Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 23:08:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053605.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_SRR053605 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053605.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 23:08:34 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053605.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,816,345
Mapped reads	5,183,336 / 58.79%
Unmapped reads	3,633,009 / 41.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	133 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,209,594 / 13.72%
Duplication rate	17.95%
Clipped reads	682,798 / 7.74%

2.2. ACGT Content

Number/percentage of A's	73,249,645 / 30.19%
Number/percentage of C's	45,170,961 / 18.62%
Number/percentage of T's	73,734,282 / 30.39%
Number/percentage of G's	50,345,721 / 20.75%
Number/percentage of N's	102,199 / 0.04%
GC Percentage	39.37%

2.3. Coverage

Mean	0.0784

Standard Deviation	0.6212

2.4. Mapping Quality

Mean Mapping Quality	44.65

2.5. Mismatches and indels

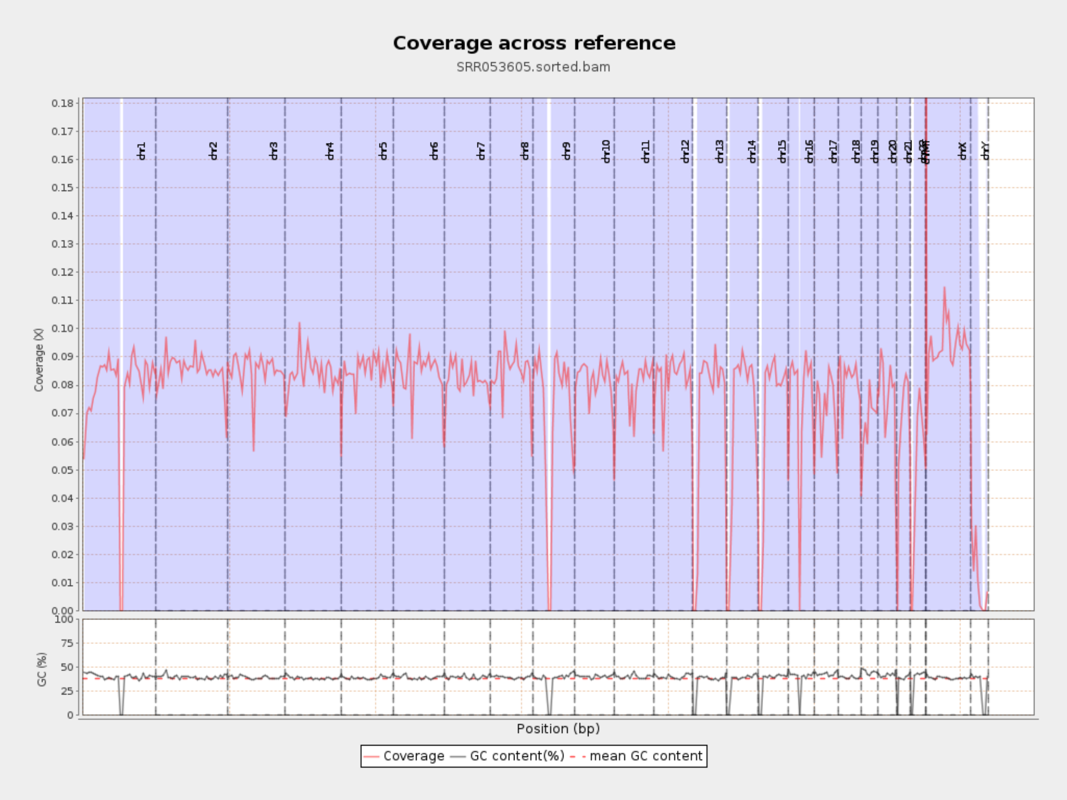
General error rate	1.06%
Mismatches	2,559,507
Insertions	13,381
Mapped reads with at least one insertion	0.26%
Deletions	36,463
Mapped reads with at least one deletion	0.7%
Homopolymer indels	46.03%

2.6. Chromosome stats

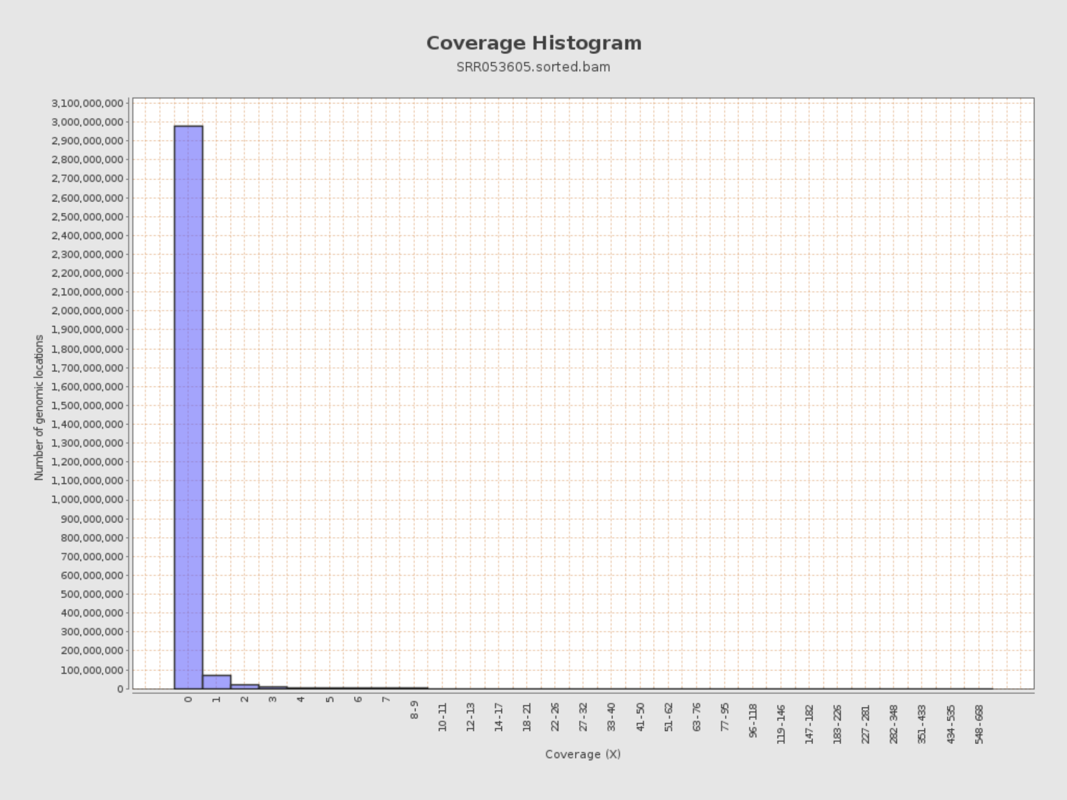
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19243467	0.0772	0.6519
chr2	243199373	20782744	0.0855	0.8122
chr3	198022430	16893158	0.0853	0.5943
chr4	191154276	16195273	0.0847	0.6189
chr5	180915260	15334781	0.0848	0.5861
chr6	171115067	14635239	0.0855	0.6445
chr7	159138663	13049918	0.082	0.6942

chr8	146364022	12431799	0.0849	0.6358
chr9	141213431	9918020	0.0702	0.556
chr10	135534747	11140386	0.0822	0.6353
chr11	135006516	10927702	0.0809	0.6175
chr12	133851895	11122159	0.0831	0.5864
chr13	115169878	8048649	0.0699	0.5293
chr14	107349540	7451597	0.0694	0.5652
chr15	102531392	6928880	0.0676	0.5143
chr16	90354753	6566516	0.0727	0.5536
chr17	81195210	5924699	0.073	0.5317
chr18	78077248	6405631	0.082	0.6787
chr19	59128983	4001279	0.0677	0.58
chr20	63025520	4900427	0.0778	0.5699
chr21	48129895	3072353	0.0638	0.5421
chr22	51304566	2461655	0.048	0.4311
chrMT	16571	11033	0.6658	1.8307
chrX	155270560	14566074	0.0938	0.6818
chrY	59373566	640162	0.0108	0.2228

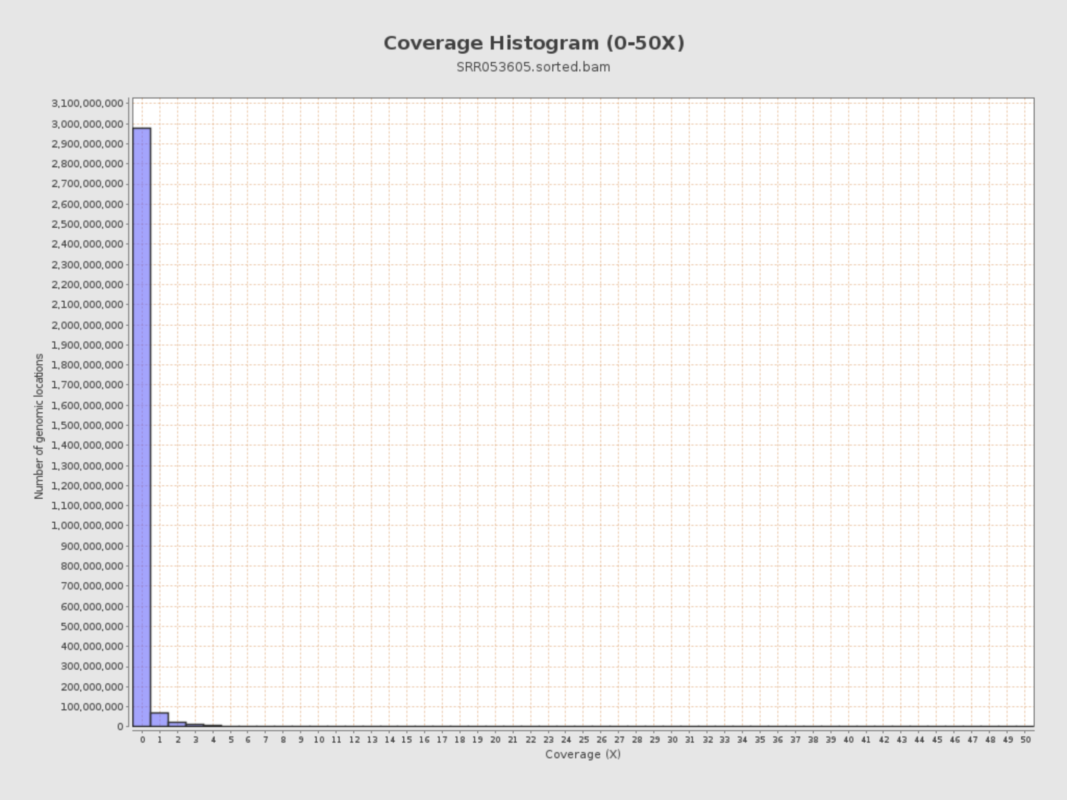
3. Results : Coverage across reference



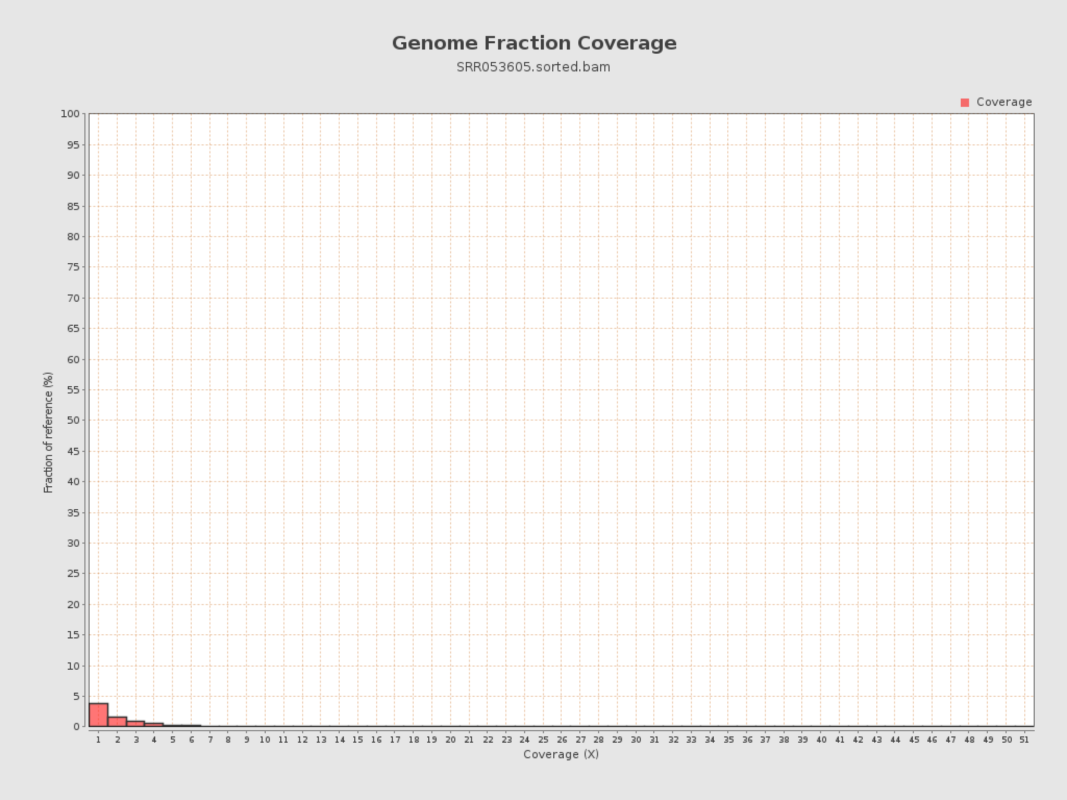
4. Results : Coverage Histogram



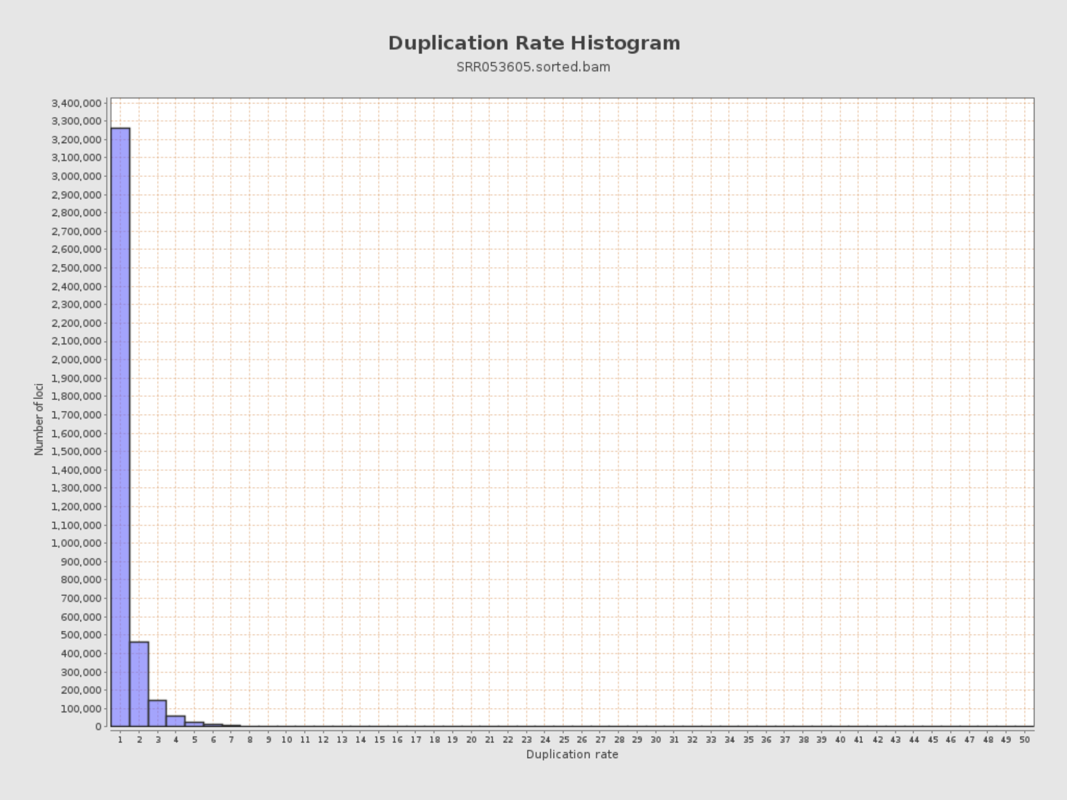
5. Results : Coverage Histogram (0-50X)



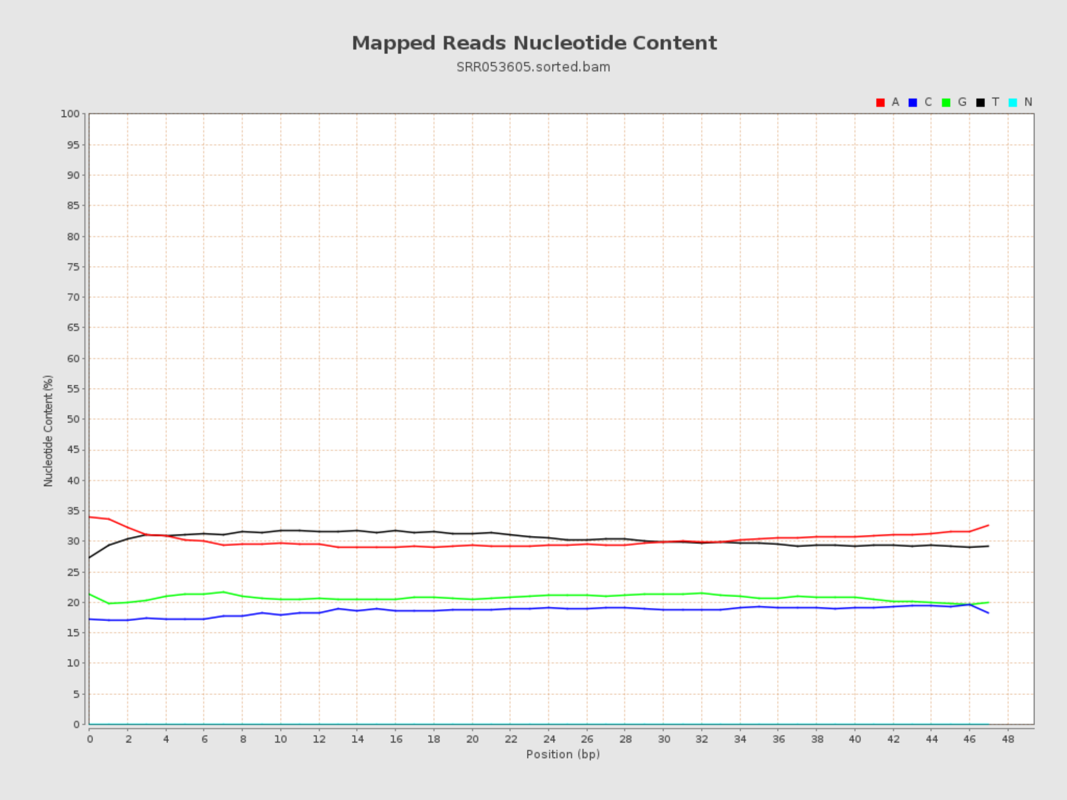
6. Results : Genome Fraction Coverage



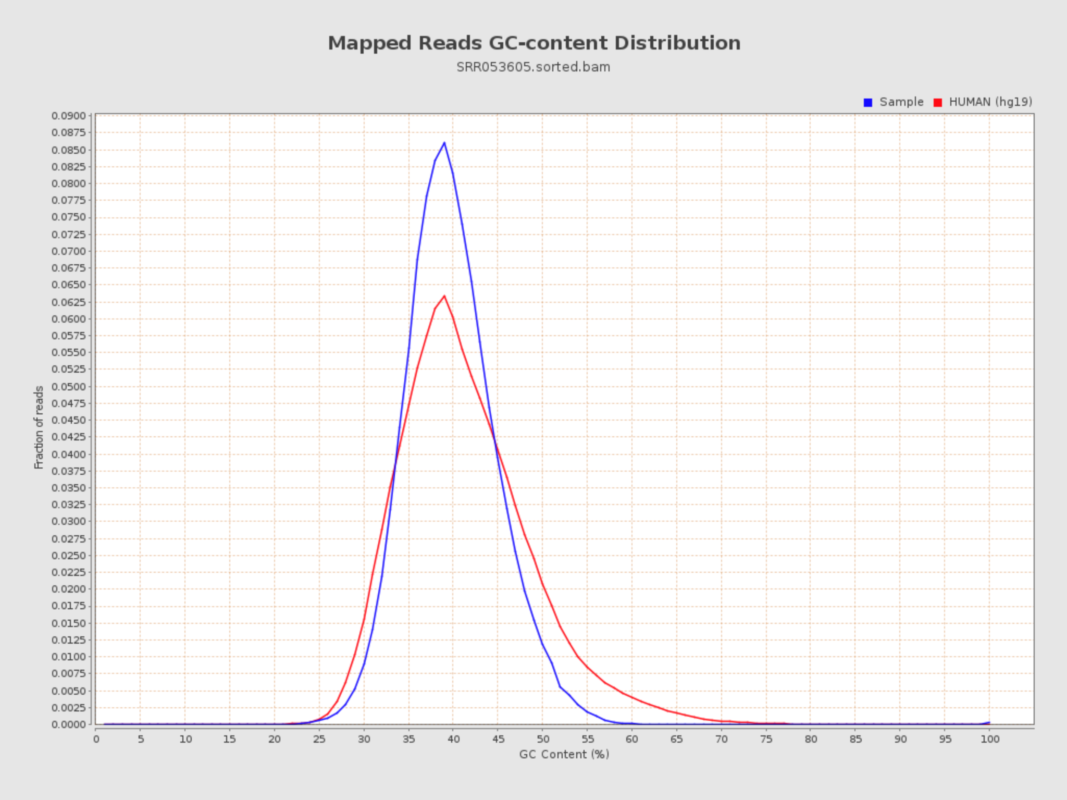
7. Results : Duplication Rate Histogram



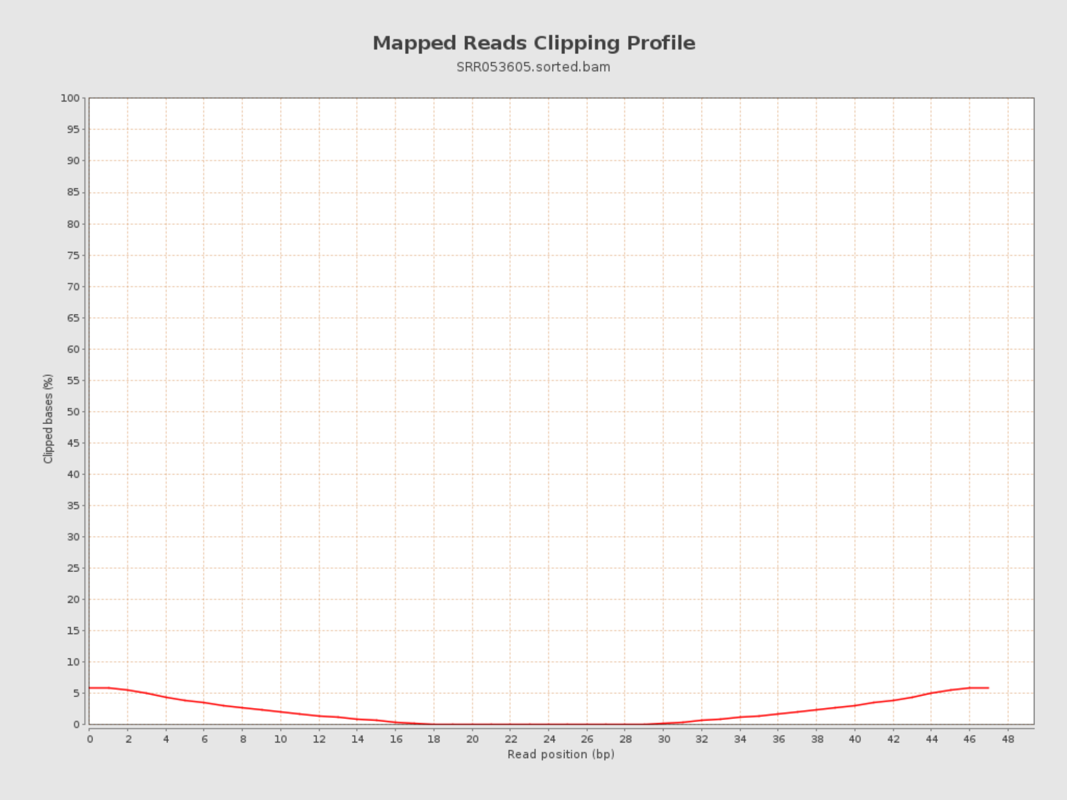
8. Results : Mapped Reads Nucleotide Content



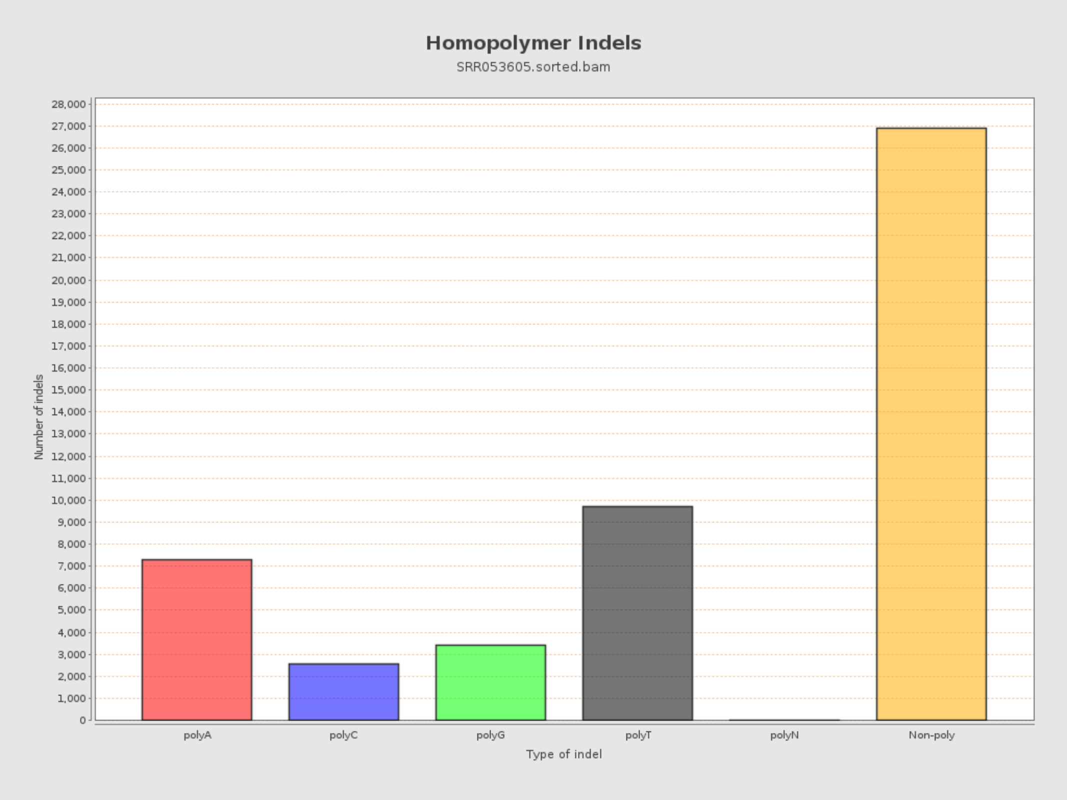
9. Results : Mapped Reads GC-content Distribution



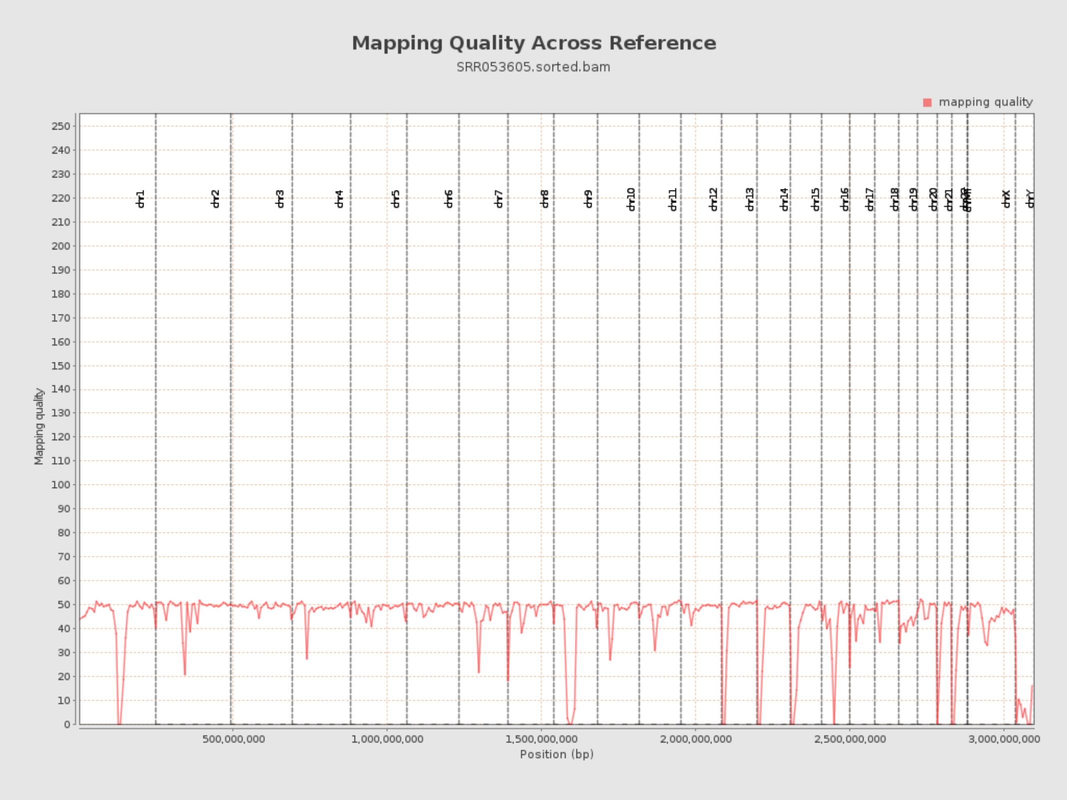
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram