Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 06:36:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054606.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_SRR054606 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054606.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 06:36:08 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054606.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,125,263
Mapped reads	5,670,088 / 79.58%
Unmapped reads	1,455,175 / 20.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	165 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	850,273 / 11.93%
Duplication rate	11.26%
Clipped reads	389,597 / 5.47%

2.2. ACGT Content

Number/percentage of A's	80,810,537 / 30.08%
Number/percentage of C's	50,053,762 / 18.63%
Number/percentage of T's	82,171,918 / 30.59%
Number/percentage of G's	55,605,412 / 20.7%
Number/percentage of N's	2,498 / 0%
GC Percentage	39.33%

2.3. Coverage

Mean	0.0868

Standard Deviation	0.6173

2.4. Mapping Quality

Mean Mapping Quality	45.89

2.5. Mismatches and indels

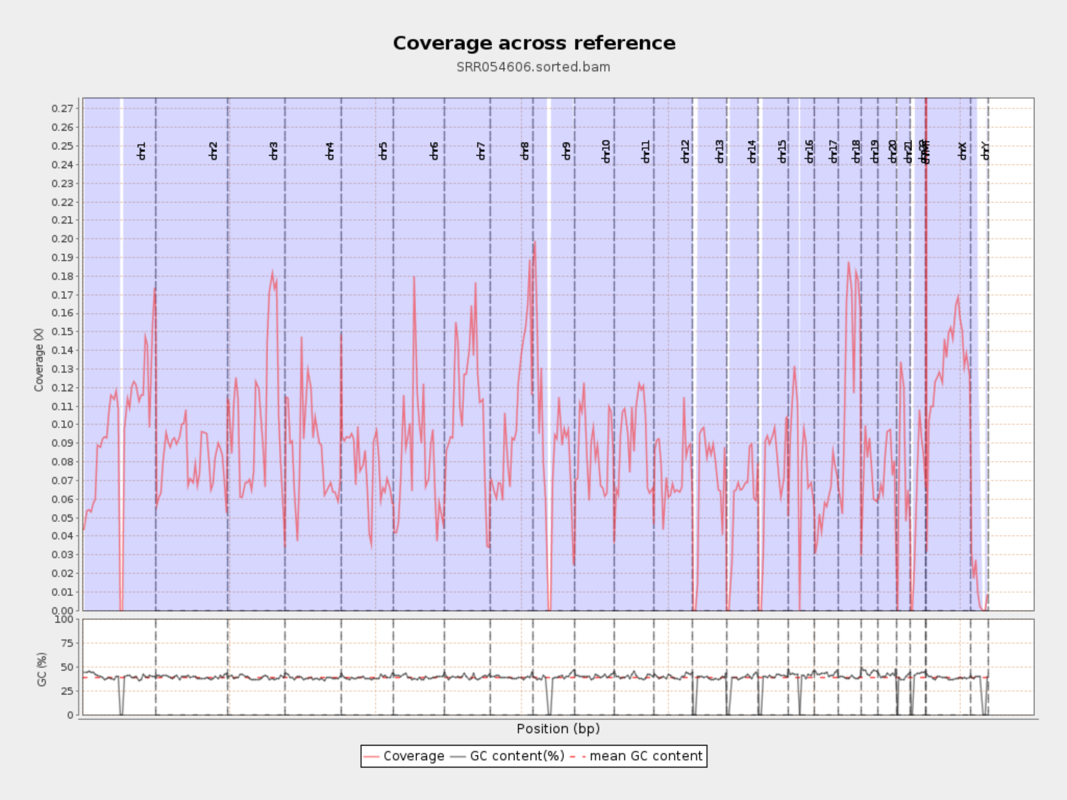
General error rate	0.51%
Mismatches	1,358,646
Insertions	11,444
Mapped reads with at least one insertion	0.2%
Deletions	37,744
Mapped reads with at least one deletion	0.66%
Homopolymer indels	48.98%

2.6. Chromosome stats

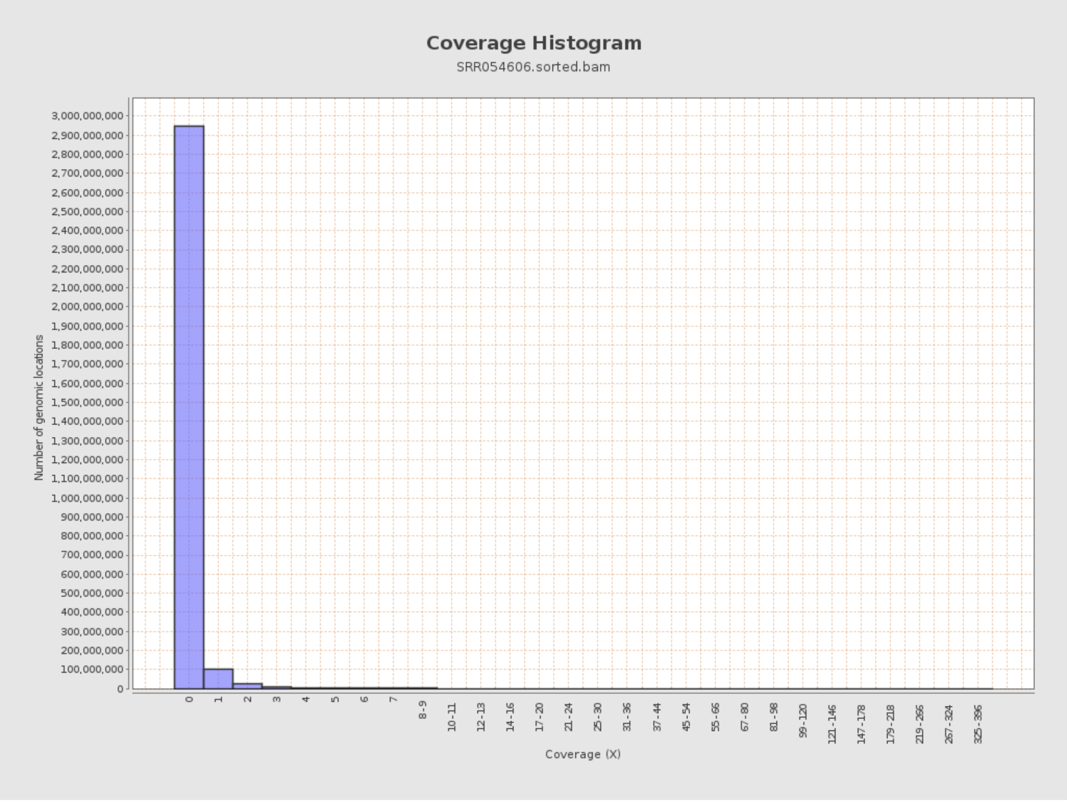
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24165800	0.097	0.7003
chr2	243199373	19932185	0.082	0.6327
chr3	198022430	20487596	0.1035	0.6416
chr4	191154276	16599736	0.0868	0.5971
chr5	180915260	13871946	0.0767	0.5223
chr6	171115067	14021754	0.0819	0.5962
chr7	159138663	17566248	0.1104	0.7464

chr8	146364022	15017053	0.1026	0.6869
chr9	141213431	12338121	0.0874	0.6126
chr10	135534747	11645822	0.0859	0.6095
chr11	135006516	12315425	0.0912	0.6169
chr12	133851895	10112689	0.0756	0.5155
chr13	115169878	7802953	0.0678	0.4891
chr14	107349540	6196972	0.0577	0.5042
chr15	102531392	7200359	0.0702	0.5023
chr16	90354753	7328672	0.0811	0.5897
chr17	81195210	4686717	0.0577	0.4307
chr18	78077248	10453315	0.1339	0.8285
chr19	59128983	4366765	0.0739	0.601
chr20	63025520	4826006	0.0766	0.5458
chr21	48129895	3527328	0.0733	0.6001
chr22	51304566	3092311	0.0603	0.4556
chrMT	16571	24861	1.5003	3.3968
chrX	155270560	20460787	0.1318	0.7959
chrY	59373566	658597	0.0111	0.2385

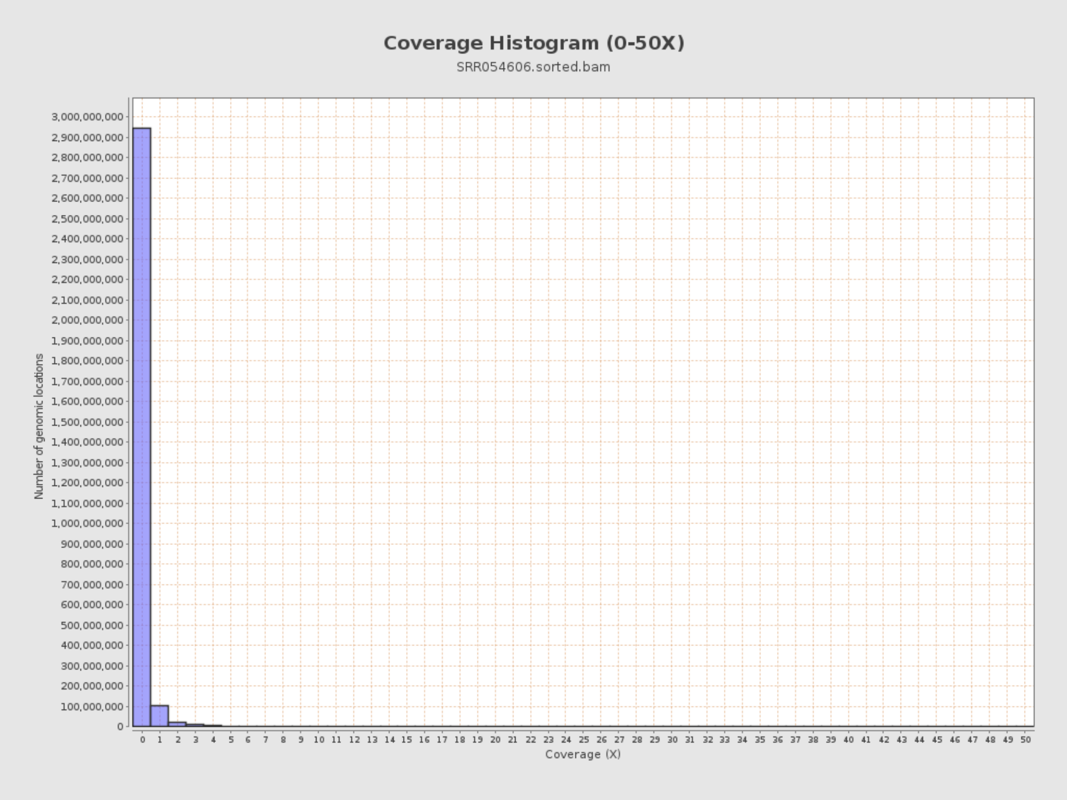
3. Results : Coverage across reference



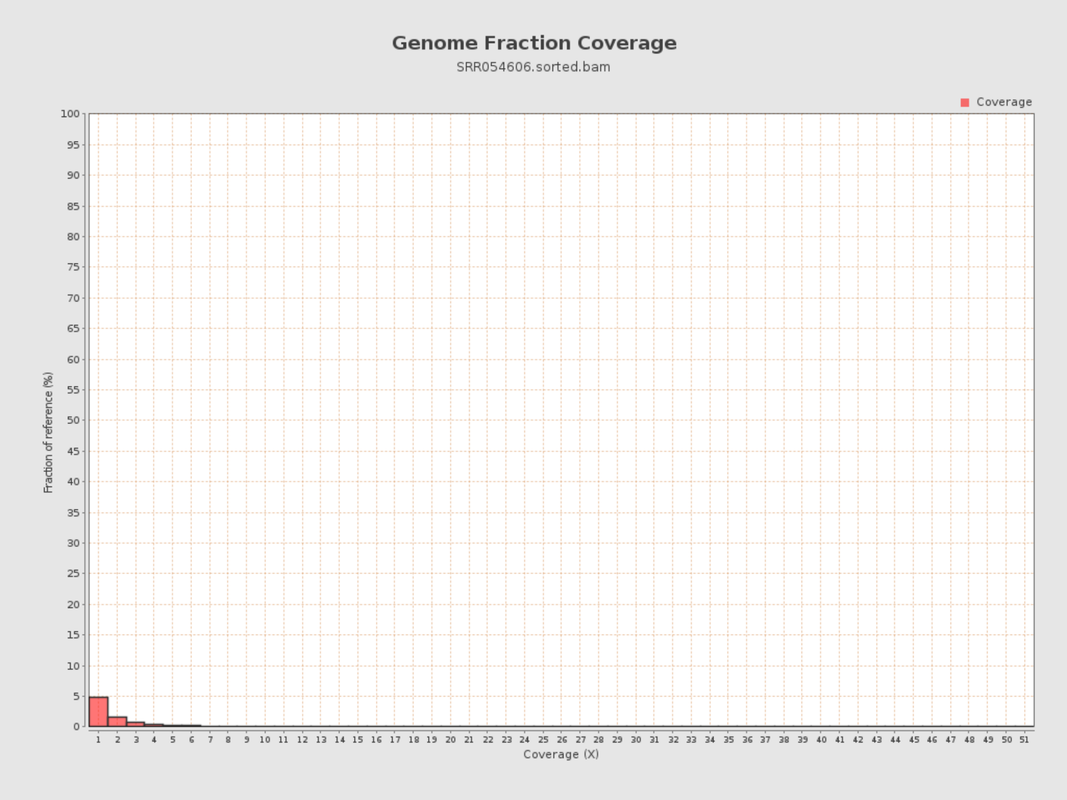
4. Results : Coverage Histogram



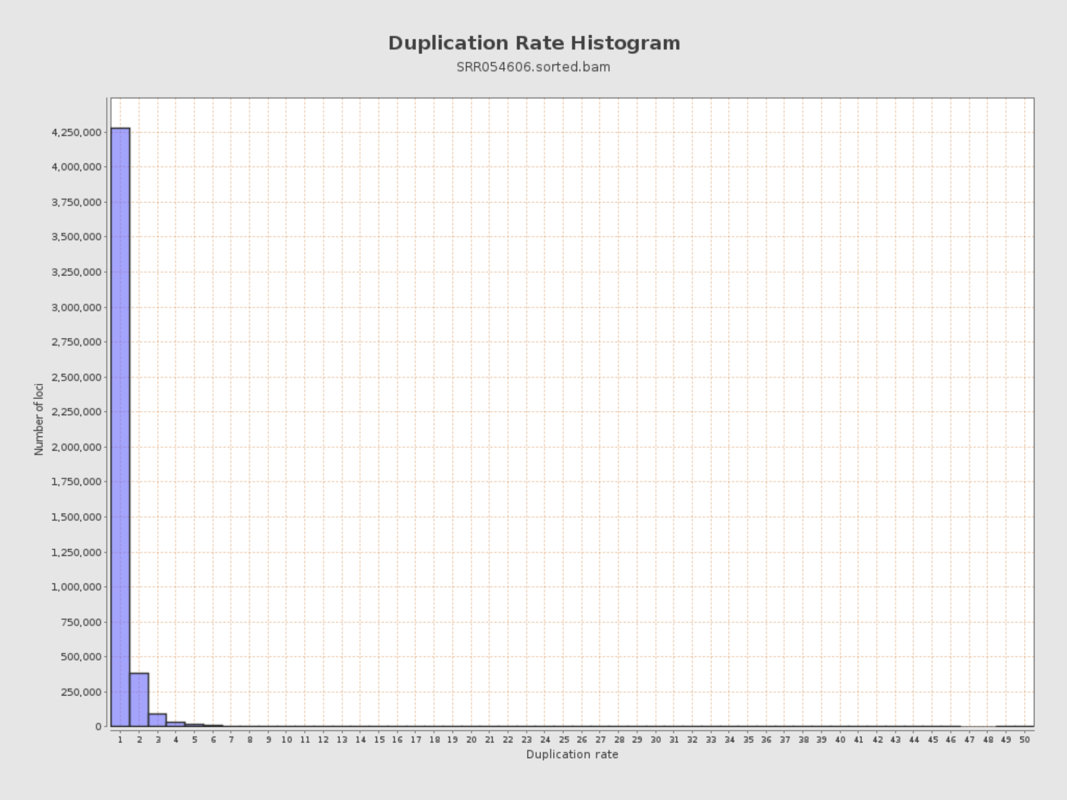
5. Results : Coverage Histogram (0-50X)



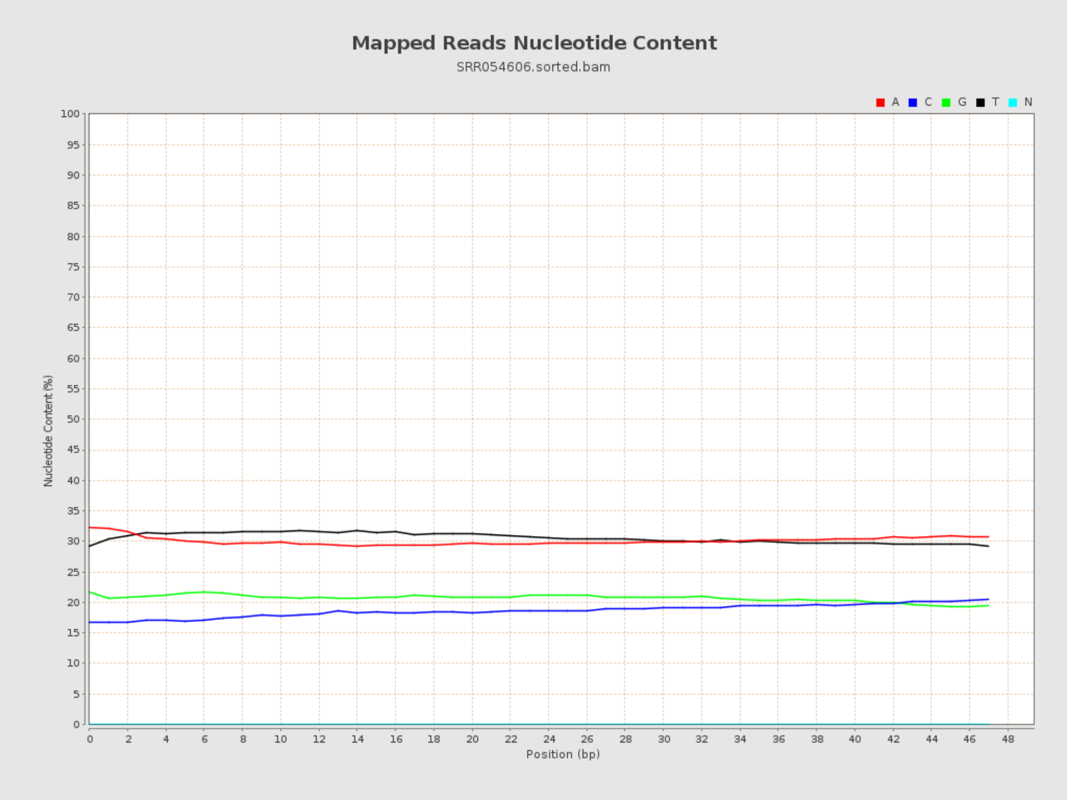
6. Results : Genome Fraction Coverage



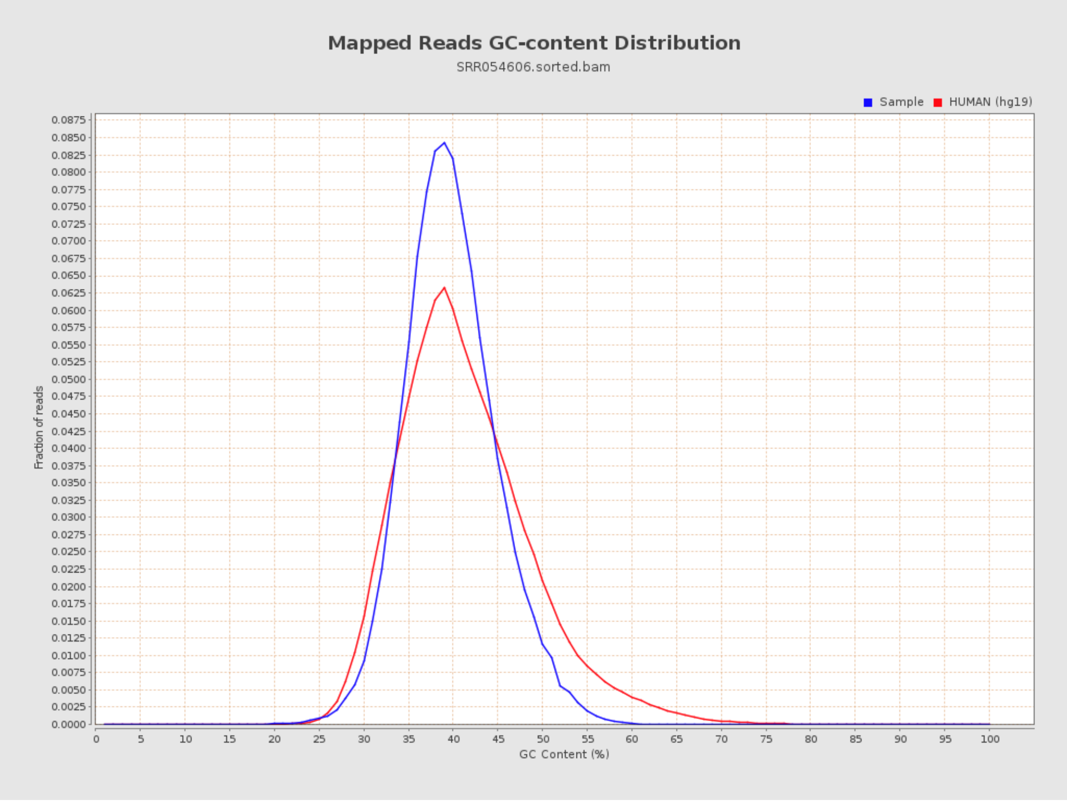
7. Results : Duplication Rate Histogram



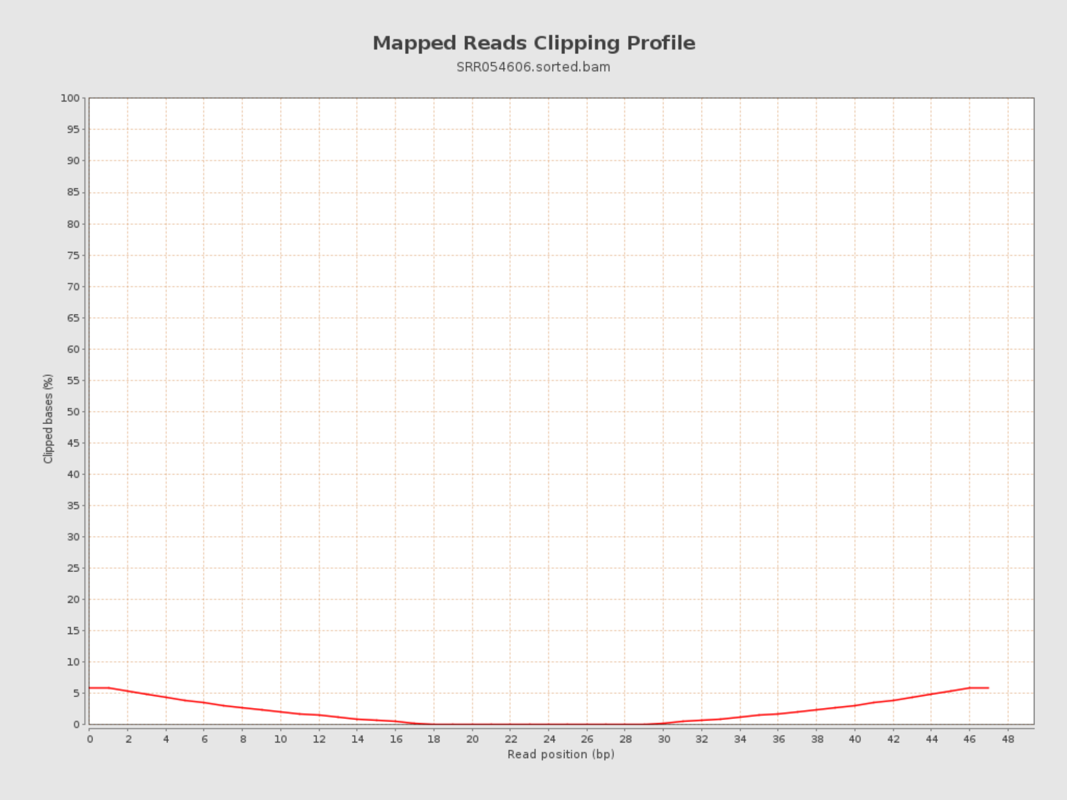
8. Results : Mapped Reads Nucleotide Content



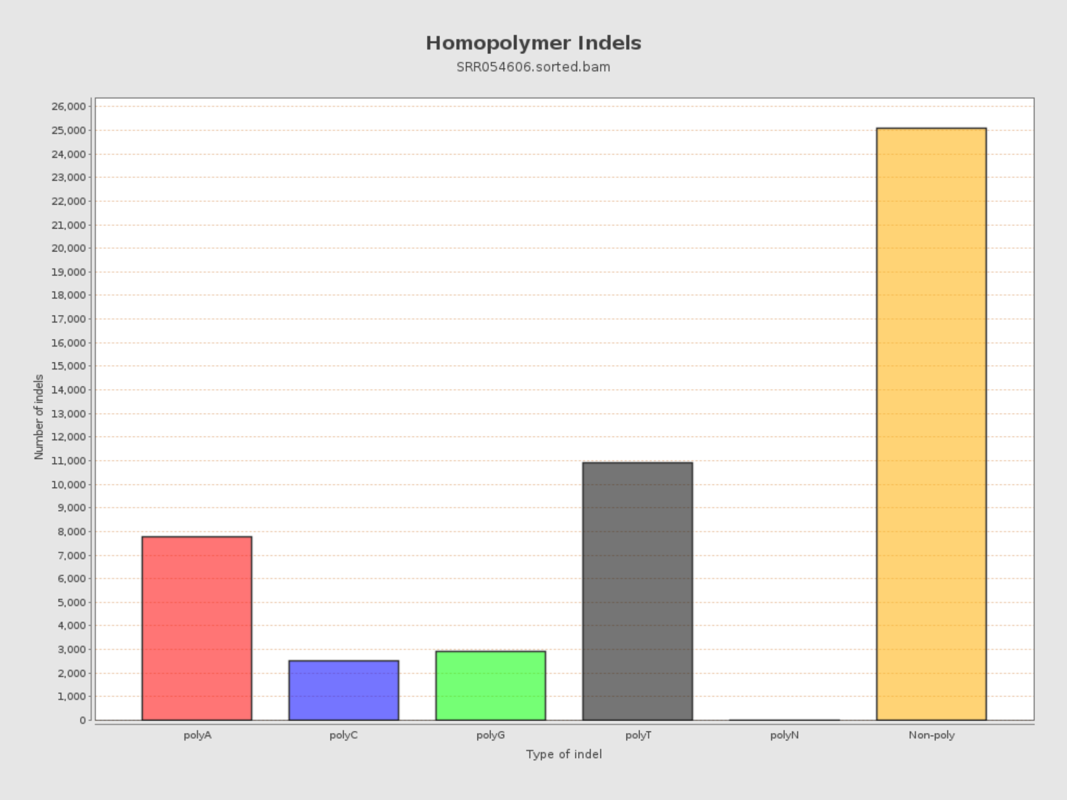
9. Results : Mapped Reads GC-content Distribution



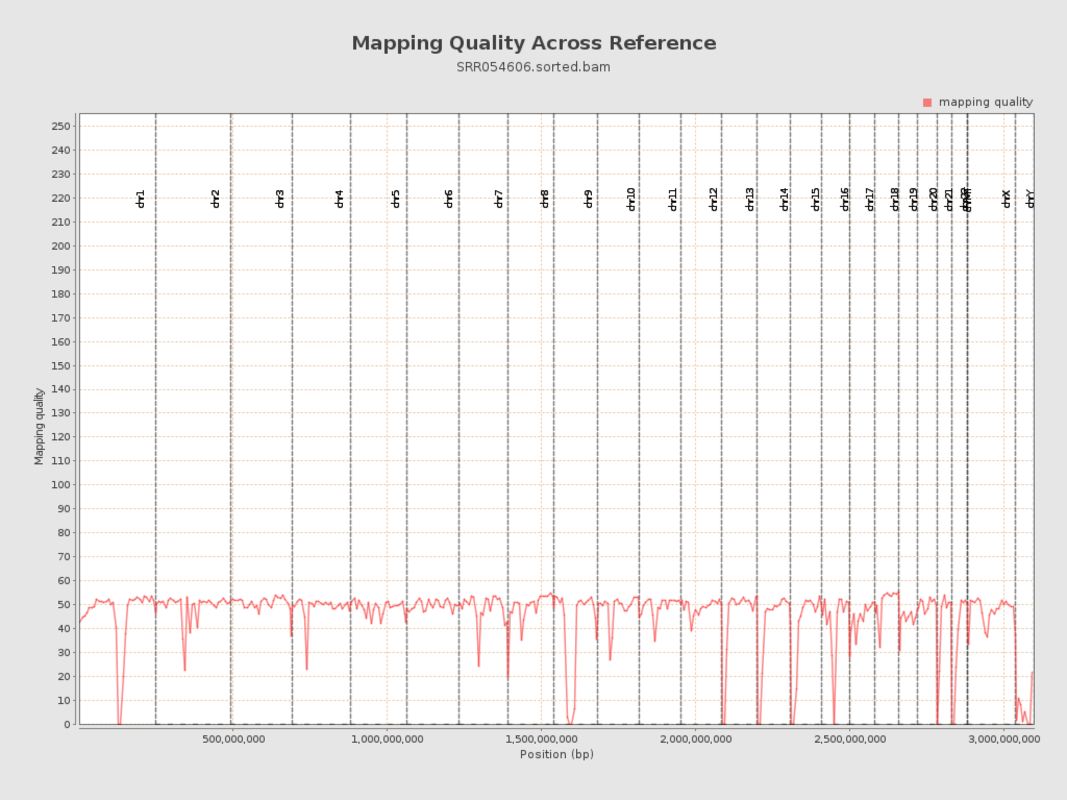
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram