Supplementary Table 1

Table S1 Functional proteins associated R-spondin (Homo sapiens) and their protein IDs analyzed in this study.

Seq No.	**Protein**	**Protein/ Gene ID**	**Protein length**	**Other Information**
1	R-spondin-1	NP_001033722.1	263 aa	DEFINITION: R-spondin-1 isoform 1 precursor [Homo sapiens]. ACCESSION: NP_001033722 VERSION: NP_001033722.1 GI:84490388
2	R-spondin-2	NP_848660.3	243 aa	DEFINITION: R-spondin-2 isoform 1 precursor [Homo sapiens]. ACCESSION: NP_848660 VERSION : NP_848660.3 GI:222446611
3	R-spondin-3	NP_116173.2	272 aa	DEFINITION R-spondin-3 precursor [Homo sapiens]. ACCESSION NP_116173 VERSION NP_116173.2 GI:18490982
4	R-spondin-4	NP_001025042.2	234 aa	DEFINITION R-spondin-4 isoform 1 precursor [Homo sapiens]. ACCESSION: NP_001025042 XP_297816 VERSION: NP_001025042.2 GI:83722284

Supplementary Table 2

Table S2 (Rspo)s and their genes

No	Gene/Locus	Gene ID	Gene Location	Protein (Gene product)
1	*RSPO1*	Gene ID: 284654	Chromosome: 1; 1p34.3 (38076821..38100595)	R-spondin 1
2	*RSPO2*	Gene ID: 340419	Chromosome: 8; 8q23.1 (108911544..109095913)	R-spondin 2
3	*RSPO3*	Gene ID: 84870	Chromosome: 6; 6q22.33 (127439844..127520626)	R-spondin 3
4	*RSPO4*	Gene ID: 343637	Chromosome: 20;20p13 (939095..982907)	R-spondin 4

Supplementary Table S3- (Rspo)s and their compositional analysis, charge distribution analysis, repetitive structures, and cysteine positions

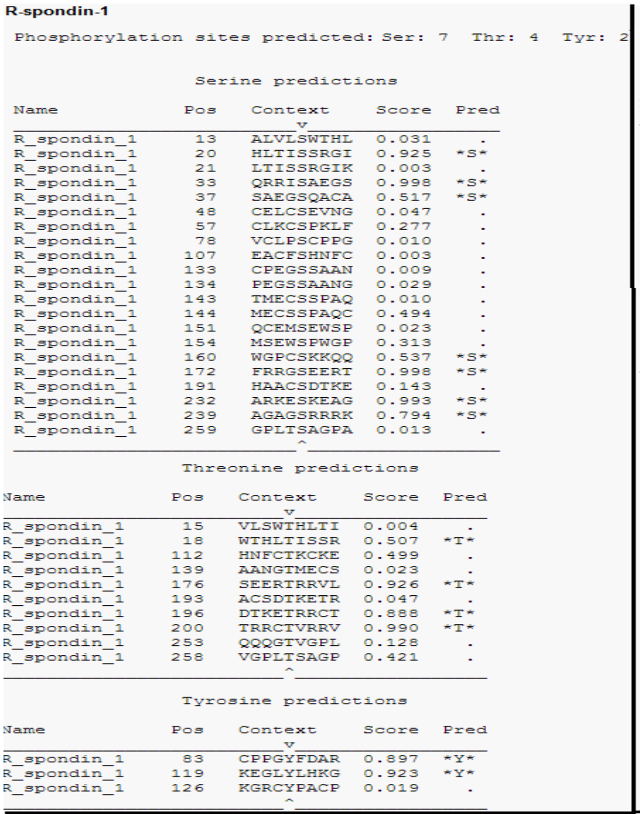
Name	Mol. wt. (kdal)	Compositional analysis of amino acids	Charge Distribution Analysis	Repetitive Structures	cysteine positions
R-spondin-1	29.0 kdal	A : 19(7.2%); C++: 23(8.7%); D- : 5(1.9%); E : 18(6.8%); F : 5(1.9%) G : 26(9.9%); H : 6(2.3%); I : 7(2.7%); K : 19(7.2%); L : 17(6.5%) M : 4(1.5%); N : 9(3.4%); P : 15(5.7%); Q : 15(5.7%); R+ : 27(10.3%) S : 21(8.0%); T : 10(3.8%); V : 11(4.2%); W : 3(1.1%); Y : 3(1.1%)	0+00000000 0000000000 0+00+0++0+ +000- 00000 0+00-000-0 0000+000+0 0000-+0-0+ 0000000000 0000- 0+00- 00+00+0+0- 00-0000000 00+0+- 0000 0+0+000000 - 000000000 - 0000000-0 0- 00000000 ++000000++ 00-- +0++00 00000-0000 0-0+- 0++00 0++0000-00 ++++0000++ - 000+000++ -0+- 00000+ +++0000000 0000000000 000	A. SEPARATED, TANDEM, AND PERIODIC REPEATS: amino acid alphabet. Repeat core block length: 4 Aligned matching blocks: [129- 132] CPEG [206- 209] CPEG [212- 215] RRKG [241- 244] RRKG B. SEPARATED AND TANDEM REPEATS: 11-letter reduced alphabet. (i= LVIF; += KR; -= ED; s= AG; o= ST; n= NQ; a= YW; p= P; h= H; m= M; c= C) Repeat core block length: 8	6,40,44,47,53,56,79,94,97,102,105,111,125,129,142,148,159,166,190,199

R-spondin-2	28.3 kdal	A : 10(4.1%); C++: 24(9.9%); D : 9(3.7%); E : 15(6.2%); F : 13(5.3%) G : 17(7.0%); H : 7(2.9%); I : 8(3.3%); K : 21(8.6%); L- : 13(5.3%) M : 7(2.9%); N : 10(4.1%); P : 9(3.7%); Q : 9(3.7%); R+ : 27(11.1%) S : 16(6.6%); T : 11(4.5%); V- : 7(2.9%); W : 4(1.6%); Y : 6(2.5%)	000+000000 000000-000 0000+0++0+ +000000000 +000000+-0 000+000+00 000++-00+0 00- 0000000 00000+00- 0 0+00+0+0-0 0- 0000+-00 0+0+000000 +0+00--00- 00000- -00- 00-00-0000 0-00000+00 +0000+000- 0+0+000++0 0+-0000000 0- 0++0+000 +00000++00 +0+- ++0+++ +++00-+00- 00000000-+ 000	*A. SEPARATED, TANDEM, AND PERIODIC REPEATS: amino acid alphabet.* Repeat core block length: 4 *B. SEPARATED AND TANDEM REPEATS: 11-letter reduced alphabet.* (i= LVIF; += KR; -= ED; s= AG; o= ST; n= NQ; a= YW; p= P; h= H; m= M; c= C) Repeat core block length: 8	15,21,46,52,55,74,78,93,96,101,104,110,113,124,128,141,145,156,163,187,196,203
R-spondin-3	30.9 kdal	A- : 7(2.6%); C++: 22(8.1%); D : 7(2.6%); E : 18(6.6%); F : 8(2.9%) G : 21(7.7%); H : 7(2.6%); I : 12(4.4%); K+ : 33(12.1%); L- : 14(5.1%) M : 5(1.8%); N : 15(5.5%); P : 13(4.8%); Q : 14(5.1%); R : 20(7.4%) S : 22(8.1%); T : 14(5.1%); V	000+000000 000000-000 00000+0++0 ++00000000 000000000- 0000000+0+ 00000-+000 +000000000 0000000+00 - 00+00+0+0 -0- 0000+00 00+0+00000 000+00-000 -00- 000000 -0000000-0 0-00000000 ++0+0000++ 00- 0+0+-00 00000+0000 0000- 0++00 00+++00+0- +0++0+-+++ ++00+0-0+- 000- 0+00-0 0+-00-0+-0 +000++++00 -	A. SEPARATED, TANDEM, AND PERIODIC REPEATS: amino acid alphabet. Repeat core block length: 4 Aligned matching blocks: [93- 99] NK__CTKCK [107- 115] NKNFCTKCK B. SEPARATED AND TANDEM REPEATS: 11-letter reduced alphabet. (i= LVIF; += KR; -= ED; s= AG; o= ST; n= NQ; a= YW; p= P; h= H; m= M; c= C) Repeat core block length: 8	41,45,48,54,57,76,80,95,102,105,111,114,125,129,142,148,159,166,190,199

		: 11(4.0%); W : 3(1.1%); Y : 6(2.2%)	+0+000000 00		
R-spondin-4	26.2 kdal	A : 11(4.7%); C++: 23(9.8%); D : 7(3.0%); E : 14(6.0%); F : 6(2.6%) G+ : 27(11.5%); H : 5(2.1%); I : 7(3.0%); K : 15(6.4%); L : 20(8.5%) M : 2(0.9%); N : 6(2.6%); P : 16(6.8%); Q : 14(6.0%); R++: 27(11.5%) S : 10(4.3%); T : 10(4.3%); V- : 7(3.0%); W : 3(1.3%); Y : 4(1.7%)	0+00000000 00000-0000 0++++00000 0000000000 00--000000 00+00000++ -00+000+00 0-00000000 +00-00+0++ 00000-0000 0-000+0++0 0000+0+000 0000000000 00+-000-0- 0000000000 0000+00000 000-0+0+-0 0+000--000 00000-0++0 000+0000-+ 0000++0++- ++0++-++0- ++0-0+0+00 0000	A. SEPARATED, TANDEM, AND PERIODIC REPEATS: amino acid alphabet. Repeat core block length: 4 Aligned matching blocks: [67- 76] GKCLHDCPPG [116- 125] GKCLPTCPPG [208- 211] RKDR [214- 217] RKDR B. SEPARATED AND TANDEM REPEATS: 11-letter reduced alphabet. (i= LVIF; += KR; -= ED; s= AG; o= ST; n= NQ; a= YW; p= P; h= H; m= M; c= C) Repeat core block length: 8	6,35,38,41,47,50,73,88,91,95,98,104,118,122,135,139,150,157,181,190

Supplementary Table 4

Table S4- Phosphorylation sites of (Rspo)s



R-spondin-1

```
 Phosphorylation sites predicted: Ser: 7  Thr: 4  Tyr: 2


                     Serine predictions

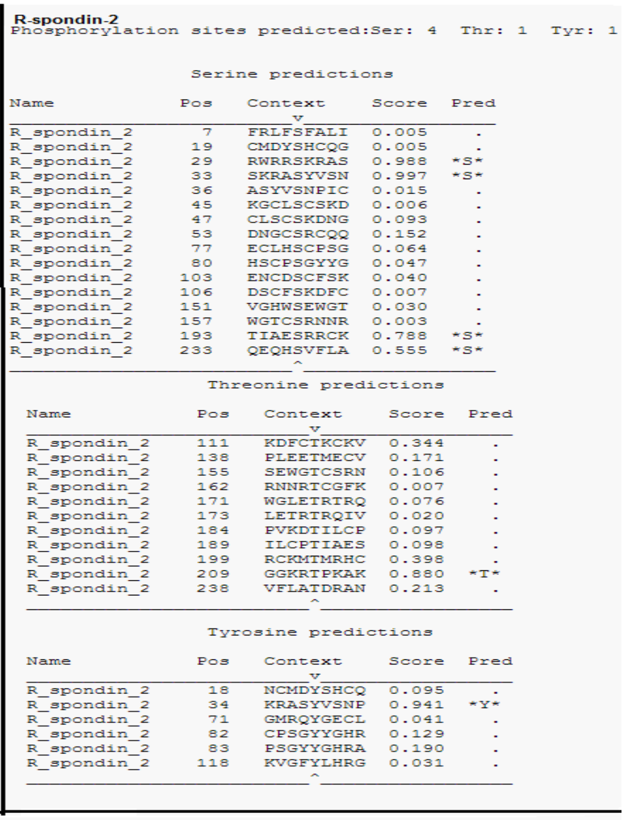
 Name             Pos    Context     Score   Pred
 _______________________________v___________________
 R_spondin_1       13    ALVLSWTHL   0.031     .
 R_spondin_1       20    HLTISSRGI   0.925   *S*
 R_spondin_1       21    LTISSRGIK   0.003     .
 R_spondin_1       33    QRRISAEGS   0.998   *S*
 R_spondin_1       37    SAEGSQACA   0.517   *S*
 R_spondin_1       48    CELCSEVNG   0.047     .
 R_spondin_1       57    CLKCSPKLF   0.277     .
 R_spondin_1       78    VCLPSCPPG   0.010     .
 R_spondin_1      107    EACFSHNFC   0.003     .
 R_spondin_1      133    CPEGSSAAN   0.009     .
 R_spondin_1      134    PEGSSAANG   0.029     .
 R_spondin_1      143    TMECSSPAQ   0.010     .
 R_spondin_1      144    MECSSPAQC   0.494     .
 R_spondin_1      151    QCEMSEWSP   0.023     .
 R_spondin_1      154    MSEWSPWGP   0.313     .
 R_spondin_1      160    WGPCSKKQQ   0.537   *S*
 R_spondin_1      172    FRRGSEERT   0.998   *S*
 R_spondin_1      191    HAACSDTKE   0.143     .
 R_spondin_1      232    ARKESKEAG   0.993   *S*
 R_spondin_1      239    AGAGSRRRK   0.794   *S*
 R_spondin_1      259    GPLTSAGPA   0.013     .
 _______________________________^___________________

                    Threonine predictions

Name             Pos    Context     Score   Pred
_______________________________v___________________
R_spondin_1       15    VLSWTHLTI   0.004     .
R_spondin_1       18    WTHLTISSR   0.507   *T*
R_spondin_1      112    HNFCTKCKE   0.499     .
R_spondin_1      139    AANGTMECS   0.023     .
R_spondin_1      176    SEERTRRVL   0.926   *T*
R_spondin_1      193    ACSDTKETR   0.047     .
R_spondin_1      196    DTKETRRCT   0.888   *T*
R_spondin_1      200    TRRCTVRRV   0.990   *T*
R_spondin_1      253    QQQGTVGPL   0.128     .
R_spondin_1      258    VGPLTSAGP   0.421     .
_______________________________^___________________

                    Tyrosine predictions

Name             Pos    Context     Score   Pred
_______________________________v___________________
R_spondin_1       83    CPPGYFDAR   0.897   *Y*
R_spondin_1      119    KEGLYLHKG   0.923   *Y*
R_spondin_1      126    KGRCYPACP   0.019     .
_______________________________^___________________
```



R-spondin-2

```
Phosphorylation sites predicted:Ser: 4  Thr: 1  Tyr: 1

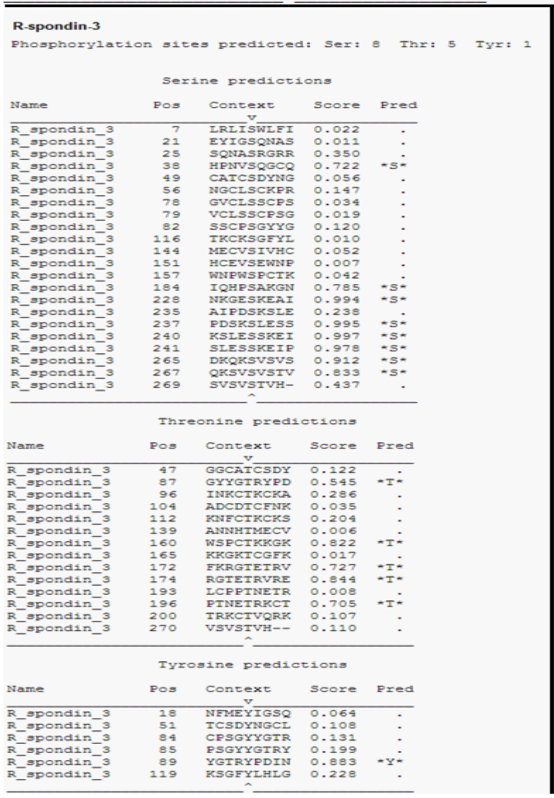

                     Serine predictions

Name             Pos    Context     Score   Pred
_______________________________v___________________
R_spondin_2        7    FRLFSFALI   0.005     .
R_spondin_2       19    CMDYSHCQG   0.005     .
R_spondin_2       29    RWRRSKRAS   0.988   *S*
R_spondin_2       33    SKRASYVSN   0.997   *S*
R_spondin_2       36    ASYVSNPIC   0.015     .
R_spondin_2       45    KGCLSCSKD   0.006     .
R_spondin_2       47    CLSCSKDNG   0.093     .
R_spondin_2       53    DNGCSRCQQ   0.152     .
R_spondin_2       77    ECLHSCPSG   0.064     .
R_spondin_2       80    HSCPSGYYG   0.047     .
R_spondin_2      103    ENCDSCFSK   0.040     .
R_spondin_2      106    DSCFSKDFC   0.007     .
R_spondin_2      151    VGHWSEWGT   0.030     .
R_spondin_2      157    WGTCSRNNR   0.003     .
R_spondin_2      193    TIAESRRCK   0.788   *S*
R_spondin_2      233    QEQHSVFLA   0.555   *S*
_______________________________^___________________
                     Threonine predictions

  Name             Pos    Context     Score   Pred
  _______________________________v___________________
  R_spondin_2      111    KDFCTKCKV   0.344     .
  R_spondin_2      138    PLEETMECV   0.171     .
  R_spondin_2      155    SEWGTCSRN   0.106     .
  R_spondin_2      162    RNNRTCGFK   0.007     .
  R_spondin_2      171    WGLETRTRQ   0.076     .
  R_spondin_2      173    LETRTRQIV   0.020     .
  R_spondin_2      184    PVKDTILCP   0.097     .
  R_spondin_2      189    ILCPTIAES   0.098     .
  R_spondin_2      199    RCKMTMRHC   0.398     .
  R_spondin_2      209    GGKRTPKAK   0.880   *T*
  R_spondin_2      238    VFLATDRAN   0.213     .
  _______________________________^___________________

                     Tyrosine predictions

  Name             Pos    Context     Score   Pred
  _______________________________v___________________
  R_spondin_2       18    NCMDYSHCQ   0.095     .
  R_spondin_2       34    KRASYVSNP   0.941   *Y*
  R_spondin_2       71    GMRQYGECL   0.041     .
  R_spondin_2       82    CPSGYYGHR   0.129     .
  R_spondin_2       83    PSGYYGHRA   0.190     .
  R_spondin_2      118    KVGFYLHRG   0.031     .
  _______________________________^___________________
```



R-spondin-3

```
Phosphorylation sites predicted: Ser: 8  Thr: 5  Tyr: 1


                    Serine predictions

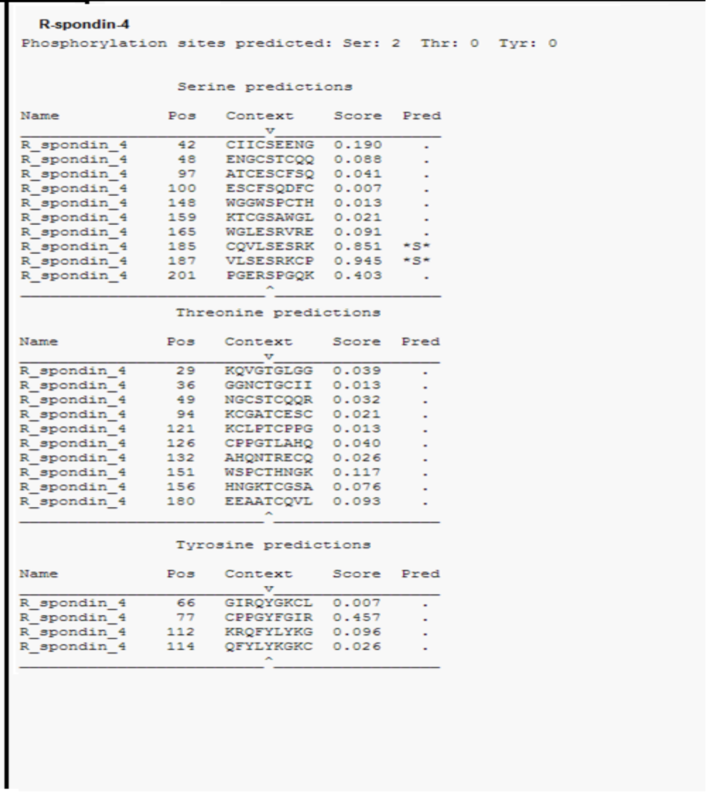
Name             Pos    Context     Score   Pred
_______________________________v___________________
R_spondin_3        7    LRLISWLFI   0.022     .
R_spondin_3       21    EYIGSQNAS   0.011     .
R_spondin_3       25    SQNASRGRR   0.350     .
R_spondin_3       38    HPNVSQGCQ   0.722   *S*
R_spondin_3       49    CATCSDYNG   0.056     .
R_spondin_3       56    NGCLSCKPR   0.147     .
R_spondin_3       78    GVCLSSCPS   0.034     .
R_spondin_3       79    VCLSSCPSG   0.019     .
R_spondin_3       82    SSCPSGYYG   0.120     .
R_spondin_3      116    TKCKSGFYL   0.010     .
R_spondin_3      144    MECVSIVHC   0.052     .
R_spondin_3      151    HCEVSEWNP   0.007     .
R_spondin_3      157    WNPWSPCTK   0.042     .
R_spondin_3      184    IQHPSAKGN   0.785   *S*
R_spondin_3      228    NKGESKEAI   0.994   *S*
R_spondin_3      235    AIPDSKSLE   0.238     .
R_spondin_3      237    PDSKSLESS   0.995   *S*
R_spondin_3      240    KSLESSKEI   0.997   *S*
R_spondin_3      241    SLESSKEIP   0.978   *S*
R_spondin_3      265    DKQKSVSVS   0.912   *S*
R_spondin_3      267    QKSVSVSTV   0.833   *S*
R_spondin_3      269    SVSVSTVH-   0.437     .
_______________________________^___________________

                   Threonine predictions

Name             Pos    Context     Score   Pred
_______________________________v___________________
R_spondin_3       47    GGCATCSDY   0.122     .
R_spondin_3       87    GYYGTRYPD   0.545   *T*
R_spondin_3       96    INKCTKCKA   0.286     .
R_spondin_3      104    ADCDTCFNK   0.035     .
R_spondin_3      112    KNFCTKCKS   0.204     .
R_spondin_3      139    ANNHTMECV   0.006     .
R_spondin_3      160    WSPCTKKGK   0.822   *T*
R_spondin_3      165    KKGKTCGFK   0.017     .
R_spondin_3      172    FKRGTETRV   0.727   *T*
R_spondin_3      174    RGTETRVRE   0.844   *T*
R_spondin_3      193    LCPPTNETR   0.008     .
R_spondin_3      196    PTNETRKCT   0.705   *T*
R_spondin_3      200    TRKCTVQRK   0.107     .
R_spondin_3      270    VSVSTVH--   0.110     .
_______________________________^___________________

                   Tyrosine predictions

Name             Pos    Context     Score   Pred
_______________________________v___________________
R_spondin_3       18    NFMEYIGSQ   0.064     .
R_spondin_3       51    TCSDYNGCL   0.108     .
R_spondin_3       84    CPSGYYGTR   0.131     .
R_spondin_3       85    PSGYYGTRY   0.199     .
R_spondin_3       89    YGTRYPDIN   0.883   *Y*
R_spondin_3      119    KSGFYLHLG   0.228     .
_______________________________^___________________
```



R-spondin-4

```
Phosphorylation sites predicted: Ser: 2  Thr: 0  Tyr: 0


                     Serine predictions

Name             Pos    Context     Score   Pred
_______________________________v___________________
R_spondin_4       42    CIICSEENG   0.190     .
R_spondin_4       48    ENGCSTCQQ   0.088     .
R_spondin_4       97    ATCESCFSQ   0.041     .
R_spondin_4      100    ESCFSQDFC   0.007     .
R_spondin_4      148    WGGWSPCTH   0.013     .
R_spondin_4      159    KTCGSAWGL   0.021     .
R_spondin_4      165    WGLESRVRE   0.091     .
R_spondin_4      185    CQVLSESRK   0.851   *S*
R_spondin_4      187    VLSESRKCP   0.945   *S*
R_spondin_4      201    PGERSPGQK   0.403     .
_______________________________^___________________

                    Threonine predictions

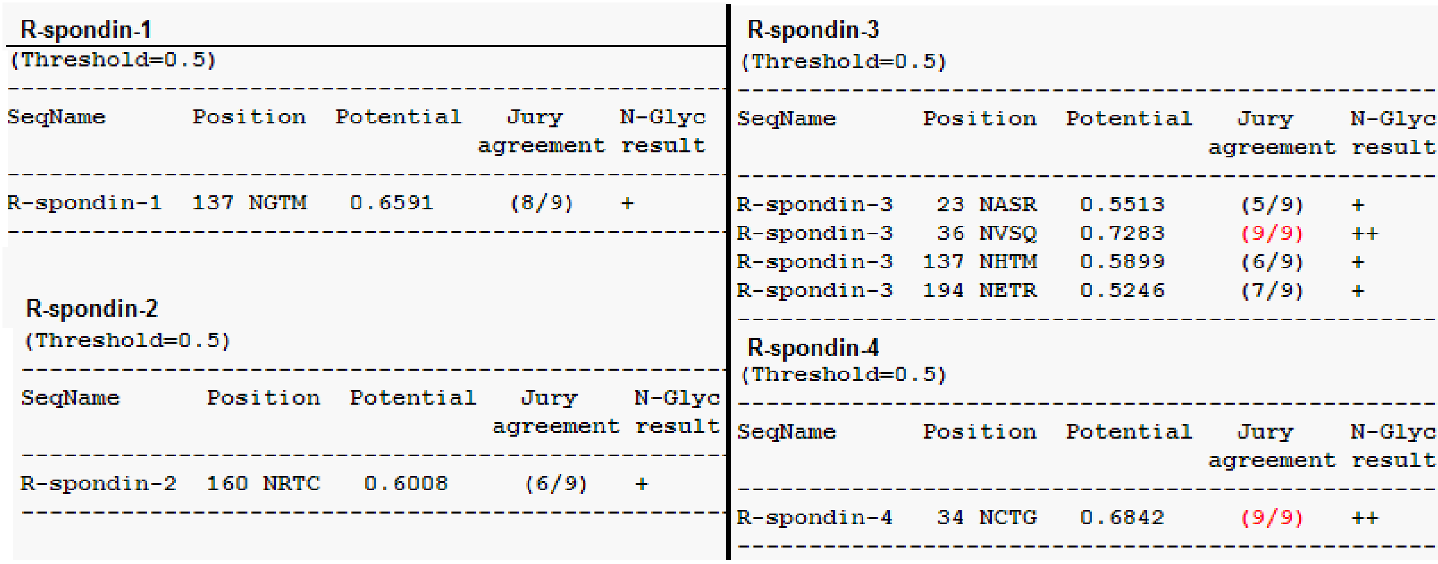
Name             Pos    Context     Score   Pred
_______________________________v___________________
R_spondin_4       29    KQVGTGLGG   0.039     .
R_spondin_4       36    GGNCTGCII   0.013     .
R_spondin_4       49    NGCSTCQQR   0.032     .
R_spondin_4       94    KCGATCESC   0.021     .
R_spondin_4      121    KCLPTCPPG   0.013     .
R_spondin_4      126    CPPGTLAHQ   0.040     .
R_spondin_4      132    AHQNTRECQ   0.026     .
R_spondin_4      151    WSPCTHNGK   0.117     .
R_spondin_4      156    HNGKTCGSA   0.076     .
R_spondin_4      180    EEAATCQVL   0.093     .
_______________________________^___________________

                    Tyrosine predictions

Name             Pos    Context     Score   Pred
_______________________________v___________________
R_spondin_4       66    GIRQYGKCL   0.007     .
R_spondin_4       77    CPPGYFGIR   0.457     .
R_spondin_4      112    KRQFYLYKG   0.096     .
R_spondin_4      114    QFYLYKGKC   0.026     .
_______________________________^___________________
```

Supplementary Table 5

Table S5- N-glycosylation sites of (Rspo)s



R-spondin-1

```
(Threshold=0.5)
----------------------------------------------------------------------
SeqName         Position  Potential   Jury     N-Glyc
                                    agreement  result
----------------------------------------------------------------------
R-spondin-1  137 NGTM    0.6591      (8/9)     +
----------------------------------------------------------------------
```

R-spondin-2

```
(Threshold=0.5)
----------------------------------------------------------------------
SeqName         Position  Potential   Jury     N-Glyc
                                    agreement  result
----------------------------------------------------------------------
R-spondin-2  160 NRTC    0.6008      (6/9)     +
----------------------------------------------------------------------
```

R-spondin-3

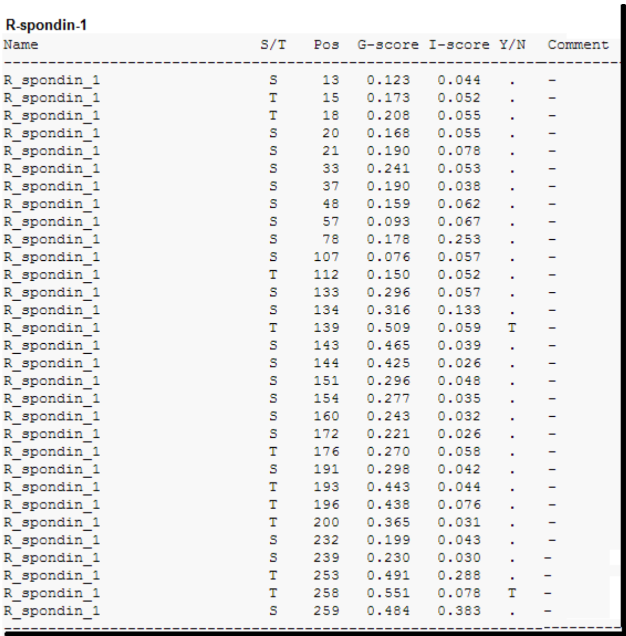
```
(Threshold=0.5)
----------------------------------------------------------------------
SeqName         Position  Potential   Jury     N-Glyc
                                    agreement  result
----------------------------------------------------------------------
R-spondin-3   23 NASR    0.5513      (5/9)     +
R-spondin-3   36 NVSQ    0.7283      (9/9)     ++
R-spondin-3  137 NHTM    0.5899      (6/9)     +
R-spondin-3  194 NETR    0.5246      (7/9)     +
----------------------------------------------------------------------
```

R-spondin-4

```
(Threshold=0.5)
----------------------------------------------------------------------
SeqName         Position  Potential   Jury     N-Glyc
                                    agreement  result
----------------------------------------------------------------------
R-spondin-4   34 NCTG    0.6842      (9/9)     ++
----------------------------------------------------------------------
```

Supplementary Table 6

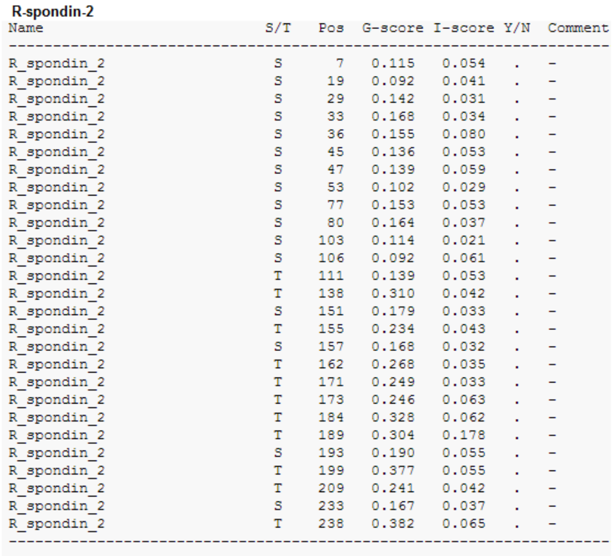
Table S6- O-glycosylation sites of (Rspo)s



R-spondin-1

```
Name                           S/T   Pos  G-score I-score Y/N   Comment
-----------------------------------------------------------------------

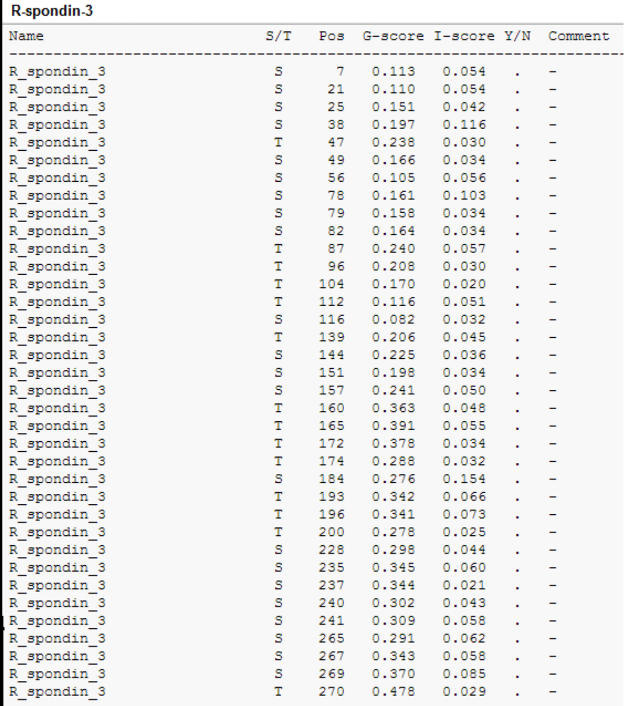
R_spondin_1                     S     13   0.123   0.044   .    -
R_spondin_1                     T     15   0.173   0.052   .    -
R_spondin_1                     T     18   0.208   0.055   .    -
R_spondin_1                     S     20   0.168   0.055   .    -
R_spondin_1                     S     21   0.190   0.078   .    -
R_spondin_1                     S     33   0.241   0.053   .    -
R_spondin_1                     S     37   0.190   0.038   .    -
R_spondin_1                     S     48   0.159   0.062   .    -
R_spondin_1                     S     57   0.093   0.067   .    -
R_spondin_1                     S     78   0.178   0.253   .    -
R_spondin_1                     S    107   0.076   0.057   .    -
R_spondin_1                     T    112   0.150   0.052   .    -
R_spondin_1                     S    133   0.296   0.057   .    -
R_spondin_1                     S    134   0.316   0.133   .    -
R_spondin_1                     T    139   0.509   0.059   T    -
R_spondin_1                     S    143   0.465   0.039   .    -
R_spondin_1                     S    144   0.425   0.026   .    -
R_spondin_1                     S    151   0.296   0.048   .    -
R_spondin_1                     S    154   0.277   0.035   .    -
R_spondin_1                     S    160   0.243   0.032   .    -
R_spondin_1                     S    172   0.221   0.026   .    -
R_spondin_1                     T    176   0.270   0.058   .    -
R_spondin_1                     S    191   0.298   0.042   .    -
R_spondin_1                     T    193   0.443   0.044   .    -
R_spondin_1                     T    196   0.438   0.076   .    -
R_spondin_1                     T    200   0.365   0.031   .    -
R_spondin_1                     S    232   0.199   0.043   .    -
R_spondin_1                     S    239   0.230   0.030   .   -
R_spondin_1                     T    253   0.491   0.288   .   -
R_spondin_1                     T    258   0.551   0.078   T   -
R_spondin_1                     S    259   0.484   0.383   .   -
-----------------------------------------------------------------------
```



R-spondin-2

```
Name                           S/T   Pos  G-score I-score Y/N   Comment
-----------------------------------------------------------------------

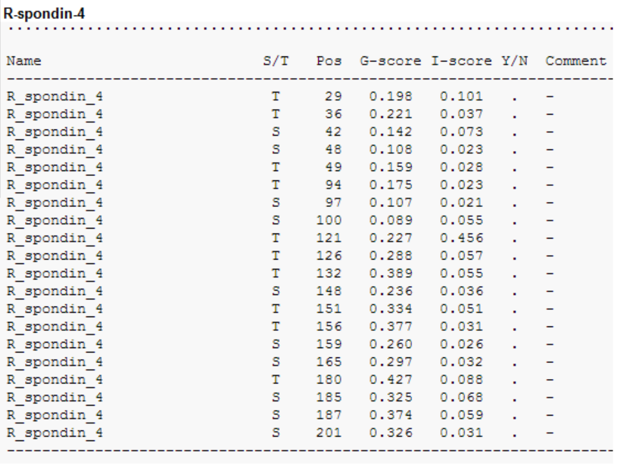
R_spondin_2                     S      7   0.115   0.054   .    -
R_spondin_2                     S     19   0.092   0.041   .    -
R_spondin_2                     S     29   0.142   0.031   .    -
R_spondin_2                     S     33   0.168   0.034   .    -
R_spondin_2                     S     36   0.155   0.080   .    -
R_spondin_2                     S     45   0.136   0.053   .    -
R_spondin_2                     S     47   0.139   0.059   .    -
R_spondin_2                     S     53   0.102   0.029   .    -
R_spondin_2                     S     77   0.153   0.053   .    -
R_spondin_2                     S     80   0.164   0.037   .    -
R_spondin_2                     S    103   0.114   0.021   .    -
R_spondin_2                     S    106   0.092   0.061   .    -
R_spondin_2                     T    111   0.139   0.053   .    -
R_spondin_2                     T    138   0.310   0.042   .    -
R_spondin_2                     S    151   0.179   0.033   .    -
R_spondin_2                     T    155   0.234   0.043   .    -
R_spondin_2                     S    157   0.168   0.032   .    -
R_spondin_2                     T    162   0.268   0.035   .    -
R_spondin_2                     T    171   0.249   0.033   .    -
R_spondin_2                     T    173   0.246   0.063   .    -
R_spondin_2                     T    184   0.328   0.062   .    -
R_spondin_2                     T    189   0.304   0.178   .    -
R_spondin_2                     S    193   0.190   0.055   .    -
R_spondin_2                     T    199   0.377   0.055   .    -
R_spondin_2                     T    209   0.241   0.042   .    -
R_spondin_2                     S    233   0.167   0.037   .    -
R_spondin_2                     T    238   0.382   0.065   .    -
-----------------------------------------------------------------------
```



R-spondin-3

```
Name                           S/T   Pos  G-score I-score Y/N   Comment
-----------------------------------------------------------------------

R_spondin_3                     S      7   0.113   0.054   .    -
R_spondin_3                     S     21   0.110   0.054   .    -
R_spondin_3                     S     25   0.151   0.042   .    -
R_spondin_3                     S     38   0.197   0.116   .    -
R_spondin_3                     T     47   0.238   0.030   .    -
R_spondin_3                     S     49   0.166   0.034   .    -
R_spondin_3                     S     56   0.105   0.056   .    -
R_spondin_3                     S     78   0.161   0.103   .    -
R_spondin_3                     S     79   0.158   0.034   .    -
R_spondin_3                     S     82   0.164   0.034   .    -
R_spondin_3                     T     87   0.240   0.057   .    -
R_spondin_3                     T     96   0.208   0.030   .    -
R_spondin_3                     T    104   0.170   0.020   .    -
R_spondin_3                     T    112   0.116   0.051   .    -
R_spondin_3                     S    116   0.082   0.032   .    -
R_spondin_3                     T    139   0.206   0.045   .    -
R_spondin_3                     S    144   0.225   0.036   .    -
R_spondin_3                     S    151   0.198   0.034   .    -
R_spondin_3                     S    157   0.241   0.050   .    -
R_spondin_3                     T    160   0.363   0.048   .    -
R_spondin_3                     T    165   0.391   0.055   .    -
R_spondin_3                     T    172   0.378   0.034   .    -
R_spondin_3                     T    174   0.288   0.032   .    -
R_spondin_3                     S    184   0.276   0.154   .    -
R_spondin_3                     T    193   0.342   0.066   .    -
R_spondin_3                     T    196   0.341   0.073   .    -
R_spondin_3                     T    200   0.278   0.025   .    -
R_spondin_3                     S    228   0.298   0.044   .    -
R_spondin_3                     S    235   0.345   0.060   .    -
R_spondin_3                     S    237   0.344   0.021   .    -
R_spondin_3                     S    240   0.302   0.043   .    -
R_spondin_3                     S    241   0.309   0.058   .    -
R_spondin_3                     S    265   0.291   0.062   .    -
R_spondin_3                     S    267   0.343   0.058   .    -
R_spondin_3                     S    269   0.370   0.085   .    -
R_spondin_3                     T    270   0.478   0.029   .    -
```



R-spondin-4

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.......................................................................

Name                           S/T   Pos  G-score I-score Y/N   Comment
-----------------------------------------------------------------------

R_spondin_4                     T     29   0.198   0.101   .    -
R_spondin_4                     T     36   0.221   0.037   .    -
R_spondin_4                     S     42   0.142   0.073   .    -
R_spondin_4                     S     48   0.108   0.023   .    -
R_spondin_4                     T     49   0.159   0.028   .    -
R_spondin_4                     T     94   0.175   0.023   .    -
R_spondin_4                     S     97   0.107   0.021   .    -
R_spondin_4                     S    100   0.089   0.055   .    -
R_spondin_4                     T    121   0.227   0.456   .    -
R_spondin_4                     T    126   0.288   0.057   .    -
R_spondin_4                     T    132   0.389   0.055   .    -
R_spondin_4                     S    148   0.236   0.036   .    -
R_spondin_4                     T    151   0.334   0.051   .    -
R_spondin_4                     T    156   0.377   0.031   .    -
R_spondin_4                     S    159   0.260   0.026   .    -
R_spondin_4                     S    165   0.297   0.032   .    -
R_spondin_4                     T    180   0.427   0.088   .    -
R_spondin_4                     S    185   0.325   0.068   .    -
R_spondin_4                     S    187   0.374   0.059   .    -
R_spondin_4                     S    201   0.326   0.031   .    -
-----------------------------------------------------------------------
```