

**Supplementary Table 2. Genes, amplified transcripts, and QPCR primers used in this study.**

Gene Name	NCBI Transcripts Amplified	Primers
MAGEA1	NM_004988.4	AGTAGTAGGTTTCTGTTCTATTGGG TACTTATTCCTACTGCTGTTATTATCC
MAGEA2	NM_005361.2, NM_175742.1, NM_175743.1, NM_153488.3	GAGGACAGTGTCTTCGCAC GGTTCTCCACCGATCTTTAGTG
MAGEA3	NM_005362.3	GCTGAGTGTGTTAGAGGTGTT AGGGGTGGGTAGGAAATGT
MAGEA4	NM_001011548.1, NM_002362.4, NM_001011549.1, NM_001011550.1	GCAATGGAGGGCGACAGC CAATCTTGGGTGAGCAGTTCC
MAGEA6	NM_005363.2, NM_175868.1	GCTGAGTGTGTTAGAGGTGTT CAGGAGTGGGTAGGAAATGC
MAGEA9	NM_005365.4, NM_001080790.1	GTTCCCTTGCTATTGGGTGATTTG TTCTCTGCTATGTTATCTTGTC
MAGEA10	NM_001011543.1, NM_021048.3	TCCGTCGTTGCTTCCCTTC TCGGCTCCTTCATTTGATACTTG
MAGEA12	NM_005367.4	CTGAGTGTGTTGGAGGCATC GGTGGGTAGGAAATGTGAGGT
MAGEB (1,2,3,4,6,10,18)	NM_173523.2, NM_002365.3, NM_002367.2, NM_182506.2, NM_002363.3, NM_177404.1, NM_177415.1, NM_173699.2, NM_002364.3, NM_001099921.1	GCAGGTGCCCAACAGTGATCC AGGACTTTCATCTTGCTGGTTTCAGC
MAGEB1	NM_002363.3, NM_177404.1, NM_177415.1	GCTTTGAGAGATGAGGAAGAGAG GGGAGGACCTGCTGAATGG
MAGEB2	NM_002364.3	TGCCTTCCCAACCCATTACG AGAATCTGCCTAAGACCTCATTG
MAGEB3	NM_002365.3	CCACGCCTAGTGAAGTTGAAG CCTCCAGTAACACCCAGTCC
MAGEB4	NM_002367.2	GTGGTTTGTCTTACTCAGTTCAG TCTCCCTCATCTCTTAAAGTCTTC
MAGEB6	NM_173523.2	GCCGACAGCAGTAACACC TCTCTCTACCTCATCTATCAAAGC
MAGEB18	NM_173699.2	AGAGGCTTTGAGGGATGAGG CACTACTTAGAATGTTGACTGCTC
MAGEC1	NM_005462.3	TCTGGGATGTGCTGAGTGG ACGAGGAGGAGAAGAGTTGG
MAGEC2	NM_016249.2	GGAGGGAGCACTTCGTCTATG AGGATGGAAGGAACTAGGAACAG
MAGEC3	NM_138702.1, NM_177456.2	CCCACAACCACTCCTATTTTC GCACTCAACACTTCCCAGATG
GAGE (1,2,3,4,6,8)	NM_001098411.3, NM_001127212.1, NM_001127200.1, NM_001098405.1, NM_001098407.1, NM_001098409.1, NM_001098406.1, NM_001472.2, NM_001468.3, NM_001040663.1, NM_021123.2, NM_001477.1, NM_012196.1, NM_001474, NM_001476, U_19144	AAGGGGAACCAGCAACTCAAC GGACCATCTTCACACTCACACC
BAGE (1,2,3,4,5)	NM_001187.1, NM_182482.2, NM_182481.1, NM_181704.1, NM_182484.1	TGGAGGTTGGAGCCTGAAG GCACAAGGATAATGATACATCTGG
SAGE	NM_018666.2	GATAGTAATGAATTTGCGGTAGGC GGAGATATTTGTGGTGTATTTGGC
HAGE	NM_018665.1	ATGGTGGTGGAAATAGAGATGAAC GAGGCGATGAACGAATGAGG
PAGE (2,5)	NM_207339.2, NM_001013435.1, NM_130467.3, NM_001015038.1	GAGTCTTCCCAGCCAGTTG AGTTGGTGGTTCCTCTTCTTG
RAGE	NM_014226.1	AGAACAGTCCCTAAAGCAAGAG TCTGACCACTCCCGAAAGC
CAGE	NM_182699.2	ATCAAGAGCGAGCAGTAGAGG GTCTTCCCTGTCCTCCCAATG
XAGE1A-E	NM_001097591.1, NM_001097595.1, NM_001097602.1, NM_133431.2, NM_001097603.1	GTGAGTGAGAGTGAAGAGGAACC GCCGTGACGAGACAAGAAGG
LAGE (CTAG) (1,2)	NM_172377.2, NM_020994.2, NM_139250.1, NM_001327.1	GGTCATGCCTCCTCCCCTAG TGTAAGCCGTCCTCCTCCAG

LAGE2 (CTAG1/NY-ESO)	NM_139250.1, NM_001327.1	CGCCTGCTTGAGTTCTACC CAGTCAGTCGGATAGTCAGTATG
SSX (1,2,3a,4a,5,6,7,8,9)	NM_021015.3, NM_175723.1, NM_173357.2, NM_005636.3, NM_175698.1, NM_005635.2, NM_003147.4, NM_021014.2, NM_001034832.2, NM_173358.2, NM_174962.3, XR_041312.1	GCCCAAGAAGCCAGCAGAGG GCAGTCTGTGGGTCCAGGC
CSAG(1,2,3)	NM_153478.1, NM_001102576.1, NM_001080848.2, NM_004909.3, NM_001129826.1, NM_001129828.1	CGCTGGTCTGGTGAAGATGTC GAGTGGCTGGATAGTGTGGC
IL-13R $\alpha$ 2	NM_000640.2	ATCATCAGAGAACAAGCCTATCAG GCAGTCACCAAGGTAGTATCATC
hTERT	NM_198253.2, NM_198255.2	GTATGGCTGCGTGGTGAAC GGTGAGACTGGCTCTGATGG
p53	NM_000546.4, NM_001126112.1, NM_001126113.1, NM_001126114.1, NM_001126115.1, NM_001126116.1, NM_001126117.1	CAATAGGTGTGCGTCAGAAGC TACATCTCCCAACATCCCTCAC
Her2/Neu	NM_004448.2, NM_001005862.1	GTGCCAGTGTGAACCAGAAG CCTCAGAAATCCACAAGACTCC
BCL-XL	NM_138578.1, NM_001191.2	CAGGCTGCTGGGATAAAGATG GGACTAGGGTGGTGTGAAC
MCL1	NM_021960.3, NM_182763.1	TTCTGTTTGTCTTACGCTTCTCTC TTGTAGTTGGTCCTAACCCCTCC
BCL2 $\alpha$	NM_000633.2	AGTGTGGTCTCCGAATGTCTG GCCTCTGTTCCTTCCCTCTAC
livin	NM_139317.1, NM_022161.2	CCGTGTCCATCGTCTTTGTG ACAGTCCAGAACAGGCAGAG
survivin	NM_001168.2, NM_001012270.1, NM_001012271.1	CTAAGCACAAAGCCATTTAAGTC TCACTCTATTCTGTCTCCTCATCC
SCP1/HOM-TES-14	NM_003176.2	ACCGTTGGGCTGTAATTGC TAGGCTCCTAACCTACACTGATTC
SPANXC	NM_022661.2	GCCGCAGACATTTGAAGAACC TCGTCTCATTACCTCGTTGG
OY-TES-1	NM_032489.2	TTTCGGGAAGTCGGTCTGTG GAGTCTTGTGGGAGGTGTGC
PLU-1	NM_006618.3	AGCCCTCACTAACAAAGAAC TTTCCTTAGATTTCTTCCAACG
RHAMM	NM_012484.1, NM_012485.1	TTCGTCTTGTGTTATTGATGTTG AGGTGATAAAGGTGAGCATTAGG
TPTE	NM_199261.2, NM_199259.2, NM_199260.2	CGGTACTTGATAACATTACAACAG TCACATCATCATAACAGAGGTAGAC
CYP1B1	NM_000104.3	TGTCAACACAGTCCAGATGTG AAATAAGCCAGGTAACCTCCAAGC
MELK	NM_014791.2	GGATGAGTGTGGGTGTGATAC GACAGATGGGCTTGATTTAGATTC
BORIS	NM_080618.2	TTGGTATAGGAGCAAGGTTTAC AGGGAAATACTACTAATCACTGG
DPPA2	NM_138815.2	GAGAGCAGAAGAGACCAATACAG GCCTCAACAGAAAACGGGAATG
BRDT	NM_207189.2, NM_001726.3	TTAGGCAAACCAGTGAACCATC TTCCGTATGAGTTCTGTGTCC
ADAM2	NM_001464.3	TTACCTCCAGATTGCTCAGTTC TGCTCATCGCTTGAATAGTCC
TSP50	NM_013270.4	TGACCAGATGACGCAGACC CCACCCAGGACCAGAACC
SPA17	NM_017425.2	GGGACACATAGCCAGAGAGG TTCACAACATCAAATCTTCTTCC
MMA	XR_040165.1	GCCAAGACCGAAAGTGCTG CTAAATATGGAACAAGTGAGAATAAC
HOMTES85	NM_016383.3	CAAGATGTCCCATTAAGTGTGTTCC TTGGCAGTTAGTTGTTAGATTAGC
SP17 (SPA17)	NM_017425.2	ACCAACTTTGATCCAGCAGAATG ACTGATGTCTCTTCTCCTTCC
KM-HN-1	NM_152775.2	TAATTGTACTGCTAACTGAACTATGC CCTGCCCTCCCTTGTAGAAG
TPBG (5T4)	NM_006670.3	AGAGGACAGACCAAGGACAAC CATTAACAGAACACCCGAGAAAC
D40	NM_170589.3, NM_144508.3	GGTGATGAAGTCTGGATGGTAG AATGGCTAATGTTCTGTGTCAGTG

<b>HCA661</b>	<b>NM_016521.2</b>	CGGCAGGTTCCAGGTCTAATG GTTGTTGTCTCCTCCTCTTCC
<b>LDHC</b>	<b>NM_002301.4, NM_017448.3</b>	TTCTCAGTATCCCTTGTGTCTTG GCCTGCTATCTTCTGTTCTCC
<b>MORC</b>	<b>NM_014429.2</b>	CGATATGTGAAGGACTACAGAATC TGCTTGACTGAGTGTGGC
<b>SGY-1</b>	<b>NM_014419.3</b>	CCTGCTGCTGCTCCTCTC CTGGTGCTCCTGGTCTCC
<b>NXF2</b>	<b>NM_017809.3, NM_022053.1, NM_001099686.1</b>	GGTCTGTCTCGCCTTAC AGACCACTCCAGTTTCATCCC
<b>FATE</b>	<b>NM_033085.2</b>	ATCATCGCCGTGCTGGTG GGGAAAGAGGAAAGAAAGAGGG
<b>LIPI</b>	<b>NM_198996.2</b>	TGTCCTCGGCTGGTTATC CCTGGCTCTTCAATCATTC
<b>CTAGE</b>	<b>NM_172241.2</b>	TGCCTTCTTCCAGTGAGAG GAGTGAGATATGTACCCAGTTG
<b>SPO11</b>	<b>NM_012444.2, NM_198265.1</b>	GCTCATCATCTCACAGTTCAG GGCAGGTAAACATAAGGTCTCC
<b>TPX1</b>	<b>NM_003296.1</b>	GGTACTGTGCTGCTCCATC CTCTCTGCTCCATCCATCTTTAG
<b>NY-SAR-35</b>	<b>NM_152578.1</b>	CAGGATGGCGGAATCTCTAAAG ACAGGTAGTAGGACAGGTAGTAGC
<b>FTHL17</b>	<b>NM_031894.1</b>	AAAGAGACTTGAGCCCAGATG ACACCTTTATTGCTTTGAGAACC
<b>TDRD1</b>	<b>NM_198795.1</b>	GAATACTGGCAAGGAATACATAGG GAGGCAGACGACAGAGAATG
<b>TDRD6</b>	<b>NM_001010870.1</b>	ATGGTATGGAGGAGATAGTGAAC TTGGTCTGCGTAAGATGCC
<b>TEX15</b>	<b>NM_031271.3</b>	AGAGAATTGGTTTGGCTGAATC CAGTTCTTTGCTTGACCTTCC
<b>HMBS</b>	<b>NM_000190.3, NM_001024382.1</b>	ACCCTAGAAACCTGCCAGAG CGAATACTCCTGAACTCCAGATGC
<b>TBP</b>	<b>NM_003194.3</b>	ATGGTGGTGTGTGAGAAGATG GATAGCAGCACGGTATGAGC
<b>GAPDH</b>	<b>NM_002046.3</b>	AGCTTGTATCAATGGAAATCCC GTGAAGACGCCAGTGGACTC

NCBI transcripts amplified were identified using the NCBI primer blast tool. Some reactions amplify multiple transcripts due to the presence of alternatively spliced transcripts, other reactions amplify several related gene family members, these reactions are typically identified because the gene name is followed by several numbers, indicating individual family members, for example, BAGE (1,2,3,4,5). The top QPCR primer is the 5' or forward primer; the bottom primer is the 3' or reverse primer.