

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 19:49:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013288.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_SRR6013288 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013288.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 19:49:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013288.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,765,274
Mapped reads	1,455,093 / 82.43%
Unmapped reads	310,181 / 17.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,578 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	86,562 / 4.9%
Duplication rate	4.88%
Clipped reads	763,789 / 43.27%

2.2. ACGT Content

Number/percentage of A's	25,302,642 / 26.93%
Number/percentage of C's	16,895,362 / 17.98%
Number/percentage of T's	30,380,237 / 32.34%
Number/percentage of G's	21,366,547 / 22.74%
Number/percentage of N's	1,148 / 0%
GC Percentage	40.73%

2.3. Coverage

Mean	0.0304

Standard Deviation	0.2973
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2.4. Mapping Quality

Mean Mapping Quality	45.17
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2.5. Mismatches and indels

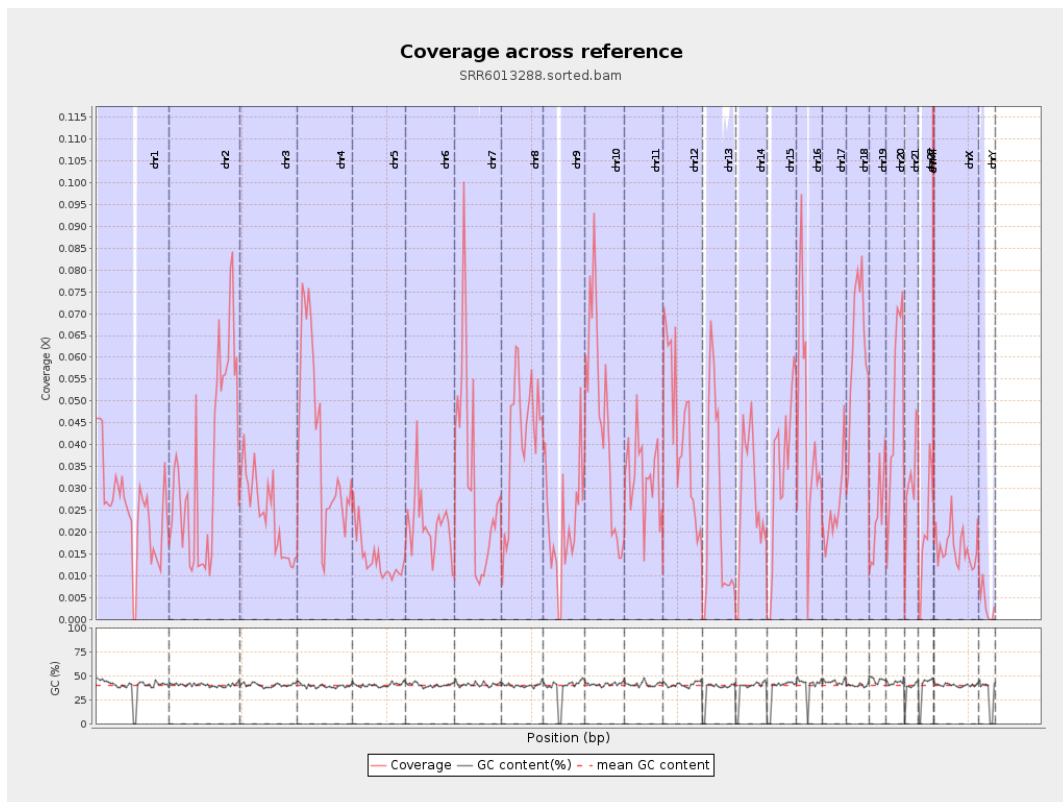
General error rate	0.8%
Mismatches	743,323
Insertions	6,626
Mapped reads with at least one insertion	0.45%
Deletions	28,691
Mapped reads with at least one deletion	1.95%
Homopolymer indels	45.55%

2.6. Chromosome stats

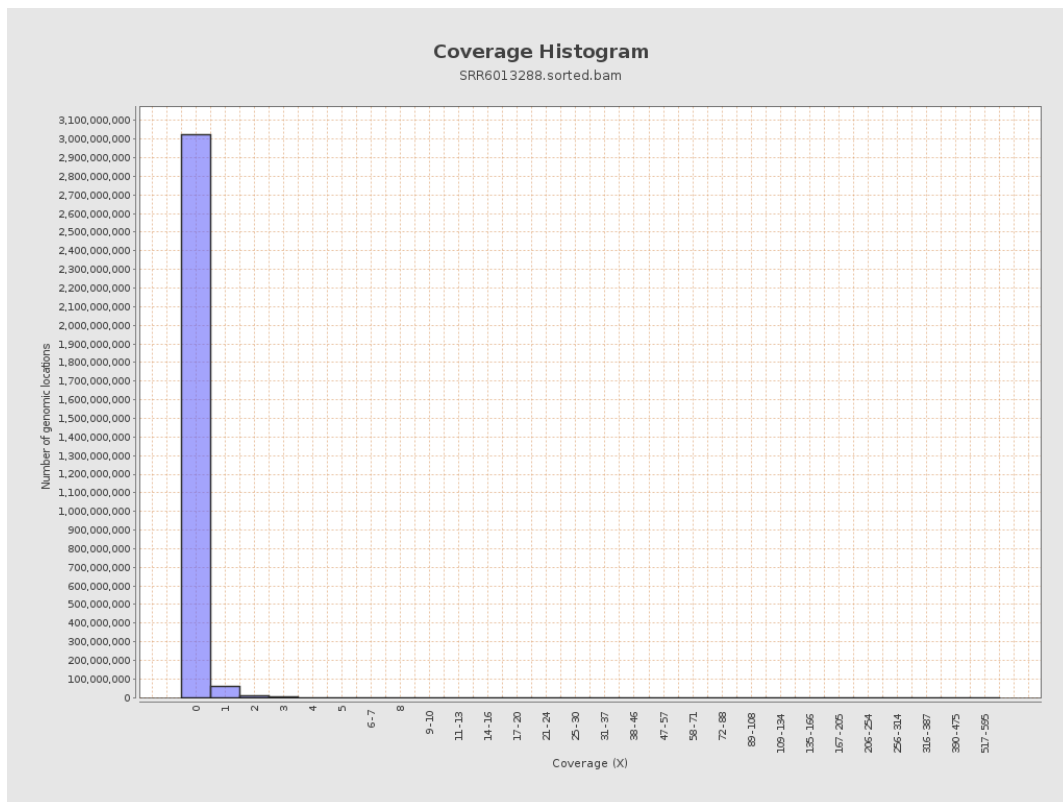
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6254833	0.0251	0.2955
chr2	243199373	8630285	0.0355	0.4014
chr3	198022430	4722211	0.0238	0.1871
chr4	191154276	7681500	0.0402	0.2504
chr5	180915260	2523381	0.0139	0.1443
chr6	171115067	3698214	0.0216	0.2026
chr7	159138663	5090932	0.032	0.5288

chr8	146364022	6090727	0.0416	0.4404
chr9	141213431	3012644	0.0213	0.2815
chr10	135534747	6111735	0.0451	0.3493
chr11	135006516	4346299	0.0322	0.2597
chr12	133851895	5752481	0.043	0.2574
chr13	115169878	2740089	0.0238	0.188
chr14	107349540	2982226	0.0278	0.211
chr15	102531392	3502566	0.0342	0.2277
chr16	90354753	3962389	0.0439	0.2646
chr17	81195210	2115873	0.0261	0.2001
chr18	78077248	4884996	0.0626	0.5292
chr19	59128983	1438204	0.0243	0.274
chr20	63025520	3093831	0.0491	0.2769
chr21	48129895	1531765	0.0318	0.2213
chr22	51304566	1052385	0.0205	0.1708
chrMT	16571	19056	1.15	1.2807
chrX	155270560	2555213	0.0165	0.1761
chrY	59373566	201464	0.0034	0.0817

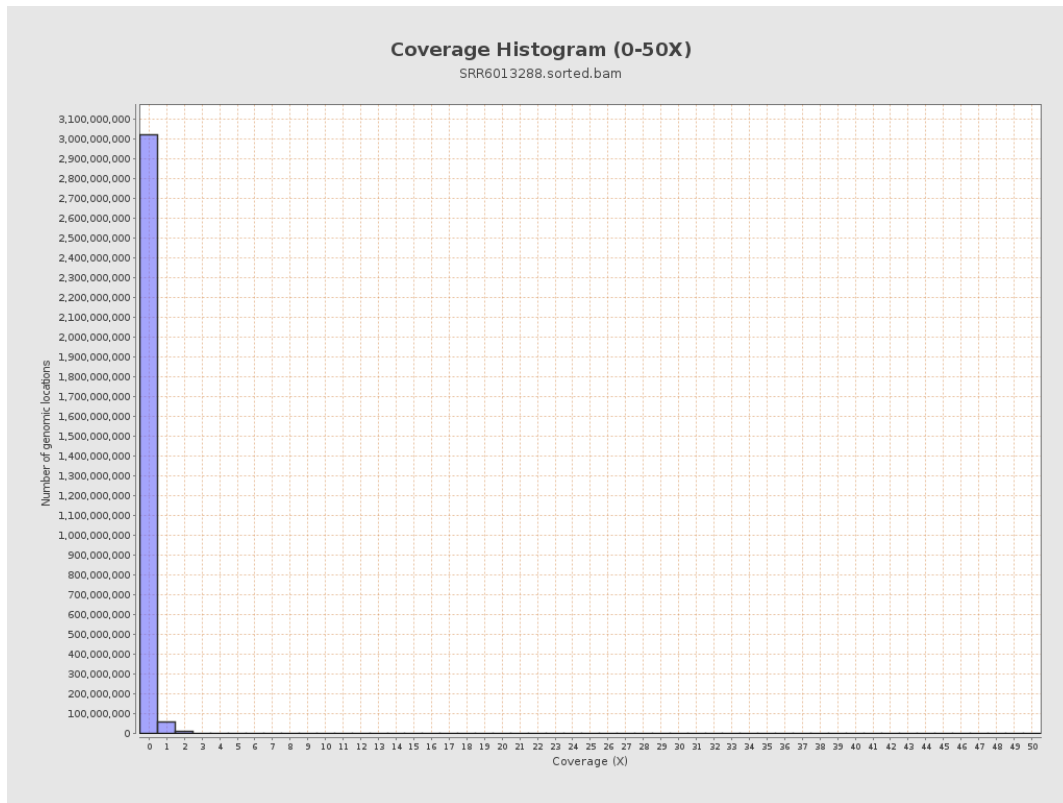
3. Results : Coverage across reference



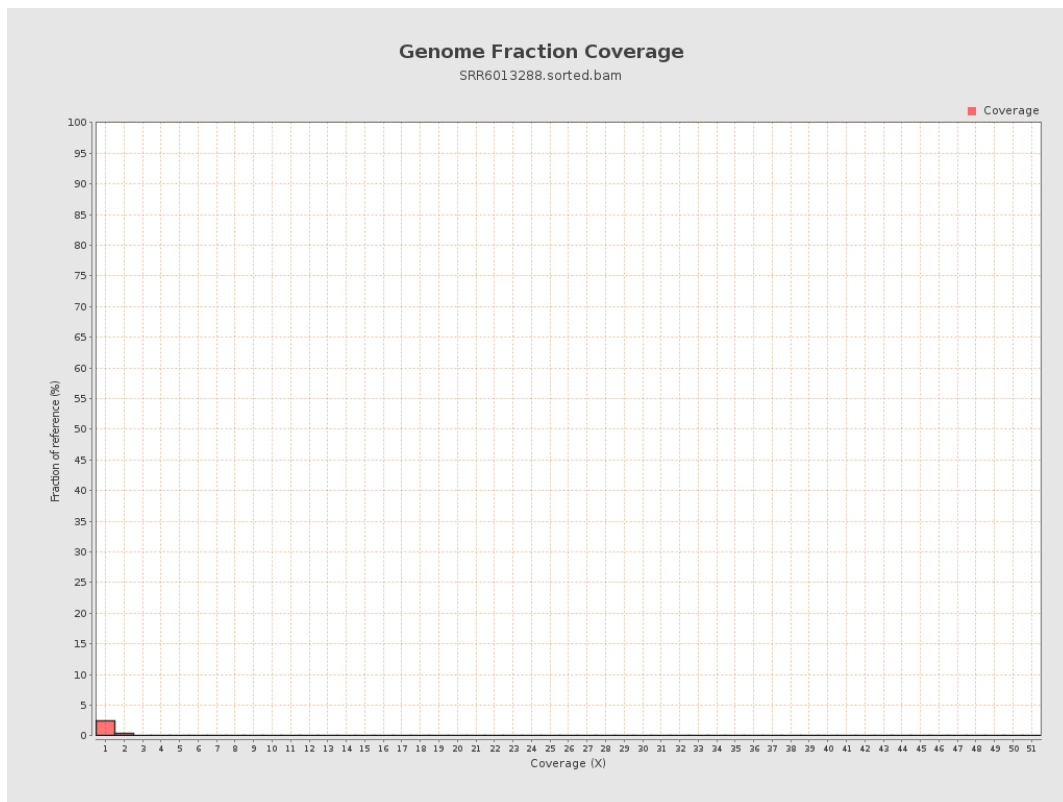
4. Results : Coverage Histogram



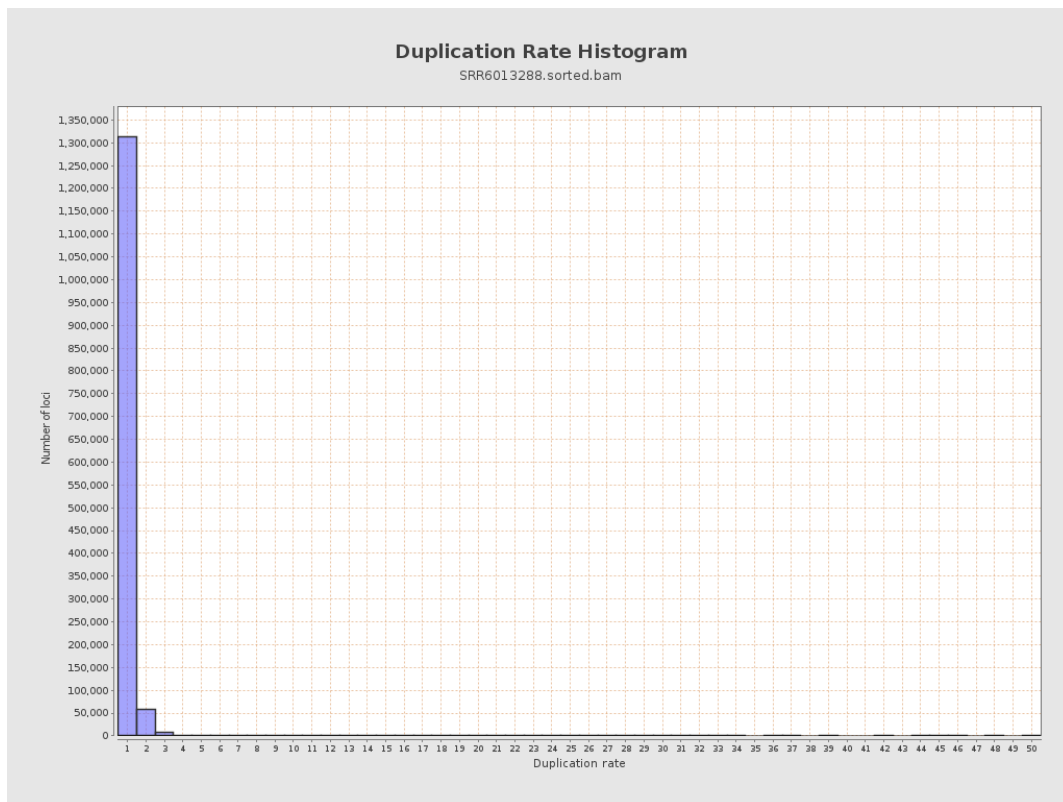
5. Results : Coverage Histogram (0-50X)



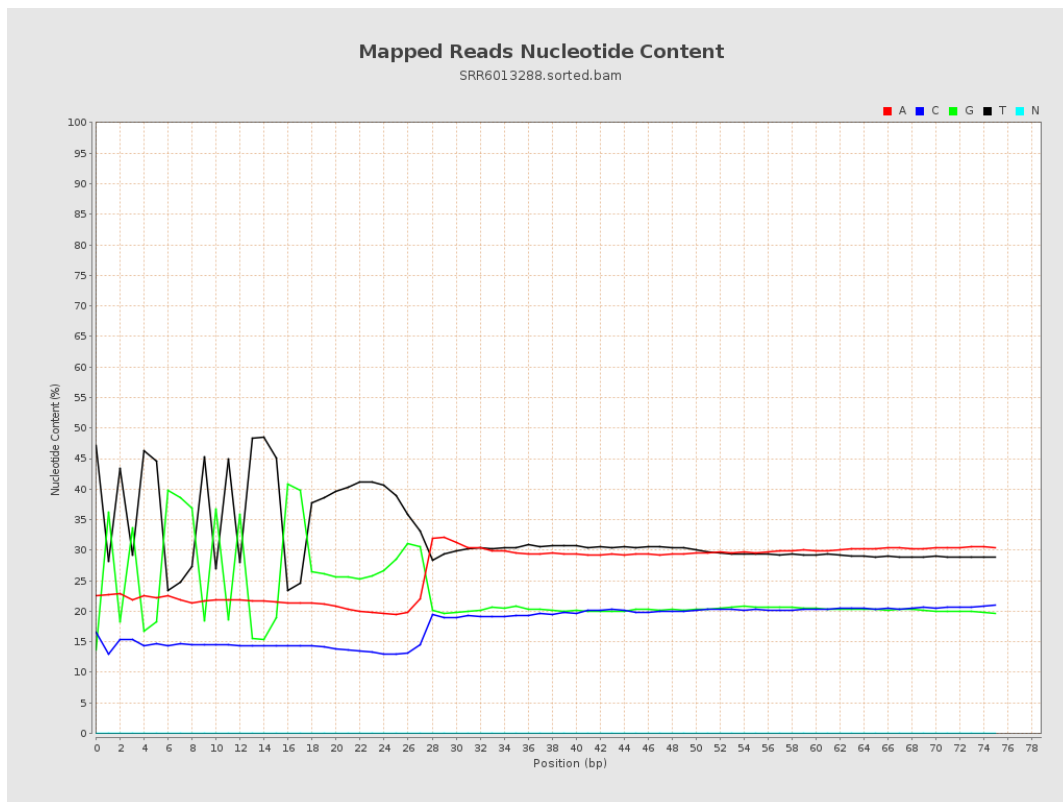
6. Results : Genome Fraction Coverage



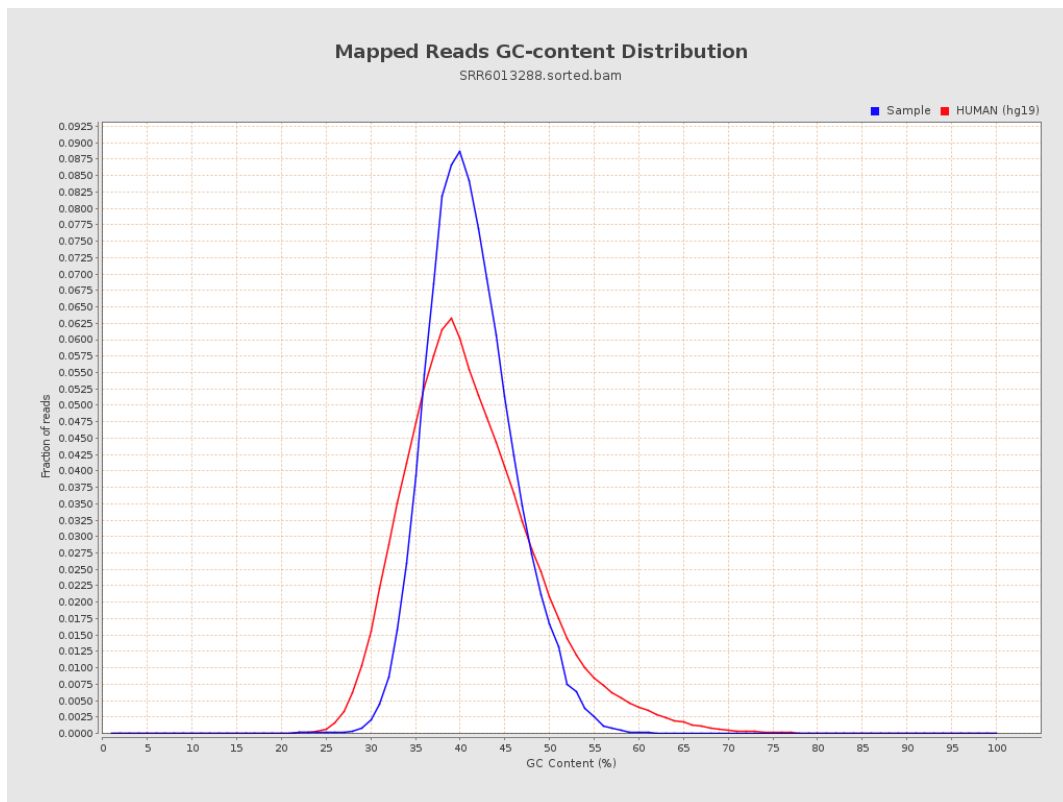
7. Results : Duplication Rate Histogram



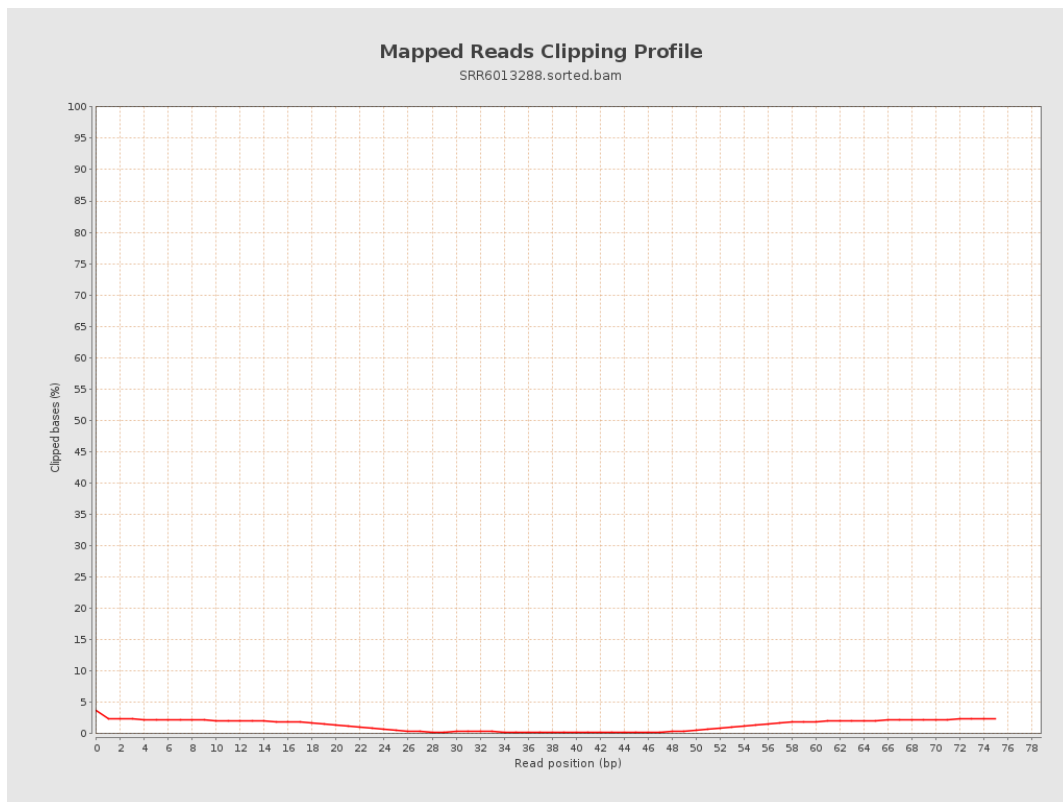
8. Results : Mapped Reads Nucleotide Content



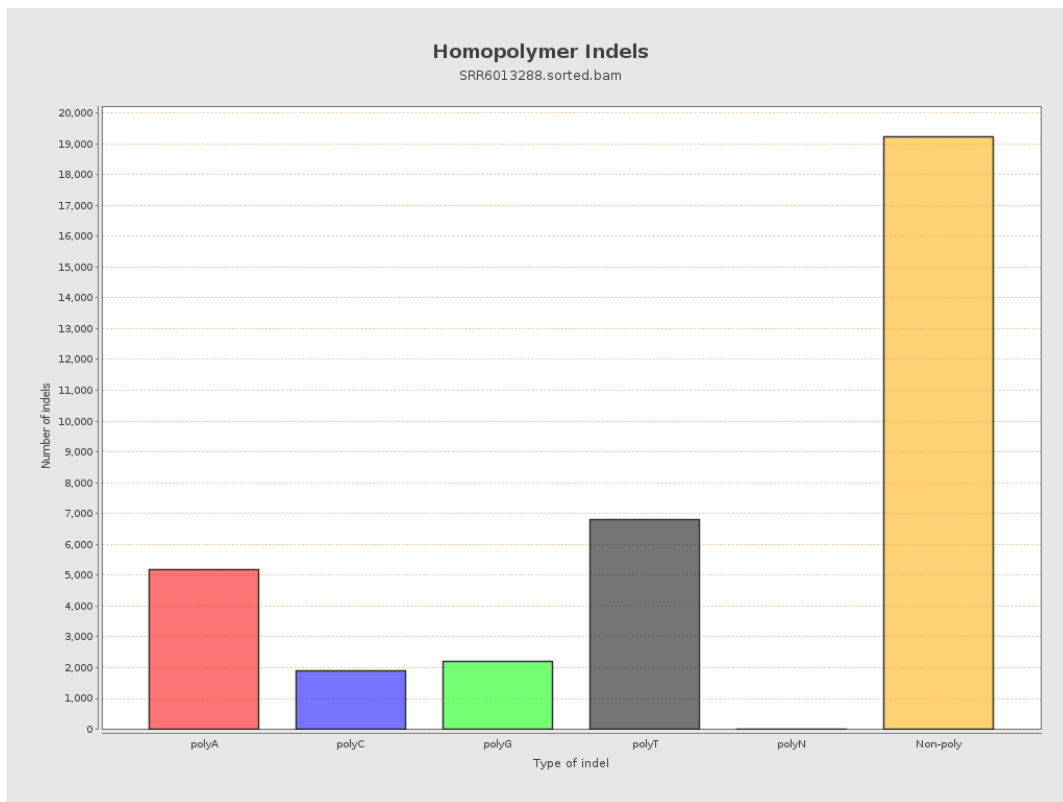
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

