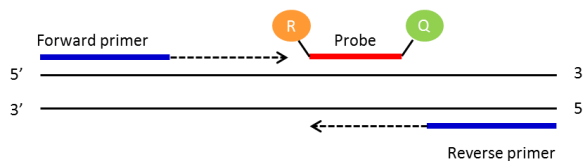




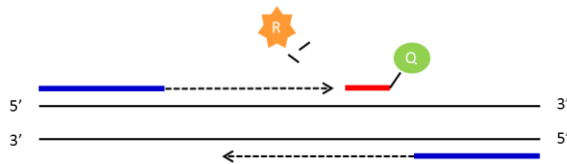
FTO-KO-FLOX Genotyping Strategy

Introduction

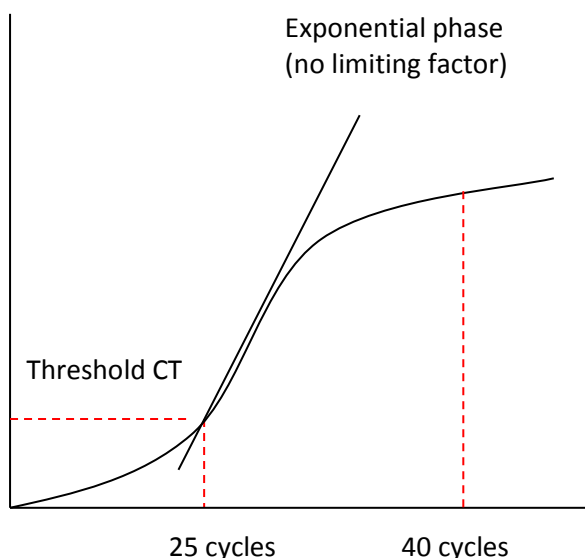
Standard PCR is the amplification of DNA between a pair of primers. Quantitative PCR employs the same principal as standard PCR, although it actually monitors the progress of the DNA synthesis as it occurs. The progress of the reaction is measured by using a Taqman probe. This is a short DNA oligo that is complimentary to part of the DNA sequence between the forward and reverse primers. At the 5' end of the probe there is a fluorescent reporter (R) and at the 3' end a quencher (Q). Whilst they are in close contact with each other there is no fluorescent signal.



As the forward primer is extended the reporter is cleaved from the probe resulting in a fluorescent signal being detected. Once the primer extends enough to release the quencher this signal is blocked. By using probes with different fluorescent signals multiple PCR assays can be multiplexed and run together.



PCR reaction plot



The number of cycles the PCR takes to reach a set threshold is known as the CT value. This is inversely correlated to the amount of template DNA in the sample.

e.g. CT 25 = 2 x template DNA
CT 26 = 1 x template DNA
CT above 30 = no template represented in the sample

CT value can be used to determine how many copies of a particular allele samples have.



Group: Diabetes
 Mutation type:
 Mutant allele: FTO-KO-FLOX-MUT1
 WT allele: FTO-KO-FLOX- WT1
 Assay Type: 2qPCR copy count Taqman assays

FTO-KO-FLOX- MUT1 (FAM labelled probe)

AACATCGATAAGCTTGATATCGAATCCGAAGTTCCTATTCTCTAGAAAGTATAGGAACTTCATCAGTCAGGTA
 CATAATATAACTTCGTATAATGTATGCTATACGAAGTTATTAGGTGGATCCACTAGTTCTAGAGCGGCCGCCTA
 GG

Primer 1 = TCCGAAGTTCCTATTCTCTAGAAAGTA
 Primer 2 = GCCGCTCTAGAACTAGTGGATC
 Probe = TCATCAGTCAGGTACATAATATAAC

FTO-KO-FLOX- WT1 (FAM labelled probe)

GGTGGACAGGTCAGCCGTGGCAGTGTACAGCTATAGCTGCGAAGGTACAGTCTGCTCTGGGGAAAGCATG
 CTCGATGGCAGTGTGGCCAGAGCCTCTGAGGCTCTGAGGATGAGTAAGCACTCGTGTCTGTGTGTTGGG
 TGTGCTTTTCCTTTCCTGGCCGGTCTCACCAGTATATCTGCAGAGCACCCCTCTCCCCATCTAATCCTCTCTGG
 CTCATTGTTCCATCGTGCGCAGAAT

Primer 1 = GGCTCTGAGGATGAGTAAGCA
 Primer 2 = GACCGGCCAGGAAAGGAAAG
 Probe = CACTCGTGTCTGTGTGTTGGGTGTC

Dot1l internal control (VIC labelled)

CCTAGCCATGGTGTGTTGTGTGTCCAGTTCATGAGGCAAGCCTACAGCCTTCATCATTCTACAGTTGCCTTCAT
 TACCCTACAGTCCACTTCTCCAGTGGAGCTGGGCCTGTGCAAACAGTGGGCAGTGGATGTGAAGGGCAGGAAGC
 TCATAGGGTGACTGGCCAACCCAGGGAAGCCGGAGTGTGCGTCTTCTGTTTCCCTTGTCTTTTCCCCTCTAGTC
 GTTTTCTGTTAGTAGTTGGCATCCTTATGCTTCATCTTACAGTCCGACTTGAGAGCTGGCCCTGAATGGTCGTGCT
 GGGGC AAGGCTTTATTTTCAGGCGTAGCACACATGGTGGCCAATGGGACTCTGTAGGATCTGCCACACCCATCAG
 GTGTGCAGGGAGACAGAGCTGAGTCAGGCTCCAGCTCTGGGGAATATGTTGAGTCACCACCTCTGTAGGGTGGTT
 GTGCATCATAGAACAAGAGGACTTTGGGGTGTCACTGTGGTTGTTGGGTCCAACCTGTGCATCTTTTCTCTTTTCAG
 GACAAGCACCATGATGCTG

Primer 1 = GCCCCAGCAGCACCATT
 Primer 2 = TAGTTGGCATCCTTATGCTTCATC
 Probe = CCAGCTCTCAAGTCG



qPCR master mix

ABI GTX Taqman master mix	5 μ l
Primers Dot1L_2F (20 μ M)	0.225 μ l
Primers Dot1L_R (20 μ M)	0.225 μ l
Probe DotL_2M (5 μ M)	0.2 μ l
FAM Assay (probe 5 μ M & primers 15 μ M each)	0.3 μ l
Water	1.55 μ l
ALIQUOT 7.5μl	
DNA	2.5 μ l
(1/10 dilution of ABI Sample-to-SNP prep)	

Example

