Table S1. Primers used for semi-quantitative PCR analysis.

Gene	Accession Number	Region amplified (aa)	Size of product (bp)	Primer sequence
HOXA1	U10421	511 to 663	153	F: 5’ CTGGCCCTGGCTACGTATAA 3’ R: 5’ TCCAACTTTCCCTGTTTTGG 3’
HOXA2	NM_006735	1027 to 1202	176	F: 5’ TTCAGCAAAATGCCCTCTCT 3’ R: 5’ TAGGCCAGCTCCACAGTTCT 3’
HOXA3	NM_030661	1525 to 1751	227	F: 5’ ACCTGTGATAGTGGGCTTGG 3’ R: 5’ ATACAGCCATTCCAGCAACC 3’
HOXA4	NM_002141	633 to 903	271	F: 5’ CCCTGGATGAAGAAGATCCA 3’ R: 5’ AATTGGAGGATCGCATCTTG 3’
HOXA5	NM_019102	796 to 988	193	F: 5’ CCGGAGAATGAAGTGGAAAA 3’ R: 5’ ACGAGAACAGGGCTTCTTCA 3’
HOXA6	NM_024014	361 to 518	158	F: 5’ AAAGCACTCCATGACGAAGG 3’ R: 5’ TCCTTCTCCAGCTCCAGTGT 3’
HOXA7	NM_006896	38 to 322	285	F: 5’ TGGTGTAAATCTGGGGGTGT 3’ R: 5’ TCTGATAAAGGGGGCTGTTG 3’
HOXA9	NM_152739	653 to 855	203	F: 5’ AATAACCCAGCAGCCAACTG 3’ R: 5’ ATTTTCATCCTGCGGTTCTG 3’
HOXA10	NM_018951	1040 to 1198	159	F: 5’ ACACTGGAGCTGGAGAAGGA 3’ R: 5’ GATCCGGTTTTCTCGATTCA 3’
HOXA11	NM_005523	800 to 1078	279	F: 5’ CGCTGCCCCTATACCAAGTA 3’ R: 5’ GTCAAGGGCAAAATCTGCAT 3’
HOXA13	NM_000522	1061 to 1236	176	F: 5’ GGATATCAGCCACGACGAAT 3’ R: 5’ ATTATCTGGGCAAAGCAACG 3’
HOXB1	NM_002144	176 to 332	157	F: 5’ TTCAGCAGAACTCCGGCTAT 3’ R: 5’ CCTCCGTCTCCTTCTGATTG 3’
HOXB2	NM_002145	9 to 267	259	F: 5’ CTCCCAAAATCGCTCCATTA 3’ R: 5’ GAAAGGAGGAGGAGGAGGAA 3’
HOXB3	NM_002146	1970 to 2268	299	F: 5’ TATGGCCTCAACCACCTTTC 3’ R: 5’ AAGCCTGGGTACCACCTTCT 3’
HOXB4	NM_024015	593 to 747	155	F: 5’ TCTTGGAGCTGGAGAAGGAA 3’ R: 5’ GTTGGGCAACTTGTGGTCTT 3’
HOXB5	NM_002147	1543 to 1731	189	F: 5’ AAGGCCTGGTCTGGGAGTAT 3’ R: 5’ GCATCCACTCGCTCACTACA 3’
HOXB6	NM_156037	151 to 334	184	F: 5’ ATTTCCTTCTGGCCCTCACT 3’ R: 5’ GGAAGGTGGAGTTCACGAAA 3’
HOXB7	NM_004502	143 to 391	249	F: 5’ CAGCCTCAAGTTCGGTTTTC 3’ R: 5’ CGGAGAGGTTCTGCTCAAAG 3’
HOXB8	NM_024016	964 to 1228	265	F: 5’ GTAGGCTTCAGCTGGGACTG 3’

				R: 5’ GGGAGCCTTTGCTTAAATCC 3’
HOXB9	NM_024017	533 to 730	198	F: 5’ TAATCAAAGACCCGGCTACG 3’ R: 5’ CTACGGTCCCTGGTGAGGTA 3’
HOXB13	NM_006361	154 to 387	234	F: 5’ CTTGGATGGAGCCAAGGATA 3’ R: 5’ CCGCCTCCAAAGTAACCATA 3’
HOXC4	NM_014620	1121 to 1396	276	F: 5’ CGCTCGAGGACAGCCTATAC 3’ R: 5’ GCTCTGGGAGTGGTCTTCAG 3’
HOXC5	NM_019953	555 to 822	268	F: 5’ CAGTTACACGCGCTACCAGA 3’ R: 5’ AGAGAGGAAAGGCGAAAAGG 3’
HOXC6	NM_004503	774 to 963	190	F: 5’ AAGAGGAAAAGCGGGAAGAG 3’ R: 5’ GGTCCACGTTTGACTCCCTA 3’
HOXC8	NM_022658	390 to 539	150	F: 5’ CTCAGGCTACCAGCAGAACC 3’ R: 5’ TTGGCGGAGGATTTACAGTC 3’
HOXC9	NM_006897	704 to 893	190	F: 5’ AGACGCTGGAACTGGAGAAG 3’ R: 5’ AGGCTGGGTAGGGTTTAGGA 3’
HOXC10	NM_017409	982 to 1270	289	F: 5’ CGCCTGGAGATTAGCAAGAC 3’ R: 5’ GGTCCCTTGGAAGGAGAGTC 3’
HOXC11	NM_014212	353 to 538	186	F: 5’ CGGAACAGCTACTCCTCCTG 3’ R: 5’ CAGGACGCTGTTCTTGTTGA 3’
HOXC12	NM_173860	654 to 833	180	F: 5’ CAAGCCCTATTCGAAGTTGC 3’ R: 5’ GCTTGCTCCCTCAACAGAAG 3’
HOXC13	NM_017416	1840 to 2009	170	F: 5’ GTGGAAATCCAAGGAGGACA 3’ R: 5’ TTGTTGAGGGACCCACTCTC 3’
HOXD1	NM_024501	929 to 1160	232	F: 5’ TTCAGCACCAAGCAACTGAC 3’ R: 5’ TAGTGGGGGTTGTTCCAGAG 3’
HOXD3	NM_006898	492 to 667	176	F: 5’ CAGCCTCCTGGTCTGAACTC 3’ R: 5’ ATCCAGGGGAAGATCTGCTT 3’
HOXD4	NM_014621	23 to 195	173	F: 5’ TCAAATGTGCCATAGCAAGC 3’ R: 5’ TCCATAGGGCCCTCCTACTT 3’
HOXD8	NM_019558	1167 to 1456	290	F: 5’ TCAAATGTTTCCGTGGATGA 3’ R: 5’ GCTCTTGGGCTTCCTTTTTC 3’
HOXD9	NM_014213	1803 to 2038	236	F: 5’ TCCCCCATGTTTCTGAAAAG 3’ R: 5’ GGGCTCCTCTAAGCCTCACT 3’
HOXD10	NM_002148	364 to 517	154	F: 5’ GCTCCTTCACCACCAACATT 3’ R: 5’ AAATATCCAGGGACGGGAAC 3’
HOXD11	NM_021192	302 to 554	253	F: 5’ GGGGCTACGCTCCCTACTAC 3’ R: 5’ GCTGCCTCGTAGAACTGGTC 3’
HOXD12	NM_021193	113 to 313	201	F: 5’ CGCTTCCCCCTATCTCCTAC 3’ R: 5’ CTTCGGGCGCATAGAACTTA 3’

HOXD13	NM_000523	868 to 1132	265	F: 5’ GGGGATGTGGCTCTAAATCA 3’ R: 5’ AACCTGGACCACATCAGGAG 3’
GAPDH	NM_002046	103 to 463	361	F: 5’ ATGGGGAAGGTGAAGGTCGGA 3’ R: 5’ GAGATGATGACCCTTTTGGC 3’
FDXR	J03826	601 to 827	227	F: 5’ TCCTACTGACCCCACCTGAG 3’ R: 5’ CTGGAGACCCAAGAAATCCA 3’
TFRC	M11507	1346 to 1524	179	F: 5’ AAAATCCGGTGTAGGCACAG 3’ R: 5’ TTAAATGCAGGGACGAAAGG 3’
MT2A	BC070289	125 to 310	186	F: 5’ GCAAATGCAAAGAGTGCAAA 3’ R: 5’ ATCCAGGTTTGTGGAAGTCG 3’
P4HA1	NM_000917	628 to 811	184	F: 5’ GGCAGCCAAAGCTCTGTTAC 3’ R: 5’ GGCTTGTTCCATCCACAGTT 3’
PSAP	NM_002778	997 to 1149	153	F: 5’ TGGTGGAGCCCATTAAGAAG 3’ R: 5’ GCTTCGAGCACATTTTGTCA 3’
TM7SF2	BC038353	552 to 775	224	F: 5’ CGCTTTCATCTTCAGCCTCT 3’ R: 5’ GCTCTGCCTCCTTCATCAAC 3’
GADD45A	NM_001924	197 to 355	158	F: 5’ GCCTGTGAGTGAGTGCAGAA 3’ R: 5’ CCCCACCTTATCCATCCTTT 3’

---

*aa = amino acids, ** bp = base pairs, F = forward primer, R = reverse primer, FDXR = Adrenodoxin reductase, MT2A = Metallothionein, P4H1 = prolyl 4-hydroxylase, alpha polypeptide I, PSAP = Prosaposin, TM7SF2 = Transmembrane superfamily member 2.