Appendix 1. Full-length and proximal promoter fluorescence data, genomic fragment locations, and primer sequences.

Fluorescence Data:

Gene	Fragment	Size (bp)	Genomic Location (Mus; mm8)	eGFP	MFI
CAR2 (R)	1500	1502	chr3:14861967-14863468	4.04	2.29
NM_0098011	500+UTR	1530	chr3:14861967-14863496	3.20	1.59
	500bp	500	chr3:14862969-14863468	4.73	2.05
	500bp+UTR	528	chr3:14862969-14863496	5.78	2.79
	ECR	396	chr3:14863073-14863468	4.54	1.94
	ECR+UTR	424	chr3:14863073-14863496	4.32	1.84
	UTR †	28	chr3:14863468-14863496	nd	nd
CD44	1500	1502	chr2:102704015-102702514	1.74	1.07
NM_009851	1500+UTR	1830	chr2:102704015-102702186	5.90	3.15
	500bp	501	chr2:102703014-102702514	1.88	0.99
	500bp+UTR	829	chr2:102703014-102702186	5.86	2.89
	ECR (CD44M3, App. 2)	332	chr2:102703728-102702514	0.82	0.83
	ECR+UTR §(+898)	1543	chr2:102703728-102702186	4.26	2.18
	UTR (CD44M2, App. 2)	313	chr2:102702500-102702188	7.04	2.72
GFAP	1500	1502	chr11:102714722-102713221	3.07	1.23
NM_010277	1500+UTR	1515	chr11:102714722-102713208	3.75	1.44
	500bp	501	chr11:102713721-102713221	3.78	1.23
	500bp+UTR	514	chr11:102713721-102713208	4.06	1.35
	ECR	95	chr11:102713412-102713318	1.30	0.88
	ECR+UTR §(+96)	205	chr11:102713412-102713208	4.15	1.38
	UTR †	14	chr11:102713222-102713208	nd	nd
GLUL (R)	1500	1523	chr1:155660644-155662166	6.10	3.20
NM_008131	1500+UTR	1637	chr1:155660644-155662280	7.28	3.37
	500bp	498	chr1:155661669-155662166	8.09	2.85
	500bp+UTR	612	chr1:155661669-155662280	7.22	3.06
	ECR	280	chr1:155661887-155662166	6.98	2.49
	ECR+UTR	394	chr1:155661887-155662280	7.33	2.97
	UTR	118	chr1:155662163-155662280	2.04	1.10
PDGFRA (R)	1500	1520	chr5:75432521-75434040	2.15	0.99
NM_011058	1500+UTR	1634	chr5:75432521-75434154	3.23	1.23
	500bp	500	chr5:75433541-75434040	2.04	0.93
	500bp+UTR	614	chr5:75433541-75434154	4.39	1.59
	ECR	871	chr5:75433170-75434040	2.39	1.07
	ECR+UTR	985	chr5:75433170-75434154	3.81	1.41
	UTR	114	chr5:75434041-75434154	4.33	1.80

Appendix 1 (Cont.).

Fluorescence Data (Cont.):

Gene	Fragment	Size (bp)	Genomic Location (Mus; mm8)	eGFP	MFI
RLBP1	1500	1500	chr7:79259798-79258299	0.76	0.87
NM_020599	1500+UTR ‡	1711	chr7:79259798-79258088	4.75	2.20
	500bp	501	chr7:79258799-79258299	1.07	1.02
	500bp+UTR ‡	712	chr7:79258799-79258088	7.32	3.57
	ECR	145	chr7:79258994-79258850	1.49	0.84
	ECR+UTR ‡,§(+551)	907	chr7:79258994-79258088	6.48	3.10
	UTR‡	211	chr7:79258298-79258088	2.09	1.37
S100B (R)	1500	1515	chr10:75696054-75697568	1.57	1.00
NM_009115	1500+UTR	1621	chr10:75696054-75697674	4.08	1.93
	500bp	501	chr10:75697068-75697568	1.77	1.12
	500bp+UTR	607	chr10:75697068-75697674	6.1	2.42
	ECR	412	chr10:75697157-75697568	1.97	1.20
	ECR+UTR	518	chr10:75697157-75697674	6.45	2.46
	UTR	106	chr10:75697569-75697674	4.43	1.82
SLC1A3	1500	1516	chr15:8659461-8657946	1.82	1.30
NM_148938	1500+UTR ‡	1908	chr15:8659461-8657554	1.16	1.04
	500bp	500	chr15:8658445-8657946	5.22	2.43
	500bp+UTR ‡	892	chr15:8658445-8657554	3.19	1.53
	ECR	129	chr15:8658074-8657946	2.42	1.05
	ECR+UTR ‡	521	chr15:8658074-8657554	4.54	1.69
	UTR‡	392	chr15:8657945-8657554	4.36	1.55
VIM (R)	1500	1506	chr2:13490297-1349180	4.63	2.09
NM_011701	1500+UTR	1988	chr2:13490297-1349228	7.19	3.79
	500bp	502	chr2:13491301-1349180	5.38	1.72
	500bp+UTR	984	chr2:13491301-1349228	7.07	3.50
	ECR (VIMM3, App. 2)	198	chr2:13491543-1349174	4.16	1.53
	ECR+UTR §(+64)	742	chr2:13491543-1349228	7.32	3.38
	UTR (VIMM2, App. 2)	480	chr2:13491805-1349228	6.55	3.48

Appendix 1 (cont.).

Primer Data:

Gene	Fragment	REN	Forward Primer (5′-3′)	REN	Reverse Primer (5′-3′)
CAR2 (R)	1500	PacI/HpaI	TTAATTAAGTTAACTCCCTAGCAGGAGCCTGGCTC	BlpI/SdaI	GCTAAGCCCTGCAGGAAGTTGTCGTCCGTCTAG
NM_0098011	500+UTR	PacI/HpaI	TTAATTAAGTTAACTCCCTAGCAGGAGCCTGGCTC	BlpI/SdaI	GCTAAGCCCTGCAGGGGTCACGCCGGTGATTGGG
	500bp	PacI/HpaI	TTAATTAAGTTAACGCTCCAGGATCCCCGCTC	BlpI/SdaI	GCTAAGCCCTGCAGGAAGTTGTCGTCCGTCTAG
	500bp+UTR	PacI/HpaI	TTAATTAAGTTAACGCTCCAGGATCCCCGCTC	BlpI/SdaI	GCTAAGCCCTGCAGGGGTCACGCCGGTGATTGGG
	ECR	PacI/HpaI	TTAATTAAGTTAACCAGCTCTGGGAAGCGGAG	BlpI/BamHI	GCTAAGCGGATCCAAGTTGTCGTCCGTCTAG
	ECR+UTR	PacI/HpaI	TTAATTAAGTTAACCAGCTCTGGGAAGCGGAG	BlpI/SdaI	GCTAAGCCCTGCAGGGGTCACGCCGGTGATTGGG
	UTR †	---	---	---	---
CD44	1500	PacI/BmtI	TTAATTAAGCTAGCACTCGGAACAAATGCAATTCTTACGA	BlpI/BamHI	GCTAAGCGGATCCCAGCCCCCGTGCGCCCAC
NM_009851	1500+UTR	PacI/BmtI	TTAATTAAGCTAGCACTCGGAACAAATGCAATTCTTACGA	BlpI/BamHI	GCTAAGCGGATCCGGCGTGCTGGATGAAACGGA
	500bp	PacI/BmtI	TTAATTAAGCTAGCAAGGATTTAAGAAATTGG	BlpI/BamHI	GCTAAGCGGATCCCAGCCCCCGTGCGCCCAC
	500bp+UTR	PacI/BmtI	TTAATTAAGCTAGCAAGGATTTAAGAAATTGG	BlpI/BamHI	GCTAAGCGGATCCGGCGTGCTGGATGAAACGGA
	ECR	PacI/RsrII	TTAATTAACGGTCCGAGTGCCTAGACCAAACCA	BlpI/AscI	GCTAAGCGGCGCGCCCGGGGAAAATCGTATGTA
	ECR+UTR §	PacI/RsrII	TTAATTAACGGTCCGAGTGCCTAGACCAAACCA	BlpI/BamHI	GCTAAGCGGATCCGGCGTGCTGGATGAAACGGA
	UTR	HpaI	GTTAACGGCGGCCATTCTCTTCTGTCC	BamHI	GGATCCCGTGCTGGATGAAACGGAGGG
GFAP	1500	PacI/BmtI	TTAATTAAGCTAGCTTGAGCTGGGAGCTTGTACTGCAC	BlpI/BamHI	GCTAAGCGGATCCTGCTGGCTCCTGGGATGTCAG
NM_010277	1500+UTR	PacI/BmtI	TTAATTAAGCTAGCTTGAGCTGGGAGCTTGTACTGCAC	BlpI/BamHI	GCTAAGCGGATCCCCTGCCCTGCCTCTGCTGG
	500bp	PacI/BmtI	TTAATTAAGCTAGCGCACATACATGTGTTGAGACCAGAGG	BlpI/BamHI	GCTAAGCGGATCCTGCTGGCTCCTGGGATGTCAG
	500bp+UTR	PacI/BmtI	TTAATTAAGCTAGCGCACATACATGTGTTGAGACCAGAGG	BlpI/BamHI	GCTAAGCGGATCCCCTGCCCTGCCTCTGCTGG
	ECR	PacI/HpaI	TTAATTAAGTTAACGCTGGTGTTCCCAAGAAAGCCTT	BlpI/SdaI	GCTAAGCCCTGCAGGGGTGGAGCTGGGCCCCAG
	ECR+UTR §	PacI/HpaI	TTAATTAAGTTAACGCTGGTGTTCCCAAGAAAGCCTT	BlpI/BamHI	GCTAAGCGGATCCCCTGCCCTGCCTCTGCTGG
	UTR †	---	---	---	---
GLUL (R)	1500	PacI/BmtI	TTAATTAAGCTAGCCCTCATGGTAAAACGCTTCACACAG	BlpI/BamHI	GCTAAGCGGATCCTCTGCAGGGTCGCTGGCTG
NM_008131	1500+UTR	PacI/BmtI	TTAATTAAGCTAGCCCTCATGGTAAAACGCTTCACACAG	BlpI/BamHI	GCTAAGCGGATCCTACCAGAGCGGTGGCCGG
	500bp	PacI/BmtI	TTAATTAAGCTAGCTCTCTCTCTCTCCCCGCG	BlpI/BamHI	GCTAAGCGGATCCTCTGCAGGGTCGCTGGCTG
	500bp+UTR	PacI/BmtI	TTAATTAAGCTAGCTCTCTCTCTCTCCCCGCG	BlpI/BamHI	GCTAAGCGGATCCTACCAGAGCGGTGGCCGG
	ECR	PacI/BmtI	TTAATTAAGCTAGCCTTAAGAACGCAAGCTGC	BlpI/BamHI	GCTAAGCGGATCCTCTGCAGGGTCGCTGGCTG
	ECR+UTR	PacI/BmtI	TTAATTAAGCTAGCCTTAAGAACGCAAGCTGC	BlpI/BamHI	GCTAAGCGGATCCTACCAGAGCGGTGGCCGG
	UTR	PacI/BmtI	TTAATTAAGCTAGCGCGGAGAATGGGAGTA	BlpI/BamHI	GCTAAGCGGATCCTACCAGAGCGGTGGCCGG
PDGFRA (R)	1500	PacI/BmtI	TTAATTAAGCTAGCAAGTAATAGTGAGCAGGGCAGTCACC	BlpI/BamHI	GCTAAGCGGATCCAACAGTAATGGGCTCAAA
NM_011058	1500+UTR	PacI/BmtI	TTAATTAAGCTAGCAAGTAATAGTGAGCAGGGCAGTCACC	BlpI/BamHI	GCTAAGCGGATCCCTTCTCCTTCTATGTCAATTTGCAAAGAA
	500bp	PacI/BmtI	TTAATTAAGCTAGCGACTGTCTATAGAAAGGA	BlpI/BamHI	GCTAAGCGGATCCAACAGTAATGGGCTCAAA
	500bp+UTR	PacI/BmtI	TTAATTAAGCTAGCGACTGTCTATAGAAAGGA	BlpI/BamHI	GCTAAGCGGATCCCTTCTCCTTCTATGTCAATTTGCAAAGAA
	ECR	PacI/BmtI	TTAATTAAGCTAGCCCATCAAGATGCAGAGGG	BlpI/BamHI	GCTAAGCGGATCCAACAGTAATGGGCTCAAA
	ECR+UTR	PacI/BmtI	TTAATTAAGCTAGCCCATCAAGATGCAGAGGG	BlpI/BamHI	GCTAAGCGGATCCCTTCTCCTTCTATGTCAATTTGCAAAGAA
	UTR	PacI/BmtI	TTAATTAAGCTAGCGGAGCTTGAGGGAGAGAAAC	BlpI/BamHI	GCTAAGCGGATCCCTTCTCCTTCTATGTCAATTTGCAAAGAA

Appendix 1 (cont.).

Primer Data (cont.):

Gene	Fragment	REN	Forward Primer (5′-3′)	REN	Reverse Primer (5′-3′)
RLBP1	1500	PacI/HpaI	TTAATTAAGTTAACCTTGCACTTCTAAGATCTGGGACTTGG	BlpI/BamHI	GCTAAGCGGATCCGGGATAGAAGGATTAATATG
NM_020599	1500+UTR ‡	PacI/HpaI	TTAATTAAGTTAACCTTGCACTTCTAAGATCTGGGACTTGG	BlpI/BamHI	GCTAAGCGGATCCCTCCACTCCTGTTTTATTTAAGGGGAA
	500bp	PacI/HpaI	TTAATTAAGTTAACGGGAGAAAAGACTGTTGT	BlpI/BamHI	GCTAAGCGGATCCGGGATAGAAGGATTAATATG
	500bp+UTR ‡	PacI/HpaI	TTAATTAAGTTAACGGGAGAAAAGACTGTTGT	BlpI/BamHI	GCTAAGCGGATCCCTCCACTCCTGTTTTATTTAAGGGGAA
	ECR	PacI/RsrII	TTAATTAACGGTCCGCTTTACACCCACATATCTG	BlpI/AscI	GCTAAGCGGCGCGCCCAGAGAATATCTGAGGGC
	ECR+UTR ‡,§	PacI/RsrII	TTAATTAACGGTCCGCTTTACACCCACATATCTG	BlpI/BamHI	GCTAAGCGGATCCCTCCACTCCTGTTTTATTTAAGGGGAA
	UTR‡	HpaI/PacI	GTTAACTTAATTAAAACAAGGGACGGTCAAGACT	BlpI/BamHI	GCTAAGCGGATCCCTCCACTCCTGTTTTATTTAAGGGGAA
S100B (R)	1500	PacI/RsrII	TTAATTAACGGTCCGACACACAGGGGTTTGAAGATCTCTCC	BlpI/SdaI	GCTAAGCGGCGCGCCGGCTTGGCGCAGTCCACTG
NM_009115	1500+UTR	PacI/RsrII	TTAATTAACGGTCCGACACACAGGGGTTTGAAGATCTCTCC	BlpI/AscI	GCTAAGCGGCGCGCCCTCCTGGTCACCTTTGCTGCTG
	500bp	PacI/RsrII	TTAATTAACGGTCCGTGCATGCTGGTCCCTGAGAATACT	BlpI/AscI	GCTAAGCGGCGCGCCGGCTTGGCGCAGTCCACTG
	500bp+UTR	PacI/RsrII	TTAATTAACGGTCCGTGCATGCTGGTCCCTGAGAATACT	BlpI/AscI	GCTAAGCGGCGCGCCCTCCTGGTCACCTTTGCTGCTG
	ECR	PacI/RsrII	TTAATTAACGGTCCGCAGGAGGGGACCAGGAAGCTG	BlpI/AscI	GCTAAGCGGCGCGCCGGCTTGGCGCAGTCCACTG
	ECR+UTR	PacI/RsrII	TTAATTAACGGTCCGCAGGAGGGGACCAGGAAGCTG	BlpI/AscI	GCTAAGCGGCGCGCCCTCCTGGTCACCTTTGCTGCTG
	UTR	PacI/RsrII	TTAATTAACGGTCCGCACACCCAGTTCTCTCTGCA	BlpI/AscI	GCTAAGCGGCGCGCCCTCCTGGTCACCTTTGCTGCTG
SLC1A3	1500	RsrII/HpaI	CGGTCCGGTTAACCTGTTTATCAGGCCCAAGACAGACTCTT	AscI/SdaI	GGCGCGCCCCTGCAGGCTGGAAGTCCGGATTAGAAC
NM_148938	1500+UTR ‡	RsrII/HpaI	CGGTCCGGTTAACCTGTTTATCAGGCCCAAGACAGACTCTT	AscI/SdaI	GGCGCGCCCCTGCAGGCTTTTCTGACTCTGGGATGGGAGG
	500bp	RsrII/HpaI	CGGTCCGGTTAACACTCCTGAAAACGGGGAT	AscI/SdaI	GGCGCGCCCCTGCAGGCTGGAAGTCCGGATTAGAAC
	500bp+UTR ‡	RsrII/HpaI	CGGTCCGGTTAACACTCCTGAAAACGGGGAT	AscI/SdaI	GGCGCGCCCCTGCAGGCTTTTCTGACTCTGGGATGGGAGG
	ECR	RsrII/HpaI	CGGTCCGGTTAACTGCTACAACAGTTGTGTG	AscI/BamHI	GGCGCGCCGGATCCCTGGAAGTCCGGATTAGAAC
	ECR+UTR ‡	RsrII/HpaI	CGGTCCGGTTAACTGCTACAACAGTTGTGTG	AscI/SdaI	GGCGCGCCCCTGCAGGCTTTTCTGACTCTGGGATGGGAGG
	UTR‡	HpaI/RsrII	GTTAACCGGTCCGCGTCCATGTGTGTGAGCGCT	AscI/SdaI	GGCGCGCCCCTGCAGGCTTTTCTGACTCTGGGATGGGAGG
VIM (R)	1500	RsrII/HpaI	CGGTCCGGTTAACAAAGAAAGGCACAGCAGGAGAGCT	AscI/BamHI	GGCGCGCCGGATCCCTAGGCGCGCTGGTAGGAGG
NM_011701	1500+UTR	RsrII/HpaI	CGGTCCGGTTAACAAAGAAAGGCACAGCAGGAGAGCT	AscI/BamHI	GGCGCGCCGGATCCGGCTTCGAAGGTGGGCTGG
	500bp	RsrII/HpaI	CGGTCCGGTTAACGGAGAACTCTCCACACTTCCCCAAC	AscI/BamHI	GGCGCGCCGGATCCCTAGGCGCGCTGGTAGGAGG
	500bp+UTR	RsrII/HpaI	CGGTCCGGTTAACGGAGAACTCTCCACACTTCCCCAAC	AscI/BamHI	GGCGCGCCGGATCCGGCTTCGAAGGTGGGCTGG
	ECR	HpaI/RsrII	GTTAACCGGTCCGTGAACTGAGTCCGTTAGATCAGGGG	BamHI/AscI	GGATCCGGCGCGCCTGGGTGGGGAGATCCGAGAG
	ECR+UTR §	HpaI/RsrII	GTTAACCGGTCCGTGAACTGAGTCCGTTAGATCAGGGG	AscI/BamHI	GGCGCGCCGGATCCGGCTTCGAAGGTGGGCTGG
	UTR	HpaI/RsrII	GTTAACCGGTCCGCCACGCCCCTTTGGCCCAGT	AscI/BamHI	GGCGCGCCGGATCCGGCTTCGAAGGTGGGCTGG

We identified and cloned the full-length promoters (~1500 bp), proximal promoter regions (~500 bp), the most proximal evolutionarily conserved regions (ECRs) to the transcription start site for each of nine genes identified in the literature as being potential or known Müller cell markers: CAR2, CD44, CRALBP, GFAP, GLUL, PDGFRA, S100B, SLC1A3, and VIM. The sequences were cloned either including or excluding the UTR, and then evaluated with fluorescent microscopy and flow cytometry. The Appendix shows the eGFP expression and the mean fluorescent intensity, with values normalized and expressed as fold change relative to pFTM3GW. Restriction endonuclease is abbreviated REN. The “†” symbol identifies small UTRs that were not individually tested. The “‡” symbol denotes very large UTRs; only the ~200 bp regions immediately following the TSS were analyzed. eGFP and MFI values are shown as fold change relative to pFTM3GW vector alone. An (R) denotes that gene is arranged in a “reversed” orientation (3′-5′) relative to the chromosome’s centromere. The “§” symbol denotes ECR not located immediately proximal to the TSS, and some intervening sequence was included in ECR+UTR constructs. “NM”numbers immediately below the gene acronym refer to RefSeq mRNA ID numbers.