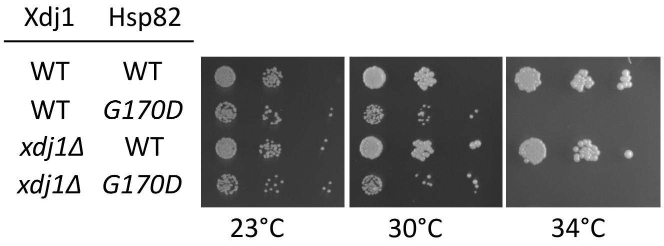
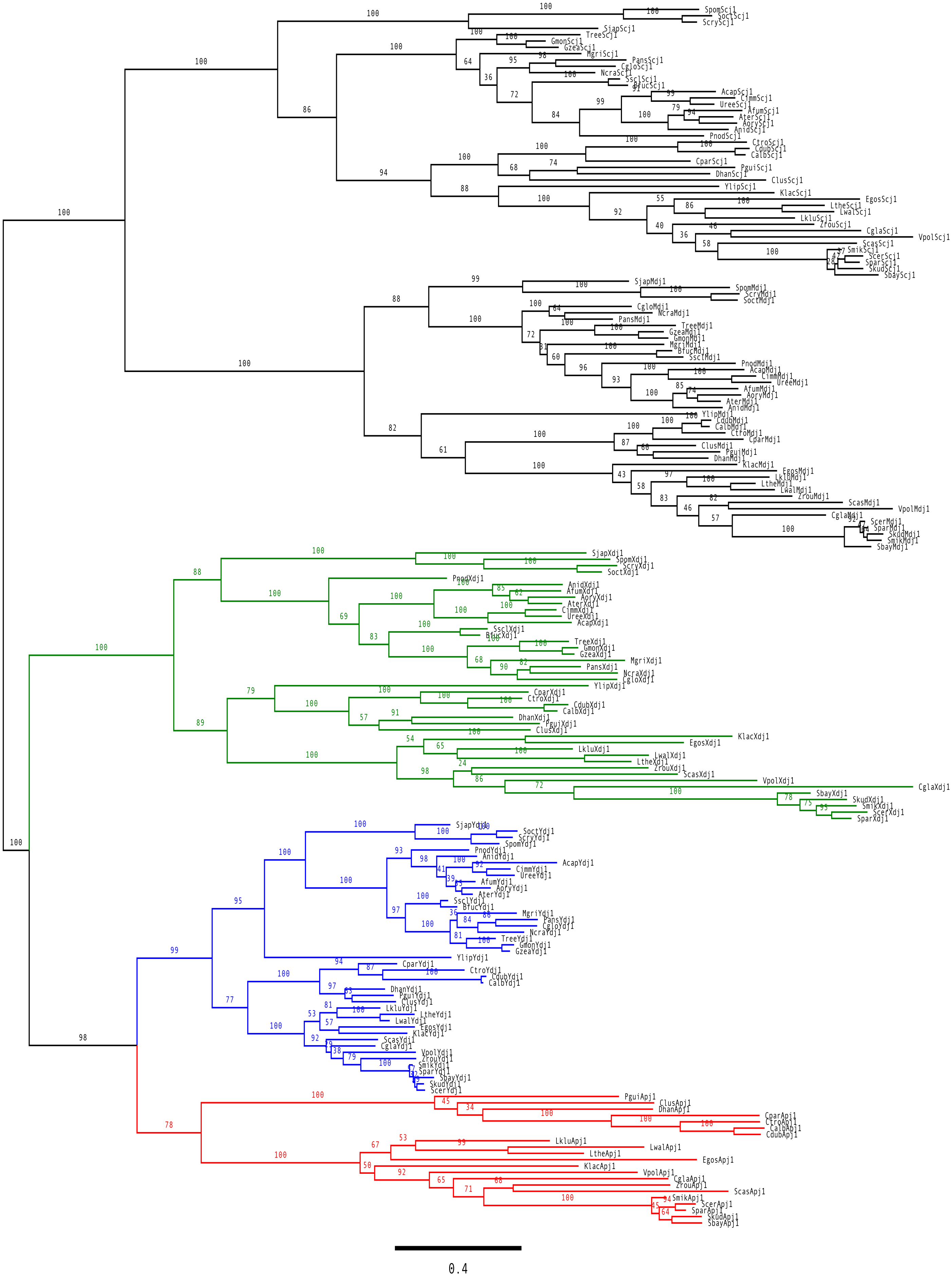
ID	Sequence	frequency
X2	FELRWMSEEPWV	8
X4	FSITLQSMHPWR	1
X12	VEIRFLTSYPWV	2
X20	LTIEAVSESPWR	1
Y1	GFIELIEWTALY	4
Y2	LSLEYISWGPYS	1
Y3	GRFSLVVRGILW	1
Y4	WQLNFSSPPLYN	1
Y5	STIYFSHPEASK	2
Y6	YTIHLSLPHRLG	1
Y10	WTIQFSSPGNLM	1
Y11	YVINFSPDHQLV	2
Y15	ATICFSSCGPQS	1
Y16	YTIHPSAGSDDP	1
Y18	QIIYLSSPEVSL	1

Supplementary Figure S5. Dodecapeptides presented on phage display isolates recovered in biopanning experiments with Xdj1 or Ydj1. The letter prefix in each ID number (left column) indicates the protein target used (X for Xdj1, Y for Ydj1). The deduced amino acid sequence of the peptide displayed at the N-terminus of M13 coat protein III is displayed in the center column. Frequency refers to the number of independent isolates obtained for each specific sequence.



Supplementary Figure S6. No obvious synthetic genetic interaction of *xdj1*Δ with Hsp90 mutant. 5μl of ten fold serial dilution of *hsc82Δ hsp82Δ* or *xdj1Δ hsc82Δ hsp82Δ* cells expressing either pRS314-*GPD*-Hsp82 (WT) or the *ts* allele of Hsp90, pRS314-*GPD*-$\mathrm{Hsp82}_{G170D}$ (G170D) were spotted on Trp omission plates and incubated at indicated temperatures for 3 days. Similar results (data not shown) were found using the strain background in which the original genomic wide screen was performed (Zhao R et al 2005).

Zhao R, Davey M, Hsu YC, Kaplanek P, Tong A, Parsons AB, Krogan N, Cagney G, Mai D, Greenblatt J, Boone C, Emili A, Houry WA (2005) Navigating the chaperone network: an integrative map of physical and genetic interactions mediated by the hsp90 chaperone. *Cell* **120:** 715-727


SpomScj1
SoctScj1
ScryScj1
SjapScj1
TreeScj1
GmonScj1
GzeaScj1
MgriScj1
PansScj1
CgloScj1
NcraScj1
SsclScj1
BfucScj1
AcapScj1
CimmScj1
UreeScj1
AfumScj1
AterScj1
AoryScj1
AnidScj1
PnodScj1
CtroScj1
CdubScj1
CalbScj1
CparScj1
PguiScj1
DhanScj1
ClusScj1
YlipScj1
KlacScj1
EgosScj1
LtheScj1
LwalScj1
LkluScj1
ZrouScj1
CglaScj1
VpolScj1
ScasScj1
SmikScj1
ScerScj1
SparScj1
SkudScj1
SbayScj1
SjapMdj1
SpomMdj1
ScryMdj1
SoctMdj1
CgloMdj1
NcraMdj1
PansMdj1
TreeMdj1
GzeaMdj1
GmonMdj1
MgriMdj1
BfucMdj1
SsclMdj1
PnodMdj1
AcapMdj1
CimmMdj1
UreeMdj1
AfumMdj1
AoryMdj1
AterMdj1
AnidMdj1
YlipMdj1
CdubMdj1
CalbMdj1
CtroMdj1
CparMdj1
ClusMdj1
PguiMdj1
DhanMdj1
KlacMdj1
EgosMdj1
LkluMdj1
LtheMdj1
LwalMdj1
ZrouMdj1
ScasMdj1
VpolMdj1
CglaMdj1
ScerMdj1
SparMdj1
SkudMdj1
SmikMdj1
SbayMdj1
SjapXdj1
SpomXdj1
ScryXdj1
SoctXdj1
PnodXdj1
AnidXdj1
AfumXdj1
AoryXdj1
AterXdj1
CimmXdj1
UreeXdj1
AcapXdj1
SsclXdj1
BfucXdj1
TreeXdj1
GmonXdj1
GzeaXdj1
MgriXdj1
PansXdj1
NcraXdj1
CgloXdj1
YlipXdj1
CparXdj1
CtroXdj1
CdubXdj1
CalbXdj1
DhanXdj1
PguiXdj1
ClusXdj1
KlacXdj1
EgosXdj1
LkluXdj1
LwalXdj1
LtheXdj1
ZrouXdj1
ScasXdj1
VpolXdj1
CglaXdj1
SbayXdj1
SkudXdj1
SmikXdj1
ScerXdj1
SparXdj1
SjapYdj1
SoctYdj1
ScryYdj1
SpomYdj1
PnodYdj1
AnidYdj1
AcapYdj1
CimmYdj1
UreeYdj1
AfumYdj1
AoryYdj1
AterYdj1
SsclYdj1
BfucYdj1
MgriYdj1
PansYdj1
CgloYdj1
NcraYdj1
TreeYdj1
GmonYdj1
GzeaYdj1
YlipYdj1
CparYdj1
CtroYdj1
CdubYdj1
CalbYdj1
DhanYdj1
PguiYdj1
ClusYdj1
LkluYdj1
LtheYdj1
LwalYdj1
EgosYdj1
KlacYdj1
ScasYdj1
CglaYdj1
VpolYdj1
ZrouYdj1
SmikYdj1
SparYdj1
SbayYdj1
SkudYdj1
ScerYdj1
PguiApj1
ClusApj1
DhanApj1
CparApj1
CtroApj1
CalbApj1
CdubApj1
LkluApj1
LwalApj1
LtheApj1
EgosApj1
KlacApj1
VpolApj1
CglaApj1
ZrouApj1
ScasApj1
SmikApj1
ScerApj1
SparApj1
SkudApj1
SbayApj1
0.4

Supplementary Figure S7. Fully resolved maximum-likelihood tree of the amino acid sequences of Ydj1, Xdj1, Apj1, Scj1 and Mdj1 used in the main text as Figure 6. All bootstrap values are shown above their respective branches. Species names and their codes are listed in Fig. S1.