Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 23:14:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506013.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_SRR1506013 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506013.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 23:14:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506013.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,460,041
Mapped reads	4,668,411 / 72.27%
Unmapped reads	1,791,630 / 27.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	193 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	304,485 / 4.71%
Duplication rate	4.88%
Clipped reads	763,670 / 11.82%

2.2. ACGT Content

Number/percentage of A's	63,311,712 / 29.21%
Number/percentage of C's	45,248,443 / 20.88%
Number/percentage of T's	62,106,680 / 28.66%
Number/percentage of G's	45,313,581 / 20.91%
Number/percentage of N's	732,769 / 0.34%
GC Percentage	41.79%

2.3. Coverage

Mean	0.07

Standard Deviation	0.6678

2.4. Mapping Quality

Mean Mapping Quality	43.5

2.5. Mismatches and indels

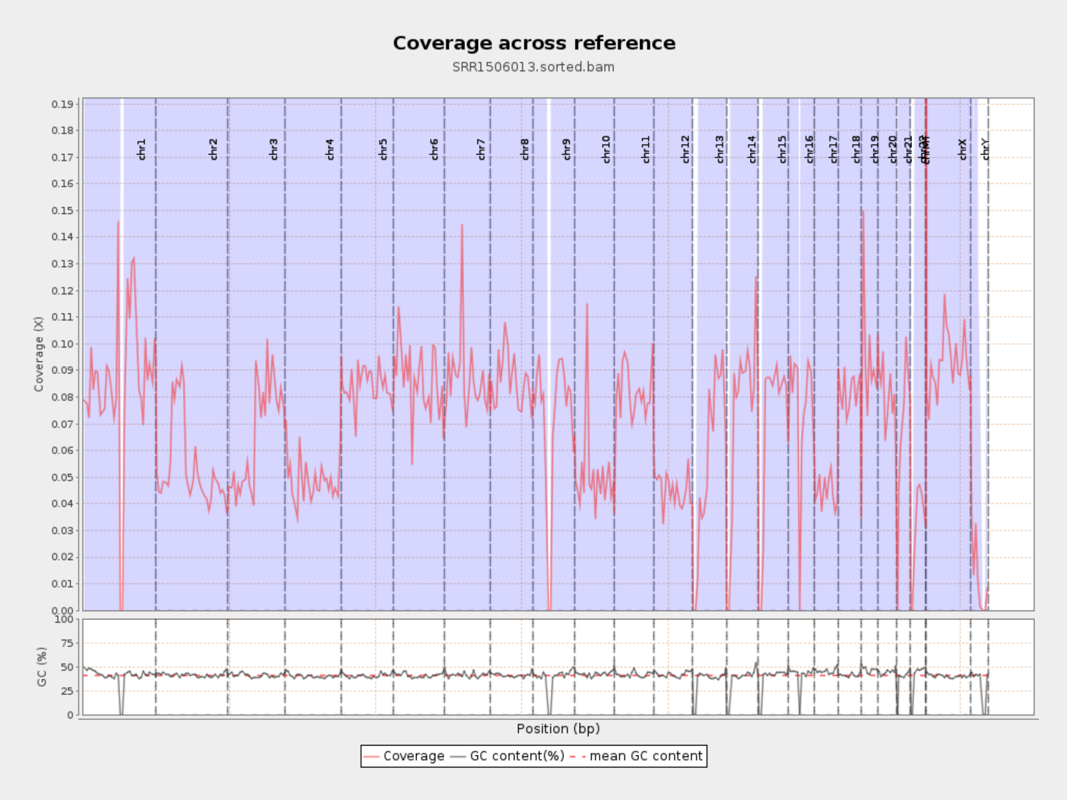
General error rate	0.81%
Mismatches	1,746,546
Insertions	9,390
Mapped reads with at least one insertion	0.2%
Deletions	31,457
Mapped reads with at least one deletion	0.67%
Homopolymer indels	44.11%

2.6. Chromosome stats

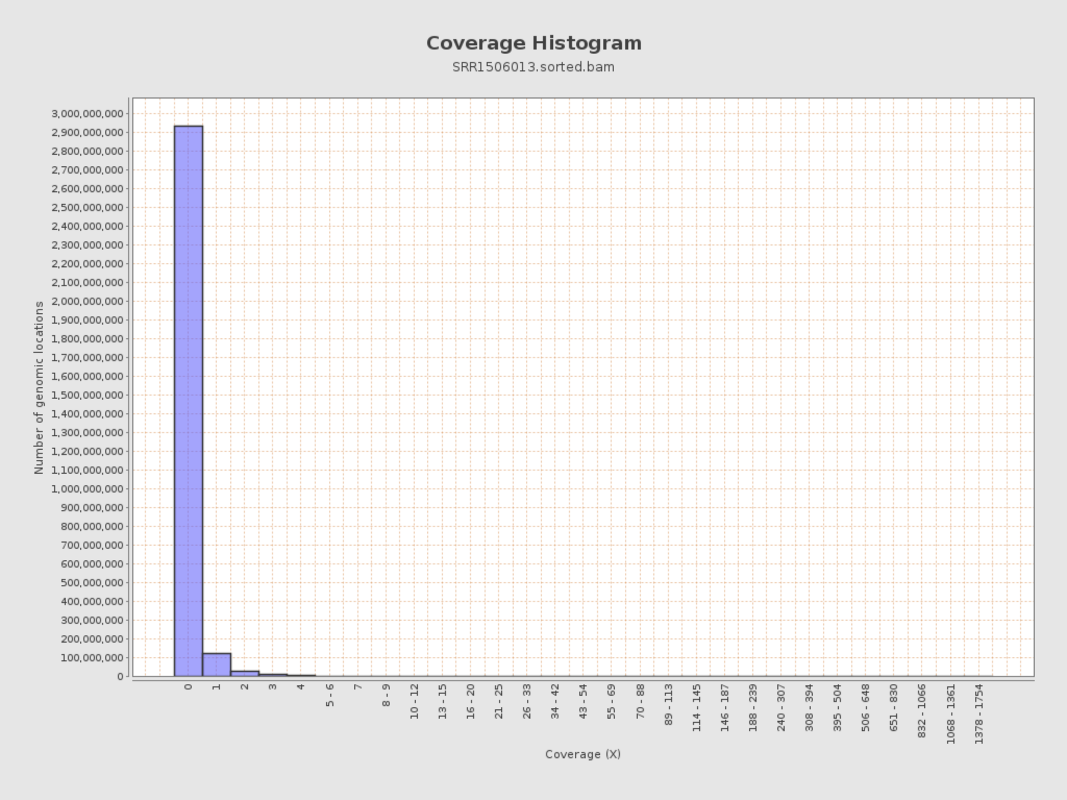
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21521264	0.0863	1.3023
chr2	243199373	13212257	0.0543	0.4449
chr3	198022430	12902735	0.0652	0.3311
chr4	191154276	9330399	0.0488	0.2957
chr5	180915260	15255388	0.0843	0.3787
chr6	171115067	14870680	0.0869	0.4393
chr7	159138663	13903811	0.0874	0.927

chr8	146364022	12620665	0.0862	0.6645
chr9	141213431	10104971	0.0716	0.4315
chr10	135534747	6901834	0.0509	0.6048
chr11	135006516	10972900	0.0813	0.505
chr12	133851895	6048473	0.0452	0.2896
chr13	115169878	6622540	0.0575	0.3077
chr14	107349540	8045268	0.0749	1.7091
chr15	102531392	7075112	0.069	0.3388
chr16	90354753	6719727	0.0744	0.402
chr17	81195210	3625181	0.0446	0.3179
chr18	78077248	6404728	0.082	0.5965
chr19	59128983	5566531	0.0941	0.9204
chr20	63025520	5064255	0.0804	0.4047
chr21	48129895	3311209	0.0688	0.3737
chr22	51304566	1583966	0.0309	0.2255
chrMT	16571	19442	1.1733	1.6583
chrX	155270560	14372563	0.0926	0.4371
chrY	59373566	701477	0.0118	0.1859

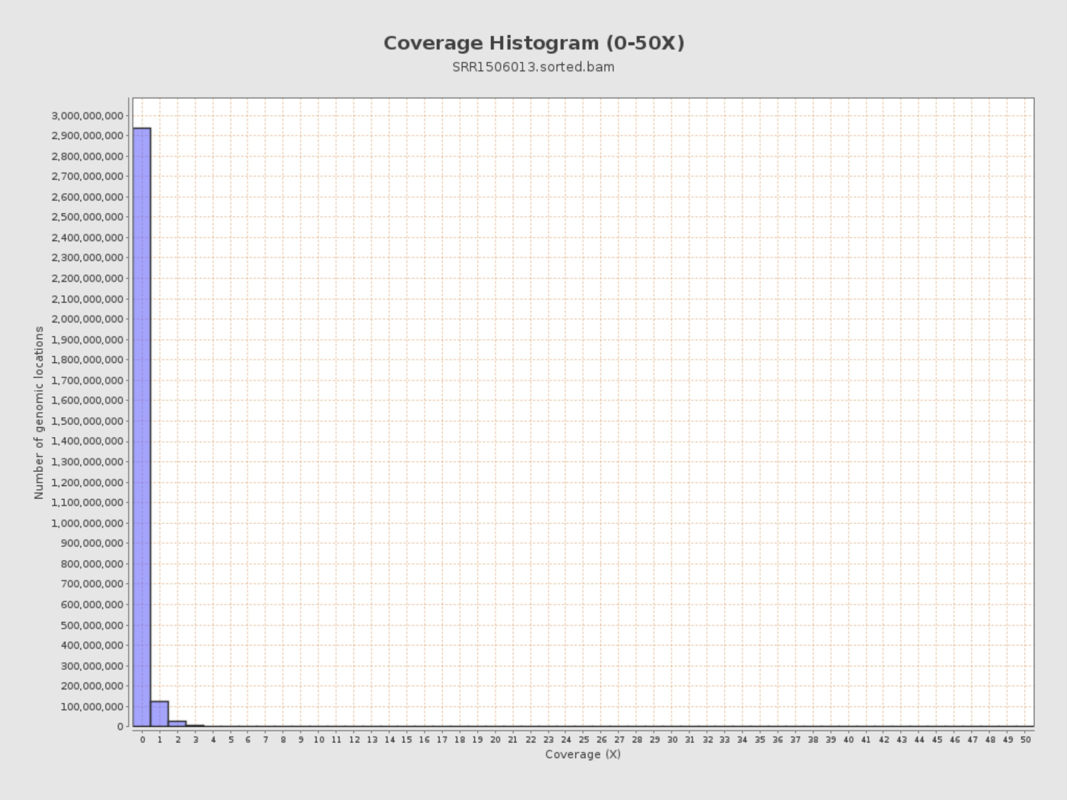
3. Results : Coverage across reference



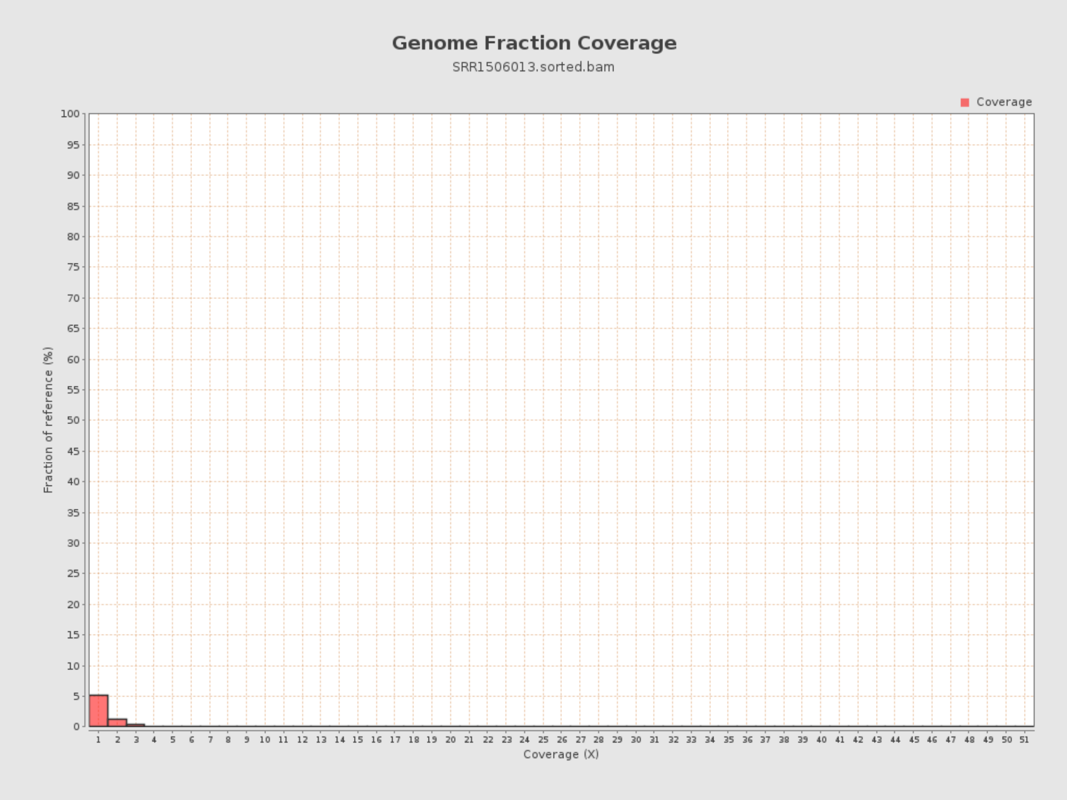
4. Results : Coverage Histogram



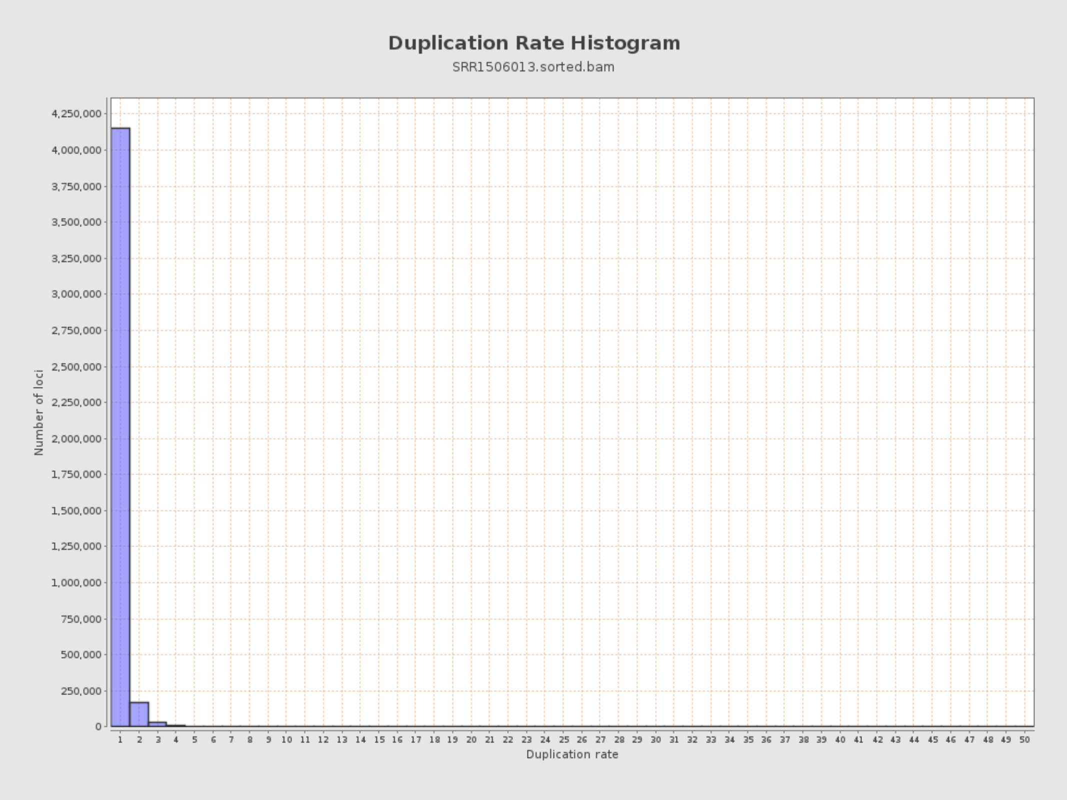
5. Results : Coverage Histogram (0-50X)



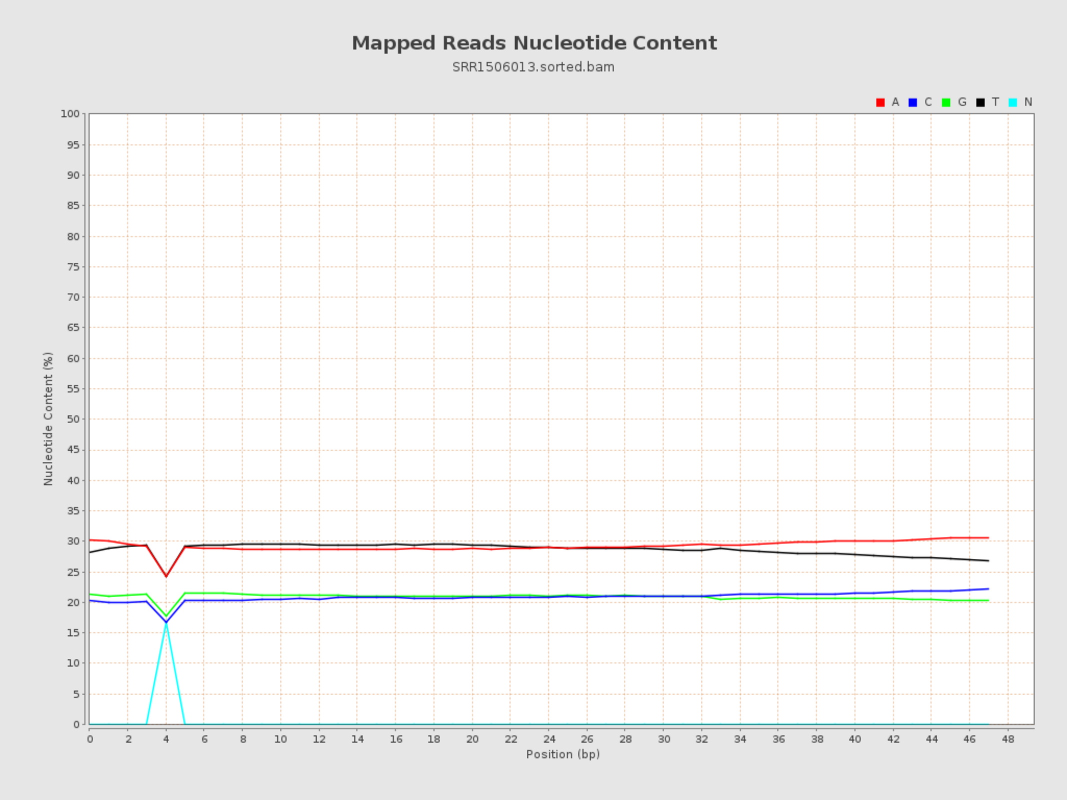
6. Results : Genome Fraction Coverage



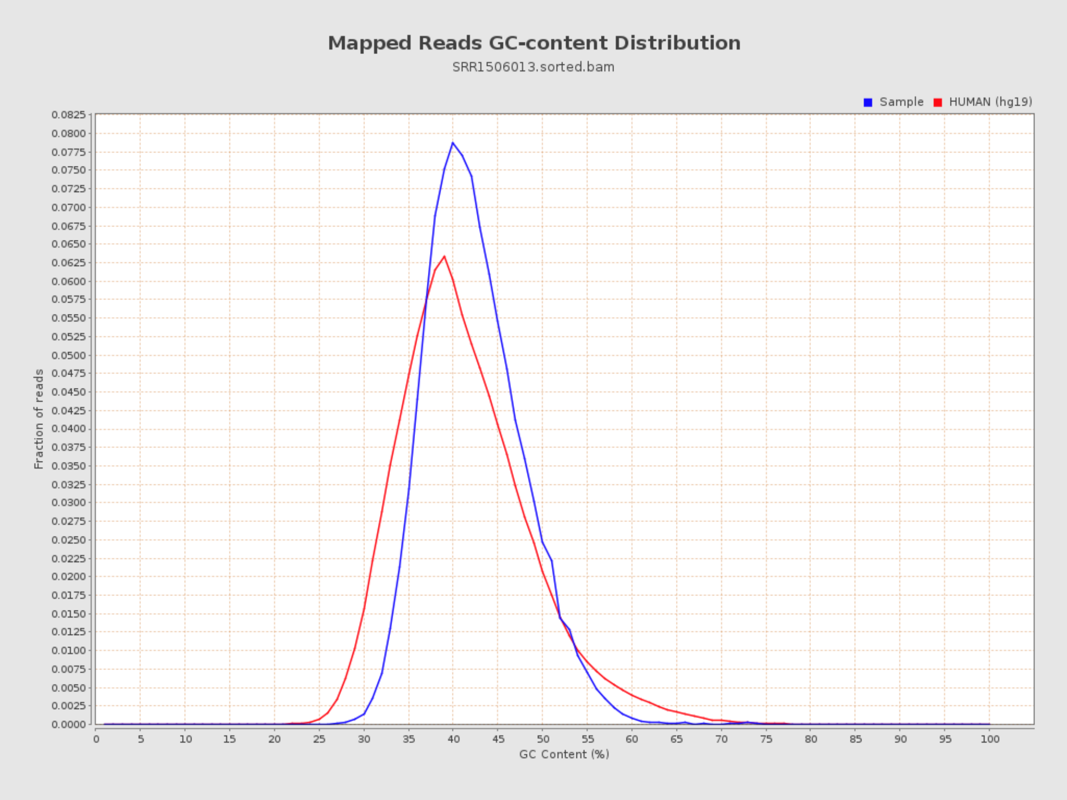
7. Results : Duplication Rate Histogram



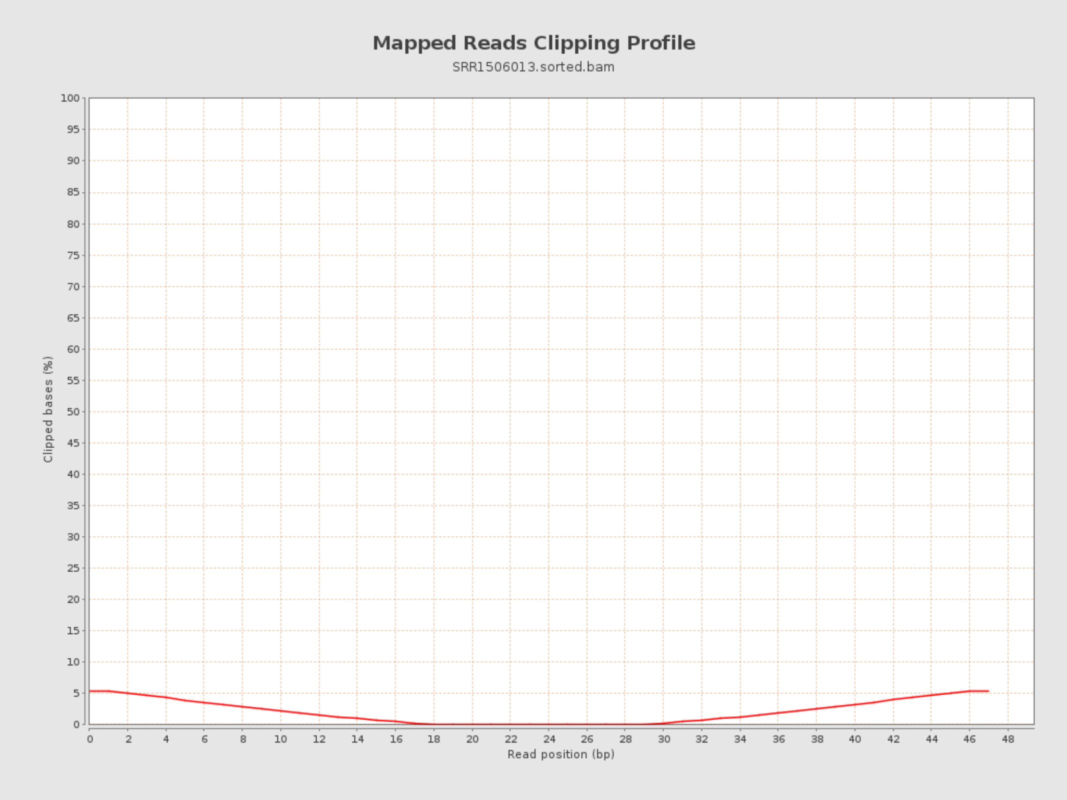
8. Results : Mapped Reads Nucleotide Content



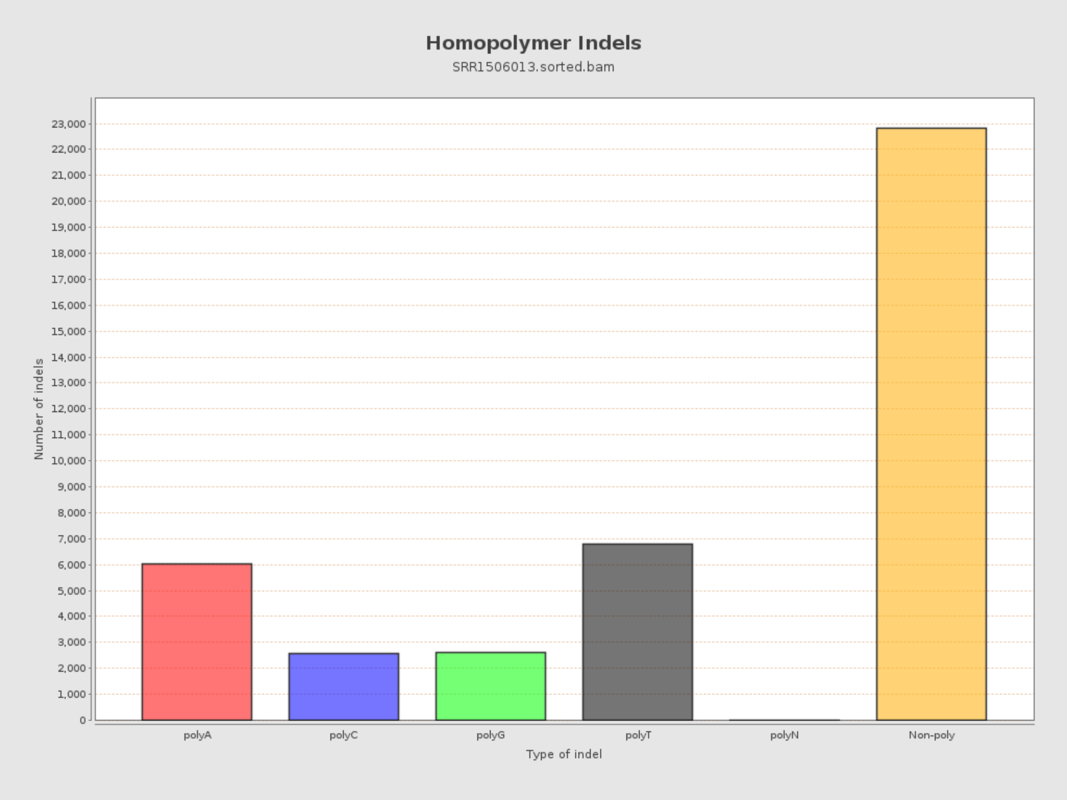
9. Results : Mapped Reads GC-content Distribution



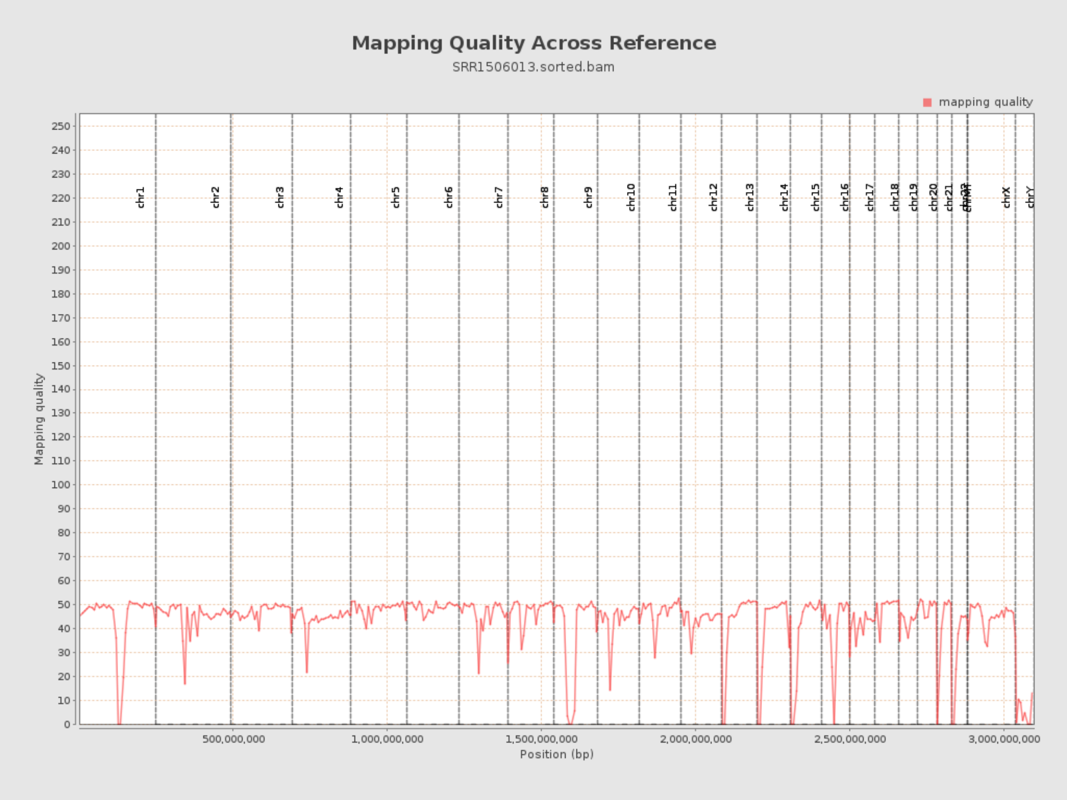
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram