

H3K4me3	Total Reads	Aligned reads	% Alignment	Unique Reads	% Unique
29d_ChIP	72,651,120	56,515,347	78%	12,471,170	22%
29d_input	241,859,534	129,130,261	60%	68,163,423	53%
35d_ChIP	94,549,362	65,914,502	70%	15,235,440	23%
35d_input	256,832,423	136,813,852	59%	67,497,500	49%
42d_ChIP	79,935,864	54,513,086	69%	13,123,594	24%
42d_input	219,636,473	127,612,919	62%	66,732,566	52%
57d_ChIP	150,759,372	83,983,773	56%	19,116,262	23%
57d_input	232,064,371	131,234,324	62%	66,787,863	51%

H3K9ac	Total Reads	Aligned reads	% Alignment	Unique Reads	% Unique
30d_ChIP	72,033,414	52,750,857	80%	11,019,515	21%
30d_input	88,614,150	60,738,145	78%	16,030,599	26%
34d_ChIP	72,232,723	54,470,143	81%	10,605,940	19%
34d_input	92,834,798	61,939,766	77%	26,812,313	43%
42d_ChIP	81,732,114	62,777,923	82%	6,623,315	11%
42d_input	88,141,553	61,854,129	78%	6,449,022	10%

Supplemental Table 2. Read and Alignment Summary for ChIP-seq Libraries.