Fig. S3a (gag)

- 22Rv1 clone
- Chronic fatigue syndrome patient
- Prostate cancer patient
Figure S3c (env)

22Rv1 clone
Chronic fatigue syndrome patient
Prostate cancer patient

Figure S3. Bayesian maximum clade credibility phylogeny of 22Rv1 cell line derived XMRV clones, patient derived XMRV sequences and other murine leukaemia viruses based on the (a) gag, (b) pol and (c) env genetic regions only. Xenotropic MLV (MLV-X), polytropic MLV (PMLV), and modified polytropic MLV (MPMLV) were added as controls. Sequences derived from prostate cancer patients (VP and WO) and chronic fatigue syndrome patients (WPI) are indicated by red and yellow circles respectively. Gene sequences derived from 22Rv1 clones are indicated by blue squares. The trees are rooted by the mid-point.
rooting method. Bayesian posterior probabilities > 0.95 (*) and of 1.00 (**) are indicated on
the corresponding branches. The branching order of the sequences within the XMRV clusters
is not statistically supported and therefore cannot be determined unambiguously from these
trees. For this reason we have reconstructed a Bayesian phylogeny from the fragments
together with the full-length XMRV sequences (Fig. 2). The scale bar represents the number
of nucleotide substitutions per site.