

**Supplementary Table 1** - RNA helicases from *P. falciparum* with Gene Ids, annotations as referred in the PlasmoDB database, and names for putative helicases confirmed based on BLAST search.

<b>S. No.</b>	<b>Gene Id</b>	<b>Database annotation</b>	<b>Given name</b>
1	PFD1060w	U5.snRNP	U5.snRNP
2	PF11_0053	PfSNF2L	PfSNF2L
3	PFE1085w	DEAD-box	DDX1
4	PF14_0655	helicase 45	DDX2A
5	PF08_0096	RNA helicase	DDX3X
6	PFC0915w	RNA helicase	DDX6
7	PF14_0081	DNA-repair helicase	DDX11
8	MAL13P1.134	DEAD-box	DDX12
9	PFI0480w	helicase with Zn-finger motif	DDX13
10	PF14_0437	helicase	DDX17
11	PFF1500c	DEAD/DEAH-box	DDX18
12	PFE0215w	helicase	DDX21
13	PFL2475w	DEAD/DEAH-box	DDX27
14	MAL7P1.113	DEAD-box	DDX31
15	PFB0445c	UAP56	DDX39
16	PFE1390w	RNA-helicase 1	DDX41
17	PFE0430w	RNA helicase	DDX46
18	PFB0860c	DEAD/DEAH-box	DDX47
19	PFD1070w	eIF	eIF4A3
20	MAL8P1.19	RNA helicase	DDX54
21	PFI0165c	DEAD/DEAH-box	DDX60
22	PF10_0294	RNA helicase	DHX8
23	PFI0860c	RNA helicase	DHX15
24	MAL13P1.322	splicing factor	DHX38
25	PFF1140c	DEAD-box	SUPV3L1
26	PFF0100w	RNA helicase	SKIV2L2

**Supplementary Table 2** - DNA helicases from *P. falciparum* with Gene Ids, annotations as referred in the PlasmoDB database, and names for putative helicases confirmed based on BLAST search.

<b>S.No.</b>	<b>Gene Id</b>	<b>Database annotation</b>	<b>Given name</b>
1	PFI0910w	DNA helicase	BLM
2	PF14_0278	DNA helicase	WRN
3	PF14_0177	MCM2	MCM2
4	PFE1345c	MCM3	MCM3
5	PF13_0095	MCM4-related	MCM4
6	PFL0580w	MCM5	MCM5
7	PF13_0291	Replication licensing factor	MCM6
8	PF07_0023	MCM7	MCM7
9	PFL0560c	MCM protein	MCM8
10	PF13_0291	Replication licensing factor	MCM9
11	PF10_0369	DNA repair helicase rad25 DNA excision-repair	XPB
12	PFI1650w	helicase	XPD
13	PFB0730w	DEAD/DEAH box helicase	HELLS
14	PF08_0048	ATP-dependent helicase	INOC1
15	PF11_0071	RuvB DNA helicase	RuvB
16	PF13_0330	DNA helicase	RuvB-like

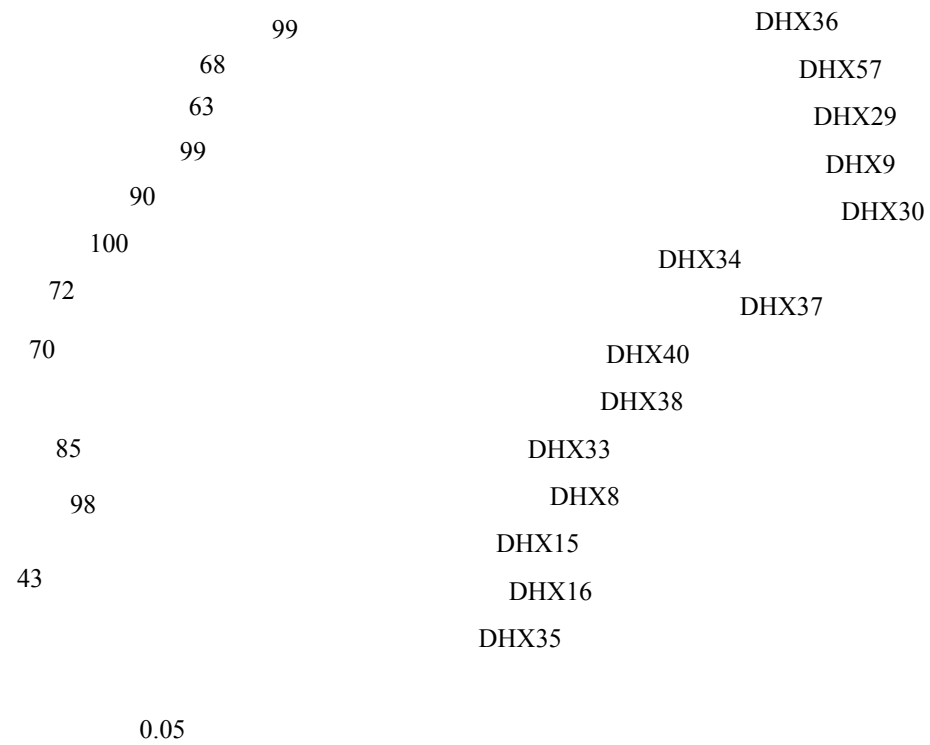
## **Legends for supplementary figures**

**Supplementary Figure 1:** Phylogenetic relationships of 14 DHX are constructed on entire protein sequences with MEGA4 alignment program. The phylogenetic tree is bootstrapped for 100 replicates. The bootstrap values at each node are indicated with numbers. The un-rooted tree is scaled for 0.05 substitutions per sequence position.

**Supplementary Figure 2:** Phylogeny for 37 DDX-type RNA helicases is built based on entire protein sequences with MEGA4 software. Bootstrap for 100 replicates; scale = 0.05 substitutions per sequence position.

**Supplementary Figure 3:** Phylogeny of RecQ helicase members drawn with MEGA4 software to scale 0.1 with 100 bootstrap replicates. Note that RecQ2, RecQ3 and RecQ4 are also called as Bloom (BLM), Werner (WRN), and Rothmund-Thomson syndrome (RTS) respectively.

**Supplementary Figure 4:** Phylogenetic analysis of MCM (2-7, 8, 9) proteins constructed on entire protein sequences with MEGA4 software. Scale is 0.05, bootstrap for 100 replicates.



**Supplementary Fig. 1**

		100	DDX2A
		100	DDX2B
	78		DDX48
		100	DDX19A
			DDX19B
	89	100	DDX25
		100	DDX39
	62		BAT1
71			DDX20
40			DDX6
			DDX21
		100	DDX50
		100	DDX3X
			DDX3Y
20	100		DDX4
		100	DDX5
	62	71	DDX17
			DDX43
		100	DDX53
	21		DDX46
24			DDX23
33	17		DDX42
	35		DDX41
			DDX52
	66		DDX59
			DDX27
	58		DDX54
		97	DDX10
	99		DDX18
67			DDX55
			DDX31
16	66		DDX56
			DDX51
24			DDX28
	96		DDX47
			DDX49
69			DDX24



**Supplementary Fig. 3**



**Supplementary Fig. 4**