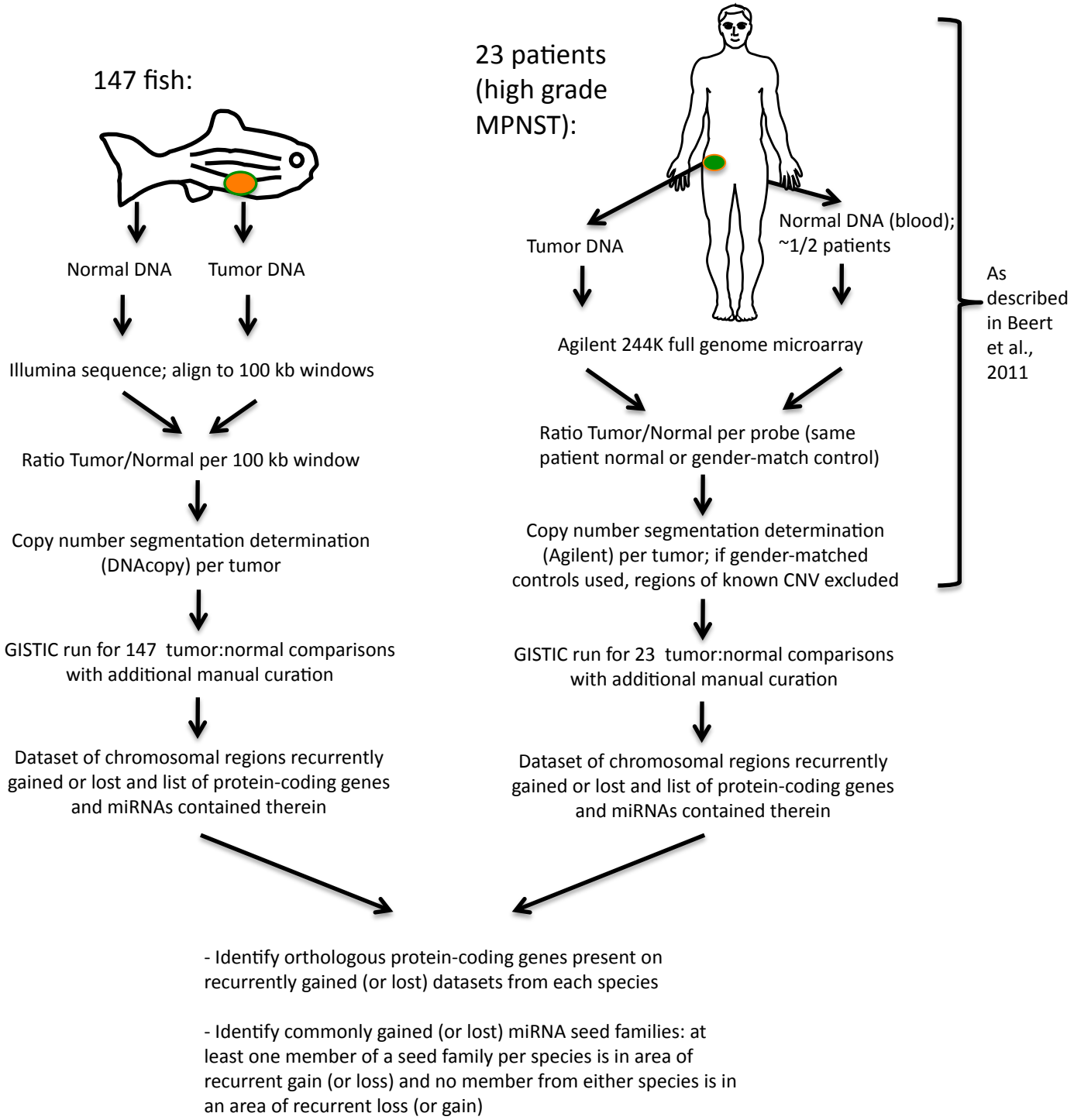
Figure S2


147 fish:
Normal DNA
Tumor DNA
Illumina sequence; align to 100 kb windows
Ratio Tumor/Normal per 100 kb window
Copy number segmentation determination (DNAcopy) per tumor
GISTIC run for 147 tumor:normal comparisons with additional manual curation
Dataset of chromosomal regions recurrently gained or lost and list of protein-coding genes and miRNAs contained therein
23 patients (high grade MPNST):
Tumor DNA
Normal DNA (blood); ~1/2 patients
Agilent 244K full genome microarray
Ratio Tumor/Normal per probe (same patient normal or gender-match control)
Copy number segmentation determination (Agilent) per tumor; if gender-matched controls used, regions of known CNV excluded
GISTIC run for 23 tumor:normal comparisons with additional manual curation
Dataset of chromosomal regions recurrently gained or lost and list of protein-coding genes and miRNAs contained therein
As described in Beert et al., 2011
- Identify orthologous protein-coding genes present on recurrently gained (or lost) datasets from each species
- Identify commonly gained (or lost) miRNA seed families: at least one member of a seed family per species is in area of recurrent gain (or loss) and no member from either species is in an area of recurrent loss (or gain)