# Figure S2. Alignment of Usp9 amino acid sequences

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1    MTATTRGSPVGGNDGQGQAPDGQSQPPLPQNQTSSPNSSNENSPVSPPDDQGQGDSPTPLEEEEPAFPHTELAKLDDMINRPRWVVPVLPKGELEVLLEA   zebrafish
1    MTATTRGSPVGGNDNQGQAPDGQSQPPLQQNQTSSPDSSNENSPATPPEQGQGDAPPQLEDEEPAFPHTDLAKLDDMINRPRWVVPVLPKGELEVLLEA    human
1    MTATTRGSPVGGNDSQGQAPDGQSQPPLQQNQTSSPDSSNENSPATPPDEQGQGDAPPQLEDEEPAFPHTDLAKLDDMINRPRWVVPVLPKGELEVLLEA   chicken

101  AIDLCKKGIDVKCEACQRFFRDGLTISFTKILTDEAVSGWKFEIHRCIINNAHRLVELCVTKLSQDWFPLLELLAMATNPHCKFHIYNGTRPSETVPAGV
101  AIDLSKKGLDVKSEACQRFFRDGLTISFTKILTDEAVSGWKFEIHRCIINNTHRLVELCVAKLSQDWFPLLELLAMAINPHCKFHIYNGTRPCESVSSSV
101  AIDLSKKGLDVKSEACQRFFRDGLTISFTKILTDEAVSGWKFEIHRCIINNTHRLVELCVAKLSQDWFPLLELLAMAINPHCKFHLYNGTRPSETVPAGV

201  QLAEDELFARPPDPRSPKGWLVDLINKFGTLNGFQTLHDRFMSGQALNVQIIAALIKPFGQCYEFLTLHTVKKYFLPIIEMVPQFLENLTDDELKKEAKN
201  QLPEDELFARSPDPRSPKGWLVDLNKFGTLNGFQILHDRFINGSALNVQIIAALIKPFGQCYEFLTLHTVKKYFLPIIEMVPQFLENLTDDELKKEAKN
201  QLAEDELYARPPDPRSPKGWLVDLINKFGTLNGFQILHDRFMSGSALNVQIIAALIKPFGQCYEFLTLHTVKKYFLPIIEMVPQFLENLTDDELKKEAKN

301  EAKNDALSMIIKSLKNLASRVPGQEETVKNLEIFRLKMILRLLQISSFNGKMNALNEVNKVISSVSYYTHRHGNPEEEEWLTAERMAEWIQQNNILSIVL
301  EAKNDALSMIIKSLKNLASRVPGQEETVKNLEIFRLKMILRLLQISSFNGKMNALNEVNKVISSVSYYTHRHGNPEEEEWLTAERMAEWIQQNNILSIVL
301  EAKNDALSMIIKSLKNLASRVPGQEETVKNLEIFRLKMILRLLQISSFNGKMNALNEVNKVISSVSYYTHRHGNPEEEEWLTAERMAEWIQQNNILSIVL

401  RDSLHQPQYVEKLEKILRFVIKEKALTQDLDNIWAAQAGKHEAIVKNVHDLLAKLAWDFSPEQLDHLFDCFKESWTNASKKQREKLLELIRRLAEDDKD
401  RDSLHQPQYVEKLEKILRFVIKEKALTQDLDNIWAAQAGKHEAIVKNVHDLLAKLAWDFSPEQLDHLFDCFKASWTNASKKQREKLLELIRRLAEDDKD
401  RDSLHQPQYVEKLEKILRFVIKEKALTQDLDNIWAAQAGKHEAIVKNVHDLLAKLAWDFSPEQLDHLFDCFKASWTNASKKQREKLLELIRRLAEDDKD

501  GVMAHKVLNLLWNLAHSDDVPVDIMDQALSAHIKILDYSCSQDRDTQKMQWIDRFIEELRTNDKWVIPALKQIREICSLFGEAPQNLS-----QTQRSPH
501  GVMAHKVLNLLWNLAHSDDVPVDIMDLALSAHIKILDYSCSQDRDTQKIQWIDRFIEELRTNDKWVIPALKQIREICSLFGEAPQNLSSSRFSQTQRSPH
501  GVMAHKVLNLLWNLAHSDDVPVDIMDQALSAHIKILDYSCSQDRDTQKIQWIDRFIEELRTNDKWVIPALKQIREICSLFGEAPQNLS-----QTQRSPH

596  VFYRHDLINQLQHNHALVTLVAENLSAYMENMRQFSKEHADFDPQTVRPGSRYSHVQEVQERLNFLRFLLKDGQLWLCAPQAKQIWKCLAENAVFLCDRE
601  VFYRHDLINQLQHNHALVTLVAENLATYMESMRLYARDHEDYDPQTVRLGSRYSHVQEVQERLNFLRFLLKDGQLWLCAPQAKQIWKCLAENAVYLCDRE
596  VFYRHDLINQLQHNHALVTLVAENLSAYMESMRQYAKEHGEYDPQTVRPGSRYSHVQEVQERLNFLRFLLKDGQLWLCAPQAKQIWKCLAENAVYLCDRE

696  ACFKWYSKLMGDEPDLDPDINKDFFENNVLQLDPSLLTENGMKCFERFFKAVNCREGKLVAKRRAYMMDDLELIGLDYLWRVVIQGSDDIASRAIDLLKE
701  ACFKWYSKLMGDEPDLDPDINKDFFESNVLQLDPSLLTENGMKCFERFFKAVNCREGKLVAKRRAYMMDDLELIGLDYLWRVVIQSNDDIASRAIDLLKE
696  ACFKWYSKLMGDEPDLDPDINKDFFENNVLQLDPSLLTENGMKCFERFFKAVNCREGKLVAKRRAYMMDDLELIGLDYLWRVVIQGNDDIANRAIDLLKE

796  IYTNLGPKLQANQVEIHEDFIQSCFDRLKASYDTLCVLDGDKDSINCARQEAIRMVRVLTVLREYITECDSDYHEERTILPMSRAFRGKHITLVVRFPNQ
801  IYTNLGPRLQVNQVVIHEDFIQSCFDRLKASYDTLCVLDGDKDSVNCARQEAVRMVRVLTVLREYINECDSDYHEERTILPMSRAFRGKHLSFVVRFPNQ
796  IYTNLGPRLQVNQVVIHEDFIQSCFDRLKASYDTLCVLDGDKDSINCARQEAIRMVRVLTVLREYINECDSDYHEERTILPMSRAFRGKHITLVVRFPNQ

896  GRQVDDLDIWSHTNDTIGSVRRCILNRIKANSTHTKIELFIGGEIIDPADDRKLIGQLNLKDKTLITAKLTQVSANMPSSPDSSSDSSTGSPGNHGNHYS
901  GRQVDDLEVWSHTNDTIGSVRRCILNRIKANVAHTKIELFVGGELIDPADDRKLIGQLNLKDKSLITAKLTQISSNMPSSPDSSSDSSTGSPGNHGNHYS
896  GRQVEDLDIWSHTNDTIGQVRRCILNRIKANSAHTKVELFIGGELVDPADDRKLIGQLNLKDKTLITAKLTQINSNMPSSPDSSSDSSTGSPGNHGNHYS

996  DGPNPEVESCLPGVIMSLHVRYISFLWQVADLGCNLNMPLLRDGARVLMKLMPPDNATVENLRAICLDHAKLGENSLSPTLDSRFFGPSPSQVLYLIEVV
1001 DGPNPEVESCLPGVIMSLHPRYISFLWQVADLGSCNLNMPLLRDGARVLMKLMPPDSTTIEKLRAICLDHAKLGESSLSPSLDSLFFGPSASQVLYLTEVV
996  DGPNPEVESCLPGVIMSLHPRYISFLWQVADLGSLNMPLLRDGARVLMKLMPPDNTTVEKLRAICLDHAKLGESSLSPSLDSLFFGPSASQVLYLTEVV

1096 YALLMPASGTLGEDASDFQYNFLKSGGLPLVLSMLTRNNFLPNADMETRRGAYLNALKIAKLLLTAVGFGHVKSVAEACQPVVEGTIPVSPINQTTHDQA
1101 YALLMPAGAPLADDSSDFQFHFLKSGGLPLVLSMLTRNNFLPNADMETRRGAYLNALKIAKLLLTAIGYGHVRAVAEACQPGVEGVNPMTQINQVTHDQA
1096 YALLMPASAPLGEDASDFQYNFLKSGGLPLVLSMLTRNNFLPNADMETRRGAYLNALKIAKLLLTAIGYGHVRAVAEACQPVVEGTSTVSPINQATHDQA

1196 LVLQNALQNIPNPSAECMLRNVAIRLAQQISDENFFQASKYIPDICVIRAVQKIVWASGCGSVQHVFSSNEEISKIYEKTNAGNEPDAEDEQVCCEALEV
1201 VVLQSALQSIPNPSSECMLRNVSVRLAQQISDE----ASRYMPDICVIRAIQKIIWASGCGSLQLVFSPNEEITKIYEKTNAGNEPDLEDEQVCCEALEV
1196 VVLQNALQNIPNPTSECMLRNVAIRLAQQISDE----ASKYIPDICVIRAVQKIVWASGCGSVQLVFSSNEEISKIYEKTNAGNEPDMEDEQVCCEALEV

1296 MTLCFALMPTALDALSKEKAWQTFIIDLLLHCQSKSVRQMAQEQFFLMATRCCMGHRPLLFFITLLFTVLGSTAKERAKHAADYFTLLRHLLNYAFNSNI
1297 MTLCFALIPTALDALSKEKAWQTFIIDLLLHCHSKTVRQVAQEQFFLMCTRCCMGHRPLLFFITLLFTVLGSTARERAKHSGDYFTLLRHLLNYAYNSNI
1292 MTLCFALIPTALDALSKEKAWQTFIIDLLLHCHSKIVRQMAQEQFFLMATRCCMGQRPLLFFITLLFTVLGSTARERAKHSGDYFTLLRHLLNYAYNSNI

1396 NLPNAEVLLNNEIDWLKRIRDEVKRTGEPGVEETILEGHIGVTKELLAFQTPEKKFYIGCEKGGASLIKELVDDFLFPASNVYLQYMKSGEFPTEQAIPV
1397 NVPNAEVLLNNEIDWLKRIRDDVKRTGETGIEETILEGHLGVTKELLAFQTSEKKFHIGCEKGGANLIKELDDFIFPASNVYLQYMRNGELPAEQAIPV
1392 NVPNAEVLLNNEIDWLKRIRDEVKRTGETGVEETILEGHLGVTKELLAFQTPEKKYHIGCEKGGANLIKELIDDFIFPASNVYLQYMRNGELPAEQAIPV

1496 CSTPATINAGFELLVALAIGCVRNLKQIVDTLTDMYYLG-----CEPLTEWEYLPPVGPRPTKGFVGLKNAGATCYMNSVIQQLYMIPPIRNGILAIEGT
1497 CGSPPTINAGFELLVALAVGCVRNLKQIVDSLTEMYIGTAITTCEALTEWEYLPPVGPRPKGFVGLKNAGATCYMNSVIQQLYMIPSIRNGILAIEGT
1492 CSSPATINAGFELLVALAVGCVRNLKQIVDTLTEMYYIGTAITTCEALTEWEYLPPVGPRPKGFVGLKNAGATCYMNSVIQQLYMIPAIRNGILAIEGT
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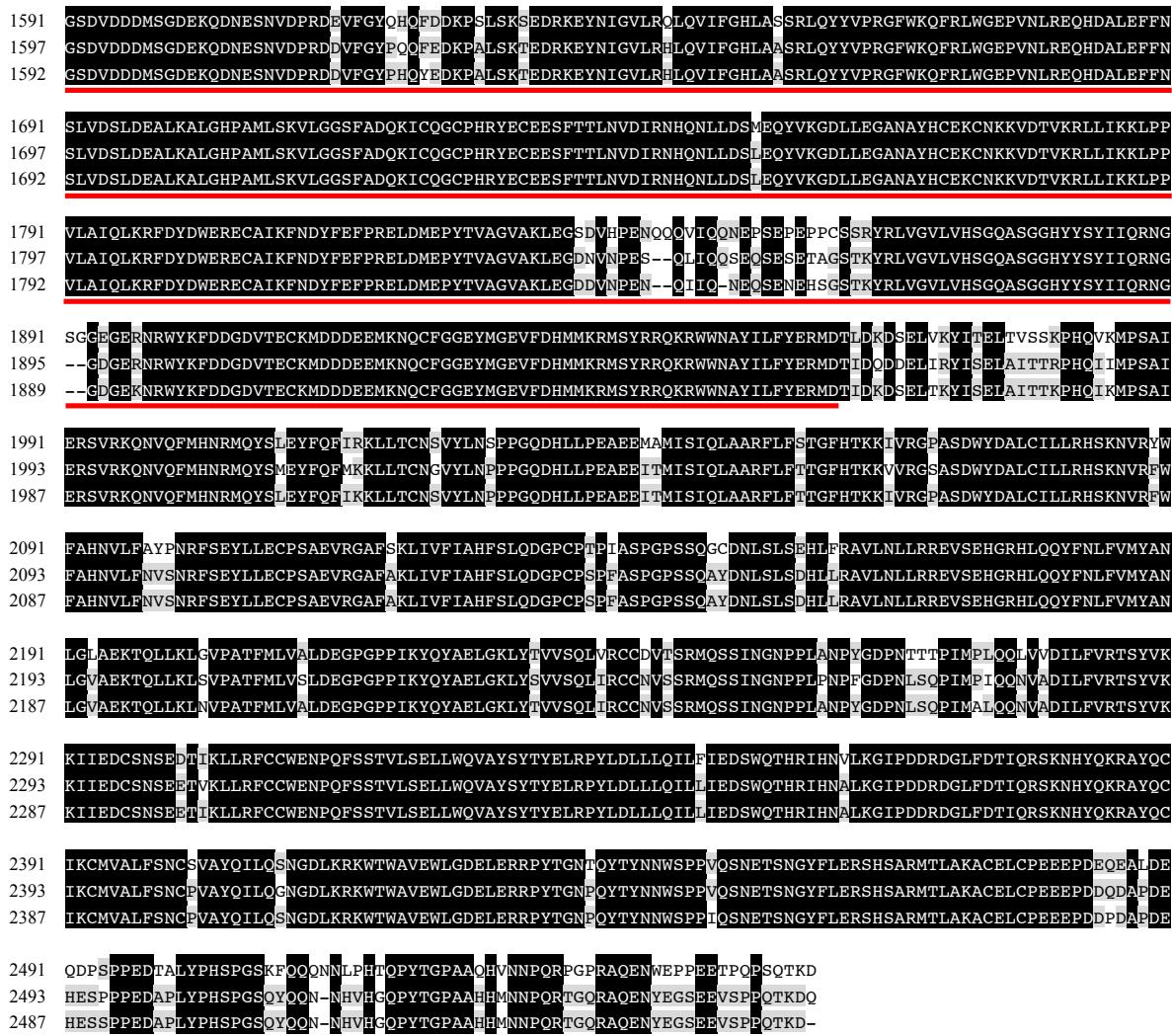
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1591 GSDVDDDMSGDEKQDNESNVDPRDEVFGYQHQFDDKPSLSKSEDRKEYNIGVLRQLQVIFGHLASSRLQYYVPRGFWKQFRLWGEPVNLREQHDALEFFN
1597 GSDVDDDMSGDEKQDNESNVDPRDDVFGYPQQFEDKPALSKTEDRKEYNIGVLRHLQVIFGHLAASRLQYYVPRGFWKQFRLWGEPVNLREQHDALEFFN
1592 GSDVDDDMSGDEKQDNESNVDPRDDVFGYPHQYEDKPALSKTEDRKEYNIGVLRHLQVIFGHLAASRLQYYVPRGFWKQFRLWGEPVNLREQHDALEFFN

1691 SLVDSLDEALKALGHPAMLSKVLGGSFADQKICQGCPHRYECEESFTTLNVDIRNHQNLLDSMEQYVKGDLLEGANAYHCEKCNKKVDTVKRLLIKKLPP
1697 SLVDSLDEALKALGHPAMLSKVLGGSFADQKICQGCPHRYECEESFTTLNVDIRNHQNLLDSLEQYVKGDLLEGANAYHCEKCNKKVDTVKRLLIKKLPP
1692 SLVDSLDEALKALGHPAMLSKVLGGSFADQKICQGCPHRYECEESFTTLNVDIRNHQNLLDSLEQYVKGDLLEGANAYHCEKCNKKVDTVKRLLIKKLPP

1791 VLAIQLKRFDYDWERECAIKFNDYFEFPRELDMEPYTVAGVAKLEGSDVHPENQQQVIQQNEPSEPEPPCSSRYRLVGVLVHSGQASGGHYYSYIIQRNG
1797 VLAIQLKRFDYDWERECAIKFNDYFEFPRELDMEPYTVAGVAKLEGDNVNPES--QLIQQSEQSESETAGSTKYRLVGVLVHSGQASGGHYYSYIIQRNG
1792 VLAIQLKRFDYDWERECAIKFNDYFEFPRELDMEPYTVAGVAKLEGDDVNPEN--QIIQ-NEQSENEHSGSTKYRLVGVLVHSGQASGGHYYSYIIQRNG

1891 SGGEGERNRWYKFDDGDVTECKMDDDEEMKNQCFGGEYMGEVFDHMMKRMSYRRQKRWWNAYILFYERMDTDKDSELVKYITELTVSSKPHQVKMPSAI
1895 --GDGERNRWYKFDDGDVTECKMDDDEEMKNQCFGGEYMGEVFDHMMKRMSYRRQKRWWNAYILFYERMDTIDQDDELIRYISELAITTRPHQIIMPSAI
1889 --GDGEKNRWYKFDDGDVTECKMDDDEEMKNQCFGGEYMGEVFDHMMKRMSYRRQKRWWNAYILFYERMDTIDKDSELTKYISELAITTKPHQIKMPSAI

1991 ERSVRKQNVQFMHNRMQYSLEYFQFIRKLLTCNSVYLNSPPGQDHLLPEAEEMAMISIQLAARFLFSTGFHTKKIVRGPASDWYDALCILLRHSKNVRYW
1993 ERSVRKQNVQFMHNRMQYSMEYFQFMKKLLTCNGVYLNPPPGQDHLLPEAEEITMISIQLAARFLFTTGFHTKKVVRGSASDWYDALCILLRHSKNVRFW
1987 ERSVRKQNVQFMHNRMQYSLEYFQFIKKLLTCNSVYLNPPPGQDHLLPEAEEITMISIQLAARFLFTTGFHTKKIVRGPASDWYDALCILLRHSKNVRFW

2091 FAHNVLFAYPNRFSEYLLECPSAEVRGAFSKLIVFIAHFSLQDGPCPTPIASPGPSSQGCDNLSLSEHLFRAVLNLLRREVSEHGRHLQQYFNLFVMYAN
2093 FAHNVLFNVSNRFSEYLLECPSAEVRGAFAKLIVFIAHFSLQDGPCPSPFASPGPSSQAYDNLSLSDHLLRAVLNLLRREVSEHGRHLQQYFNLFVMYAN
2087 FAHNVLFNVSNRFSEYLLECPSAEVRGAFAKLIVFIAHFSLQDGPCPSPFASPGPSSQAYDNLSLSDHLLRAVLNLLRREVSEHGRHLQQYFNLFVMYAN

2191 LGLAEKTQLLKLGVPATFMLVALDEGPGPPIKYQYAELGKLYTVVSQLVRCCDVTSRMQSSINGNPPLANPYGDPNTTTPIMPLQQLVVDILFVRTSYVK
2193 LGVAEKTQLLKLSVPATFMLVSLDEGPGPPIKYQYAELGKLYSVVSQLIRCCNVSSRMQSSINGNPPLPNPFGDPNLSQPIMPIQQNVADILFVRTSYVK
2187 LGVAEKTQLLKLNVPATFMLVALDEGPGPPIKYQYAELGKLYTVVSQLIRCCNVSSRMQSSINGNPPLANPYGDPNLSQPIMALQQNVADILFVRTSYVK

2291 KIIEDCSNSEDTIKLLRFCCWENPQFSSTVLSELLWQVAYSYTYELRPYLDLLLQILFIEDSWQTHRIHNVLKGIPDDRDGLFDTIQRSKNHYQKRAYQC
2293 KIIEDCSNSEETVKLLRFCCWENPQFSSTVLSELLWQVAYSYTYELRPYLDLLLQILLIEDSWQTHRIHNALKGIPDDRDGLFDTIQRSKNHYQKRAYQC
2287 KIIEDCSNSEETIKLLRFCCWENPQFSSTVLSELLWQVAYSYTYELRPYLDLLLQILLIEDSWQTHRIHNALKGIPDDRDGLFDTIQRSKNHYQKRAYQC

2391 IKCMVALFSNCSVAYQILQSNGDLKRKWTWAVEWLGDELERRPYTGNTQYTYNNWSPPVQSNETSNGYFLERSHSARMTLAKACELCPEEEPDEQEALDE
2393 IKCMVALFSNCPVAYQILQGNGDLKRKWTWAVEWLGDELERRPYTGNPQYTYNNWSPPVQSNETSNGYFLERSHSARMTLAKACELCPEEEPDDQDAPDE
2387 IKCMVALFSNCPVAYQILQSNGDLKRKWTWAVEWLGDELERRPYTGNPQYTYNNWSPPIQSNETSNGYFLERSHSARMTLAKACELCPEEEPDDPDAPDE

2491 QDPSPPEDTALYPHSPGSKFQQQNNLPHTQPYTGPAAQHVNNPQRPGPRAQENWEPPEETPQPSQTKD
2493 HESPPPEDAPLYPHSPGSQYQQN-NHVHGQPYTGPAAHHMNNPQRTGQRAQENYEGSEEVSPPQTKDQ
2487 HESSPPEDAPLYPHSPGSQYQQN-NHVHGQPYTGPAAHHMNNPQRTGQRAQENYEGSEEVSPPQTKD-
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**Figure S2.** Alignment of Usp9 amino acid sequences. Alignment of zebrafish Usp9 (*Danio rerio*, our sequence), human Usp9 (*Homo sapiens*, XP_005272733.1) and chicken Usp9 (*Gallus gallus*, XP_416773.2). Zebrafish Usp9 bears 90.04% and 92.58% amino acids identity to its counterparts of human and chicken, respectively. Red line indicates the region of ubiquitin-specific protease (USP) domain.