

RNAseq: total RNA - mapping to rRNA

- ▶ Bowtie
- ▶ default parameters; seed length=20

time points	replicate/fraction	reads processed	reads with at least one reported alignment	reads that failed to align
H000	3T 9857	195,142,147	606,071 (0.31%)	194,536,076 (99.69%)
H003	3T 9858	228,007,097	358,919 (0.16%)	227,648,178 (99.84%)
H006	3T 9859	205,192,909	210,924 (0.10%)	204,981,985 (99.90%)
H009	3T2 12108	234,362,396	459,906 (0.20%)	233,902,490 (99.80%)
H012	3T 9861	238,762,142	430,559 (0.18%)	238,331,583 (99.82%)
H018	3T 9862	247,231,837	332,775 (0.13%)	246,899,062 (99.87%)
H024	3T 9863	190,819,879	632,948 (0.33%)	190,186,931 (99.67%)
H036	3T 9864	199,228,591	467,549 (0.23%)	198,761,042 (99.77%)
H048	3T 9865	237,498,238	297,460 (0.13%)	237,200,778 (99.87%)
H072	3T 9866	198,547,041	435,281 (0.22%)	198,111,760 (99.78%)
H120	3T 9867	188,463,246	407,446 (0.22%)	188,055,800 (99.78%)
H168	3T 9868	188,881,331	311,610 (0.16%)	188,569,721 (99.84%)

RNAseq: cytoplasmic RNA, replicate 2 - mapping to rRNA

time points	replicate/ fraction	reads processed	reads with at least one reported alignment	reads that failed to align
H0	2C 8986 GATCAG	257,846,202	316,467 (0.12%)	257,529,735 (99.88%)
H3	2C 8987 TGACCA	237,513,579	2,322,516 (0.98%)	235,191,063 (99.02%)
H6	2C 8988 GGCTAC	235,077,950	193,401 (0.08%)	234,884,549 (99.92%)
H9	2C 8989 GTGGCC	237,757,279	256,874 (0.11%)	237,500,405 (99.89%)
H12	2C 8990 CAGATC	215,516,242	2,071,865 (0.96%)	213,444,377 (99.04%)
H18	2C 8991 CTTGTA	216,092,121	2,279,149 (1.05%)	213,812,972 (98.95%)
H24	2C 8992 GTGGCC	228,494,199	2,251,337 (0.99%)	226,242,862 (99.01%)
H36	2C 8993 GTTTCG	219,459,365	2,006,856 (0.91%)	217,452,509 (99.09%)
H48	2C 8994 CGTACG	244,242,968	14,073,098 (5.76%)	230,169,870 (94.24%)
H72	2C 8995 GAGTGG	253,169,280	4,850,580 (1.92%)	248,318,700 (98.08%)
H120	2C 8996 ACTGAT	232,833,724	615,524 (0.26%)	232,218,200 (99.74%)
H168	2C 8997 ATTCCT	244,162,541	865,797 (0.35%)	243,296,744 (99.65%)

RNAseq: cytoplasmic RNA, replicate 3 - mapping to rRNA

time points	replicate/ fraction	reads processed	reads with at least one reported alignment	reads that failed to align
H0	3C 9539 ANNANG	5,161,163	50,673 (0.98%)	5,110,490 (99.02%)
H0	3C 9539 ATCACG	214,529,718	2,096,719 (0.98%)	212,432,999 (99.02%)
H0	3C 9539 ATCANG	5,406,153	53,359 (0.99%)	5,352,794 (99.01%)
H3	3C 9540 CGATGT	247,342,206	28,370,609 (11.47%)	218,971,597 (88.53%)
H6	3C 9541 TTAGGC	254,402,862	1,260,028 (0.50%)	253,142,834 (99.50%)
H9	3C 9542 TGACCA	276,241,892	907,865 (0.33%)	275,334,027 (99.67%)
H12	3C 9543 ACAGTG	271,639,838	2,702,223 (0.99%)	268,937,615 (99.01%)
H18	3C 9544 GCCAAT	253,765,795	1,828,108 (0.72%)	251,937,687 (99.28%)
H24	3C 9911 CAGATC	206,068,185	1,019,721 (0.49%)	205,048,464 (99.51%)
H36	3C 9912 ACTTGA	223,125,889	403,131 (0.18%)	222,722,758 (99.82%)
H48	3C 9913 GATCAG	205,925,914	584,810 (0.28%)	205,341,104 (99.72%)
H72	3C 9914 TAGCTT	211,495,548	558,631 (0.26%)	210,936,917 (99.74%)
H120	3C 9915 GGCTAC	163,026,270	2,519,889 (1.55%)	160,506,381 (98.45%)
H120	3C 9915 GNCTAC	23,350,129	362,078 (1.55%)	22,988,051 (98.45%)
H168	3C 9916 CTTGTA	200,282,793	1,675,590 (0.84%)	198,607,203 (99.16%)