

# Kawaji et al. Suppl. Fig 4

## MDS00121

8430425A16Ri k 2 WFLGFELRTFRITVGLTRRALYLSSP  
 2410002E02Ri k 366 WLLGFELLTFGRAVGCSYPLSH-LTSP  
 C330014021Ri k 2 WLLGFELLTFGRAVGCSYPLSH-LTTP  
 3110029G23Ri k 2 WLLGFELWTFGRAVGCSYPLSH-LTSP  
 4833408D11Ri k 2 WLLGFELRTFRRAVRCGYPLSH-LTSP  
 1700047E10Ri k 2 WLLGFELRTFGRAVGCSYLLSH-LTSP  
 8030488J09Ri k 2 WLLGFELRTFRRAVGCALNHRAF---SP

## MDS00139

4930572J10Ri k 46 EVVLSATSPAPCLPACHHASLPQNNGLNL  
 8030455M16Ri k 32 DVELSAP-PTPCLPGCY---LVDGNGLNL

## MDS00129

1190005P17Ri k 147 FIPALKRMRQVDLCEFKASL  
 5730583A19Ri k 3 LI PALNRORROADLCKFEDSQ  
 5530601I19Ri k 117 LVPAPRRORWAYLCEFKASL  
 8430415L13Ri k 16 LI PALGRORQAMLCEFOTIL  
 1110012D08Ri k 3 LVPVLGRHRROADPCEFKASL  
 2010001A14Ri k 17 LI PALRRORQVDLCEFLANL  
 1500037F05Ri k 52 LI PALRRQGOAGLCEFKASL

## MDS00137

Msh3 174 HAFSRPARKNAANRNLLWOKLYCLHLOEPE  
 4930423020Ri k 29 YTRSRPARKNTANQNLROSFTAYIFRSKK  
 1700020M10Ri k 19 HAFSRPARKNATNRNLLROKLYCLHLOEPE  
 4930425F17Ri k 28 HTFTIRPARKDATNRNLLROKLYCLHLOEPE

False positive motifs MDS00121, MDS00129, MDS00137 and MDS00139. The alignments are based on putative translations of RIKEN clones that contained repeat elements in the predicted coding region. Msh3 is derived from DDBJ accession AK011426.