Soluble Siglec-14 glycan-recognition protein is generated by alternative splicing and suppresses myeloid inflammatory responses

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Supporting information

Included materials:

Legends for Table S1, Table S2, and Table S3 (Tables are provided separately as Excel files)

Table S1. List of proteins identified by proximity labeling of FLAG-Siglec-14/THP-1, labeled with anti-FLAG-HRP and biotin-tyramide.
Proteins were identified by LC-MS^2 and quantified with MaxQuant software. Proteins that were identified only as post-translationally modified form(s), identified in the reversed database, or considered possible contaminants, were excluded from the list. Subsequently, the proteins that fulfilled all the following criteria were selected: (1) proteins whose abundance in the sample purified from labeled FLAG-Siglec-14/THP-1 was 10 times or more that from labeled EV/THP-1; (2) proteins identified with three or more unique peptides; and (3) proteins that are known or predicted to be membrane proteins.

Table S2. Summary of transcriptome analysis data with Affymetrix DNA array.
Human monocyte-derived macrophages were incubated in the presence or absence of recombinant soluble Siglec-14, and purified RNA samples from these cells were subjected to transcriptome analysis using GeneChip Human Genome U133 Plus 2.0 array (Affymetrix), as described in Experimental Procedures. Transcripts that fulfilled all the following criteria were selected: (1) transcripts with gene symbols; (2) transcripts that showed hybridization signals in both samples; (3) transcripts whose abundances were changed by a factor of 2 or more (i.e., log2 ratio > 1 or < -1) in the cells treated with soluble Siglec-14. Literature information was sought in PubMed database using the following query: "macrophage AND (M1 OR M2) AND [gene symbol]", and key statements from relevant papers were quoted.

Table S3. Sequences of primers and probes used for PCR and quantitative reverse transcription-PCR (qRT-PCR).