**Code for alignment and obtained alignment rates**

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10\_S250\_L004\_R1.fastq.gz

10\_S250\_L004\_R2.fastq.gz

Aligning with HISAT2 sample 10\_S250\_L004

hisat2 -p 35 --dta-cufflinks -x /IndexedGenomesHisat/hg38\_tran/genome\_tran -1 /data/10\_S250\_L004\_R1.fastq.gz -2 /data/10\_S250\_L004\_R2.fastq.gz -S 10\_S250\_L004.sam

56433063 reads; of these:

 56433063 (100.00%) were paired; of these:

 6386886 (11.32%) aligned concordantly 0 times

 42841687 (75.92%) aligned concordantly exactly 1 time

 7204490 (12.77%) aligned concordantly >1 times

 ----

 6386886 pairs aligned concordantly 0 times; of these:

 2109648 (33.03%) aligned discordantly 1 time

 ----

 4277238 pairs aligned 0 times concordantly or discordantly; of these:

 8554476 mates make up the pairs; of these:

 5119999 (59.85%) aligned 0 times

 2223511 (25.99%) aligned exactly 1 time

 1210966 (14.16%) aligned >1 times

95.46% overall alignment rate

11\_S251\_L004\_R1.fastq.gz

11\_S251\_L004\_R2.fastq.gz

hisat2 -p 35 --dta-cufflinks -x /IndexedGenomesHisat/hg38\_tran/genome\_tran -1 /data/11\_S251\_L004\_R1.fastq.gz -2 /data/11\_S251\_L004\_R2.fastq.gz -S 11\_S251\_L004.sam

59478851 reads; of these:

 59478851 (100.00%) were paired; of these:

 5879118 (9.88%) aligned concordantly 0 times

 45391240 (76.31%) aligned concordantly exactly 1 time

 8208493 (13.80%) aligned concordantly >1 times

 ----

 5879118 pairs aligned concordantly 0 times; of these:

 2083753 (35.44%) aligned discordantly 1 time

 ----

 3795365 pairs aligned 0 times concordantly or discordantly; of these:

 7590730 mates make up the pairs; of these:

 4837559 (63.73%) aligned 0 times

 1660178 (21.87%) aligned exactly 1 time

 1092993 (14.40%) aligned >1 times

95.93% overall alignment rate

13\_S252\_L004\_R1.fastq.gz

13\_S252\_L004\_R2.fastq.gz

hisat2 -p 35 --dta-cufflinks -x /IndexedGenomesHisat/hg38\_tran/genome\_tran -1 /data/13\_S252\_L004\_R1.fastq.gz -2 /data/13\_S252\_L004\_R2.fastq.gz -S 13\_S252\_L004.sam

33962651 reads; of these:

 33962651 (100.00%) were paired; of these:

 3286733 (9.68%) aligned concordantly 0 times

 26192074 (77.12%) aligned concordantly exactly 1 time

 4483844 (13.20%) aligned concordantly >1 times

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 3286733 pairs aligned concordantly 0 times; of these:

 1172770 (35.68%) aligned discordantly 1 time

 ----

 2113963 pairs aligned 0 times concordantly or discordantly; of these:

 4227926 mates make up the pairs; of these:

 2824018 (66.79%) aligned 0 times

 823979 (19.49%) aligned exactly 1 time

 579929 (13.72%) aligned >1 times

95.84% overall alignment rate

3\_S246\_L004\_R1.fastq.gz

3\_S246\_L004\_R2.fastq.gz

hisat2 -p 35 --dta-cufflinks -x /IndexedGenomesHisat/hg38\_tran/genome\_tran -1 /data/3\_S246\_L004\_R1.fastq.gz -2 /data/3\_S246\_L004\_R2.fastq.gz -S 3\_S246\_L004.sam >>

63940404 reads; of these:

 63940404 (100.00%) were paired; of these:

 7715457 (12.07%) aligned concordantly 0 times

 45754804 (71.56%) aligned concordantly exactly 1 time

 10470143 (16.37%) aligned concordantly >1 times

 ----

 7715457 pairs aligned concordantly 0 times; of these:

 2164409 (28.05%) aligned discordantly 1 time

 ----

 5551048 pairs aligned 0 times concordantly or discordantly; of these:

 11102096 mates make up the pairs; of these:

 7368161 (66.37%) aligned 0 times

 2029616 (18.28%) aligned exactly 1 time

 1704319 (15.35%) aligned >1 times

94.24% overall alignment rate

4\_S247\_L004\_R1.fastq.gz

4\_S247\_L004\_R2.fastq.gz

hisat2 -p 35 --dta-cufflinks -x /IndexedGenomesHisat/hg38\_tran/genome\_tran -1 /data/4\_S247\_L004\_R1.fastq.gz -2 /data/4\_S247\_L004\_R2.fastq.gz -S 4\_S247\_L004.sam

63796481 reads; of these:

 63796481 (100.00%) were paired; of these:

 7967789 (12.49%) aligned concordantly 0 times

 46010159 (72.12%) aligned concordantly exactly 1 time

 9818533 (15.39%) aligned concordantly >1 times

 ----

 7967789 pairs aligned concordantly 0 times; of these:

 2277931 (28.59%) aligned discordantly 1 time

 ----

 5689858 pairs aligned 0 times concordantly or discordantly; of these:

 11379716 mates make up the pairs; of these:

 7569764 (66.52%) aligned 0 times

 2063537 (18.13%) aligned exactly 1 time

 1746415 (15.35%) aligned >1 times

94.07% overall alignment rate

5\_S248\_L004\_R1.fastq.gz

5\_S248\_L004\_R2.fastq.gz

hisat2 -p 35 --dta-cufflinks -x /IndexedGenomesHisat/hg38\_tran/genome\_tran -1 /data/5\_S248\_L004\_R1.fastq.gz -2 /data/5\_S248\_L004\_R2.fastq.gz -S 5\_S248\_L004.sam

72329430 reads; of these:

 72329430 (100.00%) were paired; of these:

 8208543 (11.35%) aligned concordantly 0 times

 52901434 (73.14%) aligned concordantly exactly 1 time

 11219453 (15.51%) aligned concordantly >1 times

 ----

 8208543 pairs aligned concordantly 0 times; of these:

 2417971 (29.46%) aligned discordantly 1 time

 ----

 5790572 pairs aligned 0 times concordantly or discordantly; of these:

 11581144 mates make up the pairs; of these:

 7943478 (68.59%) aligned 0 times

 2052220 (17.72%) aligned exactly 1 time

 1585446 (13.69%) aligned >1 times

94.51% overall alignment rate

6\_S249\_L004\_R1.fastq.gz

6\_S249\_L004\_R2.fastq.gz

hisat2 -p 35 --dta-cufflinks -x /IndexedGenomesHisat/hg38\_tran/genome\_tran -1 /data/6\_S249\_L004\_R1.fastq.gz -2 /data/6\_S249\_L004\_R2.fastq.gz -S 6\_S249\_L004.sam

57540831 reads; of these:

 57540831 (100.00%) were paired; of these:

 6474361 (11.25%) aligned concordantly 0 times

 42192855 (73.33%) aligned concordantly exactly 1 time

 8873615 (15.42%) aligned concordantly >1 times

 ----

 6474361 pairs aligned concordantly 0 times; of these:

 2095618 (32.37%) aligned discordantly 1 time

 ----

 4378743 pairs aligned 0 times concordantly or discordantly; of these:

 8757486 mates make up the pairs; of these:

 5524286 (63.08%) aligned 0 times

 1839508 (21.00%) aligned exactly 1 time

 1393692 (15.91%) aligned >1 times

95.20% overall alignment rate