

a.			
AGERv7	-----TRRGGANCR-----LCGRIRAGNSSPGDGRPGDSR----	303	
AGERv5	WPPIPATGPRKAVLSASAS---SNQARRGQLQVRGLIKSG-----	321	
AGERv8	-----NQARRGQLQVRGLIKSG-----	291	
AGERv3	VLILPEIGPDQGTYSVATHSSHGPQESRAVSISIIPEGEEPTAGSVGSGSLGTLALA	330	
AGERv1	VLILPEIGPDQGTYSVATHSSHGPQESRAVSISIIPEGEEPTAGSVGSGSLGTLALA	344	
AGERv2	VLILPEIGPDQGTYSVATHSSHGPQESRAVSISIIPEGEEPTAGSVGSGSLGTLALA	360	
AGERv4	VLILPEIGPDQGTYSVATHSSHGPQESRAVSISIIPEGEEPTAGEGFD---KVREA	356	
AGERv6	VLILPEIGPDQGTYSVATHSSHGPQESRAVSISIIPEGEEPTAGEGFD---KVREA	340	
AGERv9	VLILPEIGPDQGTYSVATHSSHGPQESRAVSISIIPEGEEPTAGEGFD---KVREA	340	
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b.			
IFNGR1v2	-----MLLKSPEN--SLLQFQFKYGVPTPTNVTIESYNMNPVYWEYQIMPQVPVFT	50	
IFNGR1v1	MALLFLLPLVMQVSRAMETADLGPSSVPTPTNVTIESYNMNPVYWEYQIMPQVPVFT	60	
IFNGR1v3	-----MNPVYWEYQIMPQVPVFT-----	19	

d.			
IFNGR2v1	MRPTLLWSLLLLLVFAAAAAAPPAQLTLETYQEWNCNSAATHDPLSQLPAPQHPKIRLY	60	
IFNGR2v2	MRPTLLWSLLLLLVFAAAAAAPP-----DPLSQLPAPQHPKIRLY	41	

e.			
IL17RcV1	MPVPWFLLSLALGRSPVVLSELERLVGPQDATHCSPVSELPWGEERLVQFLAQQLSLA	60	
IL17RcV9	MPVPWFLLSLALGRSPVVLSELERLVGPQDATHCSP-----	35	

f.			
IL17RcV1	PVTAATARTALSGLSGADGRREERGRKSWVCLSLGGSGNTEPQKGLSCLRWSDILCL	120	
IL17RcV9	-----GLSCLRWSDILCL-----	49	

IL17RcV1	PGDIVPAPGVPVLAHLQTELVLRQKQETDCDCLRVAVHLAVHNEEPEDEKFGGAA	180	
IL17RcV9	PGDIVPAPGVPVLAHLQTELVLRQKQETDCDCLRVAVHLAVHA-----	94	

IL17RcV1	DSGVVEPRNASLQAQVLSFQAYPTARCVLLVQVPAALVQFGVSGVSWYDCFEAALGS	240	
IL17RcV9	-----SLQAQVLSFQAYPTARCVLLVQVPAALVQFGVSGVSWYDCFEAALGS	144	

IL17RcV1	EVR IWSYTPQRYEKLNHTQQLPDCRGLVWNSIPSCWALPWLNVSDAGDNVHLVNVSE	300	
IL17RcV9	EVR IWSYTPQRYEKLNHTQQLP-----ALPWLNVSDAGDNVHLVNVSE	189	

g.			
MYD88v5	IRQLETQADPTGRLLDAAWQGRPGASVGRLLLELLTKLGRDDVLELGPISGAAGMMLSLM	120	
MYD88v2	IRQLETQADPTGRLLDAAWQGRPGASVGRLLLELLTKLGRDDVLELGPISGAAGMMLSLM	120	
MYD88v3	IRQLETQADPTGRLLDAAWQGRPGASVGRLLLELLTKLGRDDVLELGPISGAAGMMLSLM	108	

MYD88v5	ITCRARNVTSRPNLHSAASLQVPIRS-----	146	
MYD88v2	QEEAEKP---LQVAADVSSPRTAELAGITLDDPLGHMPERFDAFICVCPDIOFVQE	177	
MYD88v3	-----IGHMPERFDAFICVCPDIOFVQE-----	132	

MYD88v5	MIRQLEQTNVRLKLCVSDRDLVPGTCVWSIASLEIEKRCRRMNVVSDVYLSQKECDFQT	146	
MYD88v2	MIRQLEQTNVRLKLCVSDRDLVPGTCVWSIASLEIEKRCRRMNVVSDVYLSQKECDFQT	237	
MYD88v3	MIRQLEQTNVRLKLCVSDRDLVPGTCVWSIASLEIEKRCRRMNVVSDVYLSQKECDFQT	192	

MYD88v5	-----	146	
MYD88v2	KFALSLSPGAHQKRLIPIKYKAMKKEFPSILRFITVCDYTNPCTKSWFTRLAKALSPL	296	
MYD88v3	KFALSLSPGAHQKRLIPIKYKAMKKEFPSILRFITVCDYTNPCTKSWFTRLAKALSPL	251	

h.			
PDGFRv1v2	DIQRSLYDRFASYKKSMLGWAGVGTGRCQRLNSHAQAQALLAGRPLLSGLP-----	807	
PDGFRv1v3	DIORSLYDRFASYKKSMLDSEVKNL-----LSDDNSE---GLTLDDLSTFYOVARG	818	

PDGFRv1v2	-----	807	
PDGFRv1v3	MEFLASKNCVHRDLAARNVLLAQKIVKICDFGLARDIMHDSNVVSKGSTFLPVKWMAP	878	

i.			
PDGFRv1v2	MRLPGAMPALALKEGELLSSLLLELPQISQGLVWTPPGPELVNVSSTFVTCSGSAPV	60	
PDGFRv1v3	-----	0	

PDGFRv1v2	VWERMSEPPQEMAKAQDGTSSVLTNLTLGLDTGEYFCHNDSRGLTDERKRLYIFV	120	
PDGFRv1v3	---MSQEPPEMAKQDGTSSVLTNLTLGLDTGEYFCHNDSRGLTDERKRLYIFV	56	

PDGFRv1v2	PDPTVGLFNDAAEELFIFLTEITEITIPCRVTDPLVLTLEHKKGDVALPVPYDHRGFS	180	
PDGFRv1v3	PDPTVGLFNDAAEELFIFLTEITEITIPCRVTDPLVLTLEHKKGDVALPVPYDHRGFS	116	
	-----MITNVAFLVSLRTEATSAPK-----	21	
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PDGFRv1v2	GIFEDRSYICKTTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCIVIGN	240	
PDGFRv1v3	GIFEDRSYICKTTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCIVIGN	176	
	--LGTGRWILMPTMSTDSRVSPLSGLMRSVSSINVSNAVQTVVRQGENITLMCIVIGN	79	
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j.			
TGFB1v1	TTDKVIHNSMCIAEIDLIPDRPFVPCAPSSKTSVTTTYCCNQDHCNIEIPLTT---VK	116	
TGFB1v3	TTDKVIHNSMCIAEIDLIPDRPFVPCAPSSKTSVTTTYCCNQDHCNIEIPLTTGPFVSK	120	
TGFB1v2	TTDKVIHNSMCIAEIDLIPDRPFVPCAPSSKTSVTTTYCCNQDHCNIEIPLTT-----	114	

TGFB1v1	SSPGLGPVLEAAVIAGPVCVCSILMLMVIYCHNRTVIHHRVNEEDPSLDRPFISEGTT	176	
TGFB1v3	SSPGLGPVLEAAVIAGPVCVCSILMLMVIYCHNRTVIHHRVNEEDPSLDRPFISEGTT	180	
TGFB1v2	SSPGLGPVLEAAVIAGPVCVCSILMLMVIYCHNRTVIHHRVNEEDPSLDRPFISEGTT	114	

TGFB1v1	LKDLIYDMTTSGSGSLPLLQRTIARTIVLQESIGKGRFGEVWRGKWRGEEVAVKIFSS	236	
TGFB1v3	LKDLIYDMTTSGSGSLPLLQRTIARTIVLQESIGKGRFGEVWRGKWRGEEVAVKIFSS	240	
TGFB1v2	-----GLPLLQRTIARTIVLQESIGKGRFGEVWRGKWRGEEVAVKIFSS	159	

k.			
TGFB2v1	MGRGLLRGLWPLHIVLWTRIASTIPPHVQKSDVEMEAQKDEIICPCNRTAHLRHINND	60	
TGFB2v2	MGRGLLRGLWPLHIVLWTRIASTIPPHVQK-----VNIND	35	

Figure S1. Splicing isoform amino acid alignments of target genes studied. Confirmed RefSeq sequences (NM_XXXX) were aligned using the program Clustal X.