Sample	Total reads	Aligned reads	% Alignment
29d-1	50,585,318	47,809,911	95%
29d-2	56,317,560	52,160,493	93%
29d-3	74,709,300	70,289,777	94%
35d-1	61,640,834	56,589,865	92%
35d-2	59,127,761	56,810,411	96%
35d-3	74,084,899	69,345,945	94%
42d-1	49,651,744	47,583,338	96%
42d-2	64,098,111	59,183,060	92%
42d-3	65,807,180	60,144,918	91%
57d-1	68,197,891	61,300,159	90%
57d-2	59,962,671	57,633,192	96%
57d-3	55,578,330	53,576,333	96%

Supplemental Table 1. Read and Alignment Summary for RNA-seq Libraries.