Supplementary Information

Exome sequencing of serous endometrial tumors identifies recurrent somatic

mutations in chromatin-remodeling and ubiquitin ligase complex genes

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Supplementary Note

NIH Intramural Sequencing Center (NISC)

Contributions from NISC were made by Betty Benjamin, Robert Blakesley, Gerry Bouffard, Shelise Brooks, Holly Coleman, Mila Dekhtyar, Michael Gregory, Xiaobin Guan, Jyoti Gupta, Joel Han, April Hargrove, Shi-ling Ho, Taccara Johnson, Richelle Legaspi, Sean Lovett, Quino Maduro, Cathy Masiello, Baishali Maskeri, Jenny McDowell, Casandra Montemayor, James Mullikin, Betsy Novotny, Morgan Park, Nancy Riebow, Karen Schandler, Brian Schmidt, Christina Sison, Mal Stantripop, James Thomas, Meg Vemulapalli, and Alice Young.

Clinical data

A determination was made by the NIH Office for Human Subjects Research Protections (OHSRP) that this research was not "human subjects research" per the Common Rule (45 CFR 46).

Genotype and variant calling

The MPG ("Most Probable Genotype") genotype caller takes as its input a set of sequence reads aligned to an orthologous reference sequence. These sequence reads are assumed to be (1) correctly aligned to the reference, and (2) derived from one or two copies of a modified reference sequence, as would be the case in re-sequencing reads from non-repetitive regions of a diploid individual. In addition, if base quality estimates are provided, these are assumed to be accurate reflections of the probability that the read sequence actually represents the sample. The MPG algorithm is implemented in a perl

script called "bam2mpg", which reads BAM formatted files, and outputs predicted genotypes and scores at all regions of the genome covered by at least one read.

Any variation between a set of aligned sequence reads and the reference sequence can be specified by its flanking reference coordinates and a list of all of the observed sequences between them (which we will refer to as "alleles"). For example, a single nucleotide variant (SNV) can be specified by giving the coordinates to the left and right of the changed base, and all possible bases at that location (e.g., hg18 chr1:16,901,843-16,901,845, T/C). A deletion-insertion variant (DIV) can also be specified by giving the coordinates of the outer boundaries of the feature, with a list of all possible sequences seen between those two boundaries (e.g., hg18 chr1:145,232,693-145,232,694, -/AT represents an insertion of the sequence "AT" between the two coordinates listed). For variants predicted by MPG, the reference sequence is always included in the list of possible alleles.

As a simplification, we can assume that the read bases seen in a resequencing experiment are independently sequenced with equal probability from each of two chromosomes (in the case of autosomes, or one in cases where only one chromosome is present), and are then chosen from a random distribution in which sequencing errors occur with a total probability e_k . Given a group of aligned sequence reads at a variant site, we can calculate the posterior probability of all possible genotypes at that position using Bayes theorem. For a simple variant with only two possible alleles (the reference and a variant sequence), the genotypes considered are homozygous reference, heterozygous, and homozygous non-reference. If we denote the posterior probability of one of M possible genotypes G_i , given N observed read sequences $A_1, ..., A_N$ as $P(G_i | A_1, ..., A_N)$, the likelihood of observing $A_1, ..., A_N$ as $P(A_1, ..., A_N | G_i)$, and the prior probability of a site having the genotype G_i as $P(G_i)$, then the desired posterior probabilities of the different genotypes can be calculated using the equation

$$P(G_i|A_1,...,A_N) = \frac{P(A_1,...,A_N|G_i)P(G_i)}{\sum_{j=1}^{M} P(A_1,...,A_N|G_j)P(G_j)}$$

where

$$P(A_1,\ldots,A_N|G_j) = \prod_{k=1}^N P(A_k|G_j)$$

and

$$P(A_k | G_j) = (1 - e_k) \left(\frac{1}{2} \left(\delta_{G_{j,1},A_k} + \delta_{G_{j,2},A_k} \right) \right) + e_k \left(\frac{1}{2} \left((1 - \delta_{G_{j,1},A_k}) + (1 - \delta_{G_{j,2},A_k}) \right) \right).$$

The calculation is simplified by noting that for any two possible genor

The calculation is simplified by noting that for any two possible genotypes, $\begin{pmatrix} P(G | A = A) \end{pmatrix} = \frac{N}{N} f_{A} (f_{A} = f_{A}) \begin{pmatrix} (G = A) \end{pmatrix} = \begin{pmatrix} (G = A) \end{pmatrix} =$

$$\log\left(\frac{P(G_i|A_1,\ldots,A_N)}{P(G_j|A_1,\ldots,A_N)}\right) = \sum_{k=1} \left\{\log\left(P(A_k|G_i)\right) - \log\left(P(A_k|G_j)\right)\right\} + \log\left(P\left(\frac{G_i}{G_j}\right)\right).$$

The last term in this last equation is the log of the ratio of the prior probabilities, and is assumed by MPG to be the same for all non-reference genotypes compared to the reference (and 0 for all other combinations of genotypes). This value can be passed as a parameter to bam2mpg, and its default value is 3, corresponding to a reference genotype that is expected to be 1000 times more probable than any non-reference genotype.

Once the most probable genotype is determined, it is reported by bam2mpg, along with its "MPG score", which is the value of $\log(P(G_i|A)/P(G_j|A))$ when G_i is the most probable genotype and G_j is the second most probable genotype. We have found empirically that when calculated from well-aligned Illumina reads, genotypes with MPG scores of 10 or greater agree with Infineum genotypes about 99.8% of the time.

The "MPV", or "Most Probable Variant", score is an alternative scoring method which scores a site's genotype call as the log ratio of posterior probabilities of the most probable genotype compared to the homozygous reference genotype (as opposed to the second most probable genotype, as above). This assesses the probability that any variant is present, and is more suitable when variant detection, rather than exact genotype prediction, is the goal. Supplementary Figure 1 Number of somatic variants called by exome sequencing of 13 serous endometrial tumors in a mutation discovery screen

Supplementary Figure 2 Distribution of 1,544 exonic and splice junction somatic mutations identified by exome sequencing of 13 primary serous endometrial tumors

Supplementary Figure 3 Sequence chromatograms showing somatic mutations in *CHD4*, identified in primary endometrial cancers

Supplementary Figure 4 Somatic mutations in *MAP3K4*, *ABCC9*, and *CYP4X1* in serous endometrial cancers

Supplementary Figure 5 Distribution of somatic mutations in *CHD4*, *FBXW7*, and *SPOP* relative to the microsatellite instability and *MSH6* mutation status

Supplementary Figure 6 CHD4 expression in endometrial cancer cell lines

Supplementary Figure 7 Cross-species conservation of CHD4

Supplementary Figure 8 Alignment of CHD4 and closely related family members

Supplementary Figure 9 Partial, structure-based, sequence alignment of the ATPase/helicase and helicase domains of CHD4 to the Snf2 domains of SMARCA2, SMARCAL1, and SMARCA4

Supplementary Figure 10 Distribution of somatic variants called by whole exome sequencing according to score and coverage

Supplementary Table 2 Depth of whole exome sequencing coverage

Supplementary Table 3 Exonic somatic mutation rate of the 13 serous endometrial tumors included in the exome discovery screen

Supplementary Table 6 Distribution of somatic variants called by whole exome sequencing among 12 tumors in the discovery screen Supplementary Table 7 Nine genes with validated mutations in more than one tumor in the discovery screen

Supplementary Table 8 Frequency of *TP53*, PIK3CA, and PPP2R1A among serous endometrial tumors

Supplementary Table 9 Overall frequency of somatic mutations in combined discovery and prevalence screens of *CHD4*, *SPOP*, *FBXW7*, *ABCC9*, *CYP4X1*, *MAP3K4*, *TP53*, *PIK3CA* and *PPP2R1A*

Supplementary Table 10 Mutation rate of individual genes in 52 serous tumors, compared to the background mutation rate for serous endometrial cancers

Supplementary Table 12 MSI status and *MSH6* status of tumors with *CHD4*, *FBXW7*, and *SPOP* mutations

Supplementary Table 14 Networks identified by Ingenuity Pathway Analysis

Supplementary Table 15 Estimated power to detect somatically mutated genes in a discovery screen of 12 tumors



Supplementary Figure 1. Number of somatic variants called by exome sequencing of 13 serous endometrial tumors in a mutation discovery screen. After filtering on coverage and score, there were 1,522 exonic (nonsynonymous and synonymous) somatic variants and 22 somatic splice junction variants among 13 tumors. One tumor (T155) appeared to be hypermutated.



Supplementary Figure 2. Distribution of 1,544 exonic and splice junction somatic mutations identified by exome sequencing of 13 primary serous endometrial tumors. (a) Number of nonsynonymous mutations (dark orange), synonymous mutations (light orange), and splice junction mutations (black) in each tumor. T155 (red) is hypermutated, relative to the other 12 tumors. (b) Mutation signatures of the 12 non-hypermutated tumors, and (c) Mutation signature of T155, a hypermutated tumor. The percentage of mutations that were insertions-deletions (in-dels), transitions, or transversions is displayed. The percentage of nucleotide substitutions that occurred within the context of a CpG dinucleotide, relative to all exonic/splice junction mutations, is indicated.



Supplementary Figure 3. Sequence chromatograms showing somatic mutations in *CHD4*, identified in primary endometrial cancers. Mutated nucleotide positions in the tumor (T) DNA are indicated by arrows. Nucleotide sequences of the matched normal (N) DNAs are shown for reference.



Supplementary Figure 4. Somatic mutations in MAP3K4, ABCC9, and CYP4X1 in serous endometrial cancers. Schematic representation of the MAP3K4, ABCC9, and CYP4X1 proteins showing the relative positions of individual somatic mutations identified among primary serous endometrial tumors.



Supplementary Figure 5. Oncoprints displaying the distribution of somatic mutations in *CHD4*, *FBXW7*, and *SPOP* relative to the microsatellite instability (MSI) status, and the mutational status of *MSH6*, among (a) serous, (b) clear cell, (c) endometrioid, and (d) mixed histology endometrial tumors. Each blue bar represents an individual tumor (T). Nonsynonymous somatic mutations and MSI are indicated by the red bars. Only tumors that had somatically mutated *CHD4*, *FBXW7*, or *SPOP* are displayed.



Supplementary Figure 6. CHD4 is endogenously expressed in endometrial cancer cell lines. Western blots showing CHD4 levels (top) and actin levels (bottom).

Α		Lys72Argfs*128
	22	
CHD4_Human CHD4_Chimp	22	ALLNNSLPPPHPENEEDPEEDLSETETPKLKKKKKKKKFKKP-RDPKIPKSKRQKKERMLLCRQLGDSSGEGPEFVEEEEEVALRSDSEGSDTTPGKKKKKKLGPKKEK 126 LKRDHSLPPPHPENEEDPEEDLSETETPKLKKKKKKKKPKP-RDPKIPKSKRQKKELGDSSGEGPEFVEEEEEVALRSDSEGSDTTPGKKKKKKLGPKKEK 119
CHD4_Rhesus	22	ALLNNSLPPPHPENEEDPEEDLSETETPKLKKKKKPKKP-RDPKIPKSKROKKERMLLCROLGDSSGEGPEFVEEEEEVALRSDSEGSDYTPGKKKKKKLGPKKEK 126
CHD4_Dog CHD4 isol Rat	22	ALLNNSLPPPHPENEEDDEEDDSEAETPALKKKKKKKKFKP-KDPKIPKSKKQKKERMLLCKQLGDSSGEGPEFVEEEEEVALKSDSEGSDTTPGKKKKKKLGPKKEK 126 ALLNNSLPPPHPENEDDPEEDDSEAETPKLKKKKKKKKKPKKP-RDPKIPKSKRQKKERLLLCRQLGDSSGEGPEFVEEDEEAALRSDSEGSDTTPGKKKKKKLGPKKEK 126
CHD4_iso2_Rat	22	ALLNNSLPPPHPENEDDPEEDLSEAETPKLKKKKKKKKPKKP-RDPKIPKSKROKKERLLLCROLGDSSGEGPEFVEEDEEAALRSDSEGSDYTPGKKKKKKLGPKKEK 126
CHD4_Mouse CHD4_Cow	22	ALLNNSLPPPHPENEEDPDEDLSEAETPALKKKKKKFKKP-KDPKIPKSKKQKKELGDSSGEGPEFVEEEEEVALKSDSEGSDTTPGKKKKKKLGPKKEK 119 ALLNNSLPPPHPENEEDPEEDLSEAETPKLKKKKKKKKPKKP-RDPKIPKSKRQKKERLLLCRQLGDSSGEGPEFVEEEEEVALKSDSEGSDTTPGKKKKKKLGPKKEK 126
CHD4_Xenopus	18	VMLNSSIHQDDDDLDEDLSEVEAPKIKKKKKKKKKA-KESKATKVKRQKKEEIDDSSGEGNDYGDDDG-GPIRSDSEGSDYTPGKKKKKKLAQKREK 111
let-418_C.elegans	; 01	DFEHRSVMQEEDDLEEELSENDAPKVKKKKKKKKKSKESKGSKRNKSKREEIGISSPEPGEGPDLDDGEEDRSESEGSDITPGRKKKKKASTAKDK 105 GSVTQDATEETEEEEEQEQGDEAGPSERKRSSRKKGGKGGKKGS 62
		-
В		Val558Phe Arg572Gln
		** :* : * **:*****: :** :*****: :*: **:* ::::: * * ** *
CHD4_Human CHD4 Chimp	518 431	PVPRPPDADPNTPSPKPLEGRPERQFFVKWQGMSYWHCSWVSELQLELHCQVMFRNYQRKNDMDEPPSGDFGGDEEKSRKRKNKDPKFA 606 PVPRPPDADPNTPSPKPLEGRPEROFFVKWOGMSYWHCSWVSELOLELHCOVMFRNYORKNDMDEPPSGDFGGDEEKSRKRKNKDPKFA 519
CHD4_Rhesus	518	PVPRPPDADPNTPSPKPLEGRPEROFFVKWQGMSYWHCSWVSELQLELHCOVMFRNYQRKNDMDEPPSGDFGGDEEKSRKRKNKDPKFA 606
CHD4_Dog CHD4 iso1 Rat	518 518	PVPRPPDADPNTPSPKPLEGRPERQFFVKWQGMSYWHCSWVSELQLELHCQVMFRNYQRKNDMDEPPSGDFGGDEEKSRKRKNKDPKFA 606 PVPRPPDADPNTPSPKPLEGRPEROFFVKWOGMSYWHCSWVSELOLELHCOVMFRNYORKNDMDEPPSGDFGGDEEKSRKRKNKDPKFA 606
CHD4_iso2_Rat	518	PVPRPPDADPNTPSPKPLEGRPEROFFVKWOGMSYWHCSWVSELOLELHCOVMFRNYORKNDMDEPPSGDFGGDEEKSRKRKNKDPKFA 606
CHD4_Mouse CHD4 Cow	509 519	PVPRPPDADPNTPSPKPLEGRPERQFFVKWQGMSYWHCSWVSELQLELHCQVMFRNYQRKNDMDEPPSGDFGGDEEKSRKRKNKDPKFA 599 PVPRPPDADPNTPSPKPLEGRPEROFFVKWOGMSYWHCSWVSELOLELHCOVMFRNYORKNDMDEPPSGDFGGDEEKSRKRKNKDPKFA 606
CHD4_Xenopus	507	PVPRPADADPEAPPPKPLEGRPEREFFVKWQAMSYLHCSWVTELQLELHCQVMFRNYQRKNDMDEPPAGDYGGDD-EEKSRKRKNKDPKYL 596
CHD4_Zebrafish let-418 C.elegans	500 387	PVPRPSDLPTDAPDPTPLAGRPEREFFVKWQNMSYWHCSWVTELQLEIHCQVMFRNYQRKNDMDEPPPIDFGGEGEEEKSDKRKKKDPTYA 590 PLEAGKEASSDDAMLKPPRKMEPRREREFFVKWKYLSYWOCSWVSEMLLEVHFRMLTLLYWRKNDSDAPPEFEESVTSRHHSDNDPY 479
C		Arg817Gln del874Glu_Arg877Trp Leu912Val
		******** ****** ***** *.**** *.********
CHD4_Human CHD4 Chimp	801 714	MYVVTYVGDKDSRAIIRENEFSFEDNAIRGGKKASRMKKEASVKFHVLLTSYELITIDMAILGSIDWACLIVDERHRLKNNOSKFFRVLNGYSLOHKLLLTGTPLQNNLEELFHLLNFLTPE 922 MYVVTYVGDKDSRAIIRENEFSFEDNAIRGGKKASRMKKEASVKFHVLLTSYELITIDMAILGSIDWACLIVDEAHRLKNNOSKFFRVLNGYSLOHKLLLTGTPLONNLEELFHLLNFLTPE 835
CHD4_Rhesus	801	MYVVTYVGDKDSRAII <mark>R</mark> ENEFSFEDNAIRGGKKASRMKKEASVKFHVLLTSYELITIDMAILGSIDWACLIVD <mark>EAHR</mark> LKNNQSKFFRVLNGYSLQHKLLLTGTPLQNNLEELFHLLNFLTPE 922
CHD4_Dog CHD4 isol Rat	801 801	MYVVTYVGDKDSRAIIRENEFSFEDNAIRGGKKASRMKKEASVKFHVLLTSYELITIDMAILGSIDWACLIVDEAHRLKNNOSKFFRVLNGYSLOHKLLLTGTPLQNNLEELFHLLNFLTPE 922 MYVVTYVGDKDSRAIIRENEFSFEDNAIRGGKKASRMKKEASVKFHVLLTSYELITIDMAILGSIDWACLIVDEAHRLKNNOSKFFRVLNGYSLOHKLLLTGTPLONNLEELFHLLNFLTPE 922
CHD4_iso2_Rat	801	MYVVTYVGDKDSRAIIRENEFSFEDNAIRGGKKASRMKKEASVKFHVLLTSYELITIDMAILGSIDWACLIVDEAHRLKNNQSKFFRVLNGYSLQHKLLLTGTPLQNNLEELFHLLNFLTPE 922
CHD4_Mouse CHD4 Cow	794 801	MYVVTYVGDKDSRAIIRENEFSFEDNAIRGGKKASRMKKEASVKFHVLLTSYELITIDMAILGSIDWACLIVDEAHRLKNNQSKFFRVLNGYSLQHKLLLTGTPLQNNLEELFHLLNFLTPE 915 MYVVTYVGDKDSRAIIRENEFSFEDNAIRGGKKASRMKKEASVKFHVLLTSYELITIDMAILGSIDWACLIVDEAHRLKNNOSKFFRVLNGYSLOHKLLLTGTPLONNLEELFHLLNFLTPE 922
CHD4_Xenopus	791	MYVVTYVGDKDSRAVIRENEFSFEDNAIRGGKKASRMKKEASVKFHVLLTSYELITIDMAILGSIDWACLVVDEAHRLKNNQSKFFRVLNGYSLQHKLLLTGTPLQNNLEELFHLLNFLTPE 912
CHD4_Zebrafish let-418 C.elegans	786	MYVVTYVGDKDSRAVIRENEFSFENNAIRGGKKPSKMKKEASVKFHVLLTSYELITIDTAVLGSIDWACLVVDEAHRLKNNQSKFFRILNNYPLQHKLLLTGTPLQNNLEELFHLLNFLTPE 907 FYVVTYVGLRDARVULREHEFSFVEGAVRSGPKASKMKTTENMKFHVLLTSYETINMDKTILSSIEWGALVVDEAHRLKNNOSLFFKNLNEYTHYRVLLTGTPLONNLEELFHLLNFLSKE 798
		His1151Arg Arg1162Gln,
П		Arg1105Gln del1152Asn Arg1162Trp Leu1215Pro
D		*.* * ****:***** ** *******************
CHD4_Human CHD4_Chimp	1098	GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222 GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1135
CHD4_Rhesus	1098	GGITGMARQEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDMARDDQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222
CHD4_Dog CHD4_iso1_Bat	1098 1098	GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222 GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222
CHD4_iso2_Rat	1098	GITGIN ROEAIDRFNAPGAQOFCFLLSTRAGGLGINLATADTVIIYDSDWNFHNDIQAFSRAHR GQNKKVMIYRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKOELDDILKFG 1222
CHD4 Mouse		
CHD4 Cow	1091	GGITGNMRQEAIDRFNAPGAQOFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1215 GGITGNMRQEAIDRFNAPGAQOFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGONKKVMIYRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKOFLDDILKFG 1222
CHD4_Cow CHD4_Xenopus	1091 1098 1088	GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1215 GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222 GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVVIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1212
CHD4_Cow CHD4_Xenopus CHD4_Zebrafish let-418_C.elegans	1091 1098 1088 1083 5 974	GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1215 GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222 GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1212 GGITGGMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1212 GGITGGMRDEAIDRFNAPGAQQFVFLLSTRAGGLGINLATADTVIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1217 GSIMQQMRDEAIDRFNAPGAQQFVFLLSTRAGGLGINLATADTVIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMLNHLVNRAGLGGKETG SSIMQQMRDEAIDRFNAPGAQQFVFLLSTRAGGLGINLATADTVIYDSDWNPHNDIQAFSRAHRIGQNKVMIYRFVTRASVEERITQVAKKKMLLNHLVVRGLGSKTG-SMSKQELDDILKFG 1207
CHD4_Cow CHD4_Xenopus CHD4_Zebrafish let-418_C.elegans	1091 1098 1088 1083 5 974	GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1215 GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222 GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVVIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222 GGITGMRDEAIDRFNAPGAPQFVFLLSTRAGGLGINLATADTVVIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1227 GSITGMRDEAIDRFNAPGAPQFVFLLSTRAGGLGINLATADTVVIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSIMGQMRDDAIDRYNAPGAQQFIFLLSTRAGGLGINLATADTVVIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTKASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1207
CHD4_Cow CHD4_Xenopus CHD4_Zebrafish let-418_C.elegans	1091 1098 1088 1083 ; 974	GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIVDSDWNPHNDIQAFSRAHRIGQNKKVMIVRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1215 GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIVDSDWNPHNDIQAFSRAHRIGQNKKVMIVRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222 GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIVDSDWNPHNDIQAFSRAHRIGQNKKVMIVRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1220 GGITGMRQEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVVIVDSDWNPHNDIQAFSRAHRIGQNKKVMIVRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSITGMRQEAIDRFNAPGAQQFIFLLSTRAGGLGINLATADTVVIVDSDWNPHNDIQAFSRAHRIGQNKKVMIVRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSIMGQMRDDAIDRFNAPGAQQFIFLLSTRAGGLGINLATADTVVIVDSDWNPHNDIQAFSRAHRIGQNKKVMIVRFVTKKSVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSIMGQMRDDAIDRYNAPGAQQFIFLLSTRAGGLGINLATADTVIIVDSDWNPHNDIQAFSRAHRIGQNKKVMIVRFVTKKSVEERITSVAKKKMLLHLVVRAGLGGKEGKTMSKTELDDVLRWG 1099
CHD4_Cow CHD4_Xenopus CHD4_Zebrafish let-418_C.elegans E	1091 1098 1088 1083 ; 974	GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRLGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1215 GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRLGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222 GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRLGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222 GGITGMRQEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRLGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1220 GGITGMRQEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRLGQNKKVMIYRFVTKASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSIMGQMRQDAIDRYNAPGAQQFIFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRLGQNKKVMIYRFVTKKSVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSIMGQMRQDAIDRYNAPGAQQFIFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRLGQNKKVMIYRFVTKKSVEERITSVAKKKMLLHLVVRAGLGGKEGKTMSKTELDDVLRWG 1099 GJY1334Val Arg1338Lys *** *********************************
CHD4_Cow CHD4_Xenopus CHD4_Zebrafish let-418_C.elegans E CHD4_Human CHD4_Chimp	1091 1098 1088 1083 974 1295 1208	GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRLGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1215 GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRLGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222 GGITGMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRLGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1220 GGITGMRDEAIDRFNAPGAQQFVFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRLGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSIMGQMRDEAIDRFNAPGAQQFFILLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRLGQNKKVMIYRFVTKKSVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSIMGQMRDDAIDRYNAPGAQQFFIFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRLGQNKKVMIYRFVTKKSVEERITSVAKKKMLLHLVVRAGLGGKEGKTMSKTELDDVLRWG 1099 Gly1334Val Arg1338Lys *** . *:**::* . ***********************
CHD4_Cow CHD4_Xenopus CHD4_Zebrafish let-418_C.elegans E CHD4_Human CHD4_Chimp CHD4_Rhesus CHD4_Rhesus	1091 1098 1088 1083 974 1295 1208 1295 1295	GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRLGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1215 GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRLGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222 GGITGMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRLGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222 GGITGMRQEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRLGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1227 GGITGMRQEAIDRFNAPGAQQFFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRLGQNKKVMIYRFVTKASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSIMGQMRDDAIDRYNAPGAQQFIFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRLGQNKKVMIYRFVTKKSVEERITSVAKKKMLLNHLVVRAGLGGKEGKTMSKTELDDVLRWG 1099
CHD4_Cow CHD4_Xenopus CHD4_Zebrafish let-418_C.elegans E CHD4_Human CHD4_Chimp CHD4_Rhesus CHD4_lso1_Rat	1091 1098 1088 1083 974 1295 1208 1295 1295 1295	GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1215 GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222 GGITGNMRDEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222 GGITGMRDEAIDRFNAPGAPQFVFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1217 GGITGMRDEAIDRFNAPGAPQFVFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSIMGQMRDAIDRYNAPGAQQFIFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTKASVEERITQVAKKKMLLNUVVRAGLGSKTG-SMSKQELDDILKFG 1207 GSIMGQMRDAIDRYNAPGAQQFIFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGQNKKVMIYRFVTKKSVEEKITSVAKKKMLLNUVVRAGLGGKEGKTMSKTELDDVLRWG 1099
CHD4_Cow CHD4_Xenopus CHD4_Zebrafish let-418_C.elegans E CHD4_Human CHD4_Chimp CHD4_Chimp CHD4_Rhesus CHD4_Dog CHD4_iso1_Rat CHD4_iso2_Rat CHD4_iso2_Rat	1091 1098 1088 1083 974 1295 1208 1295 1295 1295 1295 1295	GGITGNMR DEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHR LGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1215 GGITGNMR DEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHR LGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222 GGITGNMR DEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHR LGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222 GGITGMR DEAIDRFNAPGAPQFVFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHR LGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1227 GGITGMR DEAIDRFNAPGAPQFVFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHR LGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1220 GGITGMR DEAIDRFNAPGAPQFVFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHR LGQNKKVMIYRFVTRASVEERITQVAKKKMLLNLVVRPGLGSKTG-SMSKQELDDILKFG 1227 GSIMGQMR DAIDRYNAPGAQQFIFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHR LGQNKKVMIYRFVTRASVEERITQVAKKKMLLNUVVRAGLGGKEGKTMSKTELDDVLRWG 1099
CHD4_Cow CHD4_Xenopus CHD4_Zebrafish let-418_C.elegans E CHD4_Human CHD4_Chimp CHD4_Chimp CHD4_Rhesus CHD4_Dog CHD4_iso1_Rat CHD4_iso2_Rat CHD4_Mouse CHD4_Cow	1091 1098 1088 1083 974 1295 1205 1295 1295 1295 1295 1295 1295	GGITGNMR DEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHR LGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1215 GGITGNMR DEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHR LGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222 GGITGNMR DEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHR LGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1212 GGITGMR DEAIDRFNAPGAPQFVFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHR LGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1220 GSIMGQMR DDAIDRFNAPGAPQFVFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHR LGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSIMGQMR DDAIDRYNAPGAQQFIFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHR LGQNKKVMIYRFVTRASVEERITQVAKKKMLLNUVRAGLGGKEGKTMSKTELDDVLKWG 1099
CHD4_Cow CHD4_Xenopus CHD4_Zebrafish let-418_C.elegans E CHD4_Human CHD4_Chimp CHD4_Chimp CHD4_Rhesus CHD4_lso1_Rat CHD4_lso2_Rat CHD4_iso2_Rat CHD4_Cow CHD4_Cow CHD4_Cow CHD4_Cow CHD4_Cows CHD4_Cows	1091 1098 1088 1083 974 1295 1208 1295 1295 1295 1295 1295 1295 1288 1295 1288 1295 1283 1270	GGITGNNR DEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHR LGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1215 GGITGNNR DEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHR LGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222 GGITGNNR DEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHR LGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222 GGITGNNR DEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHR LGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1220 GSINGQMR DEAIDRFNAPGAPQFVFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHR LGQNKKVMIYRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1220 GSINGQMR DEAIDRFNAPGAPQFVFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHR LGQNKKVMIYRFVTRASVEERITQVAKKKMLLNUVRAGLGGKEGKTMSKTELDDVLRWG 1099
CHD4_Cow CHD4_Xenopus CHD4_Zebrafish let-418_C.elegans E CHD4_Human CHD4_Chimp CHD4_Chimp CHD4_hkesus CHD4_Dog CHD4_iso1_Rat CHD4_iso2_Rat CHD4_Mouse CHD4_Cow CHD4_Zebrafish let-418_C.elegans	1091 1098 1088 1083 974 1295 1295 1295 1295 1295 1295 1295 1295	GGITONM DEATDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIVDSDNNPHNDIQAFSRAHRIGQNKKVNIVRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1215 GGITONM DEATDRFNAPGAQQFCFLLSTRAGGLGINLATADTVVIVDSDNNPHNDIQAFSRAHRIGQNKKVNIVRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1212 GGITONM DEATDRFNAPGAQQFCFLLSTRAGGLGINLATADTVVIVDSDNNPHNDIQAFSRAHRIGQNKKVNIVRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1212 GGITGMN DEATDRFNAPGAQQFCFLLSTRAGGLGINLATADTVVIVDSDNNPHNDIQAFSRAHRIGQNKKVNIVRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1212 GGITGMN DEATDRFNAPGAQQFCFLLSTRAGGLGINLATADTVVIVDSDNNPHNDIQAFSRAHRIGQNKKVNIVRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1217 GSIMGONDOATDRYNAPGAQQFFIFLLSTRAGGLGINLATADTVIVDSDNNPHNDIQAFSRAHRIGQNKKVNIVRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSIMGONDOATDRYNAPGAQQFFIFLLSTRAGGLGINLATADTVIVDSDNNPHNDIQAFSRAHRIGQNKKVNIVRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSIMGONDOATDRYNAPGAQQFFIFLLSTRAGGLGINLATADTVIVDSDNNPHNDIQAFSRAHRIGQNKKVNIVRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSIMGONDOATDRYNAPGAQQFFIFLSTRAGGLGINLATADTVIVDSDNNPHNDIQAFSRAHRIGQNKKVNIVRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSIMGONSODATDRYNAPGAQQFFIFLSTRAGGLGINLATADTVIVDSDNNPHNDIQAFSRAHRIGQNKKVNIVRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSIMGONSODATDRYNAPGAQQFFIFLSTRAGGLGINLATADTVIVDSONNPHNDIQAFSRAHRIGQNKKVNIVRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG SMSKQELDDILKFG 1207 GSIMGONSODATDRYNAPGAQQFFIFLSTRAGGLGINLATADTVIVDSONNPHNDIQAFSRAHRIGQNKKVNIVRFVTRASVEERITQVAKKKMLTHLVVRGGSSKGTS EEEVER-EIIKQEE-SVDPDYWEKLLRHHYEQQQEDLARNICKGKRIRKQVNYNDGSQEDR 1353 EEEVER-EIIKQEE-SVDPDYWEKLLRHHYEQQQEDLARNICKGKRIRKQVNYNDGSQEDR 1353 EEEVER-EIIKQEE-SVDPDYWEKLLRHHYEQQQEDLARNICKGKRIRKQVNYNDGSQEDR 1353 EEEVER-EIIKQEE-SVDPDYWEKLLRHHYEQQQEDLARNICKGKRIRKQVNYNDGSQEDR 1353 EEEVER-EIIKQEE-SVDPDYWEKLLRHHYEQQQEDLARNICKGKRIRKQVNYNDGSQEDR 1353 EEEVER-EIIKQEE-SVDPDYWEKLLRHHYEQQQEDLARNICKGKRIRKQVNYNDGSQEDR 1354 EEEVER-EIIKQEE-SVDPDYWEKLLRHHYEQQQEDLARNICKGKRIRKQVNYNDGSQ
CHD4_Cow CHD4_Zebrafish let-418_C.elegans E CHD4_Human CHD4_Chimp CHD4_Rhesus CHD4_iso1_Rat CHD4_iso1_Rat CHD4_iso2_Rat CHD4_iso2_Rat CHD4_Zebrafish let-418_C.elegans	1091 1098 1088 1083 974 1295 1295 1295 1295 1295 1295 1288 1295 1288 1295 1283 1270 1180	GGITGNNEDELDRFNAPGAQOFCFLLSTRAGGLGINLATADTVIIJOSDWNFHNDIQAFSRAHRIGONKKWNIYRFVTRASVEERITQVAKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1215 GGITGNNEDEALDRFNAPGAQOFCFLLSTRAGGLGINLATADTVIIJOSDWNFHNDIQAFSRAHRIGONKKWNIYRFVTRASVEERITQVAKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222 GGITGNNEDEALDRFNAPGAQOFCFLLSTRAGGLGINLATADTVIIJOSDWNFHNDIQAFSRAHRIGONKKWNIYRFVTRASVEERITQVAKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1223 GGITGNMEDEALDRFNAPGAQOFCFLLSTRAGGLGINLATADTVIIJOSDWNFHNDIQAFSRAHRIGONKKWNIYRFVTRASVEERITQVAKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1227 GSITGNMEDEALDRFNAPGAQOFCFLLSTRAGGLGINLATADTVIIJOSDWNFHNDIQAFSRAHRIGONKKWNIYRFVTRASVEERITQVAKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSINGQMEDALDRFNAPGAQOFIFLLSTRAGGLGINLATADTVIIJOSDWNFHNDIQAFSRAHRIGONKKWNIYRFVTRASVEERITQVAKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSINGQMEDALDRFNAPGAQOFCFLLSTRAGGLGINLATADTVIIJOSDWNFHNDIQAFSRAHRIGONKKWNIYRFVTRASVEERITGVAKKMMLTHLVVRAGLGGSKTG-SMSKQELDDILKFG 1207 GSINGQMEDALDRFNAPGAQOFCFLLSTRAGGLGINLATADTVIIJOSDWNFHNDIQAFSRAHRIGONKKWNIYRFVTRASVEERITGVAKKMMLTHLVVRAGLGGSKTG-SMSKQELDDILKFG 1207 GSINGQMEDALDRFNAPGAQOFCFLSTRAGGLGINLATADTVIIJOSDWNFHNDIQAFSRAHRIGONKKWNIYRFVTRASVEERITGVAKKMMLHUVVRAGLGGSKTG-SMSKQELDDILKFG 1207 GSINGQMEDALDRFNAPGAQOFCFLSTRAGGLGINLATADTVIIJOSDWNFHNDIQAFSRAHRIGONKKWNIYRFVTRASVEERITGVAKKMMLHUVVRAGLGGSKTG-SMSKQELDDILKFG 1207 GSINGQMEDALDRFNAPGAQOFCFLSTRAGGLGINLATADTVIIJOSDWNFHNDIQAFSRAHRIGONKKWNIYRFVTRASVEERITGVAKKMMLHUVVRAGLGGSKTG-SMSKQELDDILKFG 1207 GSINGQMEDALDRFNAPGAQOFCFLSTRAGGLGINLATADTVIIJOSDWNFHNDIQAFSRAHRIGONKKWNIYRFVTRASVEERITGVAKKMULHUVVRAGLGGSKTG-SMSKQELDDILKFG 1207 GSINGQMEDALDRFNAPGAQOFCLSKTGKKKKKKKKKKKKVNYNDGSQER 1353 EEEVER-EIIKQEE-SVDPDYWELLKHHVEQQOEDLARNIGKKKKTRKVVNYNDGSQER 1353 EEEVER-EIIKQEE-SVDPDYWELLKHHVEQQOEDLARNIGKKKKTRKVVNYNDGSQER 1328 EEEVER-EIIKQEE-SVDPDYWELLKHHVEQQOEDLARNIGKKKKTRKVVNYNDGSQER 1328 EEEVER-EIIKQEE-SVDPDYWELLKHHVEQQOEDLARNIGKKKKTRKVVNYNDGSQER 1328 EEEVER-EIIKQEE-SVDPDYWELLKHHVEQDRETELQKLKKKVKKKKKKKKKKKKVNYNDGSQER 1328 EEEVER-EIIKKEE-SVDPDYWELLKHHVEQDRETELQKLKKKKKKKKKKVKKKKKKKKKKKKTLL SATSTONCK
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CHD4_Cow CHD4_Zenopus CHD4_Zebrafish let-418_C.elegans E CHD4_Human CHD4_Chimp CHD4_Chimp CHD4_Rhesus CHD4_Dog CHD4_iso1_Rat CHD4_iso2_Rat CHD4_Joog CHD4_iso2_Rat CHD4_Cow CHD4_Zebrafish let-418_C.elegans F CHD4_Human	1091 1098 1088 1083 974 1295 1208 1295 1295 1295 1295 1295 1295 1283 1270 1180	GGTGGNKEDEAIDEFNAPGAQQFCFLLSTRAGGLGINLATADTVIIVDSDNNPHNDIQAFSRAHKIGQNKKVMIVRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1215 GGTGGNKEDEAIDEFNAPGAQQFCFLLSTRAGGLGINLATADTVVIVDSDNNPHNDIQAFSRAHKIGQNKKVMIVRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1212 GGTGGMKEDEAIDEFNAPGAQQFCFLLSTRAGGLGINLATADTVVIVDSDNNPHNDIQAFSRAHKIGQNKKVMIVRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1212 GGTGGMKEDEAIDEFNAPGAQQFCFLLSTRAGGLGINLATADTVVIVDSDNNPHNDIQAFSRAHKIGQNKKVMIVRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1212 GGTGGMKEDEAIDEFNAPGAQQFCFLLSTRAGGLGINLATADTVVIVDSDNNPHNDIQAFSRAHKIGQNKKVMIVRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSTGGMKEDEAIDEFNAPGAQQFIFLLSTRAGGLGINLATADTVVIVDSDNNPHNDIQAFSRAHKIGQNKKVMIVRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSTGGMKEDEAIDEFNAPGAQQFIFLLSTRAGGLGINLATADTVVIVDSDNNPHNDIQAFSRAHKIGQNKKVMIVRFVTRASVEERITQVAKKKMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSTGGMKEDEAIDEFNAPGAQQFIFLLSTRAGGLGINLATADTVVIVDSDNPHNDIQAFSRAHKIGQNKKVMIVRFVTRASVEERITQVAKKKMLINHLVVRAGLGSKTG-SMSKQELDDILKFG 1207 GSTGGMKEDEAIDEFNAPGAQQFIFLLSTRAGGLGINLATADTVIVDSDNPHNDIQAFSRAHKIGQNKKVMIVRFVTRASVEERITQVAKKKMLINHLVVRAGLGSKTG-SMSKQELDDILKFG 1207 GSTGGMKEDEAIDEFNAPGAQQFIFLLSTRAGGLGINLATADTVIVDSDNPHNDIQAFSRAHKIGQNKKVMIVRFVTRASVEERITQVAKKKMLINHLVVRAGLGSKTG-SMSKQELDDVLRWG 1099
CHD4_Cow CHD4_Xenopus CHD4_Zebrafish let-418_C.elegans E CHD4_Human CHD4_Chimp CHD4_Chimp CHD4_iso1_Rat CHD4_iso2_Rat CHD4_iso2_Rat CHD4_Cow CHD4_Zebrafish let-418_C.elegans F CHD4_Human CHD4_Chimp	1091 1098 1088 1083 974 1295 1208 1295 1295 1295 1295 1295 1295 1295 1295	GGITGMM RDEAIDEFNAPGAQOFCFLLSTRAGGLGINLATADTVI IVDSDWNPHND 1QAFSRAHRIGQMKKVMI IRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1212 GGITGMM RDEAIDEFNAPGAQOFCFLLSTRAGGLGINLATADTVI IVDSDWNPHND 1QAFSRAHRIGQMKKVMI IRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222 GGITGMM RDEAIDEFNAPGAQOFCFLLSTRAGGLGINLATADTVI IVDSDWNPHND 1QAFSRAHRIGQMKKVMI IRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1222 GGITGMM RDEAIDEFNAPGAQOFCFLLSTRAGGLGINLATADTVI IVDSDWNPHND 1QAFSRAHRIGQMKKVMI IRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSIMGMR DAIDEFNAPGAQOFCFLLSTRAGGLGINLATADTVI IVDSDWNPHND 1QAFSRAHRIGQMKKVMI IRFVTRASVEERITQVAKKKMLINLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSIMGMR DAIDEFNAPGAQOFCFLLSTRAGGLGINLATADTVI IVDSDWNPHND 1QAFSRAHRIGQMKKVMI IRFVTRASVEERITQVAKKKMLINLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSIMGMR DAIDEFNAPGAQOFCFLLSTRAGGLGINLATADTVI IVDSDWNPHND 1QAFSRAHRIGQMKKVMI IRFVTKKSVEEKITSVAKKKMLINLVVRPGLGSKTG-SMSKQELDDILKFG 1207 GSIMGMR DAIDEFNAPGAQOFCFLLSTRAGGLGINLATADTVI IVDSDWNPHND 1QAFSRAHRIGQMKKVMI IRFVTKKSVEEKITSVAKKKMLINLVVRGLGSKTG-SMSKQELDDILKFG 1207 GSIMGMR DAIDEFNAPGAQOFCFLSTRAGGLGINLATADTVI IVDSDWNPHND 1QAFSRAHRIGQMKKVMI IRFVTKKSVEEKITSVAKKKMLINLVVRGLGSKTG-SMSKQELDDILKFG 1207 GSIMGMR DAIDEFNAPGAQOFFLSTRAGGLGINLATADTVI IVDSDWNPHND 1QAFSRAHRIGQMKKVMI IRFVTKKSVEEKITSVAKKMLINLVVRGLGSKTG-SMSKQELDDILKFG 1207 GSIMGMR DAIDEFNAPGAQOFFLSTRAGGLGINLATADTVI IVDSDWNPHND 1QAFSRAHRIGQMKKVMI IRFVTKKSVEEKITSVAKKMLINLVVRGLGSKTG-SMSKQELDDILKFG 1207 GSIMGMR DAIDEFNAPGAQOFFLSTRAGGLGINLATADTVI IVDSDWNPHND 1QAFSRAHRIGQMKKVMI IRFVTKKSVEEKITSVAKKMLINLVVRGLGSKTG-SMSKQELDDILKFG 1207 GSIMGMR DAIDEFNAPGAQOFFLSTRAGGLGINLTATOTI IVDSDWNPHND 1QAFSRAHRIGQMKKVMI IRFVTKKSVEEKITSVAKKMLINLVVRGGGEK 1353 EEEVER-SIIKQEE-SVDPDYWELLRHTEQQQEDLANNI KKGKRI RKQVNYNDGSQEDR 1353 EEEVER-SIIKQEE-SVDPDYWELLRHTEQQQEDLANNI KKGKRI RKQVNYNDGSQEDR 1326 EEEVER-SIIKQEE-SVDPDYWELLRHTEQQQEDLANNI KKGKRI RKQVNYNDGSQEDR 1326 EEEVER-SIIKQEE-SVDPDYWELLRHTEQQQELANNI KKGKRI RKQVNYNDGSQEDR 1326 EEEVER-SIIKQEESTVIKEDEKEPDPDYWELLKHKMEQQEDLANNI KKKGKRI KKQVNYNDGSQEDR 1326
CHD4_Cow CHD4_Zenopus CHD4_Zebrafish let-418_C.elegans E CHD4_Human CHD4_Chimp CHD4_Chimp CHD4_Rhesus CHD4_Dog CHD4_iso1_Rat CHD4_iso2_Rat CHD4_Mouse CHD4_Cow CHD4_Zebrafish let-418_C.elegans F CHD4_Human CHD4_Chimp CHD4_Chimp CHD4_Chimp CHD4_Rhesus CHD4_Dog	1091 1098 1088 1083 974 1295 1208 1295 1295 1295 1295 1295 1295 1295 1283 1270 1180 1570 1483 1570	GGTGMM ODEAIDEFNAPGAQQFCFLLSTRAGGLGINLATADTVIIIDSDWNFMDIQAFSRAHEGQNKKWNIIRFVTRASVEERITQVAKKNMLTHLUVNPGLGSKTG-SNSKQELDDILKFG 1215 GGTGMM ODEAIDEFNAPGAQQFCFLLSTRAGGLGINLATADTVIIIDSDWNFMDIQAFSRAHEGQNKKWNIIRFVTRASVEERITQVAKKNMLTHLUVNPGLGSKTG-SNSKQELDDILKFG 1212 GGTGMM ODEAIDEFNAPGAQQFCFLLSTRAGGLGINLATADTVVIIDSDWNFMDIQAFSRAHEGQNKKWNIIRFVTRASVEERITQVAKKNMLTHLUVNPGLGSKTG-SNSKQELDDILKFG 1217 GGTGMM ODEAIDEFNAPGAQQFCFLLSTRAGGLGINLATADTVVIIDSDWNFMDIQAFSRAHEGQNKKWNIIRFVTRASVEERITQVAKKNMLTHLUVNPGLGSKTG-SNSKQELDDILKFG 1207 GSTMGM ODAIDEFNAPGAQQFFILLSTRAGGLGINLATADTVVIIDSDWNFMDIQAFSRAHEGQNKKWNIIRFVTRASVEERITQVAKKNMLTHLUVNPGLGSKTG-SNSKQELDDILKFG 1207 GSTMGM ODAIDEFNAPGAQQFFILSTRAGGLGINLATADTVVIIDSDWNFMDIQAFSRAHEGQNKKWNIIRFVTKASVEERITQVAKKNMLTHLUVNPGLGSKTG-SNSKQELDDILKFG 1207 GSTMGM ODAIDEFNAPGAQQFFILSTRAGGLGINLATADTVVIIDSDWNFMDIQAFSRAHEGQNKKWNIIRFVTKASVEERITQVAKKNMLTHLUVNPGLGSKTG-SNSKQELDDILKFG 1207 GSTMGM ODAIDEFNAPGAQQFFILSTRAGGLGINLATADTVVIIDSDWNFMDIQAFSRAHEGQNKKWNIIRFVTKASVEERITQVAKKNMLTHLUVNPGLGSKTG-SNSKQELDDILKFG 1207 GSTMGM ODAIDEFNAPGAQQFFILSTRAGGLGINLATADTVVIIDSDWNFMDIQAFSRAHEGQNKKWNIIRFVTKASVEERITQVAKKNMLTHLUVNPGLGSKTG-SNSKQELDDILKFG 1207 GSTMGM ODAIDEFNAPGAQQFFILSTRAGGLGINLATADTVVIIDSDWNFMDIQAFSRAHEGQNKKWNIIRFVTKASVEERITQVAKKNMLTHLUVNPGLGSKTG-SNSKQELDDILKFG 1207 GSTMGM ODAIDEFNAPGAQQFFILSTRAGGLGINLATADTVVIIDSDWNFMDIQAFSRAHEGQNKKWNIIRFVTKASVEERITQVAKKNMLTHLUVNPGLGSKTG-SNSKQELDDILKFG 1207 FEEVER-SIIKQEE-SVDPDTWELLEHHTEQQQEDLARNLEKGNETRKQWNYNDGSQEDR 1353 EEEVER-SIIKQEE-SVDPDTWELLEHHTEQQQEDLARNLEKGNETRKQWNYNDGSQEDR 1353 EEEVER-SIIKQEE-SVDPDTWELLEHHTEQQQEDLARNLEKGNETRKQWNYNDGSQEDR 1353 EEEVER-SIIKQEE-SVDPDTWELLEHHTEQQQEDLARNLEKGNETRKQWNYNDGSQEDR 1328 EEEEETERVIKEDEKEPDPDTWEKLLEHHTEQQQEDLARNLEKGNETKKQWNYNDGSQEDR 1328 EEEEETERVIKEDEKEPDPDTWEKLLEHHTEQQQEDLARNLEKGNETKKQWNYNDGSQEDR 1328 EEEEETERVIKEDEKEPDPDTWEKLLEHHTEQQQEDLARNLEKGNETKKQWNYNDGSQEDR 1328 EEEEETERVIKEDEKEPDPDTWEKLLEHHTEQQAPAASEDEKVVVEPPEGEEKVEKAEVKERTEEPMET-EPKGAADVEKVEKSKDILTIVVEDKEEKKE 1666
CHD4_Cow CHD4_Zenopus CHD4_Zebrafish let-418_C.elegans E CHD4_Human CHD4_Chimp CHD4_Chimp CHD4_Rhesus CHD4_Dog CHD4_iso1_Rat CHD4_Mouse CHD4_Gow CHD4_Zebrafish let-418_C.elegans F CHD4_Lomp CHD4_Zebrafish let-418_C.elegans	1091 1098 1088 1083 974 1295 1208 1295 1295 1295 1295 1295 1295 1283 1270 1180 1570 1483 1570	GGTGMMEDEAIDERNAPGAQOFCHLSTRAGGLGINLATADTVIIIDSDMNTHNDIQAFSRAHKIGQNKKUMIIKPYTRASVEERITQVAKKKMULTILUVRPGLGSKTG-SMSKOE DDILKFG 1215 GGTGMMEDEAIDERNAPGAQOFCHLSTRAGGLGINLATADTVIIIDSDMNTHNDIQAFSRAHKIGQNKKUMIIKPYTRASVEERITQVAKKKMULTILUVRPGLGSKTG-SMSKOE DDILKFG 1212 GGTGMMEDEAIDERNAPGAQOFCHLSTRAGGLGINLATADTVIIIDSDMNTHNDIQAFSRAHKIGQNKKUMIIKPVTRASVEERITQVAKKKMULTILVVRPGLGSKTG-SMSKOE DDILKFG 1212 GGTGMMEDEAIDERNAPGAQOFCHLSTRAGGLGINLATADTVIIIDSDMNTHNDIQAFSRAHKIGQNKKUMIIKPVTRASVEERITQVAKKMULTNLVVRPGLGSKTG-SMSKOE DDILKFG 1212 GGTGMMEDEAIDERNAPGAQOFIHLSTRAGGLGINLATADTVIIIDSDMNTHNDIQAFSRAHKIGQNKKUMIIKPVTKASVEERITQVAKKMULTNLVVRPGLGSKTG-SMSKOE DDILKFG 1207 GSTMGUDEDAIDERNAPGAQOFIHLSTRAGGLGINLATADTVIIIDSDMNTHNDIQAFSRAHKIGQNKKUMIIKPVTKASVEERITQVAKKMULTNLVVRGLGSKTG-SMSKOE DDILKFG 1207 GSTMGUDEDDIDRVARGAQOFIHLSTRAGGLGINLATADTVIIIDSDMNTHNDIQAFSRAHKIGQNKKUMIIKPVTKKSVEERITQVAKKMULTNLVVRGLGSKTG-SMSKOE DDILKFG 1207 GSTMGUDEDDIDRVARGAQOFIHLSTRAGGLGINLATADTVIIIDSDMNTHNDIQAFSRAHKIGQNKKUMIKPVTKKSVEERITQVAKKMULTNLVVRGLGSKTG-SMSKOE DDILKFG 1207 GSTMGUDEDDIDRVAKKAMIKTURGGUDELARNICKKKIKKUKUNIKPVTKKSVEERITSVAKKMULTNLVVRGLGSKTG-SMSKOE DDILKFG 1207 GTGTGMEDESVDPJVWKLLRHYEQQOEDLARNICKKKIKKUKUVNDGSGEDR 1353 EEEVER-SIIKQEE-SVDPJVWKLLRHYEQQOEDLARNICKKKIKKUVNTUGSQEDR 1353 EEEVER-SIIKQEE-SVDPJVWKLLRHYEQQOEDLARNICKKKIKKUVNTUGSQEDR 1353 EEEVER-SIIKQEE-SVDPJVWKLLRHYEQQOEDLARNICKKKIKKUVNTUGSQEDR 1353 EEEVER-SIIKQEE-SVDPJVWKLLRHYEQQOEDLARNICKKKIKKUVNTUGSQEDR 1353 EEEVER-SIIKQEE-SVDPJVWKLLRHYEQQOEDLARNICKKKIKKUVNTUGSQEDR 1341 EEEVER-SIIKQEE-SVDPJVWKKLLRHYEQQOEDLARNICKKKIKKUVNTUGSQEDR 1328 EEEEETETVIKEDEKEPDPJVWKKLLRHYEQQOEDLARNICKKKIKKUVNTUGSQEDR 1328 EEEEETETVIKEDEKEPDPJVWKKLLRHYEQQOEDLARNICKKKIKKUVNTUGSQEDR 1320 SCHSTONGOVEKKUSTAPFATIGCTQAPAPASEDEKVVEPPSGEEKVKKAEVKKEREEFEPHET-EFKGAADVEKVEEKSADLDIFJVVEDKEEKKEE 1666 SIKKEESSIGGEKVKSTAPFATIGCTQAPAPASEDEKVVEPPSGEEKVKKAEVKEREEFEPHET-EFKGAADVEKVEEKSADLDIFJVVEDKEEKKEE 1666 SIKKEESSIGGEKVKSTAPFATIGCTQAPAPASEDEKVVEPPSGEEKVKKAEVKEREEFEPHET-EFKGAADVEKVEEKSADLDIFJVVEDKEEKKEE 1664
CHD4_Cow CHD4_Zenopus CHD4_Zebrafish let-418_C.elegans E CHD4_Human CHD4_Chimp CHD4_Chimp CHD4_Rhesus CHD4_loog CHD4_iso1_Rat CHD4_Mouse CHD4_Cow CHD4_Zebrafish let-418_C.elegans F CHD4_Human CHD4_Chimp CHD4_Chimp CHD4_Chimp CHD4_Chimp CHD4_Senopus CHD4_Chimp CHD4_Senopus CHD4_Chimp CHD4_Hesus CHD4_Dog CHD4_iso1_Rat CHD4_iso2_Rat CHD4_iso2_Rat	1091 1098 1088 1083 974 1295 1295 1295 1295 1295 1295 1295 1295	GGITOMMEDEALDERNAPGAQOPCELLSTRAGGLOINLATADTVIITDESDNNPHNDIQAFSRAHKIGONKKVNITRFVTRASVEERITQVAKKNMLTHLVVRPGLOSKTG-SMSKOELDDILKFG 1212 GGITOMMEDEALDERNAPGAQOPCELLSTRAGGLOINLATADTVIITDESDNNPHNDIQAFSRAHKIGONKKVNITRFVTRASVEERITQVAKKNMLTHLVVRPGLOSKTG-SMSKOELDDILKFG 1222 GGITOMMEDEALDERNAPGAQOPCELSTRAGGLOINLATADTVIITDESDNNPHNDIQAFSRAHKIGONKKVNITRFVTRASVEERITQVAKKNMLTHLVVRPGLOSKTG-SMSKOELDDILKFG 1222 GGITOMMEDEALDERNAPGAQOPCELSTRAGGLOINLATADTVIITDESDNNPHNDIQAFSRAHKIGONKKVNITRFVTRASVEERITQVAKKNMLTHLVVRPGLOSKTG-SMSKOELDDILKFG 1212 GGITOMMEDEALDERNAPGAQOPTELSTRAGGLOINLATADTVIITDESDNNPHNDIQAFSRAHKIGONKKVNITRFVTRASVEERITQVAKKNMLTHLVVRPGLOSKTG-SMSKOELDDILKFG 1207 GSTMOQMEDEALDERNAPGAQOPTELSTRAGGLOINLATADTVIITDESDNNPHNDIQAFSRAHKIGONKKVNITRFVTKASVEERITSVAKKNMLTHLVVRPGLOSKTG-SMSKOELDDILKFG 1207 GSTMOQMEDEALDERNAPGAQOPTELSTRAGGLOINLATADTVIITDESDNNPHNDIQAFSRAHKIGONKKVNITRFVTKASVEERITSVAKKNMLTHLVVRPGLOSKTG-SMSKOELDDILKFG 1207 GSTMOQMEDEALDERNAPGAQOPTELSTRAGGLOINLATADTVIITDESDNNPHNDIQAFSRAHKIGONKKVNITRFVTKASVEERITSVAKKNMLTHLVVRPGLOSKTG-SMSKOELDDILKFG 1207 GSTMOQMEDEALDERNAPGAQOPTELSTRATGGLOINLATADTVIITDESDNNPHNDIQAFSRAHKIGONKKVNITRFVTKASVEERITSVAKKKNMLTHLVVRPGLOSKTG-SMSKOELDDILKFG 1207 GSTMOQMEDEALDERNAPGAQOPTELSTRATGGLOINLATADTVIITDESDNNPHNDIQAFSRAHKIGONKKVNITRFVTKASVEERITSVAKKKNMLTHLVVRPGLOSKTG-SMSKOELDDILKFG 1207 GGITOMMEDEALDERNAPGAQOPTELSTRATGGLOINLATADTVIITDESDNNPHNDIQAFSRAHKIGONKKVNITRFVTRASVEERITSVAKKKNULHLUVRPGLOSKTG-SMSKOELDDILKFG 1207 GEINGOMEDEALDERNAPGAQOFTELSKTGATGKGKGKKVNINDGOEDR 1353 EEEVER-EIIKQEE-SVDPJYMEKLLAHHYEQQOEDLANNI KKKKR RKQVNYNDGSQEDR 1353 EEEVER-EIIKQEE-SVDPJYMEKLLAHHYEQQOEDLANNI KKKKR RKQVNYNDGSQEDR 1353 EEEVER-EIIKQEE-SVDPJYMEKLLAHHYEQQOEDLANNI KKKKR RKQVNYNDGSQEDR 1353 EEEVER-EIIKQEE-SVDPJYMEKLLAHHYEQQOEDLANNI KKKRK RKQVNYNDGSQEDR 1353 EEEVER-EIIKQEE-SVDPJYMEKLLAHHYEQQOEDLANNI KKKRK RKQVNYNDGSQEDR 1353 EEEVER-EIIKQEE-SVDPJYMEKLLAHHYEQQOEDLANNI KKKRK RKQVNYNDGSQEDR 1353 EEEVER-EIIKQEE-SVDPJYMEKLLAHHYEQQOEDLANNI KKKRK RKQVYNDGSQEDR 1353 EEEVER-EIIKQEE-SVDPJYMEKLLAHYEQQOEDLANNI KKKRK RKQVYNDGSGENE 1220 SK
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CHD4_Cow CHD4_Zebrafish let-418_C.elegans E CHD4_Human CHD4_Chimp CHD4_Chimp CHD4_Rhesus CHD4_Dog CHD4_iso1_Rat CHD4_loog CHD4_iso2_Rat CHD4_Zebrafish let-418_C.elegans F CHD4_Rhesus CHD4_Chimp CHD4_Rhesus CHD4_Chimp CHD4_Rhesus CHD4_So1_Rat CHD4_Jo3 CHD4_So2_Rat CHD4_So2_Rat CHD4_So2_Rat CHD4_Mouse CHD4_CHD4_So2 CHD4_Zebrafish	1091 1098 1088 1083 974 1295 1295 1295 1295 1295 1295 1295 1295	GGITONNE DEALDERNAPGAQQFCFLISTRAGGLGINLATADTVIITUSDNAPHADIQAFSAAHKIGGNKKWIITKPVTRASVEERITQVAKKKWLTHLVVRGLGSKTG-SMSKQELDDILKFG 1212 GGITONNE DEALDERNAPGAQQFCFLISTRAGGLGINLATADTVIITUSDNAPHADIQAFSAAHKIGGNKKWIITKPVTRASVEERITQVAKKKWLTHLVVRGLGSKTG-SMSKQELDDILKFG 1212 GGITONNE DEALDERNAPGAQQFCFLISTRAGGLGINLATADTVIITUSDNAPHADIQAFSAAHKIGGNKKWIITKPVTRASVEERITQVAKKKWLTHLVVRGLGSKTG-SMSKQELDDILKFG 1212 GGITONNE DEALDERNAPGAQQFCFLISTRAGGLGINLATADTVIITUSDNAPHADIQAFSAAHKIGGNKKWIITKPVTRASVEERITQVAKKKWLTHLVVRGLGSKTG-SMSKQELDDILKFG 1212 GGITONNE DEALDERNAPGAQQFFFLISTRAGGLGINLATADTVIITUSDNAPHADIQAFSAAHKIGGNKKWIITKPVTRASVEERITQVAKKKWLINLIVVRGLGSKTG-SMSKQELDDILKFG 1212 GITOGNE DEALDERNAPGAQQFFFLISTRAGGLGINLATADTVIITUSDNAPHADIQAFSAAHKIGGNKKWIITKPVTRASVEERITQVAKKKWLINLIVVRGLGSKTG-SMSKQELDDILKFG 1210 SMGQKDDAIDATNAPGAQQFFFLISTRAGGLGINLATADTVIITUSDNAPHADIQAFSAAHKIGGNKKWIITKPVTRASVEERITQVAKKKWLINLIVVRGLGSKTG-SMSKQELDDILKFG 1210 SMGQKDDAIDATNAPGAQQFFFLISTRAGGLGINLATADTVIITUSDNAPHADIQAFSAAHKIGGNKKWIITKPVTRASVEERITQVAKKKWLINLIVVRGLGSKTG-SMSKQELDDILKFG 1210 SMGQKDDAIDATNAPGAQQFFFLISTRAGGLGINLATADTVIITUSDNAPHADIQAFSAAHKIGGNKKWIITKPVTRASVEERITQVAKKKWLINLIVVRAGLGSKTG-SMSKQELDDILKFG 1210 SMGQKDDAIDATNAPGAQQFFFLISTRAGGLGINLATADTVIITUSDNAPHADIQAFSAA SEEVER-EIIKQEE-SVDPTWEKLLKHYSQQEDLARULGSKTKKKWINNOSGEDR 1353 EEEVER-EIIKQEE-SVDPTWEKLLKHYSQQEDLARULGSKTKKKWINNOSGEDR 1353 EEEVER-EIIKQEE-SVDPTWEKLLKHYSQQEDLARULGSKTKKKWINNOSGEDR 1353 EEEVER-EIIKQEE-SVDPTWEKLLKHYSQQEDLARULGSKTKKKWINNOSGEDR 1341 EEEVER-EIIKQEE-SVDPTWEKLLKHYSQQEDLARULGSKKKKKWINNOSGEDR 1341 EEEVER-EIIKQEE-SVDPTWEKLLKHYSQQEDLARULGSKKKKKWINNOSGEDR 1328 EEEETEVEVKESTADFTAIECTQAPAPASEDEKVVEPPEGEEKVEKAEVKERTEEPMET-EPKGAADVKVEEKSADLTFIVVEDKEEKKEE 1666
CHD4_Cow CHD4_Zebrafish let-418_C.elegans E CHD4_Human CHD4_Chimp CHD4_Chimp CHD4_Rhesus CHD4_Dog CHD4_isol_Rat CHD4_isol_Rat CHD4_douse CHD4_Zebrafish let-418_C.elegans CHD4_Chimp CHD4_Rhesus CHD4_Chimp CHD4_Rhesus CHD4_Sol_Rat CHD4_Sol_Rat CHD4_Sol_Rat CHD4_Sol_Rat CHD4_Zebrafish let-418_C.elegans	1091 1098 1088 1083 974 1295 1295 1295 1295 1295 1295 1295 1295	GGITONK DEAT DEFNARGAGOTCFLISTRAGGGINLATAPTVI I TDSDWIPHDE DAFSRAHEG GONKKVWI TRYVTRASVEERI TOVAKKWMLTHLUVREOLGSKTG-SMSROED DI LKFG 1215 GGITONK DEAT DEFNARGAGOTCFLISTRAGGGINLATAPTVI I TDSDWIPHDE DAFSRAHEG GONKKVWI TRYVTRASVEERI TOVAKKWMLTHLUVREOLGSKTG-SMSROED DI LKFG 1212 GGITONK DEAT DEFNARGAGOTCFLISTRAGGINLATAPTVI I TDSDWIPHDE DAFSRAHEG GONKKVWI TRYVTRASVEERI TOVAKKWMLTHLUVREOLGSKTG-SMSROED DI LKFG 1212 GGITONK DEAT DEFNARGAGOTCFLISTRAGGINLATAPTVI I TDSDWIPHDE DAFSRAHEG GONKKVWI TRYVTRASVEERI TOVAKKWMLTHLUVREOLGSKTG-SMSROED DI LKFG 1207 GSIMGQHEDDAI DRYNAPGAQOTCFLISTRAGGINLATAPTVI I TDSDWIPHDE DAFSRAHEG GONKKVWI TRYVTRASVEERI TOVAKKWMLTHLUVREOLGSKTG-SMSROED DU LKFG 1099 GIV1334Val Arg1338Lys *** *********************************
CHD4_Cow CHD4_Zenopus CHD4_Zebrafish let-418_C.elegans E CHD4_Human CHD4_Chimp CHD4_Ahesus CHD4_Dog CHD4_iso1_Rat CHD4_Mouse CHD4_Zebrafish let-418_C.elegans F CHD4_Human CHD4_Ahesus CHD4_Zebrafish let-418_C.elegans CHD4_iso2_Rat CHD4_Jiso2_Rat CHD4_Ahesus CHD4_So3_Rat CHD4_So3	1091 1098 1088 1083 974 1295 1295 1295 1295 1295 1295 1295 1295	GUTENNKEESIIDERNAAGAQOFCFLISTRAGGLGINLATADTUTUISDINNIKKU IQAFSAARKI GQNKKVWIIYRVTRASVEERIIYVAKKNOLTILUVRPGLGSKTG-SNSKQE DDILKKG 1212 GUTENNKEESIIDERNAAGAQOFCFLISTRAGGLGINLATADTVIIIDSDINNIKU IQAFSAARKI GQNKKVWIIYRVTRASVEERIIYVAKKNOLTILUVRPGLGSKTG-SNSKQE DDILKG 1222 GUTENNKEESIIDERNAAGAQOFCFLISTRAGGLGINLATADTVIIIDSDINNIKU IQAFSAARKI GQNKKVWIIYRVTRASVEERIIYVAKKNOLTILUVRPGLGSKTG-SNSKQE DDILKG 1207 GSITGNKEESIIDERNAAGAQOFCFLISTRAGGLGINLATADTVIIIDSDINNIKU IQAFSAARKI GQNKKVWIIYRVTRASVEERIIYVAKKNOLTILUVRPGLGSKTG-SNSKQE DDILKG 1207 GSITGNKEESIIDERNAAGAQOFFLISTRAGGLGINLATADTVIIIDSDINNIKU IQAFSAARKI GQNKKVWIIYRVTRASVEERIIYVAKKNOLTILUVRAGLGKEGKTNSKTE DDVLRUG 1099 MILLINGES-SVDPOYNELLAHINEGODILARNI KGAFT KNOWINDGSQEDR 1353 EERVER-EIIKQEE-SVDPOYNEKLLAHINEGODELARNI KGAFT KNOWINDGSQEDR 1353 EERVER-EIIKQEES-SVDPOYNEKLLAHINEGODELARNI KGAFT KNOWINDGSQEDR 1353 EERVER-EIIKQEES-SVDPOYNEKLLAHINEGODELARNI KGAFT KNOWINDGSQEDR 1354 EERVER-EIIKQEES-SVDPOYNEKLLAHINEGODELARNI KGAFT KNOWINDGSQEDR 13
CHD4_Cow CHD4_Zenopus CHD4_Zebrafish let-418_C.elegans E CHD4_Human CHD4_Chimp CHD4_Ahesus CHD4_Dog CHD4_iso1_Rat CHD4_iso2_Rat CHD4_Zenopus CHD4_Zenopus CHD4_Zenopus CHD4_Zebrafish let-418_C.elegans F CHD4_Human CHD4_Chimp CHD4_Rhesus CHD4_oog CHD4_iso1_Rat CHD4_iso2_Rat CHD4_iso2_Rat CHD4_iso2_Rat CHD4_iso2_Rat CHD4_iso2_Rat CHD4_iso2_Rat CHD4_Cow CHD4_Zebrafish let-418_C.elegans	1091 1098 1088 1083 974 1295 1295 1295 1295 1295 1295 1295 1295	GGITGINKSELIDERTARAGQQCFCFLISTRAGGLGINLATDTVIIIDSDWINKBOIQAFSRAHEGONKKVNIITEVTRASVEERITQVAKKMOLTHLUVREGASKTG-SHSKED DDILKFG 1212 GGITGINKSELIDERTARAGQQCFCFLISTRAGGLGINLATDTVIIIDSDWINKBOIQAFSRAHEGONKKVNIITEVTRASVEERITQVAKKMOLTHLUVREGASKTG-SHSKED DDILKFG 1212 GGITGINKSELIDERTARAGQQFFFLISTRAGGLGINLATDTVIIDSDWINKBOIQAFSRAHEGONKKVNIITEVTRASVEERITQVAKKMOLTHLUVREGASKTG-SHSKED DDILKFG 1212 GGITGINKGELIDERTARAGQQFFFLISTRAGGLGINLATDTVIIDSDWINKBOIQAFSRAHEGONKKVNIITEVTRASVEERITQVAKKMOLTHLUVREGASKTG-SHSKED DDILKFG 1212 GGITGINKGELIDERTARAGQQFFFLISTRAGGLGINLATDTVIIDSDWINKBOIQAFSRAHEGOKKKVNIITEVTKKSVEERITQVAKKMOLTHLUVREGASKTG-SHSKED DDILKFG 1212 GGITGINGKEGASTIDERTARAGGLGINLATDTVIIDSDWINKBOIGAFSRAHEGOKKKVNIITEVTKKSVEERITQVAKKMOLTHLUVREGASKTG-SHSKED DDILKFG 1210 GSITGONGREGASTOFFNAFGAQOFFFLISTRAGGLGINLATDTVIIDSDWINKBOIGAFSRAHEGOKKKVNIITEVTKKSVEERITQVAKKMOLTHLUVREGASKTG-SHSKED DDILKFG 1210 GSITGONGREGASTOFFNAFGAQOFFFLISTRAGGLGINLATDTVIIDSDWINKBOIGAFSRAHEGOKKKVNIITEVTKKSVEERITQVAKKKNULLNILVVRGGASKTG-SHSKED DDILKFG 1210 GSITGONGREGASTOFFNAFGAQOFFFLISTRAGGLGINLATDTVIIDSDWINKBOIGAFSRAHEGOKKKVNIITEVTKKSVEERITQVAKKKNULLNILVVRGGASKTG-SHSKED DDILKFG 1210 GSITGONGREGASTOFFNAFGAQOFFFLISTRAGGLGINLATGOKK KKVNINDGSGED 1353 EEEVEN-EIIKQEE-VUDPUWELLEHHTEQOCOLAANLIGKKE KKVNINDGSGED 1353 EEEVEN-EIIKQEE-SVDPUWELLEHHTEQOCOLAANLIGKKE KKVVNINDGSGED 1353 EEEVEN-EIIKQEE-SVDPUWELLEHHTEQOCOLAANLIGKKE KKVVNINDGSGED 1353 EEEVEN-EIIKQEE-SVDPUWELLEHHTEQOCOLAANLIGKKE KKVVINDGSGED 1353 EEEVEN-EIIKQEE-SVDPUWELLEHHTEQOCOLAANLIGKKE KKVVINDGSGED 1353 EEEVEN-EIIKQEE-SVDPUWELLEHHTEQOCOLAANLIGKKE KKVVINDGSGED 1353 EEEVEN-EIIKQEE-SVDPUWELLEHHTEQOCOLAANLIGKKE KKVINTKOKGED 1240 SCILSESSCOKKVKSADPETAICTQAPAASEDEKVVVEPPGGEEKVKAKVKERTEEMET-EFKGADVEKVEEKSKIDLTPIVVEKKEKKEE 1666
CHD4_Cow CHD4_Zebrafish let-418_C.elegans E CHD4_Human CHD4_Chimp CHD4_Khesus CHD4_Dog CHD4_iso1_Rat CHD4_iso2_Rat CHD4_iso2_Rat CHD4_Wouse CHD4_Zebrafish let-418_C.elegans F CHD4_Chimp CHD4_Rhesus CHD4_Dog CHD4_Rhesus CHD4_Dog CHD4_So1_Rat CHD4_Dog CHD4_iso2_Rat CHD4_So2_Rat CHD4_So2_Rat CHD4_So2_Rat CHD4_So2_Rat CHD4_So2_Rat CHD4_Zebrafish let-418_C.elegans	1091 1098 1088 1083 974 1295 1208 1295 1295 1295 1295 1295 1295 1295 1295	GGITGINKSELIDRRINGEGUGTLETRAGGIGINLATDTVIIIDSDNIPHKOIGAPSRAHEGONKKVNIIRPVTRASVEERITQVAKKOMLINUVRGGSKTG-SNEKGEDDILKTG 1212 GGITGINKSELIDRRINGEAGOPCFLISTRAGGIGINLATDTVIIIDSDNIPHKOIGAPSRAHEGONKKVNIIRPVTRASVEERITQVAKKOMLINUVRGGSKTG-SNEKGEDDILKTG 1212 GGITGINKSELIDRRINGEAGOPCFLISTRAGGIGINLATDTVIIIDSDNIPHKOIGAPSRAHEGONKKVNIIRPVTRASVEERITQVAKKOMLINUVRGGSKTG-SNEKGEDDILKTG 1212 GGITGINKGEAIDRRINGEAGOPCFLISTRAGGIGINLATDTVIIIDSDNIPHKOIGAPSRAHEGONKKVNIIRPVTRASVEERITQVAKKOMLINUVRGGSKTG-SNEKGEDDILKTG 1212 GGITGINKGEAGOPTFLISTRAGGIGINLATDTVIIIDSDNIPHKOIGAPSRAHELGONKKVNIIRPVTRASVEERITQVAKKOMLINUVRGGSKTG-SNEKGEDDILKTG 1212 GSINGQARDDAIDRINAPGAQOFIFLISTRAGGIGINLATDTVIIIDSDNIPHKOIGAPSRAHELGONKKVNIIRPVTRASVEERITQVAKKOMLINUVRGGSKTG-SNEKGEDDILKTG 1212 GSINGQARDDAIDRINAPGAQOFIFLISTRAGGIGINLATDTVIIIDSDNIPHKOIGAPSRAHELGONKKVNIIRPVTRASVEERITQVAKKOMLINUVRGGSKTG-SNEKGEDDILKTG 1212 GSINGQARDDAIDRINAPGAQOFIFLISTRAGGIGINLATDTVIIIDSDNIPHKOIGAPSRAHELGONKKVNIIRPVTRASVEERITQVAKKOMLINUVRGGSKTG-SNEKGEDDILKTG 1212 GSINGQARDDAIDRINAPGAQOFIFLISTRAGGIGINLATOVIIIDSDNIPHKOIGAPSRAHELGONKKVNIIRPVTRASVEERITQVAKKOMLINUVRGGSKTG-SNEKGEDDILKTG 1212 GGITGNAGEGE-SVDPDYWELLRINHEGOGEDIARLIGKKRI RKQVNYNDGSGEDR 1353 EEEVER-SIIKQEE-SVDPDYWELLRINHEGOGEDIARLIGKKRI RKQVNYNDGSGEDR 1353 EEEVER-SIIKQEE-SVDPDYWELLRINHEGOGEDIARLIGKKRI RKQVNYNDGSGEDR 1353 EEEVER-SIIKQEE-SVDPDYWELLRINHEGOGEDIARLIGKKRI RKQVNYNDGSGEDR 1353 EEEVER-SIIKQEE-SVDPDYWELLRINHEGOGEDIARLIGKKRI RKQVNYNDGSGEDR 1353 EEEVER-SIIKQEE-SVDPDYWELLRINHEGOGEDIARLIGKKRI RKQVNYNDGSGEDR 1353 EEEVER-SIIKQEE-SVDPDYWELLRINHEGOGEDIARLIGKKRI RKQVNYNDGSGEDR 1328 EEEVER-SIIKGEE-SVDPDYWELLRINHEGOGEDIARLIGKKRI RKQVNYNDGSGEDR 1328 EEEVER-SIIKGEE-SVDPDYWELLRINHEGOGEDIARLIGKKRI RKQVNYNDGSGEDR 1328 EEEVER-SIIKGEESVEKAPTATICTOJAPAASEDEKVVEPEFGEEKVEKAEVERTEEMET-EPKGAADVEKVEKKRI DILTPIVVEDKEEKKEE 1666
CHD4_Cow CHD4_Zebrafish let-418_C.elegans E CHD4_Human CHD4_Chimp CHD4_Khesus CHD4_Dog CHD4_hiso1_Rat CHD4_iso2_Rat CHD4_iso2_Rat CHD4_Zebrafish let-418_C.elegans F CHD4_Zebrafish let-418_C.elegans CHD4_Chimp CHD4_Rhesus CHD4_Dog CHD4_iso2_Rat CHD4_iso2_Rat CHD4_Dog CHD4_Sol_Rat CHD4_Chimp CHD4_Sol_Rat	1091 1098 1088 1083 974 1295 1208 1295 1295 1295 1295 1295 1295 1295 1295	GGITOMINGELIDERNAPGAQOPCFLISTRAGGLATILATIDTVI ITDSINNITNO JQAFSRAHE GONKKWI IYRYTRASVEENI TQVAKKNMUTHLIVRPGLGSKTG-SMSKQE DDILKFG 1215 GGITOMINGELIDERNAPGAQOPCFLISTRAGGLATILATIDTVI IDSINNITNO JQAFSRAHE GONKKWI IYRYTRASVEENI TQVAKKNMUTHLIVRPGLGSKTG-SMSKQE DDILKFG 1215 GGITOMINGELIDERNAPGAQOPCFLISTRAGGLATILATIDTVI IDSINNITNO JQAFSRAHE GONKKWI IYRYTRASVEENI TQVAKKNMUTHLIVRPGLGSKTG-SMSKQE DDILKFG 1207 GSITAGOME GLIDERNAPGAQOPTILISTRAGGLATILATIDTVI IDSINNITNO JQAFSRAHE GONKKWI IYRYTRASVEENI TQVAKKNMUTHLIVRPGLGSKTG-SMSKQE DDILKFG 1207 GSITAGOME GLIDERNAPGAQOPTILISTRAGGLATILATIDTVI ITDSINNITNO JQAFSRAHE GONKKWI IYRYTRASVEENI TQVAKKNMUTHLIVRPGLGSKTG-SMSKQE DDILKFG 1207 GSITAGOME GLIDERNAPGAQOPTILISTRAGGLATILATIDTVI ITDSINNITNO JQAFSRAHE GONKKWI IYRYTRASVEENI TQVAKKNMUTHLIVRPGLGSKTG-SMSKQE DDILKFG 1207 GSITAGOME GLIDERNAPGAQOPTILISTRAGGLATILKANG IKRQVITINGOSGEDR 1353 BEEVEN-EIIKQEE-SVDPDINEKLLAHINITQQQDLAANI, KAKI KRQVITINGOSGEDR 136 BEEVEN-EIIKQEE-SVDPDINEKLLAHINITQQQDLAANI, KAKI KRQVITINGOSGEDR 136 BEEVEN-EIIKQEE-SVDPDINEKLLAHINITQQQDLAANI, KAKI KRQVITINGOSGEDR 136 BEEVEN-EIIKGEE-SVDPDINEKLLAHINITQQQDLAANI, KAKI KRQVITINGOSGEDR 136 BEEVEN-EIIKGE
CHD4_Cow CHD4_Zebrafish let-418_C.elegans E CHD4_Human CHD4_Chimp CHD4_Khesus CHD4_Chimp CHD4_houg CHD4_iso1_Rat CHD4_iso2_Rat CHD4_Wouse CHD4_Zebrafish let-418_C.elegans F CHD4_Rhesus CHD4_Chimp CHD4_Rhesus CHD4_iso1_Rat CHD4_iso2_Rat CHD4_doug CHD4_Zebrafish let-418_C.elegans CHD4_iso2_Rat CHD4_iso2_Rat CHD4_iso2_Rat CHD4_iso2_Rat CHD4_iso2_Rat CHD4_Zebrafish let-418_C.elegans G CHD4_Zebrafish let-418_C.elegans	1091 1098 1088 1083 974 1295 1208 1295 1295 1295 1295 1295 1295 1295 1295	GGITOMONE DEPRANGAQOP CYLLSTRAGGLINLARADY VITOSIMMENDIQAS SAMETI GONKAWITEPYTRASVERTIQVAKKMOLLNILVVRPGLGSKTG-SKRSQEDDILLEP 1212 GGITOMONE SALDBYANGAQOP CYLLSTRAGGLINLARADY VITOSIMMENDIQAS SAMETI GONKAWITEPYTRASVERTIQVAKKMOLLNILVVRPGLGSKTG-SKRSQEDDILLEP 1222 GGITOMONE SALDBYANGAQOP CYLLSTRAGGLINLARADY VITOSIMMENDIQAS SAMETI GONKAWITEPYTRASVERTIQVAKKMOLLNILVVRPGLGSKTG-SKRSQEDDILLEP 1212 GGITOMONE SALDBYANGAQOP CYLLSTRAGGLINLARADY VITOSIMMENDIQAS SAMETI GONKAWITEPYTRASVERTIQVAKKMOLLNILVVRPGLGSKTG-SKRSQEDDILLEP 1207 GSITKOGNEDA DRYNAGAQOP CYLLSTRAGGLINLARADY VITOSIMMENDIQAS SAMETI GONKAWITEPYTRASVERTIQVAKKMOLLNILVVRPGLGSKTG-SKRSQEDDILLEP 1207 GSITKOGNEDA DRYNAFAGOP COLLARITISCOGLINA
CHD4_Cow CHD4_Zebrafish let-418_C.elegans E CHD4_Human CHD4_Chimp CHD4_Khesus CHD4_Chimp CHD4_hiso1_Rat CHD4_iso2_Rat CHD4_iso2_Rat CHD4_Zebrafish let-418_C.elegans F CHD4_Zebrafish let-418_C.elegans CHD4_Zebrafish let-418_C.elegans CHD4_iso1_Rat CHD4_hiso1_Rat CHD4_ARhesus CHD4_Zebrafish let-418_C.elegans G CHD4_Zebrafish let-418_C.elegans CHD4_Zebrafish let-418_C.elegans	1091 1098 1088 1083 974 1295 1208 1295 1295 1295 1295 1295 1295 1295 1295	GGITGINGERALDBFNANGAQOPCFLLSTRAGG.GINLARADTVITDSDIMTENDIQASSALET GONKTWITEPTRASVERITQVAKKMOLTNUTVEPGGESKTG-SUSSQEDDILLEP122 GGITGING GALDBFNANGAQOPCFLLSTRAGG.GINLARADTVITDSDIMTENDIQASSALET GONKTWITEPTRASVERITQVAKKMOLTNUTVEPGGESKTG-SUSSQEDDILLEP122 GGITGING GALDBFNANGAQOPCFLLSTRAGG.GINLARADTVITDSDIMTENDIQASSALET GONKTWITEPTRASVERITQVAKKMOLTNUTVEPGGESKTG-SUSSQEDDILLEP122 GGITGING GALDBFNANGAQOPCFLLSTRAGG.GINLARADTVITDSDIMTENDIQASSALET GONKTWITEPTRASVERITQVAKKMOLTNUTVEPGGESKTG-SUSSQEDDILLEP122 GGITGING GALDBFNANGAQOPCFLLSTRAGG.GINLARADTVITDSDIMTENDIQASSALET GONKTWITEPTRASVERITQVAKKMOLTNUTVEPGGESKTG-SUSSQEDDILLEP122 GGITGING GALDBFNANGAQOPCFLLSTRAGG.GINLARADTVITDSDIMTENDIQASSALET GONKTWITEPTRASVERITQVAKKMOLTNUTVEPGGESKTG-SUSSQED ED1266 GSINGOLGON DATABAGAQOPTFLLSTRAGG.GINLARADTVITDSDIMTENDIQASSALET GONKTWITEPTRASVERITGVAKKMOLTNUTVEPGGESKTG-SUSSQED SUSSGEDDILLEP126 GSINGOLGON DATABAGAQOPTFLLSTRAGG.GINLARADTVITDSDIMTENDIQASSALET GONKTWITEPTRASVERITGVAKKMOLTNUTVEPGGESKTG-SUSSQED SUSSGEDILLEP126 GSINGOLGON DATABAGAQOPTFLLSTRAGG.GINLARADTVITDSDIMTENDIQASSALET GONKTWITEPTRASVERITGVAKKMOLTNUTVEFGGESKTG-SUSSQED SUSSGEDILLEP126 GSINGOLGON DATABAGAQOPTFLLSTRAGG.GINLARADTVITDSDIMTENDIQASSALET GEVENA ETIKGES-SUPPOPTRELLARIHTEQOGEDLARILLEGON KROWTNOGGEDER 1353 EEEVENA ETIKGES-SUPPOPTRELLARIHTEGODEDLARILLEGON KROWTNOGGEDER 1353 EEEVENA ETIKGES-SUPPOPTRELLARIHTEG
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CHD4_Cow CHD4_Xenopus CHD4_Zebrafish let-418_C.elegans E CHD4_Human CHD4_Chimp CHD4_Rhesus CHD4_Dog CHD4_Iso1_Rat CHD4_iso2_Rat CHD4_Cow CHD4_Zebrafish let-418_C.elegans F CHD4_Rhesus CHD4_Chimp CHD4_Rhesus CHD4_iso1_Rat CHD4_iso1_Rat CHD4_iso2_Rat CHD4_iso2_Rat CHD4_iso1_Rat CHD4_Zebrafish let-418_C.elegans G CHD4_Zebrafish let-418_C.elegans CHD4_Zebrafish let-418_C.elegans	1091 1098 1088 1083 1083 1083 1083 1083 1083 1091 1088 1083 1083 1295 1570 1558 1570 1558 15763 15763 15763 15785 1882 1910 1898 1885 1882 1900 1898 1885	GGITGING DE ALDEPHA PAQQO'CILLSTRAGGLINLATADTVI UTUBUMINPO (QAFSARABE GONKIVNI TREVTAS SVERTQVAKKMBUTLI UVEPCLOSKTG-SNSKOE DD LLKP 1222 GGITGING DE ALDEPHA PAQQO'CILLSTRAGGLINLATADTVI UTUBUMINPO (QAFSARABE GONKIVNI TREVTAS SVERTQVAKKMBUTLI UVEPCLOSKTG-SNSKOE DD LLKP 1222 GGITGING DE ALDEPHA PAQQO'CILLSTRAGGLINLATADTVI UTUBUMINPO (QAFSARABE GONKIVNI TREVTAS SVERTQVAKKMBUTLI UVEPCLOSKTG-SNSKOE DD LLKP 1222 GGITGING DE ALDEPHA PAQQO'TILLSTRAGGLINLATADTVI UTUBUMINPO (QAFSARABE GONKIVNI TREVTAS SVERTQVAKKMBUTLINUVPCLOSKTG-SNSKOE DD LLKP 1220 GSINGONG DATUBHA PAQQO'TILLSTRAGGLINLATADTVI UTUBUMINPO (QAFSARABE) GONKIVNI TREVTAS SVERTQVAKKMBUTLINUVPCLOSKTG-SNSKOE DD LLKP 1220 GSINGONG DATUBHA PAQQO'TILLSTRAGGLINLATADTVI UTUBUMINPO (QAFSARABE) GONKIVNI TREVTAS SVERTQUAKKMBUTLINUVPCLOSKTG-SNSKOE DD LLKP 1220 GSINGONG DATUBHA PAQQO'TILLSTRAGGLINLATADTVI UTUBUMINPO (QAFSARABE) GONKIVNI TREVTAS SVERTUBUKKMBUTLINUVPLOSKTG-SNSKOE DD LLKP 1200 GSINGONG DATUBAL AND (GAN RAVOVINTUS (QAFSARABE) GONKIVNI TREVTAS SVERTUBUKKMBUTLINUVPLOSKTG-SNSKOE DD LLKP 1200 GSINGONG DATUBAL AND (GAN RAVOVINTUS (QAFSARABE) GONKIVITATVITAS SVERTUBUKKMBUTLINUVPLOSKTG-SNSKOE DD LLKP 1200 GSINGONG DATUBAL AND (GAN RAVOVINTUS (QAFSARABE) GONKIVALI TREVTAS SVERTUBUKKMBUTLINUVPLOSKTG-SNSKOE DD LLKP 1200 GSINGONG DATUBAL AND (GAN RAVOVINTUS (QAFSARAVOVINTUS (QAFSARABE) 1353 EEEVEN-E IIK (QEE-SVDPDYWKLLARHITSQOEDLANNIC GAN RAVOVINTUS (QEED 1353 EEEVEN E IIK (QEE-SVDPDYWKLLARHITSQOEDLANNIC GAN RAVOVIN
CHD4_Cow CHD4_Zebrafish let-418_C.elegans E CHD4_Human CHD4_Chimp CHD4_Chimp CHD4_Rhesus CHD4_Dog CHD4_iso1_Rat CHD4_lso2_Rat CHD4_Cow CHD4_Zebrafish let-418_C.elegans F CHD4_Khesus CHD4_Chimp CHD4_Khesus CHD4_iso1_Rat CHD4_iso2_Rat CHD4_iso2_Rat CHD4_iso2_Rat CHD4_Sebrafish let-418_C.elegans G CHD4_Zebrafish let-418_C.elegans G CHD4_Khesus CHD4_Zebrafish let-418_C.elegans	1091 1098 1088 1083 1083 1083 1083 1083 1091 1088 1083 1295 1283 1570 1570 1570 1570 1570 1571 1570 1570 1570 1570 1570 1570 1570 1570 1570 1570 1570 1570 <t< td=""><td>GGITGSMEDEALDERNAPAQQCCFLLSTRAGGGUNLATADYTITUSDNMEND (JAPSBARD CONKWLITEVTRASVEERITQVAKKOULTIUVURGLOSKT-BISKQD DULKP 1215 GGITGSMEDEALDERNAPAQQCCFLLSTRAGGUNLATADYTITUSDNMEND (JAPSBARD CONKWLITEVTRASVEERITQVAKKOULTIUVURGLOSKT-BISKQD DULKP 1212 GGITGSMEDEALDERNAPAQQCFLLSTRAGGUNLATADYTITUSDNMEND (JAPSBARD CONKWLITEVTRASVEERITQVAKKOULTIUVURGLOSKT-BISKQD DULKP 1212 GGITGSMEDEALDERNAPAQQCFLLSTRAGGUNLATADYTITUSDNMEND (JAPSBARD CONKWLITEVTRASVEERITQVAKKOULTIUVURGLOSKT-BISKQD DULKP 1212 GGITGSMEDEALDERNAPAQQCFLLSTRAGGUNLATADYTITUSDNMEND (JAPSBARD CONKWLITEVTRASVEERITQVAKKOULTIUVURGLOSKT-BISKQD DULKP 1212 GGITGSMEDEALDERNAPAQQCFLLSTRAGGUNLATADYTITUSDNMEND (JAPSBARD CONKWLITEVTRASVEERITGVAKKOULTIUVURGLOSKT-BISKQD DULKP 1212 GGITGSMEDEALDERNAPAQQCFLLSTRAGGUNLATADYTITUSDNMEND (JAPSBARD CONKWLITEVTRASVEERITGVAKKOULTIUVURGLOSKT-BISKQD DULKP 1212 GGITGSMEDEALDERNAPAQQCFLLSTRAGGUNLATADYTITUSDNMEND (JAPSBARD CONKWLITEVTRASVEERITGVAKKOULTIUVURGLOSKT-BISKQD DULKP 1212 GGITGSMEDEALDERNAPAQQCFLSTRAGGUNLATADYTITUSDNMEND (JAPSBARD JAPSBARD CONKWLITED) EEEVER-SITUGES-SVPDYNKLIAHITSQQCELANN KKKRIKKVVIINGGUNLASS EEEVER-SITUGES-SVPDYNKLIAHITSQQCELANN KKKRIKKVVIINGGUNLASS EEEVER-SITUGES-SVPDYNKLIAHITSQQCELANN KKKRIKKVVIINGGUNLASS EEEVER-SITUGES-SVPDYNKLIAHITSQQCELANN KKKRIKKVVIINGGUNLASS EEEVER-SITUGES-SVPDYNKLIAHITSQQCELANN KKKRIKKVVIINGSGEN 133 EEEVER-SITUGES-SVPDYNKLIAHITSQQCELANN KKKRIKKVVIINGSGEN 134 EEEVER-SITUGES-SVPDYNKLIAHITSQQCELANN KKKRIKKVVIINGSGEN 134 EEEVER-SITUGES-SVPDYNKLIAHITSQQCELANN KKKRIKKVVIINGSGEN 134 EEEVER-SITUGESKVSTAAFTIICTQAPAA SEDEKVVEREPREEVEREPREEVEREPREE-EFKGAVURVINGSGEN 124 EEEVER-SITUGESKVSTAAFTIICTQAPAA SEDEKVVEREPREEVEREPREEVEREPREEMENT-EFKGAVURVINGKKRIKE 1556 SURVERVEREKKERTETSSEALKKRYCPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPA</td></t<>	GGITGSMEDEALDERNAPAQQCCFLLSTRAGGGUNLATADYTITUSDNMEND (JAPSBARD CONKWLITEVTRASVEERITQVAKKOULTIUVURGLOSKT-BISKQD DULKP 1215 GGITGSMEDEALDERNAPAQQCCFLLSTRAGGUNLATADYTITUSDNMEND (JAPSBARD CONKWLITEVTRASVEERITQVAKKOULTIUVURGLOSKT-BISKQD DULKP 1212 GGITGSMEDEALDERNAPAQQCFLLSTRAGGUNLATADYTITUSDNMEND (JAPSBARD CONKWLITEVTRASVEERITQVAKKOULTIUVURGLOSKT-BISKQD DULKP 1212 GGITGSMEDEALDERNAPAQQCFLLSTRAGGUNLATADYTITUSDNMEND (JAPSBARD CONKWLITEVTRASVEERITQVAKKOULTIUVURGLOSKT-BISKQD DULKP 1212 GGITGSMEDEALDERNAPAQQCFLLSTRAGGUNLATADYTITUSDNMEND (JAPSBARD CONKWLITEVTRASVEERITQVAKKOULTIUVURGLOSKT-BISKQD DULKP 1212 GGITGSMEDEALDERNAPAQQCFLLSTRAGGUNLATADYTITUSDNMEND (JAPSBARD CONKWLITEVTRASVEERITGVAKKOULTIUVURGLOSKT-BISKQD DULKP 1212 GGITGSMEDEALDERNAPAQQCFLLSTRAGGUNLATADYTITUSDNMEND (JAPSBARD CONKWLITEVTRASVEERITGVAKKOULTIUVURGLOSKT-BISKQD DULKP 1212 GGITGSMEDEALDERNAPAQQCFLLSTRAGGUNLATADYTITUSDNMEND (JAPSBARD CONKWLITEVTRASVEERITGVAKKOULTIUVURGLOSKT-BISKQD DULKP 1212 GGITGSMEDEALDERNAPAQQCFLSTRAGGUNLATADYTITUSDNMEND (JAPSBARD JAPSBARD CONKWLITED) EEEVER-SITUGES-SVPDYNKLIAHITSQQCELANN KKKRIKKVVIINGGUNLASS EEEVER-SITUGES-SVPDYNKLIAHITSQQCELANN KKKRIKKVVIINGGUNLASS EEEVER-SITUGES-SVPDYNKLIAHITSQQCELANN KKKRIKKVVIINGGUNLASS EEEVER-SITUGES-SVPDYNKLIAHITSQQCELANN KKKRIKKVVIINGGUNLASS EEEVER-SITUGES-SVPDYNKLIAHITSQQCELANN KKKRIKKVVIINGSGEN 133 EEEVER-SITUGES-SVPDYNKLIAHITSQQCELANN KKKRIKKVVIINGSGEN 134 EEEVER-SITUGES-SVPDYNKLIAHITSQQCELANN KKKRIKKVVIINGSGEN 134 EEEVER-SITUGES-SVPDYNKLIAHITSQQCELANN KKKRIKKVVIINGSGEN 134 EEEVER-SITUGESKVSTAAFTIICTQAPAA SEDEKVVEREPREEVEREPREEVEREPREE-EFKGAVURVINGSGEN 124 EEEVER-SITUGESKVSTAAFTIICTQAPAA SEDEKVVEREPREEVEREPREEVEREPREEMENT-EFKGAVURVINGKKRIKE 1556 SURVERVEREKKERTETSSEALKKRYCPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPA

Supplementary Figure 7. Cross-species conservation of CHD4 showing residues mutated in endometrial cancer (red).

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Lys72Argfs*128

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CHD4	20	ALLNNSLPPPHPENEEDPEED	LSETETPKLKK	KKKPKKF	PRDPKI	PKSKRQK	KKERMLLCRQLGD	SSGEGPE	VEEEEEVA	LRSDSEGSDYT-	-PGKKKKKK	119
CHD3_iso_1	20	ISFPPGLCWGDRMPDKDDIR	LLPSALGVKKR	KRGPKKÇ	XENKP	GKPRKR	K <mark>KR</mark>	DSEEEE	GSERDEYR	EKSESGGSEYGT	GPGRKRRRK	106
CHD3_iso_2	20	ISFPPGLCWGDRMPDKDDIR	LLPSALGVKKR	KRGPKKÇ	KENKP	GKPRKRK	KKR	DSEEEE	GSERDEYR	EKSESGGSEYGT	GPGRKRRRK	106
CHD3_iso_3	69	GCHLFPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	LLPSALGVKKR	KRGPKKÇ	KENKP	GKPRKR	KKR	DSEEEF	GSERDEYR	EKSESGGSEYGT	GPGRKRRRK	165
CHD5	19	MENEDEMSEEEDGGLEAFDD	FFPVEPVSLPK	KKKPKKI	LKENKC	-KGKRK	к <mark>ке</mark>	GSNDEI	LSENEEDLE	EKSESEGSDYS-	-PNKKKKKK	102

В		Val558Phe Arg572Gln	
	506		610
CHD4 CHD3 iso 1	508	LINANGYFSFIVYRF-FUDIAFNIFSGRFGARAGETYLWYGINSIMCSWYCSWACSULLLIAUUNTUL GARMMULFFSGFFG-GULL-ASKARAMUJFA-ALMEL	619
CHD3_iso_2	513	LHWRWGEPPVAVPAPQQ-ADGNPDVPPPRPLQGRSEREFFVKWVGLSYWHCSWAKELQLEIFHLVMYRNYQRKNDMDEPPPLDYGSGEDDGKSDKRKVKDPHYAEMEE	619
CHD3_iso_3 CHD5	572 473	LHWRWGEPVAVPAPQQ-ADGNPDVPPPRPLQGRSEREFFVKWQGLSWHCSWAKLQLEIFHLVMVRNYQRKNDMDEPPPLDVGSGDDGKSDKKKVKDPH1AEMEE LHWRWFEPDAPPMVGI, GGDNUFBAL, DPDKPLGCIPREFFVKWQGLSVHCSWAKELOLEI, HLVMVWFNYQRKNDMDEPPPPDVGSGDEDGKSEKKKNKDPLAKMEE	678 580

C		Arg8 <u>1</u> 7Gln		del874Glu	Arg877Trp	Leu9	2Val	
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CHD4 CHD3 iso 1	801	MYVVTYVGDKDSRAIIR EVVVTYVGDKDSRAIIR EVVVTYVGDKDSRAIIR EVVVTYVGDKDSRAIIR	SRMKKEASVKFHVLLTSYELITIDMAILG	SIDWACLIVDEA	HRLKNNQSKFFRVLNO	YSLQHKLLLTGTPLQNNLEEL	FHLLNFLTPE 9	22
CHD3_iso_2	811	FYVVTYTGDKDSRAIIRENEFSFEDNAIKGGKKAN	FKMKREAQVKFHVLLTSYELITIDQAALG	SIRWACLVVDEA	HRLKNNQSKFFRVLNO	GYKIDHKLLLTGTPLQNNLEEI	FHLLNFLTPE 9	32
CHD3_iso_3	870	FYVVTYTGDKDSRAIIRENEFSFEDNAIKGGKKA	FKMKREAQVKFHVLLTSYELITIDQAALG	SIRWACLVVDEA	HRLKNNQSKFFRVLNO	YKIDHKLLLTGTPLQNNLEE	FHLLNFLTPE 9	91
CHD5	115	FIVVTITGDKESRSVI <mark>R</mark> ENEFSFEDNAIRSGKKVI	RMKKEVQIKFHVLLTSYELITIDQAILG	SIEWACLVVDEA	HRLKNNQSKFFRVLNS	SYKIDYKLLLTGTPLQNNLEE <mark>L</mark>	FHLLNFLTPE 8	96
			His1151Arg	Arg1162G	iln,			
			del1152Asn	Arg1162T	rp			
D		Arg1105Gln		-			Leu1215	5Pro
		***** ****	* * * * * * * * * * * * * * * * * * *	**** :****	* * * * * * * * * * * * * * * * * *	*********************	*:******	********
CHD4	1098	GGITGNMRQEAIDRFNAPGAQQFCFLLSTRAGGL	JINLATADTVIIYDSDWNPHNDIQAFSRA	HRIGONKKVMIY	RFVTRASVEERITQV	AKKKMMLTHLVVRPGLGSKTGS	MSKQELDDILKF	GTEELFKDEAT 1232
ChD5_180_1	1100	GGIIGALAURTAIDAT MAPGAQQF CF LLSTRAGGLG	SINLAIADIVIII DODWNPHNDIQAF SKA	INT GOVINK MITT	KF VIKASVEERI 1QVF	AKKKPIPILI HL V V KPGLGSKAGS	LISKAPPDDICKL	GIGGLFRDENE 1242

CHD3 19	50 I	1108	GGITGALKQEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIFDSDWNPHNDIQAFSRAHKIGQANKVMIYRFVTRASVEERITQVAKRKMMLTHLVVRPGLGSKAGSMSKQELDDILKFGTEELFKDENE 1242
CHD3 is	so 2	1108	GGITGAL ROEAIDRFNAPGAQOFCFLLSTRAGGLGINLATADTVIIFDSDWNPHNDIQAFSRAHRIGQANKVMIYRFVTRASVEERITQVAKRKMMLTHLVVRPGLGSKAGSMSKQELDDIL KFGTEELFKDENE 1242
CHD3 is	io 3	1167	GGITGAL ROEAIDRFNAPGAOOFCFLLSTRAGGLGINLATADTVIIFDSDWNPHNDIOAFSRAHRIGOANKVMIYRFVTRASVEERITOVAKRKMMLTHLVVRPGLGSKAGSMSKOELDDILKFGTEELFKDENE 1301
CHD5	-	1072	GGITGGIRGEAIDRFNAPGAOOFCFLISTRAGGIGINIATADTVIIYDSDWNPHNDIOAFSRAHRIGONKKWMIYRFVTRASVEERITOVAKRKMMLTHLVVRPGLGSKSGSMTKOELDDIKKGTEELFKDDVE 1206

E		Gly1334Val Arg1338Gln	
		** <u>*</u> *********************************	
CHD4	1295	EEEVEREIIKQEESVDPDYWEKLLRHHYEQQQEDLARNL <mark>G</mark> KGK <mark>R</mark> IRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEEGDE	1375
CHD3_iso_1	1299	IEEIEREIIKQEENVDPDYWEKLLRHHYEQQQEDLARNICKGKRVRKQVNYNDAAQEDQDNQSEYSVGSEEEDE	1372
CHD3_iso_2	1299	IEEIEREIIKQEENVDPDYWEKLLRHHYEQQQEDLARNICKGKRVRKQVNYNDAAQEDQDNQSEYSVGSEEEDE	1372
CHD3_iso_3	1358	IEEIEREIIKQEENVDPDYWEKLLRHHYEQQQEDLARNL <mark>G</mark> KGK <mark>R</mark> VRKQVNYNDAAQEDQDNQSEYSVGSEEEDE	1431
CHD5	1301	VEEVEREIIKQEENVDPDYWEKLLRHHYEQQQEDLARNL <mark>G</mark> KGK <mark>R</mark> IRKQVNYNDASQEDQEWQDELSDNQSEYSIGSEDEDE	1381

Ser1570Asn					Ala1649Val						
	*	□	* :: .	*.	: *:	. ::.	: 3	* .:			
1550	QPNTPAPVPPAEDGIKIEEN	SLKE-EESIEG	EKEVKST-AP	ETAIECTQAP	APASEDEKVV	VEPPEGEEKVE	KAEVKERTI	EEPMETEPKG	AADVEKVEEKS	AIDLTPIVVEDKEEKKEE	1667
1 1551	CTSKPATPAPSEKGEGIRTP	LEKEEAENQEE	KPEKNSRIGE	KMETEADAPS	PAPSLGERLE	PRKIPLEDEVE	GVPGEMEPI	EPGYRGDREK	SATESTPGERG	EEKPLDGQEHRERPEGETGDLGKRED	7 1678
2 1551	CTSKPATPAPSEKGEGIRTP	LEKEEAENQEE	KPEKNSRIGE	KMETEADAPS	PAPSLGERLE	PRKIPLEDEVE	GVPGEMEPI	EPGYRGDREK	s	ED'	7 1644
3 1610	CTSKPATPAPSEKGEGIRTP	LEKEEAENQEE	KPEKNSRIGE	KMETEADAPS	PAPSLGERLE	PRKIPLEDEVE	GVPGEMEPI	EPGYRGDREK	SATESTPGERG	EEKPLDGQEHRERPEGETGDLGKRED	/ 1737
1559	LPAPLGLPDKMEAQLGYMDE	KDPG–AQKPRQ	PLEVQALPAA	LDRVESEDKH	ESPASKERAR	EERPEETEKAF	PSPEQLPRI	EEVLPEKEKI	LDKLELSLIHS	RGDSTKAE	1674
		-								-	
	1550 1 1551 2 1551 3 1610 1559	Ser15 1550 OPNTPAPVPPAEDGIKIEEN 1551 CTSKPATPAPSEKGEGIRTF 21551 CTSKPATPAPSEKGEGIRTF 31610 CTSKPATPAPSEKGEGIRTF 1559 LPAPLGLPDKMEAQLGYMDE	Ser1570Asn * : 1550 OPNTPAPVPPAEDGIKIEENSLKE-EESIEG 1551 CTSKPATPAPSEKGEGIRTPLEKEEAENQEE 21551 CTSKPATPAPSEKGEGIRTPLEKEEAENQEE 31610 CTSKPATPAPSEKGEGIRTPLEKEEAENQEE 1559 LPAPLGLPDKMEAQLGYMDEKOPG-AQKPRO	Ser1570Asn * :*: 1550 OPNTPAPVPPAEDGIKIEENSLKE-EESIEGEKEVKST-AP 1551 CTSKPATPAPSEKGEGIRTPLEKEEAENQEEKPEKNSRIGE 21551 CTSKPATPAPSEKGEGIRTPLEKEEAENQEEKPEKNSRIGE 31610 CTSKPATPAPSEKGEGIRTPLEKEEAENQEEKPEKNSRIGE 1559 LPAPLGLPDKMEAQLGYMDEKOPG-AQKPROPLEVQALPAA	Ser1570Asn * :*: 1550 OPNTPAPVPPAEDGIKIEENSLKE-EESIEGEKEVKST-APETAIECTQAP 1551 CTSKPATPAPSEKGEGIRTPLEKEEAENQEEKPEKNSRIGEKMETEADAPS 21551 CTSKPATPAPSEKGEGIRTPLEKEEAENQEEKPEKNSRIGEKMETEADAPS 31610 CTSKPATPAPSEKGEGIRTPLEKEEAENQEEKPEKNSRIGEKMETEADAPS 1559 LPAPLGLPDKMEAQLGYMDEKOPG-AQKPROPLEVQALPAALDRVESEDKH	Ser1570Asn * :: *: *: *: *: *: *: *: *: *: *: *: *:	Ser1570Asn * : *:: *: *: .: *: .: *: .: *: :: *: ::: 1550 OPNTPAPVPPAEDGIKIEENSLKE-EESIEGEKEVKST-APETAIECTQAPAPASEDEKVVVEPPEGEEKVE 1551 CTSKPATPAPSEKGEGIRTPLEKEEAENQEEKPEKNSRIGEKMETEADAPSPAPSLGERLEPRKIPLEDEVI 21551 CTSKPATPAPSEKGEGIRTPLEKEEAENQEEKPEKNSRIGEKMETEADAPSPAPSLGERLEPRKIPLEDEVI 31610 CTSKPATPAPSEKGEGIRTPLEKEEAENQEEKPEKNSRIGEKMETEADAPSPAPSLGERLEPRKIPLEDEVI 1559 LPAPLGLPDKMEAQLGYMDEKDPG-AQKPROPLEVQALPAALDRVESEDKHESPASKERAREERPEETEKA	Ser1570Asn * :: *: *: *: :: *: :: :: :: : 1550 OPNTPAPVPPAEDGIKIEENSLKE-EESIEGEKKEVKST-APETAIECTQAPAPASEDEKVVVEPPEGEEKVEKAEVKERT 1551 CTSKPATPAPSEKGEGIRTPIEKEEAENQEEKPEKNSRIGEKMETEADAPSPAPSLGERLEPRKIPLEDEVPGVPGEMEPI 21551 CTSKPATPAPSEKGEGIRTPIEKEEAENQEEKPEKNSRIGEKMETEADAPSPAPSLGERLEPRKIPLEDEVPGVPGEMEPI 31610 CTSKPATPAPSEKGEGIRTPIEKEEAENQEEKPEKNSRIGEKMETEADAPSPAPSLGERLEPRKIPLEDEVPGVPGEMEPI 1559 LPAPLGLPDKMEAQLGYMDEKOPG-AQKPROPLEVQALPAALDRVESEDKHESPASKERAREERPEETEKAPPSPEQLPRI	Ser1570Asn * *	Ser1570Asn Ala16 *	Ser1570Asn Ala1649Val *

G		Glu1902Lys	

CHD4	1859	ELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAPEPTPQQVAQQQQVAQQQQVAQAAAAAAAA	1912
CHD3_iso_1	L 1870	${\tt ellsdmkadvtrlpatlsrippiaarlqmsersilsrlaskgt} phptpayppgyatppgygaafsaapvgalaaganysqmpagsfitaatngppvlvkkekemvgalvsdgldrkepragevicidd$	2000
CHD3_iso_2	2 1836	ELLSDMKADVTRLPATLSRIPPIAARLQMSERSILSRLASKGT <mark>B</mark> PHPTPAYPPGPYATPPGYGAAFSAAPVGALAAAGANYSQMPAGSFITAATNGPPVLVKKEKEMVGALVSDGLDRKEPRAGEVICIDD	1966
CHD3_iso_3	3 1921	ELLSDMKADVTRLPATLSRIPPIAARLQMSERSILSRLASKGT <mark>B</mark> PHPTPAYPPGPYATPPGYGAAFSAAPVGALAAAGANYSQMPAGSFITAATNGPPVLVKKEKEMVGALVSDGLDRKEPRAGEVICIDD	2059
CHD5	1866	ELLSDMKADVTRLPSMLSRIPPVAARLQMSERSILSRLTNRAGDPTIQQGAFGSSQMYSNNFGPNFRGPGPGGIVNYNQMPLGPYVTDI	1954

Supplementary Figure 8. Alignment of CHD4 and closely related family members. CHD4 residues mutated in endometrial cancer are indicated in red.



Supplementary Figure 9. Partial, structure-based, sequence alignment of the ATPase/helicase and helicase domains of CHD4 to the Snf2 domains of SMARCA2, SMARCAL1, and SMARCA4. Five resides (blue boxes) that are somatically mutated in CHD4 in endometrial cancer, are conserved in SMARCA2, SMARCAL1, and SMARCA4 and undergo pathogenic germline mutations in patients with Nicolaides-Baraister syndrome (SMARCA2), Schimke immuno-osseous dysplasia (SMARCAL1), and Coffin-Siris syndrome (SMARCA4) (references 20-22).



Supplementary Figure 10. Distribution of somatic variants called by whole exome sequencing (WES) according to score and coverage. (a-c) Dot plots showing thresholds (orange lines) used to filter the calls to achieve a balance between specificity and sensitivity of somatic mutation detection. Dot plots display variants called as somatic by WES, according to their validation status by Sanger sequencing before (d) and after (e) filtering on score and coverage. Each point represents an individual variant; the validation status of variants is somatic (black), germline (red), not evaluated (light blue), or not detectable in the tumor (dark blue).

				Augusta dauth of sources for	No. of targeted bases with	% of targeted bases with
Sample	No. of bases targeted	No. of bases covered	% of targeted bases covered	Average depth of coverage for	sufficient coverage and quality	sufficient coverage and quality
				alighed reads	for variant calling	for variant calling
Tumor samples						
T27	37,640,396	37,041,467	98.41%	100.8	35,861,300	91.69%
T33	51,499,639	49,957,360	97.01%	150.4	48,506,495	91.33%
T45	37,640,396	36,951,637	98.17%	105.1	35,684,195	90.73%
T47	51,499,639	49,876,467	96.85%	94.8	48,142,085	89.19%
T56	51,499,639	49,879,322	96.85%	120.2	48,411,478	89.69%
T65	51,499,639	49,730,719	96.57%	75.4	48,505,619	87.06%
T69	51,499,639	49,892,083	96.88%	119.2	48,444,093	89.71%
T70	51,499,639	49,785,681	96.67%	74.8	47,969,296	87.07%
T75	51,499,639	49,733,051	96.57%	69.8	47,526,230	86.89%
T80	37,640,396	36,722,341	97.56%	70.8	35,832,195	85.89%
T154	51,499,639	49,935,941	96.96%	126.6	48,398,890	90.34%
T155	51,499,639	49,903,701	96.90%	128.5	48,066,638	89.87%
T162	51,499,639	49,951,052	96.99%	101.9	48,173,519	89.11%
Matched norma	al samples					
N27	37,640,396	36,984,288	98.26%	102.5	36,035,725	91.15%
N33	51,499,639	50,040,094	97.17%	124.4	48,552,347	90.79%
N45	37,640,396	36,952,879	98.17%	81.4	35,757,557	89.81%
N47	51,499,639	49,903,532	96.90%	95.2	47,995,032	89.60%
N56	51,499,639	49,953,739	97.00%	117.5	48,103,183	90.63%
N65	51,499,639	50,067,103	97.22%	72.4	47,414,952	89.91%
N69	51,499,639	50,036,195	97.16%	127.4	48,131,346	90.64%
N70	51,499,639	49,900,106	96.89%	80.6	47,435,488	88.89%
N75	51,499,639	49,746,618	96.60%	69.5	47,379,192	87.47%
N80	37,640,396	36,968,802	98.22%	117	34,836,598	91.21%
N154	51,499,639	49,968,334	97.03%	116.2	48,323,669	90.51%
N155	51,499,639	49,892,810	96.88%	108.9	48,121,062	89.54%
N162	51,499,639	50,010,023	97.11%	105.5	47,950,781	89.82%
Weighted						
average of			97.13%	102.6		89.53%
all tumors						

Supplementary Table 2: Depth of whole exome sequencing coverage

Tumor ID	No. of exonic synomymous somatic mutations	No. of exonic non synonymous somatic mutations	Total no of exonic somatic mutations	No. of covered bp within coding exons	Mutation rate	Grubbs' Test for outliers approximate P value
T27	3	8	11	26,679,401	4.123.E-07	9.079
Т33	20	34	54	30,495,201	1.771.E-06	10.558
T45	7	22	29	26,319,267	1.102.E-06	9.822
T47	27	62	89	29,912,229	2.975.E-06	11.909
Т56	8	41	49	30,175,714	1.624.E-06	10.395
T65	10	32	42	29,351,564	1.431.E-06	10.183
Т69	3	24	27	30,162,216	8.952.E-07	9.598
Т70	15	36	51	29,345,612	1.738.E-06	10.522
T75	10	28	38	29,122,936	1.305.E-06	10.044
Т80	11	37	48	25,471,115	1.884.E-06	10.684
T154	18	35	53	30,266,338	1.751.E-06	10.536
T162	4	21	25	29,980,154	8.339.E-07	9.531
T155	203	803	1006	30,070,801	3.345.E-05	6.59E-13
All Tumors	339	1183	1522	377,352,548	4.033.E-06	Not applicable
Non Hypermutated Tumors	136	380	516	347,281,747	1.486.E-06	Not applicable

Supplementary Table 3: Exonic somatic mutation rate of the 13 serous endometrial tumors included in the exome discovery screen

	No. of variants called by exome sequencing (No. of variants confirmed by Sanger seque								
Tumor	Exonic v	variants	Calico lunction variante	Total					
	Synonymous	Nonsynonymous	- Splice Junction variants	Iotal					
T27	3 (1)	8 (5)	2 (0)	13 (6)					
T33	20 (11)	34 (32)	1 (1)	55 (44)					
T45	7 (4)	22 (18)	0 (0)	29 (22)					
T47	27 (24)	62 (55)	0 (0)	89 (79)					
T56	8 (6)	41 (31)	0 (0)	49 (37)					
T65	10 (7)	32 (28)	2 (2)	44 (37)					
T69	3 (3)	24 (21)	3 (3)	30 (27)					
Т70	15 (13)	36 (31)	1 (1)	52 (45)					
T75	10 (10)	28 (26)	1 (1)	39 (37)					
T80	11 (11)	37 (32)	0 (0)	48 (43)					
T154	18 (16)	35 (27)	1 (1)	54 (44)					
T162	4 (3)	21 (15)	0 (0)	25 (18)					
Total	136 (109)	380 (321)	11 (9)	527 (439)					
Average no. of variants/tumor	11.3 (9.1)	31.7 (26.8)	0.9 (0.8)	43.9 (36.6)					
Average no. of nonsynonymous and									
splice junction variants/tumor		32	.6 (27.5)						

Supplementary Table 6: Distribution of somatic variants called by whole exome sequencing among 12 tumors in the discovery screen

Gene Name	Transcript Accession Id	Tumor	Nucleotide Change	Amino Acid Change	Mutation Assessor Prediction
TP53	uc002gij.2	T47	c.1009C>T	p.Arg337Cys	Medium
TP53	uc002gij.2	Т33	c.1025G>C	p.Arg342Pro	Medium
TP53	uc002gij.2	T69	c.614A>G	p.Tyr205Cys	High
TP53	uc002gij.2	T56	c.309C>A	p.Tyr103*	-
TP53	uc002gij.2	T154	c.1045G>T	p.Glu349*	-
TP53	uc002gij.2	T162	c.814G>C	p.Val272Leu	Medium
TP53	uc002gij.2	T65	c.476C>T	p.Ala159Val	Medium
TP53	uc002gij.2	T65	c.475G>T	p.Ala159Ser	High
TP53	uc002gij.2	T70	c.742C>T	p.Arg248Trp	High
TP53	uc002gij.2	T80	c.422G>A	p.Cys141Tyr	High
РІКЗСА	uc003fjk.1	T80	c.263G>A	p.Arg88GIn	Medium
РІКЗСА	uc003fjk.1	T75	c.3172A>T	p.lle1058Phe	Low
РІКЗСА	uc003fjk.1	T75	c.3207A>G	p.*1069insWKDN	-
РІКЗСА	uc003fjk.1	T69	c.3132T>A	p.Asn1044Lys	Low
FBXW7	uc003ims.1	T80	c.1385C>T	p.Ser462Phe	Medium
FBXW7	uc003ims.1	T80	c.1322G>C	p.Arg441Pro	Medium
FBXW7	uc003ims.1	T47	c.1436G>A	p.Arg479Gln	Medium
FBXW7	uc003ims.1	T162	c.1436G>A	p.Arg479Gln	Medium
FBXW7	uc003ims.1	T69	c.2065C>T	p.Arg689Trp	Low
CHD4	uc001qpo.1	Т33	c.3485G>A	p.Arg1162Gln	High
CHD4	uc001qpo.1	T154	c.1672G>T	p.Val558Phe	Medium
CHD4	uc001qpo.1	T56	c.3460_3462delATT	p.Asn1152del	-
SPOP	uc002ipg.1	T56	c.240C>G	p.Ser80Arg	Medium
SPOP	uc002ipg.1	T80	c.280C>G	p.Pro94Ala	Low
SPOP	uc002ipg.1	T154	c.362G>A	p.Arg121Gln	Medium
PPP2R1A	uc002pyp.1	T70	c.771G>T	p.Trp257Cys	Medium
PPP2R1A	uc002pyp.1	T65	c.1757T>C	p.Leu586Pro	Medium
PPP2R1A	uc002pyp.1	T154	c.767C>T	p.Ser256Phe	Medium
PPP2R1A	uc002pyp.1	T69	c.536C>G	p.Pro179Arg	Medium
MAP3K4	uc003qtq.1	T80	c.4165G>A	p.Glu1389Lys	High
MAP3K4	uc003qtq.1	T65	c.4077delC	p.Cys1359Alafs*8	-
ABCC9	uc001rfh.1	T70	c.2185G>T	p.Val729Phe	High
ABCC9	uc001rfh.1	T75	c.3381G>A	p.Met1127Ile	Low
CYP4X1	uc001cqr.1	T75	c.1036G>C	p.Val346Leu	Low
CYP4X1	uc001cqr.1	T56	c.211G>A	p.Glu71Lys	Low

Supplementary Table 7: Nine genes with validated mutations in more than one tumor in the discovery screen

(-) Not evaluated by Mutation Assessor

Gene Name (RefSeq ID; UCSC Transcript Accession ID^)	Mutation frequency in serous tumors	Tumor	Histology	Nucleotide Change	Amino Acid Change	Mutation type
TP53	71% (37/52)	T164	Serous	c.251delC	p.Pro84Leufs*38	Deletion
(NM 00112611		T56	Serous	c.309C>A	p.Tyr103*	Nonsense
4; uc002gij.2)		T52	Serous	c.377A>G	p.Tyr126Cys	Missense
		T45	Serous	c.395A>G	p.Lys132Arg	Missense
		T50	Serous	c.399_400insTT	p.Met133_Phe134insFfs*35	Insertion
		T10 (OM-2009-C1)	Serous	c.406C>G	p.Gln136Glu	Missense
		Т80	Serous	c.422G>A	p.Cys141Tyr	Missense
		T41	Serous	c.434T>C	p.Leu145Pro	Missense
		T65	Serous	c.475G>T	p.Ala159Phe	Missense
		T65	Serous	c.476C>T	p.Ala159Phe	Missense
		T29	Serous	c.536A>G	p.His179Arg	Missense
		T165	Serous	c.538G>T	p.Glu180*	Nonsense
		T69	Serous	c.614A>G	p.Tyr205Cys	Missense
		T55	Serous	c.637C>T	p.Arg213*	Nonsense
		T163	Serous	c.641A>G	p.His214Arg	Missense
		T83	Serous	c.722C>G	p.S241Cys	Missense
		T185	Serous	c.722C>T	p.S241Phe	Missense
		T75	Serous	c.731G>T	p.G244Val	Missense
		T71	Serous	c.733G>A	p.G245Ser	Missense
		T78	Serous	c.733G>A	p.G245Ser	Missense
		T76	Serous	c.734G>A	p.G245Asp	Missense
		T51	Serous	c.739delA	p.Asn247Thrfs*98	Deletion
		T23	Serous	c.742C>G	p.Arg248Trp	Missense
		T66	Serous	c.742C>T	p.Arg248Trp	Missense
		T70	Serous	c.742C>T	p.Arg248Trp	Missense
		T8 (OM-2511-C1)	Serous	c.743G>A	p.Arg248GIn	Missense
		T68	Serous	c.763A>T	p.Ile255Phe	Missense
		T112	Serous	c.764T>C	p.Ile255Thr	Missense
		T162	Serous	c.814G>C	p.Val272Leu	Missense
		T114	Serous	c.817C>T	p.Arg273Cys	Missense
		T167	Serous	c.818G>A	p.Arg273His	Missense
		T185	Serous	c.818G>A	p.Arg273His	Missense
		T30	Serous	c.824G>T	p.Cvs275Phe	Missense
		T166	Serous	c.830G>T	p.Cvs277Phe	Missense
		T53	Serous	c.841G>A	p.Asp281Asp	Missense
		T107	Serous	c 841G>C	n Asn281His	Missense
		T75	Serous	c 844C>T	n Arg282Trn	Missense
		T47	Serous	c 1009C>T	n Arg337Cvs	Missense
		т33	Serous	c 1025G>C	n Arg342Pro	Missense
		T154	Serous	c 1045G>T	n Glu349*	Nonsense
РІКЗСА	31% (16/52)	T75	Serous	c.3207A>G	p.*1069 *1069insTrpLysAspAsn*	Insertion
NM 006218.1:		T3 (OM-1323-C1)	Serous	c.241G>A	p.Glu81Lvs	Missense
uc003fik.1) ‡		T10 (OM-2009-C1)	Serous	c.1634A>C	p.Glu545Ala	Missense
, ·		T41	Serous	c.42 64delinsTCCAA	p.Leu15 Val22insProlle	Insertion
		T29	Serous	c.1624G>A	p.Glu542Lvs	Missense
		T49	Serous	c 1624G>C	n Glu542Gln	Missense
		T53	Serous	c 1637A>C	n Gin546i vs	Missense
		T68	Serous	c 263G>A	n Arg88GIn	Missense
		T68	Serous	c 323G>A	n Arg108His	Missense
		T60	Serous	c 3132T\A	p.Arg100113	Missense
		T71	Serous	c 10020-V	n Glu365Lvs	Missense
		T74	Serous	C 2120CVT	p.610303Lys	Missense
		T74	Serous	c 278G\A	n Argozeln	Missense
		T74	Serous	C 332GNT	n Lys111Acn	Missense
		174	Serour	C 2172A-T	p.Lys111ASH	Missense
		T76	Serous	C 1257CNA	p.ile1030File	Missonso
		170	Serous	C 221ASC	p.Glu455Lys	Missonso
		1/0	Sorous	C.331A20	p.Lys1110lu	Missonss
		1/9	Serous	L.5U/3A/G	p.mituzsaia	Missense
		180	Serous	C.203G>A	p.Arg88GIN	iviissense
000204 *	250/ /42/52)	101	Serous	C.314UA>G	p.H104/Arg	iviissense
PPP2KIA	25% (13/52)	151	Serous	C.536C>G	p.Pro1/9Arg	IVIISSENSE
(INIVI_U14225;		109	Serous	C.536C>G	p.Pro1/9Arg	iviissense
ucuu2pyp.1)		183	Serous	C.536C>G	p.Pro1/9Arg	IVIISSENSE
		1107	Serous	c.536C>G	p.Pro179Arg	Missense
		T164	Serous	c.536C>G	p.Pro179Arg	Missense
		T50	Serous	c.767C>G	p.Ser256Phe	Missense
		T108	Serous	c.767C>G	p.Ser256Phe	Missense
		T154	Serous	c.767C>G	p.Ser256Phe	Missense
		T76	Serous	c.770C>G	p.Trp257Ser	Missense
		T23	Serous	c.771C>G	p.Trp257Cys	Missense
		T55	Serous	c.771C>G	p.Trp257Cys	Missense
		T70	Serous	c.771C>G	p.Trp257Cys	Missense
		170				
		T65	Serous	c.1757T>C	p.Leu586Pro	Missense

Supplementary Table 8: Frequency of TP53, PIK3CA, and PPP2R1A among serous endometrial tumors

	nistological subtype										
Gene	Serous	Clear cell	Endometrioid	Endometrioid	Endometrioid	Endometrioid	Mixed Histology				
			All grades	Grade 1 or Grade 2	Grade 2/3	Grade 3					
CHD4	17% (9/52)	4% (1/23)	7% (5/67)	11% (5/46)	0% (0/4)	0% (0/17)	11% (2/18)				
FBXW7	29% (15/52)	13% (3/23)	10% (7/67)	15% (7/46)	0% (0/4)	0% (0/17)	11% (2/18)				
SPOP	8% (4/52)	9% (2/23)	0% (0/67)	0% (0/46)	0% (0/4)	0% (0/17)	0% (0/18)				
CHD4/FBXW7/SPOP	40% (21/52)	26% (6/23)	15% (10/67)	22% (10/46)	0% (0/4)	0% (0/17)	17% (3/18)				
ABCC9	6% (3/52)	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.				
CYP4X1	4% (2/52)	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.				
MAP3K4	6% (3/52)	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.				
TP53	71% (37/52)	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.				
РІКЗСА	31% (16/52)	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.				
PPP2R1A	25% (13/52)	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.				

Supplementary Table 9: Overall frequency of somatic mutations in combined discovery and prevalence screens of CHD4, SPOP, FBXW7, ABCC9, CYP4X1, MAP3K4, TP53, PIK3CA and PPP2R1A

				Average background mutation rate in 12 discovery screen tumors (excluding T155)					xcluding T155)	Average background mutation rate all 13 discovery screen tumors					
Gene Name	No. of covered bp within coding sequence	No. of somatic mutations	Number of genes assayed in discovery screen	Background mutation rate calculated from discovery screen data	Expected number of mutations based on background mutation rate	Poisson P- value (one- tailed) for observed number of mutations	Rank of P-value	q-value (False Discovery Rate)	CaMP-like Score (-log_10(q))	Background mutation rate calculated from discovery screen data	Expected number of mutations based on background mutation rate	Poisson P- value (one- tailed) for observed number of mutations	Rank of P-value	q-value (False Discovery Rate)	CaMP-like Score (-log_10(q))
FBXW7	2121	20	21441	1.486E-06	0.1638746	5.3515E-37	1	1.15E-32	31.940	4.033E-06	0.4448477	5.2452E-28	1	1.12E-23	22.949
CHD4	5244	10	21441	1.486E-06	0.4051667	8.3511E-13	2	8.95E-09	8.048	4.033E-06	1.0998498	2.6138E-08	2	2.80E-04	3.553
SPOP	1122	4	21441	1.486E-06	0.0866890	3.7957E-08	3	2.71E-04	3.567	4.033E-06	0.2353226	4.9455E-06	3	3.53E-02	1.452
TSPYL2	1725	3	21441	1.486E-06	0.1332785	1.1820E-05	4	6.34E-02	1.198	4.033E-06	0.3617927	5.3543E-04	4	2.87	-0.458
ABCC9	4647	4	21441	1.486E-06	0.3590408	3.6912E-05	5	1.58E-01	0.801	4.033E-06	0.9746381	3.2857E-03	5	14.09	-1.149
MAP3K4	4672	4	21441	1.486E-06	0.3609723	3.7855E-05	6	1.35E-01	0.869	4.033E-06	0.9798815	3.3607E-03	6	12.01	-1.080
KDM4B/JMJD2B	2973	3	21441	1.486E-06	0.2297026	9.6595E-05	7	2.96E-01	0.529	4.033E-06	0.6235419	3.8454E-03	7	11.78	-1.071
CYP4X1	1527	2	21441	1.486E-06	0.1179805	2.5059E-04	9	5.97E-01	0.224	4.033E-06	0.3202652	4.3143E-03	8	11.56	-1.063
TRIM16	1692	2	21441	1.486E-06	0.1307289	3.3769E-04	11	6.58E-01	0.182	4.033E-06	0.3548715	5.7216E-03	9	13.63	-1.135
ARID1A	5718	4	21441	1.486E-06	0.4417893	9.7245E-05	8	2.61E-01	0.584	4.033E-06	1.1992642	7.7267E-03	10	16.57	-1.219
YEATS4	681	1	21441	1.486E-06	0.0526160	1.3366E-03	12	2.39	-0.378	4.033E-06	0.1428295	9.2790E-03	11	18.09	-1.257
EP300	7148	4	21441	1.486E-06	0.5522753	2.7107E-04	10	5.81E-01	0.236	4.033E-06	1.4991851	1.8538E-02	12	33.12	-1.520
BAZIB	4452	2	21441	1.486E-06	0.3439745	5.2525E-03	13	8.66	-0.938	4.033E-06	0.9337398	6.8526E-02	13	113.02	-2.053
CTCF	2181	1	21441	1.486E-06	0.1685104	1.2699E-02	14	19.45	-1.289	4.033E-06	0.4574318	7.7581E-02	14	118.82	-2.075
HDAC7	2491	1	21441	1.486E-06	0.1924619	1.6307E-02	15	23.31	-1.368	4.033E-06	0.5224496	9.7087E-02	15	138.78	-2.142

Supplementar	v Table 10: Mutation rate of individual	genes in 52 serous tumors	. compared to thecalculated back	ground mutation rate for serous endometrial cancers
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The background mutation rates are calculated based on the tumors that were in the discovery screen; the mutation rate of individual genes is based on 52 tumors (12 in the discovery screen tumors and 40 prevalence screen tumors).

Supplementary Table 12: MSI status and MSH6 status of endometrial tumors with CHD4, FBXW7, and SPOP mutations

Pair-wise comparison	Frequency in Serous Tumors *	Frequency in Clear Cell Tumors	Frequency in Endometrioid Tumors **	Frequency in Mixed Histology Tumors
CHD4 mutant/MSI STABLE-MSH6 WILDTYPE	9 of 48 (18.8%)	1 of 18 (5.5%)	3 of 41 (7.3%)	1 of 15 (6.7%)
CHD4 mutant/MSI UNSTABLE-MSH6 MUTANT	0 of 3 (0%)	0 of 5 (0%)	2 of 25 (8.0%)	1 of 3 (33.3%)
P-value	1	1	1	0.3137
FBXW7 mutant/MSI STABLE-MSH6 WILDTYPE	14 of 48 (29.2%)	1 of 18 (5.5%)	3 of 41 (7.3%)	1 of 15 (6.7%)
FBXW7 mutant/MSI UNSTABLE-MSH6 MUTANT	1 of 3 (33.3%)	2 of 5 (40%)	4 of 25 (16%)	1 of 3 (33.3%)
P-value	1	0.1073	0.4122	0.3137
SPOP mutant/MSI STABLE-MSH6 WILDTYPE	4 of 48 (8.3%)	2 of 18 (11.1%)	0 of 41 (0%)	0 of 15 (0%)
SPOP mutant/MSI UNSTABLE-MSH6 MUTANT	0 of 3 (0%)	0 of 5 (0%)	0 of 25 (0%)	0 of 3 (0%)
P-value	1	1	1	1

P-value (Fisher's Exact test of significance, 2-tailed) * The MSI status for 1 of 52 serous tumors could not be determined

** The MSI status for 1 of 67 endometrioid tumors could not be determined

Network ID	Molecules in Network	Score	Focus Molecules	s Top Functions
	Actin,ARHGEF2,ATM,CHD4,CHKA,Creb,CTCF (includes EG:10664),Cyclin E,CYP11B2,DMD,EP300,FBXW7,FLNA,hCG,Histone h3,Histone			
1	h4,LHCGR,MAGEC2/MAGEC3,mediator,NUMA1,PEX2 (includes			
	EG:19302),PLAA,POLR1A,RFX5,Rnr,SIN3A,SLC26A3,SMC3,SMC4,TIP60,TP53 (includes EG:22059),TRRAP,TSPYL2,YEATS4,ZBTB33	38	26	DNA Replication, Recombination, and Repair, Gene Expression, Cancer
	AMPH,ANO3,ANXA5,CD3,CDCA7,CDH11,DSG3,ERBB2,ERK,ERK1/2,Focal adhesion kinase,GPER,GRM1,HGF,IL2RG,IRS4 (includes			
2	EG:16370),ITCH,ITGA3,MAP2K1/2,MAP4K4,Mapk,Mek,NFkB (complex),P38 MAPK,p85 (pik3r),PI3K			
	(complex),PIK3CA,PPP2R1A,PPP2R2A,PUS7,RNF128,SPDEF,SPTB,TCR,TLR7	32	23	Cellular Movement, Cell Morphology, Tissue Morphology
3	ABCA3,AGTR1,ATAD2,C3,CCND1,CDCA7,DNMT3B,DPY30,EMR3,ESR1,EZH2,FH0D3,GPR77,HAMP,HDAC7,HFE2,HK3,HNRNPH2,KANSL1,			
	KCNA1,KCNQ5,LIMCH1,MGA,MLI,NEO1,NRF1,PNRC1,RBMS3,RECK,SLC9B2,SRPK2,TGFBR2,TGM2,TMPO,WDFY3	18	16	Developmental Disorder, Hematological Disease, Hereditary Disorder
	AKRLC3,CLDDJ,CCDC82,CEP63,CUL/A1,CKMP1,CLDSP2,DISC1,D51,E6FR,EKB82,estrogen			
4	receptor, GKMS, HUC, HFE, HM13, HSPAS, JUN, KHSKP, KIF1A, KK17, MAPKTA, MPHOSPH9, PCDH7, PCDHA9, PGK (includes	47	15	Endersity Custom Development and Evention Creall Malexula Dischargister, Cell Custo
	EG:1860/)/PTPKK,SBUS,SMRDJ,SOKCSJ,SPAGJ6,SPOCKJ,STNELI, INXB,WNTSB	1/	15	Endocrine System Development and Function, Small Molecule Biochemistry, Cell Cycle
E	ADDINIJACSENJACI OLIJACVIZAJADCI I JANAR I ZANINSTEJANI IDAR SJJAN I IDAR SJAN I TO ZDUNI ANTO DALAO DRVV DI CI 1 DDEI AA DDICORE DTCCO DA			
5	(complex), county disert is proved by the sector of the se	15	14	Antigon Procontation, Collular Movement, Hematological System Development and Eurotion
	6555, (GS5, AFD1, SFT) BICS, FT MICS, F	15	14	Antigen Presentation, Celiular Movement, nematological system Development and Function
6	(includes EG:15978) Jam KDAB MARK9 MARCKS11 MRC1 (includes EG:100286774) NF1 (includes			
	EG:18015).NOV.PLEK.POLI.PPP2CA.PPP2R3A.SGOL1.SMTN.SPAG4.TGFB1 (includes EG:21803).TYMP.ZFP36L1	14	13	Embryonic Development, Organ Development, Organismal Development
_	ACTL6A, ADAM9, ADNP, ARID1A, ATP6AP1, BAF110, CCNC, CD46, CDK5, CSPG4, CTSB, EXT2, FAN1, FHL2, ITGA10, ITGB1, LIG3, MSH6, PDP1, PHLC)		
7	B1,PMS2,POU5F1,PPAP2B,PRPF6,PRPF4B,SALL4,SERPINE2,SLC3A2,Smad2/3,SMARCA4,SMARCC2,STAT3,SYVN1,TRPM3,WDR45	12	12	Cellular Compromise, Nervous System Development and Function, Tissue Development
	ANLN,BAZ1B,CHEK1,DBF4 (includes			
8	EG:10926),DDX11/DDX12P,E2F4,ERCC8,EXOSC8,FANCE,KIAA0101,KIF1B,KISS1,MARK1,MCM5,MED14,PANX3,PCNA,PKN2,PTPRN2,RAD			
	50,RAD51AP1,RBBP8,RINT1,RNA polymerase II,RRM1,RRM2,RUNX2,SHPRH,SND1,SPAG7,SVIL,TLN1,YWHAG,ZNF83,ZNF451	12	12	DNA Replication, Recombination, and Repair, Cancer, Reproductive System Disease
	ACHE,ADORA2B,AKAP2/PALM2-AKAP2,BIRC6,CASP1,CASP9 (includes EG:100140945),CCL18,CFB,CNTN1,DIABLO,DSC3 (includes			
9	EG:13507),FNDC3A,GCLM,IGHM,IGL@,LAMA3,LAMB3,LAMP3,MAFF,MOAP1,MS4A1,NFKB2,OASL,RPS13,RXRA,SEC16A,SERPINB1,SERP	I		
	NB9,SFMBT2,SLAMF7,STAB1,TNF,TNIP3,TREM1,ZFP91	11	11	Cell Death, Antigen Presentation, Cell Morphology
	ADAMTS9,Akt,ASGR1,ATP6V0D1,BAG4,CDC37L1,DNAJB1,FGFR4,GDNF,HDAC8,Hsp70,Hsp90,IgG,IRS4 (includes			
10	EG:16370),Jnk,KCNA5,KIF26B,KRT31,MDK,mir-			
	29,MTOR,NDFIP1,NQO1,PACRG,PEA15,PIK3CB,PRR5,Rar,SIAH1,SMG5,SNCAIP,STIP1,STK3,STK4,TRIM16	9	10	Cardiovascular System Development and Function, Embryonic Development, Organismal Development
	ACTN4,AIAP1,AXIN1,CDH1,CDK17,CDK5R1,CPB2,CTNNA3,CTNNB1,CUL3 (includes			
11	EG:26554),CYP24A1,DAXX,DBH,DIXDC1,FAM123B,GUCY2F,Hdac,HNF1A,HSD17B2,KLK6,LD1-cholesterol,LRP2,LRP1 (includes	0	10	Cell To Cell Constitution and Internation. Times Development Development and Undersided Context Development and Evention
12	EG:16971]/IMAP3K4,MISAZ,MUKGT,PAFAHZ,PI3K P85,PKD1,PTPKF,SLC12A6,SLT2,SIMAU4,SPOP,THBD	9	10	Cell-to-Cell Signaling and Interaction, Itsue Development, Renal and Orological System Development and Functio
12	PDAT (Includes Ed:18609),5226L	1	1	Cell Morphology, Developmental Disorder, Digestive System Development and Function
14		1	1	Coll Dooth, Nutritional Discoso, Tissue Marabolany
14		1	1	Cellular Function and Maintenance. Cellular Movement. Hematological System Development and Function
16	NGI YI BAD28	1	1	Digestive System Development and Function Protein Degradation Protein Synthesis
17	Nuclear factor 1 SIC25A5	1	1	Molecular Transport, Nucleic Acid Metabolism, Small Molecule Biochemistry
18	ABCC9 KCN111	1	1	Molecular Transport, Cardiovascular Disease, Endocrine System Development and Function
19	NRK,ZNF217	1	1	Cellular Development, Reproductive System Disease, Cardiovascular System Development and Function
20	FOXL2,TCEB3B	1	1	Cellular Development, Dermatological Diseases and Conditions, Developmental Disorder
21	GNPAT,PEX7 (includes EG:18634)	1	1	Lipid Metabolism, Small Molecule Biochemistry, Connective Tissue Disorders
22	NDUFS3,NUBPL	1	1	Hereditary Disorder, Metabolic Disease, Cellular Assembly and Organization
23	RHAG,RHCE/RHD,SLC4A1	1	1	Cellular Assembly and Organization, Hematological Disease, Cell-To-Cell Signaling and Interaction
24	VPS11,VPS18,VPS16 (includes EG:296159)	1	1	Cell Cycle, Cellular Assembly and Organization, Cellular Function and Maintenance

Actual mutation frequency of gene "G" in	Power to detect one tumor with a mutation in	Power to detect two tumors with a mutation in
serous endometrial cancer	gene "G" in a discovery screen of 12 tumors	gene "G" in a discovery screen of 12 tumors
8%	63.20%	24.90%
10%	71.80%	34.10%
15%	85.80%	55.70%
20%	93.10%	72.50%

Supplementary	/ Table 15: Estimated	power to detect somatically	/ mutated genes in a (discovery screen of 12 tumors