

Dataset S1.

a) Quality check results of the ChIP-seq dataset.

<u>H3K4me1</u>					<u>H3K4me3</u>				<u>H3K9me3</u>			
Sample ID	Total Sequences (M)	Unmapped reads (M)	PERCENT DUPLICATION (%)	VALID READS (M)	Total Sequences (M)	Unmapped reads (M)	PERCENT DUPLICATION (%)	VALID READS (M)	Total Sequences (M)	Unmapped reads (M)	PERCENT DUPLICATION (%)	VALID READS (M)
88	32.8	0.5	43.8	18.2	38.7	1.04	56.7	16.3	67.9	1.45	22.2	51.7
316	41.4	0.5	38.7	25.1	31.9	0.32	30.2	22	87.6	1.78	25.7	63.8
335	48.2	0.7	49.8	23.8	29.7	0.43	33.2	19.6	74.1	2.36	40.1	43
341	42.2	0.6	40.6	24.7	29.4	0.56	43	16.4	66.5	1.49	19.1	52.6
343	43.5	0.6	51.6	20.8	29.8	0.47	28.9	20.9	49.2	1.1	19.2	38.9
368	51.6	0.5	54.6	23.2	37.7	0.61	45.2	20.3	61.4	1.52	43.3	34
384	37.4	0.8	62	13.9	30.1	0.42	32	20.2	59.3	1.24	22	45.3

<u>H3K27ac</u>					<u>H3K27me3</u>				<u>H3K36me3</u>			
Samples	Total Sequences (M)	Unmapped reads (M)	PERCENT DUPLICATION (%)	VALID READS (M)	Total Sequences (M)	Unmapped reads (M)	PERCENT DUPLICATION (%)	VALID READS (M)	Total Sequences (M)	Unmapped reads (M)	PERCENT DUPLICATION (%)	VALID READS (M)
88	40.4	0.5	37.9	24.8	48.4	2.81	78.4	9.8	62.5	0.55	15.2	52.5
316	39.7	0.39	28.4	28.1	53.1	0.69	52.2	25.1	64.4	0.53	18.9	51.8
335	44.6	0.83	52.3	20.9	51.3	0.76	64.9	17.7	84.2	1	21.8	65.1
341	35.8	0.62	54.9	15.9	52.6	0.71	52.6	24.6	70.2	0.97	22.6	53.6
343	36.9	0.51	44.5	20.2	52	0.87	58.8	21.1	50	0.61	18	40.5
368	45.5	0.91	52.6	21.1	51.5	0.74	56.7	22	63.4	0.87	28.7	44.6
384	47.1	1.5	80.1	9.1	49.3	0.86	59.5	19.6	68.3	0.63	16.3	56.6

b) Hi-C read information and quality checks.

Samples are unstimulated controls, or have been TNF stimulated (_TNF rows).

Sample ID	Joint	Total Reads (M)		Unique Alignments (M)		Paired Reads (M)	Valid Pairs (M)	Percentage Mapped (%)
		R1	R2	R1	R2			
SF_412	Wrist	103	103	80	79	63	51	61.85
SF_412_TNF	Wrist	110	110	88	87	71	61	64.88
SF_415A	Wrist	112	112	84	83	64	48	57.2
SF_415A_TNF	Wrist	591	591	467	463	371	347	62.91
SF_415B	MCP (Hand)	56	56	41	41	30	20	54.31
SF_415B_TNF	MCP (Hand)	96	96	76	75	60	51	62.16
SF_420	Shoulder	120	120	94	92	72	63	60.64
SF_420_TNF	Shoulder	291	291	230	222	174	154	59.95
SF_424	MCP (Hand)	79	79	63	62	51	46	64.63
SF_424_TNF	MCP (Hand)	83	83	67	66	54	48	64.57
SF_427	Knee	419	419	321	316	249	170	59.39
SF_427_TNF	Knee	277	277	213	209	166	115	60.1
SF_429	Shoulder	291	291	236	233	193	164	66.26
SF_429_TNF	Shoulder	301	301	245	241	201	163	66.95

c) Capture Hi-C read information and quality checks.

Samples are unstimulated controls or have been TNF stimulated (_TNF rows).

Sample ID (capture Hi-C)	Joint	Total Reads (M)		Unique Alignments (M)		Paired Read (M)	Valid Pairs (M)	Percentage Mapped (%)
		R1	R2	R1	R2			
SF_412	Wrist	203	203	158	155	125	104	61.8
SF_412_TNF	Wrist	332	332	266	262	218	189	65.73
SF_415A	Wrist	247	247	187	186	143	124	57.93
SF_415A_TNF	Wrist	155	155	123	122	100	94	64.55
SF_415B	MCP (Hand)	336	336	239	237	173	122	51.7
SF_415B_TNF	MCP (Hand)	310	310	250	247	200	172	64.78
SF_420	Shoulder	217	217	177	175	143	127	65.98
SF_420_TNF	Shoulder	156	156	128	126	103	92	66.05
SF_424	MCP (Hand)	173	173	144	141	117	105	67.52
SF_424_TNF	MCP (Hand)	154	154	126	125	104	95	67.51
SF_427	Knee	218	218	161	159	124	92	56.84
SF_427_TNF	Knee	216	216	167	164	131	99	60.6
SF_429	Shoulder	216	216	175	173	145	124	67.11
SF_429_TNF	Shoulder	252	252	206	202	171	141	68.04

d) ATAC-seq read information and quality checks.

Samples are unstimulated controls, or have been TNF stimulated (_TNF rows).

Sample ID (ATAC)	READ PAIRS EXAMINED (M)	READ PAIR DUPLICATES (M)	PERCENT DUPLICATION (%)	ESTIMATED LIBRARY SIZE (M)
SF_346	94.3	68.5	72.7	26.5
SF_346_TNF	85.3	37.7	44.1	66.4
SF_415B	75.1	47.9	63.8	29.6
SF_415B_TNF	73.7	27	36.7	75.5
SF_420	78.9	57.1	72.3	22.5
SF_420_TNF	67.3	54	80.3	13.3
SF_424	72.8	59.2	81.3	13.7
SF_424_TNF	90.1	59.3	65.8	33.1
SF_427	81.6	55.1	67.5	28.1
SF_427_TNF	63.3	42.7	67.5	21.8
SF_429	95.3	59.9	62.8	38.8
SF_429_TNF	65.8	32.7	49.7	41.9

e) RNA-seq data quality and alignment summary.

Samples are unstimulated controls or have been TNF stimulated (_TNF rows).

Sample ID	Total bases (M)	Aligned bases (M)	Coding bases (%)	UTR bases (%)	Intronic bases (%)	Intergenic bases (%)	Usable bases (%)
SF_292	10092.8	9943.9	16.7	18.8	27.3	37.2	35
SF_292_TNF	7794.8	7673.9	10.6	16.2	27.2	46.1	26.3
SF_336	8206.8	8072	10.4	20.3	25.5	43.8	30.2
SF_336_TNF	7983.2	7846.4	12.6	18.8	26.6	42	30.9
SF_346	7263.5	7130.7	9.9	16.2	27.3	46.6	25.6
SF_346_TNF	6830.9	6705.5	11.3	18.4	26.6	43.6	29.2
SF_407	6360.5	6251	20.4	20.5	24.5	34.6	40.2
SF_407_TNF	8051.5	7954.8	6.7	17.1	28.1	48.1	23.5
SF_415B	4927.7	4858.9	6	16.2	27.6	50.2	22
SF_415B_TNF	8369.4	8271.4	6.2	17.1	28.8	47.9	22.9
SF_435	8165.7	8052.1	5.2	15.9	27	52	20.7
SF_435_TNF	10682.4	10529.9	6	17	29.2	47.7	22.7

f) CAGE-seq data quality and alignment summary.

Samples are unstimulated controls or have been TNF stimulated (_TNF rows).

Sample ID	Total Reads (M)	rRNA-Filtered (M)	BWA-Mapped (M)	HISAT2-Mapped (M)	Total Mapped (M)	Percentage Mapped (%)
SF_276	25.8	8.7	14.3	1.7	16.0	62.1
SF_276_TNF	25.4	7.6	15.2	1.4	16.6	65.5
SF_415	24.9	4.7	17.7	1.6	19.3	77.6
SF_415_TNF	20.7	4.3	13.9	1.4	15.3	74.2
SF_420	25.0	6.2	16.0	1.5	17.4	69.8
SF_420_TNF	25.3	5.6	17.0	1.5	18.5	73.0
SF_424	24.9	7.6	14.6	1.7	16.4	65.8
SF_424_TNF	27.5	14.2	10.6	1.6	12.2	44.5
SF_427	24.3	7.5	14.1	1.6	15.7	64.6
SF_427_TNF	23.6	5.9	15.2	1.4	16.6	70.2
SF_429	25.6	7.7	15.0	1.8	16.8	65.8
SF_429_TNF	25.0	5.2	17.3	1.6	18.9	75.5
SF_460	20.8	4.8	13.8	1.4	15.2	73.1
SF_460_TNF	24.0	4.7	16.5	1.6	18.1	75.6

BWA = Burrows-Wheeler Aligner