## Primers sequences for TP53 SNPs

From Garritano et al., Human mutation, 2009

Detailed haplotype analysis at the TP53 locus in p.R337H mutation carriers in the population of Southern Brazil: evidence for a founder effect.

<u>Garritano S, Gemignani F, Palmero El, Olivier M, Martel-Planche G, Calvez-Kelm FL, Brugières L, Regla Vargas F, Renzo Brentani R, Ashton-Prolla P, Landi S, Tavtigian SV, Hainaut P, Waddington Achatz MI.</u>

International Agency for Research on Cancer (IARC), Lyon, Rhône, 69372, France.

Due to patterns of migration, selection, and population expansion, founder effects are common among humans. In Southern Brazil, a recurrent TP53 mutation, p.R337H is detected in families with cancer predisposition. We have used whole locus resequencing and high density SNP genotyping to refine TP53 locus haplotype definitions. Haplotyping of 12 unrelated p.R337H carriers using a set of 29 tag SNPs, revealed that all subjects carried the same haplotype and presence of the mutation on this haplotype was confirmed by allele-specific PCR. The probability that this haplotype occurs independently in all index cases was of 3.1x10(-9), demonstrating a founder effect. Analysis of the patterns of 103 tumors diagnosed in 12 families showed that the presence of p.R337H is associated with multiple cancers of the Li-Fraumeni Syndrome (LFS) spectrum, with relatively low penetrance before the age of 30 but a lifetime risk comparable to classical LFS. The p.R337H families are mostly distributed along a road axis historically known as the main route used by merchants of Portuguese origin in the XVIII and XIX century. This historical circumstance and the relatively low penetrance before the age of 30 may have contributed to the maintenance of this pathogenic mutation in a large, open population. (c) 2009 Wiley-Liss, Inc.

|            |                          |                           | Amplicon  |
|------------|--------------------------|---------------------------|-----------|
| SNPs       | Forward sequence 5' > 3' | Reverse sequence 5' > 3'  | size (bp) |
| rs2287499  | ACTCTGTTTCCAGGGGAGTG     | GGTTGTCCCCAGATCCTGT       | 93        |
| rs17551157 | CTACGCTCCCCCTACCGAGT     | AAGAGGTGCAAGACCTGCTG      | 94        |
| rs17883353 | GGGCGACAAGAACGAAAC       | ACAACATGAACGAATGTCAGA     | 113       |
| rs17882227 | TGGCCTTTTGAGTTGTTTCC     | CGCAATTCCCCTCCTAAGTA      | 125       |
| rs17885845 | GGAATTGCGAGTTTGGAAGT     | CTAATGTCCGGAAGGCTGTG      | 146       |
| rs9903378  | TTCAGTATTTGCCTTGTCCTGTT  | CCATAAAGGTCCTAAAAGAAAATG  | 100       |
| rs17881035 | TTAACCCCAGGGTCATGAAG     | TGACTCCTACACCTCACACCA     | 135       |
| rs11656607 | GCAGGGGATCATTTGAGG       | TGGCTTCGAAAACAAGTTGG      | 290       |
| rs5819163  | ACATTACCCCCATACAATGA     | GTGGCTGCTGGTATCAGTCTT     | 120       |
| rs2078486  | AGTGGGGGTGGGAGCAGTA      | TGCAATTGTTCTATTTCACTTGTTC | 94        |
| rs1642782  | AAGATGCTGGTCCACACAGG     | ACCTGCTTGGGCTCAATAAA      | 104       |
| rs12944939 | GTTAACAGGAGGTGGGAGCA     | AGAGACAGGGCTTTGCATGT      | 132       |
| rs8079544  | CAGCCATTCTTTCCTGCTC      | CTTCCAACCCTGGGTCAC        | 108       |
| rs1642785  | CCCCTCTGAGTCAGGAAACA     | TCCCACAGGTCTCTGCTAGG      | 114       |

| rs17878362, rs17883323         | TTCCTGAAAACAACGTTCTGG | GGGGACTGTAGATGGGTGAA  | 134 |
|--------------------------------|-----------------------|-----------------------|-----|
| rs1042522                      | GAAGACCCAGGTCCAGATGA  | TGGTAGGTTTTCTGGGAAGG  | 146 |
| rs1794287                      | TCCCAGCACTCTCAAAGAGG  | CTCCATCTCCTGGCCTCA    | 194 |
| rs1625895                      | GGGTTAAGGGTGGTTGTCAG  | TTGCACATCTCATGGGGTTA  | 97  |
| rs12947788                     | CTGGAAGACTCCAGGTCAGG  | TGATGAGAGGTGGATGGGTAG | 135 |
| rs12949655                     | CCAGGCTGGTCTCTAGCCTAC | TAGCAGGCGCTTGTAGTCCT  | 357 |
| rs858528, rs1641548, rs1641549 | CAGTCGAGCCAGGCACAG    | TGTGCCTCGTTTCTTTTCTTT | 359 |
| rs6503048                      | TAATCCCAGCTACCTACTCG  | CAATGCTTTGAAGGGCCTAA  | 282 |
| rs17880560, rs1614984          | GCTCCATTCATAACTCAGGA  | CCGTAATCCTTGGTGAGAGG  | 130 |
| rs9894946, rs17883532          | TCAAAGGGCTTCTTGGGATA  | AAGAGAGCAGTGGGTGATGG  | 138 |
| rs17886760                     | ATCACCCACTGCTCTCTTGG  | CACCCACTGGACCCTAACAC  | 104 |