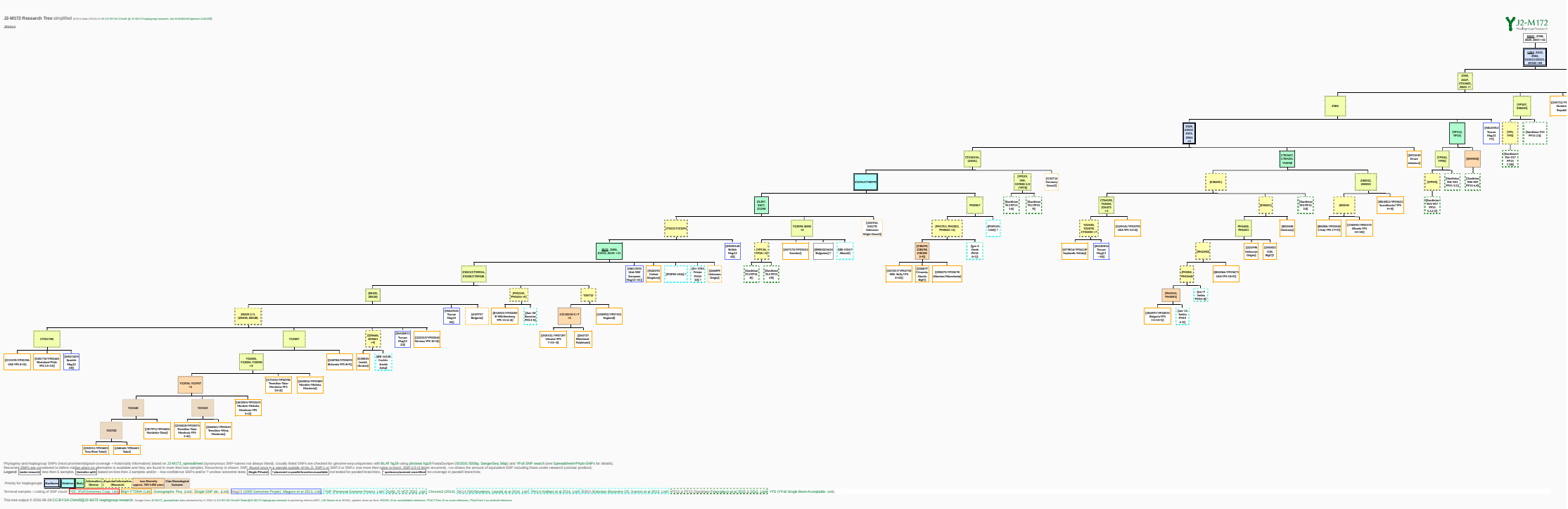
J2-M172 Research Tree simplified
J2-M172
Y-DNA Haplogroup Research
Phylogeny and Haplogroup SNPs (most prominent/good coverage + historically informative) based on J2-M172_spreadsheet (synonymous SNP-names not always listed). Usually listed SNPs are checked for genome-wide-uniqueness with BLAT hg19 using ybrowse hg19 FastaDumper (ISOGG, 500bp, SangerSeq, bAsp) 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 than two samples. Recurrency is shown: SNP_Round (once in a sample outside of his J1, SNP1) or SNP-2 or SNP+ (not more than twice in macro, SNP-1/+1 if more recurrent). +xx shows the amount of equivalent SNP including those under research (unclear position).
Legend: [under research] less than 5 samples, [tentative split] based on less than 3 samples and/or – low-confidence SNPs and/or ? unclear ancestral state, [Single/Private] not tested for parallel branches, * = placement in parallel/tentative/unconfirmed, *upstream placement unconfirmed no-coverage in parallel branches;
Priority for Haplogroup: Backbone, Essential, Basic, Informative, Expected Informative, Low Diversity (Diverse) (approx. 700-1400 years), Clan Chronological Subclade
Terminal samples / Linking of SNP values: FGC, Full Genomes Corp. (Ltd.), Big Y-700+ (Ltd.), Cartographic Proj. (Ltd.), Single SNP etc. (Ltd.), Illig13 (1000 Genomes Project, Magoon et al 2013, Ltd.), YHC (Personal Genome Project, Lim+ 2014, Cr.YHC 2014, Ltd.), Chrom2 (2014), HGDP (CEPH-Human Genome Diversity Cell Line Panel, Li et al 2008, Ltd.), YFS (YFull Single Best+Acceptable, Ltd.).
This tree output © 2016-09-28 CC-BY-SA ChrisR@J2-M172 Haplogroup research
Google Docs: J2-M172_spreadsheet; data maintained by © 2016 CC-BY-SA ChrisR+Team@J2-M172 Haplogroup research & partnering Admins (MAT, L26 (Sacha et al, M160), updates: close-up here: M2360 (if as unestablished reference, YFull YTree J2 as cross-reference, PhyloTree? as external reference.