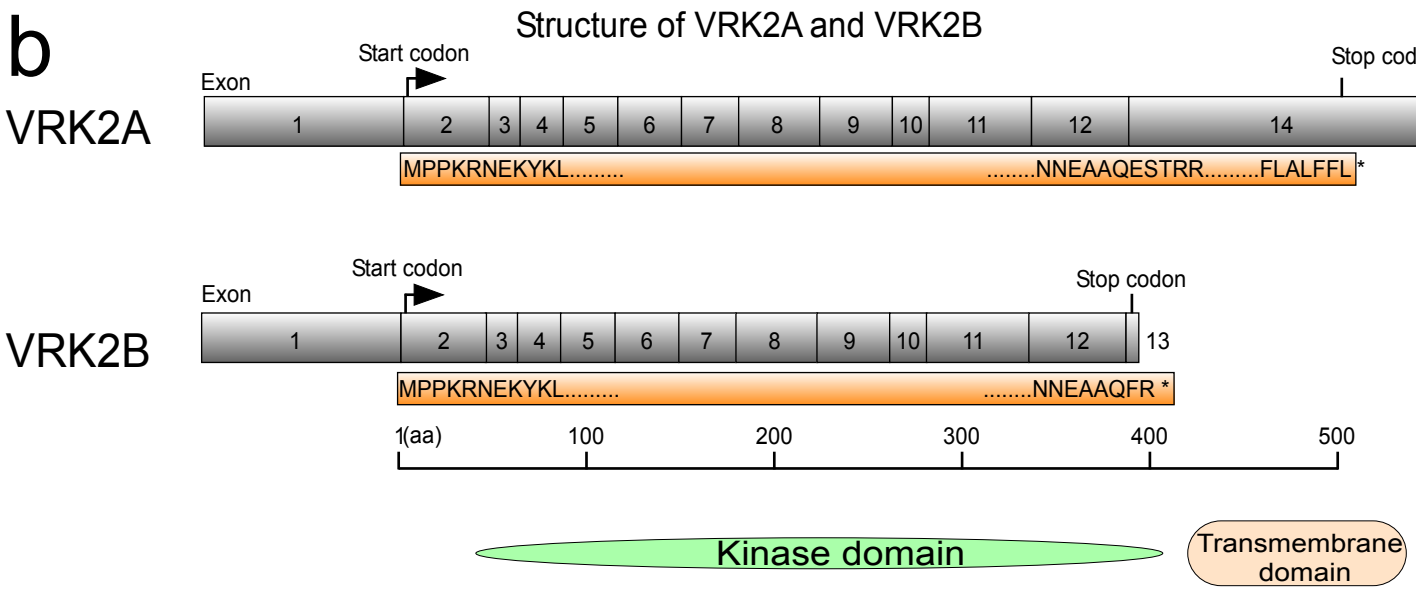
Supplemental data 2 (Fig. 1 & 2 related)

a

```
VRK1  ------------------------------------------------------------
VRK2  ------------------------------------------------------------
VRK3  MISFCPDCGKSIQAAFKFCPYCGNSLPVEEHVGSQTFVNPHVSSFQGSKRGLNSSFETSP

VRK1  ------------------------------------------------------------
VRK2  ------------------------------------------------------------
VRK3  KKVKWSSTVTSPRLSLFSDGDSSESEDTLSSSERSKGSGSRPPTPKSSPQKTRKSPQVTR

VRK1  ---------MPRVKAAQAGRQSSAKRHLAEQFAVGEIITDMAKKEWKVGLPIGQGGFGCI
VRK2  -----------------MPPKRNEKYKLPIPFPEGKVLDDMEGNQWVLGKKIGSGGFGLI
VRK3  GSPQKTSCSPQKTRQSPQTLKRSRVTTSLEALPTGTVLTDKSGRQWKLKSFQTRDNQGIL
                          :  .          :.  *  :: *   .:* :      .. * :
                                  61K
VRK1  YLADMNSSESVGS--DAPCVVKVEPSDNGPLFTELKFYQRAAKPEQIQKWIRTRKLKYLG
VRK2  YLAFPTNKPEK----DARHVVKVEYQENGPLFSELKFYQRVAKKDCIKKWIERKQLDYLG
VRK3  YEAAPTSTLTCDSGPQKQKFSLKLDAKDGRLFNEQNFFQRAAKPLQVNKWKKLYSTPLLA
      * *  ...        :   .       .:* **.* :*:**.**   ::** .  .   *.

VRK1  VPKYWGSGLHDKNGKSYRFMIMDRFGSDLQKIYEA-NAKRFSRKTVLQLSLRILDILEYI
VRK2  IPLFYGSGLTEFKGRSYRFMVMERLGIDLQKISGQ-NGT-FKKSTVLQLGIRMLDVLEYI
VRK3  IPTCMGFGVHQDK---YRFLVLPSLGRSLQSALDVSPKHVLSERSVLQVACRLLDALEFL
      :*   * *: :  :   ***:::  :* .**.          :.. :***:. *:** **::
                169K
VRK1  HEHEYVHGDIKASNLLLNYKNPDQVYLVDYGLAYRYCPEGVHKEYKEDPKRCHDGTIEFT
VRK2  HENEYVHGDVKAANLLLGYKNPDQVYLADYGLSYRYCPNGNHKQYQENPRKGHNGTIEFT
VRK3  HENEYVHGNVTAENIFVDPEDQSQVTLAGYGFAFRYCPSGKHVAYVEGSRSPHEGDLEFI
      **:*****::.* *:::.  :: .** *..**:::****.* *  * *.. :  *:* :**

VRK1  SIDAHNGVAPSRRGDLEILGYCMIQWLTGHLPWEDNLKDPKYVRDSKIRYRENIASLMDK
VRK2  SLDAHKGVALSRRSDVEILGYCMLRWLCGKLPWEQNLKDPVAVQTAKTNLLDELPQSVLK
VRK3  SMDLHKGCGPSRRSDLQSLGYCMLKWLYGFLPWTNCLPNTEDIMKQKQKFVDKPGPFVGP
      *:* *:* .  ***.*:: *****::** * *** : * :.   :    * .   ::     :

VRK1  CFPEKNKPGEIAKYMETVKLLDYTEKPLYENLRDILLQGLKAIGSKDDGK---------L
VRK2  WAPSGSSCCEIAQFLVCAHSLAYDEKPNYQALKKILNPHGIPLGPLDFSTKGQSINVHTP
VRK3  CGHWIRPSETLQKYLKVVMALTYEEKPPYAMLRNNLEALLQDLR----------------
                 : :::  .   * * *** *   *:. *       :

VRK1  DLSVVENGGLKAKTITKKRKKEIEESKEPG-----------VEDTEWSNTQTEEAIQTRS
VRK2  NSQKVDSQKAATKQVNKAHNRLIEKKVHSERSAESCATWKVQKEEKLIGLMNNEAAQEST
VRK3  -VSPYDPIGLPMVP-----------------------------------------------
        .   :

VRK1  RTRKRVQK-----------------------------------------------------
VRK2  RRRQKYQESQEPLNEVNSFPQKISYTQFPNSFYEPHQDFTSPDIFKKSRSPSWYKYTSTV
VRK3  -------------------------------------------------------------

VRK1  ---------------------------------------------------
VRK2  STGITDLESSTGLWPTISQFTLSEETNADVYYYRIIIPVLLMLVFLALFFL
VRK3  ---------------------------------------------------
```

Transmembrane Domain Kinase Domain ATP binding site kinase active site

b