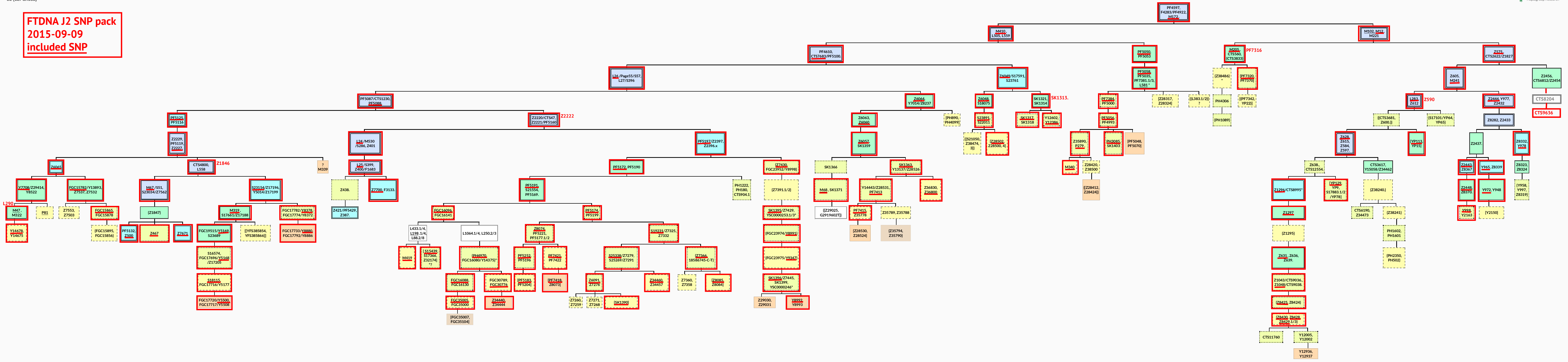
J2-M172 Research Tree simplified (0.91.0 beta ©2015-09-09 CC-BY-SA ChrisR @ J2-M172 Haplogroup research)

J2 (J2Pan15a)

FTDNA J2 SNP pack
2015-09-09
included SNP



Phylogeny and Haplogroup SNPs (two most prominents/good-coverage + historically informative/recurrent) based on J2-M172_spreadsheet (synonymous SNP-names not always listed). Usually listed SNPs are checked for genome-seq-uniqueness with BLAT 1kbp and YFull SNP search (see Spreadsheet>Phylo-SNPs for details)
Recurrent SNPs are considered to define clades when no alternative is available and they are found in more then two samples. Recurrency is shown: SNP. (found once in a sample outside of Hg J), SNP.1 or SNP.2 or SNP.x (not more then twice in Hg's), SNP.1/3 (3 times recurrent).
Legend: [under research] {tentative split} (Single/Private) ? placement vs parallel branches unavailable * upstream placement uncertified

Priority for Haplogroups: Backbone | Skeleton | Body | Informative Diverse | Expected Informative (Research) | Low Diversity approx. 700-1400 years | Clan/Genealogical Surname

Terminal samples / Listing of SNP count: FGC (Full Genomes Corp), BigY FTDNA, Genographic Proj., Single SNP etc., Mag13 (1000 Genomes Project, Magoon et al 2013), PGP (Personal Genome Project), GoNL (Y-VCF 2012), Chromo2 (2014), SK14 (SK/Stoneking, Lippold et al 2014), PH14 (Hallast et al 2014), EB15 (Estonian Biocentre CG, Karmin et al 2015), PF15 & PF13 (Sardinian Francalacci et al 2015 & 2013), YFS (YFull Single Best+Acceptable).