

*D. melanogaster* Northern probe PCR primers

cDNA ID	cDNA length, bp	Probe length, bp	5' probe primer	3' probe primer
AT08427	1808	1000	GGCCATAGCCTTGTACGTGT	CCGTGAAGCTTTGCTGTGTA
AT11392	994	807	CACCCTCTGCACAGCAGATA	ATTGTTGCCCCCAATTTGTA
AT13310	606	50	GCAATTGACCCATGCAATTT	GCTCGGAAGAAATTTCCATCA
AT14266	781	718	GCTAAATTAAGGCGATTGTAAGG	CCCGACACGCTGTTTCTTAT
AT21289	1415	997	GACGTCACAGCAAGGACTCA	GCAAATGCCGTGAGGATAAT
AT22150	1080	982	AATAGGCTCGAGCAGATGGA	GGAATACAATGCGCCCTAGA
AT24650	578	507	CGAACTCAGGACGCTCTTCT	CGCTTGTACATTTTGCCTAAG
AT27057	840	727	AGTGAATAATCCAACCCGACT	CCATGGGATAAGCCCTCGAAT
AT28783	1553	974	ATCGAAGACACCTTGGATGG	GAAAGAATTGCCAGCGAGAC
AT31442	1111	901	AACATTTTCGTCGGGTTCTG	AGCCCAATTTATCCCCTGTG
GH03576	931	710	TTGAATCGGAATCAGTGTGC	TGAAAGTCTGAGCAAACCAA
GH05108	1094	959	GAGGATGTGGAGGATGAGGA	CTGTTCCAAAATTGCTGTGG
GH05710	1211	1037	GGGAAACGCTGCAAAAGACTA	GCACATGTATGGCGATTGTC
GH06385	1190	948	AACATTTTCGTCGGGTTCTG	CAACAACGGCAACAGCTCTA
GH08923	2462	1100	GTGCGGATAATGCTTGGTTT	CTGTTGGGGGAATTTGCTTA
GH14469	695	615	ACCACGTGTGCCATTTC	ACGTCCACTTTTCTGGCATC
GH22170	743	702	GCGTTCACGCGACTCGTA	TTTTGCTTTTTAGCGCTCGT
GH25188	827	733	ATGGAACCCAGAACCAAGC	TGGGCGCCATATATTTTGAT
GH25505	2811	1021	CTACACTGCCAGCAACGAAA	TCGATCTGATTTCCGGGTAGG
GH26692	1674	923	GCCAATTGCCGAAGAGAATA	ACCGATTGGTAAAGCGCTAA
GH26828	2335	949	TGGCGAGTTGATGCGATTAG	TAAAACTCCTCGAAGCGGAGA
GH27201	4554	986	TGCTGCTGTGAAAATTCCTG	ACACCACCCAGCGAGAATAC
GM01028	1157	974	AACATTTGCATGTGTTGGGTA	TTTTTAAGGGTTGGACAACCG
GM01206	1214	977	CGAATGCAAACAGAGAACCA	TTTATTTCAATTCGAGGTTGG
GM02923	1035	819	CAACTATTTGCCAGCGCTTA	AATTTCTCATACGCGTGTCA
GM03003	1884	1060	TGGAGTCAAAGCGGATAC	GACAGCGGACGTGGCTATT
GM03661	1159	947	TCGCCACTTGTTTTAAACGA	TTTTTGCTCAACGGGACAAT
GM03914	1046	890	CCCCTCGTCTCTACTTCCAA	TGCAGTGATTCGGTGTGAT
GM04921	1159	951	ATCAATTTAGCCGCCTTGTG	TTGCTGAAATGCAAAACAAA
GM07040	3544	969	TTGACGACAGGCAAACTCAG	AAATGGGCGTAAAAGTGTGC
GM07077	1385	1067	CGCTGTTCTCATTTGCGATA	CCAATGCGCATACATTGTTC
GM07658	2095	939	TTGCAACTGCAATAGCCAAC	AGTTTTTGGCACCACCAAG
GM07660	853	701	ATCGAAAAGACGAGCGACAAA	TCGTACAAAATGTTCAAACAACA
GM07702	850	800	GATGGCAAGCCAACAACAAC	GGGTATTGTCACTTCCGGTACA
GM09444	653	507	TCCAGAGCAGACGGAAAAGT	CTTCGGTGTGGGGTGTITTT
GM09534	912	877	CCCCTCTCGCTCTAACCTCT	TTTCCCATTTCTCTTTATTCTCG
GM09668	834	604	TGTAGCAAAAACAAAACCATGT	TGCTCGAATATTTGCTAGATTTTG
GM10787	1695	932	ACCGGTTAGAGAGCGCATAA	AGCGTGTCTGTTTGGTGTG
GM12657	708	518	CCAGACTCATCCCCACTCAT	AGGGATGACAATTTGGCTTG
GM24362	450	402	AATGACGGGTTGATTGACTTG	ACGCGGAAAATTTGTTATCTGC
HL05775	1890	1033	TGCCCTAAAGATCGAAAACG	TCGCTTGCTATCGCTATTCA
LD11130	1187	923	AGTAACATGCGTGGCCAAAT	CTGTTGGGGGAATTTGCTTA
LD11162	1549	1057	CGGTTCCCGAACAACCTAAA	GTGTGCGTATCGGTTGTTTTG
LD13184	2222	958	AAGAAGGACGCTCTTGGTCA	CCAAATGCAATGATGTCTCG
LD16711	1672	1064	ATTCATTGCGCCAAGTTTTG	AGTTACGCCAGAGCCAGAAA
LD23922	1721	924	CTTCTCGTGAGCATCGACA	TTCTTTTCCCTGCCCTTTTT
LD28571	3302	951	CGCCTATGCTTAGGTTACAGC	CTAGGCGGTTAGTCCCTCT
LD30889	1069	920	AAACCAAAATCCACATGCAC	CAGCAACACCAGCGATTAGA
LD38553	1317	996	ACGCGTACACAACACAAGGA	ATGGCGAAAAGCTAAAAGA
LP01161	527	444	CATGGCTTCAACCATCTCATT	TGGGCGTATGAGGGATTTTA
LP03188	553	404	GAGAGGTTCCGGGAACAGGAG	GTTTGGTGGGTGATGGATG
LP06491	403	302	AGAGCAATCGGCATTGTTG	TATCGGCTCAAAATCGGCTA
LP11739	1222	1008	CCTCCAGAAACTGTGCGATT	CCGTTGCTTCACTGTGTTTT
LP12023	313	243	GAAACGAGTTTTGGCTCTGC	AGGCGGTGGTTTGCATAAG
RE21847	3191	1052	ATTAAGCCAGGCCAACAAATG	AACGACAACCACATCGACAA
RE28911	1005	973	AGTTGAGCCAAAGCITTTCA	TTCTTGCAAGTTTGTGTTGC
RE45760	758	615	TTCCCTTTGTAATTCATAACATCA	GATGGACAGATCGCACGAC
RE54004	562	506	CAGTCGAAAACGGAGTGTCA	GCGTTTTGTTGTTAGCCGTAA
RE63504	331	290	CGTCCAGACCAGAAGGAAAA	GGAACCTTGGCGAAAATCTA
RE65113	1062	959	ATTGCTGTTCTGCCCTGTTT	TTTGGGGAACAAGCTCTCTG
RE66017	3461	912	GCGAAACGCTTCTAGTTTTG	TTCCGATCTTGTGACCATCA
RH09485	518	420	CAGCTCTGTGCAGCTCATT	TTTATGCCACGACACTGAAAA
RH45340	407	309	AGGCAACTAGCAGCTCGAAT	TCCTTCAAGGCTTGCACATA
RH57193	981	861	AGCTGATTGGAGCGGAGTT	CTCCGAGGTGATCACAGCTT
RH62702	2049	939	TTAACCTGTGTGTGCCAAA	TATCACTTTGCGTGCCTCTG
RH62830	326	305	CTAAAGTCTCGTCGCGTGTG	TTTTGGATGGATGAAATACGC
RH63361	424	301	TGCATTTTCTAGTTGCCAAG	TCGACGAGATCCTTAGGAGTG
SD03144	3956	1029	CTGGTTGTCTGACTGGCTGA	CTGGTGCCTTCACTGCTAAA
SD04448	2301	965	TGGAGCACTTGATGAAAACG	TTCAGCTCACACCTTCATGC
SD05379	1391	1041	GTGATGAGGTGGGAAGCAAC	CGGTTCTACCGAGTGTGT
SD10988	1415	927	GCTTCTGTGTTTCTCTGTC	ATGTTTTCTGCCTTGCCACT
SD25037	1560	1100	GATTCCCAGACCGAATCAGA	AGGTGGGTGAGATCTTGTGG