

Appendix 2. Additional evolutionarily conserved region fluorescence data, genomic fragment locations, and primer sequences.

Fluorescence Data:

Gene	ECR Name	Size (bp)	Genomic Location (mm8 or rn4)	eGFP \ddagger	MFI \ddagger
CD44 (R)	CD44M1 @	809	chr2:102702500-102701692	1.08	1.22
Mus (mm8)	CD44M2 (CD44 UTR, App. 1)	313	chr2:102702500-102702188	1.78	1.55
NM_009851	CD44M3 (CD44 ECR, App. 1)	271	chr2:102703667-102703397	nd	nd
CD44 (R)	CD44R1 @	461	chr3:88110547-88110087	nd	nd
Rat (rn4)	CD44R2 #	191	chr3:88110547-88110357	2.01	1.53
NM_012924	CD44R3 #	133	chr3:88110787-88110655	nd	nd
	CD44R4 #	275	chr3:88111610-88111336	0.78	0.97
	CD44R5 #	149	chr3:88112907-88112759	nd	nd
	CD44R6 #	109	chr3:88113048-88112940	nd	nd
	CD44R7	360	chr3:88023302-88022943	nd	nd
	CD44R8	499	chr3:88022170-88021672	nd	nd
	CD44R9	171	chr3:88018602-88018432	nd	nd
	CD44R10	534	chr3:88114796-88114263	nd	nd
	CD44R11	376	chr3:88118124-88117749	nd	nd
	CD44R12	431	chr3:88110787-88110357	1.72	1.46
	CD44R13	290	chr3:88113048-88112759	nd	nd
VIM	VIMM1 @	1168	chr2:13491974-13493141	nd	nd
Mus (mm8)	VIMM2 (VIM UTR, App. 1)	306	chr2:13491974-13492279	2.35	1.77
NM_011701	VIMM3 (VIM ECR, App. 1)	198	chr2:13491543-13491740	nd	nd
	VIMM4	411	chr2:13490800-13491210	nd	nd
	VIMM5	390	chr2:13490066-13490455	nd	nd
	VIMM6	379	chr2:13489059-13489437	1.31	0.07
VIM	VIMR1 @	1280	chr17:87846950-87847923	1.27	1.13
Rat (rn4)	VIMR2 #†^	409	chr17:87846950-87847358	2.91	2.09
NM_031140	VIMR3 #	189	chr17:87846629-87846817	nd	nd
	VIMR4 #	440	chr17:87845881-87846320	nd	nd
	VIMR5 #	330	chr17:87845056-87845385	nd	nd
	VIMR6 #	360	chr17:87844033-87844392	0.54	0.74
	VIMR7	471	chr17:87855342-87855812	2.33	1.49
	VIMR8	311	chr17:87855502-87855812	2.56	1.90
	VIMR9	405	chr17:87861245-87861649	nd	nd
	VIMR10	356	chr17:87841950-87842305	nd	nd

Appendix 2 (Cont.).

Primer Data:

ECR Name	REN	Forward Primer (5'-3')	REN	Reverse Primer (5'-3')
CD44M1 @	HpaI	<u>GTTAACGGCGGCCATTCTCTTCTGTCC</u>	BamHI	<u>GGATCCCTCTGGCCTGTAGCTATGTGCACA</u>
CD44M2	BamHI	<u>GGATCCCGTGCTGGATGAAACGGAGGG</u>		
CD44M3	BmtI	<u>GCTAGCATGAATAAATGGATGGACAGGTGGC</u>	BstEII	<u>GGTTACCCGGGGAAAATCGTATGTAAAATTGC</u>
CD44R1 @	HpaI	<u>GTTAACGCCTTTCTCTTTTGCGGGGAAG</u>	BamHI	<u>GGATCCCAACCCAGAGGCATCCAGCTG</u>
CD44R2 #	HpaI	<u>GTTAACGCCTTTCTCTTTTGCGGGGAAG</u>	BamHI	<u>GGATCCCCTCGGAAGTTGGCCGTGG</u>
CD44R3 #	BmtI	<u>GCTAGCTTTTCTCAGCTCCTCCCTAAGATTAAGTC</u>	BstEII	<u>GGTTACCGAGTCTTAGGACCTCGCCCCCTC</u>
CD44R4 #	RsrII	<u>CGGTCCGATGAATAAATGGATGGGAGGTGA</u>	AscI	<u>GGCGCGCCAAATCCAGGGGAAATAATTTAAAATCACA</u>
CD44R5 #	AsiSI	<u>CGGATCGCTATTCCTCATCCATAGTTTGCCAAACC</u>	SwaI	<u>ATTTAAATTGAATACAAAGCACTTTAGAATTTGCCAG</u>
CD44R6 #	PacI	<u>TTAATTAAGCTCTGGCCTCTATGTCTTTACTGAAG</u>	BlpI	<u>GGTTAGCGATTCTCTTTGGTGGAGGAGAGGG</u>
CD44R7	PacI	<u>TTAATTAAGCCAGTTGGTACTTGAATCAGTTCCC</u>	BlpI	<u>GCTTAGCGGTGGAACATTTTCTCCTTTTTTGTG</u>
CD44R8	RsrII	<u>CGGTCCGTTCTAGCTAGATAAAAATGAATGCTTCCAGAAG</u>	AscI	<u>GGCGCGCTGTCTCTGACTTCTCCATATTCAGACAGTC</u>
CD44R9	HpaI	<u>GTTAACTGTTGAAAGATTTTTCACGACTTAAGGG</u>	BamHI	<u>GGATCCTCCCAAATAGACACTTGCATGTGTCTAC</u>
CD44R10	AsiSI	<u>GCGATCGCATGGCCAATTTAGAATCTAGGTTCCCTCTATC</u>	SwaI	<u>ATTTAAATGCTCTTACAGAAACGCCAGGGC</u>
CD44R11	PacI	<u>TTAATTAATCCAGTGATACAGGCTTTGGCC</u>	BlpI	<u>GCTTAGCGCTCTTCTAACAATGTCAATTTTACCCC</u>
CD44R12	HpaI	<u>GTTAACTTTTCTCAGCTCCTCCCTAAGATTAAGTC</u>	BamHI	<u>GGATCCCCTCGGAAGTTGGCCGTGG</u>
CD44R13	RsrII	<u>CGGTCCGGCTCTGGCCTCTATGTCTTTACTGAAG</u>	AscI	<u>GGCGCGCTGAATACAAAGCACTTTAGAATTTGCCAG</u>
VIMM1 @	HpaI	<u>GTTAACAGTAACAGGACTGTGCTTGATACCCCTACA</u>	BamHI	<u>GGATCCTTTGCCATCTCTTTGTCTGGAACC</u>
VIMM2	HpaI	<u>GTTAACAGTAACAGGACTGTGCTTGATACCCCTACA</u>	BamHI	<u>GGATCCCGAAGGTGGGCTGGCTTGC</u>
VIMM3	BmtI	<u>GCTAGCTGAACTGAGTCCGTTAGATCAGGGG</u>	BstEII	<u>GGTTACCTGGGTGGGAGATCCGAGAG</u>
VIMM4	RsrII	<u>CGGTCCGTTTGTCTTTGTGGACAGTTGTCCG</u>	AscI	<u>GGCGCGCTCCCTCCCTCCTTCCCTCCC</u>
VIMM5	AsiSI	<u>GCGATCGCCACTGCCCTGGGATCTACAAACTATG</u>	SwaI	<u>ATTTAAATGCCGTTTAGAGACACGTGCAGG</u>
VIMM6	PacI	<u>TTAATTAATTACCCACCATCTCAGTTCTAATATTCGAAG</u>	BlpI	<u>GCTTAGCAAGAAAAAAAAACAGTCTATGAGCATAGCTTT</u>
VIMR1 @	HpaI	<u>GTTAACCGCGATCCCTTCTTTCTCAGCAC</u>	BamHI	<u>GGATCCCCTTTGCCATCTCTTTGTCTGGAAC</u>
VIMR2 #†^	HpaI	<u>GTTAACCGCGATCCCTTCTTTCTCAGCAC</u>	BamHI	<u>GGATCCGCTTTCGAAGGACGAGGTGGCC</u>
VIMR3 #	BmtI	<u>GCTAGCGGTACGACCACCCCAAACCTCTG</u>	BstEII	<u>GGTTACCGGTGGGTGGGAGATCTGTGAG</u>
VIMR4 #	RsrII	<u>CGGTCCGTTTGTCTGTGCACAGTTGTCTCCG</u>	AscI	<u>GGCGCGCCCATTCCTCCAGACCACAAAAG</u>
VIMR5 #	AsiSI	<u>GCGATCGCCCTGGGATCAACACACCATGTA</u>	SwaI	<u>ATTTAAATACTCTTTGAAGCAAACCTCATCTGAGTC</u>
VIMR6 #	PacI	<u>TTAATTAAGTTTCTAACGTTACACGAGAAGGATC</u>	BlpI	<u>GCTTAGCTTTTACAAGAAAACAGTCTATGAGCATAGCTTT</u>
VIMR7	BmtI	<u>GCTAGCACTTCTGTCTGATTAGGGTCGCCCTC</u>	BstEII	<u>GGTTACCGAAGTGAAGAGAGTCTGTTCCGATATTGT</u>
VIMR8	BmtI	<u>GCTAGCTCGTATCTTAGAAAAAAGAGCTTTCAAGTGCCTTACTGC</u>	BstEII	<u>GGTTACCGAAGTGAAGAGAGTCTGTTCCGATATTGT</u>
VIMR9	HpaI	<u>GTTAACCCCTGACAACCTGTGTGCAAAAATCAC</u>	BamHI	<u>GGATCCCGCTCACTCTCCTGGCTCCC</u>
VIMR10	PacI	<u>TTAATTAACTCCCAGTTCATCTCAAACAACATG</u>	BlpI	<u>GCTTAGCATGATGGAGATCAGAAAATGCATACAG</u>

Additional evolutionarily conserved regions (ECR) from CD44 and vimentin (VIM) were further studied; 32 sequences were PCR amplified from C57BL/6J mouse and Sprague-Dawley rat genomic DNAs, cloned into the pFTMGW vector, and transfected into cultured rat Müller

cells. The sequences were initially screened by fluorescence microscopy. Subsequently, eGFP positive constructs were analyzed by flow cytometry. The Appendix shows the eGFP expression and the mean fluorescent intensity (MFI), with values normalized and expressed as fold change relative to pFTMGW alone. Restriction endonuclease is abbreviated REN. The “†” symbol identifies referenced in Geller et al. (2007) [22] as Vim409. The “‡” (nd) denotes flow cytometry was not performed on constructs showing eGFP expression qualitatively similar to vector (pFTMGW) alone. eGFP and MFI values are shown as fold change in expression relative to pFTMGW vector alone. An (R) denotes that gene is arranged in a “reversed” orientation (3'-5') relative to the chromosome's centromere. The “#” symbol represents that tested in combination with VIMR2 or CD44R2; Figure 6. The “^” symbol denotes cloned and tested in reverse orientation; Figure 6. The “@” denotes sequence includes the 5' UTR, the first protein coding exon, and part of the first intron. “NM” numbers immediately below the gene acronym refer to RefSeq mRNA ID numbers.