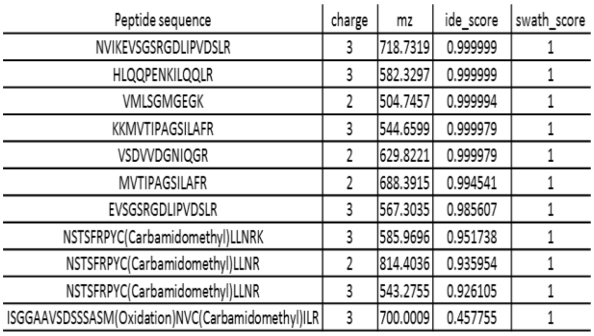
Figure S2

A



Peptide sequence	charge	mz	ide_score	swath_score
NVIKEVSGSRGDLIPVDSLR	3	718.7319	0.999999	1
HLQQPENKILQQLR	3	582.3297	0.999999	1
VMLSGMGEGK	2	504.7457	0.999994	1
KKMVTIPAGSILAFR	3	544.6599	0.999979	1
VSDVVDGNIQGR	2	629.8221	0.999979	1
MVTIPAGSILAFR	2	688.3915	0.994541	1
EVSGSRGDLIPVDSLR	3	567.3035	0.985607	1
NSTSFRPYC(Carbamidomethyl)LLNRK	3	585.9696	0.951738	1
NSTSFRPYC(Carbamidomethyl)LLNR	2	814.4036	0.935954	1
NSTSFRPYC(Carbamidomethyl)LLNR	3	543.2755	0.926105	1
ISGGAAVSDSSSASM(Oxidation)NVC(Carbamidomethyl)ILR	3	700.0009	0.457755	1

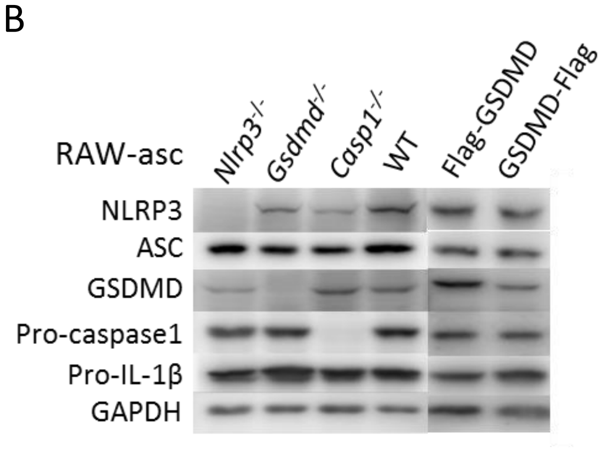


Figure S2. Identification of GSDMD by MS and characterization of RAW-asc derived cells. A. Peptide information of GSDMD identified by quantitative MS analysis. Peptide sequences, modifications, charges and mz were showed. Ide_score means iprophet probability, and swath_score means the probability of the peptide existing in the SWATH-MS file. The time-dependent increase in the amounts of these peptides in NLRP3 immuno-complex was revealed by Group-DIA and the data of xxxxxxx peptide is showed in Fig. 1A. B. Gene deletion of *Nlrp3*, *Casp1, Gsdmd* in RAW-asc cells and reconstitution of GSDMD expression in *Gsdmd*$^{-/-}$ RAW-asc cells were confirmed by immunobloting with corresponding antibodies.