Supplementary Data: Supplementary Tables and Figures

Convergent evolution of cysteine-rich keratins in hard skin appendages of terrestrial vertebrates

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Content

Supplementary Table S1. Keratin genes of the chicken (*Gallus gallus*)

Keratin type	**Name[1]**	**Genomic DNA sequence**	**Gene start[2]**	**Gene end[2]**	**Gene name (GenBank)**	**Gene**	**Protein[3]**	**Differences between new gene prediction and GenBank (GCF_000002315.5)[4]**
		(acc. nr.)	**(nucl. nr.)**	**(nucl. nr.)**		**(GenBank ID)**	**(acc. nr.)**	
type I	K222	NC_006114.5	7326273	7321193	KRT222	420046	NP_001182406.1	
type I	K12	NC_006114.5	7335707	7329801	n.a.	n.a.	n.a.	
type I	K20	NC_006114.5	7340108	7336399	KRT40	420045	NP_001264910.1	
type I	K23	NC_006114.5	7359178	7349963	KRT23	420044	XP_418167.4	
type I	K15	NC_006114.5	7366321	7362226	KRT15	408040	NP_001001312.2	
type I	K19	NC_006114.5	7373828	7369522	KRT19	395861	NP_990340.2	
type I	K9L1	NC_006114.5	7384221	7380438	LOC100857659	100857659	XP_003642867.2	GenBank gene prediction comprises 2 coding sequences
type I	K9L2	NC_006114.5	7391904	7388878	LOC100857659	100857659	XP_004948661.2	GenBank gene prediction comprises 2 coding sequences
type I	K9L3	NC_006114.5	7398958	7394346	KRT10	771977	XP_001235182.3	
type I	K9L4	NC_006114.5	7409440	7405257	KRT9L	420041	XP_418163.4	
type I	HAS1 (K9LC1)	NC_006114.5	7417651	7413171	LOC772080	772080	XP_001233972.1	
type I	HAS2 (K9LC2)	NC_006114.5	7426921	7422075	KRTC42L	420039	XP_418162.6	
type I	HAS3 (K9LC3)	NC_006114.5	7434663	7432253	LOC771995	771995	XP_003642868.1	
type I	K14L1	NC_006114.5	7442528	7438886	KRT14	408039	NP_001001311.2	
type I	K14L2	NC_006114.5	7449377	7445505	KRT17	100858439	NP_001264913.1	
type I	K18	NC_008465.4	5401187	5408382	KRT18	101749333	XP_025001434.1	
type II	K80	NC_008465.4	5202555	5188564	KRT80	431302	XP_428853.4	
type II	K7	NC_008465.4	5216450	5224940	KRT7	395772	NP_990263.1	
type II	K84L	NC_008465.4	5233503	5230255	LOC426897	426897	XP_015155864.2	
type II	K5L3	NC_008465.4	5245539	5241947	KRT75	408042	NP_001001314.2	
type II	K5L2	NC_008465.4	5254375	5249671	KRT6A	408041	NP_001001313.2	
type II	K5L1	NC_008465.4	5267020	5260881	KRT5	407779	NP_001001195.1	
type II	HBS1 (K78LC1)	NC_008465.4	5287405	5280968	KRT75L4	100858302	XP_015155859.1	
type II	HBS2 (K78LC2)	NC_008465.4	5305881	5300187	LOC768978	768978	XP_015155862.1	
type II	HBS3 (K78LC3)	NC_008465.4	5316137	5311299	LOC107055419	107055419	XP_025001374.1	
type II	K78LT	NC_008465.4	5335060	5322171	LOC431300	431300	partially identical: XP_025001353.1	Prediction is uncertain, multiple frame-shift mutations, hypothetical amino acid sequence is shown in Suppl. Fig. S1
type II	K78L4	NC_008465.4	5351881	5348560	KRT75L2	431299	XP_428850.2	
type II	K78L3	NC_008465.4	5360226	5356373	KRT71	768881	XP_001232027.4	
type II	K78L2	NC_008465.4	5369524	5365170	KRT75L1	768880	XP_015155860.1	
type II	K78L1	NC_008465.4	5379290	5374907	LOC112529929	112529929	XP_001231586.2	
type II	K8	NC_008465.4	5396641	5388108	KRT8	426896	XP_015128103.2	

Notes: [1] Keratins were named according to orthology to human proteins. K9-like cysteine-rich keratins (K9LC) are termed HAS and K78-like cysteine-rich keratins (K78LC) are termed HBS keratins. HAS, hard acidic sauropsid-specific; HBS, hard basic sauropsid-specific; L, like; LT, long tail.

[2] Gene start and end indicate the start and stop codon of the coding sequence. Introns are not indicated.

[3] Accession numbers (acc. nr.) of protein amino acid sequences predicted in GenBank.

[4] Genome sequence assembly: GRCg6a (GCF_000002315.5).

acc., accession; n.a., not available in the genome sequence assembly; nucl., nucleotide; nr., number.

Supplementary Table S2. Keratin genes of the Chinese alligator (*Alligator sinensnis)*

Keratin type	Name[1]	Genomic DNA sequence (acc. nr.)	Gene start[2] (nucl. nr.)	Gene end[2] (nucl. nr.)	Gene name (GenBank)	Gene (GenBank ID)	Protein[3] (acc. nr.)	Differences between new gene prediction and GenBank (GCF_000455745.1)[4]
type I	K222	NW_005842040.1	395100	404167	KRT222	102385505	XP_006022588.2	
type I	K24	NW_005842040.1	366765	376063	LOC102378366	102378366	XP_025058718.1	
type I	K10L	NW_005842040.1	335322	345003	LOC102378129	102378129	XP_025058719.1	Corrected exon 1: start at nucl. 335322
type I	K12	NW_005842040.1	303666	309983	LOC102377886	102377886	XP_006022639.1	
type I	K20	NW_005842040.1	275299	289066	KRT20	102385271	XP_006022587.1	
type I	K23	NW_005842040.1	178687	214213	LOC102377411	102377411	XP_006022637.2	
type I	K36L1	NW_005842040.1	127867	137534	LOC102377177	102377177	XP_006022636.1	Exon 1: start at nucl. 6043 relative to GenBank prediction; end of exon 6
type I	K36L2	NW_005842040.1	116254	122570	LOC102376945	102376945	XP_006022635.2	Corrected exon 1: starts at nucl 116254, exon 7 with premature stop codon
type I	K36L3	NW_005842040.1	100211	104304	LOC102376692	102376692	XP_025058710.1	
type I	K15L	NW_005842040.1	76246	84026	LOC102385021	102385021	XP_006022586.1	
type I	K19	NW_005842040.1	62672	69119	LOC102384765	102384765	XP_006022585.1	
type I		NW_005842040.1						
type I	K9L1	NW_005842040.1	30264	35981	LOC102384514	102384514	XP_006022584.1	
type I	K9L	NW_005842040.1	3318	14074	LOC102376455	102376455	XP_025058716.1	Incomplete start, inactivating mutation: frame shift at nucl. 11877
type I	K9L2	NW_005843869.1	11069	17220	LOC102379508	102379508	XP_006039283.2	
type I	K9L3	NW_005842585.1	1032077	1036258	LOC102369678	102369678	XP_006032846.1	
type I	K9L4	NW_005842585.1	1012386	1018971	LOC102373165	102373165	XP_025070308.1	
type I	K9L5	NW_005842585.1	985187	992565	LOC102369323	102369323	XP_025070304.1	
type I	HAS1 (K9LC1)	NW_005842585.1	947406	954479	LOC102368806	102368806	XP_006032843.1	
type I	HAS2 (K9LC2)	NW_005842585.1	925915	931931	LOC102369067	102369067	XP_006032844.1	
type I	K14L1	NW_005842585.1	878298	886416	LOC102368390	102368390	XP_006032841.1	
type I	K14L2	NW_005842585.1	864255	870926	LOC102367973	102367973	XP_006032839.1	
type I	K117	NW_005842585.1	819205	826538	LOC102372666	102372666	XP_025070287.1	
type I	K18	NW_005842452.1	1162577	1158980	KRT18	102375632	XP_006030669.1	
type II	K80	NW_005842526.1	782023	782023	KRT80	102371067	XP_006031790.2	
type II	K7	NW_005842526.1	829141	829141	LOC102371330	102371330	XP_006031791.1	
type II	K84L1	NW_005842526.1	845249	845249	LOC102377597	102377597	XP_006031815.1	
type II	K84L2	NW_005842526.1	860922	860922	LOC102377836	102377836	XP_025069161.1	Last exon with sequence gap, corrected to 860920..861200
type II	K5L4	NW_005842526.1	870439	870439	LOC102371761	102371761	XP_006031793.1	
type II	K5L3	NW_005842526.1	893670	893670	LOC102372247	102372247	XP_006031794.2	This GenBank gene prediction combines 2 coding sequences. Besides the gene indicated here, another gene starts at nucl. 888065, frame shift: nucl. 887772, premature stop: nucl. 887601
type II	K5L2	NW_005842526.1	919981	919981	LOC102372665	102372665	XP_006031796.1	
type II	K5L1	NW_005842526.1	935435	935435	LOC102378082	102378082	XP_006031817.1	
type II	HBS1 (K78LC1)	NW_005842526.1	955663	955663	LOC102373417	102373417	XP_006031800.1	
type II	HBS2 (K78LC2)	NW_005842526.1	977316	977316	LOC102378317	102378317	XP_025069184.1	
type II	HBS3	NW_005842526.1	992203	992203	LOC102378551	102378551	XP_025069194.1	
type II	K78LT	NW_005842526.1	1027861	1027861	LOC102373665	102373665	XP_006031801.1	Predicted exon 7: 1031791..1032015, predicted exon 8: 1031021..1031049, exon 9: 1027860..1030907 then frameshift
type II	K78L6	NW_005842526.1	1060335	1060335	LOC102374427	102374427	XP_014379207.1	Predicted exon 7: 1120942..1121156, exon 8: 1120411..1120445
type II	K78L5	NW_005842526.1	1089374	1089374	LOC102379545	102379545	XP_025069173.1	
type II	K78L4	NW_005842526.1	1105253	1105253	LOC102380041	102380041	XP_014379196.1	
type II	K78L3	NW_005842452.1	1279629	>1284625	LOC102380269	102380269	XP_006030688.1	Incomplete, exon 6 ends at nucl. 1284625, exons 7 and 8 are missing because of a gap in the genome sequence
type II	K78L2	NW_005842452.1	1260757	1265945	LOC102380036	102380036	XP_014378646.1	
type II	K78L1	NW_005842452.1	1250240	1256757	LOC106722579	106722579	XP_014378640.1	
type II	K8L	NW_005842452.1	1201934	1209453	LOC102379785	102379785	XP_006030686.1	
type II	K8	NW_005842452.1	1183482	1192777	KRT8	102375882	XP_006030670.1	

Notes: [1] Keratins were named according to orthology to human proteins. K9-like cysteine-rich keratins (K9LC) are termed HAS and K78-like cysteine-rich keratins (K78LC) are termed HBS keratins.
HAS, hard acidic sauropsid-specific; HBS, hard basic sauropsid-specific; L, like; LT, long tail.

[2] Gene start and end indicate the start and stop codon of the coding sequence. Introns are not indicated.

[3] Accession numbers (acc. nr.) of protein amino acid sequences predicted in GenBank.

[4] Genome assembly: ASM45574v1 (GCF_000455745.1).
acc., accession; n.a., not available in the genome sequence assembly; nucl., nucleotide; nr., number.

Supplementary Table S3. Keratin genes of the turtle (*Chrysemys picta bellii*)

Keratin type	**Name**[1]	**Genomic DNA sequence**	**Gene start**[2]	**Gene end**[2]	**Gene name (GenBank)**	**Gene**	**Protein**[3]	**Differences between new gene prediction and GenBank (GCF_000241765.3)**[4]
		(acc. nr.)	**(nucl. nr.)**	**(nucl. nr.)**		**(GenBank ID)**	**(acc. nr.)**	
type I	K222	NW_007359872.1	6017079	6007457	KRT222	101946940	XP_023956555.1	
type I	K24	NW_007359872.1	6026071	6020015	KRT24	101946677	XP_023956552.1	
type I	K12	NW_007359872.1	6059837	6053610	LOC101946402	101946402	XP_023956546.1	
type I	K20	NW_007359872.1	6079302	6066953	KRT20	101946118	XP_023956553.1	
type I	K23	NW_007359872.1	6118243	6103446	KRT23	101944292	XP_008160960.2	
type I	K15	NW_007359872.1	6154671	6144684	LOC101944027	101944027	XP_023956548.1	
type I	K19	NW_007359872.1	6169782	6164037	LOC101945842	101945842	XP_005294164.1	Prediction ends after intermediate filament domain
type I	K9L	NW_007359872.1	6203574	6194703	LOC101943762	101943762	XP_023956544.1	
type I	HAS1 (K9LC1)	NW_007359872.1	6239064	6229334	LOC101945565	101945565	XP_023956574.1	
type I	HAS2 (K9LC2)	NW_007359872.1	>6251969	6247249	LOC101943485	101943485	XP_023956575.1	Incomplete, corrected exon 1 (starts in unsequenced region: nucl: >6251969), exon 6 (end at nucl: 6247238) is last exon of prediction, corrected exon 6: , exons 7 and 8 in unsequenced region
type I	K14L1	NW_007359872.1	6284793	6277519	LOC101943211	101943211	XP_023956549.1	
type I	K14L2	NW_007359872.1	6296382	6291231	LOC112058843	112058843	XP_023956551.1	
type I	K117	NW_007359872.1	6333434	6327757	LOC101942920	101942920	XP_023956554.1	
type I	K18	NW_007281365.1	3188404	3195817	KRT18	101944455	XP_005291938.1	
type II	K80	NW_007281365.1	2707507	2683757	KRT80	101937727	XP_005292004.1	
type II	K7	NW_007281365.1	2731398	2750824	LOC101942365	101942365	XP_005291931.1	
type II	K84L	NW_007281365.1	2774533	2760328	LOC101942824	101942824	XP_005291933.1	
type II	K5L4	NW_007281365.1	2797015	2782059	LOC101943098	101943098	XP_005291934.1	
type II	K5L3	NW_007281365.1	2812964	2806768	LOC101943376	101943376	XP_008167740.1	
type II	K5L2	NW_007281365.1	2839118	2828979	LOC101943657	101943657	XP_005291936.1	
type II	K5L1	NW_007281365.1	2863680	2855514	LOC101938008	101938008	XP_008167741.1	
type II	HBS1 (K78LC1)	NW_007281365.1	2897943	2888267	LOC101938278	101938278	XP_023962088.1	
type II	HBS2 (K78LC2)	NW_007281365.1	2934586	2926151	LOC101938554	101938554	XP_023962089.1	
type II	K78L4	NW_007281365.1	2974357	2958939	LOC101938825	101938825	XP_023962090.1	
type II	K78L3	NW_007281365.1	2996774	2982340	LOC101939086	101939086	XP_005292009.1	
type II	K78L2	NW_007281365.1	3019456	3013010	LOC101943933	101943933	XP_023962091.1	
type II	K78L1	NW_007281365.1	3040012	3030390	LOC101939351	101939351	XP_008167744.1	
type II	K8L	NW_007281365.1	3108702	3091209	LOC101939638	101939638	XP_005292011.1	
type II	K8	NW_007281365.1	3135778	3124174	KRT8	101944191	XP_005291937.1	

Notes: [1] Keratins were named according to orthology to human proteins. K9-like cysteine-rich keratins (K9LC) are termed HAS and K78-like cysteine-rich keratins (K78LC) are termed HBS keratins.
HAS, hard acidic sauropsid-specific; HBS, hard basic sauropsid-specific; L, like; LT, long tail.

[2] Gene start and end indicate the start and stop codon of the coding sequence. Introns are not indicated.

[3] Accession numbers (acc. nr.) of protein amino acid sequences predicted in GenBank.

[4] Genome assembly used for predictions: Chrysemys_picta_bellii-3.0.3 (GCF_000241765.3).

acc., accession; n.a., not available in the genome sequence assembly; nucl., nucleotide; nr., number.

Supplementary Table S4. Keratin genes of the lizard (*Anolis carolinensis*)

Keratin type	**Name[1]**	**Genomic DNA sequence (acc. nr.)**	**Gene start[2] (nucl. nr.)**	**Gene end[2] (nucl. nr.)**	**Gene name (GenBank)**	**Gene (GenBank ID)**	**Protein[3] (acc. nr.)**	**Differences between new gene prediction and GenBank (GCF_000090745.1)[4]**
type I	K222	NC_014781.1	70386110	70363387	KRT222	100563084	XP_003222508.1	Coding sequence is not disrupted in GenBank. Mutation was not confirmed by our amplification and sequencing.
type I	K24	NC_014781.1	70404011	70392422	LOC100552076	100552076	XP_008111591.1	
type I	K24L	NC_014781.1	70423458	70411566	LOC103279244	103279244	XP_008111590.1	
type I	K12L	NC_014781.1	70454294	70429996	LOC100552270	100552270	XP_016850071.1	
type I	K12	NC_014781.1	70467003	70460684	LOC100552468	100552468	XP_003222621.1	
type I	K20	NC_014781.1	70488252	70472744	LOC107982248	107982248	XP_016850072.1	Corrected exon 1: nucl: 70488252..70488500, frameshift at nucl. 70488278; not predicted to encode a keratin.
type I	K23	NC_014781.1	70552329	70519742	krt23	100552665	XP_008111584.1	
type I	K36L1	NC_014781.1	70598936	70591466	LOC100337549	100337549	NP_001280052.1	
type I	K36L2	NC_014781.1	70614366	70606275	krt36	100337543	NP_001280048.1	
type I	K15	NC_014781.1	70630952	70621017	LOC100552862	100552862	XP_008111595.1	
type I	K19	NC_014781.1	70661136	70648031	LOC100563808	100563808	XP_008111599.1	
type I	K9L1	NC_014781.1	70711123	70702384	LOC100553064	100553064	XP_008111598.2	
type I	K9L2	NC_014781.1	70743419	70729212	LOC100553253	100553253	XP_016850073.1	
type I	HAS1 (K9LC1)	NC_014781.1	70773480	70763471	LOC100553450	100553450	XP_016850077.1	Exon in LOC107983006, predicted exon 2: nucl. 7077943..70770861 and exon 3: nucl. 70768746..70768590, corrected exon 4: starts at nucl. 70768463
type I	n.a.	NC_014781.1	70773480	70772921	LOC107983006	107983006	XP_016850076.1	exon 1 of HAS1; corrected range: 70773480..70772921
type I	HAS2 (K9LC2)	NC_014781.1	70784815	70777029	LOC100337544	100337544	NP_001280049.1	
type I	HAS3 (K9LC3)	NC_014781.1	70807056	70799064	LOC100553650	100553650	XP_003222627.3	
type I	HAS4 (K9LC4)	NC_014781.1	70828115	70819171	LOC100553851	100553851	XP_016850078.1	
type I	K14L1	NC_014781.1	70856045	70844971	LOC100564200	100564200	XP_003222513.1	
type I	K14L2	NC_014781.1	70875350	70865556	LOC100564396	100564396	XP_003222514.1	
type I	K117	NC_014781.1	70935269	70919125	LOC100554046	100554046	XP_008111601.1	
type I	K18	NW_003338797.1	1886076	1901530	KRT18	100567731	XP_003224490.1	
type II	K80	NC_014777.1	95942323	95982372	LOC100562605	100562605	XP_008102289.1	
type II	K7	NC_014777.1	95891088	95868214	LOC100567055	100567055	XP_003217023.1	
type II	K84L1	NC_014777.1	95865739	95849903	LOC100562411	100562411	XP_016846291.1	
type II	K84L2	NC_014777.1	95839095	95825623	LOC100337546	100337546	NP_001280051.1	
type II	K84L3	NC_014777.1	95817465	95802462	LOC100562208	100562208	XP_003217080.2	
type II	K84L4	NC_014777.1	95799482	95789077	LOC100337545	100337545	NP_001280050.1	
type II	K5L4	NC_014777.1	95777143	95758353	LOC100562008	100562008	XP_008102284.2	
type II	K5L3	NC_014777.1	95731292	95720930	LOC100566287	100566287	XP_003217019.1	
type II	K5L2	NC_014777.1	95702695	95689880	LOC100566088	100566088	XP_003217018.1	
type II	K5L1	NC_014777.1	95685012	95666735	LOC100561812	100561812	XP_003217078.1	
type II	HBS1 (K78LC1)	NC_014777.1	95656070	95645086	LOC100561620	100561620	XP_003217077.2	
type II	HBS2 (K78LC2)	NC_014777.1	95623784	95610121	LOC100561422	100561422	XP_003217076.3	
type II	HBS3 (K78LC3)	NC_014777.1	95587325	95566790	LOC100561224	100561224	XP_003217075.2	
type II	K78LT	NC_014777.1	95532173	95523420	LOC100560827	100560827	XP_016846726.1	
type II	K78L5	NC_014777.1	95512139	95490960	LOC100560629	100560629	XP_016846727.1	
type II	K78L4	NC_014777.1	95457122	95440262	LOC100560433	100560433	XP_003217072.1	
type II	K78L3	NC_014777.1	95436358	95421422	LOC100560234	100560234	XP_008102271.2	
type II	K78L2	NC_014777.1	95413159	95401878	LOC100560037	100560037	XP_003217070.1	
type II	K78L1	NC_014777.1	95385652	95370266	LOC100565886	100565886	XP_003217017.1	
type II	K8	NW_003338797.1	1781585	1779090	KRT8	100566434	XP_003224483.1	

Notes: [1] Keratins were named according to orthology to human proteins. K9-like cysteine-rich keratins (K9LC) are termed HAS and K78-like cysteine-rich keratins (K78LC) are termed HBS keratins.
HAS, hard acidic sauropsid-specific; HBS, hard basic sauropsid-specific; L, like; LT, long tail.

[2] Gene start and end indicate the start and stop codon of the coding sequence. Introns are not indicated.

[3] Accession numbers (acc. nr.) of protein amino acid sequences predicted in GenBank.

[4] Genome assembly used for predictions: AnoCar2.0 (GCF_000090745.1).

acc., accession; n.a., not available in the genome sequence assembly; nucl., nucleotide; nr., number.

Supplementary Table S5. Keratin genes of the snake (*Protobothrops mucrosquamatus*)

Keratin type	**Name[1]**	**Genomic DNA sequence (acc. nr.)**	**Gene start[2] (nucl. nr.)**	**Gene end[2] (nucl. nr.)**	**Gene name (GenBank)**	**Gene (GenBank ID)**	**Protein[3] (acc. nr.)**	**Differences between new gene prediction and GenBank (GCF_001527695.1)[4]**
type I	K222	NW_015386388.1	4579705	4563973	KRT222	107303117	XP_015687800.1	
type I	K24	NW_015386388.1	4593683	4585551	KRT24	107303090	XP_015687766.1	
type I	K24L	NW_015386388.1	4610502	4601245	LOC107303091	107303091	XP_015687767.1	Named K10-like in GenBank
type I	K10L1	NW_015386388.1	4628673	4615542	LOC107303119	107303119	XP_015687801.1	
type I	K10L2	NW_015386388.1	4639339	4631362	LOC107303022	107303022	XP_015687687.1	Incomplete N-terminus
type I	K20L	NW_015386388.1	4668627	4658157	LOC107303120	107303120	XP_015687802.1	Incomplete N-terminus
type I	K23	NW_015386388.1	4728213	4703693	LOC107303092	107303092	XP_015687768.1	
type I	K15	NW_015386388.1	4782878	4774150	LOC107303093	107303093	XP_015687770.1	
type I	K19	NW_015386388.1	4810269	4799955	LOC107303094	107303094	XP_015687772.1	
type I	K9L	NW_015386388.1	4852795	4844127	LOC107303023	107303023	XP_015687689.1	
type I	HAS1 (K9LC1)	NW_015386388.1	4946558	4939829	LOC107303121	107303121	XP_015687803.1	
type I	HAS2 (K9LC2)	NW_015386388.1	4974935	4966799	LOC107303122	107303122	XP_015687805.1	
type I	K14L1	NW_015386388.1	5009323	5000237	LOC107303095	107303095	XP_015687773.1	
type I	K14L2	NW_015386388.1	5025051	5018341	LOC107303123	107303123	XP_015687806.1	Incomplete N- and C-termini
type I	K117	NW_015386388.1	5088974	5072974	LOC107303024	107303024	XP_015687690.2	
type I	K18	NW_015386810.1	591188	599294	KRT18	107288181	XP_015672253.1	
type II	K80	NW_015387607.1	203655	243569	n.a.	n.a.	n.a.	Identified by BLAST between *Krt7* and *Faim2*
type II	K7	NW_015387607.1	281992	301511	LOC107292791	107292791	XP_015677400.1	
type II	K5L2	NW_015387607.1	380309	370750	LOC107292792	107292792	XP_015677401.1	
type II	K5L1	NW_015387607.1	415254	402945	LOC107292794	107292794	XP_015677404.1	
type II	HBS1 (K78LC1)	NW_015387607.1	438703	430012	LOC107292789	107292789	XP_015677398.1	
type II	HBS2 (K78LC2)	NW_015386143.1	23602	12950	LOC107284963	107284963	XP_015668587.1	Sequence ends after exon 6
type II	HBS3 (K78LC3)	NW_015386143.1	56136	42413	LOC107285009	107285009	XP_015668640.1	
type II	HBS4 (K78LC4)	NW_015386143.1	93963	74922	LOC107284973	107284973	XP_015668597.1	
type II	K78LT	NW_015386143.1	131703	122663	LOC107284982	107284982	XP_015668608.1	
type II	K78L4	NW_015386143.1	161149	148418	LOC107284991	107284991	XP_015668619.1	
type II	K78L3	NW_015386143.1	205835	180432	LOC107285020	107285020	XP_015668651.1	
type II	K78L2	NW_015390075.1	40293	45677	LOC107298626	107298626	XP_015683489.1	Sequence ends after exon 5
type II	K78L1	NW_015390075.1	17942	29969	LOC107298627	107298627	XP_015683491.1	Incomplete
type II	K8	NW_015386810.1	534700	518951	KRT8	107288180	XP_015672252.1	

Notes: [1] Keratins were named according to orthology to human proteins. K9-like cysteine-rich keratins (K9LC) are termed HAS and K78-like cysteine-rich keratins (K78LC) are termed HBS keratins.
HAS, hard acidic sauropsid-specific; HBS, hard basic sauropsid-specific; L, like; LT, long tail.

[2] Gene start and end indicate the start and stop codon of the coding sequence. Introns are not indicated.

[3] Accession numbers (acc. nr.) of protein amino acid sequences predicted in GenBank.

[4] Genome assembly used for predictions: P.Mucros_1.0 (GCF_001527695.1).

acc., accession; n.a., not available in the genome sequence assembly; nucl., nucleotide; nr., number.

Supplementary Table S6. Keratin genes of the frog (*Xenopus tropicalis*)

Keratin type	Name[1]	Genomic DNA sequence (acc. nr.)	Gene start[2] (nucl. nr.)	Gene end[2] (nucl. nr.)	Gene name (GenBank)	Gene (GenBank ID)	Protein[3] (acc. nr.)	Differences between new gene prediction and GenBank (GCF_000004195.3)[4]
type I	K222	NW_016683386.1	1124475	1105206	krt222	100488319	XP_004918751.1	
type I	Frog1-02	NW_016683386.1	1154939	1150145	LOC100487269	100487269	XP_002940698.2	Corrected head domain
type I	Frog1-03	NW_016683386.1	1171666	1168635	krt10	100487422	XP_012808327.1	
type I	Frog1-04	NW_016683386.1	1201989	<1197543	LOC100158585	100158585	NP_001121485.1	
type I	Frog1-05	NW_016683386.1	1240852	1233754	LOC100488172	100488172	XP_002940703.2	Incomplete at both ends
type I	Frog1-06	NW_016683386.1	1254262	1245094	krt24	496660	NP_001011224.1	
type I	Frog1-07	NW_016683386.1	1272369	1264944	LOC101731128	101731128	XP_004918844.3	Incomplete
type I	Frog1-08	NW_016683386.1	1331129	1323043	xak-c	100486967	XP_002940696.1	
type I	Frog1-09	NW_016683386.1	1347940	1343996	krt12	100144436	NP_001116496.1	
type I	Frog1-10	NW_016683386.1	1369802	1364487	xk81a1	100145042	NP_001120056.1	
type I	Frog1-11	NW_016683386.1	1390695	1385231	LOC549413	549413	NP_001016659.1	
type I	Frog1-12	NW_016683386.1	1423486	1440842	LOC101730713	101730713	XP_004918757.1	Incomplete
type I	Frog1-13	NW_016683386.1	1455161	1449470	krt16	100499212	XP_004918756.1	
type I	Frog1-14	NW_016683386.1	>1473684	1462819	krt14	100127859	XP_012808153.1	
type I	Frog1-15	NC_030686.1	1610298	1573905	LOC100491563	100491563	XP_002939081.2	One exon is missing
type I	Frog1-16	NC_030686.1	1678655	1672884	krt35	100491736	XP_002939082.3	
type I	Frog1-17	NC_030686.1	1696854	1688820	krt15	100379888	XP_002939083.2	
type I	Frog1-18	NC_030686.1	1711958	1703070	LOC100490379	100490379	XP_004918754.1	
type I	Frog1-19	NC_030686.1	1738209	1727533	krt19	394514	XP_012827034.1	
type I	Frog1-20	NC_030686.1	1788322	1780124	LOC100490554	100490554	XP_012808156.1	Incomplete
type I	Frog1-21	NC_030686.1	1797326	1791399	LOC100490729	100490729	XP_002939076.3	
type I	Frog1-22	NC_030686.1	1812174	1807464	krt17	100490897	XP_002939077.1	
type I	K117	NC_030686.1	>1861983	1857265	krt70	448098	NP_001006687.1	Start of gene in sequence gap, first exon missing
type I	K18	NC_030678.1	144892767	144889352	krt18	394541	NP_988944.1	
type II	K80	NC_030678.1	145340325	145358155	krt80	100316911	NP_001163982.1	
type II	Frog2-02	NC_030678.1	145282277	145276908	krt5.7	100101751	XP_002935788.2	
type II	Frog2-03	NC_030678.1	145241155	145245991	krt5.3	100491329	XP_012813652.1	
type II	Frog2-04	NC_030678.1	145192735	145197334	krt5.2	779830	NP_001072377.1	
type II	Frog2-05	NC_030678.1	145173996	145182744	krt5.5	100489468	XP_002935776.1	
type II	Frog2-06	NC_030678.1	145153628	145161984	krt75	100491159	XP_002935786.2	
type II	Frog2-07	NC_030678.1	145145209	145150875	krt5.6	100489309	XP_002935775.1	
type II	Frog2-08	NC_030678.1	145131141	145137134	LOC100490994	100490994	XP_002935785.1	
type II	Frog2-09	NC_030678.1	145117276	145123151	LOC100490820	100490820	XP_002935784.2	
type II	Frog2-10	NC_030678.1	145095169	145106302	krt6a	100490652	XP_017947337.1	
type II	Frog2-11	NC_030678.1	145072999	145077895	LOC100489158	100489158	XP_002935774.1	
type II	Frog2-12	NC_030678.1	145055578	145062037	krt5.4	448361	NP_001006716.1	
type II	Frog2-13	NC_030678.1	145023433	145028461	krt6	100144701	NP_001166034.1	
type II	K8	NC_030678.1	144954443	144962883	krt8	431676	NP_001002797.1	

Notes: [1] Keratins were named according to orthology to human proteins or according to type and position of the gene (Figure 1) ("Frog-type-position").

[2] Gene start and end indicate the start and stop codon of the coding sequence. Introns are not indicated.

[3] Accession numbers (acc. nr.) of protein amino acid sequences predicted in GenBank.

[4] Genome assembly used for predictions: Xenopus_tropicalis_v9.1 (GCF_000004195.3).

acc., accession; n.a., not available in the genome sequence assembly; nucl., nucleotide; nr., number.

Supplementary Table S7. Keratin genes of the platypus (*Ornithorhynchus anatinus*)

Keratin type	**Name**[1]	**Genomic DNA sequence (GenBank acc. nr.)**	**Gene ID (GenBank)**	**Protein (GenBank acc. nr.)**	**Number of cysteine residues**	**Notes**
type I	K222	NC_041738.1	100074593	XP_028930428.1	2	
type I	K224	NC_041738.1	100091675	XP_028930435.1	1	
type I	K24L4	NC_041738.1	100091681	XP_001512134.1	6	
type I	K24L3	NC_041738.1	100091690	XP_028931081.1	6	
type I	K24L2	NC_041738.1	100091696	XP_028931091.1	6	
type I	K24L1	NC_041738.1	100091718	XP_028931269.1	2	sequence incomplete
type I	K25	NC_041738.1	100091723	XP_001520523.2	12	
type I	K26	NC_041738.1	100091728	XP_001512895.1	15	
type I	K27	NC_041738.1	100091669	XP_001513002.1	11	
type I	K28	NC_041738.1	100091735	XP_001520530.1	12	
type I	K10L2	NC_041738.1	100091742	XP_028931907.1	6	
type I	K10L1	NC_041738.1	100091750	XP_007662432.2	2	sequence incomplete
type I	K20L2	NC_041738.1	100091766	XP_028931908.1	1	
type I	K12	NC_041738.1	100081910	XP_028931359.1	2	
type I	K20L1	NC_041738.1	114815072	XP_028931098.1	4	
type I	K23	NC_041738.1	100091772	XP_007662433.2	5	
type I	K39	NC_041738.1	100091780	XP_028931100.1	27	
type I	K40	NC_041738.1	100091796	XP_007662434.2	35	
type I	K33a	NC_041738.1	114815087	XP_028931270.1	28	
type I	K33b	NC_041738.1	100074485	XP_007655203.1	23	
type I	K34	NC_041738.1	100074443	XP_001505493.2	30	
type I	K31	NC_041738.1	100088880	XP_001518440.1	32	
type I	K37	NC_041738.1	100088890	XP_001518445.2	26	
type I	K38	NC_041738.1	100083777	XP_028931108.1	19	
type I	K32	NC_041738.1	100083755	XP_007661319.2	25	
type I	K36	NC_041738.1	100083734	XP_001514298.2	10	sequence incomplete
type I	K13	NC_041738.1	100079550	XP_001510496.2	7	
type I	K15	NC_041738.1	100086149	n.a.	n.a.	pseudogene
type I	K19	NC_041738.1	107547508	XP_028931283.1	0	
type I	K9	NC_041738.1	100082561	XP_028931280.1	5	
type I	K14	NC_041738.1	100077389	XP_001511728.2	6	
type I	K16	NC_041738.1	114815097	XP_028931325.1	9	
type I	K17	NC_041738.1	100092093	XP_028932116.1	4	
type I	K18	NC_041737.1	114814771	XP_028930001.1	2	
type II	K80	NC_041737.1	100086395	XP_028929028.1	12	
type II	K7	NC_041737.1	100087958	XP_028929030.1	0	
type II	K81L2	NC_041737.1	103164921	XP_007654211.2	n.a.	sequence incomplete
type II	K81L	NC_041737.1	100092864	XP_028929027.1	33	
type II	K83L2	NC_041737.1	100092929	XP_028929031.1	34	
type II	K83L1	NC_041737.1	100092926	XP_028929024.1	31	
type II	K85L2	NC_041737.1	103164923	XP_028928757.1	18	
type II	K85L1	NC_041737.1	100089219	XP_028929033.1	25	
type II	K84	NC_041737.1	100090360	XP_028929015.1	19	
type II	K82	NC_041737.1	103164922	XP_028929034.1	21	sequence incomplete
type II	K75	NC_041737.1	114814612	XP_028929009.1	4	
type II	K6aL	NC_041737.1	100092858	XP_001514525.1	10	
type II	K5L	NC_041737.1	103168998	XP_028929007.1	4	
type II	K6AL	NC_041737.1	114814567	n.a.	n.a.	pseudogene
type II	K71	NC_041737.1	100092898	XP_028929017.1	9	
type II	K72	NC_041737.1	100092892	XP_007654210.1	10	
type II	K73	NC_041737.1	100092888	XP_028928758.1	12	
type II	K74	NC_041737.1	100092881	XP_001521385.3	10	
type II	K2L2	NC_041737.1	100092878	XP_028929018.1	4	
type II	K2L1	NC_041737.1	114814568	XP_028928759.1	6	
type II	K1	NC_041737.1	114814611	XP_028929002.1	3	
type II	K77	NC_041737.1	103164924	XP_028929014.1	7	
type II	K76	NC_041737.1	100073951	XP_028929006.1	2	
type II	K3L2	NC_041737.1	114814569	XP_028928760.1	4	
type II	K3L1	NC_041737.1	100074276	XP_001505912.1	7	
type II	K4	NC_041737.1	100078666	XP_028929023.1	9	
type II	K79	NC_041737.1	100088469	XP_028929019.1	10	
type II	K78	NC_041737.1	100084867	XP_028928761.1	8	
type II	K8	NC_041737.1	100078521	XP_001507306.1	0	

Notes: [1] Keratins were named according to orthology to human proteins. K, keratin; L, like.
Genome sequence assembly used for predictions: mOrnAna1.p.v1 (GCF_004115215.1).
n.a., not applicable

Supplementary Table S8. Number of cysteine residues in keratins of the kiwi (*Apteryx australis mantelli*)

Keratin type	Name	Protein (GenBank acc. nr.)	Number of cysteine residues
type I	K222	XP_025928687.1	3
type I	K12	XP_013801838.1	1
type I	K20	XP_013801841.1	0
type I	K23	XP_013801848.1	5
type I	K36L	XP_013801846.1	18
type I	K15	XP_013801843.1	6
type I	K19	XP_013801844.1	1
type I	K9L1	XP_013801847.1	5
type I	K9L2	XP_013801845.1	5
type I	K9L3	XP_013801842.1	9
type I	K9L4	XP_013801836.1	12
type I	HAS1 (K9LC1)	XP_013801837.1	28
type I	HAS2 (K9LC2)	XP_013801835.1	18
type I	HAS3 (K9LC3)	XP_013801834.1	21
type I	K14L1	XP_013801867.1	2
type I	K14L2	XP_013801833.1	10
type I	K18	XP_013805088.1	0
type II	K80	XP_013810925.1	9
type II	K7	XP_013810923.1	0
type II	K84L	XP_013810920.1	18
type II	K5L4	XP_013810918.1	6
type II	K5L3	XP_013810922.1	10
type II	K5L2	XP_013810921.1	3
type II	K5L1	XP_013810917.1	3
type II	HBS1 (K78LC1)	XP_013810916.1	35
type II	HBS2 (K78LC2)	XP_013810915.1	27
type II	HBS3 (K78LC3)	XP_013810914.1	16
type II	K78LT	XP_013810912.1	9
type II	K78L5	XP_013810911.1	11
type II	K78L4	XP_013810926.1	8
type II	K78L3	XP_013810927.1	8
type II	K78L2	XP_013810928.1	8
type II	K78L1	XP_013810929.1	7
type II	K8	XP_013813947.1	2

Notes: Keratins were named according to orthology to chicken proteins.

K, keratin; L, like; HA/BS, hard acidic/basic sauropsid-specific.

Genome sequence assembly: AptMant0 (GCF_001039765.1).

Supplementary Table S9. Number of cysteine residues in keratins of the ostrich (*Struthio camelus australis*)

Keratin type	Name	Genomic DNA/cDNA sequence (acc. nr.)	Gene ID (GenBank)	Protein (GenBank acc. nr.)	Number of cysteine residues	Notes
type I	K222	NW_009272154.1	104152437	XP_009686054.1	3	
type I	K12	NW_009272154.1	104152438	XP_009686056.1	1	
type I	K20	NW_009272154.1	104152454	XP_009686074.1	1	
type I	K23	NW_009272154.1	104152435	XP_009686053.1	3	
type I	K15	NW_009272154.1	104152453	XP_009686073.1	6	
type I	K19	NW_009272154.1	104152434	XP_009686052.1	1	sequence incomplete
type I	K9L1	NW_009272154.1	104152433	XP_009686051.1	7	
type I	K9L2	NW_009272154.1	104152452	XP_009686072.1	7	
type I	K9L3	NW_009272154.1	104152432	XP_009686050.1	8	
type I	K9L4	NW_009272154.1	104152431	XP_009686049.1	11	
type I	HAS1 (K9LC1)	NW_009272154.1	104152430	XP_009686048.1	28	
type I	HAS2 (K9LC2)	NW_009272154.1	104152429	XP_009686047.1	26	
type I	HAS3 (K9LC3)	NW_009272154.1	104152451	XP_009686071.1	17	sequence incomplete
type I	K14L1	NW_009272154.1	104152428	XP_009686045.1	2	
type I	K14L2	NW_009272154.1	104152450	XP_009686070.1	2	
type I	K18	NW_009270297.1	104152322	XP_009685921.1	0	
type II	K80	NW_009270297.1	104152362	XP_009685973.1	10	
type II	K7	NW_009270297.1	104152373	XP_009686015.1	0	
type II	K5L4	NW_009270297.1	104152571	XP_009686271.1	8	
type II	K5L3	NW_009270297.1	104152351	XP_009685961.1	3	
type II	K5L2	NW_009270297.1	104152346	XP_009685948.1	3	
type II	K5L1	NW_009270297.1	104152560	XP_009686260.1	1	
type II	HBS1 (K78LC1)	NW_009270297.1	104152550	XP_009686249.1	27	Gene ID: 2 incomplete coding sequences
type II	HBS2 (K78LC2)	NW_009270297.1	104152550	XP_009686249.1	19	Gene ID: 2 incomplete coding sequences
type II	K78LT	NW_009270297.1	104152547	XP_009686235.1	7	sequence incomplete
type II	K78L	NW_009270297.1	104152337	XP_009685942.1	12	
type II	K8	n.a.	n.a.	n.a.	n.a.	

Notes: Keratins were named according to orthology to chicken proteins.
K, keratin; L, like; HA/BS, hard acidic/basic sauropsid-specific.
Genome sequence assembly: ASM69896v1 (GCF_000698965.1).
n.a., not available.

Supplementary Table S10. Keratin genes of the zebra finch (*Taeniopygia guttata*)

Keratin type	**Name[1]**	**Genomic DNA sequence (acc. nr.)**	**Gene ID (GenBank)**	**Protein[3] (GenBank acc. nr.)**	**Number of cysteine residues**	**Notes**
type I	K222	NC_044239.1	101233916	XP_004174708.1		
type I	K12	NC_044239.1	100229407	XP_012426581.1	1	
type I	K20	NC_044239.1	100226488	XP_002194074.3	0	
type I	K23	NC_044239.1	101233949	XP_004174709.2	9	
type I	K15	NC_044239.1	100223619	XP_002194098.1	5	
type I	K19	NC_044239.1	100227535	XP_002197015.2	0	
type I	K9L1	NC_044239.1	101233334	XP_030112293.1	11	
type I	K9L2	NC_044239.1	100220698	XP_002194122.4	10	
type I	K9L3	NC_044239.1	100228906	XP_030112121.1	9	
type I	K9L4	NC_044239.1	100230285	XP_030112123.1	10	
type I	HAS1 (K9LC1)	NC_044239.1	100227476	XP_012426580.2	28	
type I	HAS2 (K9LC2)	NC_044239.1	100224590	XP_002194209.3	27	
type I	HAS3 (K9LC3)	NC_044239.1	100221664	XP_030112003.1	25	
type I	K14L1	NC_044239.1	100231284	XP_030112001.1	3	Gene ID: 2 coding sequences
type I	K14L2	NC_044239.1	100231284	XP_012426586.2	3	Gene ID: 2 coding sequences
type I	K18	NC_044242.1	115491360	XP_030115101.1	0	
type II	K80	NC_044242.1	115491353	XP_030115077.1	5	
type II	K7	NC_044242.1	100224644	XP_030115482.1	0	
type II	K5L4	NC_044242.1	100224585	XP_002195031.2	10	
type II	K5L3	NC_044242.1	100227468	XP_002195007.1	8	
type II	K5L2	NC_044242.1	100230278	XP_002194692.1	3	
type II	K5L1	NC_044242.1	100230328	XP_030115537.1	1	exon 1: nucl. 333626 - 332934
type II	HBS1 (K78LC1)	NC_044242.1	115491512	XP_030115539.1	35	
type II	HBS2 (K78LC2)	NC_044242.1	100217876	XP_030115112.1	36	
type II	K78LT	NC_044242.1	100226538	XP_030115078.1	75	
type II	K78L4	NC_044242.1	100229354	XP_030115113.1	15	
type II	K78L3	NC_044242.1	100232294	XP_002191799.3	14	
type II	K78L2	NC_044242.1	115491354	XP_030115084.1	11	
type II	K78L1	NC_044242.1	101233849	XP_004175950.2	15	
type II	K8	NC_044242.1	115491358	XP_030115098.1	0	

Notes: Keratins were named according to orthology to chicken proteins.

K, keratin; L, like; HA/BS, hard acidic/basic sauropsid-specific.

Genome assembly used for predictions: bTaeGut1_v1.p (GCF_003957565.1).

Supplementary Table S11. Keratin genes of the Tibetan frog (*Nanorana parkeri*)

Keratin type	Name	Genomic DNA sequence	Gene ID	Protein	Number of cysteine residues	Notes
		(acc. nr.)	(GenBank)	(GenBank acc. nr.)		
type I	K222	NW_017306323.1	108804307	XP_018431528.1	4	
type I	Nanorana1_02	NW_017306323.1	108804320	XP_018431537.1	9	
type I	Nanorana1_03	NW_017306323.1	108804334	XP_018431542.1	4	
type I	Nanorana1_04	NW_017306323.1	108804356	XP_018431567.1	6	
type I	Nanorana1_05	NW_017306323.1	108804339	XP_018431544.1	12	
type I	Nanorana1_06	NW_017306323.1	108804340	XP_018431545.1	6	
type I	Nanorana1_07	NW_017306323.1	108804351	XP_018431561.1	3	
type I	Nanorana1_08	NW_017306323.1	108804364	XP_018431575.1	2	
type I	Nanorana1_09	NW_017306510.1	108787107	XP_018412066.1	4	
type I	Nanorana1_10	NW_017306510.1	108787113	XP_018412076.1	5	
type I	Nanorana1_11	NW_017306510.1	108787108	XP_018412067.1	3	
type I	Nanorana1_12	NW_017306510.1	108787122	XP_018412088.1	0	
type I	Nanorana1_13	NW_017306510.1	108787106	XP_018412065.1	0	
type I	Nanorana1_14	NW_017306510.1	108787114	XP_018412078.1	1	
type I	Nanorana1_15	NW_017306510.1	108787118	XP_018412084.1	0	
type I	Nanorana1_16	NW_017306510.1	108787115	XP_018412079.1	2	
type I	Nanorana1_17	NW_017306510.1	108787105	XP_018412064.1	6	
type I	Nanorana1_18	NW_017306510.1	108787121	XP_018412087.1	1	
type I	Nanorana1_19	NW_017306510.1	108787104	XP_018412063.1	4	sequence incomplete
type I	Nanorana1_20	NW_017306510.1	108787103	XP_018412061.1	4	
type I	Nanorana1_21	NW_017306510.1	108787102	XP_018412060.1	4	
type I	Nanorana1_22	NW_017306510.1	108787101	XP_018412059.1	4	
type I	Nanorana1_23	NW_017306510.1	108787100	XP_018412058.1	6	
type I	Nanorana1_24	NW_017306510.1	108787099	XP_018412057.1	7	
type I	Nanorana1_25	NW_017306510.1	108787123	XP_018412089.1	3	
type I	Nanorana1_26	NW_017306510.1	108787098	XP_018412056.1	3	
type I	Nanorana1_27	NW_017306510.1	108787097	XP_018412055.1	5	
type I	Nanorana1_28	NW_017306510.1	108787096	XP_018412053.1	3	
type I	Nanorana1_29	NW_017306510.1	108787095	XP_018412052.1	3	
type I	Nanorana1_30	NW_017306510.1	108787094	XP_018412051.1	3	
type I	Nanorana1_31	NW_017306510.1	108787086	XP_018412042.1	5	
type I	Nanorana1_32	NW_017306510.1	108787124	XP_018412090.1	4	
type I	Nanorana1_33	NW_017306510.1	108787093	XP_018412050.1	6	
type I	Nanorana1_34	NW_017306510.1	108787092	XP_018412049.1	8	Gene ID: 3 coding sequences
type I	Nanorana1_35	NW_017306510.1	108787092	XP_018412049.1	0	Gene ID: 3 coding sequences
type I	Nanorana1_36	NW_017306510.1	108787092	XP_018412049.1	3	Gene ID: 3 coding sequences
type I	Nanorana1_37	NW_017306510.1	108787091	XP_018412048.1	2	
type I	Nanorana1_38	NW_017306510.1	108787090	XP_018412046.1	3	
type I	Nanorana1_39	NW_017306510.1	108787089	XP_018412045.1	8	
type I	Nanorana1_40	NW_017306510.1	108787088	XP_018412044.1	2	
type I	Nanorana1_41	NW_017306510.1	108787119	XP_018412085.1	0	
type I	Nanorana1_42	NW_017306510.1	108787087	XP_018412043.1	2	
type I	Nanorana1_43	NW_017306510.1	108787116	XP_018412080.1	0	
type I	Nanorana1_44	NW_017306510.1	108787111	XP_018412073.1	4	
type I	Nanorana1_45	NW_017306510.1	108787112	XP_018412075.1	3	
type I	Nanorana1_46	NW_017306510.1	108787120	XP_018412086.1	1	
type I	Nanorana1_47	NW_017306510.1	108787109	XP_018412069.1	2	
type I	Nanorana1_48	NW_017306510.1	108787117	XP_018412082.1	2	K117 ortholog
type I	Nanorana1_K18	NW_017307321.1	108796078	XP_018422969.1	1	
type II	Nanorana2_K80L	NW_017307900.1	108799101	XP_018426427.1	5	
type II	Nanorana2_02	NW_017307900.1	108799102	XP_018426428.1	0	
type II	Nanorana2_03	NW_017307900.1	108799100	XP_018426426.1	3	
type II	Nanorana2_04	NW_017307900.1	108799097	XP_018426424.1	9	
type II	Nanorana2_05	NW_017307900.1	108799098	XP_018426425.1	5	
type II	Nanorana2_06	NW_017307530.1	108797348	XP_018424432.1	5	
type II	Nanorana2_07	NW_017307530.1	108797347	XP_018424431.1	4	
type II	Nanorana2_08	NW_017307530.1	108797345	XP_018424429.1	7	
type II	Nanorana2_09	NW_017307530.1	108797344	XP_018424428.1	5	
type II	Nanorana2_10	NW_017307530.1	108797356	XP_018424444.1	4	
type II	Nanorana2_11	NW_017307530.1	108797342	XP_018424426.1	2	
type II	Nanorana2_12	NW_017307530.1	108797355	XP_018424443.1	8	
type II	Nanorana2_13	NW_017307530.1	108797352	XP_018424442.1	5	
type II	Nanorana2_14	NW_017307530.1	108797349	XP_018424436.1	5	isoform x3
type II	Nanorana2_15	NW_017307530.1	108797351	XP_018424441.1	1	
type II	Nanorana2_16	NW_017307530.1	108797341	XP_018424425.1	1	
type II	Nanorana2_17	NW_017307530.1	108797350	XP_018424440.1	4	
type II	Nanorana2_18	NW_017307530.1	108797339	XP_018424423.1	13	
type II	Nanorana2_19	NW_017307530.1	108797340	XP_018424424.1	8	sequence incomplete
type II	Nanorana2_20	NW_017307321.1	108796077	XP_018422968.1	4	
type II	Nanorana2_K8	NW_017307321.1	108796080	XP_018422973.1	0	

Notes: Names indicate the keratin type and the position of the gene in the cluster, unless a name is suggested by GenBank.
Genome assembly used for predictions: ASM93562v1 (GCF_000935625.1).

Supplementary Table S12. Number of cysteine residues in keratins of the axolotl (*Ambystoma mexicanum*)

Keratin type	Name[1]	cDNA sequence (acc. nr.)[2]	Number of cysteine residues
type I	K17L	isotig63037	1
type I	K9L	isotig132511	2
type I	K15L1	istog85088	0
type I	K15L2	contig317039	2
type I	K15L3	contig327242	2
type I	K19L	isotig36490	0
type I	K24L1	contig365045	1
type I	K24L2	isotig29543	0
type I	K24L3	JK974491.1	1
type I	K24L4	isotig81597	4
type I	K18L1	contig330148	0
type I	K18L2	contig321256	1
type II	K80L	isotig85003	0
type II	K7L	isotig199907	3
type II	K5L1	isotig198655	1
type II	K5L2	isotig204938	1
type II	K5L3	isotig64160	0
type II	K5L4	isotig122526	4
type II	K8	isotig64108	2

Notes: [1] Preliminary names were given according to orthology to human proteins.
K, keratin; L, like.

[2] Sequences from: https://ambystoma.uky.edu/quick-links/blast - tBLASTn on V4.0-isotigs+Contigs

Supplementary Table S13. Number of cysteine residues in keratins of the caecilian (*Microcaecilia unicolor*)

Keratin type	Name[1]	Protein (GenBank acc. nr.)	Number of cysteine residues
type I	K23	XP_030077854.1	2
type I	K117	XP_030076825.1	0
type I	K17L	XP_030076598.1	1
type I	K19L	XP_030076445.1	0
type I	K15L	XP_030076444.1	2
type I	K24L1	XP_030077816.1	1
type I	K24L2	XP_030077793.1	1
type I	K24L3	XP_030077100.1	2
type I	K24L4	XP_030077098.1	2
type I	K24L5	XP_030076687.1	1
type I	K24L6	XP_030076596.1	1
type I	K24L7	XP_030076337.1	2
type I	K24L8	XP_030076336.1	4
type I	K24L9	XP_030076250.1	1
type I	K24L10	XP_030076248.1	1
type I	K24L11	XP_030076246.1	1
type I	K24L12	XP_030076243.1	1
type I	K20L1	XP_030076749.1	1
type I	K20L2	XP_030076338.1	1
type I	K18L1	XP_030066300.1	4
type I	K18L2	XP_030061931.1	3
type II	K80	XP_030054078.1	3
type II	K7L	XP_030054077.1	2
type II	K5L1	XP_030054076.1	1
type II	K5L2	XP_030054074.1	4
type II	K5L3	XP_030054073.1	3
type II	K5L4	XP_030054072.1	2
type II	K5L5	XP_030054071.1	2
type II	K5L6	XP_030054068.1	6
type II	K5L7	XP_030054066.1	5
type II	K5L8	XP_030054064.1	5
type II	K5L9	XP_030054063.1	3
type II	K8	XP_030054059.1	1

Notes: [1] Keratins were named according to orthology to human proteins.
K, keratin; L, like.
Genome sequence assembly: ASM69896v1 (GCF_000698965.1).

Supplementary Table S14. Number of cysteine residues in keratins of zebrafish *(Danio rerio)*

Name[1]	Protein (GenBank acc. nr.)	Number of cysteine residues	Notes
Danio_26CYS	NP_001002392.1	26	alternative name: krt95
Danio_02	NP_001003480.1	0	
Danio_03	NP_001017588.1	2	
Danio_04	NP_001034908.1	0	
Danio_05	NP_001035449.1	4	
Danio_06	NP_001038375.1	2	
Danio_07	NP_001070122.1	4	
Danio_08	NP_001070922.1	0	
Danio_09	NP_001076492.1	1	
Danio_10	NP_001096111.1	0	
Danio_11	NP_001107814.1	0	
Danio_12	NP_001186881.1	0	
Danio_13	NP_571182.1	0	
Danio_14	NP_571183.1	1	
Danio_K4	NP_571584.2	0	
Danio_K5	NP_571231.2	0	
Danio_K8	NP_956374.1	1	
Danio_K17	NP_001076574.1	0	
Danio_K18	NP_848524.1	0	
Danio_K18b	NP_956862.1	1	
Danio_K24	NP_998688.2	0	
Danio_K91	NP_001003445.1	0	
Danio_K92	NP_001017824.1	0	
Danio_K97	NP_001002383.1	0	

Notes: [1] Danio_26CYS contains 26 cysteine residues. Other keratins were numbered arbitrarily or according to GenBank.

Genome sequence assembly: GCF_000002035.6

A

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>Chicken_K12
MDCGSPICPALLRAWQNSPALWSTMALSVRSSVGPRQFSSRSSLGGGSLRLSGNSTGGGFGGSGLGFGGG
SAGGFGAASVLGSGSGFSGGFGSSVGSGFGGGFASGSGGGYGSGSGGGFGGGFGSGFGSGSGIIFGGGFG
SGAAPGLGGGFGIGGGGDGGLLSGSKKETMQNLNDRLAAYLDKVRSLEDANTELERKIREWYEKNGPGAA
VPGSGNDYSKYYPIIEDLRNKIINATIDNARIILQVDNARLAADDFRLKYENEVALRQSVEADINGLRRV
LDELTLTRADLEMQIESLNEELAYLKKNHEEELQGLQSSAVGQVSVEMDAAPGIDLTKLLNDMRGQYEVI
AEQNRKEAEAWFNEKSGELKREISTNTEQLQSGKSEITDLKRTLQNLEIELQSQLAMKKSLEDTLAETEG
GYCAQLSQMQLQIGNLESQLLQVRADMERQSAEYQQLLDIKSRLEMEIETYRRLLDGEFVSGGQGVVFES
SSLTGSKSQTQSLDSSQDPTKTRKIKTIVEEVVDGKVVASHVKEVEEKI

>Chicken_K20
MSFSTQSSQLGTAAHLQGTAPGGSALSVRSAAVQRIQAPSVYGGAGGYGTRISSSSVRRQSSSGAFHSNI
SDNDLLLSGNEKSTMQNLNDRLAAYLERVRSLEKANSLLEKQIKEWHEKNTVGVRSDYSSYFQTIEDLQS
KIGAAQLENAKLVLQIDNAKLAADDFRLKYENELLLRQSVESDINGLLRVLDDLTLTKSDLESQIENVNE
EIVFLKKNHEEEVDRLRKQVGGSVNVEVDAAPGTDLASIMENMRRQYEEMAEKNRQEAKERFEKQTEALN
QEVAINVEQLQEQRREVTDRRQICQSLELELQTHLNMKKPLEDTLAETEARYSFQLAQIQETIAKLEAQL
RQLRADMEAQNTEYSVLLDIKTRLELEIATYRRLLEGEDVGLVQEDAVTTELEKESSKIKKIKTIVEEVI
DGKVVSSQVKEIEEKM

>Chicken_K23
MSTSQGPFQFYSGSLRGSAGCGLAQQGTSYRPPSADGASGTHTSFSSTRPLSLAAGGGASWGCFGEHHWE
SIFLGGNEKQTMQNLNDRLAAYLDKVRSLEAANAQLESCILEWHKTKSHGKRHDFNQYEQNVTDMQRQIE
DGKITNASILLQIDNANMASEDFRLKYEAEKTRRQGVQCDLENLRKELDGLTIITTDLEMEIEGLREEHI
LRRKDHEEDMEANRSSQDFKVNVKVNAPPPEDLTKILAEIREDYEAIIEKNRQSLDSWYKELSTAVSLAA
DPNPEQVQSSENEIKDLTRTLQSLDIELQAQMSKKHMLEDTLADTRNYYAVALQNMQQTISKCEEELSQL
RHDIRQQHNQYRVLLGIKTRLEKEISTYRLLLEGNVDRITRTCESKAEEYAELTNGKIKAIVHDSMNGQL
LSSTTAIHQEE

>Chicken_K15
MTTYTVQNSFASGAGGLGAAGSGSSRLSSVRVGGSYRTPSIHGGSGGRGVSISSTKYVSSVGGGYGGGSC
AGFGGGYGGGYGGFGGGAVCGLGGGAGFGGGFDAICAFGGGDGLLSGNEKITMQNLNDRLATYLQKVRAL
EDANAELEVKIRDWYQKEAPSSPARDYSNYYKIIEDLQDKILAATIDNSRVVLEIDNARLAADDFRLKHE
NELFLRQSVESDINGLRRVLDELTLSRADLEMQIESLKEELAYLKKNHEEEMKEYSNQLSGKVSVEMDAA
PGIDLTRILSEMREQYEALAEKYRKDAEAWFLTQTTELNHEVATHTEQIQSSKSEITELRRTMQSLEIEL
QSQISMKAGLEANLRDTEGRYCAQLAQIQNLITSVEEQLSEIRCDMERQNQEYRMLMDIKSRLEQEIATY
RQLLETQDSQMSGVNPKDASAAGRARGGTEDEGRSSSTRDRRHQ

>Chicken_K19
MATYSFRQTTSSVAGGPCGRSLRLGGGSFRAPSIHGGSGGRGVSVSSARFVSSGLGSGLGGGYGGAFSSS
FSAGFGGGYGGGLGSGDGLLSGNEKTTMQNLNDRLASYLDKVRALEEANSDLETKIREWYLKQGPGPARD
YSPYYKAIEDLRDQILAATIDNSKVVLQIDNARLAADDFKTKFETEQALRMSVEADINGLRRVLDELTLA
RTDLELQIENLKEELAYLKKNHEEEMSALGGQVAGQVSVEVDSAPGIDLSKILADMRDQYEHMAEKNRKD
AEAWFHSKTEELNREVAVNTEQLQSSKSEVTDLRRTLQGLEIELQSQLSMKGALESTLADTEGRYGAQLA
QIQDMIGSIEAQLAELRADMERQNSEYKMLMDIKTRLEQEIATYRQLLEGQESQLFGSLSGSPDKRDKPA
DGK

>Chicken_K9L1
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GGLGGGFGGGFAGSFGAGGDILLSGNEKITMQNLNDRLASYLDKVRRLEEDNAQLELHIREWYRKQAPSV
SKDYSSYYQTIEQLQNQIISATVDNNRMLLDIDNSKMTADDFRMKYENELVIRQSVESDVNGLRNLLDDL
THTRSSLESELESLKEELIALKRNHEEELRQLQSQTGGDVSVEVNAAPGEDLTKILNDLRNEYEQIIEKN
RREVEQWYEVKIEEVNRQVTSSSQDIQTSSHQLTELKREMQNLEIELQAQLSTKNSLENSLAETESRYGC
LLQQIQGQINSVEEELANIRCEMEGQNQEYKMLLGIKTRLEQEIAQYRALLNEGQQDLAMPQGGGRTSHS
YSSTSYSHGQSGGDKSGQTRVC

>Chicken_K9L2
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GGLGGGFGGGFAGSFGAGGDILLSGNEKITMQNLNDRLASYLDKVRRLEEDNAQLELHIREWYRKQAPSV
SKDYSSYYQTIEQLQNQIISATVDNNRMLLDIDNSKMTADDFRMKYENELVIRQTVESDINGLRNMLDDL
TLVRSSLESELESLKDELIALKRNHEEELRQLQSQTGGDVSVEVNAAPGEDLTKILNDLRNEYEQIIEKN
RREVEQWYEVKIEEVNRQVTSSSQDIQTSSHQLTELKREMQNLEIELQAQLSTKDSLENSLAETESRYGC
LLQQIQGQINSVEEELANIRCEMEGQSQEYKMLLGIKTRLEQEIAQYRALLHEGQQDLAASQGSFQGGGK
SSQSYSSSSFSQSQSGDVTGQSRVC

>Chicken_K9L3
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KSSYGGGFSSGSCGRIGRSSYGRMSGGSYGGGMGGSMGGGYGSCGGGFGGMGGGYGGGGFGGGSGGYSGG
GFSGFGGSGGFGGGSYGGGSFGGVGFGEDSGLLSTNEKLTMQNLNDRLASYMDKVRGLEEENAHLERLIR
EWYQKQGPTGSKDYSQYYRTIEELQNQIVGANVDLNRMLLDIDNTRMTVDDFRLKYETEYTLHQSVASDI
NGLRPLLDQLTLSRSDLETQFESLKEELIYLKKNHEEEMRGLQTQSSGDVNVEVNATPGTNLMEKLNEMR
CEYERLIENNRREVESWYETKMEEVNQQVHSSGQEIQSSNQQISELRREYQSLEIELQSQLSMVDSLQSN
LEDTERRYNMQLQQIQGMIGPLEEELASIRCEMESQNEEYKMLLGIKTRLEQEIAQYRALLEEGQQDLVI
PAGGMGGGMGGGRIGGGGFSGGGRGGSGSICGGMGGGIGGGSGGIGGGSGGIGGGSGGIGGGSGGSCIIG
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>Chicken_K9L4
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NNEKLTMQNLNDRLASYLDKVRSLERENARLEQLIREWYQKQGPTGRKDYSHYYTTIEDLQNQILTAAVE
TNKILLDLDNTRMTAEDFRTKYETEYGLRQNVEADINTLRPLLDSLTLSRTDLEMQFESLKEEMINLKKD
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>Chicken_HAS1
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>Chicken_HAS2
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>Chicken_HAS3
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>Chicken_K14L1
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>Chicken_K14L2
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>Chicken_K18
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>Alligator_K24
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>Alligator_K10L
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>Alligator_K12
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>Alligator_K20
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>Alligator_K36L1
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>Alligator_K36L2
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>Alligator_K36L3
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>Alligator_K15
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>Alligator_K19
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>Alligator_K9L3
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>Alligator_K9L4
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>Alligator_K9L5
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>Alligator_HAS1
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>Alligator_HAS2
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>Alligator_K14L1
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>Alligator_K117
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>Lizard_K9L2
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>Lizard_HAS4
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>Lizard_K14L1
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>Lizard_K14L2
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>Lizard_K18
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>Snake_K9L
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>Snake_HAS1
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>Snake_HAS2
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>Snake_K18
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>Xenopus1_K18
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>Xenopus1_02
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>Xenopus1_03
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>Xenopus1_04
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>Xenopus1_06
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>Xenopus1_08
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>Xenopus1_09
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>Xenopus1_10
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>Xenopus1_11
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>Xenopus1_12
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>Xenopus1_13
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>Xenopus1_14
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>Xenopus1_15
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>Xenopus1_17
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>Xenopus1_18
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>Xenopus1_20
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>Xenopus1_21
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>Xenopus1_22
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>Xenopus1_K117
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>Chicken_K5L1
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>Chicken_HBS1
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>Chicken_HBS2
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>Chicken_HBS3
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>Chicken_K78LT
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>Chicken_K78L4
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>Chicken_K78L3
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>Chicken_K78L2
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>Chicken_K78L1
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>Chicken_K8
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>Alligator_K80
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>Alligator_K7
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>Alligator_K5L4
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>Alligator_K5L2
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>Alligator_K5L1
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>Alligator_HBS1
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>Alligator_HBS2
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>Turtle_K7
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>Turtle_K5L1
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>Turtle_HBS2
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>Lizard_K5L3
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>Lizard_K5L2
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>Lizard_K5L1
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>Lizard_K78LT
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>Lizard_K78L4
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>Snake_K78L4
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KFASFIDKVRFLEQQNKMLETKWAILQEQRTARSHIEPLFEAYIGNLRRQLDCLLGEKSRLEGERKNMED
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>Frog2_04
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QQSAGRHGDDLRSTKTEISELNRMINRLRSEIDSVKKQCAKLQAAITEAEERGELALKDAKKKLADLEEA
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SSRKL

>Frog2_05
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>Frog2_07
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>Frog2_08
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>Frog2_09
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>Frog2_10
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>Frog2_11
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>Frog2_K8
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DIANKSRLEVESMYQVKYQELQASAGRHGDDLKNTKAEISELTRYTTRLQSEIDALKAQRSNLEAQIAEA
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Suppl. Fig. S1. Amino acid sequences of type I and II keratins of sauropsids and frog (*X. tropicalis*). The amino acid sequences of sauropsidian and frog type I (**A**) and type II (**B**) keratins used for comparative analysis of cysteine contents and phylogenetic analyses (Figures 1-4, Suppl. Figure S5) are shown in FASTA format. The sequences are sorted according to species and, within each species, according to the order of the corresponding genes in the type I or type II keratin gene clusters (Figures 1 and 2). Accession numbers and data about the genes are provided in Supplementary Tables S1-S6. Species: chicken (*Gallus gallus*), alligator (*Alligator sinensis*), turtle (*Chrysemys picta bellii*), lizard (*Anolis carolinensis*), snake (*Protobothrops mucrosquamatus*), western clawed frog (*Xenopus tropicalis*).

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>Platypus_K25
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>Platypus_K26
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>Platypus_K27
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>Platypus_K10L2
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>Platypus_K20L1
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>Platypus_K32
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>Platypus_K36
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>Platypus_K13
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>Platypus_K19
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>Platypus_K9
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>Nanorana1_15
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MSRGDLEIQFESLAEELAYLKKNHEEEMQIARSSATGQVNVEMDAAPGIDLTKLLNDMRADYEALADKNRREAEALFAAKSKELHQEISAGVQQ
VETTKSELTDLRRSLQGLEIELQSQLAMKKSLEDTLAETDGRYGGQLQQLQQVIGGLEEQLQQIRSDMERQSMEYRELLDIKTRLEMEIETYRR
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>Nanorana1_16
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EISDLRRTLQSLEIELQAQISMKNSLEGTLEETEGRYCAQLNQLQNQISSIEEQFQQVRSDMERQKAEYVRLLDIKTRLEMEIETYRRLLEGEL
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>Nanorana1_17
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DQLTLARAELEMQIEGLNEELVYLKKNHTEEVNEIRKQSSGSVDVEVDVAPTVNLGKAMEDMREQYAKMIEKQRLEAKFWFDKKLEDWNEEVHV
NTTELEKYRKDLTEVKQTVQNLEIHSQAEFSKKNAAEATLGNVKDQYAMQLTDLQENITHVESMLQQTRRDVNHQISEFTLLLSLKTRLEAEIA
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>Nanorana1_18
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LSLTRGDLELQIENLQEELAYLKKNHEEEVTALRQQVGGTVNVEMDAAPSVDLAKVLSDMRLECETVSEKIREDARLQFETRIEAVHREITVST
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>Nanorana1_19
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>Nanorana1_20
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>Nanorana1_21
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>Nanorana1_22
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QQRTEELNRDVASGSEQLQSVQTEVIDLNRTVQTLEIELQSQLSMTSALENTLAETEATFGAKLAQLQCLINSVESQLAQIRSDLERQNQEYRI
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>Nanorana1_23
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QLSMTSALENTLAETEATFGAQLAQLQCLINSVESQLAQVRSDLERQNQEYSILMDQKTHLEMEIATYKRLLDGQQAFAGDVSLILSKSTCDVA
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>Nanorana1_24
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RQRTEELNRDVASGSEQLQSVQTEVIDLNRTVQALEIELQSQQSFRSALENTLAETEATFGDQLAQLQCLINNVESQLAQIRSDLERQNQEYRI
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>Nanorana1_25
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>Nanorana1_26
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>Nanorana1_27
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>Nanorana1_28
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>Nanorana1_29
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>Nanorana1_30
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>Nanorana1_31
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>Nanorana1_32
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>Nanorana1_33
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>Nanorana1_34
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>Nanorana1_35
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>Nanorana1_36
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>Nanorana1_37
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>Nanorana1_38
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>Nanorana1_39
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>Nanorana1_40
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>Nanorana1_41
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EAEALFLSQAEALQNEVVTNTQQAQSVKSESTDLRRNLQGLENELQSLLSVKAGLESSVANVEDRYAAQLYQIQNIIGGIEAQLADLRSDLERQ
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>Nanorana1_42
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>Nanorana1_43
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>Nanorana1_44
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>Nanorana1_45
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>Nanorana1_46
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>Zebra_finch_K8
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>Nanorana2_05
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>Nanorana2_06
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>Nanorana2_07
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>Nanorana2_08
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>Nanorana2_09
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>Nanorana2_12
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>Nanorana2_13
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>Nanorana2_17
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>Nanorana2_19
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>Axolotl_K7L
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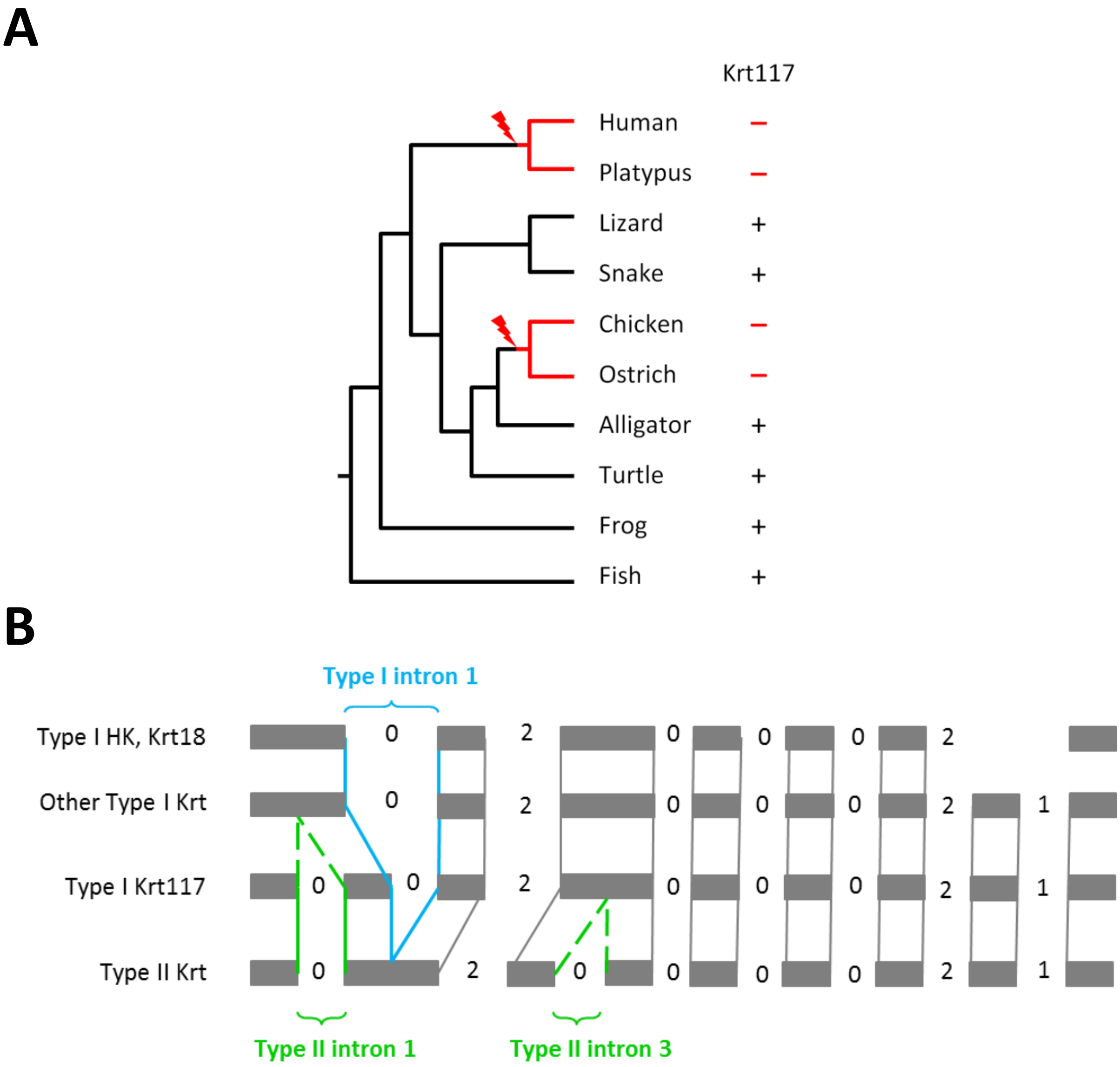
Suppl. Fig. S2. Amino acid sequences of type I and II keratins of platypus, birds, and amphibians. The amino acid sequences of type I (**A**) and type II (**B**) keratins used for comparative analysis of cysteine contents are shown in FASTA format. The sequences are sorted according to species and, within each species, according to the order of the corresponding genes in the type I or type II keratin gene clusters, unless this order is currently unknown (axolotl and caecilian). Accession numbers and data about the genes are provided in Supplementary Tables S7-S13. Preliminary names and accession numbers of zebrafish (*Danio rerio*) keratins are provided in Supplementary Table S14. Keratin amino acid sequences of species shown in Figures 1 and 2 are not included here but in Suppl. Fig. S1. Species: platypus (*Ornithorhynchus anatinus*), kiwi (*Apterix australis*), ostrich (*Struthio camelus australis*), zebra finch (*Taeniopygia guttata*), Nanorana/Tibetan frog (*Nanorana parkeri*), axolotl (*Ambystoma mexicanum*), caecilian (*Microcaecilia unicolor*).



C

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 Frog_K117  MSFSTRSISQSARFGVFASPGVNRARSVA-----GGASTVRMSSANMTSSAFA------------------ASPAFEVGV
Allig_K117  MA-SSLS-RNLFCFGVPQGPRLNWISAAGLQ---PGLLSIHGGAGSIGSYLSSASDAFVKCVPGGSYEPGIGSGASGIGL
Turtle_K117 MA-S-FS-RS----GVTLGPRLSWVRVVGLQGGVPGGLGVCGGAGSTSSRLFSGSDGIVG--------PGLGGGAREPGL
Lizard_K117 MS-TTFSSRSLSFSGSVRGPRSGSTLSIARPQTASNIYGVMNSLPPSAKDTMA------------------RRYGPETDI
 Snake_K117 MP-TTFSSHSMS-SGSIQGPRGRRLLALGRPQAVPSIHRVIRDKTRLSYGD--------------------GQGFMDTNI
            <----------------------------- encoded by exon 1 -------------------------------

            81                                                                            160
 Fish_K117  ASNGGKFTMQNLNDRLACYLEKVRSLENKNRELQLNIDEFRVKTTYI-TKDYANYFSIISDLKKKITRSCSENQNLLLQI
 Frog_K117  TSNNGKETMQNLNDRLSNYLERVRSLELANHELERKIREYLDKKAAVGSMDVSGYYKTINLLRSQINDATIDNTRLVLSI
Allig_K117  LGMNEKDTMQNLNDRLAAYLERVCSLEEANGQLEQRIQELQVKKTLARHYDPSSCFSTIAELRSQIQDESVRNSQLTLQL
Turtle_K117 LSMNEKDTMQNLNDRLAAYLETVRSLEEANGQLERQIREVYAKRAQAGCQDLSGYFSTIAELRSQIQAASTSNAQLILQI
Lizard_K117 LDINQKGTMQNLNDRLAAYLGRVHSLEESNAQLEQNIREYYAKRASAGGPDLSGYFNTLSELKAKIEQETLNNAGLLLRI
 Snake_K117 LDMNEKGTMKNLNDRLAAYLDKVLSLEKSNMQLEQNIQEFYTKQTSTGTHDMSAYFNAMIQMKSEIQKETLKNAGLLLQI
             encoded by exon 1 --><---------- encoded by exon 2 ------------><- enc. exon 3

            161                                                                           240
 Fish_K117  ESSRLAAEDFKMKSEMEINMRTTVEADLLDVRRFRDGLTLTMSSLELTLEGLNEERIPMDREHDEEMEERRRRGAGEVKV
 Frog_K117  DNAKLAADDFKIKYESELAIRTGAESDIAGLRRVLDELTLNKTDLELDIESLKEELIYLKKSHEEELAVVRSSAKGNVDV
Allig_K117  DNAKLAANDFRMKYEAELATRLGVESDIKGLRKVLDGLTEARASLQVQIESLKEELTYLQQNHGEEVAALQGHLGGSVSV
Turtle_K117 DNATLAADDFRVKFESELAIRRGGESDVAGLRKVLDEVTLSRASLQEELGSLQEELAQLQKNHGEEAAALQGRLGGSVSV
Lizard_K117 DNAKLAADDFKVKLESEVAIRLSLEGDVNGLRKVLDDVNASRASLQVQVDNLQEELVYLKRNHEEEVASLQGRLGGTVNV
 Snake_K117 DNARLAADDFRVKLESEVAMRLSLEGDLGGLRKALEELNASRASLQVQADNLQEELACLKRNHKEEVASLQGHLGGTVNV
            enc. exon 3 ><-------------- encoded by exon 4 -----------------><- enc. exon 5
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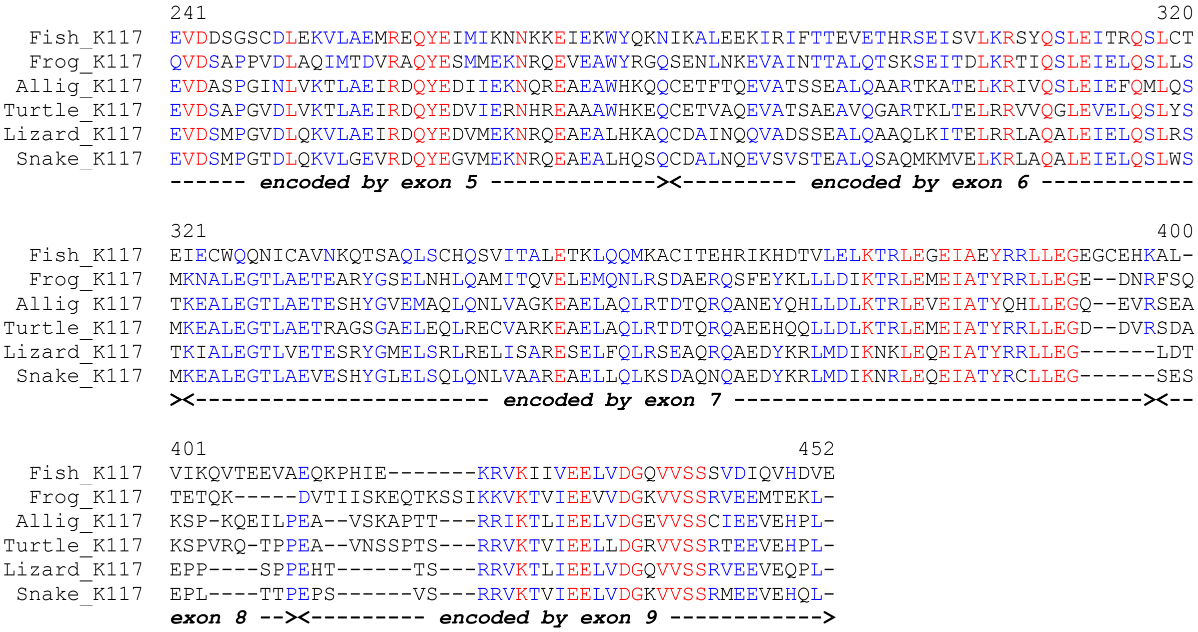

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             241                                                                          320
  Fish_K117  EVDDSGSCDLEKVLAEMREQYEIMIKNNKKEIEKWYQKNIKALEEKIRIFTTEVETHRSEISVLKRSYQSLEITRQSLCT
  Frog_K117  QVDSAPPVDLAQIMTDVRAQYESMMEKNRQEVEAWYRGQSENLNKEVAINTTALQTSKSEITDLKRTIQSLEIELQSLLS
 Allig_K117  EVDASPGINLVKTLAEIRDQYEDIIEKNQREAEAWHKQQCETFTQEVATSSEALQAARTKATELKRIVQSLEIEFQMLQS
Turtle_K117  EVDSAPGVDLVKTLAEIRDQYEDVIERNHREAAAWHKEQCETVAQEVATSAEAVQGARTKLTELRRVVQGLEVELQSLYS
Lizard_K117  EVDSMPGVDLQKVLAEIRDQYEDVMEKNRQEAEALHKAQCDAINQQVADSSEALQAAQLKITELRRLAQALEIELQSLRS
 Snake_K117  EVDSMPGTDLQKVLGEVRDQYEGVMEKNRQEAEALHQSQCDALNQEVSVSTEALQSAQMKMVELKRLAQALEIELQSLWS
             ------ encoded by exon 5 -------------><--------- encoded by exon 6 ------------

             321                                                                          400
  Fish_K117  EIECWQQNICAVNKQTSAQLSCHQSVITALETKLQQMKACITEHRIKHDTVLELKTRLEGEIAEYRRLLEGEGCEHKAL-
  Frog_K117  MKNALEGTLAETEARYGSELNHLQAMITQVELEMQNLRSDAERQSFEYKLLLDIKTRLEMEIATYRRLLEGE--DNRFSQ
 Allig_K117  TKEALEGTLAETESHYGVEMAQLQNLVAGKEAELAQLRTDTQRQANEYQHLLDLKTRLEVEIATYQHLLEGQ--EVRSEA
Turtle_K117  MKEALEGTLAETRAGSGAELEQLRECVARKEAELAQLRTDTQRQAEEHQQLLDLKTRLEMEIATYRRLLEGD--DVRSDA
Lizard_K117  TKIALEGTLVETESRYGMELSRLRELISARESELFQLRSEAQRQAEDYKRLMDIKNKLEQEIATYRRLLEG------LDT
 Snake_K117  MKEALEGTLAEVESHYGLELSQLQNLVAAREAELLQLKSDAQNQAEDYKRLMDIKNRLEQEIATYRCLLEG------SES
             ><----------------------- encoded by exon 7 --------------------------------><--

             401                                              452
  Fish_K117  VIKQVTEEVAEQKPHIE-------KRVKIIVEELVDGQVVSSSVDIQVHDVE
  Frog_K117  TETQK-----DVTIISKEQTKSSIKKVKTVIEEVVDGKVVSSRVEEMTEKL-
 Allig_K117  KSP-KQEILPEA--VSKAPTT---RRIKTLIEELVDGEVVSSCIEEVEHPL-
Turtle_K117  KSPVRQ-TPPEA--VNSSPTS---RRVKTVIEELLDGRVVSSRTEEVEHPL-
Lizard_K117  EPP----SPPEHT------TS---RRVKTLIEELVDGQVVSSRVEEVEQPL-
 Snake_K117  EPL----TTPEPS------VS---RRVKTVIEELVDGKVVSSRMEEVEHQL-
             exon 8 --><--------- encoded by exon 9 ------------>
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Suppl. Fig. S3. ***Krt117*, a keratin gene with a unique exon-intron structure, has been lost in mammals and birds.** (**A**) The presence (+) or absence (-) of *Krt117* was mapped onto a simplified phylogenetic tree of vertebrates. Gene loss events (flash symbols) were inferred from the distribution of *Krt117* in extant species. (**B**) Exon-intron structure of *Krt117* and other keratin genes. Exons are depicted as grey boxes. The numbers between the exons indicate the phase of splicing of the intron. Homologous splice sites are connected by vertical lines. Intron 1 of type I keratin genes is not conserved in type II keratin genes, whereas introns 1 and 3 of type II keratin genes are not conserved in type I keratin genes. *Krt117* has the same introns as other type I keratins but, in addition, it has an intron at a position homologous to intron 1 of type II keratins. Note that the lengths of exon symbols are not proportional to the lengths of the exons. (**C**) Amino acid sequence alignment of K117 proteins. The segments encoded by the different exons of the *Krt117* gene are indicated below the sequences. Residues identical in all species are shown with red fonts, and weakly conserved residues are shown with blue fonts. The alignment was made with the Multalin program. Species: alligator (*Alligator sinensis*, abbreviation: Allig), fish (guppy, *Poecilia reticulata*), frog (*Xenopus tropicalis*), lizard (*Anolis carolinensis*), snake (*Protobothrops mucrosquamatus*), turtle (*Chrysemys picta bellii*).

```
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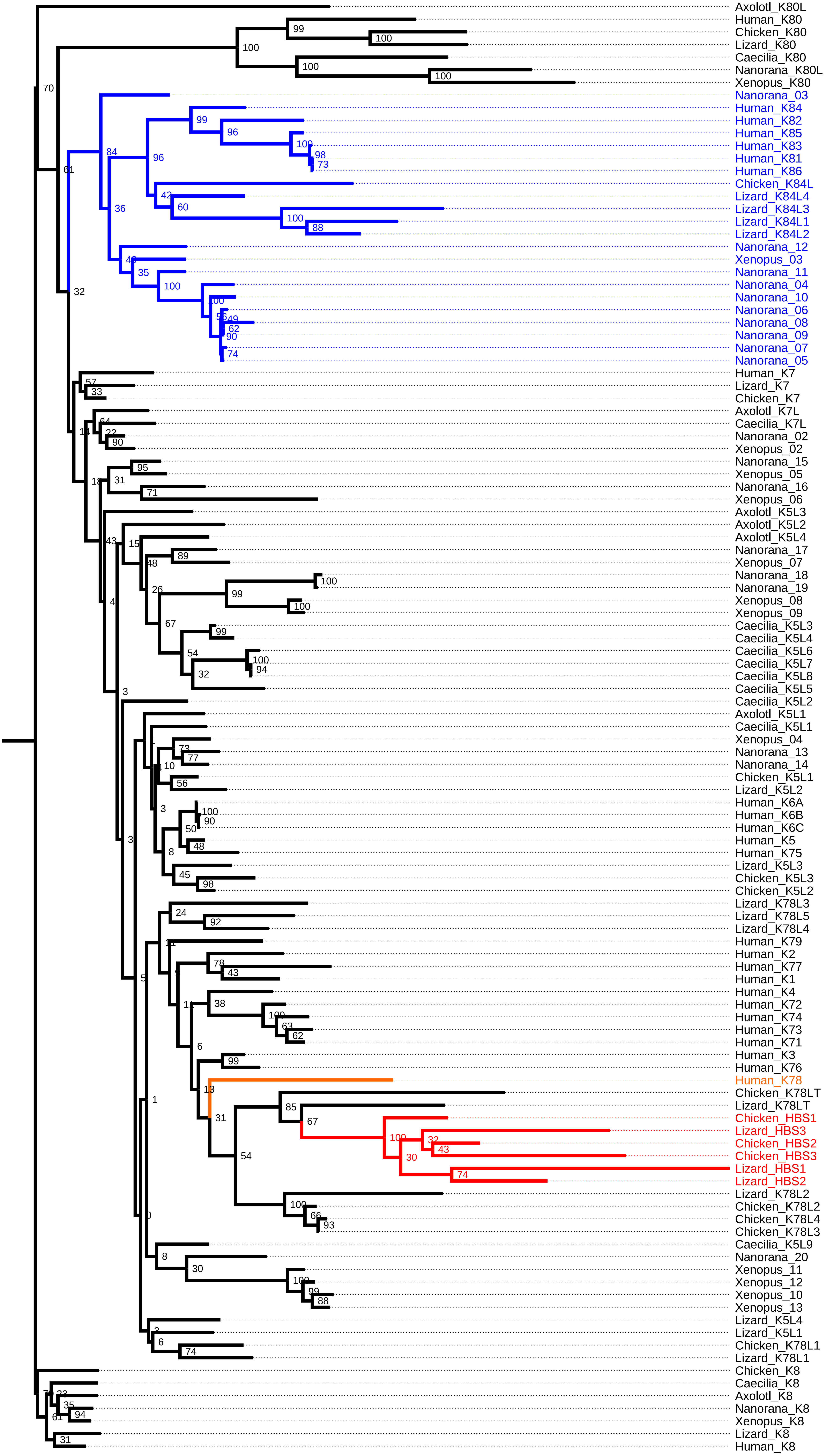
Suppl. Fig. S4. Predictions of amino acid sequences of K78LT keratins of archosaurs. The intermediate filament domains are underlined. Cysteine residues are highlighted by red shading. Glycine and serine residues, which are highly abundant in the head and tail domains, are marked by light and dark grey shading. "X"s with blue shading indicate uncertain positions corresponding to frame-shifts in the genomic DNA sequence available in GenBank. Note that the sequences of K78LT proteins of the Chinese alligator (Asi, *Alligator sinensis*), translation of GenBank gene LOC102373665 + two 3'-terminal exons) and chicken (Gga, *Gallus gallus*) (Suppl. Table S1) after these frameshift sites are hypothetical. The sequence of the American alligator (Ami, *Alligator mississippiensis*) K78LT (Suppl. Table S2) is the translation of a gene without frame-shifts.

Suppl. Fig. S5. Maximum likelihood phylogenetic analysis of type I and type II keratins of tetrapods. The phylogenetic tree was generated with PhyML. Hair keratins and orthologs are indicated with blue fonts and lines. Sauropsid-specific cysteine-rich keratins (HAS, HBS) are shown with red fonts and lines. Bootstrap values are indicated. Bayesian phylogenetitic inference yielded similar results. Amino acid sequences: Suppl. Fig. S1. Accession numbers: Suppl. Tables S1-S6.

Suppl. Fig. S6. Maximum likelihood phylogenetic analysis of type I keratins of amphibians (*X. tropicalis*, Tibetan frog, axolotl, caecilian), chicken, lizard, and human. The phylogenetic tree was generated with PhyML. Sauropsid-specific cysteine-rich keratins (HAS) are shown with red fonts and lines. Hair keratins and orthologs are indicated with blue fonts and lines. Note that hair keratin orthologs of Xenopus and Nanorana have a low cysteine content. Bootstrap values are indicated. The scale bar represents substitutions/site. Bayesian phylogenetitic inference yielded similar results. Amino acid sequences are provided in Suppl. Fig. S1 and S2. Accession numbers and information about the genes is shown in the Suppl. Tables S1-S13.



Suppl. Fig. S7. Maximum likelihood phylogenetic analysis of type II keratins of amphibians (*X. tropicalis*, Tibetan frog, axolotl, caecilian), chicken, lizard, and human. The phylogenetic tree was generated with PhyML. Sauropsid-specific cysteine-rich keratins (HBS) are shown with red fonts and lines. Hair keratins and orthologs are indicated with blue fonts and lines. Note that hair keratin orthologs of Xenopus and Nanorana have a low cysteine content. Bootstrap values are indicated. Bayesian phylogenetitic inference yielded similar results. Amino acid sequences: Suppl. Fig. S1 and S2. Accession numbers and information about the genes: Suppl. Tables S1-S13.

Suppl. Fig. S8. Maximum likelihood phylogenetic analysis of type I and type II keratins of fish (*Danio rerio*) and tetrapods (*Xenopus tropicalis*, lizard, chicken, human). The phylogenetic tree was generated with PhyML. Hair keratins and orthologs are indicated with blue fonts and lines. Sauropsid-specific cysteine-rich keratins (HAS and HBS) are shown with red fonts and lines. A fish keratin with 26 cysteine residues is highlighted by green fonts. Bootstrap values are indicated. Bayesian phylogenetitic inference yielded similar results. Accession numbers of *Danio* keratins are shown in the Suppl. Table S14.

A

```
        1                                                                                               100
E1BZZ9  ----------------------------------------------------------------------------------------------------
  HAS1  MSCNIKETITVSSKGRSSGGSCIIGGGGGARISSYAIGSGRGFSGRSYCGGVNYGGGLSVGSLAGGSYGGGNCYGNGLGFGLGGGVVVGGLGSDCLLSSC

        101                                                                                             200
E1BZZ9  ----------------------------------------------------------------------------------------------------
  HAS1  DEKVTMQNLNDRLASYLDKVKCLEKENAELECRIREWYATQGLSCEPRDYSCYYKEIEDLQNQIVCATIDNNKIILDIDNSRMAADDFRVKYETELALRQ

        201                                                                                             300
E1BZZ9  --------------------------------------------MNCLRKQSTGDVSVEVNACPGPDLRQILEDLRCQYETLIARNRKEVEDWYECKIEE
  HAS1  SVEADINGLRQVLDQLTLCRSDLEAQLESLREELCCLKKNHEEEMNCLRKQSTGDVSVEVNACPGPDLRQILEDLRCQYETLIARNRKEVEDWYECKIEE

        301                                                                                             400
E1BZZ9  VNREVITSGQEVETCNNQVTELRRQLQALEIDLQAQLSQRNNLESSLAETECQYNTLLGELQNQITCVEQQLAEIRAEIECQNQEYKTLLDVKCRLEQEI
  HAS1  VNREVITSGQEVETCNNQVTELRRQLQALEIDLQAQLSQRNNLESSLAETECQYNTLLGELQNQITCVEQQLAEIRAEIECQNQEYKTLLDVKCRLEQEI

        401                                                           466
E1BZZ9  QTYRCLLEGGQQDLIHGGGIGVGSGVGGGVIRTSHTYTTTTASHCQPQVPPCKTGDIQVTCRRICD
  HAS1  QTYRCLLEGGQQDLIHGGGIGVGSGVGGGVIRTSHTYTTTTASHCQPQVPPCKTGDIQVTCRRICD
```

B

```
        1                                                                                               100
E1C8E5  ----------------------------------------------------------------------------------------------------
  HAS2  MSSVSSGRYTTCGIGGSRGFSGRSYCGGVNYGGGLSSGSLVGGSYGGGLGAAVLGGCSGIGFSGGSARFGGGIGGGLGISLGGGVVGGGFSGDGILLSGD

        101                                                                                             200
E1C8E5  ----------------------------------------------------------------------------------------------------
  HAS2  EKVTMQNLNDRLASYLDKVRCLEQENADLECRIREWYAKQGPFCEPRDYSCYYKEIEDLQNQIVCATIDNNKIILNIDNSRMTADDFRVKYETELALRQS

        201                                                                                             300
E1C8E5  -------------------------------------------MNCLRKQSTGDVSVEVNACPGPDLRKILEEMRCQYETLIERNRKEVEDWYECKIEEV
  HAS2  VEADINGLRQVLDQLTLCRSDLEAQLESLREELCCLKKNHEEEMNCLRKQSTGDVSVEVNACPGPDLRKILEEMRCQYETLIERNRKEVEDWYECKIEEV

        301                                                                                             400
E1C8E5  NREVITSGQEVETCNNQVTELRRQLQALEIDLQAQLSQRDNLESSLAETECRYNNHLGELQTQITCVEQQLADLRAEMECQNQEYKILLDVK--------
  HAS2  NREVITSGQEVETCNNQVTELRRQLQALEIDLQAQLSQRDNLESSLAETECRYNNHLGELQTQITCVEQQLADLRAEMECQNQEYKILLDVKCRLEQEIH

        401                                                               470
E1C8E5  ----------------------------------------------------------------------
  HAS2  TYRCLLEGGQQDLIQQGGIGQLSGLGGGVARTGGIGGGGIIRTSHTYTSSAQMPSCAAAEIQVPCRRICD
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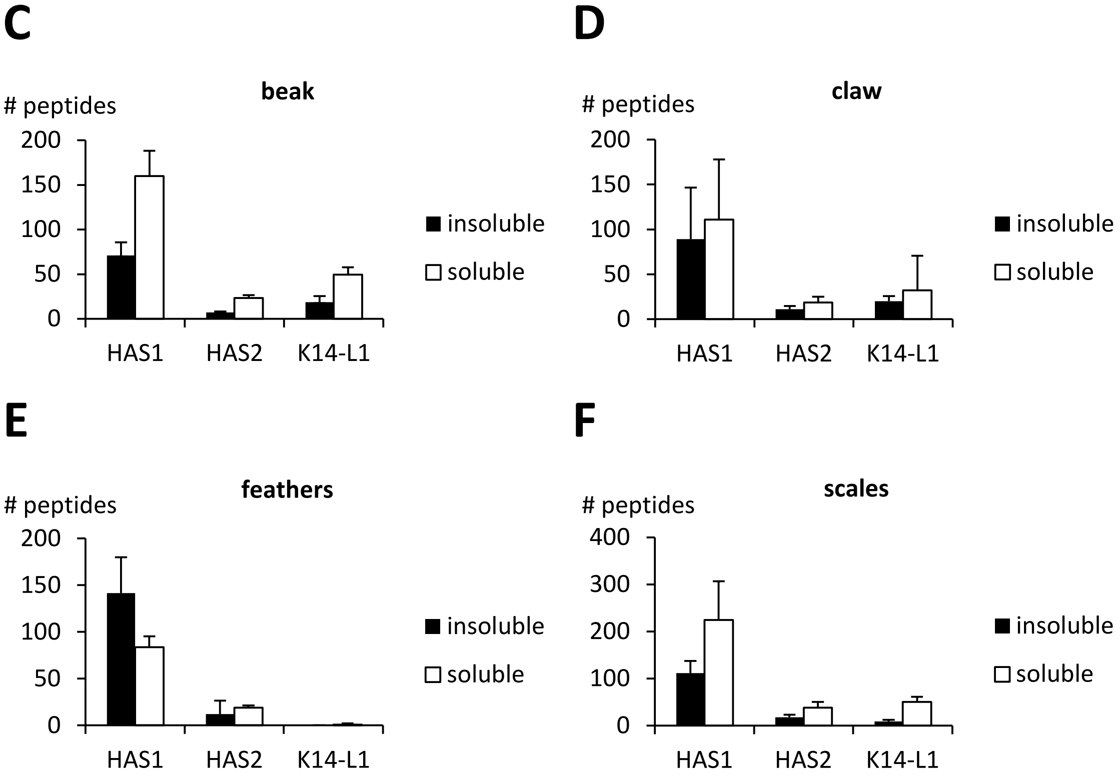
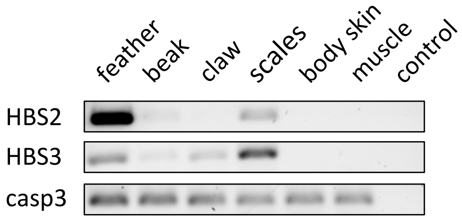
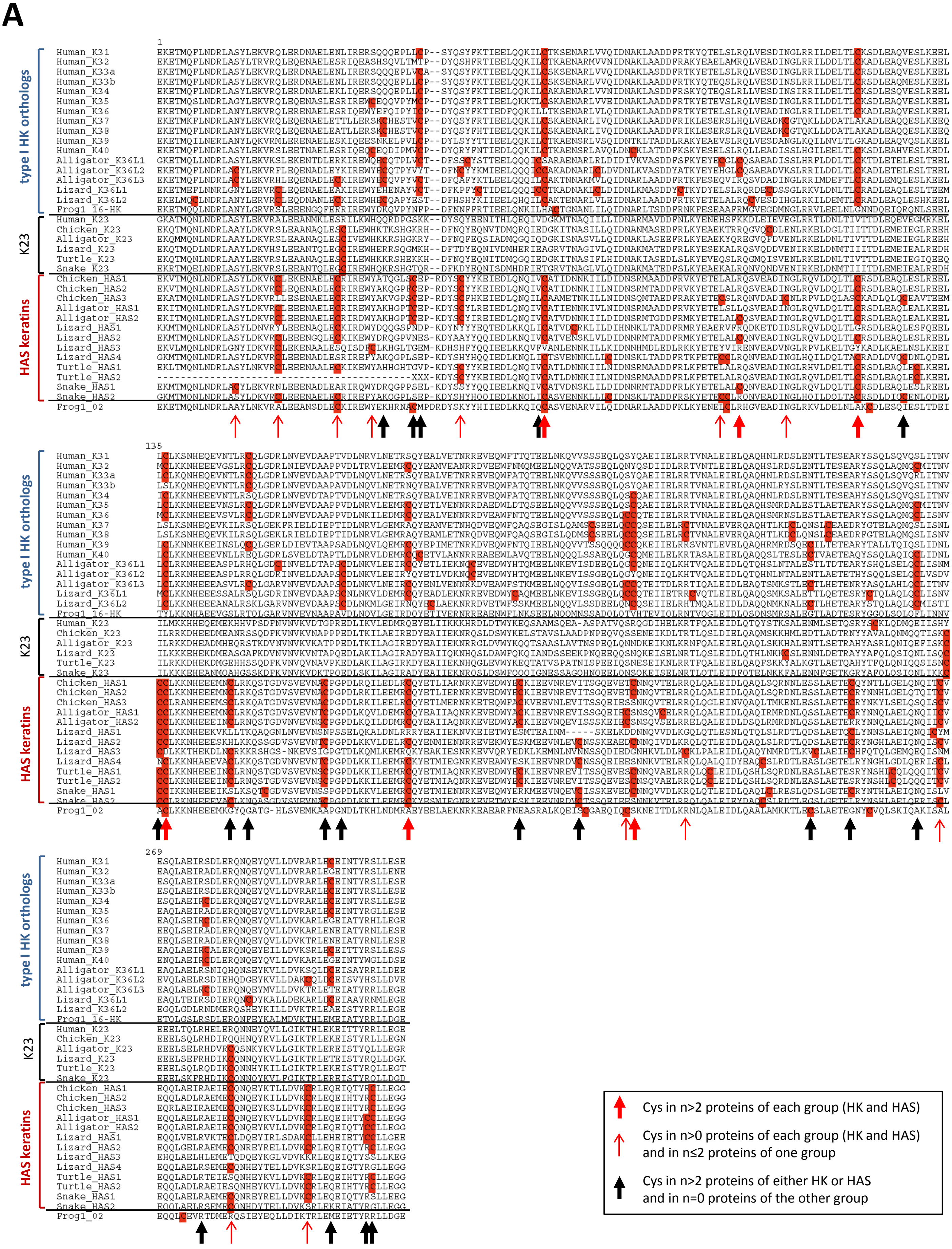


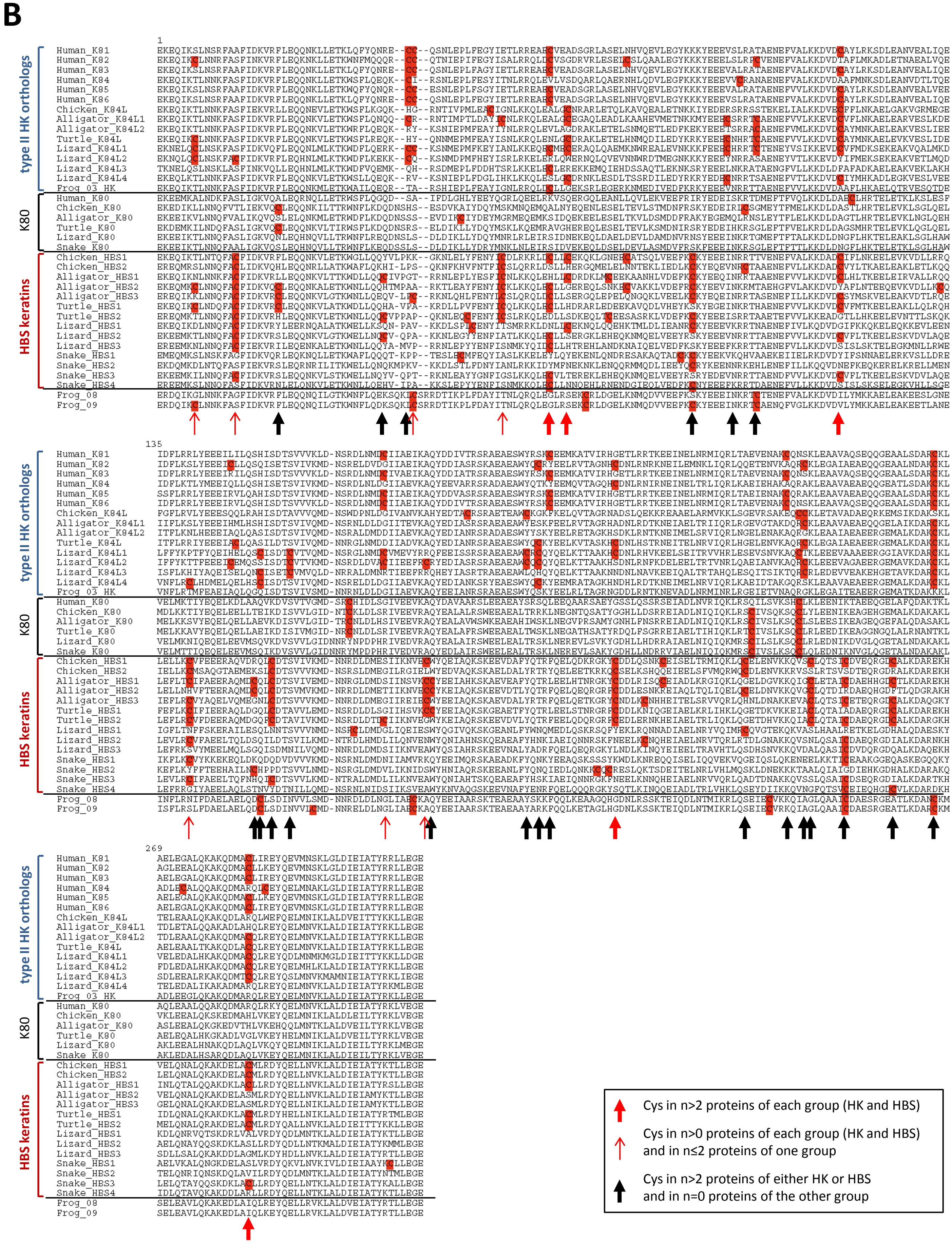
Suppl. Fig. S9. Detection of HAS1 and HAS2 keratin fragments in the proteomes of hard skin appendages of the chicken. Results of proteomic analysis of cornified chicken skin appendages (Rice et al., 2013) were re-analyzed using protein predictions as defined in the present study. Amino acid sequence alignments showed that E1BZZ9 (Uniprot accession number) and E1C8E5, that were detected by proteomics, corresponded to fragments of keratins HAS1 (**A**) and HAS2 (**B**), respectively. Red fonts mark identical residues. (**C-F**) Number of peptides detected by proteomics in cornified chicken skin appendages (soluble and insoluble fractions). Bars indicate means of n=4 samples. Error bars indicate standard deviations. Peptide counts of K14L1 (keratin 14-like 1) are shown for comparison.



Suppl. Fig. S10. Keratins HBS2 and HBS3 are differentially expressed in hard skin appendages of the chicken. Gene expression was investigated by RT-PCR analysis on RNA extracted from chicken tissues. Caspase-3 (casp3) is ubiquitously expressed and was investigated for comparison. In a control reaction, no cDNA was added to the PCR. PCR products were run on an agarose gel and DNA was visualized by GelRed fluorescent dye.



Suppl. Figure S11. Continued on the next page.



Supplementary Figure S11. Comparison of positions of cysteine residues in the intermediate filament (IF) domains of hair keratin (HK) orthologs, HAS and HBS keratins. The amino acid sequences of the IF domains of type I keratins (**A**) and type II keratins (**B**) were aligned with the Seaview program. Cysteine residues (C) are highlighted by red shading. The sequences of evolutionary ancient keratins with low to medium cysteine contents (K23 and K80) are included for comparison. Type I and type II frog (*X. tropicalis*) keratins with the highest cysteine contents are also included in the alignment. Vertical arrows indicate positions with cysteine in multiple proteins. Red arrows (definition in the boxed legends on the right) indicate likely convergent evolution towards cysteine at particular positions whereas black arrows indicate cysteine residues that are specific for either HAS or type I HK or HBS or type II HK (without consideration of cysteine in K23, K80 or frog keratins). Due to a sequence gap in the genome sequence, the sequence of turtle HAS2 is incomplete at the amino-terminus.

```
>Chicken_K12
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RLEMEIETYRRLLDGE
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>Chicken_K15
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>Human_K13
EKITMQNLNDRLASYLEKVRALEEANADLEVKIRDWHLKQSPA----SPERDYSP--YYK
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MREQYEAMAERNRRDAEEWFHAKSAELNKEVSTNTAMIQTSKTEITELRRTLQGLEIELQ
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>Human_K14
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LTLARADLEMQIESLKEELAYLKKNHEEEMNALRGQVG-GDVNVEMDAAPGVDLSRILNE
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RLEQEIATYRRLLEGE
>Human_K15
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LTLARTDLEMQIEGLNEELAYLKKNHEEEMKEFSSQLA-GQVNVEMDAAPGVDLTRVLAE
MREQYEAMAEKNRRDVEAWFFSKTEELNKEVASNTEMIQTSKTEITDLRRTMQELEIELQ
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>Human_K16
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EKVTMQNLNDRLASYLDKVRALEEANADLEVKIRDWYQRQRP-----SEIKDYSP--YFK
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>Human_K17
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RLEQEIATYRRLLEGE
>Human_K18
EKETMQSLNDRLASYLDRVRSLETENRRLESKIREHLEKKGP------QVRDWSH--YFK
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IRAQYDELARKNREELDKYWSQQIEESTTVVTTQSAEVGAAETTLTELRRTVQSLEIDLD
SMRNLKASLENSLREVEARYALQMEQLNGILLHLESELAQTRAEGQRQAQEYEALLNIKV
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>Human_K19
EKLTMQNLNDRLASYLDKVRALEAANGELEVKIRDWYQKQGP-----GPSRDYSH--YYT
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>Human_K24
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RLEVEIETYRRLLDGE
>Human_K25
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HLEKEIETYCLLIGGD
>Human_K26
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LTLCTTDLEIQCETLSEELTYLKKSHEEEMEVLQYTAG-GNVNVEMNATPGVDLTVLLNN
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FLEKEIDIYCNLLDGE
>Human_K27
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HLEKEIETYCLLIDGE
>Human_K28
EKVTMQNLNDRLASYLDNVRALEEANAELERKIKGWYEKYGPGSCR-GLDHDYSR--YHL
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>Human_K31
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>Human_K32
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AQHSLRDSLENTLTESEARYSSQLAQMQCMITNVEAQLAEIRADLERQNQEYQVLLDVRA
RLEGEINTYRSLLENE
>Human_K33a
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AQHNLRDSLENTLTESEARYSSQLSQVQRLITNVESQLAEIRSDLERQNQEYQVLLDVRA
RLECEINTYRSLLESE
>Human_K33b
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LTLCKSDLESQVESLREELICLKKNHEEEVNTLRSQLG-DRLNVEVDTAPTVDLNQVLNE
TRSQYEALVEINRREVEQWFATQTEELNKQVVSSSEQLQSCQAEIIELRRTVNALEIELQ
AQHNLRDSLENTLTESEAHYSSQLSQVQSLITNVESQLAEIRCDLERQNQEYQVLLDVRA
RLECEINTYRSLLESE
>Human_K35
EKETMQSLNDRLAGYLEKVRQLEQENASLESRIREWCEQQVP-----YMCPDYQS--YFR
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LTLCKSDLEAQVESLKEELLCLKKNHEEEVNSLRCQLG-DRLNVEVDAAPPVDLNRVLEE
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RLECEINTYRGLLESE
>Human_K36
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RLEGEIATYRHLLEGE
>Human_K37
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RLENEIATYRNLLESE
>Human_K38
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RLENEIATYRNLLESE
>Human_K39
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RLECEITTYRSLLESS
>Human_K40
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RLEGEINTYWGLLDSE
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Suppl. Fig. S12. Amino acid sequence alignment of the intermediate filament domains of type I keratins used for the phylogenetic analysis shown in Figure 3. The multiple sequence alignment is shown in fasta_aln format.

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>Chicken_K80
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RTELEVKLSGLQELMDLKKTIYEQELEELLTEI--KDISVVLGIDNTCKL-DLSRIVEEV
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LDLEILTYRKLVEGE
>Chicken_K7
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KVELEAKVDALTDEINFLRSLYEAELRELQAQI--SDTSVVLSMDNSRNL-DLDSIIAEV
KAQYEDIANRSRAEAESWYQSKFEALQVTAGKHGDDLRNTKNEITEINRVIQRLQGEIEN
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LDIEIATYRKLLEGE
>Chicken_K84L
EKEQIKTLNNKFASFIEKVRLLEQQNEVLETKWSFLKGQKH----GRNTIVPMLEACIGN
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KAELGAKVGRMEGEFGFLRVLYEEESQQLRAHI--SDTAVVVQMDNSWDP-NLDGIVANV
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>Chicken_K5L3
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KTELQARLDALLEEIDFLRALYEAELSQLQSQI--ADTSVILTMDNNRSL-DMDSIIAEV
KAQYEDIAKRSREEAESWYQSRYEELQATAGRHGDDLRSTKQEISELNRHVQRLRAEIDS
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>Chicken_K5L2
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KAQYEDIANRSRAEAESWYQTKYEELQATAGRHGDDLRSTKQEISELNRHVQRLRAEIDS
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>Chicken_K5L1
EREQIKTLNNKFASFIDKVRFLEQQNKVLETKWSLLQEQGHTV--TRKSLEPLFETYINN
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KAQYEDIANRSRAEAEAWYQNKYEELQVSAGRHGDDLRNTKMEISEINRMVQRLRNEIES
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>Chicken_HBS1
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>Chicken_HBS2
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>Chicken_HBS3
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>Chicken_K78L3
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>Chicken_K78L1
EREELKTLNNKFASFIDKVRFLEQQNKVLETKWKLLQEQSPTT--STRSLDPYFEAYISR
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>Chicken_K8
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LQKQLEMLSGDGVRLDSELRNMQDLVEDYKKRYEVEINRRTAAENEFVVLKKDVDAAYMN
KVELQAKVDSLTDEIKFFKCLYEGEITQIQSHI--SDTSIVLSMDNNRDL-DLDSIIAEV
RAQYEEIALKSKAEAETLYQTKIQELQVTAGQHGDDLKLTKAEISELNRLIQRIRSEIGN
VKKQCADLETAIADAEQRGDCALKDARAKLDELEGALHQAKEELARMLREYQELVSLKLA
LDMEIATYRKLLESE
>Human_K73
EREQIKVLNNKFASFIDKVRFLEQQNQVLETKWELLQQLDLNN--CKNNLEPILEGYISN
LRKQLETLSGDRVRLDSELRSVREVVEDYKKRYEEEINKRTTAENEFVVLKKDVDAAYTS
KVELQAKVDALDGEIKFFKCLYEGETAQIQSHI--SDTSIILSMDNNRNL-DLDSIIAEV
RAQYEEIARKSKAEAEALYQTKFQELQLAAGRHGDDLKHTKNEISELTRLIQRLRSEIES
VKKQCANLETAIADAEQRGDCALKDARAKLDELEGALQQAKEELARMLREYQELLSVKLS
LDIEIATYRKLLEGE
>Human_K74
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LRKQLETLSGDRVRLDSELRSMRDLVEDYKKRYEVEINRRTTAENEFVVLKKDADAAYAV
KVELQAKVDSLDKEIKFLKCLYDAEIAQIQTHA--SETSVILSMDNNRDL-DLDSIIAEV
RMHYEEIALKSKAEAEALYQTKIQELQLAASRHGDDLKHTRSEMVELNRLIQRIRCEIGN
VKKQRASLETAIADAEQRGDNALKDAQAKLDELEGALHQAKEELARMLREYQELMSLKLA
LDMEIATYRKLLEGE
>Human_K75
EREQIKTLNNKFASFIDKVRFLEQQNKVLETKWALLQEQGSRT--VRQNLEPLFDSYTSE
LRRQLESITTERGRLEAELRNMQDVVEDFKVRYEDEINKRTAAENEFVALKKDVDAAYMN
KVELEAKVKSLPEEINFIHSVFDAELSQLQTQV--GDTSVVLSMDNNRNL-DLDSIIAEV
KAQYEDIANRSRAEAESWYQTKYEELQVTAGRHGDDLRNTKQEISEMNRMIQRLRAEIDS
VKKQCSSLQTAIADAEQRGELALKDARAKLVDLEEALQKAKQDMARLLREYQELMNIKLA
LDVEIATYRKLLEGE
>Human_K76
EREQIKTLNNKFASFIDKVRFLEQQNKVLETKWELLQQQTTGS--GPSSLEPCFESYISF
LCKQLDSLLGERGNLEGELKSMQDLVEDFKKKYEDEINKRTAAENEFVGLKKDVDAAFMN
KVELQAKVDSLTDEVSFLRTLYEMELSQMQSHA--SDTSVVLSMDNNRCL-DLGSIIAEV
RAQYEEIAQRSKSEAEALYQTKLGELQTTAGRHGDDLRNTKSEIMELNRMIQRLRAEIEN
VKKQNANLQTAIAEAEQRGEMALKDANAKLQDLQTALQKAKDDLARLLRDYQELMNVKLA
LDVEIATYRKLLEGE
>Human_K77
EREQIMVLNNKFASFIDKVRFLEQQNQVLQTKWELLQQVNTST--GTNNLEPLLENYIGD
LRRQVDLLSAEQMRQNAEVRSMQDVVEDYKSKYEDEINKRTGSENDFVVLKKDVDAAYVS
KVDLESRVDTLTGEVNFLKYLFLTELSQVQTHI--SDTNVILSMDNNRSL-DLDSIIDAV
RTQYELIAQRSKDEAEALYQTKYQELQITAGRHGDDLKNSKMEIAELNRTVQRLQAEISN
VKKQIEQMQSLISDAEERGEQALQDAWQKLQDLEEALQQSKEELARLLRDYQAMLGVKLS
LDVEIATYRQLLEGE
>Human_K78
ETQEIRTLNNQFASFIDKVRFLEQQNKVLETKWHLLQQQGLSG--SQQGLEPVFEACLDQ
LRKQLEQLQGERGALDAELKACRDQEEEYKSKYEEEAHRRATLENDFVVLKKDVDGVFLS
KMELEGKLEALREYLYFLKHLNEEELGQLQTQA--SDTSVVLSMDNNRYL-DFSSIITEV
RARYEEIARSSKAEAEALYQTKYQELQVSAQLHGDRMQETKVQISQLHQEIQRLQSQTEN
LKKQNASLQAAITDAEQRGELALKDAQAKVDELEAALRMAKQNLARLLCEYQELTSTKLS
LDVEIATYRRLLEGE
>Human_K79
EREQIKTLNNKFASFIDKVRFLEQQNKVLETKWALLQEQGQNLGVTRNNLEPLFEAYLGS
MRSTLDRLQSERGRLDSELRNVQDLVEDFKNKYEDEINKHTAAENEFVVLKKDVDAAYMG
RMDLHGKVGTLTQEIDFLQQLYEMELSQVQTHV--SNTNVVLSMDNNRNL-DLDSIIAEV
KAQYELIAQRSRAEAEAWYQTKYEELQVTAGKHGDNLRDTKNEIAELTRTIQRLQGEADA
AKKQCQQLQTAIAEAEQRGELALKDAQKKLGDLDVALHQAKEDLTRLLRDYQELMNVKLA
LDVEIATYRKLLESE
>Human_K80
EKEEMKALNDKFASLIGKVQALEQRNQLLETRWSFLQGQDSAI----FDLGHLYEEYQGR
LQEELRKVSQERGQLEANLLQVLEKVEEFRIRYEDEISKRTDMEFTFVQLKKDLDAECLH
RTELETKLKSLESFVELMKTIYEQELKDLAAQV--KDVSVTVGMDSRCHI-DLSGIVEEV
KAQYDAVAARSLEEAEAYSRSQLEEQAARSAEYGSSLQSSRSEIADLNVRIQKLRSQILS
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>Human_K81
EKEQIKSLNSRFAAFIDKVRFLEQQNKLLETKLQFYQNREC----CQSNLEPLFEGYIET
LRREAECVEADSGRLASELNHVQEVLEGYKKKYEEEVSLRATAENEFVALKKDVDCAYLR
KSDLEANVEALIQEIDFLRRLYEEEILILQSHI--SDTSVVVKLDNSRDL-NMDCIIAEI
KAQYDDIVTRSRAEAESWYRSKCEEMKATVIRHGETLRRTKEEINELNRMIQRLTAEVEN
AKCQNSKLEAAVAQSEQQGEAALSDARCKLAELEGALQKAKQDMACLIREYQEVMNSKLG
LDIEIATYRRLLEGE
>Human_K82
EKEQIKCLNNRFASFINKVRFLEQKNKLLETKWNFMQQQRC----CQTNIEPIFEGYISA
LRRQLDCVSGDRVRLESELCSLQAALEGYKKKYEEELSLRPCVENEFVALKKDVDTAFLM
KADLETNAEALVQEIDFLKSLYEEEICLLQSQI--SETSVIVKMDNSREL-DVDGIIAEI
KAQYDDIASRSKAEAEAWYQCRYEELRVTAGNHCDNLRNRKNEILEMNKLIQRLQQETEN
VKAQRCKLEGAIAEAEQQGEAALNDAKCKLAGLEEALQKAKQDMACLLKEYQEVMNSKLG
LDIEIATYRRLLEGE
>Human_K83
EKEQIKSLNSRFAAFIDKVRFLEQQNKLLETKLQFYQNREC----CQSNLEPLFAGYIET
LRREAECVEADSGRLASELNHVQEVLEGYKKKYEEEVALRATAENEFVALKKDVDCAYLR
KSDLEANVEALIQEIDFLRRLYEEEIRILQSHI--SDTSVVVKLDNSRDL-NMDCIVAEI
KAQYDDIATRSRAEAESWYRSKCEEMKATVIRHGETLRRTKEEINELNRMIQRLTAEVEN
AKCQNSKLEAAVAQSEQQGEAALSDARCKLAELEGALQKAKQDMACLIREYQEVMNSKLG
LDIEIATYRRLLEGE
>Human_K84
EKEQIKTLNNKFASFIDKVRFLEQQNKLLETKWSFLQEQKC----IRSNLEPLFESYITN
LRRQLEVLVSDQARLQAERNHLQDVLEGFKKKYEEEVVCRANAENEFVALKKDVDAAFMN
KSDLEANVDTLTQEIDFLKTLYMEEIQLLQSHI--SETSVIVKMDNSRDL-NLDGIIAEV
KAQYEEVARRSRADAEAWYQTKYEEMQVTAGQHCDNLRNIRNEINELTRLIQRLKAEIEH
AKAQRAKLEAAVAEAEQQGEATLSDAKCKLADLECALQQAKQDMARQLCEYQELMNAKLG
LDIEIATYRRLLEGE
>Human_K85
EKEQIKSLNSRFAAFIDKVRFLEQQNKLLETKWQFYQNQRC----CESNLEPLFSGYIET
LRREAECVEADSGRLASELNHVQEVLEGYKKKYEEEVALRATAENEFVVLKKDVDCAYLR
KSDLEANVEALVEESSFLRRLYEEEIRVLQAHI--SDTSVIVKMDNSRDL-NMDCIIAEI
KAQYDDVASRSRAEAESWYRSKCEEMKATVIRHGETLRRTKEEINELNRMIQRLTAEIEN
AKCQRAKLEAAVAEAEQQGEAALSDARCKLAELEGALQKAKQDMACLLKEYQEVMNSKLG
LDIEIATYRRLLEGE
>Human_K86
EKEQIKSLNSRFAAFIDKVRFLEQQNKLLETKLQFYQNREC----CQSNLEPLFEGYIET
LRREAECVEADSGRLASELNHVQEVLEGYKKKYEEEVSLRATAENEFVALKKDVDCAYLR
KSDLEANVEALIQEIDFLRRLYEEEIRVLQSHI--SDTSVVVKLDNSRDL-NMDCIIAEI
KAQYDDIVTRSRAEAESWYRSKCEEMKATVIRHGETLRRTKEEINELNRMIQRLTAEVEN
AKCQNSKLEAAVAQSEQQGEAALSDARCKLAELEGALQKAKQDMACLIREYQEVMNSKLG
LDIEIATYRRLLEGE
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Suppl. Fig. S13. Amino acid sequence alignment of the intermediate filament domains of type II keratins used for the phylogenetic analysis shown in Figure 4. The multiple sequence alignment is shown in fasta_aln format.

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>Frog2_K80
EEAETK-LRAALATFNDKIRYLEKQREILESRW-SMIQTEE------TTQ-TDLEPQ--Y
LSYISRLLGEVKNVTQNNHQTQRQLLDMMDSVNDMKDKFEDELFRRTDVEYSFVELKKDA
DGRSLEQTELETRKQDIKEMIDLMKTVYKQELKELM-EDS--GDISVLVNME-QSCPLNL
DKVVEEVKAQYERIASWSRDEAQALSKNKLAEGVQRVGRYELELKSSRSEITHLNSKIQR
LRSEIQSIQKQCSKLEQDVSLAQTNSNMAIVDANTKVTEIQDVLLKAKQDMAKQLRDYQE
LLHVKMALDVEIAAYNLLL-EGE
>Frog2_K7
EREQIKTLNNKFASFIDKVRFLEQQNKVLETKW-ELLQNQKS-----AKA-SNVGPL--F
DAYIANLRRQLDGLTGDKGKLEGELRNMQDLVEDFKNKYEDEINKRTSAENEFVVLKKDV
DAAYMNKVELEAKMEALTDEINFLRALYEAELRELQ-EQI--SDTSVVLSMD-NNRALDM
DSIIAEVKAQYEDIANKSRANAEAVYQNKFQELQATAGRHGDDLRTTKTEISELNRAMQR
LQAEIESVKAQRAKLEAQIAEAEERGELALKDARTKLAELEAALQKAKQDMARQLREYQE
LMNVKLALDIEIATYRKLL-EGE
>Frog2_03
EKEQIKTLNNKFASFIDKVRFLEQQNKMLETKW-AILQEQR------TAR-SHIEPL--F
EAYIGNLRRQLDCLLGEKSRLEGERKNMEDIVEDFKRKYEEEVNRRTTAENEFVVLKKDV
DAAFLHKAELQTRVESQTDEVNFLRTMFEAEIAQLQ-GQI--SDTSVIVSMD-NNRNLDL
DGIIAEVKAQYEEIANRSRAEAESWYQSKYEELRLTAGRNGDDLRNTKNEVADLNRMINR
LRGEIETVNAQRGKLEGAITEAEERGEMATKDAKKKLADLEEGLQKAKQDMARQLREYQE
LMNVKLALDIEIATYRKLL-EGE
>Frog2_04
EREQIKTLNNKFASFIDKVRFLEQQNKVLETKW-NLLQEQGVK----SVK-CNIDPL--F
EAYISALRRQLDSLLSEKVRLDSDLRQMQDAVEDYKKKYEDEINKRTSVENEFVVLKKDV
DAAYMNKVELEAKLNALTDEINFLRAVYEAEIAQMQ-TQI--SDTSVVLSMD-NNRTLDL
NGIIAEVKAQYEDIANRSRAEAESWYQTKYEELQQSAGRHGDDLRSTKTEISELNRMINR
LRSEIDSVKKQCAKLQAAITEAEERGELALKDAKKKLADLEEALQKCKQEMARQLREYQE
LMNVKLSLDVEIATYRKLL-EGE
>Frog2_05
EREQIKTLNNKFASFIDKVRFLEQQNKVLETKW-SLLQEQGGQVKG-SRK-NNIDPI--F
DAYINSLKRQLDALQNDKLRLDGELRNMQDLVDDFKNKYEDEINKRTSAENEFVVIKKDV
DAAYMGKVELEAKVDALTDELNFLRTFFEAELGELQ-AQI--SDTSVVLSMD-NNRALDL
ESIIAEVKSQYEDIAKKSRAEAESVYQGKVQELQASAGEQGDVLRNTKSEISELNRKSQR
LKAEIENVKKQIAKLQASITEAEERGDLVLKDAQSKLAELEAALQKVKQDMARQLREYQE
LMNVKLALDVEIATYRKLL-EGE
>Frog2_06
EREKIKLLNNKFASFIDKVRFLEQQNKVLETKW-SLLQKQQVS----KSRSSEIESI--F
NTLITSLRSQLDSLVKDKGLLGGELQVMKDHAENFKNKFELEFKKRTADENDFVSLKKDV
DATYLIQVQLETKQKALDDELAFLRNLYKEELDGIK-QQT--AGTSVVLSMD-NSRMLDL
GDIIADVKAQYEDTTRRSKEEAEAAYQSKYQQLQLAAGQQGEDLKSSKKEISEVNRSVQK
LRNEIESVKKQIASLQVSIQDSERRGDIALRDAQEKLVNLERALQKAKQEMAQQLREYQT
LLNVKLALDVEIATYRKLL-EGE
>Frog2_07
EREQIKTLNNKFASFIDKTRFLEQQNQVLKTKW-ELLQEHGQKGV--TKR-SNIVPL--F
EAYISNLRRSLDSLLNDKHRLESDLRSTQDLVEDYKNKYEDEINKRTTAENEFVVLKKDV
DGAYMNKVELDCKVDALTDEINFLRTLYEAEVQDLQ-GQL--SDISVVLSMD-NNRALDL
DGIIAEVKCQYEEIANKSKAEAEAACAMKFQQLQATAGQHGDSLKSSKTEIADLNRMIQR
LKAEIESVKKQCANLQTSITEAEERGELAVKDAQKKLDELQEALRKAKEEMAKQLHDYQR
LMSIKLALDIEIATYKKLL-EGE
>Frog2_08
ERDQIKGLNNKFAGFIDKVRFLEQQNQILGTKW-NFLQEKSQKLC--SRR-DTIKPL--F
DAYITNLQRQLEGLRSEKCRLDGELKNMQDVVEEFKSKYEEEINKRTCTENEFVALKKDV
DILYMKKAELEAKEESLGNEINFLRNIFDAELAELQ-DCL--SDINVVLSMD-NNRDLDL
NGLIAECKAQYEEIAARSKTEAEAAYSKKFQQLKEAAGQHGDNLRSSKTEIQDLNTMIKR
LQSEIECVKKQIAGLQAAICDAESRGEATLKDANCKMSELEAVLQKAKEDLAIQLREYQE
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>Frog2_09
ERDQIKCLNNKFASFIDKVRFLEQQNQILGTKW-NFLQDKSQKLC--SRR-DTIKPL--F
DAYITNLQRQLEGLRSEKCRLDGELKNMQDVVEEFKCKYEEEINKRTCAENQFVGLKKDV
DVLYMKKAELEAKEETLANEISFLRSLFDAELAELQ-DCL--SDINVVLCMD-NNRELDL
NGLIAECKAQYEEIAARSKTEAEAAYARKFQQLKETAGLHGDNLKSSKTEIQDLNTMIKR
LQSEIECVRKQIAGLQAAICDAESRGEATLKDARCKMSELEAVLQKAKEDLAIQLKEYQE
LLRVKLALDVEIATYRTLL-EGE
>Frog2_10
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EKYIGDLNKYLSTLINEKGSLEHELKNLQGFVEDYKKKYEEEINKRTKAENDFVVVKKGV
DTAYMANRELEAKADGVTSEINFLKTLYAAELSQVH-DSV--TNTSVVLTMD-NNRDLNL
EGIIQEVKAQLELSAQRSKMEAEALYDNKYKELQRTAEGHGDSIKNSKSEIAELNRRIQR
LKAEIESTKKQIAGLNQSIAGAEEKGNLALKDAEKKIQDLEAAEKKLKEDMARQLKEYQE
LLAAKISLDVEISTYGLML-GGE
>Frog2_11
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EKYIGDLRRYLDTLINERGRLEHELKNQQDLVEEYKKKYEDEINKRTKAENDFVLLKKDV
DAAFMAKTDLEARVDGLTSEINFLRTLYAAELSQVH-EQV--TDTSVILTMD-NNRDLNL
SGIIQEVKCQYEQIAQRSKMEAEALYDNKYKELQKTVEGHGHSIKNSKAEIAELNRNIQR
LRAEIENLKKQIAGLNQSIAGAEEKGNLALKDAEKKLHDLEAAEKKLKEDMARQLKEYQE
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>Frog2_12
EREQIKTLNNKFAAYIDKVRFLEQQNKVLETKW-KLLQEQGTKGS--TKR-ASLEPL--F
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LLAAKISLDVEISTYGLML-GGE
>Frog2_13
EREQIKTLNNKFAAYIDKVRFLEQQNKVLETKW-KLLQEQGTKGS--TKR-ANLEPL--F
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DTVYMAKTELEAKVDAVTSEINFLRTLYAAELSQVH-DTV--TDTSVVLTMD-NNRDLNL
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>Frog_K8
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DEAYMNKVQLEARLEALTDEINFLRQLYEEELRELQ-SQI--SDTSVVLSMD-NNRSLDL
DGIIAEVRAQYEDIANKSRLEVESMYQVKYQELQASAGRHGDDLKNTKAEISELTRYTTR
LQSEIDALKAQRSNLEAQIAEAEERGELALKDARTKLAELEAALKNAKQDMARQLREYQE
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>Chicken_K80
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DASTLHRTELEVKLSGLQELMDLKKTIYEQELEELL-TEI--KDISVVLGID-NTCKLDL
SRIVEEVRAQYEALALRSWEEAEALTRRKLNEGNTQSATYGGHLLDSRREIADLNIQIQK
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DSIIAEVKAQYEDIANRSRAEAESWYQSKFEALQVTAGKHGDDLRNTKNEITEINRVIQR
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>Chicken_K84L
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ECFFLNKAELGAKVGRMEGEFGFLRVLYEEESQQLR-AHI--SDTAVVVQMD-NSWDPNL
DGIVANVKAHYEDTACRSRAETEAWCKGKFKELQVTAGRNADSLQEKKREAAELARMVKK
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>Chicken_K5L3
EKEQIQTLNNKFASFIDKVRFLEQENKVLETKW-ALLQEQGHK----TVR-NNIEPL--F
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DSTYMTKTELQARLDALLEEIDFLRALYEAELSQLQ-SQI--ADTSVILTMD-NNRSLDM
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>Chicken_K5L2
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DASYMNKVELQAKADALTEEINFLRALYEAELSQMQ-TQI--SDTSVVLTMD-NNRNLDL
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>Chicken_K5L1
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DGAYMNKVELQAKADGLADEINFLRALYEAELSQMQ-QQV--SDTSVVLSMD-NNRSLDL
NSIIAEVKAQYEDIANRSRAEAEAWYQNKYEELQVSAGRHGDDLRNTKMEISEINRMVQR
LRNEIESVKKQCANLQAAIAEAEERGEMALKDAKSKLAELEDALQKAKADLARQLREYQE
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>Chicken_HBS1
EKEQIKNLNNQFACFIDKVRLLEQQNKVLTTKW-ELLQQYVLP----ASR-RNLEPV--F
ENFICNLRKQLECVLGERERLENEERCLRDLVQEYKCKYEDEINKRTAAENEFVVLKKDV
DCLYLTKEELEVRVGLLRQQLEFLKCIYAEERAQMD-CQL--CDTSVIVQMD-NSRDLDM
EGIIKSVECCYEEIAQKSKAEVEAFYQTRLEELHSSRGKFCDDLRNNQSEIAELNRMIQK
LQCESDNVKKQIAALQTAICDAEQRGDCALKDARQKLVDLQTALQQAKDKMACLLRDYQE
LLNVKLALDIEIATYRTLL-EGE
>Chicken_HBS2
EKEQIKTLNTQFACFIDKVRFLEQQNKVLETKW-GLLQQYVLP----KKG-KNLELY--F
ENYICDLRKRLDCLLCEKQKLGNEECATSQLVEEFKCKYEEEINRRTTVENEFVALKKDA
DCIFLNKEELEVKVDLLRRQLELLKCVFEEERAQVD-RQL--CDTSVIVKMD-NNRDLDM
ESIIKNVECWYQEIAQKSKEEVDAFYQTRFQELQDKRGKYCDDLQSNKCEISELTRMIQK
LQCELENVKKQVSCLQTSICDVEQRGDCALKDAREKHVELQNALQKAKDELACMLRDYQE
LLNVKLALDIEIATYKTLL-EGE
>Chicken_HBS3
EREQMRSLNNQFACLIDKVQHLEQQNRLLATKW-AFLQKHIL-----PSQ-KNFKHV--F
NTFICSLQRRLDSLLHERGQMELELNNTEKLIEDLKCKYEQEVNRCTAAENEFVLLKKDA
DCVYLTKAELEAKLETLKQQIELLKCMSAQGTAEME-KSL--CDTSVVVKMD-NSRSLDM
EGILRGIELWYEDVAQKSKAELDALYRTRYQELEETKRKQCSELKSHQQEIEELSFVMQR
WQCDLENVKKRVSSLRTSVSDTEQRGDRALKDAREKHLELQNALQKAKDELACMLRDYQE
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>Chicken_K78LT
EKEQIKTLNSNFASFIDKVQCLERQNQALMTKW-ELLQQQSSRP---EES-RSITSF--F
QSYINNLQRQLDMLQSQKEQLDPEAYEMLQLVEDYKKRFEDEINKRASKEEEYVELKKEL
DSTYMRKMEFEVRVEILKQELEFLRCLYEAELSQLQ-TVV--DNTNVILSMD-NGREVNM
DGIIEEVRQEYEKIAQKGKDEVNAMYQGRYQDLQNMRVNQREQLRYTYQEIQELTRQIQR
LQPEIEIVRRENDSRQEAIRDAEQRGSSAVKDGQKKLQELENALQQAREDLARILHDYQE
LLNAKLSLDVEIAMYRSLL-EEE
>Chicken_K78L4
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>Chicken_K8
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DAAYMNKVELEAKVDALMDEINFMKMFFDAELSQMQ-THV--SDTSVVLSMD-NNRNLDL
DSIIAEVKAQYEEIANRSRTEAESWYQTKYEELQQTAGRHGDDLRNTKHEISEMNRMIQR
LRAEIDNVKKQCANLQNAIADAEQRGELALKDARNKLAELEEALQKAKQDMARLLREYQE
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>Human_K6B
EREQIKTLNNKFASFIDKVRFLEQQNKVLDTKW-TLLQEQGTK----TVR-QNLEPL--F
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DAAYMNKVELQAKADTLTDEINFLRALYDAELSQMQ-THI--SDTSVVLSMD-NNRNLDL
DSIIAEVKAQYEEIAQRSRAEAESWYQTKYEELQITAGRHGDDLRNTKQEIAEINRMIQR
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DAAYMNKVELQAKADTLTDEINFLRALYDAELSQMQ-THI--SDTSVVLSMD-NNRNLDL
DSIIAEVKAQYEEIAQRSRAEAESWYQTKYEELQVTAGRHGDDLRNTKQEIAEINRMIQR
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>Human_K6A
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DAAYMNKVELQAKADTLTDEINFLRALYDAELSQMQ-THI--SDTSVVLSMD-NNRNLDL
DSIIAEVKAQYEEIAQRSRAEAESWYQTKYEELQVTAGRHGDDLRNTKQEIAEINRMIQR
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LMNVKLALDVEIATYRKLL-EGE
>Human_K7
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DAAYMSKVELEAKVDALNDEINFLRTLNETELTELQ-SQI--SDTSVVLSMD-NSRSLDL
DGIIAEVKAQYEEMAKCSRAEAEAWYQTKFETLQAQAGKHGDDLRNTRNEISEMNRAIQR
LQAEIDNIKNQRAKLEAAIAEAEERGELALKDARAKQEELEAALQRGKQDMARQLREYQE
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>Human_K8
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DEAYMNKVELESRLEGLTDEINFLRQLYEEEIRELQ-SQI--SDTSVVLSMD-NSRSLDM
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>Human_K71
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>Human_K72
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DAAYMNKVELQAKVDSLTDEIKFFKCLYEGEITQIQ-SHI--SDTSIVLSMD-NNRDLDL
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>Human_K73
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>Human_K74
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>Human_K75
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>Human_K76
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>Human_K77
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>Human_K78
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>Human_K79
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DAAYMGRMDLHGKVGTLTQEIDFLQQLYEMELSQVQ-THV--SNTNVVLSMD-NNRNLDL
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>Human_K80
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SGIVEEVKAQYDAVAARSLEEAEAYSRSQLEEQAARSAEYGSSLQSSRSEIADLNVRIQK
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>Human_K81
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DCIIAEIKAQYDDIVTRSRAEAESWYRSKCEEMKATVIRHGETLRRTKEEINELNRMIQR
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DCIVAEIKAQYDDIATRSRAEAESWYRSKCEEMKATVIRHGETLRRTKEEINELNRMIQR
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>Human_K84
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>Human_K85
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>Frog1_K18
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>Frog1_02 13C
----MQNLNDRLAAYLNKVRALEEANSDLECKIREWYEKHRNAC---MPD-RDYSKY--Y
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DDLTLSRAELEGQLESLTEELAYLKKNHDDEVRSIKVTEA----GKVSVEMN-AAPSNDL
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LLEMKTKLEGEIATYRSLL-D--
>Frog1_04
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LLEMKTKLENEIKTYQSLL-D--
>Frog1_05
-XXXMQNLNDRLANYLDKVNALEAANAELERKIKEWYDKQPTTS---DGG-KDYSKY--Y
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>Frog1_06
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>Frog1_07
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>Frog1_08
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>Frog1_09
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>Frog1_10
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>Frog1_14
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>Frog1_16
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RT-IEELQNKILHACTGNANLILQIDNARLTSDDFRNKFESEAAFRMGVEGDMNGLRRVL
EELNLGNNDQEIQRQNLSEELTYLKKNHAEEVGSLR-TQL---GARVNVEVN-AAPAVDL
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Suppl. Fig. S14. Amino acid sequence alignment of the intermediate filament domains of keratins (type I and type II combined) used for the phylogenetic analysis shown in Supplementary Figure S5. The multiple sequence alignment is shown in fasta_aln format.