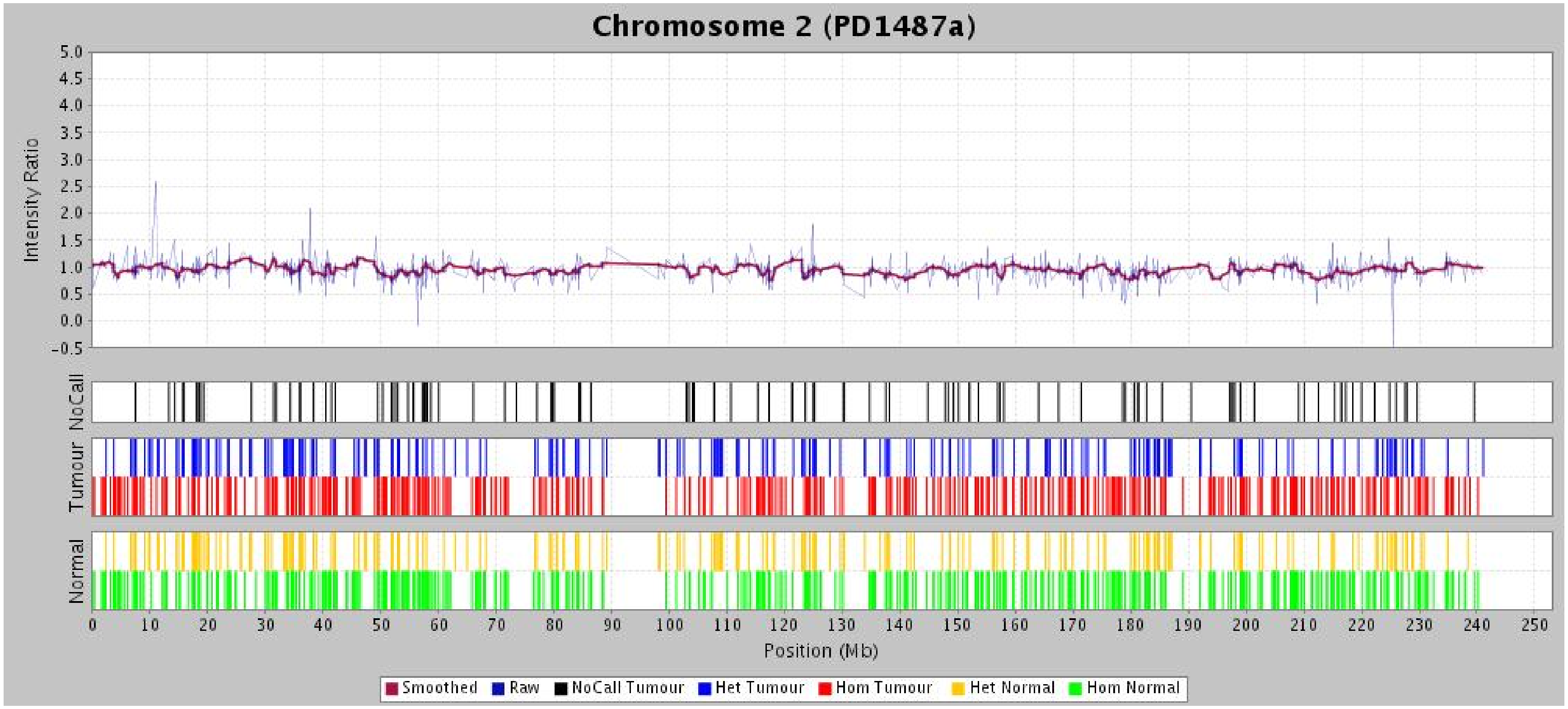
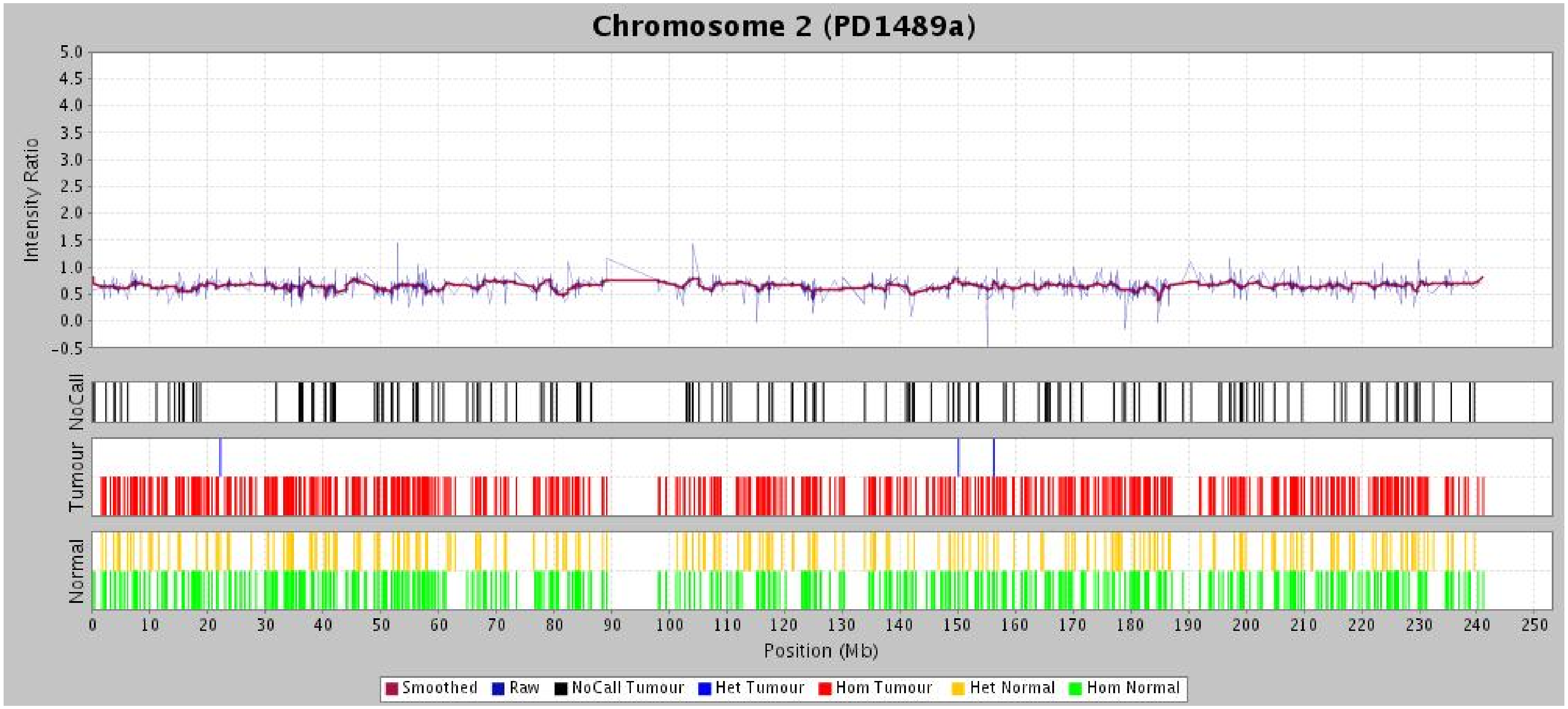


Copy number analysis of chromosome 2 for PD1487
for additional data see http://www.sanger.ac.uk/genetics/CGP/CopyNumberMapping/



Copy number analysis of chromosome 2 for PD1489
for additional data see http://www.sanger.ac.uk/genetics/CGP/CopyNumberMapping/

Conservation of A1303 in the MutS family across species*

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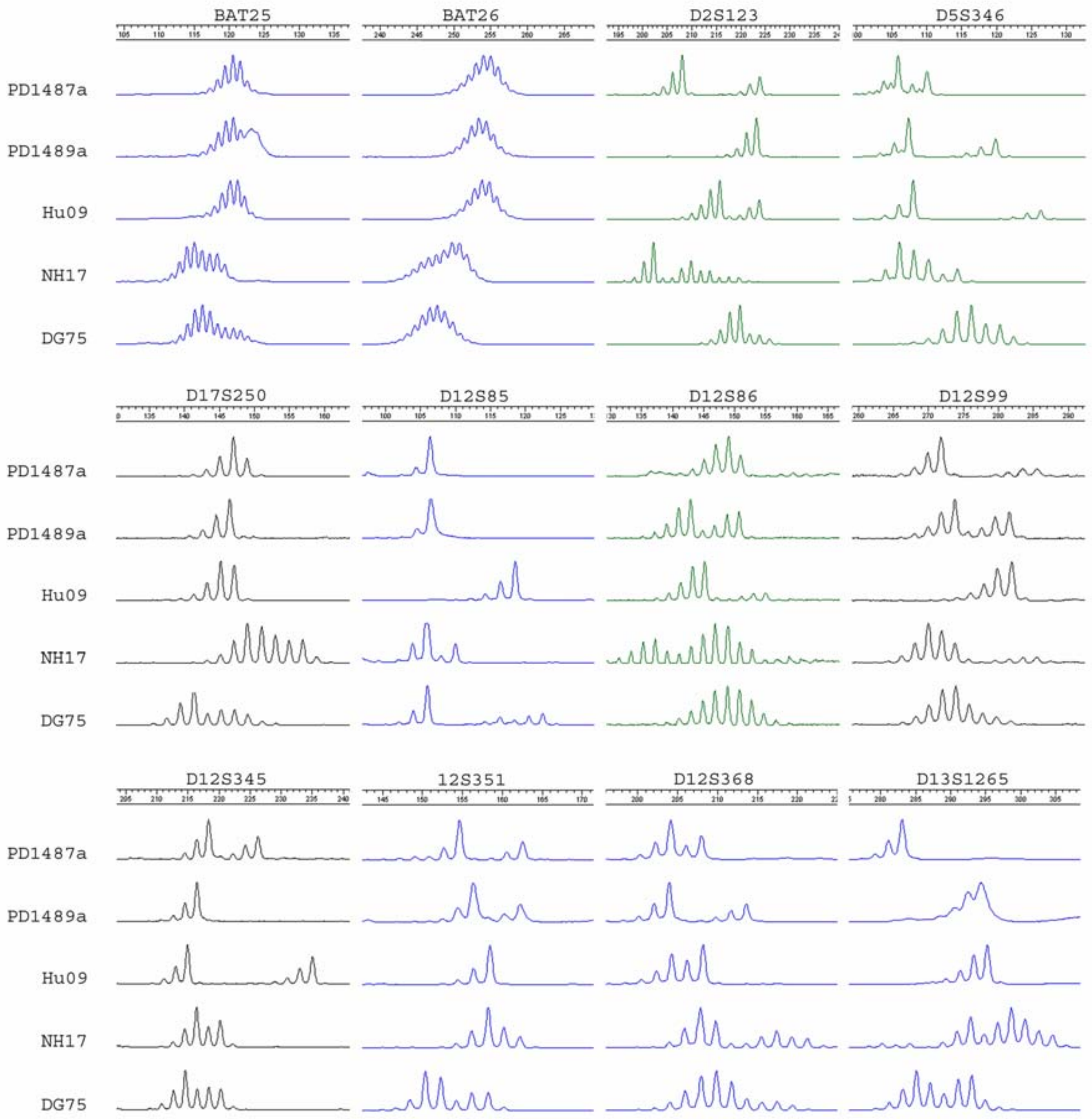
Sequence Source                                                          Accession

PD1487 mutant                1291  ............T.................  1320
Homo sapiens MSH6            1291  KGACPKSYGFNAARLANLPEEVIQKGHRKA  1320    4504191
Mus musculus                 1289  ..............................  1318    2506881
Gallus gallus                139   E...............DI...I........  168     50739005
Danio rerio                  1300  R................I..D...S..K..  1329    33504503
Xenopus laevis               1273  ................HI.D.I..V..Q..  1302    58399508
Tetraodon nigroviridis       1193   ...............S.......C.QG..  1221    47228957
Schistosoma japonicum        100    ...............L..DK.TRL.LT..  128     60602808
Trypanosoma cruzi            862    .P.GR...LYV.Q........V.SAKC..  890     70876490
Dictyostelium discoideum     1180   .V..N...LHV.SM.G..R.I.T.AEE.S  1208    66827461
Caenorhabditis elegans       1121   .I.......Y..K..GIDHQ.VRNAY     1146    15375264
Drosophila melanogaster      1116   ............K..GM.QGI.KRAY     1141    10727920
Anopheles gambiae            917    ............K..GM.TAI.KRAY     942     58383922
Plasmodium falciparum        1277  ..V....F.IHI.K..G..K.I.DLA.E.S  1306    23613078
Oryza sativa                 1159   .S......V.V....GI.AS.L.RANE.S  1187    51091562
Arabidopsis thaliana         1239   ........V.V....G..DY.L.R       1262    2104549
Schizosaccharomyces pombe    1177   .I......M.V.SM.G...K..DAAEE..  1205    3581916
Escherichia coli             764    ..AS....LAV.A..GV.K...KRARQ.   791     17017340
Salmonella typhimurium       68     ..AS....LAV.A..GV.K...KRARQ.   95      24285901
Bacillus subtilis            752   E..AD....IHV.Q..E..GDL.AR       776     7404403
```

*Position of the A1303T mutation in PD1487 is indicated. Dots indicate identity and shading hightlights the cognate position and conservation of A1303 across MutS family members from various species. Amino acid postions are given either side of the sequence and the GI accession number used in the alignment is given.

Evaluation of microsatellite instability using the NIH-NCI consensus markers and an additional seven CA dinucleotide repeats

The images are trace files from the analysis of the NIH-NCI consensus markers and an additional seven CA dinucleotide repeats to identify the extent of microsatellite instability in each sample. Samples NH17 and DG75 are known to have microsatellite instability while Hu09 does not. These facts are reflected in the trace patterns below. Gliomas PD1487a and PD1489a show no evidence of microsatellite instability in these analysis. In addition no other glioma in this study appeared to have microsatellite instability.



Additional Statistical Methods –

To assess whether the sequence context of somatic mutations differed from that expected by chance the following procedure was adopted. The expected sequence context was derived from the entire set of trinucleotides centred around all cytosines in the coding sequences of the protein kinases. 10,000 Monte-Carlo simulations of the Chi-squared statistic were used to provide an exact statistical test to compare the observed against the expected.