

Supplementary Materials

Table S1. Direct correlation between microarray data and TaqMan q-PCR data on the association between differential gene expression levels and IgE-dependent activation responses among different human mast cell responders. Human mast cell cultures derived from normal donors were classified as High, Average or Low responders according to their responses to anti-IgE stimulation. RNA samples derived from unstimulated mast cell cultures from each of the 3 responder groups, respectively, were analyzed by microarray ($n = 60$ for mast cell cultures) and TaqMan q-PCR ($n = 20$ for each selected gene).

Gene	Microarray Data Changes in gene expression levels in High responders compared with those in Low responders	TaqMan q-PCR Data Correlation curves between gene expression levels and IgE-dependent cell activation ($Y =$ slope of the fitted trend line)
AKAP12	High \uparrow vs Low	3.647
CALB2	High \uparrow vs Low	4.470
DPP44	High \downarrow vs Low	-7.501
FCGR1A	High \downarrow vs Low	-0.114
FOXF1	High \uparrow vs Low	39.101
GADD45B	High \downarrow vs Low	-24.602
IL13RA1	High \uparrow vs Low	4.006
IRF1	High \downarrow vs Low	-19.727
ITM2C	High \uparrow vs Low	12.698
NELL2	High \uparrow vs Low	4.523
PTGDR	High \downarrow vs Low	-1.751
SIGLEC8	High \downarrow vs Low	-12.877
SOCS2	High \downarrow vs Low	-20.167
SPTLC3	High \downarrow vs Low	-11.509
TMEM255B	High \uparrow vs Low	14.381

Fig. S1

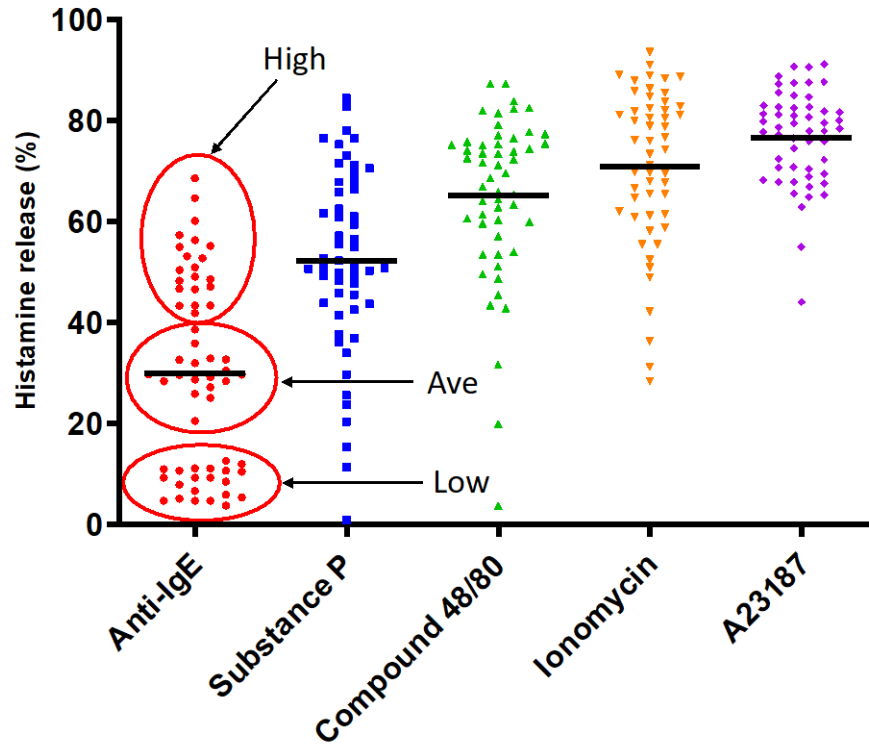


Figure S1. Anti-IgE induced degranulation responses exhibited by human mast cell cultures that were selected from High ($n = 22$), Average ($n = 17$), and Low ($n = 21$) responder groups for microarray gene expression analysis. Each dot of different colors shown in this figure represents a single normal individual donor.