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SUPPLEMENTARY DATA

Supplementary Table SII RNA sequencing sample information. (See also Fig. 2)

Sample Name	**Total reads (paired-end)**	**Total uniquely aligned reds (% of alignment)**
f-HM1-A	26442323	22412726 (84.76%)
f-HM1-B	29051269	25036031 (86.18%)
f-HM1-C	31990760	28157884 (88.02%)
f-HM2-A	28712382	25436982 (88.59%)
f-HM2-B	30903057	27268262 (88.24%)
f-HM2-C	29156866	26178620 (89.79%)
f-KS1-A	31912802	27502436 (86.18%)
f-KS1-B	30660012	27175994 (88.64%)
f-KS1-C	31596123	27970675 (88.53%)
f-KS2-A	29108090	25369597 (87.16%)
f-KS2-B	30016732	25863541 (86.16%)
f-KS2-C	31732922	28158324 (88.74%)
f-HF1-A	27263821	24200429 (88.76%)
f-HF1-B	33601566	28547861 (84.96%)
f-HF1-C	34731025	29839603 (85.92%)
ips-HM1-A	35621968	30658201 (86.07%)
ips-HM1-B	30541835	26730957 (87.52%)
ips-HM1-C	28924522	25106670 (86.80%)
ips-HM2-A	33373070	29453146 (88.25%)
ips-HM2-B	31271798	27868193 (89.12%)
ips-HM2-C	28269767	24572861 (86.92%)
ips-KS1-A	29244861	25007339 (85.51%)
ips-KS1-B	31930095	27941999 (87.51%)
ips-KS1-C	31351931	27508531 (87.74%)
ips-KS2-A	33387820	29312719 (87.79%)
ips-KS2-B	32981954	29151697 (88.39%)
ips-KS2-C	33102027	28514986 (86.14%)
ips-HF1-A	32352668	28422631 (87.85%)
ips-HF1-B	30883152	25826418 (83.63%)
ips-HF1-C	36296560	32531240 (89.63%)
HS980-A	28758729	23919947 (83.17%)
HS980-B	30366209	26270259 (86.51%)
HS980-C	33487090	29835552 (89.10%)