

PAT054993A_ST25
SEQUENCE LISTING

<110> Novartis AG
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Hao, Huaixiang
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Jiang, Xiaomo
Liu, Jun
Ng, Nicholas

<120> CANCER PATIENT SELECTION FOR ADMINISTRATION OF Wnt SIGNALING
INHIBITORS USING RNF43 MUTATION STATUS

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<151> 2012-02-28

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 His Glu Leu Pro Ser Cys Ala Cys Cys Cys Glu Pro Gln Pro Ser Pro
 705 710 715 720
 Ala Gly Pro Ser Ala Gly Ala Ala Gly Ser Ser Thr Leu Phe Leu Gly
 725 730 735
 Pro His Leu Tyr Glu Gly Ser Gly Pro Ala Gly Gly Glu Pro Gln Ser
 740 745 750
 Gly Ser Ser Gln Gly Leu Tyr Gly Leu His Pro Asp His Leu Pro Arg
 755 760 765
 Thr Asp Gly Val Lys Tyr Glu Gly Leu Pro Cys Cys Phe Tyr Glu Glu
 770 775 780
 Lys Gln Val Ala Arg Gly Gly Gly Gly Gly Ser Gly Cys Tyr Thr Glu
 785 790 795 800

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Asp Tyr Ser Val Ser Val Gln Tyr Thr Leu Thr Glu Glu Pro Pro Pro
805 810 815

Gly Cys Tyr Pro Gly Ala Arg Asp Leu Ser Gln Arg Ile Pro Ile Ile
820 825 830

Pro Glu Asp Val Asp Cys Asp Leu Gly Leu Pro Ser Asp Cys Gln Gly
835 840 845

Thr His Ser Leu Gly Ser Trp Gly Gly Thr Arg Gly Pro Asp Thr Pro
850 855 860

Arg Pro His Arg Gly Leu Gly Ala Thr Arg Glu Glu Glu Arg Ala Leu
865 870 875 880

Cys Cys Gln Ala Arg Ala Leu Leu Arg Pro Gly Cys Pro Pro Glu Glu
885 890 895

Ala Gly Ala Val Arg Ala Asn Phe Pro Ser Ala Leu Gln Asp Thr Gln
900 905 910

Glu Ser Ser Thr Thr Ala Thr Glu Ala Ala Gly Pro Arg Ser His Ser
915 920 925

Ala Asp Ser Ser Ser Pro Gly Ala
930 935

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<211> 784
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<222> (1)..(23)

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<222> (272)..(316)
<223> RING-finger domain

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Met Ser Gly Gly His Gln Leu Gln Leu Ala Val Leu Trp Pro Trp Leu
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Leu Met Ala Thr Leu His Ala Gly Phe Gly His Thr Gly Arg Val Leu
-5 -1 1 5

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Ala Ala Ala Val Glu Ser Glu Arg Ser Ala Glu Gln Lys Ala Val Ile
10 15 20 25

Arg Val Ile Pro Leu Lys Met Asp Pro Thr Gly Lys Leu Asn Leu Thr
30 35 40

Leu Glu Gly Val Phe Ala Gly Val Ala Glu Val Thr Pro Ala Glu Gly
45 50 55

Lys Leu Met Gln Ser His Pro Leu Tyr Leu Cys Asn Ala Ser Asp Asp
60 65 70

Asp Asn Leu Glu Pro Gly Phe Ile Ser Ile Val Lys Leu Glu Ser Pro
75 80 85

Arg Arg Ala Pro Arg Pro Cys Leu Ser Leu Ala Ser Lys Ala Arg Met
90 95 100 105

Ala Gly Glu Arg Gly Ala Asn Ala Val Leu Phe Asp Ile Thr Glu Asp
110 115 120

Arg Ser Ala Ala Glu Gln Leu Gln Gln Pro Leu Gly Leu Thr Lys Pro
125 130 135

Val Val Leu Ile Trp Gly Ser Asp Ala Ala Lys Leu Met Glu Phe Val
140 145 150

Tyr Lys Asn Arg Lys Ala Tyr Val Trp Ile Glu Leu Lys Glu Pro Pro
155 160 165

Ala Gly Ala Asn Tyr Asp Val Trp Ile Leu Leu Thr Val Val Gly Thr
170 175 180 185

Val Phe Val Ile Ile Leu Ala Ser Val Leu Arg Ile Arg Cys Arg Pro
190 195 200

His His Ser Arg Pro Asp Pro Leu Gln Gln Arg Thr Ala Arg Ala Ile
205 210 215

Ser Gln Leu Ala Thr Arg Arg Tyr Gln Ala Gly Cys Arg Arg Ala Arg
220 225 230

Ala Glu Trp Pro Asp Ser Gly Ser Ser Cys Ser Ser Thr Pro Val Cys
235 240 245

Ala Ile Cys Leu Glu Glu Phe Ser Glu Gly Gln Glu Leu Arg Val Ile
250 255 260 265

Ser Cys Leu His Glu Phe His Arg Thr Cys Val Asp Pro Trp Leu Tyr
270 275 280

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Gln His Arg Thr Cys Pro Leu Cys Met Phe Asn Ile Val Glu Gly Asp
285 290 295

Ser Phe Ser Gln Ala Pro Ala Ala Ser Pro Ser Tyr Gln Glu Pro Gly
300 305 310

Arg Arg Leu His Leu Ile Arg Gln His Pro Gly His Ala His Tyr His
315 320 325

Leu Pro Ser Ala Tyr Leu Leu Gly Pro Ser Arg Thr Ser Val Ala Arg
330 335 340 345

Thr Pro Arg Pro Arg Pro Phe Leu Pro Ser Gln Glu Pro Ser Met Gly
350 355 360

Ser Arg His Gln Arg Leu Pro Arg Thr Ser His Leu Arg Ala Pro Glu
365 370 375

Glu Gln Gln His Leu Ala Val Ser Pro His Pro Tyr Ala Gln Gly Trp
380 385 390

Gly Leu Asn Arg Leu Arg Cys Thr Ser Gln His Pro Ala Ala Cys Pro
395 400 405

Val Ala Leu Arg Arg Ala Arg Pro His Glu Ser Ser Gly Ser Gly Glu
410 415 420 425

Ser Tyr Cys Thr Glu Arg Ser Gly Tyr Leu Ala Asp Gly Pro Ala Ser
430 435 440

Asp Ser Ser Ser Gly Pro Cys His Gly Ser Ser Ser Asp Ser Val Val
445 450 455

Asn Cys Thr Asp Val Ser Leu Gln Gly Ile His Gly Ser Ser Ser Thr
460 465 470

Phe Arg Ser Ser Leu Ser Ser Asp Phe Asp Pro Leu Val Tyr Cys Ser
475 480 485

Pro Glu Gly Asp Leu Gln Gly Lys Gly Ile Gln Pro Ser Val Thr Ser
490 495 500 505

Arg Pro Arg Ser Leu Asp Ser Val Val Pro Arg Gly Glu Thr Gln Val
510 515 520

Ser Ser His Ile His Tyr His Arg His Arg His His His Tyr Lys Arg
525 530 535

Gln Phe Gln Trp His Gly Arg Lys Pro Gly Pro Glu Thr Gly Ile Pro
540 545 550

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Gln Ser Met Pro Ala Ala Ser His Thr Gln Leu Glu Pro Ser Leu Pro
555 560 565

Asp Gln Gln Leu Ile Thr Pro Asn Pro Thr Ala Ser Ser Met Leu Pro
570 575 580 585

Asn Pro Gln Arg Pro Arg Ala Leu Thr Glu Pro Ala Pro Gly Leu Ala
590 595 600

Glu Ala Ser Ser Pro Ser Pro Ser Pro Lys Pro Asn Pro Ser Gly Leu
605 610 615

Leu Asn Leu Gln Lys Ser Ser Leu Thr Val Arg His Pro His Arg Lys
620 625 630

Arg Arg Gly Gly Pro Ser Glu Pro Leu Pro Thr Ser Leu Pro Pro Asp
635 640 645

Leu Thr Val His Thr Ala Cys Pro Val Phe Pro His Tyr Ser Pro Arg
650 655 660 665

Leu Ala Tyr Pro Trp Pro Pro Glu Val His Pro Leu Met Phe Arg Pro
670 675 680

Pro Gly Pro Asp Arg Arg Leu Leu His Glu Val Pro Gly Pro Cys Tyr
685 690 695

Ser Ser Ser Gln Pro Val Trp Leu Tyr Leu Asn Pro Cys Gln Pro Leu
700 705 710

Gly Pro Cys Leu Pro Gly Glu Gly His Ser Lys Trp Thr Phe Asp Ser
715 720 725

Pro Glu Gly Arg Arg Cys Pro Tyr Ser His Cys Gln Val Leu Pro Ala
730 735 740 745

Gln Pro Gly Ser Glu Glu Glu Leu Glu Glu Leu Cys Glu Gln Ala Val
750 755 760

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<211> 913
<212> PRT
<213> Mus musculus

<220>
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<222> (1)..(52)

<220>
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<220>
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 <222> (1)..(52)

<220>
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 <222> (53)..(913)

<400> 6

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Arg Arg Leu Arg Arg Gly Pro Arg Gly Arg Arg Leu Pro Pro Pro Pro
 -35 -30 -25

Pro Leu Pro Leu Leu Leu Gly Leu Leu Leu Ala Ala Ala Gly Pro Gly
 -20 -15 -10 -5

Ala Ala Arg Ala Lys Glu Thr Ala Phe Val Glu Val Val Leu Phe Glu
 -1 1 5 10

Ser Ser Pro Ser Gly Asp Tyr Thr Thr His Thr Thr Gly Leu Thr Gly
 15 20 25

Arg Phe Ser Arg Ala Gly Ala Met Leu Ser Ala Glu Gly Glu Ile Val
 30 35 40

Gln Met His Pro Leu Gly Leu Cys Asn Asn Asn Asp Glu Glu Asp Leu
 45 50 55 60

Tyr Glu Tyr Gly Trp Val Gly Val Val Lys Leu Glu Gln Pro Glu Leu
 65 70 75

Asp Pro Lys Pro Cys Leu Thr Val Leu Gly Lys Ala Lys Arg Ala Val
 80 85 90

Gln Arg Gly Ala Thr Ala Val Ile Phe Asp Val Ser Glu Asn Pro Glu
 95 100 105

Ala Ile Asp Gln Leu Asn Gln Gly Ser Glu Asp Pro Leu Lys Arg Pro
 110 115 120

Val Val Tyr Val Lys Gly Ala Asp Ala Ile Lys Leu Met Asn Ile Val
 125 130 135 140

Asn Lys Gln Lys Val Ala Arg Ala Arg Ile Gln His Leu Pro Pro Arg
 145 150 155

Gln Pro Thr Glu Tyr Phe Asp Met Gly Ile Phe Leu Ala Phe Phe Val
 160 165 170

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Val Val Ser Leu Val Cys Leu Ile Leu Leu Val Lys Ile Lys Leu Lys
 175 180 185
 Gln Arg Arg Ser Gln Asn Ser Met Asn Arg Leu Ala Val Gln Ala Leu
 190 195 200
 Glu Lys Met Glu Thr Arg Lys Phe Asn Ser Lys Ser Lys Gly Arg Arg
 205 210 215 220
 Glu Gly Ser Cys Gly Ala Leu Asp Thr Leu Ser Ser Gly Ser Thr Ser
 225 230 235
 Asp Cys Ala Ile Cys Leu Glu Lys Tyr Ile Asp Gly Glu Glu Leu Arg
 240 245 250
 Val Ile Pro Cys Thr His Arg Phe His Arg Lys Cys Val Asp Pro Trp
 255 260 265
 Leu Leu Gln His His Thr Cys Pro His Cys Arg His Asn Ile Ile Glu
 270 275 280
 Gln Lys Gly Asn Pro Gly Ala Val Cys Val Glu Thr Ser Asn Leu Thr
 285 290 295 300
 Arg Gly Arg Gln Pro Arg Val Thr Leu Pro Val His Tyr Pro Gly Arg
 305 310 315
 Val His Arg Thr Asn Ala Ile Pro Ala Tyr Pro Thr Arg Thr Ser Met
 320 325 330
 Asp Ser His Gly Asn Pro Val Thr Leu Leu Thr Met Asp Arg His Gly
 335 340 345
 Glu Gln Asn Leu Tyr Ser Pro Gln Thr Pro Thr Tyr Val Arg Gly Tyr
 350 355 360
 Pro Pro Leu His Leu Asp His Thr Leu Ala Pro His Arg Cys Ser Leu
 365 370 375 380
 Glu His Arg Ala Tyr Ser Pro Ala His Pro Phe Arg Arg Pro Lys Phe
 385 390 395
 Ser Ser Arg Ser Phe Ser Lys Ala Ala Cys Phe Ser Gln Tyr Glu Thr
 400 405 410
 Met Tyr Gln His Tyr Tyr Phe Gln Gly Leu Ser Tyr Pro Glu Gln Glu
 415 420 425
 Gly Gln Thr Ile Pro Ser Val Thr Pro Arg Gly Gln Ser Arg Ala Phe
 430 435 440

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Pro Pro Ser Gly Ala Ser Ser Leu Leu Phe Pro Thr Met Val His Val
445 450 455 460

Ala Pro Pro Thr His Val Glu Ser Gly Ser Thr Ser Ser Phe Ser Cys
465 470 475

Tyr His Gly His Arg Ser Val Cys Ser Gly Tyr Leu Ala Asp Cys Pro
480 485 490

Gly Ser Asp Ser Ser Ser Asn Ser Ser Gly Gln Cys Arg Cys Ser Ser
495 500 505

Ser Asp Ser Val Val Asp Cys Thr Glu Val Ser Asn Gln Gly Val Tyr
510 515 520

Gly Ser Cys Ser Thr Phe Arg Ser Ser Leu Ser Ser Asp Tyr Asp Pro
525 530 535 540

Phe Ile Tyr Arg Ser Arg Gly Pro Ala Val His Leu Glu Gly Ser Pro
545 550 555

Pro Pro Glu Glu Leu Pro Ala Gly His Ser Gln Ser Ala Gly Arg Gly
560 565 570

Glu Pro Trp Leu Gly Pro Ala Ser Pro Ser Gly Asp Gln Leu Ser Thr
575 580 585

Cys Ser Leu Glu Met Asn Tyr Ser Ser Asn Ser Ser Leu Glu Pro Arg
590 595 600

Gly Pro Asn Ser Ser Thr Ser Glu Val Gly Leu Glu Val Ser Pro Gly
605 610 615 620

Ala Ala Leu Asp Leu Arg Arg Thr Trp Lys Gly Gly Pro Glu Gly Pro
625 630 635

Ser Cys Ala Cys Cys Phe Glu Pro Gln Pro Phe Pro Pro Gly Ser Gly
640 645 650

Ile Glu Thr Ser Ala Gly Gly Ser Ser Leu Phe Leu Gly Pro Arg Leu
655 660 665

Leu Glu Asp Cys Asn Pro Pro Ser Gly Glu Pro Gln Leu Gly Ser Ser
670 675 680

Gln Gly Leu Tyr Gly Leu His Ser Asp His Tyr Pro Arg Thr Asp Gly
685 690 695 700

Val Lys Tyr Glu Gly Leu Pro Cys Cys Phe Tyr Glu Glu Lys Gln Val
705 710 715

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Ala His Ser Ala Gly Arg Gly Asn Gly Cys Tyr Thr Glu Asp Tyr Ser
720 725 730

Val Ser Val Gln Tyr Thr Leu Thr Glu Glu Pro Pro Pro Ser Cys Tyr
735 740 745

Ala Gly Pro Arg Asp Leu Ser Gln Arg Ile Pro Ile Ile Pro Glu Asp
750 755 760

Val Asp Cys Asp Leu Gly Leu Pro Gln Asp Cys His Gly Met His Asn
765 770 775 780

His Ser Pro Trp Gly Gly Ala Leu Ser Leu Asp Val Pro Arg Leu His
785 790 795

Trp Ser Leu Gly Thr Thr Arg Glu Glu Glu Gln Ala Pro Cys Tyr Gln
800 805 810

Ala Glu Val Gln Pro Gly Cys Ser Pro Glu Glu Ala Gly Ala Ser Arg
815 820 825

Ala Ser Leu Ser Ser Ala Pro Gln Asp Thr Gln Glu Ser His Ala Leu
830 835 840

Ala Ala Glu Ala Ser Gly Pro Gly Ser Gly Pro Gly Ile Gly Thr Gly
845 850 855 860

Ala

<210> 7
<211> 19
<212> DNA
<213> Homo sapiens

<220>
<221> primer_bind
<222> (1)..(19)
<223> pGL2 (Dharmacon D-001100-01), target sequence

<400> 7
cgtagcgga atacttcga

19

<210> 8
<211> 19
<212> RNA
<213> Homo sapiens

<220>
<221> snRNA
<222> (1)..(19)
<223> RNF43-1 (Dharmacon J-007004-12), target sequence

<400> 8
gguggagucu gaaagauca 19

<210> 9
<211> 19
<212> RNA
<213> Homo sapiens

<220>
<221> snRNA
<222> (1)..(19)
<223> RNF43-2 (Dharmacon J-007004-11), target sequence

<400> 9
ggagaaagcu auugcacag 19

<210> 10
<211> 19
<212> RNA
<213> Homo sapiens

<220>
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<222> (1)..(19)
<223> CTNNB1- 1 (Dharmacon J-003482-10), target sequence

<400> 10
uaaugaggac cuauacuua 19

<210> 11
<211> 19
<212> RNA
<213> Homo sapiens

<220>
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<222> (1)..(19)
<223> CTNNB1- 2 (Dharmacon J-003482-12), target sequence

<400> 11
gguacgagcu gcuauguuc 19