



C

Sample	Mark	Number of peaks	total read	read in peaks	FRIP
T1025	H3K27ac	57480	12898446	6780203	0.52566
T1033	H3K27ac	79083	23252169	11227875	0.482874
T1087-1	H3K27ac	24964	9868799	2169127	0.219796
T1156	H3K27ac	110445	36402472	19359698	0.531824
T1175	H3K27ac	74464	28222155	11849954	0.419881
T1211-2	H3K27ac	66171	31066987	10117684	0.325673
T2542	H3K27ac	91628	26268361	10266973	0.390849
T3395	H3K27ac	71353	29813837	14364869	0.481819
T391	H3K27ac	57369	32259279	14840331	0.460033
T447	H3K27ac	62273	16511796	10594952	0.64166
T791-2	H3K27ac	66645	34200842	17422092	0.509405
T813-1	H3K27ac	79452	26769347	16614011	0.620636
T839	H3K27ac	47443	11899135	6135329	0.515611
T877	H3K27ac	50386	13253291	6569751	0.495707
T924-1	H3K27ac	99034	38174186	21101523	0.552769
T1025	H3K27me3	91945	17523244	6989698	0.398882
T1033	H3K27me3	1531	32907632	168192	0.005111
T1087-1	H3K27me3	24447	13475044	1492759	0.11078
T1156	H3K27me3	90948	23818238	6759895	0.283812
T1175	H3K27me3	64395	26637172	6755173	0.253599
T1211-2	H3K27me3	59279	32004727	6898519	0.215547
T2542	H3K27me3	566	28325631	172339	0.006084
T3395	H3K27me3	1863	25130663	222722	0.008863
T391	H3K27me3	57510	22666982	4802169	0.211857
T447	H3K27me3	85587	27760311	8445860	0.304242
T791-2	H3K27me3	31347	12101578	1567048	0.129491
T813-1	H3K27me3	13938	52702312	608480	0.011546
T839	H3K27me3	52912	13348050	2562277	0.191959
T877	H3K27me3	7	29592691	1016	3.43E-05
T924-1	H3K27me3	83485	26832708	6360990	0.237061
T1025	H3K9me3	28570	5239795	1250389	0.238633
T1033	H3K9me3	19704	37401410	1247093	0.033343
T1087-1	H3K9me3	8777	9827987	1104504	0.112384
T1156	H3K9me3	28957	20658261	1155253	0.055922
T1175	H3K9me3	50631	17941560	3001338	0.167284
T1211-2	H3K9me3	740	23536967	337744	0.01435
T2542	H3K9me3	7393	32151810	867307	0.026975
T3395	H3K9me3	26974	36299887	1695578	0.04671
T391	H3K9me3	23883	12205751	1353281	0.110872
T447	H3K9me3	89610	21470059	5073066	0.236286
T791-2	H3K9me3	90420	43887296	9374620	0.213607
T813-1	H3K9me3	72650	23474222	1681764	0.071643
T839	H3K9me3	55007	11698270	2449291	0.209372
T877	H3K9me3	71717	13963038	2888492	0.206867
T924-1	H3K9me3	42422	24931930	1518931	0.060923
5637	H3K27ac	45940	48069709	20721568	0.431073
5637	H3K27me3	81381	38545596	16184847	0.419888
5637	H3K9me3	67899	38880258	7699164	0.198022
KK47	H3K27me3	81295	2927476	53790455	0.054424
KK47	H3K27ac	42479	2641660	49789214	0.053057
L1207	H3K27ac	49958	30656612	79371958	0.38624
L1207	H3K27me3	99012	28898848	94964172	0.304313
L1207	H3K9me3	120513	19348866	74700084	0.259018
MGHU3	H3K27me3	73221	1712698	46163480	0.037101
MGHU3	H3K27ac	50734	1644454	39826658	0.041289
NHU11	H3K9me3	69783	1113263	58946442	0.018886
NHU11	H3K27me3	51400	1480880	46449018	0.031882
NHU11	H3K27ac	44280	1875773	52280305	0.035879
NHU12	H3K9me3	60671	544925	57677279	0.009448
NHU12	H3K27me3	51384	1772139	71573711	0.02476
NHU12	H3K27ac	51542	1559343	43893510	0.035526
RT112	H3K27ac	46513	47340406	1.17E+08	0.40384
RT112	H3K27me3	118688	21180874	68708970	0.032629
RT112	H3K9me3	64029	9744421	70999979	0.137245
SCaBER	H3K27me3	66506	1673182	32874254	0.050896
SCaBER	H3K27ac	48691	2606122	53174952	0.04901
SD48	H3K27ac	44822	37894501	19850888	0.523846
SD48	H3K27me3	63627	76768376	16525476	0.215264
SD48	H3K9me3	102050	39382228	6221312	0.157973

Figure S2: ChIPseq Quality controls

A) Washu Epigenome browser view of H3K27ac ChIPseq in tumors (bigwig) at 2 large windows on chromosome 4 (around FGFR3 gene) and chromosome 12 (around GAPDH gene).
 B) Macs2 Peaks number per sample for each tested histone marks. C) Fraction of Reads in Peaks statistics from MACS2 peaks.