

Table S3 Summary of Runx2 ChIP-Seq libraries

Time point	Replicate	Raw reads	Peaks	Genome coverage
Day 0	2	77,753,556	25,457	6.22 x
Day 9	2	33,414,085	60,596	2.67 x
Day 28	2	28,418,309	40,330	2.27 x

Note: genome coverage = (number of raw reads number x average fragment size)/mouse genome size. Average fragment size = 200 bp, and mouse genome size = 2.5×10^9 bp.