Table S1 LC-MS/MS Analysis of the Immunoprecipitates of anti-Suz12 and Control IgG

International Protein Index	kDa	Unique Peptide Count		% Sequence Coverage		Protein name	Peptide sequences	Protein Description
		anti-Suz12 IP	IgG	anti-Suz12 IP	IgG			
IPI00124575	137.4	5	0	5.6		Jarid2	KVLYLSLK; SVSLTTFYR; QHGEGLAGSLK; LLYQIAQAEAK; IVEPLLPPPATQISDLSK;	jumonji, AT rich interactive domain 2
IPI00123127	85.5	2	0	2.7		Ezh1	QVFQFAVK; LPTDELMNPAQK;	enhancer of zeste homolog 1 (Drosophila)
IPI00396676	83	18	0	34.1		Suz12	SYSLLFR; QPGFAFSR; ATWETILDGK; ALETDGVSGVPK; NLIAPIFLHR; STAPVAKPLATR; TFVAQMTVFDK; FIFNYVYHPK; IFYQFLYNNNTR; TITQIEEFSDVNEGEK; LPPFETFSQGPTLQFTLR; ASMSEFLESEDGEVEQQR; RLPPFETFSQGPTLQFTLR; TITQIEEFSDVNEGEKEVMK; NSESLHQENKPGSVKPAQTIAVK; NDKPSQNSENEQNSVTLEVLLVK; HGGGGGGGSGPSAGSGGGGFGGSAAAVAAAASGGK; MEHVQADHELFLQAFEKPTQIYR;	suppressor of zeste 12 homolog (Drosophila)

IPI00312722	80.5	9	0	17.6		Ezh2	EFAAALTAER; TETLNQEWK; IFEAISSMFPDK; IQPVHIMTSVSSLR; AIQTGEELFFDYR; ESSIIAPVPTEDVDTPPR; LPNNSSRPSTPTISVLESK; IFEAISSMFPDKGTAEELK; MKPNIEPPENVEWSGAEASMFR;	enhancer of zeste homolog 2 (Drosophila)
IPI00133903	73.5	1	0	4.6		Hspa9	AQFEGIVTDLIK;	heat shock protein 9
IPI00467892	66.9	11	0	21.2		Mtf2	TAELPLDK; SWPAAIPHLR; FEEGQDVLAR; VPPVPPNVAFK; LHPGELADTPK; SVGRPPGPYTR; ALQTQNSEVVK; NSITSYFGAAGR; VQYLVEWEGATAS; YEHVLEALNDYK; QTLPYSVADLEWDAGHK;	metal response element binding transcription factor 2
IPI00312600	50.2	14	0	34.9		Eed	MLALGNQVGK; WLGDLILSK; DPNLLLSVSK; FSMDFWQK; IHFPDFSTR; ESYDYNPNK; IINPITMQCIK; IKPSESNVTILGR; EVSTAPAGTDMPAAK; HYVGHGNAINELK; EGDPLVFATVGSNR; VTLYECHSQGEIR; LYVWDLEVEDPHK; MEDDIDKIKPSESNVTILGR;	embryonic ectoderm development

IPI00122698	47.8	6	0	17.6		Rbbp7	LMIWDTR; TVALWDLR; LNVWDLSK; YMPQNPHIIATK; TPSSDVLVFDYTK; IGEEQSAEDAEDGPPELLFIHGGHTAK;	retinoblastoma binding protein 7
IPI00122696	47.6	8	0	24.7		Rbbp4	LMIWDTR; TVALWDLR; LNVWDLSK; GEFGGFGSVSGK; TPSSDVLVFDYTK; ADKEAAFDDAVEER; HPSKPDPSGECNPDLR; IGEEQSPEDAEDGPPELLFIHGGHTAK;	retinoblastoma binding protein 4
IPI00223156	38.1	2	0	6.2		E130012A19Rik	GFALDTPSLR; RRPAPPPPSVQPR	RIKEN cDNA E130012A19 gene

	Table S2	**Sequences**	**For PCR Primers and shRNAs**
RT-PCR	SUZ12	Forward	CGCGAAGATGGAGAAAAGAC
		Reverse	CCGGTCCATTTCGACTAAAA
	MTF2	Forward	GGTGCTTCCAGTGCAAACGAAACT
		Reverse	TCGCTCCTTCCCATTCCACAAGAT
	esPRC2p48	Forward	CCGGCTGATGCTCTTTCTAC
		Reverse	CGGAGAGAAAAGAGGGAGGT
	JARID2	Forward	GATTGCACAAGCAGAAGCAA
		Reverse	TTGGTGTGGGTTTGTTGAGA
	EZH1	Forward	AGTGGATGCTACCCGGAAAGGAAA
		Reverse	ATGGTAGCACTGGTTGGTTCCTGA
	EZH2	Forward	TACATCCCTTCCATGCAACA
		Reverse	CCGAGAATTTGCTTCAGAGG
	Pax3	Forward	TGCCCTCAGTGAGTTCTATCAGC
		Reverse	GCTAAACCAGACCTGCACTCGGGC
	Pax7	Forward	GCTACCAGTACAGCCAGTATG
		Reverse	GTCACTAAGCATGGGTAGATG
	Brachyury	Forward	TGCTGCCTGTGAGTCATAC
		Reverse	ACAAGAGGCTGTAGAACATG
	GAPDH	Forward	TCTGGAAAGCTGTGGCGTG
		Reverse	TCCTTGGAGGCCATGTAGGC
	Tgfβr2	Forward	TCGCTCATCTCCACAGTGAC
		Reverse	CGACTCCACGTTTTCCAGAT
	Tgfβ1	Forward	GACTCTCCACCTGCAAGACC
		Reverse	CGTCAAAAGACAGCCACTCA
	Zeb2	Forward	CGGCTTCTTCATGCTTTTTC
		Reverse	CAGCTGTGCTCCACAACACT
	Snail1	Forward	GAGGACAGTGGCAAAAGCTC
		Reverse	GGAGAATGGCTTCTCACCAG
	Gata1	Forward	GATGGAATCCAGACGAGGAA
		Reverse	CAGCAGAGGTCCAGGAAAAG
	Gata3	Forward	CTGGAGGAGGAACGCTAATGG
		Reverse	CATCTTCCGGTTTCGGGTCT
	Gata4	Forward	GTCGTAATGCCGAGGGTGA
		Reverse	TCCTTCCGCATTGCAAGAG
	Lenti	Forward	gatgaactgaccaggcacta

		Reverse	gattatcggaattccctcgag
	Nanog	Forward	accaaaggatgaagtgcaag
		Reverse	agttttgctgcaactgtacg
	Oct4	Forward	agcttgggctagagaaggat
		Reverse	tcagtttgaatgcatgggag
	Sox2	Forward	tgcacatggcccagcacta
		Reverse	ttctccagttcgcagtccag
	Cripto	Forward	aacttgctgtctgaatggag
		Reverse	tttgaggtcctggtccatca
	KLF4	Forward	cagcagggactgtcaccctg
		Reverse	ggtcacatccactacgtgggat
	Nat1	Forward	ggagagtgcgattgcagaag
		Reverse	ggtcacatccactacgtggga
	HOXA9	Forward	tgtggactccttcctgctgg
		Reverse	gcatcgcttcttccgagtg
	HOXB1	Forward	ccagctatgggccttctcag
		Reverse	ggcacggctcaggtatttgt
	HOXC5	Forward	tgtgggaactatggatcggc
		Reverse	taactggttcgggaccgct
	HOXD10	Forward	gattccttgatcagtgcctgc
		Reverse	catgacagtggagctgccttc
shRNA	SUZ12	GCTGTTACCAAGCTCCGAG	
		GAGCAACATGGGAGACAAT	
	JARID2	GGTGGACACTAATACCCAT	
		GATGATGAGACGGAAGATG	
	MTF2	GCTCCCAATGAAATGGTTA	
		GGAATCAGTTTCAGAGAAT	
		GGAAGTAAGCAATGGGATA	
	esPRC2p48	GCTCGAAACTTTGGTGTTA	
		GGAAGAGAACGGAGACCTA	
		GGACCTTGGTGATGGACAA	
	CFP	GCAAGCTGACCCTGAAGTT	

CHIP	Tgfβr2	1	Forward	GTTTGCTGGTCACCCAGTCT
			Reverse	TTCTTGTCTCGTGCATCTGG
		2	Forward	GAAGCAGTGTTTGGTGCTGA
			Reverse	CATGCCTGTTGCAGAAGCTA
	HoxC5	1	Forward	CTCTGTCTCCGGGTTCTCCT
			Reverse	AGGCCAGAACTCAGTTTCCA
		2	Forward	TACAGCCCAGCCTATCTGGT
			Reverse	GCTCTTAGCCCAGGTTTCAA
		3	Forward	CCAAGCAAGAGACCTTGACC
			Reverse	ATGCGCTCTTCCCAAATAAG

Table S3 Amino Acids   **Sequences for**   **the Peptides used In the Peptide Array**

SPOT	Residue # from N-term	Mods	Grid Location		Sequence	Peptide #
H3	1 - 12	none	A	1	H H H H H H H H H H H H	1
H3	1 - 13	none	A	2	A R T K Q T A R K S T G G	2
H3	1 - 13	R2 - monoMe	A	3	A Rme T K Q T A R K S T G G	3
H3		R2 - sym diMe	A	4	A Rme2(s) T K Q T A R K S T G G	4
H3		R2 - asym diMe	A	5	A Rme2(a) T K Q T A R K S T G G	5
H3		K4 - monoMe	A	6	A R T Kme Q T A R K S T G G	6
H3		K4 - diMe	A	7	A R T Kme2 Q T A R K S T G G	7
H3		K4 - triMe	A	8	A R T Kme3 Q T A R K S T G G	8
H3		K9 - monoMe	A	9	A R T K Q T A R Kme S T G G	9
H3		K9 - diMe	A	10	A R T K Q T A R Kme2 S T G G	10
H3		K9 - triMe	B	1	A R T K Q T A R Kme3 S T G G	11
H3		K9 - ac	B	2	A R T K Q T A R Kac S T G G	12
H3		S10 - phosph	B	3	A R T K Q T A R K pS T G G	13
H3		R2 - monoMe/K4me3	B	4	A Rme T Kme3 Q T A R K S T G G	14
H3		R2 - sym diMe/K4me3	B	5	A Rme2(s) T Kme3 Q T A R K S T G G	15
H3		R2 - asym diMe/K4me3	B	6	A Rme2(a) T Kme3 Q T A R K S T G G	16
H3	5 - 20	none	B	7	Q T A R K S T G G K A P R K Q L	17
H3		S10 - phosph/K14ac	B	8	Q T A R K pS T G G Kac A P R K Q L	18

H3		K14 - ac	B	9	Q T A R K S T G G Kac A P R K Q L	19
H3		R17 - monoMe	B	10	Q T A R K S T G G K A P Rme K Q L	20
H3		R17 - sym diMe	C	1	Q T A R K S T G G K A P Rme2(s) K Q L	21
H3		R17 - asym diMe	C	2	Q T A R K S T G G K A P Rme2(a) K Q L	22
H3		K18 - ac	C	3	Q T A R K S T G G K A P R Kac Q L	23
H3		K14ac/K18ac	C	4	Q T A R K S T G G Kac A P R Kac Q L	24
H3		K9 - monoMe/K14ac	C	5	Q T A R Kme S T G G Kac A P R K Q L	25
H3		K9 - diMe/K14ac	C	6	Q T A R Kme2 S T G G Kac A P R K Q L	26
H3		K9 - triMe/K14ac	C	7	Q T A R Kme3 S T G G Kac A P R K Q L	27
H3		K9 - ac/K14ac	C	8	Q T A R Kac S T G G Kac A P R K Q L	28
H3	15 - 29	none	C	9	A P R K Q L A T K A A R K S A	29
H3		K23 - monoMe	C	10	A P R K Q L A T Kme A A R K S A	30
H3		K23 - diMe	D	1	A P R K Q L A T Kme2 A A R K S A	31
H3		K23 - triMe	D	2	A P R K Q L A T Kme3 A A R K S A	32
H3		K18 - ac	D	3	A P R Kac Q L A T K A A R K S A	33
H3		K18ac/K27 monoMe	D	4	A P R Kac Q L A T K A A R Kme S A	34
H3		K18ac/K27 - diMe	D	5	A P R Kac Q L A T K A A R Kme2 S A	35
H3		K18ac/K27 - triMe	D	6	A P R Kac Q L A T K A A R Kme3 S A	36
H3		K23 - ac	D	7	A P R K Q L A T Kac A A R K S A	37
H3		K23ac/K27 - monoMe	D	8	A P R K Q L A T Kac A A R Kme S A	38
H3		K23ac/K27 - diMe	D	9	A P R K Q L A T Kac A A R Kme2 S A	39
H3		K23ac/K27 - triMe	D	10	A P R K Q L A T Kac A A R Kme3 S A	40
H3		K18 - ac/K23 -ac	E	1	A P R Kac Q L A T Kac A A R K S A	41

H3	21 - 34	none	E	2	A T K A A R K S A P A T G G	42
H3		R26 - monoMe	E	3	A T K A A Rme K S A P A T G G	43
H3		R26 - sym diMe	E	4	A T K A A Rme2(s) K S A P A T G G	44
H3		R26 - asym diMe	E	5	A T K A A Rme2(a) K S A P A T G G	45
H3		K27 - monoMe	E	6	A T K A A R Kme S A P A T G G	46
H3		K27 - diMe	E	7	A T K A A R Kme2 S A P A T G G	47
H3		K27 - triMe	E	8	A T K A A R Kme3 S A P A T G G	48
H3		S28 - phosph	E	9	A T K A A R K pS A P A T G G	49
H3	30 - 42	none	E	10	P A T G G V K K P H R Y R	50