

Figure S1. Amino acid alignment of the IRGM proteins

Hs_IRGM	1	MNVEKASADGNLPEVTSNIKETLKIIVSRTPVNIITMAGDSGNGMSTFFISALRNTGHEGKAS
Ptr_IRGM	1	MNVEKASADGNLPEVTSNIKETLKIIVSRTPVNIITTA GHSGNGMSTFFISALRNTGHEGKAS
Ggo_IRGM	1	MNVEKASADENLPEVTSNIKETLKIIVSRTPVNIITMAGDSGNGMSTFFISALRNTGHEGKAS
PPY_IRGM	1	MSVEKASADGNLPEVTSDIKETLKIIVSRTPVNIITMAGDSGNGMSTFFISALRNTGHEGKAS
Cja_IRGM	1	MNVERASADGDLPEVVSATKESLKVIFRTPVNIITMAGDSGNSISTFFISALQIAGHEAKAS
Rh_IRGM	1	MNVEKALVGGNLPYASATNETLKIIVSRTPVNIITMAGDSGSGMNTFFISALRNTGHEGKPS
Pph_IRGM	1	MNGDKALISGNLPYEASATKETLKIIVSSTFFCIAMAE NSGSGMNTFFICALRNTGHEGKPS
IRGM9	1	MSIEKAIAGGNLPELVSAVRETVMVSRTPVNVAVT GDSGNGMSTFFINALRNIGHEEEAS
IRGM8	1	MSIEKAIAGGNLPELVSAIRETVKMSRTPVNVAVT GDSGNGMSTFFINALQNIIGHEEEAS
IRGM7	1	MSIEKAIAGGNLPEVVSATRESLKMASRTPVNVAVT GNSGNDMSTFFINPLRNIGHEEEAS
IRGM5	1	TNIEKALGDGKLLLEVSMIRETLETVSSAPVSIAVT GDSGNGMSTFFINALREIGHDEKDS
IRGM6	1	INIEKALGDGKLLLEVSMIRETLETVSSAPVSIAVT GDSGNGMSTFFINALREIGHDEKDS
IRGM4	1	MNIEKALGEGKLLDMVSVRETLETASSVPVSIAVT GDSGNGMSTFFINALRKHGHNEEDS
Irgm2	1	KRIETAVKEGEVVKVVSIVKEIITQNVSRNKIITAVT GDSGNGMSTFFINALRLIGHEEKDS
Irgm3	1	EDIGKAVTEGNLQKVIIGVKDEIQSKSRYRVIITAVT GDSGNGMSTFFINALRFIGHEEEDS
Irgm1	1	RSTERALREGKLLLELVYGIKETVATLSQIPVSIITVIT GDSGNGMSTFFINALRVIGHDEDAS

GXXXXGMS
G1

Hs_IRGM	61	PPTGLVKATQRCASYFS-SHFSNVVLWDLPGTGSATTTLENYLMEMQFNRYD-FIMVASA
Ptr_IRGM	61	PPTGLVKATQRCASYFS-SHFSNVVLWDLPGTGSATKTTLENYLMEMQFNRYD-FIMVASA
Ggo_IRGM	61	PPTGLVKATQRCASYFS-SHFANVVLWDLPGTGFATKTTLENYLMEMQFNRYD-FIMVASA
PPY_IRGM	61	PRTGLVKTQRCASYFS-SHFSNVVLWDLPGTGSATKTTLENYLMEMQFNQCD-FIMVASA
Cja_IRGM	61	PPTGLVKATQRCASYFS-SRFPNVVLWDLPGTGSATKTTLENYLMEMQFNQYD-FIMVASA
Rh_IRGM	61	PPTGLVKATQRCAPYLS-SHFNVVLWDLPGTGSATKTTLENYLMEMQFNQYD-FIMVASA
Pph_IRGM	61	PPTGLVTPQKCAPYFS-SFFPHVPRWDLPGTWSANYCLCNHYHMEMRVHOYD-FILGASA
IRGM9	61	APVGVLKTQTQTHACYLS-PHFPNVVLWDLPGTVAASLENYATEMQFSRYDFIIITASE
IRGM8	61	APVGVLKTQTQTRACYLS-PHFPNVELWDLPGTECAAQSLNYSMEMQFSRYDFIIITASE
IRGM7	61	VPVAVLKTQTQTRACYLS-PHFPNVVLWDLPGTECAAQSLNYSMEMQFSRYDFIIIVSE
IRGM5	61	APTGVVRTTQVPTCYSS-SHFPMELWDLPGTGTQSLNYLEKIHFSQYDLFIIITASE
IRGM6	61	APTGVVRTTQVPTCYSS-SHFPMELWDLPGTGTQSLNYLEKIHFSQYDLFIIITASE
IRGM4	61	APTGVVRTTQIPTCYSF-SDIPNVELWDLPGTGAATQNLLETYLEEMQFSRYDLFIIITASE
Irgm2	61	APTGVVRTTQKPTCYFS-SHFPMELWDLPGTGATAQSVESYLEEMQISTYDLIIIVASE
Irgm3	61	APTGVVRTTKKPCYSS-SDSHFPYVELWDLPGTGATAQSVESYLEEMQISTYDLIIIVASE
Irgm1	61	APTGVVRTTKTRTEYSS-SHFNVVLWDLPGTGATAQTVEDYVEEMKFSYDCLFIIITASE

DXXG
G3

Hs_IRGM	119	QFSMNHVMLAKTAEDMGKKFYIVWTKLMDLSTGALPEVQLLQ-IRENVLENL
Ptr_IRGM	119	QFSMNHVMLAKTAEDMGKKFYIVWTKLMDLSTGALPEVQLLQ-IRENVLENL
Ggo_IRGM	119	QFSMNHVMLAKTPEDMGKKFYIVWTKLMDLSTGALPEVQLLQ-IRENVLENL
PPY_IRGM	119	QFSMNQVMLAKTAEDMGKKFYIVWTKLMDLSTGALPEVQLLQ-IRENVLENL
Cja_IRGM	119	QFSMNHVILAKTIEDMGKKFYIVWTKLMDLSTGALPEVQLLQ-IRENVLESL
Rh_IRGM	119	QFSMNHVMLAKTIEDMGKKFYIVWTKLMDLSTGALPEVQLLR-IRENVLENL
Pph_IRGM	119	QFIMIHVMLDVTTDDMGYKFYIVWTSLDMDLSTGALPDVQLLH-IRLNVLENL
IRGM9	120	QFSMNHVMLAKTVEDMGKQFYIVWTKLMDLNTSALPKGQLGKIIRENILENL
IRGM8	120	QFSMNHVMLAKTVEDMGKHFYIVWTKLMDLNTSALPKGQLRQIIRENILENL
IRGM7	120	QFSMNHVILAKTMDMRKHFYIVWTKLMDLNTSALPEGQLLQIIRENILENL
IRGM5	120	QFSMNLVKKLVKAIQRQGKRFYIVWTKLDRDLSTRVLPPEEQVLQNIWENIQETL
IRGM6	120	QFSMNLVKKLVKAIQRQGKRFYIVWTKLDRDLSTRVLPPEEQVLQNIWENIQETL
IRGM4	120	QFSMNLVKKLVKSIQGGKRFYIVWTKLDRDLSTCVLSEEQLLRNIRENIRETL
Irgm2	120	QFSINHVKLAITMQRMKRFYIVWTKLDRDLSTSTFPEPOLLQSIQRNIRESL
Irgm3	121	QFSINHVKLAITMQRMKRFYIVWTKLDRDLSTSTFPEPOLLQSIQRNIRENL
Irgm1	120	QFSINHVKLSKI IQSMGKRFYIVWTKLDRDLSTSVLSEVRLLONIQENIRENL

TKXD
G4