

Rhox3

A

variant nucleotides

-29---50--203--206--450--525--546--712--746--751-

<i>rhox3A</i>	G	G	G	A	G	T	A	C	C	G
<i>rhox3B</i>	A	G	G	A	A	T	A	C	T	T
<i>rhox3C</i>	G	G	C	G	G	T	A	C	T	G
<i>rhox3D</i>	G	G	G	A	G	A	T	C	T	T
<i>rhox3E</i>	G	G	G	A	G	T	A	C	C	A
<i>rhox3F</i>	G	C	C	G	G	T	A	A	C	T
<i>rhox3G</i>	A	C	G	G	G	T	A	A	C	T
<i>rhox3H</i>	G	C	C	G	A	T	A	C	T	T

B

RHOX3A	MKPERSISNWIHSNVERAGRNL FQVNGHRSALLPELPQDYHRASRSVNGCETKMDSTQGT	60
RHOX3B	MKPERSISN-----	9
RHOX3C	MKPERSISNWIHSNVERAGRNL FQVNGHRSALLPELPQDYHRASRSV Y GCETKMDSTQGT	60
RHOX3D	MKPERSISNWIHSNVERAGRNL FQVNGHRSALLPELPQDYHRASRSVNGCETKMDSTQGT	60
RHOX3E	MKPERSISNWIHSNVERAGRNL FQVNGHRSALLPELPQDYHRASRSVNGCETKMDSTQGT	60
RHOX3F	MKPERS M SNWIHSNVE P AGRNL FQVNGHRSALLPELPQDYHRASRSVNGCETKMD N TQGT	60
RHOX3G	MKPERSISN-----	9
RHOX3H	MKPERSISNWIHSNVE P AGRNL FQVNGHRSALLPELPQDYHRASRSVNGCETKMDSTQGT	60
RHOX3A	KVLPAAEEGKNEEDGGQVESALGATAARGRGKEALNGESPAAAGTAGLVEEDRNKEDGGTK	120
RHOX3B	-----	-
RHOX3C	KVLPAAEE AR NEEDGGQVESALGATAARGRGKEALNGESPAAAGTAGLVEEDRNKEDGGTK	120
RHOX3D	KVLPAAEEGKNEEDGGQVESALGATAARGRGKEALNGESPAAAGTAGLVEEDRNKEDGGTK	120
RHOX3E	KVLPAAEEGKNEEDGGQVESALGATAARGRGKEALNGESPAAAGTAGLVEEDRNKEDGGTK	120
RHOX3F	KVLPAAEE AR NEEDGGQVESALGATAARGRGKEALNGESPAAAGTAGLVEEDRNKEDGGTK	120
RHOX3G	-----	-
RHOX3H	KVLPAAEE SR NEEDGGQVESALGATAARGRGKEALNGESPAAAGTAGLVEEDRNKEDGGTK	120
RHOX3A	GGEKNEQEVREQIPEHVEGESDQAEAPRQVPRRRLHHRFTQWQLDELERIFRMNYFLSLE	180
RHOX3B	-----	-
RHOX3C	GGEKNEQEVREQIPEHVEGESDQAEAPRQVPRRRLHHRFTQWQLDELERIFRMNYFLSLE	180
RHOX3D	GGEKNEQEVREQIPEHVEGESDQAEAPRQVPRRRLHHRFTQWQLDELERIFRMN-----	174
RHOX3E	GGEKNEQEVREQIPEHVEGESDQAEAPRQVPRRRLHHRFTQWQLDELERIFRMNYFLSLE	180
RHOX3F	GGEKNEQEVREQIPEHVEGESDQAE L RQVPRRRLHHRFTQWQLDELERIFRMNYFLSLE	180
RHOX3G	-----	-
RHOX3H	GGEKNEQEVREQIPEHVEGESDQAEAPRQVPRRRLHHRFTQWQLDELERIFRMNYFLSLE	180
RHOX3A	++ ++ + + ***** *	213
RHOX3B	-----	-
RHOX3C	ARKQLARWGMVNEAIVKRFQKRREQYRWKRL	213
RHOX3D	-----	174
RHOX3E	ARKQLARWGMVNEAIVKRFQKRREQYRWKRL	213
RHOX3F	ARKQLARWGMVNEAIVKRFQKRRE K YRWKRL	213
RHOX3G	-----	-
RHOX3H	<u>ARKQLARWGMVNEAIVKRFQKRREQYRWKRL</u>	213

Additional File 3

A. Unique nucleotide profile of predicted *rhox3A-H* transcripts. The position of the nucleotides is given relative to the published start site. B. Clustal W alignment of predicted amino acid sequence from *rhox3A-H*. Residues different from the consensus are highlighted in blue (conservative amino acid change) or red (non-conservative amino acid change). The homeobox domain is underlined with hydrophobic residues (+) crucial for homeodomain packing and residues involved in DNA binding (*) annotated.