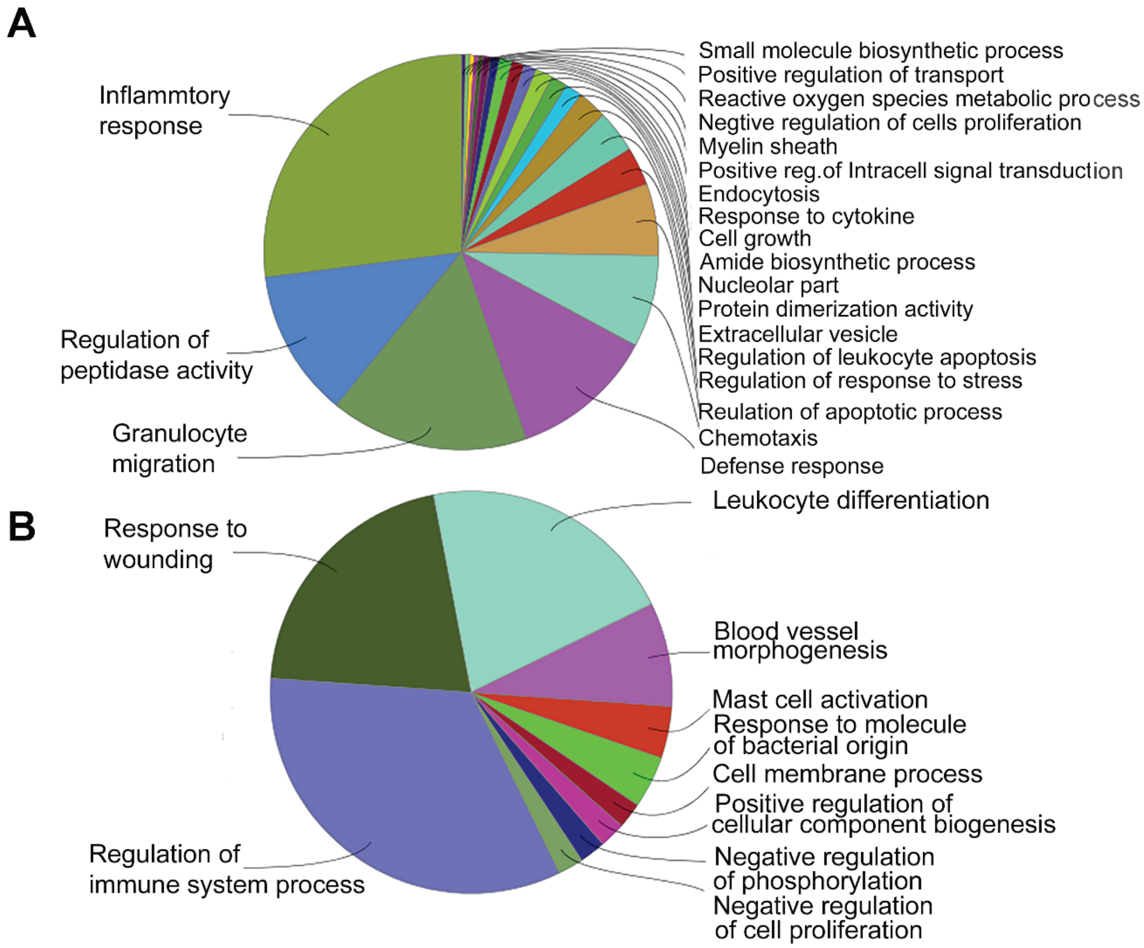
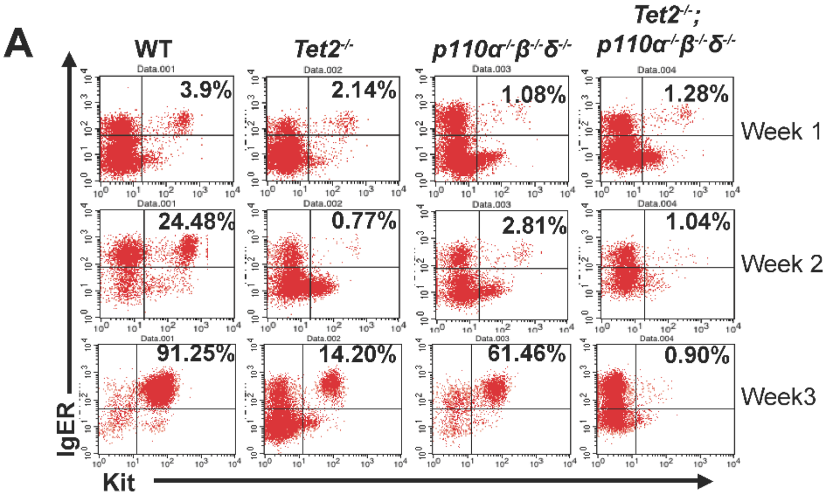
Supplementary Material



Supplementary Figure 1

Supplementary Figure 1: Biological response pathway analysis on RNA-seq obtained from wildtype and TET2 depleted BMMCs. Biological response pathway analysis was performed using Cystoscape-ClueGo gene network analysis tool. Differentially expressed genes with p-value <0.05, >1.5 fold increase **(A)**, and genes with <-1.5 fold decrease **(B)** in *Tet2*$^{-/-}$ cells compared to wildtype mast cells were considered for Cytoscape pathway analysis. Biological processes significantly (gene interactions with p-value 0.001) active in *Tet2*$^{-/-}$ cells compared to wildtype cells are shown in the pie chart (A). Biological processes significantly (gene interactions with p-value 0.001) active in wildtype mast cells but negatively regulated in *Tet2*$^{-/-}$ cells are represented in the pie chart (B).



Supplementary Figure 2

Supplementary Figure 2: Differentiation of BM cells derived from WT, *Tet2*$^{-/-}$, *p110α*$^{-/-}$*β*$^{-/-}$*δ*$^{-/-}$, and *Tet2*$^{-/-}$*:p110α*$^{-/-}$*β*$^{-/-}$*δ*$^{-/-}$ mice. **(A)** BM cells were harvested from WT, *Tet2*$^{-/-}$*, p110α*$^{-/-}$*β*$^{-/-}$*δ*$^{-/-}$, and *Tet2*$^{-/-}$*:p110α*$^{-/-}$*β*$^{-/-}$*δ*$^{-/-}$ mice and mast cells were derived *in vitro*. Cells were harvested and stained with antibodies that recognize KIT and IgE receptor after the indicated weeks followed by flow cytometry. Numbers in the top right quadrant of each dot blot indicate the percentage of BM cells that are double positive for KIT and IgE receptor expression during different times of culture. Representative of three independent experiments is shown.

Supplementary Table 1: Log2 transformed FPKM values for list of mast cell specific genes.

GENE_NAME	WT1	WT2	WT3	TET2_1	TET2_2	TET2_3
tpsb2	4227.541	1899.38	3926.57	2.775661	3.373069	3.422306
cma1	8946.757	5092.47	6749.48	17.036045	9.028786	12.128532
kit	565.3237	280.255	525.859	2.47546	2.060791	2.965605
tpsg1	105.469	71.5844	117.806	0.018415	0.062859	0
il1rl1	564.2405	338.837	468.868	16.29764	18.15447	50.835056
ms4a2	395.1983	287.464	300.28	14.088174	12.912913	46.049496
maob	85.81255	70.6525	73.2082	3.118099	1.613525	13.373298
vwa5a	295.7672	167.907	250.115	10.412058	50.089565	41.323723
cpa3	11566.28	12027	9103.38	413.66855	756.39502	2201.5444
mcpt4	12.70616	15.6556	9.06757	0.037906	0.012597	0
hpgds	25.40108	14.4097	19.4478	0.582445	2.200912	1.777329
gmpr	30.97326	23.3717	20.382	1.000246	5.598278	2.904835
hs3st1	14.08325	20.3878	14.8396	0.095879	0.049515	4.079843
ptpn13	9.518226	5.46605	6.82411	0.046565	0.042335	0.170712
mlph	6.371841	3.32371	7.70163	0.010423	0.057978	0.058204
lxn	28.06297	26.5274	24.3603	3.220151	9.135504	6.716341
cebpa	6.879161	8.95966	6.89603	12.854253	26.699945	43.441555
gdf15	15.73524	4.00878	9.88167	0.137778	3.032506	0.916795
gata1	37.40713	28.4636	28.0565	6.912234	4.878828	12.368827
cebpe	0.168928	1.582	0.11705	17.452652	2.997378	5.098306
mybbp1a	8.261993	9.23766	6.13141	16.973072	22.464828	29.485455
gata2	122.7476	69.2632	120.27	22.590857	22.68656	54.617352
rgs13	4.085579	6.39582	1.43541	0.068687	0.016327	0
dnm3	4.09146	2.24935	4.49431	0.008161	0.027731	0.010273
mpo	2.805589	9.7552	0.873	72.035454	1.345871	22.046629
mitf	14.94305	11.2094	12.7784	0.984529	8.124659	3.29243
sp140	5.184626	5.9777	4.36023	15.668153	14.238983	10.324224
arhgap6	11.83566	8.06909	19.4513	1.705597	5.387648	6.660093
stap1	24.731	28.7275	19.1458	10.243584	3.68591	10.52612
cadm1	2.635895	1.41962	3.45834	0.007755	0.058402	0.024209
pros1	25.86814	12.4394	19.675	0.804553	16.780426	7.898569
nfe2l1	15.16737	13.2499	12.3181	15.350415	40.263805	20.888157
sp110	5.037924	4.072	3.49498	8.385232	7.290154	11.580946
copz2	4.873461	4.56922	2.13402	0.08929	1.091842	0.603388
ppm1h	5.902589	10.5177	13.4255	1.483433	6.205177	4.169242
rab27b	34.83411	37.9218	39.3381	12.484581	10.106756	29.86574
ube2c	1.761392	8.81572	1.27298	12.240773	4.317343	13.085465
lif	32.41653	28.6804	37.7429	6.651708	9.426719	33.408493
nfe2	15.81934	9.36737	11.3734	21.063334	19.069208	19.495028

Supplementary Table 2: List of c-*Myc* transcription factor regulated genes in wildtype and *Tet2*$^{-/-}$ mast cells. FPKM values are indicated in the table.

GENE_NAME	WT1	WT2	WT3	TET2_1	TET2_2	TET2_3
rps6ka2	39.349419	14.076205	26.22188	0.051985	1.378382	0.409534
hspa9	35.896114	41.138832	24.551365	104.230415	272.924286	190.199829
npm1	120.554703	168.286331	82.876045	359.530426	439.483337	612.16803
hmga1	5.347586	5.928294	3.497373	32.212105	36.021149	19.097425
apex1	4.961151	7.826916	3.749486	14.354388	30.589556	29.097912
mgst1	6.950203	8.653933	3.320165	15.551988	60.326633	21.304783
hspd1	24.00625	33.675671	16.826853	59.607105	83.406067	88.514664
bcat1	0.013011	0.143847	0.00869	4.661543	4.4449	6.13234
nme1	21.834595	13.389706	5.98026	21.318218	51.104195	63.390358
id2	143.519852	93.911278	121.244873	11.406699	68.40155	39.410175
gnl3	9.394905	10.112895	6.769429	18.291555	28.531466	28.78474
rpl22	75.85054	114.362526	61.132328	171.86702	223.839508	219.677399
ncl	13.775664	32.456966	11.979703	60.991512	48.460758	79.046486
pa2g4	12.53449	16.487207	10.10388	31.047289	31.122282	38.9128
eno1	75.519997	140.95285	37.058914	207.857422	363.32724	210.073532
dkc1	4.583518	7.010841	3.251347	14.040655	11.64597	24.60947
odc1	9.934567	12.294112	7.776676	16.983675	28.590904	32.683228
srm	5.386822	13.840751	5.818141	18.239454	20.202072	40.500946
impa2	0.909723	1.645439	0.469654	5.931523	6.169487	5.905899
hspe1	33.798023	46.501884	23.371267	43.446262	106.813858	91.121964
rpl32	309.425934	512.843689	237.20192	609.852051	833.240479	1034.05225
eif3c	53.158707	59.693447	38.028057	67.265289	131.995255	103.702644
rpl26	253.259308	333.73288	173.086655	435.938812	471.081421	729.527466
rcc1	1.932782	3.246695	1.394367	4.817006	8.067264	9.781575
rps16	148.409195	216.865189	133.115082	219.132019	420.317017	357.124146
mrto4	4.051436	6.051312	3.058061	9.847059	12.874236	15.210299
cct5	47.134079	62.393803	33.682579	71.726875	103.517654	117.739716
rfc2	100.424637	72.561897	80.357475	9.096663	31.890432	63.675297
cstb	40.318695	41.849377	25.1777	27.021381	194.72644	79.921951
ppid	7.148161	7.368445	5.430848	15.574816	14.213568	20.420465
ppat	3.199576	3.649847	1.976511	6.790802	6.782664	11.257791
uprt	2.371649	2.689075	2.428601	3.622855	10.974696	8.89535
tfrc	12.987247	14.810143	9.807862	7.767103	52.496861	37.819427
tyms	2.129248	5.515958	1.490965	7.191824	11.81252	7.438531
rps5	232.747955	296.844543	203.603867	203.060898	580.711182	582.246094
timm10	4.060412	4.229712	3.035606	4.772413	14.118529	10.377941
prep	6.74133	7.82177	5.217824	9.822432	21.049515	15.362393
psmg1	5.303575	5.490014	3.62417	7.833306	10.692748	14.404034
rpl19	441.387299	518.103882	308.927979	441.288788	784.169617	962.557007
smn1	2.7895	3.184116	2.958815	6.90914	8.289955	7.365903
mettl1	0.37642	1.165568	0.362905	2.611811	4.900576	4.405966

rpl5	393.090759	509.224854	294.984497	387.518982	793.729675	879.630432
rpl27a	138.541397	160.103973	101.241234	121.544159	258.432556	286.714905
rps17	212.727417	291.216705	138.923965	254.268799	420.033966	424.899658
eif4e	8.82324	9.273637	4.825171	9.860579	20.383547	17.912714
shmt1	0.837545	1.487971	0.758242	4.836191	1.93235	5.033238
pink1	46.434666	24.242989	32.283882	5.826118	21.705904	24.482595
eif4a1	76.42128	122.104195	77.475662	111.222816	150.690552	200.06871
rps20	270.932556	315.877991	33.026726	249.886276	628.712769	640.515686
eif2s1	14.944627	18.793022	10.642443	18.341728	28.509634	30.599789
rpl9	102.050827	92.577766	70.509697	83.204918	169.14856	146.586594
ube2c	1.761392	8.815722	1.272975	12.240773	4.317343	13.085465
mthfd1	2.915982	5.1794	2.393052	5.280927	7.464284	9.485664
nme2	65.414131	93.319603	42.229214	44.691055	251.688156	112.263596
rpl27	120.474159	122.454491	92.053879	72.282753	225.088776	256.152313
exosc8	7.089818	9.049405	4.972477	15.440249	11.406604	11.26676
snrpb	42.562218	30.014606	30.798819	26.846123	83.705368	53.671585

Supplementary Table 3: Oligo Sequences for QRT-PCR primers

Primer Name	**Oligo Sequence**
β-actin f:	GTATGGAATCCTGTGGCATC
β-actin r:	AAGCACTTGCGGTGCACGAT
Gata2 f:	ACGAGGTGGATGTCTTCTA
Gata2 r:	GCTGTGCAACAAGTGTGGTC
Gata1 f:	CTTTCCCAGTCCTTTCTTCTC
Gata1 r:	GTTGCTCCACAGTTCACACAC
c-Myc f:	TTCCTCGGACTCGCTGCT
c-Myc r:	CCACAGACACCACATCAATTTC
Pu.1 f:	GGATCTGACCAACCTGGAG
Pu.1 r:	CTGCCCTAGTAGACGAAGGAG
Kit f:	GGCCTCACGAGTTCTATTTACG
Kit r:	GGGGAGAGATTTCCCATCACAC
Cebpa f:	GTGGACAAGAACAGCAACGAG
Cebpa r:	TCACTGGTCAACTCCAGCAC
Mitf f:	GTG CAG ACC CAC CTG GAA AAC
Mitf r:	AGT TAA GAG TGA GCA TAG CCA TAG
Tpsb2 f:	GCTGGGGCGACATTGATA
Tpsb2 r:	TGGGAACCTTCACTTGCTTC
Tpsg1 f:	ACTGTTTCTGGCTGTTTCTGG
Tpsg1 r:	CTTGTGCAGACGGAGGCTA
Cma1 f:	TCTTCTTACTCTTCATCTGCTGCT
Cma1 r:	CCGTGCCTCCAATGATCT
Cpa3 f:	GCTATTAATTCCTTATGGCTACACATT
Cpa3 r:	GTGGCAATCCTTGCAACTTT
Mcpt4 f:	CCATGACATCATGTTGCTGAA
Mcpt4 r:	GCTTGATAAAGTCAGAAGGACGA
Tet1 f:	GGAATGAGTTCTGAAGGAAGTGACGTG
Tet1 r:	CCAGCAACTTCTTCATATTCCACCTGA
Tet2 f:	AACCTGGCTACTGTCATTGCTCCA
Tet2 r:	AGCAGAGAAGTCCAAACATGCAGTG
Tet3 f:	ACAAGGACCAACATAACCTCTACAATGG
Tet3 r:	CCACTACTGACCTTGGCGTTCTG
Eno1 f:	GCCCTAGAACTCCGAGACAA
Eno1 r:	CAGAGCAGGCGCAATAGTTT
Odc1 f:	TCCCTCAACCCTTGACTCC
Odc1 r:	TTGACTGCCGATGTTGTATGA
Bcat1 f:	ATTCTCCCAGGAGTGACCAG
Bcat1 r:	TGTCTCTCACATACCTTAAACTCACC
Npm1 f:	GCCTCAGAACTACCTTTTCGTG
Npm1 r:	GCTTCTGCCTCTACGATGTGT
Id2 f:	GACAGAACCAGGCGTCCA

Id2 r:	AGCTCAGAAGGGAATTCAGATG
Shmt1 f:	GAGGGATATCCAGGCCAAA
Shmt1 r:	CCTGTAATGCACGCTTCTGA
Npm1 f:	GCCTCAGAACTACCTTTTCGTG
Npm1 r:	GCTTCTGCCTCTACGATGTGT
Junb f:	CCACGGAGGGAGAGAAAATC
Junb r:	AGTTGGCAGCTGTGCGTAA
Fos f:	GGGACAGCCTTTCCTACTACC
Fos r:	AGATCTGCGCAAAAGTCCTG
Pten f:	GATTACAGACCCGTGGCACT
Pten r:	ATCACCACACACAGGCAATG