Supplementary Figure S9

Location of LCRs in proteins associated with SG defects

The locations of LCRs (identified according to Li and Kahveci, 2006), within the 54 proteins associated with strong SG-defective phenotypes are shown.

Graph Based Algorithm

Low complexity regions masked by 'X':

>YBL087C | RPL23A
MSGNGAQGTKFRISLGLPVGAIMNCADNSGARNLYIIAVKGSGSRLNRLPAASLGDMVMA
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FSAGXXXXXXXXXXXXXXXXXEAEAEKEEEEAKEESDDDMGFGLFD

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XXXXXXRKELALEYLFMDATPEGFARNNALVAEKFDLDEISHXXXXXXXXXXXXXXXXPY
TTIWNNHPMGIKWFIKEAIVXXXXXXXXXXXXXXXXVILSARRKKIPARYYGQELENMEG
TIVFNDNESQNTSFWKGSDAFSTRSRSSTVTPNFYGNHLRGKNIHGGDNSSIRSDDHHAR
LRTHNTLNXXXXXXXXXXXXXXXXXXXXPFHSRMPDIKVELLHDDIIEAYEQEDLLHLEV
SDIPKFQTYIYQYSKLLFRWGLPLERVKILKVSTDFXXXXXXXXXXXXXXKKSPYNGVLT
HWIENNEFGEEKFLARNCNYCDLRVTRSSFICGNCQHVLHSSCARIWWEIGDECPSGCGC
NCPEMFDA

>YER155C | BEM2 (IPL2, SUP9, TSL1)
MKGLLWSKNXXXXXXXXXXXXXXXSHKXXXXXXXXXXXXXXXXXXXXXXXSGASPYMXXX
XXXXXXXXXXXXXDNNRDKRKSSVFPPSKQYTSTSSSQVNLGMYHSDTNTRSSRSIASTL
KDDSPSVCXXXXXXXXXXXXXXXXXXTPIAYXXXXXXXXXXXXXXXXXLSPPQSRCXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXNVIHLNSENYDTTVFKTGWVNKSHGQX
XXXXXXXXXXXXXXXXXXXXQNLRNDAYSRNRESRFYGXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXMAIDPQMLVPDYRLYRAQLKGCVLNLYKSGLNSNIKFFDPTLPASNSSIANEN
HQQKKQQTNNQAQAEALHQKQSFGQMGEPITLDLKYLSEVYPHPDLRQDSDGKIISGTIE
SLCHTVLFYPGPKQSDVPNEKSLSKTHRAVINLLLMFPLLDHFIKFLKVFNQFGLSFTKN
KSRLTNNSTQFYNISPAVDDSMTQRLALTAKTILDVFPGFLLDEPMLKTIISLLDTISLH
NDEISNNLKIKIANKHNELMKLTAFTRSLPMATSSXXXXXXXXXXXXXXXXXITTLADEV
HHINLKFDKVWAPKFDYSLLYDSKFINRRIVSLNPLVFNNDQNIHFLGRLLISHLFPTNP
EFSKKVTPKVRAELLDKWVQIGCRFEHLGDMVSWLAVATIICSIPVLRXXXWXXXXXXXX
XXXXXXXXXTIIQLXXXXXXXXXXXXXXXXXXXXXXXXFTRANVISYFGDLLIHADDLPS
DTKFKYLEKKINRTKNAFHKWQQRLQAIDSTRHKTNSTENVRDNDSPNNVVYQLWKFHLS
QPPLNIEGIMKLSVQHEPPIIDQKAYSTIGSQRSALVTGSYLPIXXXXXXXXXXXXXNT
LVGXXXXXXXXXXRXXXXXXXXXXXXXXXXXASNSHTMGSLTDDAMSSKNDNNKVTGVGK
IDGPVIKEMSSXXXXXXXXXXXXXXXXXXXXXXFHISDELVFKSVYDNDGKSRPASMVIE
TPKRFSQHSSMLINNPATPNQKMRDSLDTTGRLSKTLENMDFFNNIGQXXXXXXXXXXXX
XXXXXXLEKIFDLLVLTSNIFSKLVDTKDLENYYYHQRQRXXXXXXXXXXXXXXXXXAFV
KLTMDNDXXXXXXXXXXXXXXXXXXVLENMAKRYVGAKSCSVSISKILDRSDDSKMKINE
DTNLVSSSLYDQNFPVWDMKVTDDENINLIYMAKIQIGAAEAILHLVKNHYSDFTDDLCN
NSTLLDIIKIMEQEVSTEWPTRIANSKLQKSLPENFVIETENLLTTLTDLFHGIKSAYXX
XXXXXXXXXXXXXRIXXXXXXXXXXXXXXXXXXXXXXXXXXXMIRSFQKLHSTNYEDILE
WIYQLDNFISKKFNLVSKKDWIVLFQELELLSKESLVSFFNYPLHFKSSKLINPGYLQLH
EFEISNLFTWISTLILKDDNGTESLFFEKLPQSIKLLIKLHTSLTTFFVMEISNVNKSSS
ERLTTCKVILQILNYIRWKNGSLDLFDSXXXXXXXXXXXXIPAFIETAIAHAIISPESRN
YELSWIKASEKLSDPTKGTQNLRSISNVLEKIDDIHIKRFIEIDDVFSKNCKNLCPCPGW
FISRLLEISQFVPNMSITNSKLINFDKRRFVNNIISNVLDLIPNEREFPLDIEMSDENPS
KRTTFGRILFNNFEDVNKVYXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIEKIKREARK
LEVLLDQEKILKNSAALHQAVPKKNXXXXXXXXXXXXXXXXXYNINKNTGQTPSLGSVMES
NNSARNRRDSRASFSTNRSSVVSNSSHNGVXXXXXXXXXXXXXXXXXNTXXXXXXXXXXX
XXXXXXXKSILPSILPEVDSMQLHDXXXXXXXXXXXXXXXXXXINHRNIPAXXXAFKIVM
QNGHEYLIQTASSSDLTEWIKMIKASKRFSFHSKKYKGKTHNKIFGVPLEDVCERENTLI
PTIVVKLLEEIELRGLDEVGLYRIPXXXXXXXXXXXXXXEEGATDNSFTLEDDRWFEVNA
IAGCFKMYLRELPDSLFSHAMVNDFTXXXXXXXXXXXXXXXXXRMMNELLQKLPTCYYQT
LKRXXXXXXXXXXXXXXXXMDASNLAIVFSMSFINQEDLANSMGSRLGAVQTILQDFIKN
PNDYFKQ

>YGL105W | ARC1
MSDLVTKFESLIISKYPVSFTKEQSAQAAQWESVLKSGQIQPHLDQLNLVLRDNTFIVST
LYPTSTDVHVFEXXXXXXXXXXXXXXXXXXXXXXXRHILRWIDYMQNLLEVSSTDKLEIN
HDLDLPHEVIEKKKKAPAGGAADAAAKADEDVSKKAKKQDHPRGKPDXXXXXXXXXXXXX
XXXXXXXXXXXQQQEQQNKAPEKPKPSAIDFRVGFIQKAIKHPDADSLYVSTIDVGDEEG
PRTVCSGLVKHFPLDAMQERYXXXXCNLKPVNMRGIKSTAMVLCGSNDDKVEFVEPPKDS
KAGDKVFFEGFGDEAPMKQLNPKKKIWEHLQPHFTTNDGLEVIFKDEEEKDHPVRKLTNA
KGESFKVASIANAQVR

>YGL136C | MRM2
MILVYNRIRSIIXXXXXXXXXXXXXXXQXXXXXXXXXXXXXXXXXVQNLRSRAAFKLMQI
DDKYRLFSKNRTDQRILDLGYAPGAWSQVARQRXXXXXXXXXXXXXXXEPPHGVNSIQAN
ILAKRTHDLIRLFFSKHFQLNRHDDLHKDHGYFQNMLEEELTHVKDTELYREIFTSDDIY
ETPNTNSTLIEREKFPVDVIISDMYEPWPQTTGFWNNITNQAYFRMANTSGVSIRDHYQS
IDLCDAALVTAIDLLRPLGSFVCKLYTGXXXNLXXXXXXXXXXXXXXXXPDASRDESKET
YYIGLKKKRNVDKLDVFSNS

>YGL154C | LYS5
MVKTTEVVSEVSKVAGVRPWAGIFVVEIQEDILADEFTFEALMRTLPLASQARILNKKSF
HDXXXXXXXXXXXXXXXXIVTGLNFQELKFDKGSFGKPFLDNNRFLPFSMTIGEQYVAMF
LVKCVSTDEYQDVGIDIASPCNYGGREELELFKEVFSEREFNGLLKASDPCTIXXXXXXX
XXXXXXXXXXXXNXXXXXXXXXXXXXXXXXXXSMCITLDEVPLIFHSQWFNNEIVTICMP
KSISDKINTNRPKLYNISLSTLIDYFIENDGL

>YGR092W | DBF2
MLSKSEKNVDLLAGNMSNLSFDGHGTPGGTGLFPNQNITKRRTRPAGINDSPSPVKPSFF
PYEDTSNMDIDEVSQPDMDVSNSPKKLPPKFYERATSNKTQRVVSVCKMYFLEHYCDMFD
YVISRRQRTKQVLEYLQQQSQLPNSDQIKLNEEWSSYLQREHQVLRKRRLKPKNRDFEMI
TQVGQGGYGQVYLARKKDTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRSEWLVKL
LYAFQDLQSLYLAMEFVPGGDFRTLLINTRCLKSGHARFYISEMFCAVNALHDLGYTHRD
LKPENFLIDAKGHIKLTDFGLAAGTISNERIESMKIRLEKIKDLEFPAFTEKSIEDRRKM
YNQLREKEINYANSMVGSPDYMALEVLEGKKYDFTVDYWSLGCMLFESLVGYTPFSGSST
NETYDNLRRWKQTLRRPRQSDGRAAFSDRTWDLITRLIADPINRLRSFEHVKRMSYFADI
NFSTLRSMIPPFTPQLDSETDAGYFDDFTSEADMAKYADVFKRQDKLTAMVDDSAVSSKL
VGFTFRHRNGKQGSSGILFNGLEHSDPFSTFY

>YLR264W | RPS28B
MDSKTPVTLAKVIKVLGRTGSRGGVTQVRVEFLEDTSRTIVRNVKGPXXXXXXXXXXXXX
XXARRLR

>YOR070C | GYP1 (YOR29-21)
MGVRSAAKEMHERDHNXXXXXXXXXXXXXXXXXXASSSKKPSLYKMNTTESTSLPSGYAS
SADRDRRTSDGNFEAMAKQQASTRRTSNSYSPLRYVNPTLSTASNESPRPALLLRQHHXX
XXXXQQPRHSSSGSVGNNCSNSTEPNKKGDRYFKDLDEDWSAVIDDYNMPIPILTNGGFG
TPVAPTRTLSRKSTXXXIXXXXXXXXXXXXXXXXXXXXXXXXXLQKEKTNDSKKTQLEIE
NERDVQELNSIIQRISKFDNILKDKTIINQQDLRQISWNGIPKIHRXXXXXXXXXXXXXX
XXXXXXXXXXXXXEYRDSLKHTFSDQHSRDIPTWHQIEIDXXXXXXXXXXXXXXXXXXXX
XXXXXLWAIRHPASGYVQGINDLVTPFFETFLTEYLPPSQIDDVEIKDPSTYMVDEQITD
LEADTFWCLTKLLEQITDNYIHGQPGILRQVKNLSQLVKRIDADLYNHFQNEHVEFIQFA
FRWMNCLLMREFQMGTVIRMWDTYLSETSQEVTSSYSMSSNDIKPPXXXXXXXXXXXXXX
XKDFQSPTTALSNMTPNNAVEDSGKMRQSSLNEFHVFVCAAFLIKWSDQLMEMDFQETIT
FLQNPPTKDWTETDIEMLLXXXXXXXXXXXXXXXXXL

>YOR275C | RIM20
MSELLAIPLKRTLEVDFATELSKLXXXXXXXXXXXXXXXILKVVDARNNAIAPDISIDGL
SALKEYYVILLQLEKKFPNNQIEFTWFQTLSQKSRGTSQYSLQWEKLTIIYNIGCMYSLL
ALNSNNDAAESLKTSCLYFQNAAGCFKHVLDHQKNLETIPVVDDATLNALTSLMLAQAQE
CFWFKAVQDKHKDSLIAKLSQQIVDFYCEAINDAQRGKLIRSDWINHLKAKKAYFSAVTY
YRIALSFNEKKXXXXXXXXXXXXXXXXNESTLSSQAKFKTVVESSLKEAQRDNEFIYLQE
VXXXXXXXXXXXXXXXXXXXXXXXIKKDETLFKDLIPIEVMXXXXXXXXXXXXXXXXXRV
TNPLASLNKLLKESXXXXXXXXXXXXXXXXXLSHYXXXXXXXXXXXKNVQVQLDNIEQIL
NEEAFTDNQLRLKHGTLNWTLPESSTTNTAYYXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XNLIGSEIRLPESNDPLTNKIKMIIQERNDYIDRTRRKSSEYRILPKIITSYKKNGTVDF
EPIFIGHLKYFDEDXXXXXXXXXXXXXXXXXVNLSKKNNPGRSGIEPKKMVRIDPRELYI
EDLRYSFKLLDEVKXXXXXXXXXXXXXXXXXXNLYNEVQEYDTARRAEKARLDKSLTFED
Q

>YPL106C | SSE1 (LPG3, MSI3)
MSTPFGLDLGXXXXXXXXXXXXXXXXXXXXXXXXSTPSVVGFGPKNRYLGEXXXXXXXXX
XXXTVANLKRIIGLDYHHPDFEQESKHFTSKLVELDDKKTGXXXXXXGEKHVFSATQXXX
XXXXXXXXXXXXXXKANITDVCIAVPPWYTEEQRYNIADAARIAGLNPVRIVNDVTAAGV
SYGIFKTDLPEGEEKPRIVAFVDIGHSSYTCSIMAFKKGQLKVLGTACDXXXXXXXXXXX
XXXXXADEFKTKYKIDIRENPKAYNRILTAAEKLKKVLSANTNAPFSVESVMNDVDVSSQ
LSREELEELVKPLLERVTEPVTKALAQAKLSAEEVDFVEIIGGTTRIPTLKQSISEAFGK
PLSTTLNQDEAIAKGAAFICAIHSPTLRVRPFKFEDIHPYXXXXXXXXXXXXXXHMEVFP
AGSSFPSTKLITLNRTGDFSMAASYTDITQLPPNTPEQIANWEITGVQLPEGQDSVPXXX
XXRCDPSGLHTXXXXXXXXXXXXXXXPIPLXXXXXXXXXXXXXXXXXXXXDDLTIVAHTF
GLDAKKLNELIEKENEMLAQDKLVAETEDRKNTLXXXXXXXXXXXXXXXAPFASDAEKTK
LQGMLNKAEEWLYDEGFDSIXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXTEGDVDMD

>YDR034C | LYS14
MFESVNLDENXXXXXXXXXXXXXXXXXXXXXXXXXXXSFTNSGTSTSCFEPKNNLPSLSF
LNARAXXXXXXXXXXXXXXXXXXXIGGENVESTTSSNDGSNENXXXXXXXXXXXXXXXXX
ISQADDNGHSSLTPNPAVTSTVTDKKGNXXXXXXXXXXXXXXXXXXMKCDETKPTCWQCA
RLNRQCVYVLNPKNKKRRTSNAQRVKEFRKHSTSLDNDHNNAXXXXXXXXXXXXXXXXXX
NLSEDTTDPKPITDNGKNVPXXXXXXXXXXXXXXXXXXNGYDVNLLMQNLNDMVNMKLHD
SYLLNEELKGLDLPDLDIPELLPASNVNSSVPISFLVNNVITFNTKLSSFKLGGIHDKYL
KIFYYDCLDSIAPFFQNQGNPLRDILLSFAKNEAYLLSSILATGASIAYRKSNNLEDERN
YCAYLSHCLSLLGEQFKNESNVLNRIEPIILTVIMLAWDCIYSMNSQWRSHLKGVTDLFK
KINAGNSSKVLNVAKCWFKVMETFASISTVFGGSLIDNNDLDAIFDPYDYQYVDSLKFLN
IMTPLNEFNLLRGHKEDFDLVIKEVFKSLNTIRSTEKNYFSKEEGLFTKKLDYLLLSSQT
SSEKSKDQISYFNTQKILVEIDKQLDYEFIDKSGIIPSDNQSHPRISNIHDNAIDMVTLK
NGEEVAISXXXXXXXXXXXXXXXXXXXXXXGMPKESSTIQQVVKKIMSFFKFLDSDSPPQ
NSRTCYSNFAVLIAGLNAMDEETRAIVKRYYKINGGKFQKLTEHNLNRLEKVWYGKNQNY
RLEEQDVLTW

>YJL124C | LSM1 (SPB8)
MSANSKDRNQSNQDAKRQQQNFPKKISEGEADLYLDQYNFTTTAAIVSSVDRKIFVLLRD
GRMLFGVLRTFDQYANLILQDCVERIYFSXXXXXXXXXXXXXXXXXXXXXXXXXVDIDKE
DQPLEAMERIPFKEAWLTKQKNDEKRFKEETHKGKKMARHGIVYDFHKSDMY

>YGL045W | RIM8 (PAL3, YGL046W, ART9)
MSLLRLWNKESRAPSKIKSHGIVGSYGNSMLAHNNVKQFRIDIDEPHRVWKPNESITGEA
VIDIKRDITNVAIKLSLVCEVRVKTGNSPTSKNKRIEKTLEKSTFLYGQDYVKTAFSAKE

```
KKPHVDKTTILNGLSKGEHRFPFRIRIPRGRGMLSSIKFERGSITYFLSCTLESLNNING
LKKPEARCEREFAVIVPLDVSRLPKPKTKTVVLQSASMVQNKKNKSTEDESSSYTQLTQK
STTSNSSSSSVNSKTSPLPNKTVTISVDIPQAGFMIGEIIPIDVKIDHXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXICQSISPIYINPETLQFQSRVYLKVPLDAFSTLTTVG
KFFSFQYYIEVMVNLSKKNVVYTESNRIIGTPIGEQNGLGVENNINRIQRKMLRMVNPET
LENDSEGYESSIFFKDMVNVEKLKRLRNVTGMSIETVIGTTRSEQQQSDASIPSQSSITA
PQNSPSNLRDWLAPLNAYDSDDVPVPKYSPNDKVSVPSEDKQELEQKRLQQLESDPPPCD
DY
```

Rangeof lowcomplexityregionswithp-values:

```
>YBL087C
135-137 p-value: 0.000e+00

>YAL018C
55-71 p-value: 3.583e-01
85-99 p-value: 4.927e-02
188-213  p-value: 5.761e-02

>YDL081C
65-81  p-value: 3.416e-15

>YDL136W
73-91 p-value: 1.474e-02


>YDR076W
53-68 p-value: 1.477e-02
152-154 p-value: 0.000e+00

>YLR181C
123-137 p-value: 3.642e-03
188-203 p-value: 7.773e-03
222-238 p-value: 2.896e-01
280-293 p-value: 2.045e-01
312-327  p-value: 4.125e-01

>YML062C
260-275 p-value: 3.766e-06
345-381 p-value: 2.494e-01
385-387 p-value: 0.000e+00

>YML063W
4-19 p-value: 1.504e-04
156-165 p-value: 1.587e-01
233-246 p-value: 5.227e-03

>YML121W
6-18 p-value: 2.628e-02
106-121 p-value: 3.739e-01
147-163 p-value: 3.768e-07
222-235 p-value: 8.926e-03
270-277 p-value: 2.437e-06
```

```
>YML017W
107-133 p-value: 3.523e-03
398-417 p-value: 1.589e-06
419-449 p-value: 4.673e-14
453-488 p-value: 1.160e-35
562-584 p-value: 1.753e-06

>YNL091W
5-21 p-value: 1.289e-10
26-42 p-value: 3.116e-02
71-103 p-value: 1.281e-01
144-166 p-value: 2.604e-03
206-230 p-value: 5.133e-02
452-483 p-value: 6.255e-16
524-538 p-value: 7.998e-09
556-580 p-value: 1.163e-30
617-635 p-value: 8.642e-02
637-668 p-value: 2.712e-70
671-690 p-value: 3.957e-11
692-709 p-value: 3.856e-10
712-730 p-value: 4.682e-04
732-755 p-value: 2.592e-14
992-1006 p-value: 1.856e-16

>YNR050C
105-122 p-value: 5.315e-01
263-279 p-value: 1.706e-01

>YNR051C
457-474 p-value: 2.093e-03

>YOL039W
67-99 p-value: 7.962e-06

>YOR106W
44-59 p-value: 4.544e-02
112-117 p-value: 1.344e-01
165-179 p-value: 2.032e-20
183-195 p-value: 1.421e-01
223-227 p-value: 1.214e-04
268-282 p-value: 1.654e-07

>YOR014W
16-55 p-value: 3.184e-43
85-104 p-value: 1.504e-17
106-122 p-value: 1.466e-05
126-141 p-value: 2.916e-10
143-147 p-value: 0.000e+00
303-321 p-value: 1.686e-01
550-576 p-value: 2.590e-02
679-701 p-value: 1.310e-01
```

```
>YOR038C
68-77  p-value: 1.977e-08
153-163 p-value: 6.273e-03
250-261 p-value: 1.094e-03
286-299 p-value: 2.306e-02
335-350 p-value: 5.636e-02
364-381 p-value: 5.410e-01
416-433 p-value: 5.955e-03
464-473 p-value: 2.976e-02
532-544 p-value: 2.096e-01
651-667  p-value: 1.021e-01
705-707 p-value: 0.000e+00
781-793  p-value: 3.567e-01

>YOR078W
158-173 p-value: 3.317e-02

>YOR382W
93-143  p-value: 3.373e-04

>YOR235W
34-49 p-value: 3.428e-03

>YOR293W
20-22 p-value: 0.000e+00

>YPL157W
7-20  p-value: 1.193e-06
56-58 p-value: 0.000e+00
83-94 p-value: 1.707e-02
277-290 p-value: 1.457e-04
292-303 p-value: 3.269e-03

>YPR172W
101-131 p-value: 2.137e-07

>YFL001W
49-80 p-value: 1.432e-01
83-98 p-value: 1.005e-01
422-437 p-value: 4.083e-01

>YNL284C
78-110 p-value: 2.240e-08
130-139  p-value: 1.788e-01
192-206 p-value: 2.714e-03
232-257 p-value: 2.871e-01
271-286 p-value: 3.359e-01

>YLR238W
25-51 p-value: 4.124e-01
110-115 p-value: 0.000e+00
281-309 p-value: 1.130e-01
```

```
>YBR201W
42-59 p-value: 4.060e-01

>YBR076W
136-150 p-value: 2.179e-01
157-174 p-value: 7.746e-02

>YBR106W
108-122 p-value: 3.375e-01

>YGL174W
21-42 p-value: 1.507e-06
49-68 p-value: 2.152e-02
179-181 p-value: 0.000e+00
200-217 p-value: 3.927e-01

>YGL199C
102-119 p-value: 8.051e-02

>YGL199C
102-119 p-value: 1.043e-01

>YGL031C
101-140 p-value: 5.496e-05

>YLR234W
21-23 p-value: 0.000e+00
62-75 p-value: 9.180e-02
180-195 p-value: 4.180e-01
202-211 p-value: 3.508e-02
272-275 p-value: 8.493e-17
305-321 p-value: 1.638e-01
395-428 p-value: 1.248e-02
438-457 p-value: 2.567e-01
464-472 p-value: 4.063e-02
475-487 p-value: 2.991e-01
506-522 p-value: 9.845e-02

>YGL049C
6-24 p-value: 1.031e-20
82-94 p-value: 8.293e-10
182-197 p-value: 1.659e-02
224-256 p-value: 5.860e-02
296-314 p-value: 1.244e-03
316-343 p-value: 8.565e-04
489-502 p-value: 3.374e-05
509-531 p-value: 3.174e-05
541-558 p-value: 3.331e-02
872-887 p-value: 4.075e-02

>YBR093C
38-55 p-value: 2.487e-01
111-122 p-value: 1.869e-18
385-400 p-value: 1.942e-02
```

```
>YDR128W
51-67 p-value: 2.241e-01
219-221 p-value: 0.000e+00
266-282 p-value: 8.873e-04
340-354 p-value: 1.831e-01
392-409 p-value: 5.340e-01
640-658 p-value: 2.933e-02
689-704 p-value: 3.624e-03
708-732 p-value: 2.591e-13
755-767 p-value: 4.268e-01
770-786 p-value: 5.685e-02
823-838 p-value: 3.381e-03
861-876 p-value: 2.368e-02
969-988 p-value: 2.156e-02
1057-1070 p-value: 1.519e-03

>YER155C
10-24 p-value: 3.391e-22
28-50 p-value: 8.634e-22
58-73 p-value: 1.722e-20
129-146 p-value: 2.870e-03
152-168 p-value: 4.605e-01
177-213 p-value: 7.774e-11
240-260 p-value: 9.957e-13
279-307 p-value: 4.444e-04
576-592 p-value: 3.403e-01
709-711 p-value: 0.000e+00
713-729 p-value: 7.680e-02
735-758 p-value: 9.180e-02
885-898 p-value: 1.638e-08
904-913 p-value: 5.864e-14
915-931 p-value: 4.790e-02
972-993 p-value: 2.488e-01
1069-1086 p-value: 1.662e-01
1121-1137 p-value: 1.832e-01
1148-1165 p-value: 1.044e-06
1319-1333 p-value: 4.308e-01
1336-1362 p-value: 4.338e-05
1529-1540 p-value: 1.261e-04
1701-1730 p-value: 3.698e-02
1766-1781 p-value: 1.615e-01
1831-1847 p-value: 8.076e-07
1850-1867 p-value: 7.333e-03
1886-1903 p-value: 1.613e-01
1912-1914 p-value: 0.000e+00
2006-2019 p-value: 2.001e-04
2067-2083 p-value: 2.790e-01
2104-2119 p-value: 3.595e-01

>YGL105W
73-95 p-value: 9.144e-02
168-191 p-value: 4.887e-20
```

```
262-265 p-value: 0.000e+00

>YGL136C
13-27 p-value: 5.693e-02
29-45 p-value: 2.108e-01
94-108 p-value: 3.091e-02
269-271  p-value: 0.000e+00
274-289 p-value: 2.612e-01

>YGL154C
63-78  p-value: 9.094e-07
174-192 p-value: 7.368e-02
194-212  p-value: 4.120e-01

>YGR092W
200-232  p-value: 3.249e-02

>YLR264W
48-62 p-value: 4.527e-01

>YOR070C
17-34 p-value: 7.808e-03
119-124 p-value: 1.087e-45
195-197 p-value: 0.000e+00
199-223 p-value: 5.656e-03
287-313  p-value: 9.641e-02
341-365  p-value: 1.629e-01
527-541  p-value: 2.681e-08
620-636 p-value: 1.888e-01

>YOR275C
25-39  p-value: 3.663e-02
252-267 p-value: 2.056e-02
302-325 p-value: 1.201e-10
343-358 p-value: 1.287e-01
375-391  p-value: 4.404e-01
396-406 p-value: 6.515e-03
453-481 p-value: 1.411e-01
555-571 p-value: 3.839e-01
615-632 p-value: 4.228e-03

>YPL106C
11-34 p-value: 1.032e-01
52-63  p-value: 1.333e-01
102-107  p-value: 6.683e-01
118-134 p-value: 4.555e-02
230-245 p-value: 3.052e-02
401-414  p-value: 1.255e-02
478-482 p-value: 2.903e-04
492-505 p-value: 8.929e-06
510-530 p-value: 3.344e-04
575-589 p-value: 3.617e-05
621-685 p-value: 8.506e-13
```

>YDR034C
11-37 p-value: 1.637e-03
66-84 p-value: 3.803e-01
104-166 p-value: 4.924e-02
223-278 p-value: 9.878e-02
669-690 p-value: 1.002e-02

>YJL124C
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