

Table S2. The primer sequences of 6 WS-related genes.

fragment_name	fragment_size	primer_5'	position	sequence	primer_3'	position	sequence
mSOX10E04D	275	mSOX10E04 D_5R	chr22:38370038-3 8370059	AGCCACGAGGTAATGTCCAACA	mSOX10E04 D_3F	chr22:38369785-3 8369804	GGCTGGTCGGTGTAGTGTGG
mSOX10E03A	280	mSOX10E03 A_5R	chr22:38374171-3 8374192	CATTCACGCCAGCCCCTCTGCT	mSOX10E03 A_3F	chr22:38373913-3 8373933	CCTCTCCTGGGTGCCGGTGGT
mSOX10E03B	200	mSOX10E03 B_5R	chr22:38373977-3 8373996	GTGGGGAGGCCGAGCAAGGT	mSOX10E03 B_3F	chr22:38373797-3 8373822	GTCTCATTGCCATCCAGCCATCTC CT
mSOX10E02B	274	mSOX10E02 B_5R	chr22:38379777-3 8379796	gcgacatggcggaggAGCAG	mSOX10E02 B_3F	chr22:38379523-3 8379541	ATGGGCACCAGCGTCCAGT
mSOX10E01A	261	mSOX10E01 A_5R	chr22:38380552-3 8380574	CGGCTCAGGCTCAGTCGCTCAGT	mSOX10E01 A_3F	chr22:38380314-3 8380332	GCGGGCCAGGGAGGAGCAG
mSOX10E02A	209	mSOX10E02 A_5R	chr22:38379933-3 8379954	GGGCTGTGCCACGTCCTGTCT	mSOX10E02 A_3F	chr22:38379746-3 8379766	CCACGGGGCTCAGCTCCACCT
mSOX10E04C	243	mSOX10E04 C_5R	chr22:38369849-3 8369870	GTCTCACCACCTGGTGTGGATG	mSOX10E04 C_3F	chr22:38369628-3 8369649	GAAGGCCGAGTAGAGGCCAGAG
mSOX10E02C	277	mSOX10E02 C_5R	chr22:38379550-3 8379571	AGGCCGTCAGCCAGGTGCTCAG	mSOX10E02 C_3F	chr22:38379295-3 8379316	GCCGCCTCGGCTACCCTGAATC
mSOX10E04B	275	mSOX10E04 B_5R	chr22:38369694-3 8369715	CCGCCCCAGTTTGACTACTCT	mSOX10E04 B_3F	chr22:38369441-3 8369460	GAACAGGGCACACAGGCTGG
mSNAI2E01A	246	mSNAI2E01 A_5R	chr8:49834019-49 834050	CTGTGATTGGATCTTTCTTGCAAAA GAGAGGA	mSNAI2E01 A_3F	chr8:49833805-49 833826	ACCAGGAAGGAGCGCGGCATCT
mSNAI2E01B	269	mSNAI2E01 B_5R	chr8:49833857-49 833878	GTCCTCCCGCCGACCGTTATC	mSNAI2E01 B_3F	chr8:49833610-49 833641	TCCCTTTCAGGACACTGTTAAAAA GGAAAACA

mSNAI2E03A	235	mSNAI2E03A_5R	chr8:49831528-49831549	AGGGGAGAAGCCTTTTTCTTGC	mSNAI2E03A_3F	chr8:49831315-49831338	GCTTCGGAGTGAAGAAATGCATTC
mSNAI2E02C	277	mSNAI2E02C_5R	chr8:49833013-49833036	TGCCTTAATCTTCTCTCCCTCCCT	mSNAI2E02C_3F	chr8:49832760-49832781	CTAATGGGGCTTTCTGAGCCAC
mSNAI2E03B	251	mSNAI2E03B_5R	chr8:49831705-49831740	TAAATGCAATATTCAAGTTTATCTTAAAAATTCAGG	mSNAI2E03B_3F	chr8:49831490-49831515	AGATTTGACCTGTCTGCAAATGCTCT
mSNAI2E02B	257	mSNAI2E02B_5R	chr8:49832800-49832819	TCCCCCTCCTCCATCTGACA	mSNAI2E02B_3F	chr8:49832563-49832582	CGCCCAGGCTCACATATTCC
mSNAI2E02A	247	mSNAI2E02A_5R	chr8:49832621-49832638	CAGCTGCACTGCGATGCC	mSNAI2E02A_3F	chr8:49832392-49832409	ACAGCCAGCCCAGGGCTT
mMITFE07A	285	mMITFE07A_5F	chr3:70005561-70005588	CATGGCACTGTTACTAATAGCCTTTCCT	mMITFE07A_3R	chr3:70005814-70005845	TGAGACTAACCAAAGAAAGGTGTAAGAAGAA
mMITFE01A	255	mMITFE01A_5F	chr3:69985655-69985680	AAAAAGGCCCTTATGTGAACGTTTTCCT	mMITFE01A_3R	chr3:69985878-69985909	CACCTGATAGTGATTATATTCTAGCATTTC
mMITFE05A	208	mMITFE05A_5F	chr3:69998153-69998184	ATGGGAATTGTTCAACAGTTAATTCTGTAC	mMITFE05A_3R	chr3:69998333-69998360	ACAGAAATCTGCAGTAAGAGGCCACATTT
mMITFE04A	265	mMITFE04A_5F	chr3:69990342-69990377	AGTTTATTATTTTTGTCTCTCTTCTCTTACCCTTT	mMITFE04A_3R	chr3:69990571-69990606	CCATTTTACTATTAATACATTTAATCAGTGAACCAG
mMITFE01B	279	mMITFE01B_5F	chr3:69985798-69985829	AAATTGGAATTATAGAAAGTAGAGGGAGGGAT	mMITFE01B_3R	chr3:69986043-69986076	GTTCAAACTACATTGAATTACTTCTTATGGCAT
mMITFE08A	230	mMITFE08A_5F	chr3:70008379-70008408	GCCTCAAATCCTAAAAATATCTGTTCCT	mMITFE08A_3R	chr3:70008579-70008608	AAAAAGCAGTAACTTTACACAACTCAGGC
mMITFE09B	285	mMITFE09B_5F	chr3:70014155-70014176	CAACTCTCGATCTCACGGATGG	mMITFE09B_3R	chr3:70014418-70014439	AAGGAAGCAGTTTGTGCGAATG
mMITFE06A	287	mMITFE06A	chr3:70000914-70000914	TGCAACTTCAAACAGTTCCAACCTT	mMITFE06A	chr3:70001167-70001167	GGAAAATATATACCTTGGTTTCTG

6A		_5F	000941	CTAA	_3R	001200	TCAAATACAA
mMITFE0 9A	275	mMITFE09A _5F	chr3:70013949-70 013972	tcctctgtgctctgcctatttcag	mMITFE09A _3R	chr3:70014203-70 014223	GGTTGGCCTCAGTCCCAGTTC
mMITFE0 2B	273	mMITFE02B _5F	chr3:69987093-69 987112	CCATGTCCAAACCAGCCTGG	mMITFE02B _3R	chr3:69987344-69 987365	AGACAACAGGCTGGAATGCCAC
mMITFE0 2A	277	mMITFE02A _5F	chr3:69986906-69 986929	AAGGAAGAGCCGTCTGAAACTCAC	mMITFE02A _3R	chr3:69987159-69 987182	GTAAAGCGTAAGCATAGCCATGGG
mMITFE0 3A	251	mMITFE03A _5F	chr3:69988171-69 988194	TCAGCTTTGTGTGAACAGGTCATT	mMITFE03A _3R	chr3:69988397-69 988421	TGCTTAAGTTTTCAGGAAGGTGTG A
mEDNRB E03A	245	mEDNRBE0 3A_5R	chr13:78477770-7 8477791	GGGCATCTTATGAAACCCCCTA	mEDNRBE0 3A_3F	chr13:78477547-7 8477578	GAATTGCACAGTTTATTTTCTAAG TAACATGG
mEDNRB E08E	284	mEDNRBE0 8E_5R	chr13:78471784-7 8471805	TGCATTTTTTCGGACACTGGAAA	mEDNRBE0 8E_3F	chr13:78471522-7 8471545	TCTTTTGGGATAGCCTTTCAAACA
mEDNRB E02A	211	mEDNRBE0 2A_5R	chr13:78492350-7 8492369	CTGGGGATCATCGGGAACTC	mEDNRBE0 2A_3F	chr13:78492159-7 8492178	TCATCTCCCCGTCTCCAACC
mEDNRB E08J	287	mEDNRBE0 8J_5R	chr13:78470781-7 8470805	AGCAAAACACAGTGCAATGTTCTC A	mEDNRBE0 8J_3F	chr13:78470519-7 8470546	TGAAATTAAAGAACAAGTTTGTGG GTGA
mEDNRB E08A	260	mEDNRBE0 8A_5R	chr13:78472510-7 8472531	GGAGGAAGAGTTGGGAAAGGTG	mEDNRBE0 8A_3F	chr13:78472272-7 8472297	CATTTTGTTTTAATGACTTCGGTCC A
mEDNRB E08F	270	mEDNRBE0 8F_5R	chr13:78471558-7 8471587	TTTACATTCAGTTAAGATCAAACC TCACAA	mEDNRBE0 8F_3F	chr13:78471318-7 8471343	GGCATCTCTCCATCGTAAAGCTAT GA
mEDNRB E08B	234	mEDNRBE0 8B_5R	chr13:78472337-7 8472366	TCCGTTCCAGTAATAAATACAGCT CATCTT	mEDNRBE0 8B_3F	chr13:78472133-7 8472155	TCCCACTGATTTTCTTTCCATGC
mEDNRB E08G	288	mEDNRBE0 8G_5R	chr13:78471345-7 8471362	ATGAGGGCAGGCCCTGTG	mEDNRBE0 8G_3F	chr13:78471075-7 8471100	CCATGTCAAGCAAACCTTTTCTATT GG

mEDNRB E07A	251	mEDNRBE0 7A_5R	chr13:78474154-7 8474185	CCTTACAAAAGCACAGAAGCTACA ATGACTAC	mEDNRBE0 7A_3F	chr13:78473935-7 8473966	TGAAAGCTTATATTTGAGCCATAT TACAAAGA
mEDNRB E04B	237	mEDNRBE0 4B_5R	chr13:78477622-7 8477649	TGTGCTCTGAGTATTGACAGGTAG AAGC	mEDNRBE0 4B_3F	chr13:78477413-7 8477440	CCCAAATCAAAACAATTTCTACTG CTGT
mEDNRB E08I	290	mEDNRBE0 8I_5R	chr13:78470989-7 8471015	TGTGCGTTCCTGCCTAATTTTTATA TC	mEDNRBE0 8I_3F	chr13:78470726-7 8470755	CATATTTTAAGACCGAGTTAAAGC TCTTGG
mEDNRB E01A	252	mEDNRBE0 1A_5R	chr13:78549679-7 8549702	gaggcagctccttagtgacttaa	mEDNRBE0 1A_3F	chr13:78549451-7 8549471	GGAGTGGGCAAGTTCCAAAGA
mEDNRB E02C	267	mEDNRBE0 2C_5R	chr13:78492742-7 8492763	CTAGGCTCTGAAACTGCGGAGC	mEDNRBE0 2C_3F	chr13:78492497-7 8492514	ACCTCCGCAGGTGCCAAC
mEDNRB E04A	259	mEDNRBE0 4A_5R	chr13:78477449-7 8477476	TGGAGTAGAATTAAGGAATTGGG GTTC	mEDNRBE0 4A_3F	chr13:78477218-7 8477241	GGGGAACAGGGGAAAAATAGCTA A
mEDNRB E05A	245	mEDNRBE0 5A_5R	chr13:78475353-7 8475387	TCTTACAGAGGAGTATTAATCGTA AAAATTCTCTC	mEDNRBE0 5A_3F	chr13:78475143-7 8475175	TCATAATTATAAATTCAACCACGA GTTATCAAA
mEDNRB E06A	220	mEDNRBE0 6A_5R	chr13:78474799-7 8474826	GCCATCTTTTAAGGGTCAAACAT GGAT	mEDNRBE0 6A_3F	chr13:78474607-7 8474634	TTCTGAGTGGCATTATTTACAAA ACCA
mEDNRB E08D	283	mEDNRBE0 8D_5R	chr13:78472000-7 8472030	AATGAGCTCACTCAGAATTTCTAT TCTTTCT	mEDNRBE0 8D_3F	chr13:78471748-7 8471772	TGCTCTTTCTGTTACTCCCTCCTGA
mEDNRB E02B	279	mEDNRBE0 2B_5R	chr13:78492555-7 8492580	AGAGATAATGACGCCACCCACTAA GA	mEDNRBE0 2B_3F	chr13:78492302-7 8492321	GGACCGTTTTGCATGCACTT
mEDNRB E08H	290	mEDNRBE0 8H_5R	chr13:78471229-7 8471249	CCTCTCTACCCATGCTGTGG	mEDNRBE0 8H_3F	chr13:78470960-7 8470984	CAAGCTATCCTAAGGCACTTTGCT T
mEDNRB E02D	267	mEDNRBE0 2D_5R	chr13:78492953-7 8492972	CGGGGGAAGAAAAACAGCTG	mEDNRBE0 2D_3F	chr13:78492706-7 8492727	CATGCTGCTACCTGCTCCAGAA
mEDNRB	237	mEDNRBE0	chr13:78472156-7	AGCTACATATGACATTTTATGAGC	mEDNRBE0	chr13:78471951-7	TTCTTCCTTTATATCAGAGTCCCAT

E08C		8C_5R	8472187	TGTTTACG	8C_3F	8471979	TGAT
mPAX3E0 8A	257	mPAX3E08A _5R	chr2:223066809-2 23066830	GTCTGGAACCTACCACCACGGT	mPAX3E08 A_3F	chr2:223066574-2 23066603	AATCTTGCTCTAATTCACCTTTCT TAAGG
mPAX3E0 1A	259	mPAX3E01A _5R	chr2:223163370-2 23163391	TCGCCTTTCCGTTTCGCCTTCA	mPAX3E01 A_3F	chr2:223163133-2 23163154	GTGCCAGGGAATGGGCTTCCT
mPAX3E0 2A	193	mPAX3E02A _5R	chr2:223161825-2 23161842	TCGTGGAGATGGCCCACC	mPAX3E02 A_3F	chr2:223161650-2 23161669	AGGGGACCACAGTCTGGGAG
mPAX3E0 8B	277	mPAX3E08B _5R	chr2:223067026-2 23067049	GGGTCATAGTCTCCTGGACAGCT	mPAX3E08 B_3F	chr2:223066773-2 23066800	TTCATATGGTCTAGTCTCTGACTGC AGC
mPAX3E0 2B	227	mPAX3E02B _5R	chr2:223161968-2 23161995	TTCTTTGCTTTTTATTTTCCTCCAGT GA	mPAX3E02 B_3F	chr2:223161769-2 23161786	GACGCAGCCGTGGGACAC
mPAX3E0 7A	243	mPAX3E07A _5R	chr2:223085005-2 23085028	CTCCAAGCACTGTACACCAAAGCA	mPAX3E07 A_3F	chr2:223084786-2 23084813	ACTACTGCCTCAGGGAATTGAATA TTTG
mPAX3E0 6B	203	mPAX3E06B _5R	chr2:223086066-2 23086087	GTGCAAGATGGAGGAAGCAAGC	mPAX3E06 B_3F	chr2:223085885-2 23085906	CACCAGAGAAATCGCCTGGAAG
mPAX3E0 3A	238	mPAX3E03A _5R	chr2:223160410-2 23160427	ACCTGGCCCAGGGTACCG	mPAX3E03 A_3F	chr2:223160190-2 23160211	GCCGGGGTAATAGCGACTGACT
mPAX3E0 7B	277	mPAX3E07B _5R	chr2:223085186-2 23085213	TTAAGAAACGCAGTTTGAAGTGAA CATT	mPAX3E07 B_3F	chr2:223084937-2 23084956	GCTGGAAAATCCATGCCTGG
mPAX3E0 6A	231	mPAX3E06A _5R	chr2:223086203-2 23086225	TCTTGCATCTATTTGCCCTTTCA	mPAX3E06 A_3F	chr2:223085995-2 23086012	AGGTCCGCATGGCAGTGG
mPAX3E0 5B	269	mPAX3E05B _5R	chr2:223097176-2 23097199	ACATTGGGAATGCACTGTAGACCA	mPAX3E05 B_3F	chr2:223096931-2 23096958	GCTGTTTCTCTTTAGTGGTAAATC TGG
mPAX3E0 4A	223	mPAX3E04A _5R	chr2:223159040-2 23159057	GTGCGCTCCCTTGCTTCC	mPAX3E04 A_3F	chr2:223158835-2 23158854	ATGCCCTCCAAGTCACCCAG

mPAX3E0 5A	279	mPAX3E05A _5R	chr2:223097001-2 23097028	GATGTTTTGTCTTCTGTGCTTTTA GCC	mPAX3E05 A_3F	chr2:223096750-2 23096775	TTTCCTGTCTGGACTGAAGTAGGA CA
mEDN3E0 4A	271	mEDN3E04 A_5F	chr20:57897368-5 7897389	GAAAAACCAGCCACAGGGAAAG	mEDN3E04 A_3R	chr20:57897619-5 7897638	CCACCAAAGGCACCATTGCT
mEDN3E0 2A	242	mEDN3E02 A_5F	chr20:57876409-5 7876428	GGGTGTTGAGGGGTCTGCAC	mEDN3E02 A_3R	chr20:57876633-5 7876650	CAGGGCTTCCAGGGCTTG
mEDN3E0 3A	260	mEDN3E03 A_5F	chr20:57896022-5 7896039	GAGCAGGGAGGCCTGGGT	mEDN3E03 A_3R	chr20:57896258-5 7896281	TGCAAATGAGTGAAACTGGAGGA G
mEDN3E0 1A	185	mEDN3E01 A_5F	chr20:57875829-5 7875847	GTCCTCCTGGTCCGGTGCT	mEDN3E01 A_3R	chr20:57875995-5 7876013	CGCGACGCACATCTTCTCC
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mEDN3E0 5A	272	mEDN3E05 A_5F	chr20:57899287-5 7899308	TGGGAAGACGTTCCCTTTTCA	mEDN3E05 A_3R	chr20:57899537-5 7899558	ATGACAGAAGCCTCCCGAGACC
SOX10_E 04E	287	SOX10_E04 E_5F2	chr22:38370017-3 8370037	CAGCCACATCAAAGGTCTCCA	SOX10_E04 E_3R2	chr22:38370285-3 8370303	CCGCTGCCTGAAGGTGAAC