## **RNA STAR OUTPUT FOR GSM461177**

Galaxy31-[RNA\_STAR\_on\_data\_24,\_data\_19,\_and\_data\_18\_\_log] - Notepad File Edit Format View Help

Started mapping on Oct 28 22:24:45 Finished on Oct 28 22:24:45 Finished on Oct 28 22:32:17  Mapping speed, Million of reads per hour 83.05  Number of input reads   10428011 Average input read length   10428011 Average input reads number   10428011 Average mapped reads   10428011 Average mapped reads   10428011 Average mapped length   10428011 Number of splices: Total   10428011 Number of splices: Total   10428011 Number of splices: Total   10428011 Number of splices: GC/AG   1042946 Number of splices: GC/AG   1049940 Number of splices: AT/AC   10488 Number of splices: Non-canonical   10440 Mismatch rate per base   104894 Deletion average length   104894 Insertion average length   104894 Insertion average length   104894 Insertion average length   104894 Insertion average length   104894 Number of reads mapped to multiple loci   104894 Number of reads mapped to multiple loci   104894 Number of reads mapped to omany loci   104894 Number of reads mapped to omany loci   104894 Number of reads unmapped: too short   104994	Started job on	Oct 28 22:23:46
Mapping speed, Million of reads per hour   83.05    Number of input reads   10428011   73   10428011   1042801		
Number of input reads Average input read length UNIQUE READS:  Uniquely mapped reads number Uniquely mapped reads % Average mapped length Average mapped length Number of splices: Total Number of splices: Total Number of splices: GT/AG Number of splices: GT/AG Number of splices: GT/AG Number of splices: AT/AC Number of splices: Non-canonical Number of splices: Non-canonical Mismatch rate per base Deletion rate per base Deletion average length Insertion average length Insertion average length Insertion average length Insertion average length Number of reads mapped to multiple loci % of reads mapped to multiple loci % of reads mapped to too many loci UNMAPPED READS: Number of reads unmapped: too many mismatches Number of reads unmapped: too short Number of reads unmapped: other CHIMERIC READS:		
Number of input reads   10428011 Average input read length   73		
Average input read length   UNIQUE READS:  Uniquely mapped reads number   8666702  Uniquely mapped reads %   83.11%  Average mapped length   72.87  Number of splices: Total   952323  Number of splices: Annotated (sjdb)   943181  Number of splices: GC/AG   7149  Number of splices: AT/AC   288  Number of splices: Non-canonical   1940  Mismatch rate per base, %   0.77%  Deletion rate per base   0.00%  Deletion rate per base   0.00%  Insertion rate per base   0.00%  Insertion average length   1.48  Insertion rate per base   0.00%  Number of reads mapped to multiple loci   571324  % of reads mapped to multiple loci   574223  % of reads mapped to too many loci   574223  % of reads mapped to my mismatches   0  Number of reads unmapped: too many mismatches   0.00%  Number of reads unmapped: too short   599120  % of reads unmapped: too short   5.75%  Number of reads unmapped: other   16642  % of reads unmapped: other   16642  % of reads unmapped: other   0.16%  CHIMERIC READS:	mapping speed, million of reads per nour	83.05
UNIQUE READS:  Uniquely mapped reads number   8666702  Uniquely mapped reads %   83.11%  Average mapped length   72.87  Number of splices: Total   952323  Number of splices: Annotated (sjdb)   943181  Number of splices: GT/AG   942946  Number of splices: GT/AG   942946  Number of splices: AT/AC   288  Number of splices: Non-canonical   1940  Mismatch rate per base, %   0.77%  Deletion rate per base   0.00%  Deletion rate per base   0.00%  Insertion average length   1.48  Insertion average length   1.39  MULTI-MAPPING READS:  Number of reads mapped to multiple loci   571324  % of reads mapped to too many loci   574223  % of reads mapped to too many loci   574223  % of reads unmapped: too many mismatches   0  % of reads unmapped: too short   599120  % of reads unmapped: too short   599120  % of reads unmapped: too short   5.75%  Number of reads unmapped: other   16642  % of reads unmapped: other   16642  % of reads unmapped: other   0.16%  CHIMERIC READS:	Number of input reads	10428011
Uniquely mapped reads number   8666702		73
Uniquely mapped reads %   Average mapped length   72.87   Number of splices: Total   952323   Number of splices: Annotated (sjdb)   943181   Number of splices: GT/AG   942946   Number of splices: GC/AG   7149   Number of splices: AT/AC   288   Number of splices: Non-canonical   1940   Mismatch rate per base, %   0.77%   Deletion rate per base   0.00%   Deletion average length   1.48   Insertion rate per base   0.00%   Insertion rate per base   0.00%   Insertion average length   1.39   MULTI-MAPPING READS:  Number of reads mapped to multiple loci   571324   % of reads mapped to multiple loci   5.48%   Number of reads mapped to too many loci   574223   % of reads mapped to many mismatches   0 % of reads unmapped: too many mismatches   0.00%   Number of reads unmapped: too short   5.75%   Number of reads unmapped: too short   5.75%   Number of reads unmapped: other   16642   % of reads unmapped: other   0.16%   CHIMERIC READS:	(1) 10 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0000700
Average mapped length   72.87 Number of splices: Total   952323  Number of splices: Annotated (sjdb)   943181 Number of splices: GT/AG   942946 Number of splices: GC/AG   7149 Number of splices: AT/AC   288  Number of splices: Non-canonical   1940 Mismatch rate per base, %   0.77% Deletion rate per base   0.00% Deletion average length   1.48 Insertion rate per base   0.00% Insertion average length   1.39  MULTI-MAPPING READS:  Number of reads mapped to multiple loci   571324 % of reads mapped to multiple loci   5.48% Number of reads mapped to too many loci   574223 % of reads mapped to too many loci   574223 % of reads unmapped: too short   0.00% Number of reads unmapped: too short   5.75% Number of reads unmapped: too short   5.75% Number of reads unmapped: other   16642 % of reads unmapped: other   0.16% CHIMERIC READS:	51 NOV 1014 TO	
Number of splices: Total   952323  Number of splices: Annotated (sjdb)   943181  Number of splices: GT/AG   942946  Number of splices: GC/AG   7149  Number of splices: AT/AC   288  Number of splices: Non-canonical   1940  Mismatch rate per base, %   0.77%  Deletion rate per base   0.00%  Deletion average length   1.48  Insertion average length   1.39  MULTI-MAPPING READS:  Number of reads mapped to multiple loci   571324  % of reads mapped to multiple loci   5.48%  Number of reads mapped to too many loci   5.51%  UNMAPPED READS:  Number of reads unmapped: too many mismatches   0.00%  Number of reads unmapped: too short   5.99120  % of reads unmapped: too short   5.75%  Number of reads unmapped: other   16642  % of reads unmapped: other   0.16%  CHIMERIC READS:		
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Number of splices: Non-canonical   1940   Mismatch rate per base, %   0.77%   Deletion rate per base   0.00%   Deletion average length   1.48   Insertion rate per base   0.00%   Insertion average length   1.39   MULTI-MAPPING READS:   Number of reads mapped to multiple loci   571324   % of reads mapped to multiple loci   5.48%   Number of reads mapped to too many loci   574223   % of reads mapped to too many loci   5.51%   UNMAPPED READS:   Number of reads unmapped: too many mismatches   0   % of reads unmapped: too many mismatches   0.00%   Number of reads unmapped: too short   5.99120   % of reads unmapped: too short   5.75%   Number of reads unmapped: other   0.16%   CHIMERIC READS:		
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Number of reads unmapped: too many mismatches   0   0.00%   Number of reads unmapped: too short   599120   % of reads unmapped: too short   5.75%   Number of reads unmapped: other   16642   % of reads unmapped: other   0.16%   CHIMERIC READS:	2.() 전하면 하는 전 하는 사람들은 사람들은 사람들은 사람들은 사람들은 사람들은 사람들은 사람들은	3.31/0
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% of chimeric reads   0.00%	% of chimeric reads	0.00%

## **RNA STAR OUTPUT FOR GSM461180**

Galaxy34-[RNA\_STAR\_on\_data\_24,\_data\_22,\_and\_data\_21\_\_log] - Notepad

Started job on	Oct 29 03:23:49
Started mapping on	Oct 29 03:27:00
Finished on	Oct 29 03:33:31
Mapping speed, Million of reads per hour	102.77
Number of input reads	11161595
Average input read length   UNIQUE READS:	71
Uniquely mapped reads number	8818168
Uniquely mapped reads %	79.00%
Average mapped length	70.52
Number of splices: Total	946755
Number of splices: Annotated (sjdb)	929256
Number of splices: GT/AG	938411
Number of splices: GC/AG	5295
Number of splices: AT/AC	385
Number of splices: Non-canonical	2664
Mismatch rate per base, %	1.73%
Deletion rate per base	0.00%
Deletion average length	1.44
Insertion rate per base	0.00%
Insertion average length   MULTI-MAPPING READS:	1.34
Number of reads mapped to multiple loci	507492
% of reads mapped to multiple loci	4.55%
Number of reads mapped to too many loci	587775
% of reads mapped to too many loci	5.27%
UNMAPPED READS:	1720
Number of reads unmapped: too many mismatches	0
% of reads unmapped: too many mismatches	0.00%
Number of reads unmapped: too short	1239790
% of reads unmapped: too short	11.11%
Number of reads unmapped: other	8370
% of reads unmapped: other   CHIMERIC READS:	0.07%
Number of chimeric reads	0
% of chimeric reads	0.00%

## **MULTI QC REPORTS**





