

Primers

Target gene (bp)	Forward primer (5'-3')	Reverse primer (5'-3')
NOD1	CCTCCTCCCGTCCGTCC	TCAGAAGCAAATGATCCG
NLRC3(1~936)	ATGGAAGAGGCTTGGATCAG	CTCCGTCATGCGGTCTAC
NLRC3(676~1507)	CCCCACATCACGGAACCAAC	GATCGAATATCGCCCGTTG
NLRC3(1433~2482)	ATTTCTCCCACTTAACCATAC	CCGAGCCGTTGTCTCCTAC
NLRC3(2216~3276)	GCCCATCGGGAGCGAAAGC	TCACACCACCACCACGCAG
NLRP3(1~1024)	ATGGCAGGAGAAGAAAGCACC	AGGCCACATCTGCTTTACTG
NLRP3(676~1782)	TGCCCTCAACAGCGAATGC	GAAACTGCCAACACGCTC
NLRP3(1423~2202)	CTCTTCGCAGCGATGTTTTAC	TCACCGCAGGACACGCAGC

>NOD1-chicken

MEGHLCANLKTSVEKPLTTSPPSCIALLKVYRELLVSKIRHTQCLIDNLINNEYFSTEDAEIVVQFPTQ
ADKVRKILDLVQSKGEEVSEYFICVLQKVTDAYYELQPWLDEIGYQPSENICSKPVVNTDPVSRYCQKL
RYELGRDSKFFVLSYAQREEMLEEIYSNSIMEMVNFTNESLGEVCQLQALFDDAVGVINEDGETIYVFG
DAGIGKSILLQKIQSLWAKKQLDIGAKFFFHFRCRMFSFCKEDEAVCLKDLLFRNYCYPDQDPTEVFHH
ILQFPHTVLFTHDFGDEIYSNFDLSSVPEMCSPDEPMHPLVLLVSLLRGKLLKGSKKILTARTGTEIQR
NIIRKKVLLRGFSNSNLKEYTAMFFKDVGGQRTLVLNLQLEANPNLCSLCSVPLFCWIIFKCYEHFHSMPD
SHELDPDCSVTLTDVFLLMIEVHLNRSLKTSLLKNNTRSQAQEVFRSRKETLLALGKIAYRGMGNSIFIFE
QEEVSSANISEEDLQLGFLRTVKGYSRCDNQSTYEFHLTLQSFFTALFLVIEERVGNKELLQFFNECS
SAEAAQRTCFRVPWLKKPLTGEDPFRNNEHFHTNLFCLGILLSRSKEKLFKHLVSPAVIRKKRKTILITY
LGESMKSHLKGVTRSRLPMYNQVQVQPNFVWMLRCLYETQSEKVGKLAAKRMHANYIKLTYCNAYSADC
SAISFVVHFFQKHLALDLNNDYGVKQLLPCFSKLAVIRLSVNQITDHGARILYEELSKYQIVSYL
GLYNNQITDIGAKYVAKLIEECSSLEYVKIGANKITSEGGKCLAQAIQKSTTMFEIGMWGNQVGDGAK
AFADALRNHPRLTNVSLAFNGITTEGGKSAEALQHNDSVKIFWLTKNELDDEAAMSFAEMLKINKKL
HLWLIQNQITAKGVKYLSEALKENTAIKEVCLNGNLISQEEAKAFESEERIICF

>NLRC5-chicken-AEY11256.1

MQPTLQNDDFNLEGAVASIRPQLVEFLSHRLDWLLSASQHFLLPTAVLSGLAGVTDHREKVSVLLDLLEK
AGHATWKQFAQCLCMECDLPLEMEILLMSSAGEGNLTQKQEAQTDASDQSSVPRGLTRRRRSSPISDK
GAKQKRLDSAKEYQRLVDSICKRYGSRRAAGAAAQEPQPLAFSQAQFVNLVLRQSKASRLKERTDKPR
EDVPSAPEPEECVDTAVRVSDLFGSVVRSRGTTKVIFLFGKPGTGKTMHRICQKWAEGVLHQFLFTFL
FEFRQLNLLKRKLTLEKLLFDLFLQPEDSPDAVFQHLLENAQRTLIFDGLDEFVGNMDEVSSASKGSLN
RSSSMSISELFAELCHGNLLPGCTVLVTSRPRKVPDFLINTVDLLAEVWGFDEKVEEYVSHYFRHHSF
KEQAIHLKNNTKLLSMCQIPALCYVVCICLEYLLKHQTSVELPQMTQFYIKMLLIFINKQQGEHAG
DEEAQLNSNKAAILGLCDLALKGLEAKKLVFVYVDIPEHVKEFASLHGLLTVFEVKTNSAHPETGYAFV
HLSLQEFFAALCLMISKSVDKSHLKRKLSLKSQWTLRNEAKTGMESFHIFLSGLSSKECRTFIMLLAE
QSEAWVQDKQDAILQSLKLAATQLTGPKVIELCHCTFETQGLEVAQHIGSLLNFKYEFKNFRLTPLDM
SALVFVINSQDVTHLDFAGCPLDTCLEMLASCRNVEHLSFRSRRFGDDFAAALSKGLGEMGSLKLE
VTGGSITAAGLTDMVQALSHCLQLEEINLQDNRIQNPVKTVMELFSRMEKLLKIDLSKNSLSLNAVLL
LAKEFIACQNAELHVRKDTVIIISFSGPSGKVPRLDLKREQNKECVTPTRHLRLCLQARCLSSQHAK
IVSILQSCPHLSEVDLSDNKLGDGCSFLENLSWISISKQLNLSHNLLSVTGIYSLKAVNTCQRVVE

VEVSLYHNTAVLRFTEDEGFASPPASREEPLYPTDDQWDDKENQTPVPSKKIRLTYCRFQASDLEKLCA
VLKECGSISELDLSNNYLGDGLAQLLQFLPNLKTLSLKLNNHLSLSSVFCLAQSLCTLEHLETMDL
SLGRMQVVHLTFGDRIRLRRTSRWRRSFLVHPKHVTNGQCFRLRNCTVGPEDVTRLCQMLTQCTQLTEI
DLCGNALNDQSIERLLSFLPHFCQLTLLSIRNNTFSPCCAFLFANSINLCERIRRVEVRSSQNAFLHLR
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HNRIHQRGVHLINTFTTSGNTTEVQVSLCSKATLIKMTSRDDPRKILRLTECSFQPEHLEKLCVLE
NCTNLTECISSNNVTVDAAAGLLRSLSKTPGPLKISIEEPWVCKLSVTSLELAVQAHGNTAIMICK
EKNLFQLGVRLPHCLEKVGSVSRLNNEPEIKQACFYQRVHDKCTQLQELRWSHVELHDDTEMLVLSIL
LPLPDLKKFELTSCSFTPTGIDCLITGLQRCQAI EELNLGHMKGDAAPKLVFGLCEMPSLKRILNH
NSIGDDGCSRLAEALSSMHCMEENLGHNKIGDLGLINIAAVLLEMQNLKRIDLGNCPSPAGGEKLE
ALANCKHLEELILSRNDFGDTAVKLALCLPHMNRKILHLQHNNIGPAGGTELARALMACELLEESL
SENNLGEGERALSEGLPRFEHLRKIELRLCGITDDASKLLSRGFQQCPAVEEIIILSWNALGDGGAQVL
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>NLRP3-chicken

MAGEESTIFLEALEGLTLEDFQEFKKKLPHTDIKGGWNIGRDELEKVTHPSSLISYMGDSYGEGAAMD
AISLFEEMNQDLAEKILDEKVKEYKQKYTEHVAREFLQYKEANSCLGENLSVRDRYTNLTIAKSWDQ
HGDEPGDVSSDVTVTQTLLLEPSKDGQVPPITVLV GASGMGKMTIRKVMMEWVEGTLCQFDYVFCIDC
KELSFKEVSMVDLISKCCPQQRMPAGRILGNPEKILFIFDSFEALGLPLAQPKDELSTDPTEAKPLET
TLLSLLRRTVLPESVLIATRPAALQSLGQCLEGGHYVEILGFSPAAREEYFHRYFGNDNKADVAFRFT
RGNEVLYSLCVIPVMSWTVCTVLERELYERNQLLACSKTTTTQMIMFYLSWLMKHRVSNWQNLQQLFK
LCSLAADGIWKHKVLFEEKEIEDQGLNQPQLLSLFLNEKLEKGTDHVNVYSFSLHLQELFAAMFYVL
EDQDGMVSDSRILAKDVNMLLESYHTRSMDLNVTVRLLFGLVNPKSVEYAGEGIGCRISLQPQEDLLRW
LQTRPRGTSHPREVMKIEDLDTFHLLFETNEKSFVQSVLGSFTGIALQDVKLTLYDQAALCFCIKQWAG
LLSVTLWCSFHQQHHRQEPKGLPRQSWRQEELHSPHPLCQALGHPGSSLQSLRLQWCGLTEGDSGA
LGTLLATLPSLVHLELGDGALGDDGVRMLCAGLRQPGCQLRVLR

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MEEAWISRYRRQLMRSISPQFLEEIIGYLQRLDLLTVEEAGRAQEASSLPEQVRAVVDILAGKGSHASQ
TLQSFIEETTNSQLYPLCAEPMVQKHLESLQSFYGNLSLEIGSLQRLTNLLLVEGLTDIQQKEHDILQMEM
TKGLRNVSKSIPLEKFLPLSKVSIIPRISVTMGVAGIGKSTLVKLFVGRWAKGLINRDI MFVPLP TFR
ELNTYEKLSAERLIRSSFPHITEPNYISAGAARTLLILDGLDEFKTPLDFSN TVACTDPKKEIQVDNLI
TNIIRGNLLQEASIWVTSRPTAASQIPGGLVDRMTEIRGFRA TEMKDFLDQMFLDNKDL SGQVLHHIKA
NRSLHIMCTVPGFCRIYGSSIGYYLKNSTGQPQEMTVAPKTLSEIYSYYFKMALSSDWPERRRET
QAVNNSKKVMGSLGRLAFYGLLKRKHVFYEQDMKAYGIDLSLLHSSLCRLLLKEDMQPTTAYYFSLT
IQEFLAAIYYYYTAAKRAIFDLFTESGMSWPKLGFNLHFSAVQRSLQAEDGQLDIFVRFSLGLLSPQVN
QLLSGWLLVKDEHNSYRSQAISFLQGLNTNYV ISSQTVNTVHCLHEIQHTEIAKAVEEAMKNESLAGM
LTPVNCALAYLLQVSDVCVEETNLSNCLTYNICSLLPPLLFCHSLRLDNNQFKDNVMELLSM SVK
DCQIQRLSLAENQICNKGAKALARSMLVNRSLTVLDPRSNSIGPSGAKALADALKKNQVLLSLRLQHN
IKEEGAAALAEALLTNRRLITLHLQKNSIGAHGARKLAEALAQNC SLKELMLSSNSVGDNGSVALAEAL
KVNHSLQSLDLQSNFISNTGVSALTAALCSNKGTLNLRENSISKEGGPAIAHALRTNCTLRKDLAA
NLLHDEGGKAIALAMKENRALTSLHLQWNFIQTQAAVALAQALQSNDSLASLDLQENAI GDEGMAALAA
ALKVNTTLADLHLQVASISAAGAQLAEALMVNNSLQVLDLRGNSISVAGAKAMANALKVNRSLRWLNL
QENSLGMDGAICIAATALRGNHGLTYVNLQGNRIGQSGAKMISDAIRTNSPDCVVVV

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RYELGRDSKFFVMSYAQREEMLLEEIYSNSIMELVSFTNESLGEVCQLEALFDDAVGLINEDGETIYVFG
DAGIGKSILLQKIQSLWARKELDIGAKFFFRFCRMFSCFKEDAICLKDLLFKYNCYPDQDPTEVFHH
ILQFPHTVLFVTFDGFDEIYSNFDLSSVPEMCSPNEPIHPLVLLVSLLRGKLLKGSKKILTARTGTEIQR
NIIRKKVLLRGFSSNNLKEYTAMFFKDEGQRTLVLNQLEANPNLCSLCSVPLFCWIIFKCYEHFHSMFD
SHELPCDSVTLTDVFLLMIEVHLNRSLKTSLLKNNTRSQAEMFKSRKETLLALGKMAYKGMENSFFIFE
QEEVSSANISEGDLQLGFLRVTVKYSRCDNQSTYEFHLTLQSFFTALFLVIEEKVGAKEQLQFFNECS
STETAQPTCLRIPWLKKQLAGEDPFRNNEHFHTNLFLCGLLSRSKQKLFRLVSPAVIKRKRKTLITY
LGESMKSHLKGLTRSRLPNYNQVQVQPNFVWMLRCLYETQSEKVGKLAAKRMHANYIKLTYCNAYSADC
SAISFVVHFFQKRLALDLNNDYGVKQLLPCFSKLAVIRLSVNQVTDHGVRILYEELSKYQIVSFL
GLYNNQITDVGAKYVAKLIEECSSLEYVKIGANKITSEGGKCLAQAIQKSKTMFEIGMWGNQVGDGAK
AFAEALRNHPRLTNVSLAFNGITTEGGKSAEALQHNNSVKIFWLTKNELDDEAAMSFAEMLKVNKKLV
HLWLIQNQITAKGVKYLSEALKENTAIKEVCLNGNLISQEEAKAFENEERIICF

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MEEQGHSEMEIIPSESHSHIKLLKINRELLVTHIRNTQCLVDNLLKNDYFSAEDAEIVCACPTQPKVR
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DCSALSFLVHHFRKRLALDLNNDYGVRELQPCFSRLTVIRLSVNQITDSGVKVLCEELTKYKIVT
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DAKQQRLLDSAEKYRHLLIDSICQRYGSRRAGAAAQEPQPLAFNQAFVNLVIRQSKASRLKERTDKPR
EDVAGAPEPEECVDTAVKVSDFGVSVPSTTKVIFLFGKPGTGKTMHRIQCQKWAEGVLHQFLFTFL
FEFRQLNLLKRKLTLEKLLFDLFLQPEDSPDAVFQYLLENAQHTLIIFDGLDEFVGNMDVSSSSKGGPT
LSSRMSISELFADLCHGNLLPGCTVLVTSRPKRLPDFLLNTVDLLAEIWGFDFHEKVVEEYVSHYFHHSF
KEQAI AHLKNNTKLLSMCLIPALCYVVCICLEYLLKHQMSVELPQTMQFYIKMLLIFINKQGERAG
DEETQLNCNKKAILGLCDLALKGLEAKKLVFVYVDIPEHVKEFASLHGLLTVFEVKTSGTCP EAGYAFV
HLSLQEFFAALCLMVSKRVDKNYLKKKFSLSKSWTLKNEAKTEFMESFHIFLSGLSSKECRTFLMLLAE
QDEAWVQDKQDAIQLSKKLAATQLTGPKVIELCHCTFETQDLEVAQHIGSLLNFKYEFKNFRLTPLDM

SALV FV INSGQDLTHLDFAGCLLDIDCLEVLGCKNVEHLSFRSRRCGDDFAAALSKGLRGMGSLK KLE
LTGGSITAEGMTNLVQALSHCLQLEEINLQDNRI RDPEVKRVMELFSRMEK LKKIDLSNNNLSLNAVLI
LAKEVIACQ NATELRVRKDTV IISFSGPSGK VPRSLDLRWEENKEHVIPTRHLKLCLQDRCLSSQHAK E
IVAILQSCPCLSEVDLSGNKLGDEGCSFLLES LPWISISKQLDLSHNRLSVTGICSLKAVNTCQKVME
VQVSLCHKTAVLRFTEDREFASLPPREEPVFSTDDQQYGEENQTPTASKKIRLTYCRFQASDLEKLC AV
LKECGSISELDLSNNYLGD ELLQLFQFLPNL KMLRSLKLNQSLNSVFFLAQSLSTLEHIKTMNLS
LGHMQVVHLTFGERIRVRSTSRWRSDSFLAHPKHVANGRCFRLRDCRVGPEDVTRLCQILAQCPQLTEI
DLSGNSLSDQSIERLLSFLPYLCQLTLLSIRNNTFSRPRCTVLLINSINLCERIRMVEVRSSENAFLHLR
ASTQSQKTSCLTDCAIGQQQIEELCRVLEQHGCLAELDLSRNQLGD EGLRCLLDHLHRVPVTC SLNLS
HNRI SQDGVLHLINAFATSGNTTEVQVSLCSKATLI IKLTSRDDPRKILRLAECNFQPEHLEKLC LLLLE
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DKNLFQLGVRFPHCLEKVESVVSRLNLYKPEIKHACFYQRVREKCAQLQELRWSHVELHNDEAEMLVSI
LLPLPELKKFGLTSSSIMPTGIDYELITGLQNCQAIEELNLGHMKLSSAAIPKLVGLCEMP SLKRLILN
HNSIGNDGCSRLAEALRNMHYMEEINLSHNKIGDPGLINLAAVLLEMQNLKRIDLSGNCPSPAGGEKLM
EALAYCKHIEELILSRNGFGDRTAVKLALCLPHMTNLKILHLQHNNIGPAGGMELARALVVCELLEEIS
LSENDLGEGSIHALSEGLPCFEHLRKIDLKLCGITDDASKSLSHGFRQCPAMEEII LSWNALGDGGAQE
LASVLPGM EKLMKDLEKNRIGACGATKLAEE LAKCPEIQFIRLW DNPV PKGLAESLTSQDPRLCF SFC

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MDPVSLQLGNKNLWSWLVRLLSKDP EWLNAKVKFFLPNMDLSRNEALDPTQRVILQLNKLHAQGPATW
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DVSILDLFNTKANKGPRVTVLLGKAGMGTTLAHRLCQKWADGQLDRFQALFLFEFRQLNLI TRFLTLP
QLLFDLYLSPEADPAVFQYLEENADQVLLIFDGLDEALQPCSSKETVGPDDPGSALTLFSGLCHGTLL
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ALCQVACLCLHYHLLPGSSPGQSAALLPTMTQLYVQMV LALSPRGHLPAT SLLGLGEVALRGLETGKVI
FSAEDIPPLMAFGAAHSLT SFCIRTGPGHQETGYAFTHLSLQEFFAALHLMASPKVDKDTLTHHVTL
NSRWVLR TKARLGLSDHLP TFLAGLASRTCRPFLSHLAQRDEVWVGAKQAAVVQVLRKLATRKL TGPKV
VELCHCVGETQEPELASLIAQSLPYQLPFHNFPLTCADL ATL TNILEHRDAP IHLDFDGC PLEPHCPEA
LVGCGQVENLSFKSRKCGDAFAEALSRS LPTMGSLKMLGLAGSKITARGISHLVQALPLCPQLEEV SFQ
DNQLKDQEV LNIVEVLPCLPRLQKLDLSRNSVCMSTLLCLAKVA VTCPTVRMLQVREADLIFLLSP PTE
TAAELQGAPDLQGNDSQRKGAQSRSLTLRLQKCQLRVHDAEAL IALLQEGPHLEEVDLSGNQLEDEGCR
LMAEASQLHIARKLDLSDNGLSVAGVHCVLRAVSTCRTLAE LHSLLHKT VVLTFAQEPEEQEQIQKR
AAFLDSLMLQMPSELPLSSRRIRLTHCGFQAKHLEQLCKALGGSCHLGHLDLSGNALGDEGVAQLAQLL
PGLGPLQSLNLS ENGLSLDAVFSLAQCFSTLQWLFHLEISFESQHILLRGDRTGRDMLAAGSLPEFPAG
AQFLGFGQRCIPRSFCLRECQLEPLSLTHLCDTLEKCPGPLEVQLSCEFLSDQSLETLLHRLPQLPQLS
LLQLSQTGLSPRSPFLADIFSLCPRVQKVDLRS LRHATLHFRSNEEQEGVCCRFTGCSLSQEHVEPLC
WLLSKCKDLSQLDLSANLLGDSGLRCLLECLPQVPISGSLDLSHNSISQESALYL VETLPSCPRVREAS
VNLGSEQSFRIHFSREEEAGKTLRLSECSFRPEHVSRLATGLS QSLQLTELTLTQCCLGLEQLTILLSL
VRRPAGLFSLRVEEPWVGRAGVLTLLVEVCAQASGSVTEIS ISETQQQLCVQLEFPRQEENPEAVALRLA
HCDLGHHSLLVRQLMETCARLQQLSLSQVNLCEDDASSLLLQSLLLSSELKTFRLTSSCVSTEGLA
HLASGLGHCHHLEELDLSNNQFGEEGTKVLMGALEGKCR LKRLDLSHLP LDSSTLALLTQGLSHMTLLQ
SLSLSRNSIGDVGCHLSEALRAATSLEELGLSHNQIGDTGAQHLAA ILPGLPEL RKIDLSANSIGPAG
GVQLAESLALCRHLEELMLGCNALGDPTALGLA QGLPQHRLRVLHLPSSHLGPEGALS LAQALDGC PHVE

EISLAENNLGGVPHFCKGLPLLRQIDLVSCKIDDQTAKPLAASF_TLCPALEEILLSWNLLGDEAAAEL
AQVLPQMGR_LKRVDLEKNQITACGAWLLAEGLAQGSGIQVIRLWNNP_IPPDMAQRLQSQEPRLDFAFFD
NQPQAP