

**Table S1. Quality check RNA sample and RNA-sequencing reads.**

Sample ID	Concentration Fragment Analyzer (ng/ul)	Integrity before sequencing (RQN)	% $\geq$ Q30
818R_2h	25.89	8.90	88.91
819L_11h	61.43	8.70	88.71
820R_9h	122.13	8.80	88.95
821R_16h	26.23	9.10	89.17
822L_2h	19.94	8.10	88.76
823R_16h	102.42	8.80	88.54
824L_21h	45.01	9.30	88.53
825L_7h	106.51	9.40	88.54
830L_9h	91.26	8.70	88.68
831L_11h	53.91	8.60	88.78
832L_21h	34.11	9.10	88.79
836R_9h	31.74	9.00	88.63
837R_2h	11.74	8.70	89.27
838R_9h	52.12	8.70	88.38
839R_7h	70.59	9.10	88.65
840L_7h	113.40	9.10	88.59
841L_11h	21.68	9.10	88.91
842L_11h	12.38	9.50	88.97
843L_16h	79.09	9.60	88.92
844L_16h	88.29	9.00	88.92
845R_21h	3.33	8.20	89.98
861R_7h	6.95	8.40	88.72
862L_11h	84.59	9.00	88.55
863L_7h	42.72	9.20	88.92
870R_2h	52.81	9.30	89.12
871R_9h	47.83	9.30	89.01
882R_16h	58.13	8.00	89.14
883L_21h	60.93	8.70	88.96
888L_21h	7.05	8.30	88.84
889R_2h	17.97	9.30	88.66

RNA concentration and quality. RNA quality number (RQN) ranges from 10 (intact) to 1 (highly degraded). Q30 indicates the percentage of reads which have a base call accuracy of 99.9 %.