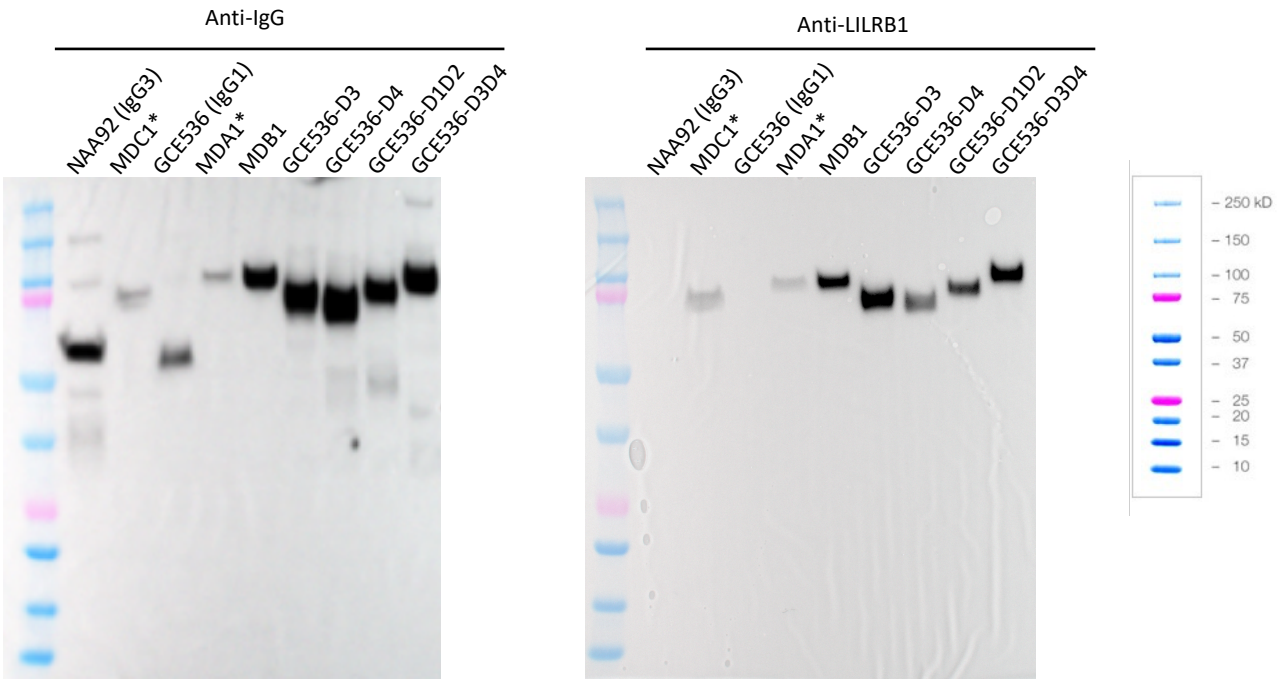
Supplementary Figure 1



Supplementary Figure 1. Original source images for western blot analysis of naturally occurring LILRB1-containing antibodies. MDC1 and MDA1 tested as culture supernatants and MDB1 tested as recombinant antibody. Shown are also IgG1 and IgG3 isotype control antibodies (GCE536 and NAA92), as well as recombinant antibodies carrying different LILRB1 domains inserted in the GCE536 VH-CH1 elbow (representative of n = 2 independent experiments).

Supplementary Table 1 | *V* gene and insert usage of representative LILRB1-containing antibodies

Donor	mAb	Isotype		Heavy chain VDJ genes (% identity to GL)					Light chain VDJ genes (% identity to GL)				Inserted LILRB1 domain	LILRB1 mutations (% identity to GL)
A	MDA1	IgG1	λ	VH3-74	(92.4)	D2-21	JH4	(87.5)	VL1-51	(95.4)	JL2	(86.1)	D3-D4	(100)
B	MDB1	IgG4	λ	VH2-5	(90.7)	D5-24	JH4	(87.5)	VL3-25	(89.6)	JL1	(86.8)	D3-D4	(100)
C	MDC1	IgG3	κ	VH7-4	(94.8)	D4-23	JH3	(94)	VK4-1	(91.9)	JK2	(91.9)	D3	(99)
C	MDC2	IgG3	κ	VH7-4	(94.8)	D4-23	JH3	(94)	VK3-20	(95.8)	JK1	(94.7)	D3	(99)

Isotype and *V(D)J* gene usage of heavy chain and light chain of mAbs containing LILRB1 domain/domains in the switch region. GL, germline.

Supplementary Table 2 | Data Collection and Refinement Statistics for cryoEM and X-ray crystallography

a

	MDB1: RIFIN-V2 EMD-22879 PDB-7KHF
Data Collection	
Microscope	FEI Titan Krios
Voltage (kV)	300
Electron dose ($e^-/Å^2$)	70.72
Detector	Gatan K2 Summit
Pixel Size (Å)	1.083
Defocus Range (μm)	-0.1 to -3.0
Magnification	81000
Reconstruction	
Software	cryoSparc
Particles	390908
Symmetry	C1
Box size (pix)	320
Resolution (Å) (FSC0.143)[$]	3.5
Refinement (Phenix) [#]	
Protein residues	3855
Chimera CC	0.85
Resolution ($FSC_{0.5}$)	3.9
EMRinger Score	2.85
R.m.s. deviations	
Bond lengths (Å)	0.008
Bond angles (°)	1.02
Validation	
Molprobity score	1.79
Clash score	7.03
Favored rotamers (%)	93.6
Ramachandran	
Favored regions (%)	94.08
Disallowed regions (%)	0

b

	LILRB1-D3D4:RIFIN.V2 (PF3D7_1373400)
PDB accession code	7KFK
Data collection	
Wavelength	1
Resolution range (Å)	50 - 2.65 (2.70 - 2.65)
Space group	P 4_2 2_1 2
Cell dimensions	
a, *b*, *c* (Å)	111.0 111.0 152.1
α, β, γ (°)	90, 90, 90
Unique reflections	28673 (1410)
Multiplicity	21.2 (16.9)
Completeness (%)	99.8 (99.9)
I / σI	29.9 (2.1)
Wilson *B*-factor	62.29
R_{merge}	0.200 (1.306)
$CC_{1/2}$	0.998 (0.896)
Refinement	
Reflections used in refinement	28615 (2663)
Reflections used for R-free	1415 (125)
R_{work}	0.23 (0.38)
R_{free}	0.27 (0.44)
Number of non-hydrogen atoms	5182
macromolecules	5009
ligands	119
solvent	54
Protein residues	679
RMS(bonds) (Å)	0.005
RMS(angles) (°)	0.88
Ramachandran favored (%)	97.74
Ramachandran outliers (%)	0.00
Average *B*-factor ($Å^2$)	64.67
macromolecules	63.83
ligands	103.85
solvent	55.61

*Values in parentheses are for highest-resolution shell.

$ Resolutions are reported according to the FSC 0.143 gold-standard criterion.
& The numbers in parenthesis are resolution values calculated using cryoSparc
# Statistics are reported for the protein residues within the complex excluding the Ab constant domains.

Supplementary Table 3 | Primers for detection of LILRB1 inserts

Name	Content	Primer 5' to 3'
MOC19	5' primer for MGAA2 V region	CAGGTGCAGCTGGTGCAATCTGGG
MOC20	5' primer for MGAA2 V region, internal to MOC19	CCTTCAGTGCCTATGCTATAAATTGG
MOC21	5' primer for MGAA2 V region, internal to MOC20	GTGCAAGGGATCCTATTAGACCTCG
MOC22	5' primer for MGAB11 V region	GAGGTCCAGCTGGTGGAGTCC
MOC23	5' primer for MGAB11 V region, internal to MOC22	CCTGTGTAGTCTCTGGATTCACC
MOC24	5' primer for MGAB11 V region, internal to MOC23	GACGCTGGTCACGGACTCCTTA
MOA120	5' primer for LILRB1 exon 7	CTAAGAAGCCATCACTCTCAGTGCAGC
MOA120.5	3' primer for LILRB1 exon 7	GCTGCACTGAGAGTGATGGCTTCTTAG
MOA121	5' primer for LILRB1 exon 7	CTACGGTGCACACAACCTCTCCTCCGAG
MOA121.5	3' primer for LILRB1 exon 7	CTCGGAGGAGAGGTTGTGTGCACCGTAG
MOA122	5' primer for LILRB1 7-8 intron	GTTCAGTCAGGGACCCAGGCTCCGCAC
MOA122.5	3' primer for LILRB1 7-8 intron	GTGCGGAGCCTGGGTCCCTGACTGAAC
MOA123	5' primer for LILRB1 7-8 intron	GGGGAGGTGTCAGCTCAGAGCAAGGTG
MOA123.5	3' primer for LILRB1 7-8 intron	CACCTTGCTCTGAGCTGACACCTCCCC
MOA124	5' primer for LILRB1 exon 8	GACAGTTCTATGACAGAGTCTCCCTCT
MOA124.5	3' primer for LILRB1 exon 8	AGAGGGAGACTCTGTCATAGAACTGTC
MOA125	5' primer for LILRB1 exon 8	GAATTCCCCATGGGTCCTGTGACCTCAG
MOA125.5	3' primer for LILRB1 exon 8	CTGAGGTCACAGGACCCATGGGGAATTC
MOA126	5' primer for VH2-5 Leader Exon 1	ATGGACACACTTTGCTCCACGCTCCTG
MOA127	5' primer for VH2-5 Leader Exon + Intron, internal to MOA126	CATGTGAGTGCTGTGGTCAGGGACTCC
MOA128	5' primer for MGZ4 VH2-5 difference, internal to MOA127	CTGGTCCTACGCTGGTGGAACGCACAC
MOA31	3' primer for IgG, Cg, -288bp	TCTTGTCCACCTTGGTGTTGCT
MOA32	3' primer for IgG, Cg, -95bp, internal to MOA45, MOA31	GTAGTCCTTGACCAGGCAGC