

ChIP sample	Input sample	Peak calling software	Confident regions threshold	Enriched regions threshold	Peaks (replicates' agreement)
YAP1_SF268_1	Input_SF268_1	Peakzilla	2680	7659	2498
YAP1_SF268_2			984	3397	
TEAD1_SF268_1	Input_SF268_2	Peakzilla	2683	8521	2652
TEAD1_SF268_2			2249	7102	
H3K27ac_SF268_1	Input_SF268_2	MACS	35517	45205	38331
H3K27ac_SF268_2			37041	46381	
YAP1_NCI-H2052_1	Input_NCI-H2052_1	Peakzilla	16388	33114	16470
YAP1_NCI-H2052_2			13113	29142	
YAP1_IMR90_1	Input_IMR90_1	Peakzilla	3553	409	1111
YAP1_IMR90_2			6884	1116	

**S1 Table. Peak calling strategy for ChIP-seq datasets.**

For YAP1 and TEAD1 datasets, confident regions were selected using peakzilla with score  $\geq 2$  and fold enrichment over input  $\geq 4$  and enriched regions with score  $\geq 1$  and fold enrichment over input  $\geq 4$ . For H3K27ac datasets, confident regions were selected using MACS with P-value  $\leq 10^{-10}$  and enriched regions with P-value  $\leq 10^{-30}$ . We defined peaks as shared between samples if confident peaks called in one sample are overlapping an enriched region in another sample and reciprocally. This ensures that a peak that is enriched in both replicates but which missed the stringent threshold for peak calling in one of them is not wrongly discarded.