Set	Gene Name	Primer 1 Sequence	Primer 2 Sequence	Fragment Size (bp)	Primer Concn (nM)
1					
	HOXA6	GAGCGCCAGATCAAGATCTGGTT	CTCCCCTGAAGCTGCGGAAGCCCC	240	45
	HOXA9	GAGAGGCAGGTCAAGATCTGGTT	GAGGTTTAGAGCCGCTTTGTGCG	217	45
	HOXA7	GAGCGCCAGATTAAGATCTGGTT	GGCCCCGGATCGGCCCCTCATTC	200	227
	HOXA2	GAGAGACAAGTGAAAGTGTGGTT	AGAAGGGCCCCAGAGACGCTAAG	182	91
	HOXA5	TTGCCTCTCCGAGAGACAAATTAAAATCTGGTT	ACTGACACTACGCGGGATCCGCTAATA	173	159
	HOXA10	ACGGACAGACAAGTGAAAATCTGGTT	GGAAGTGAAAAAACCGCGTCGCCTGG	141	45
	HOXA13	GAGCGGCAGGTCACAATCTGGTT	TTCTGAAGCGTTTCTTCAAGTTGCCTTCTTGC	128	45
	HOXA4	GAGCGCCAGGTCAAGATCTGGTT	CTTTCCCTGGTGGGCCGGCAGAGGC	124	45
	HOXA1	GAGACCCAAGTGAAGATCTGGTT	CCTTCTCGTCGTTTCCTGGCG	112	45
	HOXA3	GAGCGCCAGATCAAGATCTGGTT	CTTGGAGACTGGCCCCCCGAT	101	45
	HOXA11	GATCGTCAAGTCAAAATCTGGTT	TGGATTTGCTGAGTAGTACTGTAAACG	90	159
2					
	HOXB3	GAGCGGCAGATCAAGATCTGGTT	GGTAGTTGGAGGGCAGCGCGTAG	241	75
	HOXB5	GAGCGCCAGATCAAGATCTGGTT	GCAGGCTTGTGGGAACCGGTC	220	50
	HOXB1	GAAACACAGGTCAAGATTTGGTT	GGAAGCCCCATTGGTGGCTAGGT	205	50
	HOXB7	GAAAGACAGATCAAGATTTGGTT	CTGGGCTTCTCTTCGTCTCCCTTTCTCATG	180	175
	HOXB8	GAGAGACAGGTCAAAATCTGGTT	CTTGTCGCCCTTCTGCGCGTC	168	250
	HOXB9	GAGAGACAAGTCAAAATCTGGTT	GCACTGGCTTTGCAGTCGTCACAT	156	50
	HOXB4	GAGCGCCAGATCAAGATCTGGTT	CGCGGGGGCCTCCATTGGGC	142	100
	HOXB13	GAGCGCCAGATTACCATCTGGTT	CCAGGACACCCCCACTTTCGC	134	50
	HOXB6	GAGAGGCAGATCAAGATATGGTT	CCAGCACCTTACTCGGCCTGTTTTTCTTCC	125	50
	HOXB2	GAAAGGCAGGTCAAAGTCTGGTT	GGTCGCAGATGTCCTCCAGGG	121	250
3					
	HOXC13	GAGCGCCAGGTAACCATCTGGTT	GCGCGGTTCTTCTCTTTCCTTAACA	215	56
	HOXC6	GAGCGACAGATCAAAATCTGGTT	GGGAGAGAGGGGTGGCAGGGAC	195	111
	HOXC8	GAGAGACAAGTGAAGATCTGGTT	GGGGTCTTTCTTTTTTGCTTAGTCCTTGTT	180	194
	HOXC4	GAGAGGCAGATCAAAATCTGGTT	GTGGTCTTCAGAAGTACCCGGGGTA	150	83
	HOXC12	GACCAGCAGGTCAAGATCTGGTT	TTTGCTCTCTGCCAGGGACAGG	142	111
	HOXC9	GAGCGGCAGGTCAAAATCTGGTT	TTTCCCTTGGCTGTGCTGAGG	126	56
	HOXC11	GACCGACAAGTGAAAATTTGGTT	AAAGGGCCCGGTCTGCAG	118	556
	HOXC10	GACAGACAAGTCAAAATCTGGTT	CGCTCTCAGGTGAAATTAAAATTGGAGGT	110	278
	HOXC5	GAGAGACAGATCAAGATCTGGTT	CCCCGCTGCCTCTAAAGAGCCT	95	194
4					
	HOXD4	GAGCGCCAGATCAAGATCTGGTT	CCAGGGTCCCCACTTCTATAAGGTCG	201	83
	HOXD9	GAGAGACAGGTCAAAATCTGGTT	CTGGAGAGTTTCTGGAAATCAAGCACCAAACA	185	278
	HOXD11	GACCGGCAAGTCAAAATCTGGTT	GAGCAGGCTGGTGGGAAGG	162	194
	HOXD8	GAGAGACAGGTAAAAATCTGGTT	CTGTCTTCCTCCAGCTCTTGGGC	140	278
	HOXD13	GAGAGACAAGTGACCATTTGGTT	GACAACCGAATGGCTTCTAAGCTGTC	130	111
	HOXD10	GACAGGCAGGTCAAGATTTGGTT	TCAGACCGGCCTCAGACCTAAGA	122	111
	HOXD1	GACACGCAAGTCAAAATCTGGTT	GAAGTTGGAGGGGAGCCACAG	106	111
	HOXD12	GACCAGCAAGTCAAAATCTGGTT	CACGCGCGCGGCTAGTAG	98	194
	HOXD3	GAACGCCAGATCAAGATCTGGTT	ACTGGCTAGCCGGCGAGTGCAGGATG	94	278
5					
	GBX1	ACAGCATTTACCAGCGAGCAGCTT	CCAGAACGGCTGCTCACATTGC	191	46
	BARHL1	AGATCTCCAGCTCCAGGGACAGT	TGCGTGTCGGTGAGGTTGAGCGA	175	52
	MSX1	AAACACAAGACGAACCGTAAGCCG	GGAACCATATCTTCACCTGCGTCT	160	202
	HLXB9	CGCTCTCCTACTCGTACCCGCA	GAAGTCGGGCATCTTAGGCAGGAT	146	433
	NP_001009812	GTGTCGAGGAGGGCGTCGGAGTTT	GCGGCAGGCCTGTGAGTTGTTT	133	29
	GBX2	GCTGATGATGATGCAGCGCCCG	GGTAGCCGGTGTAGACGAAATGG	110	577
	DLX3	CATGGTGAATGGGAAGCCCAAGAA	GTACTGGGCCTTCTGGAAGCGG	100	288
	DLX1	AGTGCGCTTCAATGGCAAGGGAAA	CTGGAACCTCCGGTTCAAAGCCT	91	87
	DLX6	AAGCCTCGGACCATTTATTCCAGC	TCTGGAAGGGCCAGATACTGTGT	83	87
	DLX4	TCCGCAAGCCGAGGACCATCTACT	AGGTACTGCGTGTGCTGGAAAC	76	58
	DLX5	AGAAGACTCAGTACCTCGCCTTGC	TGTGTTTGTGTCAATCCCAGCGAG	70	87
	DLX2	AGAAGGAGGACCTTGAGCCTGAAA	GGGTTTCCGGACTTTCTTTGGCTT	65	288
	LBX1	GAGGAGCTCGCCAGCAAGACGTTTA	CTTCGGCTGCCTGCAGAACGCT	61	346
6					
	PAX7	ACTCCATCAAGCCAGGAGACAG	ATAAACAAGCAGGAGGCCCTGG	193	87
	PAX1	CGGACGCCCTCAGTAGCTTACA	ACTGGCTTCCTCCTCCGCGAGT	177	101
	PAX9	TACATGACCTACAGTGCTGCTCCT	GGAAGCCGTGACAGAATGACTACCTT	162	46
	PAX2	AATGGAGATTCCCAGAGTGGTGTG	CTGATTTGATGTGCTCTGATGCCTGG	148	58
	PAX3	GGCCAGCTGCAGTCAGAGACTAGA	TACTGCCCATATTGGTAGCCTGTG	135	46

	PAX8	ATCCTCACTCACCCTTCGCCATAA	GAGCCGACTTGCTGCAGATCCAAA	112	101
	PAX5	AGACTTCCTCCGGAAGCAGATGCG	GTGAAGATGTCTGAGTAGTGCTGCCT	102	72
	PAX4	AACCACTGGGTCCCTCCTGCTAT	AGGGCTTGAGACAGGCTTTAGGT	93	52
	PBX3	GCAAGTTTCAGGAAGAAGCCAACC	TTGTTCTGCACAGCTGCTGCTACT	85	115
	PBX4	GCGACGGAAGTGCTGAATGAGTAT	CAGCTCTTCTTTGGCTTCTTCGCT	78	72
	PAX6	TCGGTGAATGGGCGGAGTTATGAT	CATTGGCTGACTGTTCATGTGTGTC	72	72
	PBX2	GTCTCCAACTGGTTTGGCAACAAGAG	CCTCCTCTTGGAACTTTCCGATGT	67	101
	PBX1	CTATTCCCATCTCAGCAACCCTTACC	CACTTCTTGGCTAACTCCTCTTTGGC	63	101
7					
	NP_078843	GCCTTGGAAACTTTGGACCGTCTT	TTGATTGGTAGTGCAAGGCTGTGG	213	35
	CUTL1	ACAGCTCAGTCAGTGACAGCCA	GTGGCGAGGTCTTCGATGGTTT	196	35
	NP_775756	CTCACCTGGGTTTCCAAATGAAGGAC	GTTTGCTCACAAATGTCCGACAGC	180	46
	CUTL2	GGAAAGCATCCTGGGTCTGACA	TCCAGCTTCTTCATATCCCTCAGC	165	58
	TLX1	CGTCCTTCACACGCCTGCAGAT	CACTTTGTCCGCCGGTTCTGGA	151	58
	TLX3	AGCTGCAACACGACGCCTTCCAAA	TGACAGCGGGAACCTTGGAACTAT	138	288
	LASS2	AAGATGAACGCAGTGACCGGGAA	TCTTACGATGGTTGTTATTGAGGATGGG	126	87
	LASS4	ACACCACATACTACGAGTCCATCAGC	AGAATGAGGCAAGACCAGAACACG	115	72
	LASS1	AGGTCCTGTATGCCACCAGTCA	AGAGGTTCATAAGGGTGAGCAGCA	105	46
	LASS5	AGCAGCTCAGAGGAAGAAGATGTG	TCCCATGTGACCATTCACCCGATT	96	46
	LASS6	AGGACTCAGAACCTCCGGGAAAGAAT	GAGCCAGTCAGGAGATACCCGTT	88	52
	TLX2	TTCCTGCGCCAGAAGTACCTGG	TTTGACCTGTGCGTCGGTCATGC	81	577
	LASS3	TGCACGCTGATCTTGCCTATGT	GATCATGAGCTGTAGGTTGAGGAAGATG	75	72
8					
	HMX3	GAGATCATTCTGGAGGAGAGCGACT	AAGACTGTGCGCGTCTTCTTCTTG	182	231
	MSX2	ATGGCTTCTCCGTCCAAAGGCAAT	TTGTCGGACATGAGCGCCTCCA	167	231
	NKX2-4	TCTTCTCGCAGGCGCAGGTCTAC	GTTTCATCTTGTACCGGTGGTTCTGG	153	404
	MIXL1	CGGAGATTATCCTCAACCACTGTGC	ACCTTGGGAGCTAGAGTCAGAGAT	140	115
	IRX2	GTGGACTCGCTCACGGATCACT	TCGTCCTCCAGGTCGTCATACTTGT	128	288
	LHX4	ACTTTGTCTACCACCTGCACTGCT	TCTCGTAGTCTTCCTTGCACACCA	117	58
	ARX	CTGCTGAAACGCAAACAGAGGC	CTGGTGAAGACGTCCGGGTAGT	107	288
	POU6F1	ATTGCTAAGGAGCTCAACTACGACCG	TGAAAGACGTTCAGCTTGCTGGTG	98	58
	EN2	CTCGGACTCGGACAGCTCGCAA	TCCGAGTAGCGCGTACAGTAGA	90	404
	GSH1	AAGTGCTCCGAGGATGACGACGAAT	TAGGGAGTGACCGTAAGATCCCG	83	87
	TITF1	AAAGCACACGACTCCGTTCTCAGT	CCTCCATGCCCACTTTCTTGTAGCTT	77	144
	POU4F1	TCGCCGAGAAACTGGACCTCAAA	GCTTCTGCTTCTGTCTCTGGTTGC	72	144
	SHOX	TGAATGCAAAGAGAAGCGCGAGGA	TCTGTTTCAGCTTGGTCTGCCCGT	68	115
9					
	VSX1	AAGATAAGTTGGCAGGACTCTGGG	GAGTTGGAGCCTCCTTGAGCAC	199	35
	GBX2	ACTCAGCGAGGTGCAGGTGAAA	GCCTGTTCTAGCTGCTGATGCT	183	87
	LBX1	GGCCTTCACCAACCACCAGATCTAT	TCCTCCAGGTCCCGCTTGAGCTTAG	168	87
	IPF1	TAGAGCTGGAGAAGGAGTTCCTATTCAACA	CCGCGCTTCTTGTCCTCCTCCTTT	154	87
	NKX2-8	GCCTACCAGCACTTAGCATCCC	ACGGAGAGCGTTCCAGGCGTTC	141	144
	NKX3-1	TTCAGCCATCAGAAGTACCTGTCG	GGAGAGCTGCTTTCGCTTAGTCTT	129	144
	BAPX1	GCTTTAACCACCAGCGCTACCTGT	CGCTTTGTCTTGTAGCGACGGTTC	118	202
	VAX1	CCGTTAACAATGGCTGGTTCGCTA	CCCTTCTTTATTGTTGGTCCGGGAGT	108	231
	DLX3	ATGGTGAATGGGAAGCCCAAGAAG	GTACTGGGCCTTCTGGAAGCGG	99	144
	NKX2-2	AGCACATGCAGTACAACGCCCAGTACA	CAAGTCCACTGCTGGGCCTGGAC	91	87
	TLX1	TTCCAGAAGAGCCTGGCACAGC	ATTCTGCAGGGCGAAGAGCGACGA	78	404
	HMX2	TCGACCTGAAGCGCTACCTGAGCA	AGATCTTAACCTGCGTCTCGGTGA	84	46
	HLXB9	CTCAACAAGTACCTGTCGCGGCCCAA	CTGGGTCTCGGTGAGCATGAGC	69	144
10					
	TLX3	GATCTTACAGTGTGAACCTGAGCCTAGC	TGTGAAGCGGTCTTTCACGAAGC	200	231
	BARX1	AGCAGGCGGCGGTGTTCAAGTT	TTCTTGGCTTTGGTGCCTGGCT	184	115
	TLX2	GATGCTGGGTCCACACAACCTCCCA	GTAGCCCGAGGCTCCGTGGTAT	169	173
	LHX6	AGGAGCTCTGGACAAGGACGAG	TGAGCAGATATCGGTCCAGGATCTC	155	87
	ISL2	AGATCCACGACCAGTTTATCCTGC	TAGGTCTTCCCGTCTCTCACGAA	130	173
	SIX3	CTGTTGCGGGAGTGGTACCTACAG	TGCCGCCGGTTCTTAAACCAGTTGCC	119	87
	SHOX2	AAATCAAGCAGAGGCGAAGTCGGA	AGTTCCTCTCGCATGAAGGCGT	109	115
	PITX2	CGGCCGTTGAATGTCTCTTCTCCAAA	AAGAACTTGCTGCTGGCTGCCTCTTT	100	87
	HOP	TGCAGATCCGTCACAGACTAAGGA	AGCTTGGTTAAGCGGAGGAGAGAA	92	72
	NKX6-2	ACGACGACGAATACAACCGGCCC	TTCGAGGGTTTGTGCTTCTTGAGC	85	288
	GSCL	TTCAAGAACCGCCGGGCCAAAT	ACTTCTTGACGCCGGGCAGGAG	79	115
	EMX2	AGCTGGAGGAAGAAGGCTCAGATT	GGCGATTCTCCACCGGTTAATATGGT	74	72
	HHEX	AAAGGAAAGGCGGCCAGGTGAGATT	TGCGTCTCGAATTTCTTCTCCAGC	70	72
11					

	POU3F1	TACGGTAACGTGTTCTCGCAGAC	TCGATGGACGTGCGCTTCTTGC	191	469
	POU3F2	AGCATAGACAAGATCGCAGCGCAA	ACCAAACTCTCACCACCTCCTTCT	175	250
	POU6F2	GCCAAACTGAACCCTGGCCTTT	TCCCGATAAACTCGGTCAGGTTCT	160	63
	POU6F1	TCGAGAAGCTAGACATCACACCCA	TTTGCGTTTCTTGGAGGGCTCG	146	50
	POU4F1	TGAACAAGCCTGAGCTCTTCAACG	ATGGCGGCGATCTTCTCGGACG	133	250
	POU4F2	GCTCACCAAGCCTGAACTCTTCAA	TTCAGAGGAGGGCCGAGGCTGAAT	121	188
	POU2F1	TGCAACTGGGAACCTGGTATTTGC	TAACAGGGTTGCTGGTGAGCAGA	110	63
	POU3F4	ACGCATTTCCTCAAGTGTCCCAAG	TACAGAACCAGACACGCACCACTT	100	156
	POU2F2	CAGAGGAGATCCTGCTGATCGCCGAG	CGTTTCTCCTTCTGGCGCCGGTT	91	63
	POU1F1	AGATGCTCTGGAGAGACACTTTGG	CCAGATTCAGTTCTTCAGCCATCCTC	83	94
	POU5F1/L/N	TGGTCCGAGTGTGGTTCTGTAAC	TCTCGTTGTGCATAGTCGCTGCTT	70	63
	POU2F3	AAGGAGAAGCGAATCAACTGCCCT	GGGAGTTGTAGACAGGTGGTTTGA	61	94
12					
	ALX3	CTGAGGAGAAGACCTCCAAAGCTG	AATGTGCTGAAGGTCGTGCGGTTA	211	94
	VSX1	AGGAAGTGAAGATAAGTTGGCAGGAC	AGGGTGCACTTTCTTGGTCTCCT	178	50
	CHX10	TCCCAGGAGGAACTGAGGGAGAA	TCTCCGCCGGCCTGTCTTCATC	163	56
	ALX4	ATTCAGAACCCGTCCTGGCTCG	ACACTCAGGAAGTCGGTGACGCT	149	125
	CART1	TCGCCTCGGACAGATTCCAGTTA	CAAATGCATGTCCATTGGTTGCCC	124	38
	SHOX2	TACATGATGTTCCCAGCACCGCCCTT	TTGCTGGTGGTCTTGGCGGCTG	113	219
	HESX1	CCCAATGCCAGAAGAAAGAGCTTC	TGGTCTTCGGCCTCTATACCAACT	103	94
	LMX1A	GAGTGCTGGGATGGAAGGAATCAT	ATCTGAGCTGTAGACACTCTGCTCG	94	78
	ISL2	CAGTGGAGGTGCAGACGTACCA	TTGGAAGGCGGGTTGGTCCAGGT	86	78
	ISL1	TGGCTTACAGGCTAACCCAGTGGAA	CAAGGCGAAGTCGCTCAGTACTTT	73	125
	LMX1B	GAGGGCATGATGGCTTCCTACA	CTCTGTTCCATGGCCACGATCT	68	94
	CXorf43	ACTGCTGTCAGATTTACCTCCTGAATTAGA	AGGCTCCAGTGAGGCATGATTGAAA	64	156
13					
	PEPP2	AGGTCAAAGAGGAGGAAGAGGATGC	CTTCCCATAGGTGGCCAGGAACT	162	60
	PITX2	ACCCGTCTAAGAAGAAGCGGCAAA	GCTTCCGTAAGGTTGGTCCACACA	148	375
	PEPP1	CCGTGTTCTACTGCCTGAGTGTAT	GGTTCATATTACCCATGAGGCCTGGA	123	113
	ESX1L	AGAAACTTACCGTGACCTCGCTGA	GACCCTTCCGTGCCAACGTTGTTT	112	75
	O60393	ATCCTGACAGTGATAAACGCCGAG	CACTCCACCCTGCCACCAGTGA	102	113
	PITX3	CCCAGAGGACGGTTCGCTGAAA	CTCTGGAAGGTCGCCTCTAGCTC	93	263
	Q9HB31	TGGAGAGGGCGTTTGCAGCATGG	TTGGCCTCAGGAAGGCAAGTGA	85	75
	PITX1	AGACGACCCAGCCAAGAAGAAGAA	AGCTCTTGCAACTGCTGGCTTGTGAA	72	188
	PROP1	AGTCAGCCTTTGGGAGGAACCAGTA	CCAGTGTCCCGGGCAAGACTCTCT	67	113
	HOP	TCCTGGAGTACAACTTCAACAAGGTCG	CGATGAGGCACAGCGTGGTGGAAT	63	225
14					
	DMBX1	TTATGGTTCCCAGCACCGCAAACA	CCTCAGGCAGGTTGGTGCACAT	149	60
	RAX	CACCGGCGAAGCGAAACTGTCAGA	GCTGTACACGTCCGGGTAGTGGGA	136	113
	OTX2	CGTTCACTCGGGCGCAGCTAGA	CCTCGACTCGGGCAAGTTGATTT	113	113
	OTX1	CACCACCTTCACGCGTTCACAG	GTTGATCTTGAGCGCCACCTCCT	103	68
	NP_116142	AAGAAGAAGCACCGGAGGAACC	ACACATCCGGGTAGTGAGAGGC	94	188
	PRRX2	CACGTTCAACAGCAGCCAACTG	CAAGCTCCTCGCGCACAAAGGC	86	113
	PRRX1	AGCAGCGAAGGAATAGGACAACCT	GGATAGTGTGTCCGCTCAAAGACA	79	75
	PHOX2B	CAAACTCTTCACGGACCACGGC	ACTGGTGAAAGTGGTGCGGATG	73	75
	PHOX2A	TTCTTCCCAGAGCCATCCGGCCT	CTGGTGAACGTGGTGCGGATGC	68	94
	CRX	CACTGTTTGCCAAGACCCAGTACC	TTGATCTTCAGAGCCACCTCCTCA	64	75
15					
	NKX3-1	CTCACGTCCTTCCTCATCCAGGACA	CCGGTGCTCAGCTGGTCGTTCT	161	703
	BAPX1	TCAGCGAGGAGAACGAGAGCAG	TTCCTCCTCTAGGTCTTTGGAAGCG	134	469
	NKX2-3	ACTTCCACTCTGCGCCCTGCAT	ATAGGACAATTTCTCGCCCTCGTC	101	56
	HMX2	TTCGACCTGAAGCGCTACCTGA	TGGAACCAGATCTTAACCTGCGTC	92	703
	NKX2-6	AGTACCTGAGAATGGACGCAGAGC	AACCATCCAGCTTTCTGTCACCG	84	75
	NKX2-8	CTGGTTCCAGAATCATCGCTACAAGC	ATGCTGCCAGGTCAGGCGACTC	77	469
	NKX2-5	TTCACCGGCCAAGTGTGCGTCT	TCGCTGTAGGCACGTGGATAGAAGGC	66	117
	NKX2-2	TTCTACGACAGCAGCGACAACCCGTA	TACTGAAGGCCCTCGGTGCTGG	62	117
16					
	LHX2	CGGGACTTGGTTTATCACCTCAACTG	CACGTCGGCATGGTTGAAGTGTG	165	56
	LHX3	CCCAGGACTTCGTGTACCACCT	CTCGCTGCTTGGCGGTTTCGTAGT	138	281
	LHX5	TCATCCTGTACGGACCGCAGTTT	GTTCTGCTCCTCGTTCTCGTTGTT	126	141
	LHX1	CCCAGTTTGTCTCCGGATTCCCAA	CCAGGTTCTGGTCGTCATTCTCGTT	115	94
	LHX9	AAGACCAAGCGCATGCGAACCTCTTT	AAGCTGCTTGAGGTCCTTGGCAT	105	47
	LHX6	GTTATGCAGGCGCAGTTCGCGCAG	CTGGATGACTCTCCGGCTGAGG	96	469
	GSCL	GCCACCGCACCATCTTCAGCGA	TCGCGCGTACTCACGTCAGGATA	88	469
	GSC	CACCAGATGCTGCCCTACATGAAC	ACAGTGCAGCTGGTTGAGAAGC	75	234

17					
	TGIF2	AACTGGTTCATCAATGCCCGGCGGCG	CTGGCCTGAGTGAAGCGGCAT	216	214
	PBX3	AATTGGTTTGGCAACAAACGAATCAG	GGAATTTGGTGTGGTGGGCGAA	159	161
	C10orf48	AATTGGTTTGCTAATGCAAGACGTCG	GAGTCATCACTGCTTACGCTAAGCCGT	137	107
	PBX1	AACTGGTTTGGAAATAAGCGAATCCG	GCTTCCATGGGCTGACACATTGG	120	161
	PBX2	AACTGGTTTGGCAACAAGAGGATTCG	CCTGGGTGACTGACACGGCG	103	107
	PBX4	AACTGGTTTGGCAACAAAAGAATCCG	TCCACAGCCGTTTTACCCGTGTAAAT	92	107
	TGIF2LX/Y	AACTGGTTTATCAATGCTCGCAGACG	TGGCCAATGATGGGGTCGTTTC	77	107
18					
	EVX2	GGATCAAGTGCGGCGCTACCGT	GGTGGTTTCGGGCAGGTTGAGT	139	107
	IPF1	TTCACCACCACCTCCCGGCTCA	GACTTCATCCATGGGAAAGGCAGC	127	429
	EVX1	CTTCACCCGAGAGCAGATTGCG	TGATGGTGGTTTCCGGCAGGTTTA	116	107
	GSH2	ACCCAATGGCAAGAGGATGAGGA	TTCAATCCTCCGGAGTCGAGACA	106	321
	VENTX2	TAAGGAGCCAAATACCTTGCGGG	GTACTGGTGGTGCTGGAAGACG	97	107
	MEOX2	GGACAGCATTTACCAAAGAGCAAATCAG	TATCTCGTATCGCCTCAGTCTGGT	89	107
	MEOX1	TGGAGGCAGAGTTTGCCCATCATA	CGCTCAGAGAGGTCCAGGTTTAC	82	107
19					
	IRX1	ACCTGGTTCGCCAACGCGCGCCGGCG	TCGCCATCGTGCTCGTCGATCT	191	125
	IRX3	ACCTGGTTCGCCAACGCGCGCCGGCG	CCTCCAGCTCTAGCTCGCGTTTG	163	250
	IRX6	ACCTGGTTCGCCAACGCACGCCGGCG	TTCTTTGGTGTCAGCAGTTAGGCAGC	139	20
	IRX5	ACCTGGTTCGCCAACGCGCGCCGGCG	GGGCTCGTCCTCGTCGTTCTTC	129	250
	IRX2	ACCTGGTTCGCCAACGCGCGCCGGCG	CGTCCTTGCTTCTGGTAGCGTCG	118	625
	IRX4	ACCTGGTTCGCCAACGCGCGCCGGCG	TAGGGCCGCTTCTCGTCTGCG	92	125
20					
	POU4F2	GTCTGGTTCTGCAACCAGAGGCAGAA	GCTCAGTTGTTCGCTCGTTCGC	219	250
	POU4F1	GTGTGGTTTTGCAACCAGAGACAGAA	CCCCAAATGCAGGCAGGATAACG	179	250
	POU1F1	GTTTGGTTTTGCAACCGGAGGCAGAG	TGAGGAAGAGAAAGGAATGAAACGGGAGAA	155	100
	POU4F3	GTCTGGTTCTGCAACCAGAGACAGAA	GATAACCATCCCCCGAACCCG	133	250
	POU3F2	GTTTGGTTTTGTAACAGGAGACAGAA	GAGTGTCCCTACTCCCCCCGTACA	100	250
	POU6F2	GTTTGGTTCTGCAATAAGAGGCAAGC	CTCCAAAGGGACTGCCGTGGC	87	125
21					
	CDX1	GGCAAAGGAGCGCAAAGTGAACAA	GCAGAAACTCCTCTTTCACAGGCA	176	68
	BARHL2	TTGCTGGCCGAGGCAGGGAACTA	AGGAGTCCGGTACATGCTGCTG	147	61
	BARX2	GAAGCTGAAGAGAAGATGAACAGCCAGG	TCTGGTGGCTCTGCCATCTCTAA	134	136
	HLX1	AGCGTTCTCTGCACCAAACAACAG	GCTGCTGAAGCTGAAACTATTGCC	122	102
	HHEX	AGGTGCTTCTTTGGATAGCTCTCAATGTTC	TTATCGCCCTCAATGTCCACTTCC	111	102
	NANOG	GACACTGGCTGAATCCTTCCTCT	TGGGCATCATGGAAACCAGAACAC	92	68
	CDX4	TTTCAGAATCGCAGAGCCAAGGAGAG	ACTTTGCACCGAGCCTCCACTATT	84	136
	TCF2	AGTATTCCCACACCTCCCGGTTT	CATGTTGGTGAGTGTACTGATGCTGC	77	102
	TCF1	TACCAGAGCTCAGACTCCAGCAAT	AAGGTCTCGATGACGCTGTGGTT	71	68
	BARX1	TCGGAGCCGCACTGTGTTCACC	TTCTGCTTCTCGAAGCGTTTCTCC	66	205
	CDX2	ATATCGAGTGGTGTACACGGACCA	GACTGTAGTGAAACTCCTTCTCCAGC	62	153
22					
	SIX5	CTCCATCCTGGTGAACGGGAGCTT	AGAGAGGTCTTGGTCTCGCTGG	195	68
	SIX4	ACTGGTCAAGACCTATTGTCAGTCCC	GTTAGCTACCGATTGCAGAACCAAACG	150	61
	SIX6	CTCCAGCAGCAGGTCCTGTCAC	ATGGAGATGGCTGAAGTGGCCG	137	55
	SIX2	GAGAACAACGAGAACTCCAATTCTAACAGC	GGGCTGGATGATGAGTGGTCTG	125	85
	SIX1	TCCTCCTCCAACAAGCAGAACCAA	AAGGACCGAGTTCTGGTCTGGACTTT	114	102
	PKNOX2	ATGCTTGATGCCAGCAACCCAGAT	GCGATGGAGTTGGGCCAGAATCTTT	95	68
	MEIS2	CACCCTGGAATGACTATGTCAGCA	ATGAATGTCCATAACCTGTCCGCC	87	136
	PROX1	GCATTACCTCTCAGCTCATCAAGTGG	TTGACGTGCGTACTTCTCCATCTG	80	136
	MEIS1	GCCACCGGTATATTAGCTGTTTGAAAGGG	TGATCCTCCTTCTCTATCGTCTATCACC	74	170
	PKNOX1	ACGTGGACAGCCTTCAGTCTCTGT	CTGCCATCATGACCTGCTGCAC	69	68
	MEIS3	CTCTCCCAGTTCTGGTGGAGAAGAT	CCCTCTTCTTGTTTCGCCGTCGCT	65	102
23					
	CDX2	ATCTGGTTTCAGAACCGCAGAGCAAA	TGCAGGGAAGACACCGGACTCA	173	83
	TCF1	AACTGGTTTGCCAACCGGCGCAAAGA	CCTTACTGGGGGAGAGGGCAGGT	154	83
	HLX1	GTGTGGTTCCAGAACCGGCGGATGAA	GGCTGGGGCTCCTCTCGTCCTGCTCG	142	50
	CDX1	ATCTGGTTCCAAAACCGGCGGGCAAA	GGCCCCCCAGGGATGGCCCG	130	83
	CDX4	ATCTGGTTTCAGAATCGCAGAGCCAA	CTGATGGAGTCAGAGTCACTTTGCACCGAGCCTCC	107	83
	HHEX	AGGTGAGATTCTCCAACGACCAGA	ATCTTGGCCAGACGCTTCCTCT	97	250
	TCF2	AACTGGTTTGCAAACCGCAGGAAGGA	CAGGCTGTGAGTCTGGTTGGAGCTATAG	87	67
	NANOG	ACCTGGTTCCAGAACCAGAGAATGAA	TGCGTCACACCATTGCTATTCTTC	80	125
	HHEX	TGTGATCAGAGGCAAGATTTGCCCAGTGAA	GGGGAGGGCGAACATTGAGAGCTA	77	208
24					

	IRX3	AGGGAAACGCTTATGGGAGCGA	GCGCCGTCTAAGTTCTCCAAATCG	181	250
	IRX1	GCTCGCAGTATGAACTGAAGGACA	CTTGAGCGTGCTGGTGCTCTCG	152	250
	IRX5	ACACGAACTATGGCTCCTTCGGA	TTCGGGTCTTTAGCCAAAGCGT	139	417
	TGIF2LX/Y	ACAGGCAGAGTTCTTGCCTTACCA	CTTCTTCTGAAGGGTAGGCCTTAAACCG	127	188
	TGIF2	AGCAGGACAAAGAGGACTTCAGCA	AGTGTGCAGTAATGGGAGTGATGG	116	104
	C10orf48	CAAGAGCAGCTTGTTGAACCGTTACC	AGATCCCGAGTGGTTTCTTTGCCT	106	83
	IRX6	CGAATCTACCCAACGCTCTGTCTCA	ACTGCCCAGCAGTCGACTATCGTA	97	208
	IRX4	GCTGCAGGAGCACCGCAAGAAC	AGACCTGTGTGAGGGTCATCTTGGT	89	83
	TGIF	TTCCCTTGGACCTTTCTTCATCCG	AGAATCTGCACAGACTCCTTGGGT	82	125
25					
	CHX10	GTCTGGTTCCAGAACCGTCGAGCCAA	TGGCTGACTTGAGGATGGACTCG	142	188
	ALX4	GTCTGGTTCCAGAACCGAAGGGCCAA	TCATATGCAGTGGAGAAGTGGGTTCG	92	125
	ALX3	GTCTGGTTCCAGAACCGCAGAGCCAA	CAGCCGTGAAGGGGTTCCGCCCCTC	85	100
	VSX1	GTCTGGTTTCAAAACCGCAGGGCCAA	CGTACTCGGCCATCACGCTGCT	79	188
	CART1	GTTTGGTTTCAAAATCGAAGGGCCAA	GCTTTTCGCTTGTTGTATTTGGCCATAAC	72	125
	HESX1	ATTTGGTTTCAAAATCGGCGTGCAAA	CGCCATTAGAAACTGTGATTCTCTATGGG	66	188
26					
	POU6F1	GTCTGGTTCTGCAATCGGCGCCAGAC	GATGCACATGCACACGGTGGA	215	300
	POU3F4	GTCTGGTTCTGTAATCGAAGACAAAA	TGGCAAGATGTGTCTGTTTTCACGG	107	600
	POU2F2	GTCTGGTTCTGCAACCGGCGCCAGAA	CTGTAGCTGGCCGGCTTCCCT	95	120
	POU2F1	GTTTGGTTCTGTAACCGCCGCCAGAA	GCTTTAATAGGTGAGCTGCTGGTCCCAC	83	150
	POU2F3	GTCTGGTTCTGCAACCGACGCCAAAA	TGTAGACAGGTGGTTTGATGGGTGTG	79	150
27					
	EN1	ACCAAATACCCGGAGCACGGCAA	GGACGATCCGAATAACGTGTGCAGTA	137	125
	NP_689781	ACCTGGGTCTAGGCTTTGCTCA	ATGCAGGAGTGTCTGCTTCTTCC	125	83
	EMX2	AGTCGCTGGTGGCCAAGGACAG	AGCCGTTGAGGAACGGATTTATGG	114	417
	NP_940881	TTGCCAGACACCCAGTTATTCCCT	CCTTCTTGGTACTGAGAGGTCATGGT	104	104
	VAX2	GAAATTGTCCTGCCTAAGGGCCTG	AACTCCATCTCCAGGCGGTACA	95	167
	VAX1	GCTCTATCGGCTGGAGATGGAGTT	GAGAGGTTAAGCTGCCGGGCGA	87	333
	EMX1	AGCGCGCCTTCGAGAAGAACCACTA	CGTCTCGGAGAGGCTGAGACTG	80	104
	NKX6-2	AACCTTCGAGCAGACCAAGTACC	TCTCGGTCATGCCCAGCGAGTA	74	625
	NKX6-1	GCCCTGGAGAAGACTTTCGAACAA	CGAATAGGCCAAACGAGCCCTCT	69	167