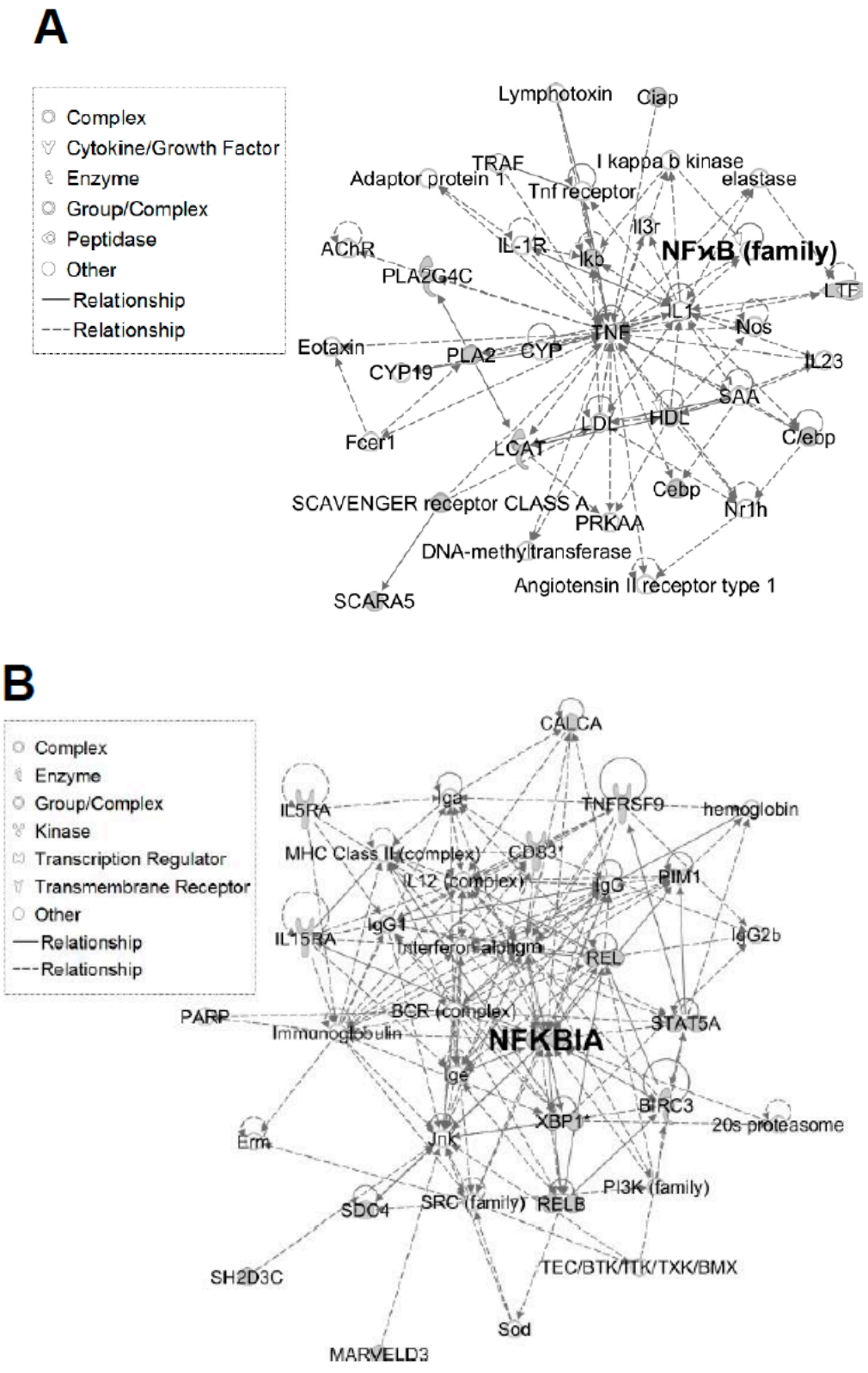

Figure S1. Ingenuity Pathway Analysis (IPA). (A) and (B) IPA representative networks showing genes regulated by S15A with NF-κB as one of the critical nodes in these networks.

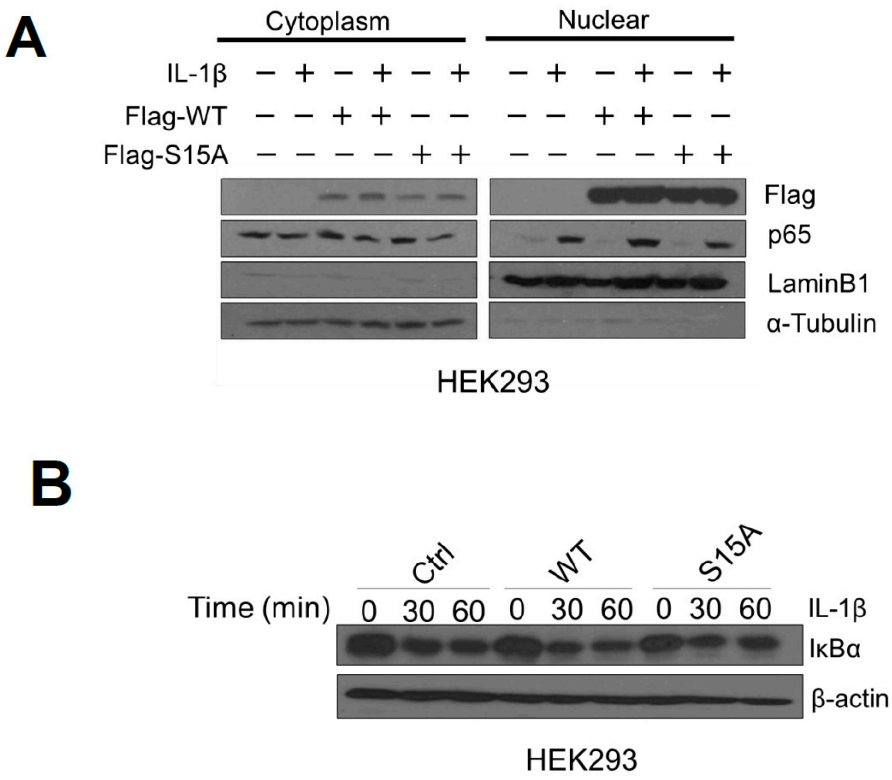

Figure S2. Effect of S15A mutant on PRMT5 subcellular localization, p65 nuclear translocation and IκB*α* degradation. (A) Cell fractionation assay, showing subcellular compartmentalization of Flag-PRMT5 and Flag-S15A in HEK293 cells. Western blot was probed with anti-FLAG, p65, LaminB1 and *α*-tubulin antibodies. (B) Western blot, showing IL-1β-induced IκB*α* degradation pattern in WTPRMT5 and S15A HEK293 cells.

ACCESSION NO.	TargetID	S15A-PRMT5 +IL-1β/WT+IL-1β
NM_001115.1	ADCY8	0.45
NM_014391.2	ANKRD1	0.38
NM_020373.2	ANO2	0.15
XR_041624.1	C10ORF85	0.36
XR_041485.1	C13ORF29	0.27
XM_001726191.1	C19ORF29OS	0.00
NM_178342.2	C3ORF35	0.50
NM_018452.3	C6ORF35	0.32
NM_145028.3	C6ORF81	0.16
NM_152786.1	C9ORF43	0.33
NM_001742.2	CALCR	0.24
NM_175931.1	CBFA2T3	0.28
NM_138414.1	CCDC101	0.41
NM_015603.1	CCDC9	0.48
NM_004591.1	CCL20	0.37
NM_207007.2	CCL4L2	0.47
NM_145057.2	CDC42EP5	0.41
NM_000735.2	CGA	0.33
NM_000737.2	CGB	0.45
NM_024111.2	CHAC1	0.00
NM_015557.1	CHD5	0.27
NM_024944.2	CHODL	0.47
NM_138429.1	CLDN15	0.49
NM_080645.2	COL12A1	0.22
NM_002089.3	CXCL2	0.29
NM_016229.3	CYB5R2	0.36
NM_000779.2	CYP4B1	0.31
NR_024064.1	DAD1L	0.39
NM_006557.4	DMRT2	0.28
NR_024595.1	DNM1P35	0.06
NM_133637.1	DQX1	0.37
NM_004428.2	EFNA1	0.48
NM_007036.2	ESM1	0.22
NM_153606.2	FAM71A	0.50
NM_001012426.1	FOXP4	0.06
NM_000148.2	FUT1	0.35

NM_002068.1	GNA15	0.40
XM_935238.1	GOLGA8F	0.45
BX109627	HS.130639	0.46
AI801879	HS.144030	0.14
BU633914	HS.25555	0.27
AK026734	HS.287720	0.34
AF339771	HS.344872	0.19
CD695721	HS.538157	0.00
AI253067	HS.541845	0.20
U10515	HS.544238	0.46
AI628074	HS.545238	0.13
NM_130770.2	HTR3C	0.28
NM_172200.1	IL15RA	0.17
NM_001012633.1	IL32	0.49
NM_000564.2	IL5RA	0.50
NM_000584.2	IL8	0.48
NM_002195.1	INSL4	0.30
XM_934728.1	KIAA0565	0.09
NM_138343.2	KLC4	0.02
NM_002774.3	KLK6	0.34
NM_004139.2	LBP	0.29
NM_001010939.1	LIPJ	0.18
NM_033029.2	LMLN	0.15
XM_001724965.1	LOC100129268	0.13
XM_001716704.1	LOC100130288	0.15
XM_001718675.1	LOC100130705	0.50
XM_001714361.1	LOC100131999	0.18
XR_038987.1	LOC100132496	0.37
XM_001724630.1	LOC100132716	0.05
XM_001726146.1	LOC100132839	0.06
XM_001721522.1	LOC100134009	0.18
XM_001720931.1	LOC100134041	0.14
XM_001715304.1	LOC100134081	0.00
XM_001721704.1	LOC100134170	0.19
XM_001714134.1	LOC100134499	0.00
NM_178514.3	LOC283487	0.26
XM_944838.2	LOC285733	0.27
XM_939888.1	LOC339742	0.49
XM_370865.4	LOC388122	0.23

XM_374766.2	LOC399715	0.11
XM_495854.3	LOC440013	0.10
XM_001717499.1	LOC642076	0.04
NR_024495.1	LOC642826	0.40
XM_927139.1	LOC643869	0.14
XM_933938.2	LOC643872	0.38
XM_928663.1	LOC645649	0.03
XR_037491.1	LOC646808	0.46
XM_943707.1	LOC649431	0.33
XM_941853.1	LOC652416	0.00
XM_928640.1	LOC653651	0.39
XM_001126803.1	LOC728185	0.36
XR_015405.1	LOC728895	0.43
XM_001130993.1	LOC729675	0.23
XM_001714434.1	LOC730376	0.40
NM_002343.2	LTF	0.01
NM_012323.2	MAFF	0.44
NM_005204.2	MAP3K8	0.39
NM_052858.3	MARVELD3	0.33
NM_033290.1	MID1	0.33
NR_030209.1	MIR518E	0.31
NM_173855.3	MORN3	0.40
NM_013404.3	MSLN	0.21
NM_003828.2	MTMR1	0.45
NM_001005474.1	NFKBIZ	0.47
NM_001080379.1	PACRG	0.01
NM_000438.3	PAX3	0.27
NM_003706.1	PLA2G4C	0.41
NM_002658.2	PLAU	0.44
XM_940486.1	PLEKHA2	0.26
NM_014330.2	PPP1R15A	0.46
NM_022114.2	PRDM16	0.11
NM_000963.1	PTGS2	0.32
NM_000963.1	PTGS2	0.40
NM_001024455.2	RGAG4	0.43
NM_184237.1	RNPC2	0.48
NM_001007098.1	SCP2	0.40
NM_000450.1	SELE	0.22
NM_013386.3	SLC25A24	0.41

NR_003237.1	SNORD113-9	0.34
XM_291729.7	TAF3	0.38
NM_031898.1	TEKT3	0.16
NM_001001524.2	TM6SF2	0.10
NM_001097620.1	TMEM184A	0.08
NM_002160.2	TNC	0.45
NM_002160.1	TNC	0.44
NM_006290.2	TNFAIP3	0.28
NM_001561.4	TNFRSF9	0.50
NM_033229.2	TRIM15	0.41
NM_020810.2	TRMT5	0.21
NM_001080419.1	UNK	0.50
NM_030570.2	UPK3B	0.39
NM_001078.2	VCAM1	0.15
NM_206923.1	YY2	0.30
NM_145271.3	ZNF688	0.18

Figure S3. Full list of genes downregulated by the S15A-PRMT5 mutation. Fold change is represented as S15A-PRMT5 +IL-1β/WT+IL-1β ≤ 0.5