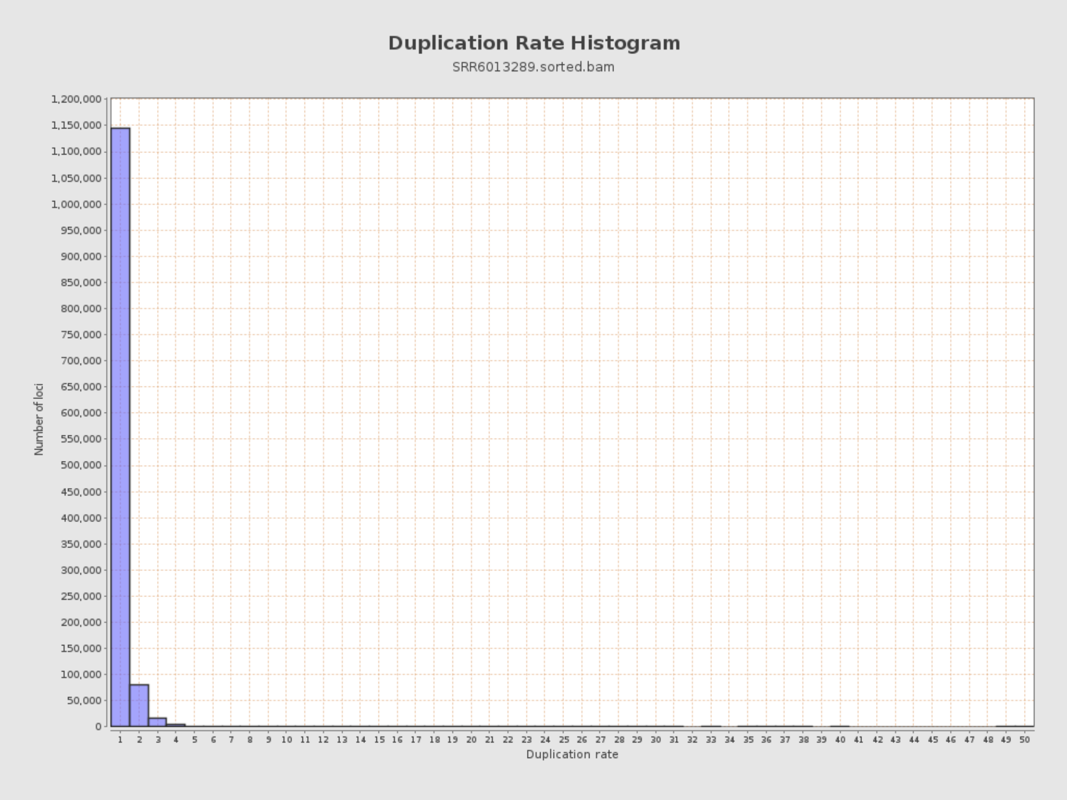
5. Results : Coverage Histogram (0-50X)



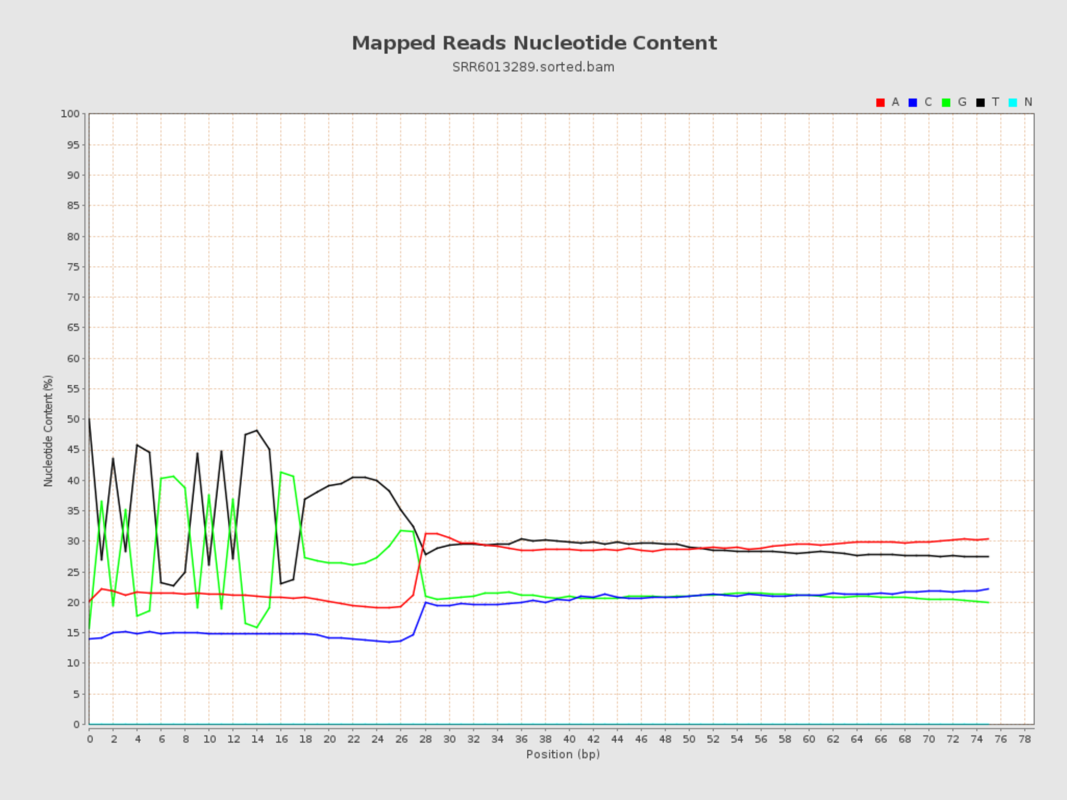
6. Results : Genome Fraction Coverage



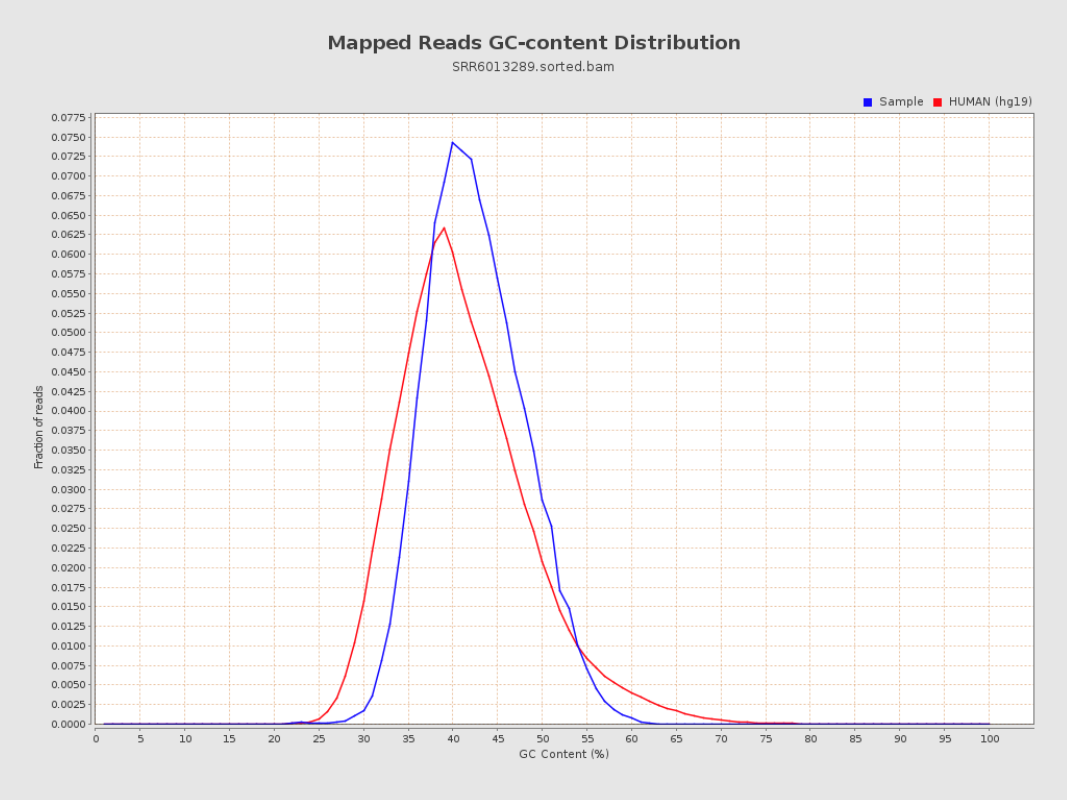
7. Results : Duplication Rate Histogram



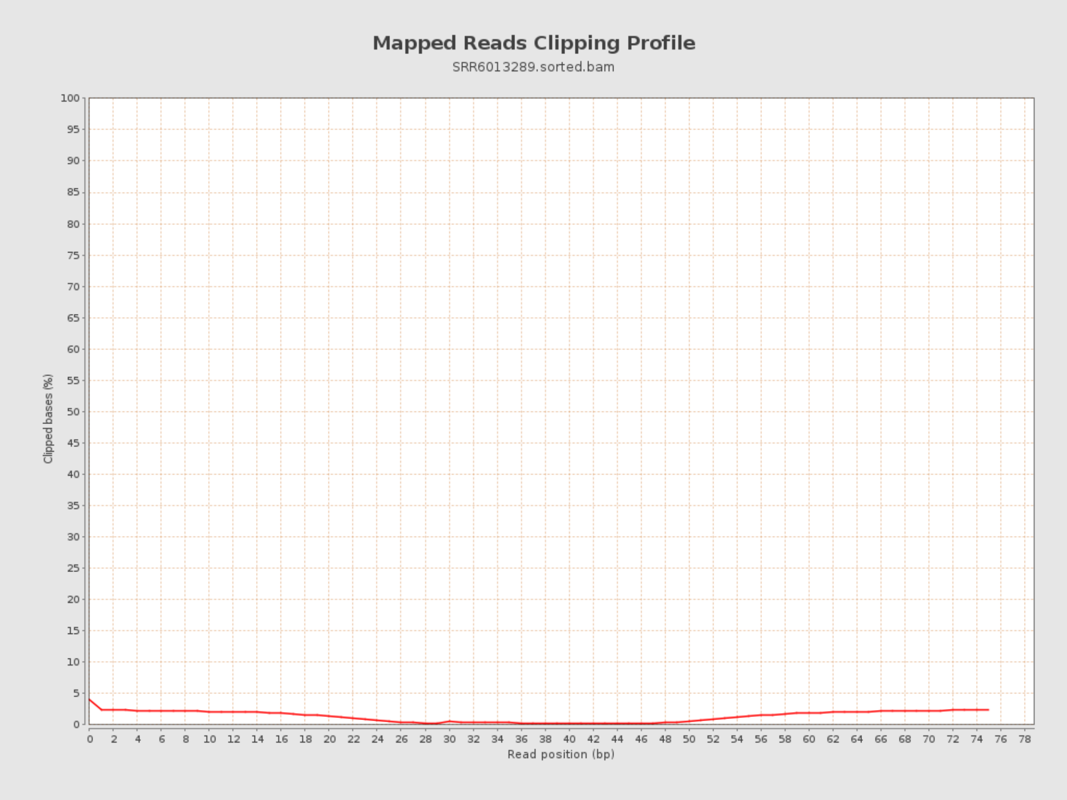
8. Results : Mapped Reads Nucleotide Content



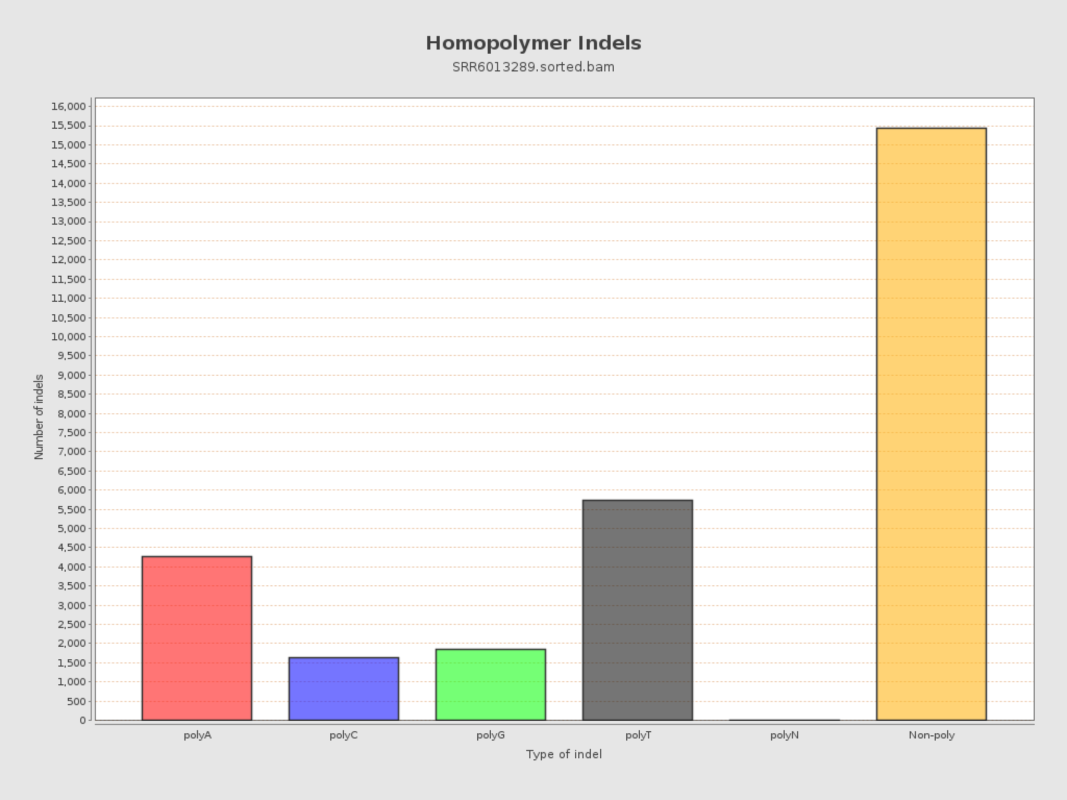
9. Results : Mapped Reads GC-content Distribution



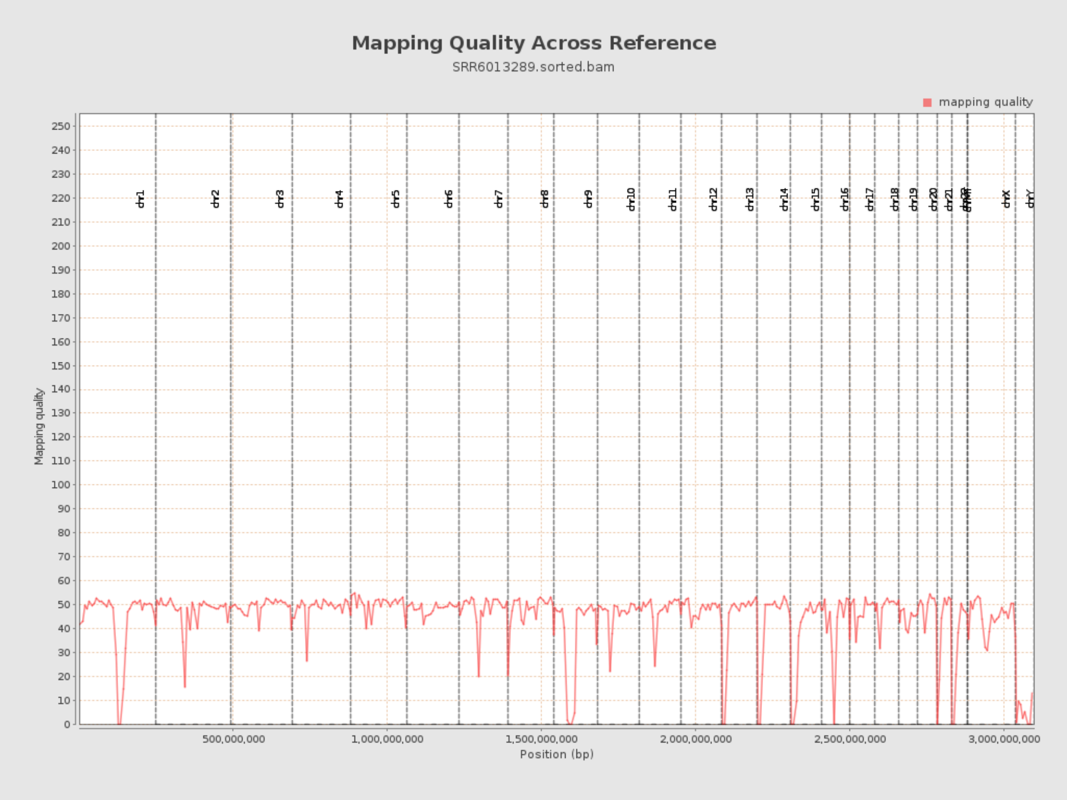
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram