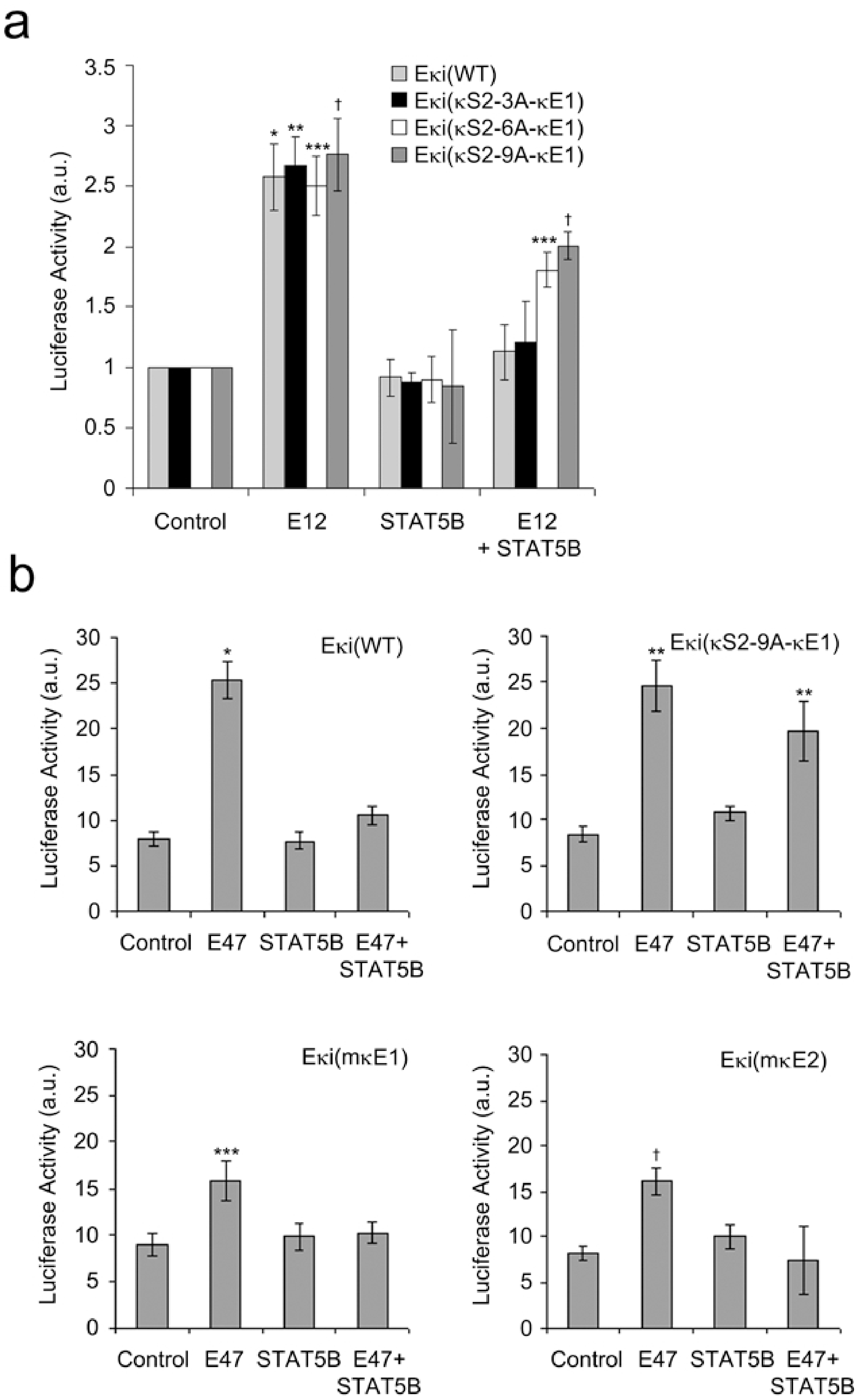
Supplementary Figure 1 Mandal *et. al.*



Supplementary Figure 2

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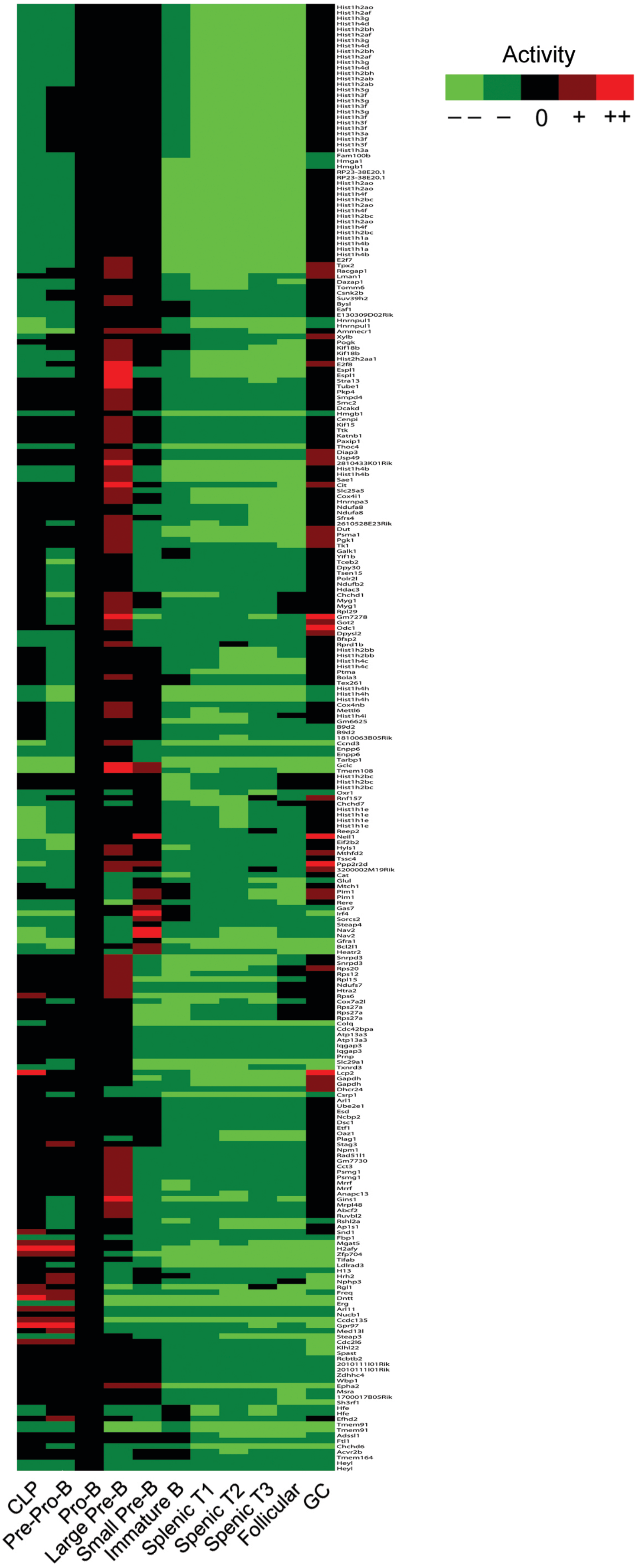

Supplementary Figure 3

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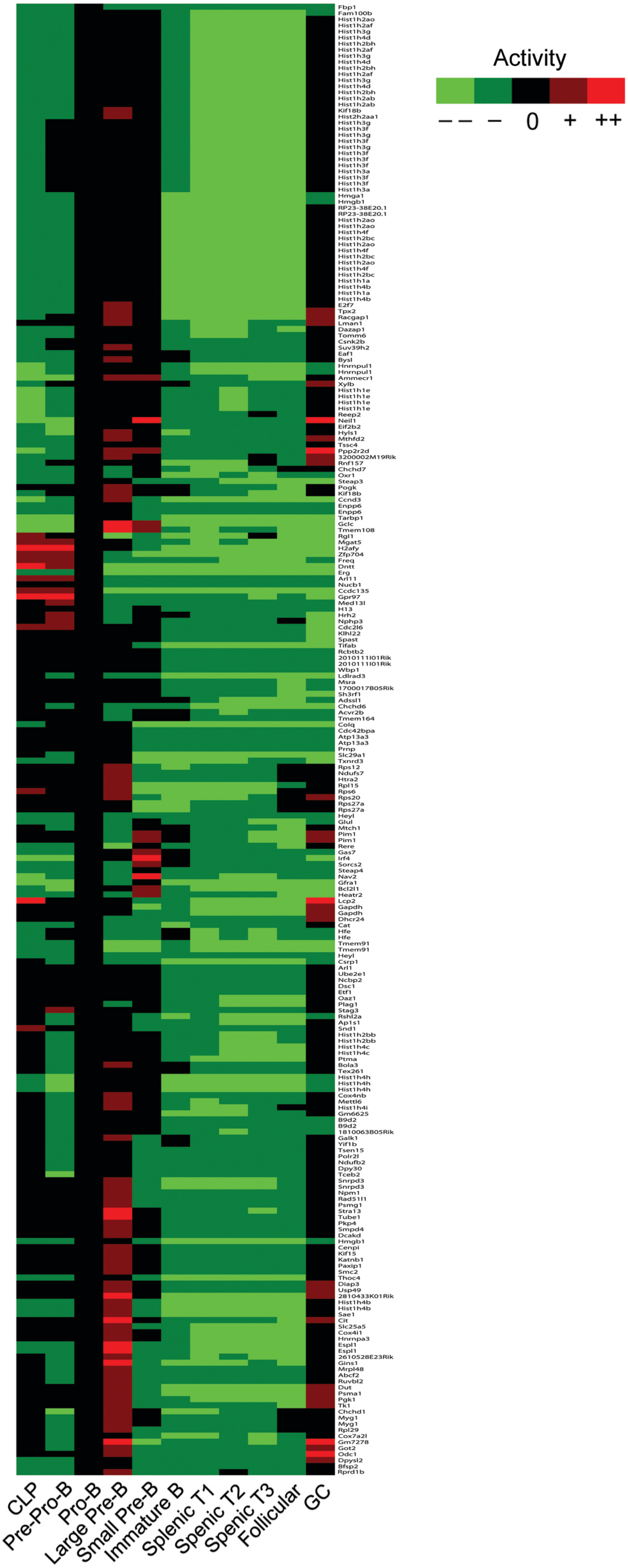

Supplementary Figure 4

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Supplementray Table 1 Mandal *et. al.*

List of probes and primers

EMSA: Biotinylated at 5’ end and non biotinylated	
κS1(WT)-F	5’- TCT ATT GTT TTT CTT GGT AAA GAA CTC T-3’
κS1(WT)-R	5’-AGA GTT CTT TAC CAA GAA AAA CAA TAG A-3’
κS1(Mut)-F	5’- TCT ATT GTT T**AA G**TT GGT AAA GAA CTC T-3’
κS1(Mut)-R	5’-AGA GTT CTT TAC CAA **CTT** AAA CAA TAG A-3’
κS2(WT)-F	5’-AGAGGGGACTTTCCGAGAGGCCATCTGGCAGTTGCTTAA -3’
κS2(WT)-R	5’-TTAAGCAACTGCCAGATG GCCTCTCGGAAAGTCCCCTCT-3’
κS2(Mut)-F	5’-AGAGGGGACT**AAG**CGAGAGGCCATCTGGCAGTTGCTTAA -3’
κS2(Mut)-R	5’-TTAAGCAACTGCCAGATG GCCTCTCG**CTT**AGTCCCCTCT-3’
κS2(CS)-F	5’-AGAGGGGACTTTCCGAGA**A**GCCATCTGGCAGTTGCTTAA -3’
κS2(CS)-R	5’-TTAAGCAACTGCCAGATGGC**T**TCTCGGAAAGTCCCCTCT-3’
STAT5 dimer-only-F	5’-GAATGTAGT**TTCAGGGAA**GAAAGGCAA-3’
STAT5 dimer-only-R	5’-TTGCCTTTCTTCCCTGAAACTACATTC-3’
STAT5 tetramer-only-F	5’-CCGGGCT**TTCAAAGAA**GCATACT**TTC**CGGAGCA-3’
STAT5-tetramer-only-R	5’- TGCTCCG**GAA**AGTATGC**TTCTTTGAA**AGCCCGG-3’
STAT5-dimer-tertramer-F	5’CCGGCT**TTCGTGGAA**TCGTGGCACTAT**GAA**CCA-3’
STAT5-dimer-tertramer-R	5’TGG**TTC**ATAGTGCCACGA**TTCCACGAA**AGCCGG-3’
κS2-end-Mut-F	5’-AGAGGGGACTTTCCGAGAGGCCA**AAA**GGCAG**GG**GCTT**TT**-3’
κS2-end-Mut-R	5’-**AA**AAGC**CC**CTGCC**TTT**TGGCCTCTCGGAAAGTC CCCTCT-3’
Pax5-F	5’-TCGAAGGGCCACTGGAGCCCATCTCCGGCACGGC-3’
Pax5-R	5’-TCGAGCCGTGCCGGAGATGGGCTCCAGTGGCCCT-3’
Oct-F	5’-TCGGGTAATTTGCATTTCTAGCT-3’
Oct-R	5’-AGCTAGAAATGCAAATTACCCGA-3’
ChIP- Quantitative PCR	
Igκ-Eκi - F	5’-TTTGACCCTTCCCTGCCAAA-3’
Igκ-Eκi - R	5’-CAACTGTAATCTGGGCCACCTG-3’
Vκ$_{21-1}$-F	5’- TTGTGCTCACCCAATCTCCAG-3’
Vκ$_{21-1}$-R	5’- GGCTGTCCTGGTTTCTGTTGG-3’
Jκ$_{1-}$ Jκ$_{2}$ -F	5’-AGGCACCAAGCTGGAAATCAA-3’
Jκ$_{1-}$ Jκ$_{2}$ -R	5’-TGCCTTGGAGAGTGCCAGAAT-3’
Jκ$_{4-}$ Jκ$_{5}$ - F	5’- GCTCGGGGACAAAGTTGGAA-3’
Jκ$_{4-}$ Jκ$_{5}$ –-R	5’- GATGCACAGGTTGCCAGGAAT-3’
Jκ$_{5}$- Eκi- F	5’- TGTTTTAATGGCCACGGTTTTG-3’
Jκ$_{5}$- Eκi- R	5’- AGAAGAGGTTGCGGACCGTTT-3’
Eκi- F	5’- GCAGGTGGCCCAGATTACAGT-3’
Eκi- R	5’- AGGGCCTTAAGCCAGGGTCT-3’
Cκ-F	5’- TCTGGAGGTGCCTCAGTCGT-3’
Cκ- R	5’-CCAACTGTTCAGGACGCCATT-3’
3’Eκ- F	5’- CCCCACCTCCATCTTGTTTGA-3’
3’Eκ- R	5’- GGGCCCAGTGACCATATCAGA-3’
Eκi (pGL3-specific)-F	5’-GGTACCGAGCTCTTACGCGT-3’
Eκi (pGL3-specific)-R	5’-GGACTATGGTTGCTGACTAATTGAGAT 3’
Ezh2- F	5’-AAACTTGCCCACCTCGGAAAT-3’
Ezh2- R	5’-CATTCAGGAGGCAGAGCACCT-3’

ChIP- Quantitative PCR (Cont.)	
B-2 Microglobulin-F	5’-AGACTGATACATACGCCTGCA-3’
B-2 Microglobulin-R	5’-GCAGGTTCAAATGAATCTTCA-3’
Igk-Germline-F	5’-GAGGGGGTTAAGCTTTCGCCTACCCAC-3’
Igk-Germline-R	5’-GTTATGTCGTTCATACTCGTCCTTGGTCAA-3’
Short Hairpin RNA Constructs	
sh-Ezh2-390 (target seq)	5’-GGCACTTTCATTGAAGAACTAA-3’
sh-Ezh2-1562 (target seq)	5’- GTGCCCTTGTGTGATAGCACAA-3’
sh-Ezh2-390 (97mer)	5’- TGCTGTTGACAGTGAGCGAGCACTTTCATTGAAGAACTAATAGTGAAGCCACAGATGTATTAGTTCTTCAATGAAAGTGCCTGCCTACTGCCTCGGA-3'
sh-Ezh2-1562 (97mer)	5'-TGCTGTTGACAGTGAGCGATGCCCTTGTGTGATAGCACAATAGTGAAGCCACAGATGTATTGTGCTATCACACAAGGGCACTGCCTACTGCCTCGGA-3'
Site directed mutagenesis	
Mut κS1-F	5’- CTGCTCATAATTCTATTGT TT**AAG**TTGGTAAAGAAC- 3’
Mut κS1-R	5’- AAACAATAGAATTATGAGCAGCCTTTCCCCCC-3’
Mut κS2-F	5’- GGCATCTCAACAGAGGGGACT**AAG**CGAGAGGCCATC-3’
Mut κS2-R	5’- AGTCCCCTCTGTTGAGATGCCAACTCTTGGGT-3’
κS2-3A spacer-F	5’- CAGAGGGGACTTTCCGAGAGG**AAA**CCATCTGGCAG - 3’
κS2-6A spacer-F	5’-CAGAGGGGACTTTCCGAGAGG**AAAAAA**CCATCTGGCAG- 3’
κS2-9A spacer-F	5’-CAGAGGGGACTTTCCGAGAGG**AAAAAAAAA**CCATCTGGCAG-3’
κS2- 3A/6A/9A spacer-R	5’- CCTCTCGGAAAGTCCCCTCTGTTGAGATGCCAAC-3’
Mut κE1-F	5’- AGAGGGGACTTTCCGAGAGGC**AAA**CTGGCAGTTGCT-3’
Mut κE1-R	5’-GCCTCTCGGAAAGTCCCCTCTGTTGAGATGCC-3’
Mut κE2-F	5’- AGTCTGCCAGTTCCTCCCAGG**AAA**GTGGCCCAGATT-3’
Mut κE2-R	5’-CCTGGGAGGAACTGGCAGACTTCACTTCTGAT -3’

Supplementary Table 2 Mandal *et. al.*

List of genes where both STAT5 and H3K27me3 bind at the regulatory sites

Chromosome no	Gene name	STAT5 binds at	H3K27 trimethylation Status
Chr2	Cstad	Intron 1	High in promoter and entire gene
Chr2	Lhx6	370bp upstream 4kb upstream	High in promoter and entire gene
Chr2	Hoxd3	Intron 1	High in promoter and entire gene
Chr2	Pax6	~20kb upstream ~9kb upstream	High in promoter and entire gene
Chr2	Cdh22	Intron 1	High in promoter and entire gene
Chr2	Matn4	1.1kb upstream (Rev strand)	High in promoter and entire gene
Chr2	Mir10b	Intron 1	High throughout the entire gene
Chr3	Mir9-1	~20kb upstream ~4.5kb upstream	High throughout the entire gene
Chr3	Adar	~14kb upstream	High in promoter and extended to intron 1
Chr4	Arhgef19	~3.576kb upstream	High throughout the entire region
Chr5	Flt1	Intron 1	High in promoter and upto 1st Exon and 1st Intron
Chr5	Tbx3	~3kb downstream	High in promoter and entire gene
Chr5	Tbx5	~29kb upstreamt	High in promoter and entire gene
Chr5	Grid2ip	~3.212kb upstream	High in promoter and entire gene
Chr6	Wnt16	Intron 3	High in promoter and low in entire gene
Chr6	Igk-Eki	Intronic kappa Enhancer	High in the entire intronic kappa enhancer
Chr6	Atoh8	Intron 2 (Rev strand)	High in promoter and entire gene
Chr6	Rimklb	Intron 1 (Rev strand)	High in promoter and the beginning of the gene
Chr7	Homer 2	~3.5kb up	High in promoter and the beginning of the gene
Chr7	Nav2	~4kb up	High in promoter and upto 1st Exon
Chr7	Fgf15	Intron 2	High in promoter and entire gene
Chr7	Mir7-2		High throughout the entire gene
Chr8	Vat1l	330bp upstream	High in promoter and entire gene
Chr8	Ncan	Intron 7	High in promoter and entire gene
Chr9	Igdcc3	Intron 2	High in promoter and entire gene
Chr9	Elov14	~322bp upstream (Rev)	Hig in promoter and beginning of gene
Chr9	Amotl2	~25kb upstream	High in promoter and beginning of the gene
ChrX	Nhs	Intron 1 of 7	Low in promoter and beginning of the gene
Chr10	Rspo3	~3kb upstream	High in promoter and beginning of the gene
Chr11	SLC47a1	Intron 14 (Rev)	High in promoter and entire gene
Chr11	SLC47a2	~9kb upstream (Rev)	High in promoter and beginning of the gene
Chr11	Osbp2	Intron 2 of 13 (Rev)	High in promoter and entire gene
Chr12	Fam150b	Intron 3 of 4	High in promoter and entire gene
Chr12	Zdhhc22	~3kb upstream	High in promoter and entire gene
Chr12	Eml1	~224bp upstream	High throughout the entire region
Chr14	Grid1	Intron 2 of 15	High in promoter and beginning of the gene
Chr14	Jph4	Intron 1 of 1 (Rev)	High in promoter and entire gene
Chr14	Htr2a	Exon 1 of 3	High in promoter
Chr16	Brwd1	~5.8kb upstream	High in promoter and beginning of the gene
Chr17	Sox8	Intronic	High throughout the entire region
Chr17	Mir715	Transcription strat site	High throughout the entire region
Chr18	Arap3	~24.5kb upstream (Rev)	High in promoter
Chr19	Pax2	~93kb upstream	High in promoter and entire gene
chr19	Dmrt2	Intron 2	High throughout the entire region

Supplementary Table 3 Mandal *et. al.*

Predicted STAT5 tetrameric binding motifs	**Number of nucleotides between two motifs**	**First motif**	**Second motif**
TTTCCTTCCCTTGAAGGTGTGGAGAAT	7	TTTCCTTCCCT	GTGTGGAGAAT
CTTCCCTTGAAGGTGTGGAGAAT	3	CTTCCCTTGAA	GTGTGGAGAAT
TTTCTGGTTTTTTCTTTCCTCCCTT	5	TTTCTGGTTTT	TTTCCTCCCTT
TTTCTTTCCTCCCTTCCTCTGGT	3	TTTCTTTCCTC	CTTCCTCTGGT
TTTCCTCCCTTCCTCTGGTATTTCTTTCCAG	10	TTTCCTCCCTT	TTTCTTTCCAG
CTTCCTCTGGTATTTCTTTCCAG	3	CTTCCTCTGGT	TTTCTTTCCAG
CTTCCTCTGGTATTTCTTTCCAGCCAA	7	CTTCCTCTGGT	TTTCCAGCCAA
TTTCCAGCCAAGATCTTGTTAGGTA	5	TTTCCAGCCAA	CTTGTTAGGTA
CTTGTTAGGTACCAAATATTCACCCGCA	8	CTTGTTAGGTA	ATTCACCCGCA
GTTCTTTAGATCTCAAAGTATACGGAAA	8	GTTCTTTAGAT	GTATACGGAAA
ATTCCACATGAAGCCACGTTCTGTTGAT	8	ATTCCACATGA	GTTCTGTTGAT
TTCCACATGAAGCCACGTTCTGTTGAT	7	TTCCACATGAA	GTTCTGTTGAT
CTTCCCCGAAATTTTCAATAATC	3	CTTCCCCGAAA	TTTCAATAATC
GTTCCGTGTCTCCGTTCACTTACT	4	GTTCCGTGTCT	GTTCACTTACT
GTTCCCTTTCGCCTTGTCCACAGAAC	6	GTTCCCTTTCG	GTCCACAGAAC
CTTCATTCAAGAACTTCTGTCCAT	4	CTTCATTCAAG	CTTCTGTCCAT
TTTCCCAAGTCCTTCTTCCCCCAGA	5	TTTCCCAAGTC	CTTCCCCCAGA
CTTCAGCTCACTCAGCTTCAGGGGTG	6	CTTCAGCTCAC	CTTCAGGGGTG
TTTCCCCACAGACACCTTCTCCCTAT or	7	TTTCCCCACA	CTTCTCCCTAT
CTTGTCTGGGGTGAGTTTCCACAGCC	6	CTTGTCTGGGG	TTTCCACAGCC
ATTCATCATAGGAGTACAGCTGACATAGCAATGGAAG	17	ATTCATCATAG	TAGCAATGGAAG
CTTCACCTGGCTCTGATCCAGAAC	4	CTTCACCTGGC	TGATCCAGAAC
GTTGGCCCGGTGCCCGCGCTCTCCGAGG	8	GTTGGCCCGGT	GCTCTCCGAGG
ATTCCTCCCATTTCCTTCCCTTCCT	5	ATTCCTCCCAT	CTTCCCTTCCT
TTTCCTTCCCTTCCTTCGGTCTGGAAC	7	TTTCCTTCCCT	CGGTCTGGAAC
CTTCCCTTCCTTCGGTCTGGAACAA	3	CTTCCCTTCCT	CGGTCTGGAAC
GTTCCCCCAGGAGTGGCCTAATATTGTCTAGAT	13	GTTCCCCCAGG	ATTGTCTAGAT
CTTCCGTTCTCCCCAGGACAGGAAG	5	CTTCCGTTCTC	AGGACAGGAAG

Predicted STAT5 tetrameric binding motifs	Number of nucleotides between two motifs	First motif	Second motif
TTTCCCCCCACCTTTCCCTGCTC	3	TTTCCCCCCAC	TTTCCCTGCTC
TTTCCCTGCTCCCTGCTTTCCACAGT	7	TTTCCCTGCTC	TTTCCACAGT
GTTCTCCCCAGGACAGGAAGTACAAGAGAAA	11	GTTCTCCCCAG	TACAAGAGAAA
GTTCAGATCAGAGGTCTGTTCCAAGGTT	8	GTTCAGATCAG	GTTCCAAGGTT
GTTCCAAGGTTCAGTAAAAGAAC	3	GTTCCAAGGTT	CAGTAAAAGAAC
TTTCCATTTCATTTGAACATGCAATTCAAACAGG	14	TTTCCATTTCA	ATTCAAACAGG
TTTCATTTGAACATGCAATTCAAACAGG	8	TTTCATTTGAA	ATTCAAACAGG
CTTCATGTAGGAACTTCAGAAGTG	4	CTTCATGTAGG	CTTCAGAAGTG
CTTCAGAAGTGGACTTTCTGTTGCT	5	CTTCAGAAGTG	TTTCTGTTGCT
CTTCTGGAAGCTGGGGTCAGTCAGGGTAAC	10	CTTCTGGAAGC	GTCAGGGTAAC
GGACTCAGAACATTTGTCATTCTGTGCGG	9	GGACTCAGAAC	ATTCTGTGCGG
CTTGGGCTGAGGATTCTGCGTCC	3	CTTGGGCTGAG	ATTCTGCGTCC
TTTCAGACACTGCTCTTGTCTCAAT	5	TTTCAGACACT	CTTGTCTCAAT
GTTCACATAACCCCTAAAAATCGGTAGTCATGAAG	15	GTTCACATAAC	GTAGTCATGAAG
GTTCAAAGAAGCCTTCAGCCCTA	3	GTTCAAAGAAG	CTTCAGCCCTA
CTTGGTAGAAATAAACTTCTGAGCAA	6	CTTGGTAGAAA	CTTCTGAGCAA
CTTCCCGCACCTCCCTGCCGCTCCACTCAGAAC	13	CTTCCCGCACC	CCACTCAGAAC
ATTCGTCTCTGTCCATTTCAAGGCGC	6	ATTCGTCTCTG	TTTCAAGGCGC
GTTGCAGTCACCCTTTCTCCTCAG	4	GTTGCAGTCAC	TTTCTCCTCAG
CTTCTCCCCAGGGGTCCTGGCAGG	4	CTTCTCCCCAG	GTCCTGGCAGG
ATTCCAGGAGTTATCTGCCTACCTCTGCCCAAG	13	ATTCCAGGAGT	CTCTGCCCAAG
GTTCTGCCGGATGCAACGTGGGAAA	5	GTTCTGCCGGA	AACGTGGGAAA
TTTCTGGTTCTTGCCTATCATTCACCTCCA	10	TTTCTGGTTCT	ATTCACCTCCA
GTTCTTGCCTATCATTCACCTCCATCACAT	5	GTTCTTGCCTA	ATTCACCTCCA
TTTCACTGTAAAGGAATGCCATTTGTCTTAAG	12	TTTCACTGTAA	TTTGTCTTAAG
TGTAAAGGAATGCCATTTGTCTTAAG	6	TGTAAAGGAAT	TTTGTCTTAAG
CTTCCGCTGCTGAGACTGGGGATTTGTAAAAC	12	CTTCCGCTGCT	ATTTGTAAAAC
CTTCTAGCAGAAGCATTAGATTGCTAAACT	10	CTTCTAGCAGA	ATTGCTAAACT
GTACAGGGAAATGCCCCTAAGATGCTGTTGAAG	13	GTACAGGGAAA	TGCTGTTGAAG
CTTCCCCATAGCATCTCAGCTGAAC	5	CTTCCCCATAG	CTCAGCTGAAC
ATTCAGAAAATGCTCTGTTCGCCAGTT	7	ATTCAGAAAAT	GTTCGCCAGTT
CTTCCGGCAATGAGGCTTACCGGACAAT	6	CTTCCGGCAAT	CTTACCGGACA

Predicted STAT5 tetrameric binding motifs	Number of nucleotides between two motifs	First motif	Second motif
ATTCCAGGAATTTGAGGTCTCCCCTGAGA	9	ATTCCAGGAAT	CTCCCCTGAGA
CTTCCATTCACATCCTCATTTGTTTATGAAC	11	CTTCCATTCAC	TGTTTATGAAC
TTTCAAAGGAAGGGTGTCCTTGAGAAG	6	TTTCAAAGGAA	GTCCTTGAGAAG
ATTCACATCCTCATTTGTTTATGAAC	6	ATTCACATCCT	TGTTTATGAAC
ATTCTATTCAGCTGAACATCACACAAG	7	ATTCTATTCAG	CATCACACAAG
CTTCTCCGGCACCCGTCTTCTTTTCATGC	7	CTTCTCCGGCA	CTTCTTTTCAT
CTCCGGCACCCGTCTTCTTTTCATGC	4	CTCCGGCACCC	CTTCTTTTCAT
GTTGATTAAAACGAGCAATCCTTTGAAG	8	GTTGATTAAAA	ATCCTTTGAAG
ATTAAAACGAGCAATCCTTTGAAG	4	ATTAAAACGAG	ATCCTTTGAAG
ATTCCTAAGCTGACATTCTCTGCCT	5	ATTCCTAAGCT	ATTCTCTGCCT
TTTCTGCATCCTTGGTCCCCTCTTGGGGTAGG	12	TTTCTGCATCG	CTTGGGGTAGG
ATCCTTGGTCCCCTCTTGGGGTAGG	5	ATCCTTGGTCC	CTTGGGGTAGG
CTTGGGGTAGGGACATGGGTTCTTGTGGA	9	CTTGGGGTAGG	GTTCTTGTGGA
CTTCTTATGTGGCCCCATCCCACAAT	6	CTTCTTATGTG	CATCCCACAAT
GTTCTGGTGACTTTCTTCATGGTGT	5	GTTCTGGTGAC	CTTCATGGTGT
CGTCCTGGAAGCCGTCCTTCCAGAGCC	7	CGTCCTGGAAG	CTTCCAGAGCC
TTTCCTGATGTCACTTGCCATAGC	4	TTTCCTGATGT	CTTGCCATAGC
CTTCTTAGTCCTATTAGGTCCTCAGCTG	8	CTTCTTAGTCC	GTCCTCAGCTG
TTTCCACATTTAATCTCACCCTCGGACT	8	TTTCCACATTT	ACCCTCGGACT
CTTTATTGACAACTGTCGTGATT	3	CTTTATTGACA	CTGTCGTGATT
ATTATTCTCACCATTGCGGGAAA	3	ATTATTCTCAC	ATTGCGGGAAA
TTTCCTGATGTCACTTGCCATAGC	4	TTTCCTGATGT	CTTGCCATAGC
TTTCCTTGTCATGCCCGTGTCCATGTTAA	9	TTTCCTTGTCA	GTCCATGTTAA
ATTCAAGGACAGATAATATATGCATGCATG	10	ATTCAAGGACA	ATGCATGCATG
TTTCCATGGTTATGTTCTTCCTTAAGG	7	TTTCCATGGTT	CTTCCTTAAGG
GTTCCGGAGGGAAAGCCGTGGCCTTCGATGCAG	13	GTTCCGGAGGG	CTTCGATGCAG
ATTCAAAAAGCATTGAGAGGCAAAGGAAT	9	ATTCAAAAAGC	GGCAAAGGAAT

Supplementary Table 4

Analysis of STAT5 tetrameric binding motifs (total no of motifs 88)

Position (First Site)	No. of As/%	No. of Ts/%	No. of Gs/%	No. of Cs/%
1	0/0	85/97	3/3	0/0
2	2/2	83/95	0/0	3/3
3	2/2	3/3	8/9	75/86
4	23/26	21/24	7/8	37/42
5	18/20	28/32	20/23	22/25
6	19/21	21/24	22/25	26/30
7	18/20	23/27	27/31	20/22
8	24/28	17/19	24/27	23/26
9	41/47	14/16	13/15	20/22
No. of bases in between two sites (number appeared/ % appeared)	3(12/14%); 4(10/11%); 5(14/16%); 6(11/13%); 7(9/10%); 8(9/10%); 9(5/6%); 10(5/6%); 11(2/2%); 12(3/3%); 13(5/6%); 14(1/1%); 15(1/1%); 17(1/1%)			
Position (Second Site)	No. of As/%	No. of Ts/%	No. of Gs/%	No. of Cs/%
1	5/6	70/80	10/11	3/3
2	3/3	59/68	8/9	18/20
3	8/9	13/14	12/14	55/63
4	21/24	32/36	11/13	24/27
5	16/18	21/24	20/23	31/35
6	21/24	29/33	23/26	15/17
7	11/13	20/23	40/45	17/19
8	48/55	4/5	16/18	20/22
9	45/51	14/16	16/18	13/15

Supplementary Table 5

Mandal *et. al.*

Sample	Reads	Fails to align	Aligned reads	Duplicate reads	Unique mapped reads
Input	30669275	920362	21329219		
H3K27me3	28968570	991113	19459871	1407177	18052694
STAT5	26487197	2414068	17282363	1518430	15763933