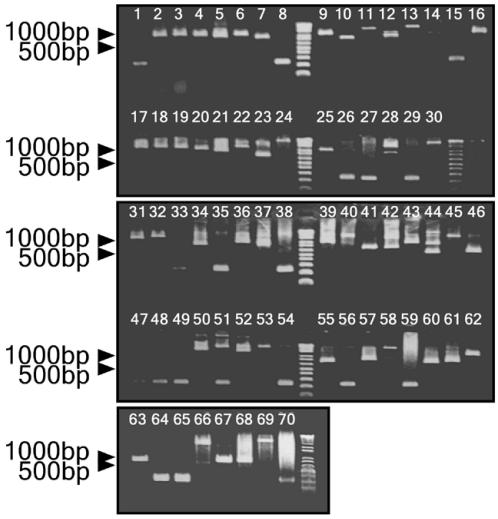
A



B

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Fig. S1. Candidate clones and sequence alignments. (A) Approximately 2.0×10^6 yeast transformants were screened and 70 primary candidates were identified as follows: Group I: >1000 bp, 16 clones; Group II: ≤1000 bp (>500 bp) 33 clones; Group III: <500 bp, 21 clones. The corresponding prey plasmids were isolated and sequenced. (B) Amino acid sequence of eEF1A2 and INT SE shows 96% similarity. The candidate $p16^{INK4a}$ binding partners were then identified by NCBI BLAST searches of the nucleotide and protein databases.

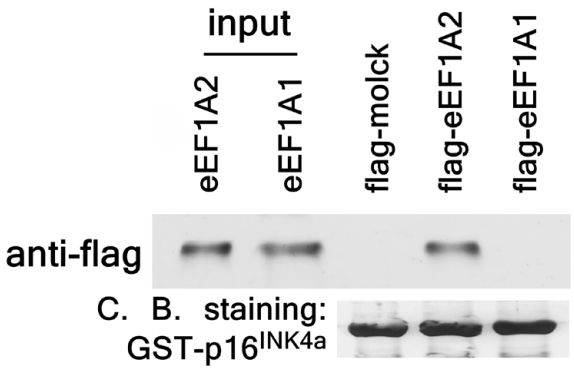

Fig. S2. Interaction between p16^{INK4a} and eEF1A2 or eEF1A1. A Flag-tagged eEF1A2 or eEF1A1 full-length or mock plasmid was incubated with an equal amount of GST-p16^{INK4a}. Bound proteins were analyzed by 12% SDS-PAGE and detected by western blotting.

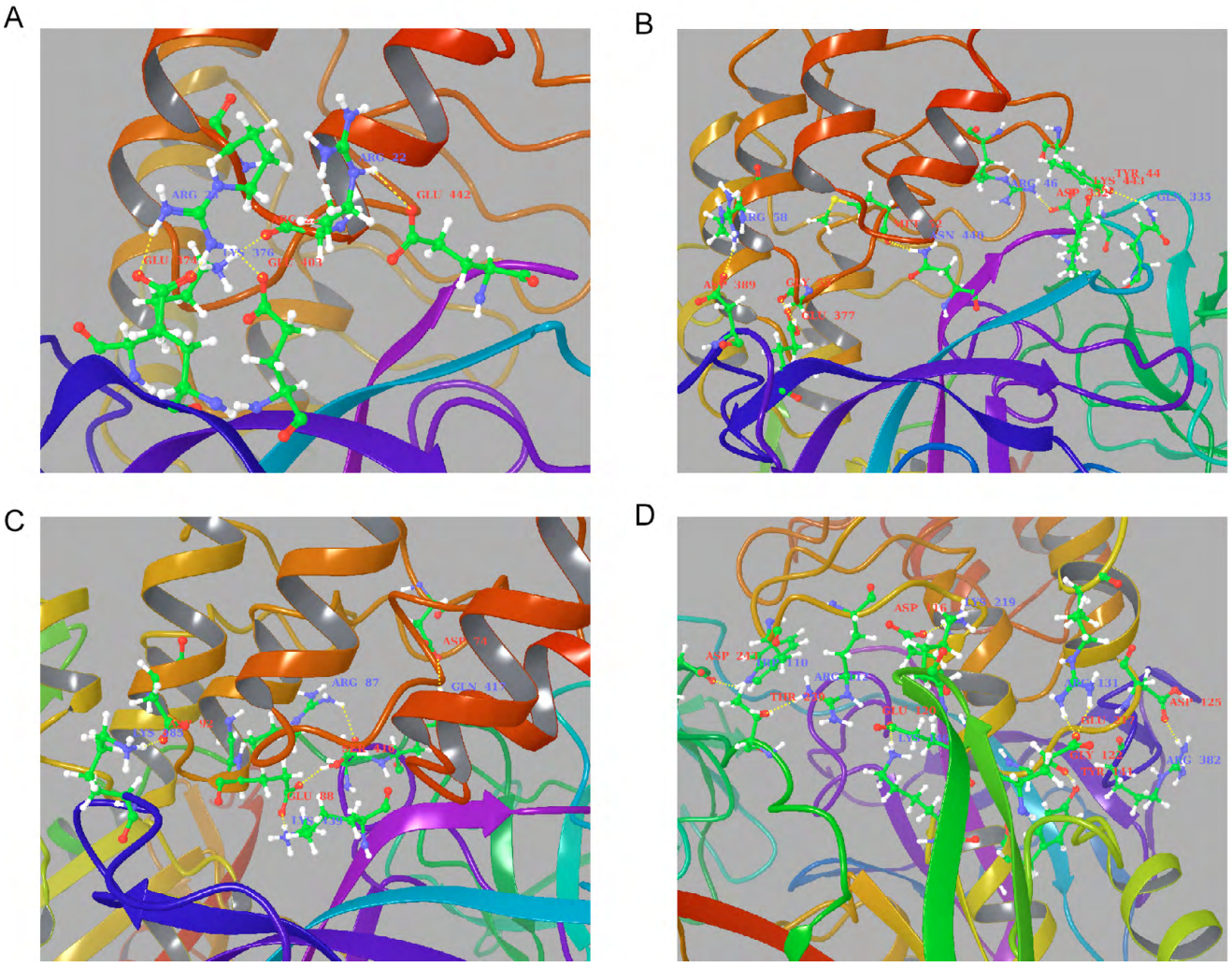

Fig. S3. Hydrogen bonding between the interface residues in the computational model of the p16^{INK4a}-eEF1A2 complex. (A) Hydrogen bonds between the residues from the first ankyrin repeat of p16^{INK4a} and those from Domain III of eEF1A2. (B) Hydrogen bonding between the residues from the second ankyrin repeat of p16^{INK4a} and those from Domain III of eEF1A2. (C) Hydrogen bonding between the residues from the third ankyrin repeat of p16^{INK4a} and those from Domain III of eEF1A2. (D) Hydrogen bonding between the residues from the fourth ankyrin repeat of p16^{INK4a} and those from Domain I of eEF1A2 (with one exception of Arg382 from Domain III). These figures were generated using the Schrödinger Maestro software program.

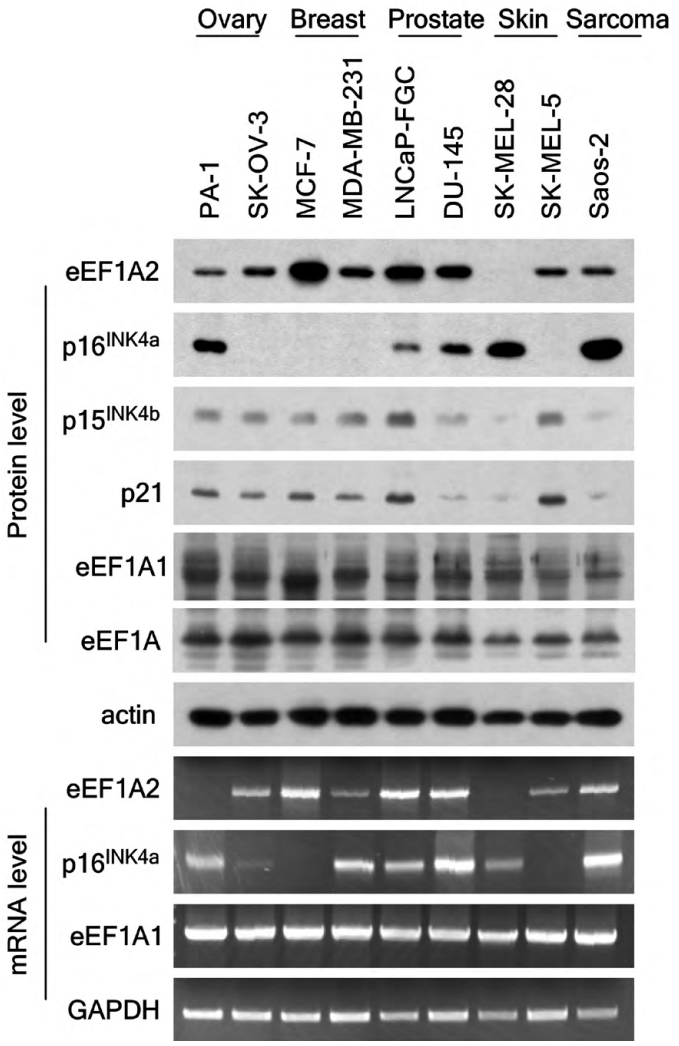

Fig. S4. Expression of eEF1A2 and p16^{INK4a} in cancer cell lines. The seven upper panels show protein expression of eEF1A2 and p16^{INK4a} and the four lower panels show mRNA levels of *eEF1A2* and *p16^{INK4a}*.

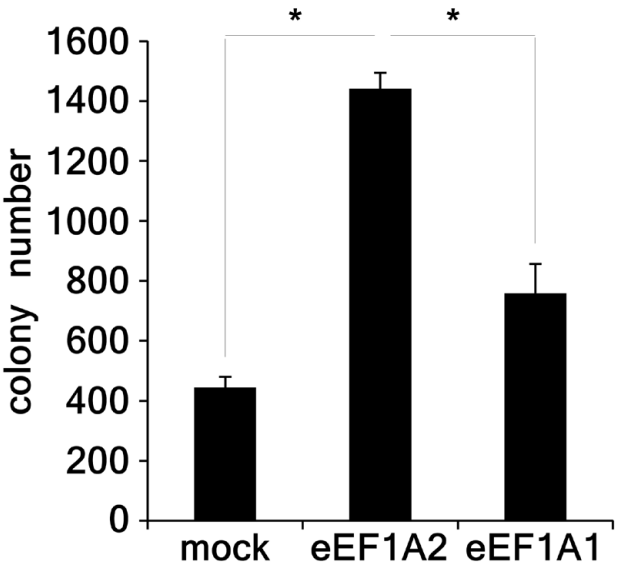

Fig. S5. Anchorage-independent cell growth in NIH3T3 cells transfected with mock, eEF1A1 or eEF1A2. Cells were stably transfected with mock, eEF1A1 or eEF1A2. Similar results were obtained from three independent experiments. Data are shown as means ± s.d.. of 3 independent experiments and the asterisk (*) indicates a significant difference (P<0.01).

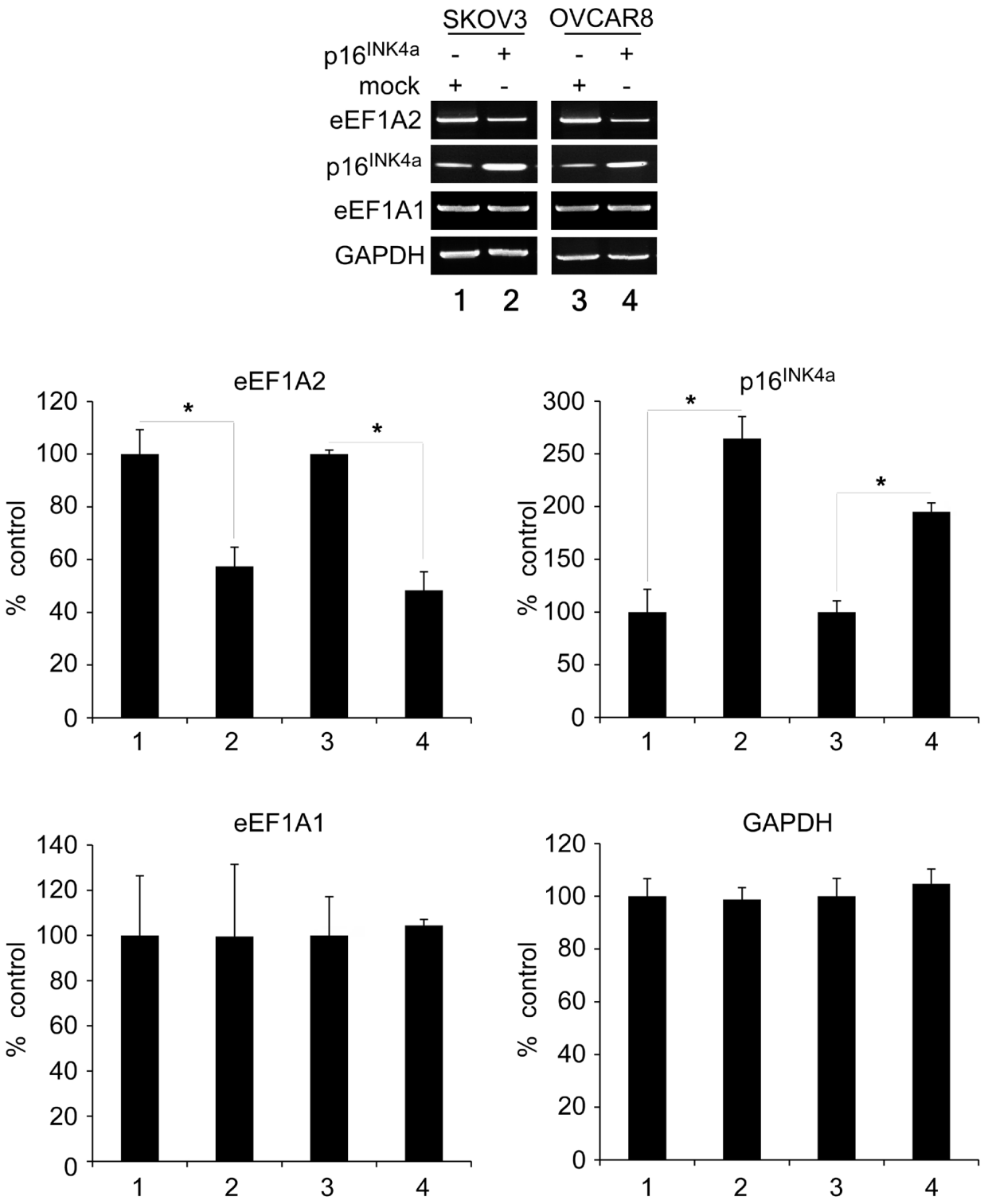

Fig. S6. The mRNA levels of eEF1A2, eEF1A1 and p16^{INK4a} in SKOV3 and OVCAR8 cells. Cells were transfected with mock or p16^{INK4a} and harvested after 48 h for preparing total RNAs. mRNA expression of *eEF1A2*, *eEF1A1* and *p16^{INK4a}* were analyzed by reverse transcriptase-PCR. Similar results were obtained from three independent experiments. Data are shown as means ± s.d. of 3 independent experiments and the asterisk (*) indicates a significant difference (P<0.01).

Table S1. Hydrogen bonds in the computational model of the p16^{INK4a}-eEF1A2 complex

Element (Atom-H)	Element (Atom-A)	Distance (<2.5 Å)	DHA angle (>120º)	HAB angle (>90º)
eEF1A2(IIII): Lys376-3HZ	P16(1st): Arg22-O	1.666	150.6	162.3
P16(1st): Arg22-HE	eEF1A2(III):Glu442-OE2	2.322	126.4	140.8
P16(1st): Arg24-1HH1	eEF1A2(III):Glu374-OE1	1.535	154.2	102.1
P16(1st): Arg24-2HH2	eEF1A2(III):Glu374-OE2	1.907	157.8	107.1
P16(1st): Arg24-2HH1	eEF1A2(III):Glu403-OE2	1.686	150.7	139.3
eEF1A2(III): Gln335-2HE2	P16(2nd): Tyr44-OH	2.356	157.1	96.9
P16(2nd): Tyr44-HH	eEF1A2(III): Lys443-O	2.008	143.8	121.3
P16(2nd): Arg46-1HH2	eEF1A2(III):Asp332-OD1	1.698	173.9	109.4
eEF1A2(III):Asn440-1HD2	P16(2nd):Met52-O	1.732	166.8	107.5
eEF1A2(III): Glu377-HE2	P16(2nd):Gly55-O	2.038	161.9	113.1
P16(2nd): Arg58-2HH1	eEF1A2(III): Asp389-OD2	1.812	155.3	162.5
eEF1A2(III): Gln417-2HE2	P16(3rd): Asp74-OD2	1.954	139.4	144.9
P16(3rd): Arg87-1HH1	eEF1A2(III): Ser416-O	2.499	130.0	120.9
eEF1A2(III): Ser416-HG	P16(3rd): Glu88-OE1	1.739	155.5	119.8
eEF1A2(III): Lys439-1HZ	P16(3rd): Glu88-OE2	1.530	176.1	119.3
eEF1A2(III): Lys385-1HZ	P16(3rd): Asp92-OD2	1.492	169.8	144.6
P16(4th): Trp110-HE1	eEF1A2(I): Asp243-OD2	1.966	136.1	103.6
P16(4th): Arg112-1HH1	eEF1A2(I): Thr239-OG1	1.914	163.5	130.1
eEF1A2(I): Lys219-3HZ	P16(4th): Asp116-OD1	1.608	172.3	157.4
eEF1A2(I): Lys146-2HZ	P16(4th): Glu120-OE1	1.447	171.2	121.6

eEF1A2(I): Tyr141-HH	P16(4^{th}): Gly122-O	1.690	166.4	127.1
eEF1A2(III): Arg382-1HH1	P16(4^{th}): Asp125(OD1)	1.790	150.8	140.4
P16(4^{th}): Arg131-1HH1	eEF1A2(I): Glu217-OE2	1.868	145.4	102.7
P16(4^{th}): Arg131-2HH2	eEF1A2(I): Glu217-OE2	1.714	151.5	143.9

The ankyrin repeats of $p16^{INK4a}$ and domains of eEF1A2 are also labeled in the table below. The hydrogen bonds are defined by default when the following distances and angle cut-offs were satisfied: 2.5 Å for H-A distance; D-H-A angle greater than 120°; and H-A-B angle greater than 90° where H is the hydrogen, A is the acceptor, D is the donor, and B is a neighbor atom bonded to the acceptor.

Note: HH is the hydrogen of the phenolic hydroxyl group of tyrosine. 2HE2 is one hydrogen in the amide side chain group of glutamine; HE2 is one carboxylic hydrogen of glutamic acid; 1HZ, 2HZ and 3HZ are the three hydrogens in the ε-ammonium group of lysine; 1HH1, 1HH2, 2HH2, 2HH1 and HE are the five hydrogens in the guanidinium side chain of arginine; O is the oxygen in the backbone amide group; OE1, OE2 are the two carboxylic oxygens of glutamic acid; OD1 and OD2 are the two carboxylate oxygens of aspartic acid.