**Genetic targets may be a promising future for osteoporosis**

**supplements**

**1.Statistical applications LRP5G171R genotypes , femur BMD**

Related-Samples McNemar Change Test was used to exams the variant significant under 95% confidence level (α ≤ .050) and studying a null hypothesis interested in LRP5G171Rgenotypes variant of distribution across femur T-score values taking into consideration all genotypes of LRP5G171R

automated cross-tab was used to identify the odd risk for femur T- score observing when LRP5G171Rgenotypes excess comparing with the possibility to observe femur T- score when LRP5G171Rgenotypes absence taking into consideration all genotypes

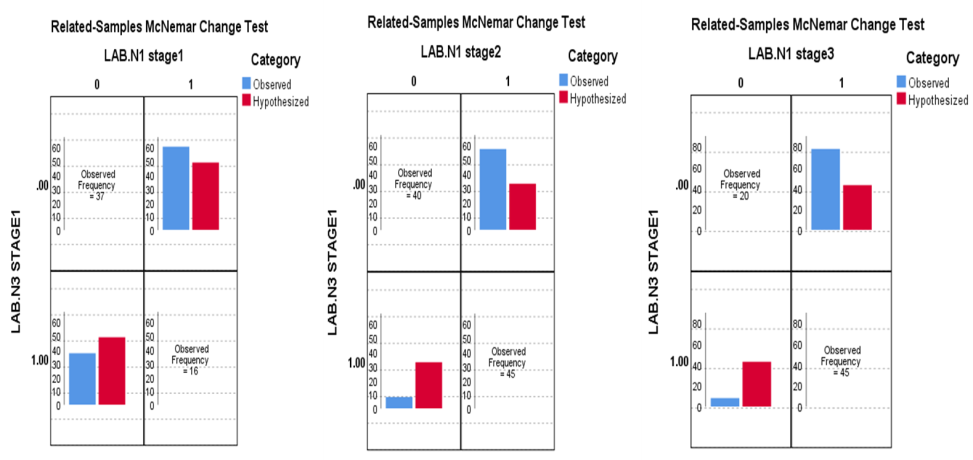
Chi-Square Tests was used to estimate the correlation between LRP5G171Rgenotypes and each of femur T- score under 95% confidence (α ≤ .050)

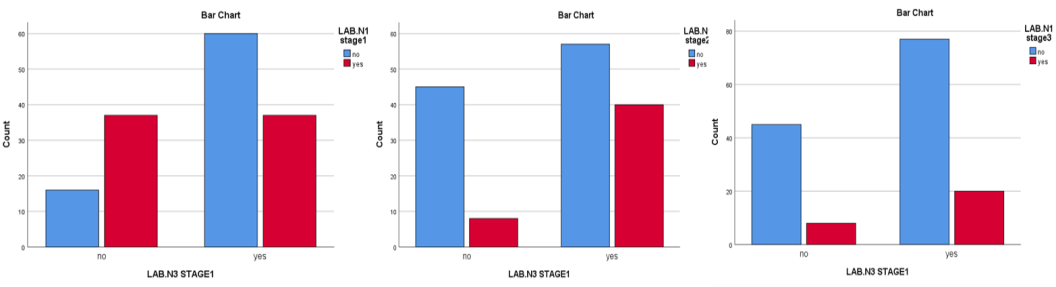
* 1. **Related-Samples McNemar Change Test**

**1.1.1.GG genotype results**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Hypothesis Test Summary** | | | | |
|  | Null Hypothesis | Test | Sig. | Decision |
|  | The distributions of different values across GG genotype and normal femur T-scoreare equally likely. | Related-Samples McNemar Change Test | .025 | Reject the null hypothesis. |
| |  |  |  |  |  | | --- | --- | --- | --- | --- | |  | The distributions of different values across GG genotype and osteopenia femur T-scoreare equally likely. | Related-Samples McNemar Change Test | .000 | Reject the null hypothesis. | | |  |  |  |  |  | | --- | --- | --- | --- | --- | |  | The distributions of different values across GG genotype and osteoporosis femur T-score are equally likely. | Related-Samples McNemar Change Test | .000 | Reject the null hypothesis. | | Asymptotic significances are displayed. The significance level is .050. | | | | | | | | | | | | | | |

Table.1: Observation hypothesis Test Summary for GG genotype, femur T-score values

Figure.1: Related-Samples McNemar Change Test between GG genotype and normal femur T-score(LAB.N1 stage1), osteopenia femur T-score(LAB.N1 stage2), osteoporosis femur T-score(LAB.N1 stage3).

Figure .2: Bar chart to the frequency between normal femur T-score(LAB.N1 stage1) osteopenia femur T-score(LAB.N1 stage2), osteoporosis femur T-score(LAB.N1 stage3) and GGgenotype.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Crosstab(GG genotype and normal femur T-score)** | | | | | | | | | | | | | | | |
| Count | | | | | | | | | | | | | | | |
|  | | normal femur T-score | | | | | | | | | | Total | | | |
| No | | | | Yes | | | | | |
| GG genotype | No | 16 | | | | 37 | | | | | | 53 | | | |
| yes | 60 | | | | 37 | | | | | | 97 | | | |
| Total | | 76 | | | | 74 | | | | | | 150 | | | |
| **Risk Estimate(GG genotype and normal femur T-score)** | | | | | | | | | | | | | | | |
|  | | | | | Value | | | | | | 95% Confidence Interval | | | | |
| Lower | | | | Upper |
| Odds Ratio for GG genotype (no / yes) | | | | | .267 | | | | | | .130 | | | | .545 |
| For cohort normal femur T-score = no | | | | | .488 | | | | | | .315 | | | | .756 |
| For cohort normal femur T-score = yes | | | | | 1.830 | | | | | | 1.344 | | | | 2.493 |
| N of Valid Cases | | | | | 150 | | | | | |  | | | |  |
| **Crosstab(GG genotype and osteopenia femur T-score)** | | | | | | | | | | | | | | | |
| Count | | | | | | | | | | | | | | | |
|  | | | osteopenia femur T-score | | | | | | | | | | Total | | |
| No | | | Yes | | | | | | |
| GG genotype | No | | 45 | | | 8 | | | | | | | 53 | | |
| Yes | | 57 | | | 40 | | | | | | | 97 | | |
| Total | | | 102 | | | 48 | | | | | | | 150 | | |
| **Risk Estimate(GG genotype and osteopenia femur T-score)** | | | | | | | | | | | | | | | |
|  | | | | Value | | | | 95% Confidence Interval | | | | | | | |
| Lower | | | | | Upper | | |
| Odds Ratio for GG genotype (no / yes) | | | | 3.947 | | | | 1.681 | | | | | 9.271 | | |
| For cohort osteopenia femur T-score = no | | | | 1.445 | | | | 1.181 | | | | | 1.768 | | |
| For cohort osteopenia femur T-score = yes | | | | .366 | | | | .185 | | | | | .723 | | |
| N of Valid Cases | | | | 150 | | | |  | | | | |  | | |
| **Crosstab(GG genotype and osteoporosis femur T-score)** | | | | | | | | | | | | | | | |
| Count | | | | | | | | | | | | | | | |
|  | | osteoporosis femur T-score | | | | | | | Total | | | | | | |
| No | | | | Yes | | |
| GG genotype | No | 45 | | | | 8 | | | 53 | | | | | | |
| yes | 77 | | | | 20 | | | 97 | | | | | | |
| Total | | 122 | | | | 28 | | | 150 | | | | | | |
| **Risk Estimate(GG genotype and osteoporosis femur T-score)** | | | | | | | | | | | | | | | |
|  | | | | | | | Value | | | 95% Confidence Interval | | | | | |
| Lower | | | | Upper | |
| Odds Ratio for GG genotype (no / yes) | | | | | | | 1.461 | | | .595 | | | | 3.589 | |
| For cohort osteoporosis femur T-score= no | | | | | | | 1.070 | | | .919 | | | | 1.245 | |
| For cohort osteoporosis femur T-score= yes | | | | | | | .732 | | | .346 | | | | 1.547 | |
| N of Valid Cases | | | | | | | 150 | | |  | | | |  | |

Table.2: Results of cross-tab and risk estimate tests were used to identify the odd risk for femur T-score values when GG genotype is absence or existed.

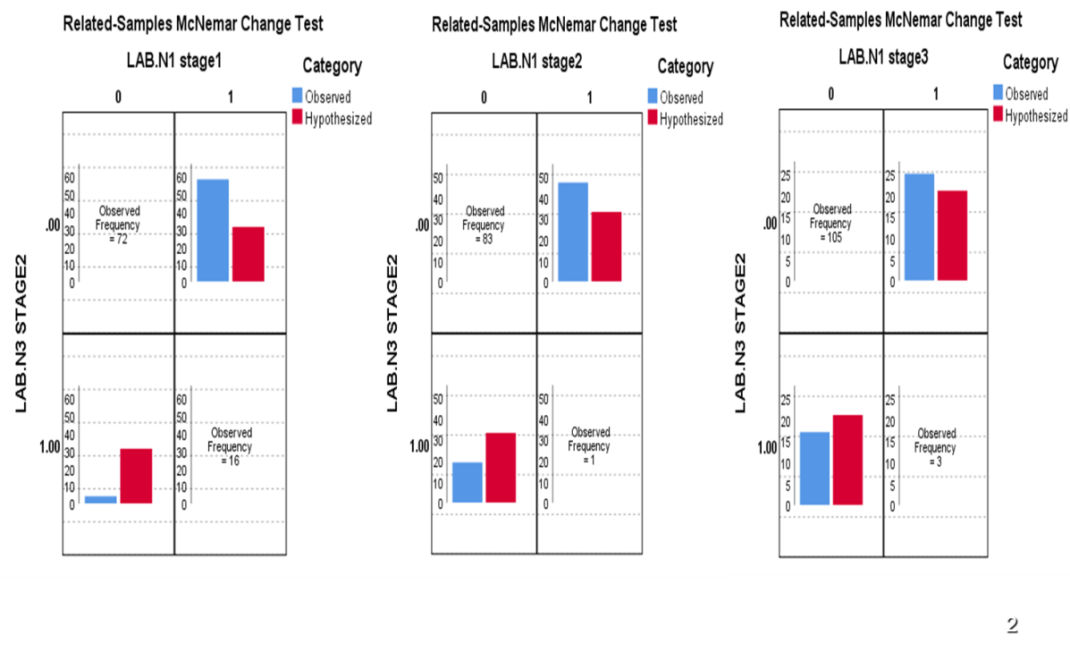
|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Chi-Square Tests (GG genotype and normal femur T-score)** | | | | | |
|  | Value | Df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 13.750a | 1 | .000 |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 26.15. | | | | | |
| b. Computed only for a 2x2 table | | | | | |
| **Chi-Square Tests( GG genotype and osteopenia femur T-score)** | | | | | |
|  | Value | Df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 10.765a | 1 | .001 |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 16.96. | | | | | |
| b. Computed only for a 2x2 table | | | | | |
| **Chi-Square Tests (GG genotype and osteoporosis femur T-score)** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | .689a | 1 | .407 |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 9.89. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

Table.3: Results of Chi-Square Tests for GG genotype and femur T-score values

**1.1.2. CC genotype results**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Hypothesis Test Summary** | | | | | |
|  | Null Hypothesis | Test | Sig. | Decision |
|  | The distributions of different values across CC genotype and normal femur T-score are equally likely. | Related-Samples McNemar Change Test | .000 | Reject the null hypothesis. |
| |  |  |  |  |  | | --- | --- | --- | --- | --- | |  | The distributions of different values across CC genotype and osteopenia femur T-score are equally likely. | Related-Samples McNemar Change Test | .001 | Reject the null hypothesis. |  |  |  |  |  |  | | --- | --- | --- | --- | --- | |  | The distributions of different values across CC genotype and osteoporosis femur T-score are equally likely. | Related-Samples McNemar Change Test | .280 | Retain the null hypothesis. | | Asymptotic significances are displayed. The significance level is .050. | | | | | | | | | | |

Table.4: Observation hypothesis Test Summary for CC genotype, femur T-score values

Figure.3: Related-Samples McNemar Change Test between CC genotype and normal femur T-score(LAB.N1 stage1), osteopenia femur T-score(LAB.N1 stage2), osteoporosis femur T-score(LAB.N1 stage3).

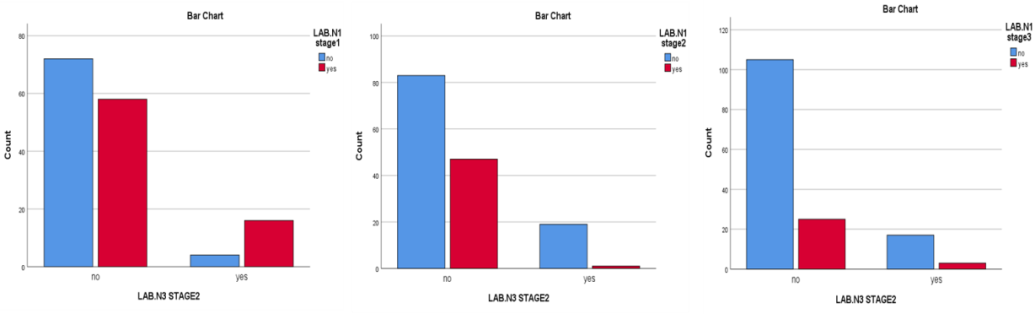


Figure.4: Bar chart to the frequency between normal femur T-score(LAB.N1 stage1), osteopenia femur T-score(LAB.N1 stage2), osteoporosis femur T-score(LAB.N1 stage3) and CC genotype.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Crosstab (CC genotype and normal femur T-score)** | | | | | | | |
| Count | | | | | | | |
|  | | normal femur T-score | | Total | | | |
| No | yes |
| CC genotype | no | 72 | 58 | 130 | | | |
| yes | 4 | 16 | 20 | | | |
| Total | | 76 | 74 | 150 | | | |
| **Risk Estimate(CC genotype and normal femur T-score)** | | | | | | | |
|  | | | | | Value | 95% Confidence Interval | |
| Lower | Upper |
| Odds Ratio for CC genotype (no / yes) | | | | | 4.966 | 1.574 | 15.665 |
| For cohort normal femur T-score = no | | | | | 2.769 | 1.137 | 6.743 |
| For cohort normal femur T-score = yes | | | | | .558 | .417 | .746 |
| N of Valid Cases | | | | | 150 |  |  |
| **Crosstab(CC genotype and osteopenia femur T-score)** | | | | | | | |
| Count | | | | | | | |
|  | | osteopenia femur T-score | | Total | | | |
| No | yes |
| CC genotype | no | 83 | 47 | 130 | | | |
| yes | 19 | 1 | 20 | | | |
| Total | | 102 | 48 | 150 | | | |
|  | |  |  |  | | | |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Crosstab(CC genotype, osteoporosis femur T-score)** | | | | |
| Count | | | | |
|  | | osteoporosis femur T-score | | Total |
| No | yes |
| CC genotype | No | 105 | 25 | 130 |
| yes | 17 | 3 | 20 |
| Total | | 122 | 28 | 150 |

|  |  |  |  |
| --- | --- | --- | --- |
| **Risk Estimate(CC genotype and osteopenia femur T-score)** | | | |
|  | Value | 95% Confidence Interval | |
| Lower | Upper |
| Odds Ratio for CC genotype (no / yes) | .093 | .012 | .717 |
| For cohort osteopenia femur T-score = no | .672 | .571 | .792 |
| For cohort osteopenia femur T-score = yes | 7.231 | 1.056 | 49.516 |
| N of Valid Cases | 150 |  |  |

|  |  |  |  |
| --- | --- | --- | --- |
| **Risk Estimate(CC genotype and osteoporosis femur T-score)** | | | |
|  | Value | 95% Confidence Interval | |
| Lower | Upper |
| Odds Ratio for CC genotype (no / yes) | .741 | .201 | 2.727 |
| For cohort osteoporosis femur T-score = no | .950 | .776 | 1.163 |
| For cohort osteoporosis femur T-score = yes | 1.282 | .426 | 3.856 |
| N of Valid Cases | 150 |  |  |

Table.5: Results of cross-tab and risk estimate tests were used to identify the odd risk for femur T-score values when CC genotype is absence or existed.

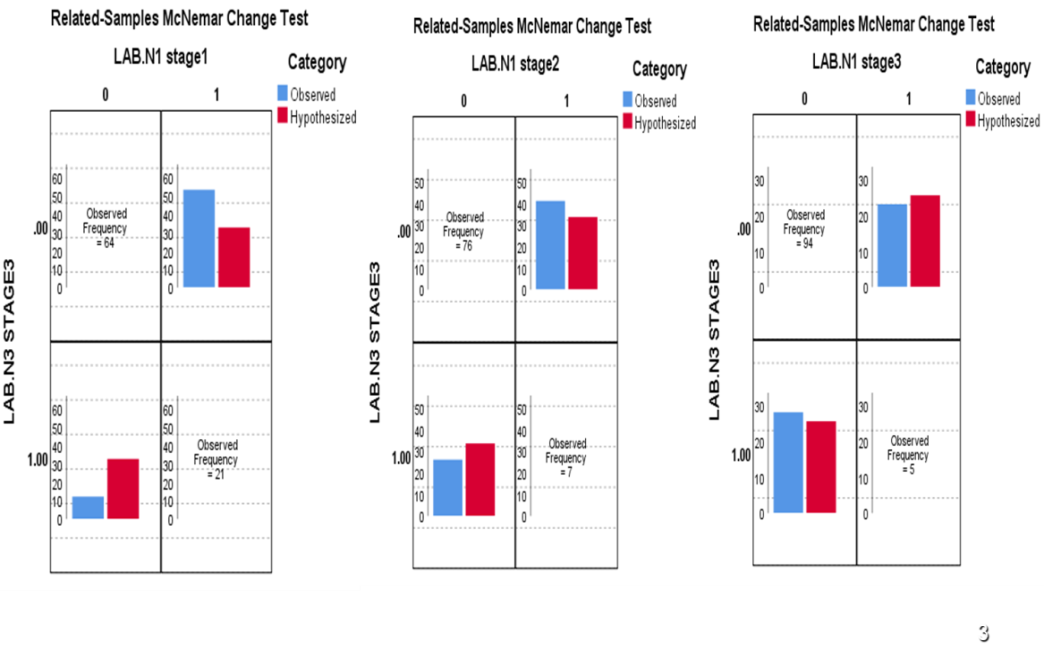
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Chi-Square Tests(CC genotype, normal femur T-score)** | | | | | | | | | | | | |
|  | Value | | | df | | | Asymptotic Significance (2-sided) | | Exact Sig. (2-sided) | | Exact Sig. (1-sided) | |
| Pearson Chi-Square | 8.683a | | | 1 | | | .003 | |  | |  | |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 9.87. | | | | | | | | | | | | |
| b. Computed only for a 2x2 table | | | | | | | | | | | | |
| **Chi-Square Tests(CC genotype, osteopenia femur T-score)** | | | | | | | | | | | | |
|  | | | Value | | | Df | | Asymptotic Significance (2-sided) | | Exact Sig. (2-sided) | | Exact Sig. (1-sided) |
| Pearson Chi-Square | | | 7.731a | | | 1 | | .005 | |  | |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 6.40. | | | | | | | | | | | | |
| b. Computed only for a 2x2 table | | | | | | | | | | | | |
| **Chi-Square Tests(CC genotype, osteoporosis femur T-score)** | | | | | | | | | | | | |
|  | | Value | | | df | | Asymptotic Significance (2-sided) | | | Exact Sig. (2-sided) | | Exact Sig. (1-sided) |
| Pearson Chi-Square | | .204a | | | 1 | | .651 | | |  | |  |
| a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is 3.73. | | | | | | | | | | | | |
| b. Computed only for a 2x2 table | | | | | | | | | | | | |

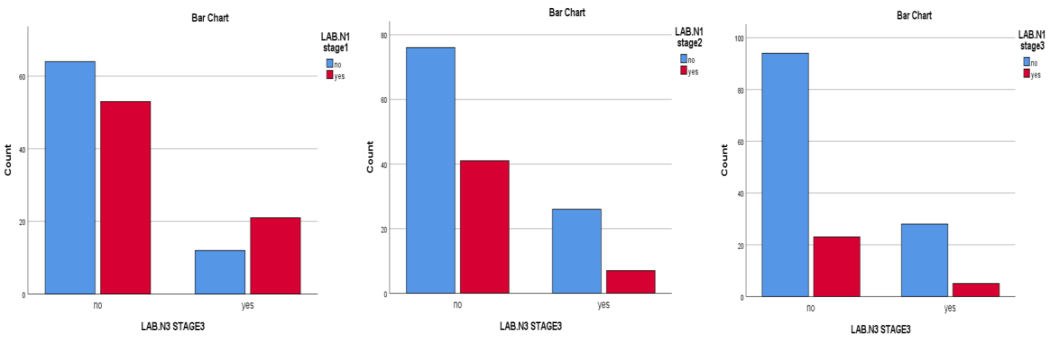
Table.6: Results of Chi-Square Tests for CC genotype and femur T-score values

**1.1.3.GC genotype results:**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Hypothesis Test Summary** | | | | |
|  | Null Hypothesis | Test | Sig. | Decision |
|  | The distributions of different values across LAB.N3 STAGE3 and LAB.N1 stage1 are equally likely. | Related-Samples McNemar Change Test | .000 | Reject the null hypothesis. |
|  | The distributions of different values across GC genotype and osteopenia femur T-scoreare equally likely. | Related-Samples McNemar Change Test | .087 | Retain the null hypothesis. |
|  | The distributions of different values across GC genotype and osteoporosis femur T-scoreare equally likely. | Related-Samples McNemar Change Test | .575 | Retain the null hypothesis. |
| Asymptotic significances are displayed. The significance level is .050. | | | | |

Table. 7: Observation hypothesis Test Summary for GC genotype, femur T-score values

Figure.5: Related-Samples McNemar Change Test between GC genotype and normal femur T-score(LAB.N1 stage1), osteopenia femur T-score(LAB.N1 stage2), osteoporosis femur T-score(LAB.N1 stage3).

Figure.6: Bar chart to the frequency between normal femur T-score(LAB.N1 stage1) osteopenia femur T-score(LAB.N1 stage2), osteoporosis femur T-score(LAB.N1 stage3) and GC genotype

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Crosstab(GC genotype, normal femur T-score)** | | | | |
| Count | | | | |
|  | | normal femur T-score | | Total |
| No | yes |
| GC genotype | no | 64 | 53 | 117 |
| yes | 12 | 21 | 33 |
| Total | | 76 | 74 | 150 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Risk Estimate(GC genotype, normal femur T-score)** | | | | | | | | | | | | |
|  | | | | Value | | | | 95% Confidence Interval | | | | |
| Lower | | | Upper | |
| Odds Ratio for GC genotype (no / yes) | | | | 2.113 | | | | .952 | | | 4.690 | |
| For cohort normal femur T-score = no | | | | 1.504 | | | | .930 | | | 2.432 | |
| For cohort normal femur T-score = yes | | | | .712 | | | | .514 | | | .986 | |
| N of Valid Cases | | | | 150 | | | |  | | |  | |
| **Crosstab(GC genotype, osteopenia femur T-score)** | | | | | | | | | | | | |
| Count | | | | | | | | | | | | |
|  | | osteopenia femur T-score | | | | | Total | | | | | |
| No | yes | | | |
| GC genotype | no | 76 | 41 | | | | 117 | | | | | |
| yes | 26 | 7 | | | | 33 | | | | | |
| Total | | 102 | 48 | | | | 150 | | | | | |
| **Risk Estimate(GC genotype, osteopenia femur T-score)** | | | | | | | | | | | | |
|  | | | | | | Value | | | 95% Confidence Interval | | | |
| Lower | | | Upper |
| Odds Ratio for GC genotype (no / yes) | | | | | | .499 | | | .199 | | | 1.248 |
| For cohort osteopenia femur T-score = no | | | | | | .824 | | | .661 | | | 1.029 |
| For cohort osteopenia femur T-score = yes | | | | | | 1.652 | | | .818 | | | 3.334 |
| N of Valid Cases | | | | | | 150 | | |  | | |  |
| **Crosstab(GC genotype, osteoporosis femur T-score)** | | | | | | | | | | | | |
| Count | | | | | | | | | | | | |
|  | | osteoporosis femur T-score | | | | | | | | Total | | |
| No | Yes | | | | | | |
| GC genotype | no | 94 | 23 | | | | | | | 117 | | |
| yes | 28 | 5 | | | | | | | 33 | | |
| Total | | 122 | 28 | | | | | | | 150 | | |
| **Risk Estimate(GC genotype, osteoporosis femur T-score)** | | | | | | | | | | | | |
|  | | | | | Value | | | | | 95% Confidence Interval | | |
| Lower | | Upper |
| Odds Ratio for GC genotype (no / yes) | | | | | .730 | | | | | .254 | | 2.096 |
| For cohort osteoporosis femur T-score = no | | | | | .947 | | | | | .799 | | 1.122 |
| For cohort osteoporosis femur T-score = yes | | | | | 1.297 | | | | | .535 | | 3.149 |
| N of Valid Cases | | | | | 150 | | | | |  | |  |

Table.8: Results of cross-tab and risk estimate tests were used to identify the odd risk for femur T-score values when LRP5G171R genotype is absence or existed.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Chi-Square Tests(GC genotype, normal femur T-score)** | | | | | | | | |
|  | | Value | Df | | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) | |
| Pearson Chi-Square | | 3.463a | 1 | | .063 |  |  | |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 16.28. | | | | | | | | |
| b. Computed only for a 2x2 table | | | | | | | | |
| **Chi-Square Tests(GC genotype, osteopenia femur T-score)** | | | | | | | | |
|  | | Value | Df | | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | | Exact Sig. (1-sided) |
| Pearson Chi-Square | | 2.263a | 1 | | .133 |  | |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 10.56. | | | | | | | | |
| b. Computed only for a 2x2 table | | | | | | | | |
| **Chi-Square Tests (GC genotype, osteoporosis femur T-score)** | | | | | | | | |
|  | Value | | | Df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | | Exact Sig. (1-sided) |
| Pearson Chi-Square | .344a | | | 1 | .557 |  | |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 6.16. | | | | | | | | |
| b. Computed only for a 2x2 table | | | | | | | | |

Table.9: Results of Chi-Square Tests for GC genotype and femur T-score values

**2.Statistical applications LRP5G171R genotypes , BMI**

Likelihood ratio test was used to determine the predictive power of BMI. Multinomial logistic regression was used to estimate the predictability under 95% confidence level (α ≤ .050) and odds ratios of CC genotype occurrence rather than GG genotype , and GC genotype occurrence rather than GG genotype with respecting the variety of BMI. Chi-Square Tests was used to estimate the correlation between each of the studied variant level with every genotype that happened to be studied under 95% confidence (α ≤ .050) with backing to and aiding by the sign of the multiple regression slope coefficient to recognize the correlation direction

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Likelihood Ratio Tests** | | | | |
| Effect | Model Fitting Criteria | Likelihood Ratio Tests | | |
| -2 Log Likelihood of Reduced Model | Chi-Square | df | Sig. |
| BMI | 149.832 | 15.658 | 8 | .048 |
| The chi-square statistic is the difference in -2 log-likelihoods between the final model and a reduced model. The reduced model is formed by omitting an effect from the final model. The null hypothesis is that all parameters of that effect are 0. | | | | |
| a. This reduced model is equivalent to the final model because omitting the effect does not increase the degrees of freedom. | | | | |

Table10: Likelihood Ratio Tests which appear the correlation between (BMI) and genotypes of LRP5rs121908669 (ϰ2 = 149.832, p = .048 <.05) .

The predictability under 95% confidence level (α ≤ .050) and odds ratios of genotypes of LRP5G171R with respecting the variety of BMI;

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Parameter Estimates** | | | | | | | | | |
| LRP5G171R genotyping | | **B** | Std. Error | Wald | df | **Sig.** | **Exp(B)** | 95% Confidence Interval for Exp(B) | |
| Lower Bound | Upper Bound |
| CC genotyping | Intercept | **3.931** | 2.439 | 2.599 | 1 | **.107** |  |  |  |
| <18.5 | **-8.244** | 5.268 | 2.449 | 1 | **.118** | **.000** | 8.626E-9 | 8.007 |
| [ 18.5- 24.9] | **-8.374** | 4.526 | 3.424 | 1 | **.064** | **.000** | 3.245E-8 | 1.643 |
| [ 25- 29.9] | **-4.712** | 1.965 | 5.750 | 1 | **.016** | **.009** | .000 | .423 |
| [30- 34.9] | **-3.280** | 1.887 | 3.024 | 1 | **.082** | **.038** | .001 | 1.518 |
| ≥35 | **0b** | . | . | 0 | **.** | **.** | . | . |
| GC genotype | Intercept | **2.851** | 1.871 | 2.322 | 1 | **.128** |  |  |  |
| <18.5 | **-2.271** | 3.037 | .559 | 1 | **.455** | **.103** | .000 | 39.708 |
| [ 18.5- 24.9] | **-2.802** | 2.702 | 1.075 | 1 | **.300** | **.061** | .000 | 12.120 |
| [ 25- 29.9] | **-1.288** | 1.599 | .649 | 1 | **.421** | **.276** | .012 | 6.333 |
| [30- 34.9] | **.650** | 1.538 | .179 | 1 | **.673** | **1.915** | .094 | 38.982 |
| ≥35 | **0b** | . | . | 0 | **.** | **.** | . | . |
| a. The reference category is: GG genotype. | | | | | | | | | |
| b. This parameter is set to zero because it is redundant. | | | | | | | | | |

Table11: Multinomial logistic regression which was used to estimate the predictability under 95% confidence level (α ≤ .050) and odds ratios of genotypes of LRP5G171R with respecting the variety of BMI

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Crosstab**(GG genotype **\* BMI<18.5)** | | | | |
| Count | | | | |
|  | | BMI<18.5 | | Total |
| no | yes |
| GG genotype | No | 51 | 2 | 53 |
| yes | 93 | 4 | 97 |
| Total | | 144 | 6 | 150 |
| **Crosstab**(GG genotype **\* BMI[18.5-24.9])** | | | | |
| Count | | | | |
|  | | BMI[18.5-24.9] | | Total |
| no | yes |
| GG genotype | no | 49 | 4 | 53 |
| yes | 56 | 41 | 97 |
| Total | | 105 | 45 | 150 |
| **Crosstab** GG genotype **\* BMI[25-29.9]** | | | | |
| Count | | | | |
|  | | BMI[25-29.9] | | Total |
| no | yes |
| GG genotype | no | 36 | 17 | 53 |
| yes | 53 | 44 | 97 |
| Total | | 89 | 61 | 150 |
| **Crosstab**(GG genotype **\* BMI[30-34.9])** | | | | |
| Count | | | | |
|  | | BMI[30-34.9] | | Total |
| no | yes |
| GG genotype | no | 32 | 21 | 53 |
| yes | 90 | 7 | 97 |
| Total | | 122 | 28 | 150 |
| **Crosstab** GG genotype **\* BMI≥35** | | | | |
| Count | | | | |
|  | | BMI≥35 | | Total |
| no | yes |
| GG genotype | no | 44 | 9 | 53 |
| yes | 96 | 1 | 97 |
| Total | | 140 | 10 | 150 |
| **Crosstab** (CC genotype **\* BMI<18.5)** | | | | |
| Count | | | | |
|  | | BMI<18.5 | | Total |
| no | Yes |
| CC genotype | no | 125 | 5 | 130 |
| yes | 19 | 1 | 20 |
| Total | | 144 | 6 | 150 |
| **Crosstab**(CC genotype **\* BMI[18.5-24.9])** | | | | |
| Count | | | | |
|  | | BMI[18.5-24.9] | | Total |
| no | yes |
| CCgenotype | no | 86 | 44 | 130 |
| yes | 19 | 1 | 20 |
| Total | | 105 | 45 | 150 |
| **Crosstab**(CC genotype **\* BMI[25-29.9])** | | | | |
| Count | | | | |
|  | | BMI[25-29.9] | | Total |
| no | yes |
| CC genotype | no | 76 | 54 | 130 |
| yes | 13 | 7 | 20 |
| Total | | 89 | 61 | 150 |
| **Crosstab**(CC genotype **\* BMI[30-34.9])** | | | | |
| Count | | | | |
|  | | BMI[30-34.9] | | Total |
| no | yes |
| CC genotype | no | 108 | 22 | 130 |
| yes | 14 | 6 | 20 |
| Total | | 122 | 28 | 150 |
| **Crosstab**(CC genotype **\* BMI≥35)** | | | | |
| Count | | | | |
|  | | BMI≥35 | | Total |
| no | Yes |
| CC genotype | no | 125 | 5 | 130 |
| yes | 15 | 5 | 20 |
| Total | | 140 | 10 | 150 |
| **Crosstab**(GC genotype **\* BMI<18.5)** | | | | |
| Count | | | | |
|  | | BMI<18.5 | | Total |
| no | Yes |
| GC genotype | no | 112 | 5 | 117 |
| yes | 32 | 1 | 33 |
| Total | | 144 | 6 | 150 |
| **Crosstab**(GCgenotype **\* BMI[18.5-24.9])** | | | | |
| Count | | | | |
|  | | BMI[18.5-24.9] | | Total |
| no | yes |
| GC genotype | no | 75 | 42 | 117 |
| yes | 30 | 3 | 33 |
| Total | | 105 | 45 | 150 |
| **Crosstab**(GC genotype **\* BMI[25-29.9])** | | | | |
| Count | | | | |
|  | | BMI[25-29.9] | | Total |
| no | yes |
| GC genotype | no | 66 | 51 | 117 |
| yes | 23 | 10 | 33 |
| Total | | 89 | 61 | 150 |
| **Crosstab**(GC genotype **\* BMI[30-34.9])** | | | | |
| Count | | | | |
|  | | BMI[30-34.9] | | Total |
| No | yes |
| GC genotype | no | 104 | 13 | 117 |
| yes | 18 | 15 | 33 |
| Total | | 122 | 28 | 150 |
| **Crosstab**(GC genotype **\* BMI≥35)** | | | | |
| Count | | | | |
|  | | BMI≥35 | | Total |
| no | Yes |
| GC genotype | no | 111 | 6 | 117 |
| yes | 29 | 4 | 33 |
| Total | | 140 | 10 | 150 |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Chi-Square Tests**(GG genotype **\* BMI<18.5)** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | .011a | 1 | .917 |  |  |
| a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 2.12. | | | | | |
| b. Computed only for a 2x2 table | | | | | |
| **Chi-Square Tests**(GG genotype **\* BMI[18.5-24.9])** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 19.675a | 1 | .000 |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 15.90. | | | | | |
| b. Computed only for a 2x2 table | | | | | |
| **Chi-Square Tests** GG genotype **\* BMI[25-29.9]** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 2.507a | 1 | .113 |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 21.55. | | | | | |
| b. Computed only for a 2x2 table | | | | | |
| **Chi-Square Tests**(GG genotype **\* BMI[30-34.9])** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 23.707a | 1 | .000 |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 9.89. | | | | | |
| b. Computed only for a 2x2 table | | | | | |
| **Chi-Square Tests** GG genotype **\* BMI≥35** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 14.013a | 1 | .000 |  |  |
| a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is 3.53. | | | | | |
| b. Computed only for a 2x2 table | | | | | |
| **Chi-Square Tests** (CC genotype **\* BMI<18.5)** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | .060a | 1 | .806 |  |  |
| a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is .80. | | | | | |
| b. Computed only for a 2x2 table | | | | | |
| **Chi-Square Tests**(CC genotype **\* BMI[18.5-24.9])** | | | | | |
|  | Value | Df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 6.868a | 1 | .009 |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 6.00. | | | | | |
| b. Computed only for a 2x2 table | | | | | |
| **Chi-Square Tests**(CC genotype **\* BMI[25-29.9])** | | | | | |
|  | Value | Df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | .307a | 1 | .579 |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 8.13. | | | | | |
| b. Computed only for a 2x2 table | | | | | |
| **Chi-Square Tests**(CC genotype **\* BMI[30-34.9])** | | | | | |
|  | Value | Df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 1.952a | 1 | .162 |  |  |
| a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is 3.73. | | | | | |
| b. Computed only for a 2x2 table | | | | | |
| **Chi-Square Tests**(CC genotype **\* BMI≥35)** | | | | | |
|  | Value | Df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 12.466a | 1 | .000 |  |  |
| a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is 1.33. | | | | | |
| b. Computed only for a 2x2 table | | | | | |
| **Chi-Square Tests**(GC genotype **\* BMI<18.5)** | | | | | |
|  | Value | Df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | .104a | 1 | .748 |  |  |
| a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.32. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Chi-Square Tests**(GCgenotype **\* BMI[18.5-24.9])** | | | | | | | | |
|  | | Value | | Df | | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | | 8.808a | | 1 | | .003 |  |  |
| a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 9.90. | | | | | | | | |
| b. Computed only for a 2x2 table | | | | | | | | |
| **Chi-Square Tests**(GC genotype **\* BMI[25-29.9])** | | | | | | | | |
|  | Value | | | Df | | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 1.883a | | | 1 | | .170 |  |  |
| a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 13.42. | | | | | | | | |
| b. Computed only for a 2x2 table | | | | | | | | |
| **Chi-Square Tests**(GC genotype **\* BMI[30-34.9])** | | | | | | | | |
|  | | | Value | Df | | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | | | 19.997a | 1 | | .000 |  |  |
| a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 6.16. | | | | | | | | |
| b. Computed only for a 2x2 table | | | | | | | | |
| **Chi-Square Tests**(GC genotype **\* BMI≥35)** | | | | | | | | |
|  | | | Value | | Df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | | | 2.023a | | 1 | .155 |  |  |
| a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is 2.20. | | | | | | | | |
| b. Comuted only for a 2x2 table | | | | | | | | |

Table.12: Results of Chi-Square Tests for GG,CC, GC genotype and BMI under 95% confidence (α ≤ .050);

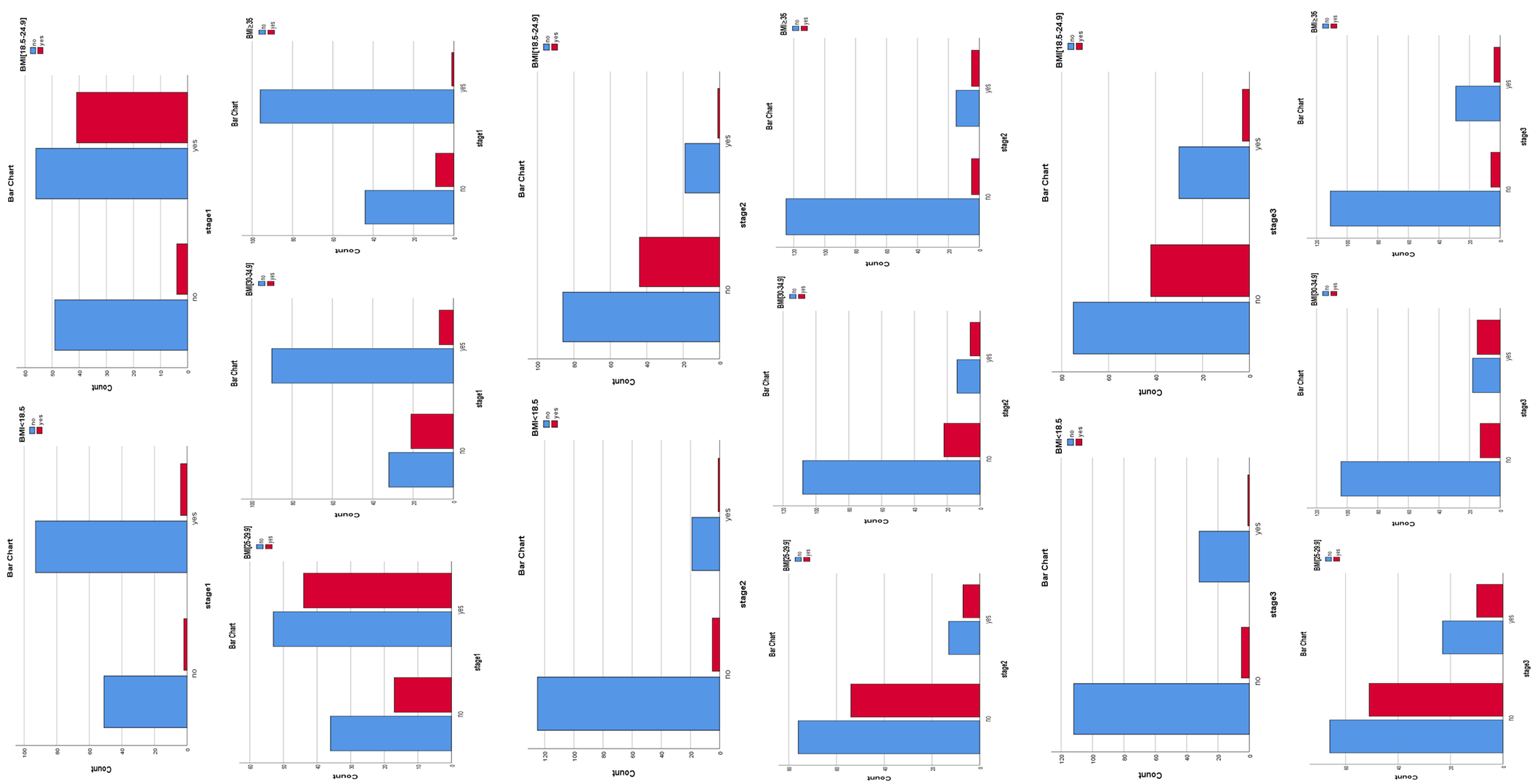


Figure .7: Bar chart to the frequency between BMI groups and GG(stage1)CC(stage2), GC(stage3) genotypes.

**3.Statistical applications LRP5G171R genotypes , Lumbar BMD**

Related-Samples McNemar Change Test was used to exams the variant significant under 95% confidence level (α ≤ .050) and studying a null hypothesis interested in LRP5G171Rgenotypes variant of distribution across lumbar T-score values taking into consideration all Laboratory value stages.

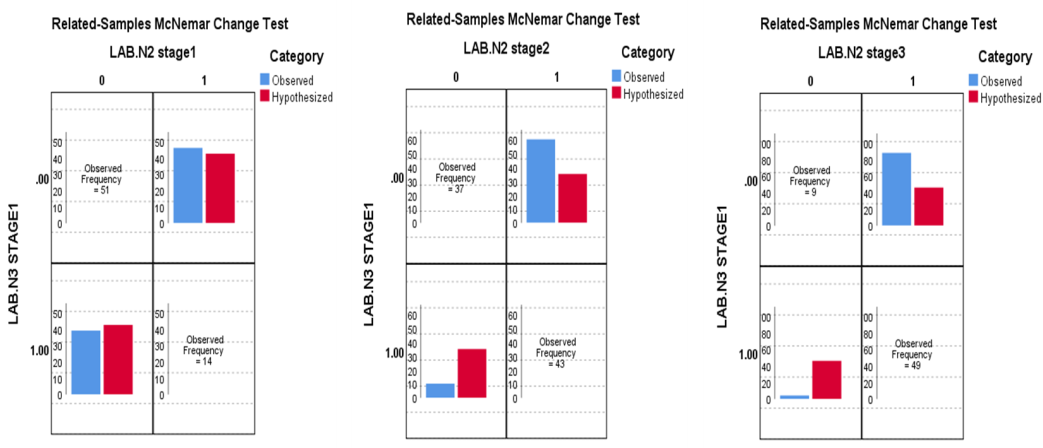
automated cross-tab to identify the odd risk for lumbar T- score observing when LRP5G171Rgenotypes excess comparing with the possibility to observe lumbar T- score when LRP5G171Rgenotypes absence taking into consideration all genotypes

Chi-Square Tests was used to estimate the correlation between LRP5G171Rgenotypes and each of lumbar T- score under 95% confidence (α ≤ .050)

**3.1. GG genotype results:**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Hypothesis Test Summary** | | | | |
|  | Null Hypothesis | Test | Sig. | Decision |
|  | The distributions of different values across GG genotype and normal lumbar T-score are equally likely. | Related-Samples McNemar Change Test | .515 | Retain the null hypothesis. |
|  | The distributions of different values across LAB.N3 STAGE1 and LAB.N2 stage2 are equally likely. | Related-Samples McNemar Change Test | .000 | Reject the null hypothesis. |
|  | The distributions of different values across GG genotype and osteoporosis lumbar T-scoreare equally likely. | Related-Samples McNemar Change Test | .000 | Reject the null hypothesis. |
| Asymptotic significances are displayed. The significance level is .050. | | | | |

Table .13: Observation hypothesis Test Summary for GG genotype, lumbar T-score values

Figure.8: Related-Samples McNemar Change Test between GG genotype and normal lumbar T-score(LAB.N1 stage1), osteopenia lumbar T-score(LAB.N1 stage2), osteoporosis lumbar T-score(LAB.N1 stage3).

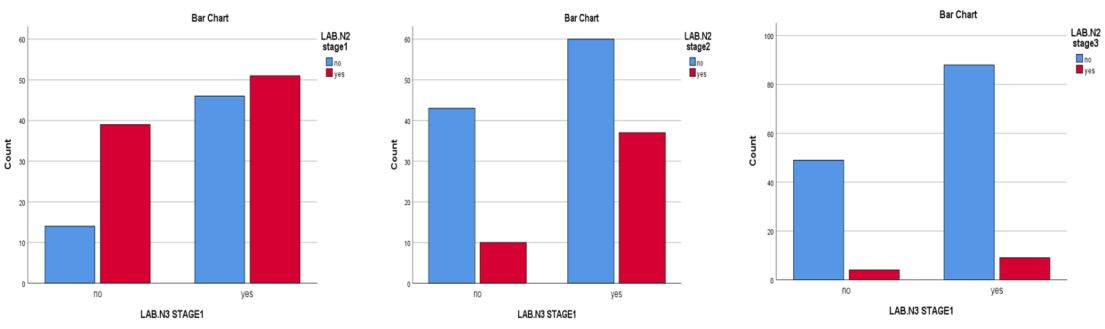


Figure .9: Bar chart to the frequency between normal lumbar T-score(LAB.N1 stage1) osteopenia lumbar T-score(LAB.N1 stage2), osteoporosis lumbar T-score(LAB.N1 stage3) and GGgenotype.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Crosstab(GG genotype and normal lumbar T-score)** | | | | | | | | | | | | | | |
| **Count** | | | | | | | | | | | | | | |
|  | | normal lumbar T-score | | | Total | | | | | | | | | |
| No | yes | |
| GG genotype | no | 14 | 39 | | 53 | | | | | | | | | |
| yes | 46 | 51 | | 97 | | | | | | | | | |
| Total | | 60 | 90 | | 150 | | | | | | | | | |
| **Risk Estimate(GG genotype and normal lumbar T-score)** | | | | | | | | | | | | | | |
|  | | | | | | Value | | | | 95% Confidence Interval | | | | |
| Lower | | | Upper | |
| Odds Ratio for GG genotype (no / yes) | | | | | | .398 | | | | .192 | | | .825 | |
| For cohort normal lumbar T-score = no | | | | | | .557 | | | | .339 | | | .915 | |
| For cohort normal lumbar T-score = yes | | | | | | 1.400 | | | | 1.092 | | | 1.794 | |
| N of Valid Cases | | | | | | 150 | | | |  | | |  | |
| **Crosstab(GG genotype and osteopenia lumbar T-score)** | | | | | | | | | | | | | | |
| **Count** | | | | | | | | | | | | | | |
|  | | osteopenia lumbar T-score | | | Total | | | | | | | | | |
| no | Yes | |
| GG genotype | no | 43 | 10 | | 53 | | | | | | | | | |
| yes | 60 | 37 | | 97 | | | | | | | | | |
| Total | | 103 | 47 | | 150 | | | | | | | | | |
| **Risk Estimate(GG genotype and osteopenia lumbar T-score)** | | | | | | | | | | | | | | |
|  | | Value | | 95% Confidence Interval | | | | | | | | | | |
| Lower | | | | Upper | | | | | | |
| Odds Ratio for GG genotype (no / yes) | | 2.652 | | 1.190 | | | | 5.906 | | | | | | |
| For cohort osteopenia lumbar T-score = no | | 1.312 | | 1.070 | | | | 1.607 | | | | | | |
| For cohort osteopenia lumbar T-score = yes | | .495 | | .268 | | | | .913 | | | | | | |
| N of Valid Cases | | 150 | |  | | | |  | | | | | | |
| **Crosstab(GG genotype and osteoporosis lumbar T-score)** | | | | | | | | | | | | | | |
| **Count** | | | | | | | | | | | | | | |
|  | | osteoporosis lumbar T-score | | | | | | | | | | Total | | |
| no | | | | | | | yes | | |
| GG genotype | no | 49 | | | | | | | 4 | | | 53 | | |
| yes | 88 | | | | | | | 9 | | | 97 | | |
| Total | | 137 | | | | | | | 13 | | | 150 | | |
| **Risk Estimate(GG genotype and osteoporosis lumbar T-score)** | | | | | | | | | | | | | | |
|  | | | | | | | Value | | | | 95% Confidence Interval | | | |
| Lower | | | Upper |
| Odds Ratio for GG genotype (no / yes) | | | | | | | 1.253 | | | | .367 | | | 4.280 |
| For cohort osteoporosis lumbar T-score = no | | | | | | | 1.019 | | | | .922 | | | 1.126 |
| For cohort osteoporosis lumbar T-score = yes | | | | | | | .813 | | | | .263 | | | 2.516 |
| N of Valid Cases | | | | | | | 150 | | | |  | | |  |

Table.14: Results of cross-tab and risk estimate tests were used to identify the odd risk for lumbar T-score values when GG genotype is absence or existed.

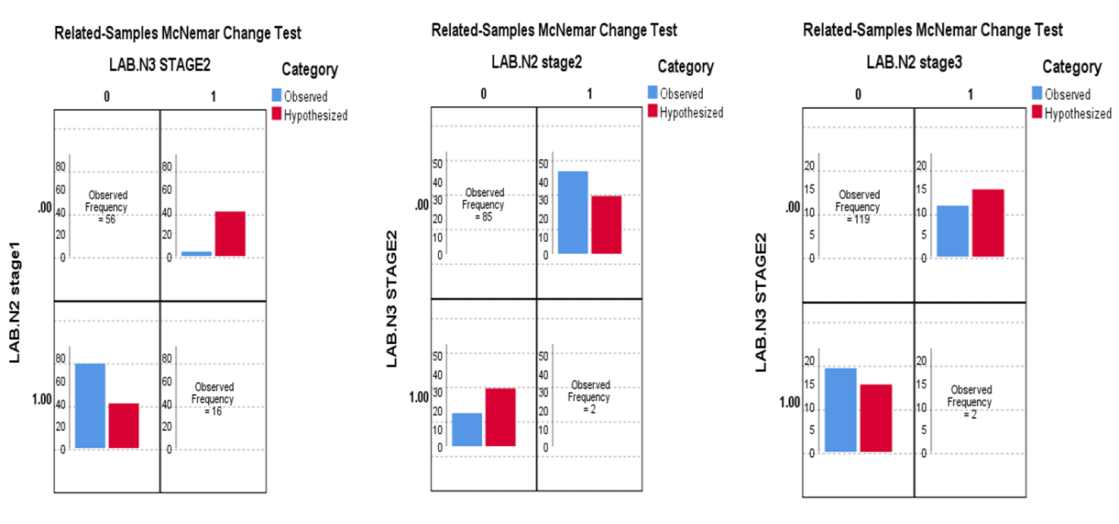
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Chi-Square Tests( GG genotype and normal lumbar T-score)** | | | | | | | | | | | | |
|  | Value | | df | | Asymptotic Significance (2-sided) | | | Exact Sig. (2-sided) | | Exact Sig. (1-sided) | | |
| Pearson Chi-Square | 6.302a | | 1 | | .012 | | |  | |  | | |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 21.20. | | | | | | | | | | | | |
| b. Computed only for a 2x2 table | | | | | | | | | | | | |
| **Chi-Square Tests( GG genotype and osteopenia lumbar T-score)** | | | | | | | | | | | | |
|  | | Value | | | df | Asymptotic Significance (2-sided) | | | Exact Sig. (2-sided) | | | Exact Sig. (1-sided) |
| Pearson Chi-Square | | 5.919a | | | 1 | .015 | | |  | | |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 16.61. | | | | | | | | | | | | |
| b. Computed only for a 2x2 table | | | | | | | | | | | | |
| **Chi-Square Tests (GG genotype and osteoporosis lumbar T-score)** | | | | | | | | | | | | |
|  | | | | Value | | df | Asymptotic Significance (2-sided) | | Exact Sig. (2-sided) | | Exact Sig. (1-sided) | |
| Pearson Chi-Square | | | | .130a | | 1 | .719 | |  | |  | |
| a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is 4.59. | | | | | | | | | | | | |
| b. Computed only for a 2x2 table | | | | | | | | | | | | |

Table.15: Results of Chi-Square Tests for GG genotype and lumbar T-score values

**3.2.CC genotype results:**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Hypothesis Test Summary** | | | | |
|  | Null Hypothesis | Test | Sig. | Decision |
|  | The distributions of different values across CC genotype,normal lumbar T-score are equally likely. | Related-Samples McNemar Change Test | .000 | Reject the null hypothesis. |
|  | The distributions of different values across CC genotypes and osteopenia lumbar T-score are equally likely. | Related-Samples McNemar Change Test | .001 | Reject the null hypothesis. |
|  | The distributions of different values across CC genotype and osteoporosis lumbar T-scoreare equally likely. | Related-Samples McNemar Change Test | .265 | Retain the null hypothesis. |
| Asymptotic significances are displayed. The significance level is .050. | | | | |

Table.16: Observation hypothesis Test Summary for CC genotype, lumbar T-score values

Figure.10: Related-Samples McNemar Change Test between CC genotype and normal lumbar T-score(LAB.N1 stage1), osteopenia lumbar T-score(LAB.N1 stage2), osteoporosis lumbar T-score(LAB.N1 stage3).

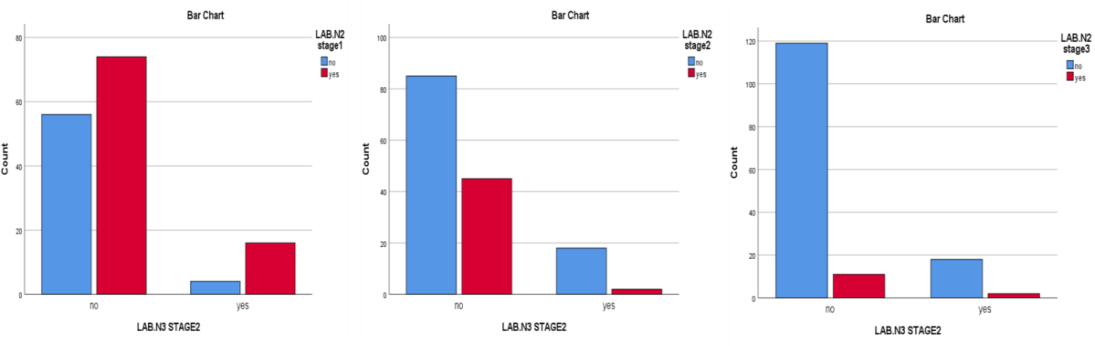


Figure.11: Bar chart to the frequency between normal lumbar T-score(LAB.N1 stage1), osteopenia lumbar T-score(LAB.N1 stage2), osteoporosis lumbar T-score(LAB.N1 stage3) and CC genotype.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Crosstab (CC genotype and normal** lumbar **T-score)** | | | | | | | |
| **Count** | | | | | | | |
|  | | normal lumbar T-score | | | | Total | |
| no | | yes | |
| CC genotype | no | 56 | | 74 | | 130 | |
| yes | 4 | | 16 | | 20 | |
| Total | | 60 | | 90 | | 150 | |
| **Risk Estimate(CC genotype and normal lumbar T-score)** | | | | | | | |
|  | | | Value | | 95% Confidence Interval | | |
| Lower | | Upper |
| Odds Ratio for CC genotype (no / yes) | | | 3.027 | | .959 | | 9.554 |
| For cohort normal lumbar T-score = no | | | 2.154 | | .877 | | 5.290 |
| For cohort normal lumbar T-score = yes | | | .712 | | .546 | | .928 |
| N of Valid Cases | | | 150 | |  | |  |
| **Crosstab (CC genotype and osteopenia lumbar T-score)** | | | | | | | |
| Count | | | | | | | |
|  | | osteopenia lumbar T-score | | | | Total | |
| no | | Yes | |
| CC genotype | no | 85 | | 45 | | 130 | |
| yes | 18 | | 2 | | 20 | |
| Total | | 103 | | 47 | | 150 | |
| **Risk Estimate(CC genotype and osteopenia lumbar T-score)** | | | | | | | |
|  | | | Value | | 95% Confidence Interval | | |
| Lower | | Upper |
| Odds Ratio for CC genotype (no / yes) | | | .210 | | .047 | | .945 |
| For cohort osteopenia lumbar T-score = no | | | .726 | | .599 | | .881 |
| For cohort osteopenia lumbar T-score = yes | | | 3.462 | | .910 | | 13.165 |
| N of Valid Cases | | | 150 | |  | |  |
| **Crosstab (CC genotype and osteoporosis lumbar T-score)** | | | | | | | |
| **Count** | | | | | | | |
|  | | osteoporosis lumbar T-score | | | | Total | |
| no | | yes | |
| CC genotype | no | 119 | | 11 | | 130 | |
| yes | 18 | | 2 | | 20 | |
| Total | | 137 | | 13 | | 150 | |
| **Risk Estimate(CC genotype and osteoporosis lumbar T-score)** | | | | | | | |
|  | | | Value | | 95% Confidence Interval | | |
| Lower | | Upper |
| Odds Ratio for CCgenotype (no / yes) | | | 1.202 | | .246 | | 5.871 |
| For cohort osteoporosis lumbar T-score = no | | | 1.017 | | .871 | | 1.188 |
| For cohort osteoporosis lumbar T-score = yes | | | .846 | | .202 | | 3.540 |
| N of Valid Cases | | | 150 | |  | |  |

Table.17: Results of cross-tab and risk estimate tests were used to identify the odd risk for lumbar T-score values when CC genotype is absence or existed.

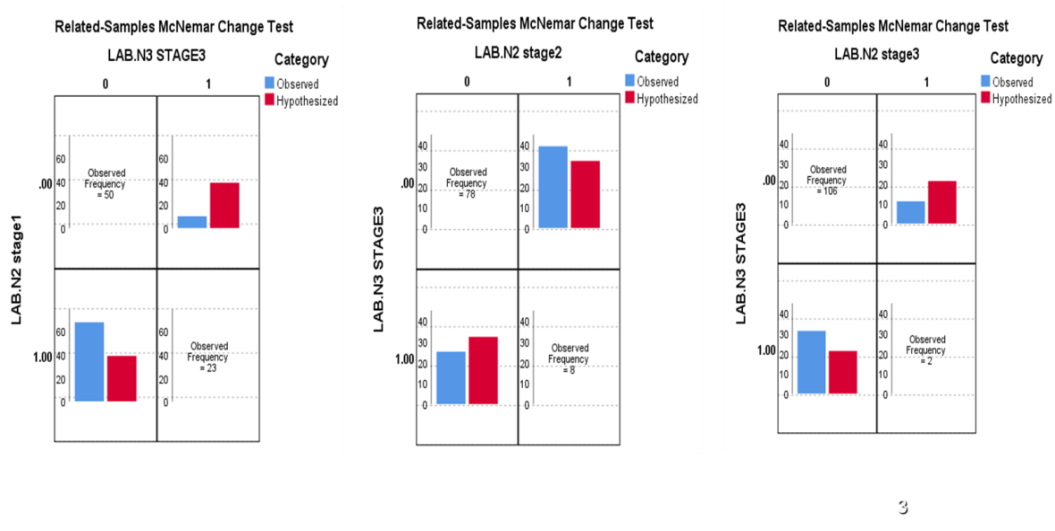
|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Chi-Square Tests(CC genotype, normal lumbar T-score)** | | | | | |
|  | Value | Df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 3.846a | 1 | .050 |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 8.00. | | | | | |
| b. Computed only for a 2x2 table | | | | | |
| **Chi-Square Tests** CC, osteopenia | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 7.731a | 1 | .005 |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 6.40. | | | | | |
| b. Computed only for a 2x2 table | | | | | |
| **Chi-Square Tests CC.** osteoporosis | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | .204a | 1 | .651 |  |  |
| a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is 3.73. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

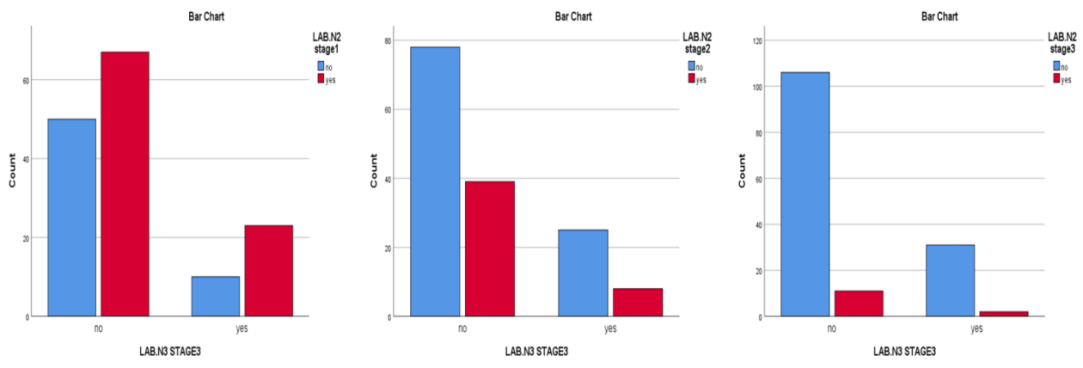
Table.18: Results of Chi-Square Tests for CC genotype and lumbar T-score values

**3.3.GC genotype results:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Hypothesis Test Summary** | | | | | |
|  | Null Hypothesis | Test | Sig. | | Decision |
|  | The distributions of different values across GC genotype and normal lumbar T-scoreare equally likely. | Related-Samples McNemar Change Test | .000 | | Reject the null hypothesis. |
|  | The distributions of different values across GC genotype and osteopenia lumbar T-scoreare equally likely. | Related-Samples McNemar Change Test | .104 | Retain the null hypothesis. | |
|  | The distributions of different values across GC genotype and osteoporosis lumbar T-scoreare equally likely. | Related-Samples McNemar Change Test | .003 | | Reject the null hypothesis. |
| Asymptotic significances are displayed. The significance level is .050. | | | | | |

Table.19: Observation hypothesis Test Summary for GC genotype, lumbar T-score values

Figure.12: Related-Samples McNemar Change Test between GC genotype and normal lumbar T-score(LAB.N1 stage1), osteopenia lumbar T-score(LAB.N1 stage2), osteoporosis lumbar T-score(LAB.N1 stage3)

Figure.13: Bar chart to the frequency between normal lumbar T-score(LAB.N1 stage1) osteopenia lumbar T-score(LAB.N1 stage2), osteoporosis lumbar T-score(LAB.N1 stage3) and GC genotype

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Crosstab (GC genotype, normal lumbar T-score)** | | | | | | | | | | | | |
| Count | | | | | | | | | | | | |
|  | | normal lumbar T-score | | | | | | | Total | | | |
| no | | | | yes | | |
| GC genotype | no | 50 | | | | 67 | | | 117 | | | |
| yes | 10 | | | | 23 | | | 33 | | | |
| Total | | 60 | | | | 90 | | | 150 | | | |
| **Risk Estimate(GC genotype, normal lumbar T-score)** | | | | | | | | | | | | |
|  | | | Value | | | | 95% Confidence Interval | | | | | |
| Lower | | | | Upper | |
| Odds Ratio for GC genotype (no / yes) | | | 1.716 | | | | .750 | | | | 3.928 | |
| For cohort normal lumbar T-score = no | | | 1.410 | | | | .807 | | | | 2.465 | |
| For cohort normal lumbar T-score = yes | | | .822 | | | | .625 | | | | 1.081 | |
| N of Valid Cases | | | 150 | | | |  | | | |  | |
| **Crosstab (GC genotype, osteopenia lumbar T-score)** | | | | | | | | | | | | |
| Count | | | | | | | | | | | | |
|  | | osteopenia lumbar T-score | | | | | | | Total | | | |
| no | | | | Yes | | |
| GC genotype | no | 78 | | | | 39 | | | 117 | | | |
| yes | 25 | | | | 8 | | | 33 | | | |
| Total | | 103 | | | | 47 | | | 150 | | | |
| **Risk Estimate(GC genotype, osteopenia lumbar T-score)** | | | | | | | | | | | | |
|  | | | | Value | | | | 95% Confidence Interval | | | | |
| Lower | | | | Upper |
| Odds Ratio for GC genotype (no / yes) | | | | .640 | | | | .264 | | | | 1.549 |
| For cohort osteopenia lumbar T-score = no | | | | .880 | | | | .698 | | | | 1.109 |
| For cohort osteopenia lumbar T-score = yes | | | | 1.375 | | | | .714 | | | | 2.648 |
| N of Valid Cases | | | | 150 | | | |  | | | |  |
| **Crosstab (GC genotype, osteoporosis lumbar T-score)** | | | | | | | | | | | | |
| Count | | | | | | | | | | | | |
|  | | osteoporosis lumbar T-score | | | | | | | Total | | | |
| no | | | | yes | | |
| GC genotype | no | 106 | | | | 11 | | | 117 | | | |
| yes | 31 | | | | 2 | | | 33 | | | |
| Total | | 137 | | | | 13 | | | 150 | | | |
| **Risk Estimate(GC genotype, osteoprosis lumbar T-score)** | | | | | | | | | | | | |
|  | | | | | Value | | | | | 95% Confidence Interval | | |
| Lower | | Upper |
| Odds Ratio for GC genotype (no / yes) | | | | | .622 | | | | | .131 | | 2.955 |
| For cohort osteoporosis lumbar T-score = no | | | | | .964 | | | | | .869 | | 1.071 |
| For cohort osteoporosis lumbar T-score = yes | | | | | 1.551 | | | | | .362 | | 6.655 |
| N of Valid Cases | | | | | 150 | | | | |  | |  |

Table.20: Results of cross-tab and risk estimate tests were used to identify the odd risk for lumbar T-score values when LRP5G171R genotype is absence or existed.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Chi-Square Tests(GC genotype, normal** lumbar **T-score)** | | | | | | | | | | | |
|  | Value | | | df | Asymptotic Significance (2-sided) | | | Exact Sig. (2-sided) | | Exact Sig. (1-sided) | |
| Pearson Chi-Square | 1.658a | | | 1 | .198 | | |  | |  | |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 13.20. | | | | | | | | | | | |
| b. Computed only for a 2x2 table | | | | | | | | | | | |
| **Chi-Square Tests(GC genotype, osteopenia lumbar T-score)** | | | | | | | | | | | |
|  | | | Value | | | df | Asymptotic Significance (2-sided) | | Exact Sig. (2-sided) | | Exact Sig. (1-sided) |
| Pearson Chi-Square | | | .989a | | | 1 | .320 | |  | |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 10.34. | | | | | | | | | | | |
| b. Computed only for a 2x2 table | | | | | | | | | | | |
| **Chi-Square Tests(GC genotype, osteoporosis lumbar T-score)** | | | | | | | | | | | |
|  | | Value | | | | Df | Asymptotic Significance (2-sided) | | Exact Sig. (2-sided) | | Exact Sig. (1-sided) |
| Pearson Chi-Square | | .363a | | | | 1 | .547 | |  | |  |
| a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is 2.86. | | | | | | | | | | | |
| b. Computed only for a 2x2 table | | | | | | | | | | | |

Table .21: Results of Chi-Square Tests for GC genotype and lumbar T-score values

**4.Statistical applications Mild OI, LOW BMD**

Related-Samples McNemar Change Test was used to exams the variant significant under 95% confidence level (α ≤ .050) and studying a null hypothesis interested in mild OI of distribution across low BMD. Chi-Square Tests was used to estimate the correlation between mild OI and each of lpw BMD(osteopenia, osteoporosis) under 95% confidence (α ≤ .050)

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Variables in the Equation** | | | | | | | | | | | |
|  | | | B | | S.E. | Wald | | df | | Sig. | Exp(B) |
| Step 1a | | mild(1) | 1.758 | | .407 | 18.612 | | 1 | | .000 | 5.800 |
| Constant | .000 | | .221 | .000 | | 1 | | 1.000 | 1.000 |
| Variable(s) entered on step 1: STAGE(2.3) "N1 and/or N2. | | | | | | | | | | | |
| **Table 3. Observation hypothesis Test Summary** | | | | | | | | | | | |
|  | Null Hypothesis | | | Test | | | Sig. | | Decision | | |
| 1 | The distributions of different values across mild and STAGE(2.3) "N1 and/or N2 are equally likely. | | | Related-Samples McNemar Change Test | | | .108 | | Retain the null hypothesis. | | |
| Asymptotic significances are displayed. The significance level is .050. | | | | | | | | | | | |

Table 22. Variables in the Equation for mild OI \* OSTEOPENIA , OSTEOPROSIS binary logistic regression

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 20.635a | 1 | .000 |  |  |
| Continuity Correctionb | 19.093 | 1 | .000 |  |  |
| Likelihood Ratio | 21.845 | 1 | .000 |  |  |
| Fisher's Exact Test |  |  |  | .000 | .000 |
| Linear-by-Linear Association | 20.498 | 1 | .000 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 23.12. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

Table 23. mild OI \* (OSTEOPENIA, OSTEOPROSIS) Chi-Square Tests

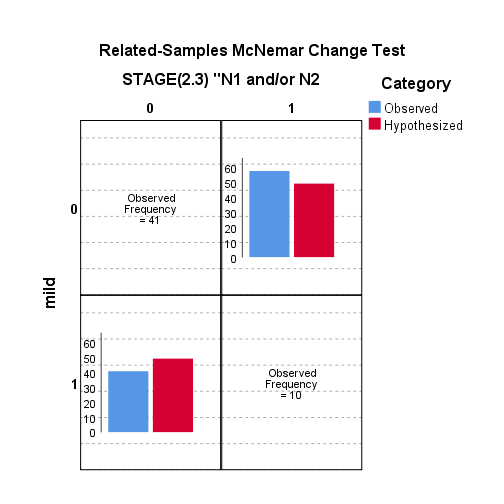


Figure 14. Related-Samples McNemar Change Test between mild and mild OI/ Low BMD( osteopenia=stage2, osteoporosis= stage 3

**5.Statistical applications (MILD OI, LOW BMD) with parameters**

Multinomial logistic regression was used to estimate the predictability under 95% confidence level (α ≤ .050) . Odds ratio test and chi –square test to estimate the relationship of (mild OI, low BMD) with parameters under 95% confidence (α ≤ .050).

**1.5. Variables in the Equation for parameter \* mild OI + low BMD binary logistic regression**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Variables in the Equation** | | | | | | | | | |
|  | | B | S.E. | Wald | df | Sig. | Exp(B) | 95% C.I.for EXP(B) | |
| Lower | Upper |
| Step 1a | [40-59] weight group | 2.868 | 1.320 | 4.717 | 1 | .030 | 17.597 | 1.323 | 234.079 |
| [60-79] weight group | .934 | .933 | 1.001 | 1 | .317 | 2.544 | .409 | 15.838 |
| [80-99] weight group | 1.686 | 1.000 | 2.841 | 1 | .092 | 5.397 | .760 | 38.334 |
| [150-159] height group | .069 | 1.128 | .004 | 1 | .951 | 1.071 | .117 | 9.782 |
| [160-169] height group | .239 | 1.029 | .054 | 1 | .816 | 1.270 | .169 | 9.549 |
| 18.5 ≥ BMI group | -2.590 | 2.039 | 1.613 | 1 | .204 | .075 | .001 | 4.083 |
| [18.5-24.9] BMI group | -1.534 | 1.462 | 1.100 | 1 | .294 | .216 | .012 | 3.790 |
| [25-29.9] BMI group | -.185 | 1.270 | .021 | 1 | .884 | .831 | .069 | 10.017 |
| [30-34.9] BMI group | -.441 | 1.172 | .142 | 1 | .706 | .643 | .065 | 6.391 |
| [40-50] age group | .501 | 1.358 | .136 | 1 | .712 | 1.650 | .115 | 23.618 |
| ]50-60] age group | 1.668 | 1.332 | 1.567 | 1 | .211 | 5.299 | .389 | 72.156 |
| ]60-70] age group | 2.839 | 1.329 | 4.563 | 1 | .033 | 17.107 | 1.264 | 231.567 |
| {11] first of Menstrual period group | 1.182 | .982 | 1.450 | 1 | .229 | 3.262 | .476 | 22.355 |
| [12] first of Menstrual period group | -.457 | 1.015 | .203 | 1 | .653 | .633 | .087 | 4.628 |
| [13] first of Menstrual period group | .884 | .944 | .876 | 1 | .349 | 2.419 | .380 | 15.389 |
| [14] first of Menstrual period group | .467 | .925 | .255 | 1 | .614 | 1.595 | .260 | 9.772 |
| [40-42] end and pre- end of Menstrual period group | .237 | .789 | .091 | 1 | .763 | 1.268 | .270 | 5.950 |
| [43-45] end and pre- end of Menstrual period group | .677 | .789 | .735 | 1 | .391 | 1.967 | .419 | 9.237 |
| [46-48] end and pre- end of Menstrual period group | -.040 | .726 | .003 | 1 | .956 | .961 | .231 | 3.988 |
| [49-51] end and pre- end of Menstrual period group | -1.103 | .755 | 2.134 | 1 | .144 | .332 | .076 | 1.458 |
| Constant | -3.591 | 1.544 | 5.410 | 1 | .020 | .028 |  |  |
| a. Variable(s) entered on step 1: [40-59] weight group, [60-79] weight group, [80-99] weight group, [150-159] height group, [160-169] height group, 18.5 ≥ BMI group, [18.5-24.9] BMI group, [25-29.9] BMI group, [30-34.9] BMI group, [40-50] age group, ]50-60] age group, ]60-70] age group, {11] first of Menstrual period group, [12] first of Menstrual period group, [13] first of Menstrual period group, [14] first of Menstrual period group, [40-42] end and pre- end of Menstrual period group, [43-45] end and pre- end of Menstrual period group, [46-48] end and pre- end of Menstrual period group, [49-51] end and pre- end of Menstrual period group. | | | | | | | | | |

Table 24. Variables in the Equation for parameter \* mild OI + low BMD binary logistic regression

**2.5. Results of Odd Ratio test for mildOI / low BMD (osteopenia = stage2, osteoporosis= stage3)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Crosstab** | | | | | |
|  | | | [170-179] height group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 87 | 22 | 109 |
| % within mild+/ stage2 - 3 | 79.8% | 20.2% | 100.0% |
| Yes | Count | 39 | 2 | 41 |
| % within mild+/ stage2 - 3 | 95.1% | 4.9% | 100.0% |
| Total | | Count | 126 | 24 | 150 |
| % within mild+/ stage2 - 3 | 84.0% | 16.0% | 100.0% |

|  |  |  |  |
| --- | --- | --- | --- |
| **Risk Estimate** | | | |
|  | Value | 95% Confidence Interval | |
| Lower | Upper |
| Odds Ratio for mild+/ stage2 - 3 (No / Yes) | .203 | .045 | .905 |
| For cohort [170-179] height group = No | .839 | .746 | .943 |
| For cohort [170-179] height group = Yes | 4.138 | 1.018 | 16.817 |
| N of Valid Cases | 150 |  |  |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Crosstab** | | | | | |
|  | | | BMI ≥ 35 | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 101 | 8 | 109 |
| % within mild+/ stage2 - 3 | 92.7% | 7.3% | 100.0% |
| Yes | Count | 39 | 2 | 41 |
| % within mild+/ stage2 - 3 | 95.1% | 4.9% | 100.0% |
| Total | | Count | 140 | 10 | 150 |
| % within mild+/ stage2 - 3 | 93.3% | 6.7% | 100.0% |

|  |  |  |  |
| --- | --- | --- | --- |
| **Risk Estimate** | | | |
|  | Value | 95% Confidence Interval | |
| Lower | Upper |
| Odds Ratio for mild+/ stage2 - 3 (No / Yes) | .647 | .132 | 3.184 |
| For cohort BMI ≥ 35 = No | .974 | .893 | 1.063 |
| For cohort BMI ≥ 35 = Yes | 1.505 | .333 | 6.793 |
| N of Valid Cases | 150 |  |  |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Crosstab** | | | | | |
|  | | | ]70-80] age group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 91 | 18 | 109 |
| % within mild+/ stage2 - 3 | 83.5% | 16.5% | 100.0% |
| Yes | Count | 40 | 1 | 41 |
| % within mild+/ stage2 - 3 | 97.6% | 2.4% | 100.0% |
| Total | | Count | 131 | 19 | 150 |
| % within mild+/ stage2 - 3 | 87.3% | 12.7% | 100.0% |

|  |  |  |  |
| --- | --- | --- | --- |
| **Risk Estimate** | | | |
|  | Value | 95% Confidence Interval | |
| Lower | Upper |
| Odds Ratio for mild+/ stage2 - 3 (No / Yes) | .126 | .016 | .980 |
| For cohort ]70-80] age group = No | .856 | .777 | .942 |
| For cohort ]70-80] age group = Yes | 6.771 | .934 | 49.107 |
| N of Valid Cases | 150 |  |  |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Crosstab** | | | | | | | | |
|  | | | [15] first of Menstrual period group | | | | Total | |
| No | | Yes | |
| mild+/ stage2 - 3 | No | Count | | 91 | | 18 | | 109 |
| % within mild+/ stage2 - 3 | | 83.5% | | 16.5% | | 100.0% |
| Yes | Count | | 38 | | 3 | | 41 |
| % within mild+/ stage2 - 3 | | 92.7% | | 7.3% | | 100.0% |
| Total | | Count | 129 | | 21 | | 150 | |
| % within mild+/ stage2 - 3 | 86.0% | | 14.0% | | 100.0% | |

|  |  |  |  |
| --- | --- | --- | --- |
| **Risk Estimate** | | | |
|  | Value | 95% Confidence Interval | |
| Lower | Upper |
| Odds Ratio for mild+/ stage2 - 3 (No / Yes) | .399 | .111 | 1.435 |
| For cohort [15] first of Menstrual period group = No | .901 | .799 | 1.015 |
| For cohort [15] first of Menstrual period group = Yes | 2.257 | .702 | 7.259 |
| N of Valid Cases | 150 |  |  |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Crosstab** | | | | | |
|  | | | [52-54] end and pre- end of Menstrual period group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 83 | 26 | 109 |
| % within mild+/ stage2 - 3 | 76.1% | 23.9% | 100.0% |
| Yes | Count | 34 | 7 | 41 |
| % within mild+/ stage2 - 3 | 82.9% | 17.1% | 100.0% |
| Total | | Count | 117 | 33 | 150 |
| % within mild+/ stage2 - 3 | 78.0% | 22.0% | 100.0% |

|  |  |  |  |
| --- | --- | --- | --- |
| **Risk Estimate** | | | |
|  | Value | 95% Confidence Interval | |
| Lower | Upper |
| Odds Ratio for mild+/ stage2 - 3 (No / Yes) | .657 | .261 | 1.658 |
| For cohort [52-54] end and pre- end of Menstrual period group = No | .918 | .771 | 1.093 |
| For cohort [52-54] end and pre- end of Menstrual period group = Yes | 1.397 | .658 | 2.968 |
| N of Valid Cases | 150 |  |  |

Table25:results of ODD ratio test for mildOI / low BMD (osteopenia = stage2, osteoporosis= stage3)

**3.5. Mild OI+/ low BMD(osteopenia =stage2, osteoporosis= stage3) \* parameters groups(chi-square test)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Crosstab** | | | | | |
|  | | | [40-59] weight group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 90 | 19 | 109 |
| % within mild+/ stage2 - 3 | 82.6% | 17.4% | 100.0% |
| Yes | Count | 30 | 11 | 41 |
| % within mild+/ stage2 - 3 | 73.2% | 26.8% | 100.0% |
| Total | | Count | 120 | 30 | 150 |
| % within mild+/ stage2 - 3 | 80.0% | 20.0% | 100.0% |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 1.645a | 1 | .200 |  |  |
| Continuity Correctionb | 1.110 | 1 | .292 |  |  |
| Likelihood Ratio | 1.574 | 1 | .210 |  |  |
| Fisher's Exact Test |  |  |  | .252 | .146 |
| Linear-by-Linear Association | 1.634 | 1 | .201 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 8.20. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Crosstab** | | | | | |
|  | | | [60-79] weight group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 59 | 50 | 109 |
| % within mild+/ stage2 - 3 | 54.1% | 45.9% | 100.0% |
| Yes | Count | 19 | 22 | 41 |
| % within mild+/ stage2 - 3 | 46.3% | 53.7% | 100.0% |
| Total | | Count | 78 | 72 | 150 |
| % within mild+/ stage2 - 3 | 52.0% | 48.0% | 100.0% |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | .724a | 1 | .395 |  |  |
| Continuity Correctionb | .445 | 1 | .505 |  |  |
| Likelihood Ratio | .724 | 1 | .395 |  |  |
| Fisher's Exact Test |  |  |  | .464 | .252 |
| Linear-by-Linear Association | .719 | 1 | .396 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 19.68. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Crosstab** | | | | | |
|  | | | [80-99] weight group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 103 | 6 | 109 |
| % within mild+/ stage2 - 3 | 94.5% | 5.5% | 100.0% |
| Yes | Count | 37 | 4 | 41 |
| % within mild+/ stage2 - 3 | 90.2% | 9.8% | 100.0% |
| Total | | Count | 140 | 10 | 150 |
| % within mild+/ stage2 - 3 | 93.3% | 6.7% | 100.0% |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | .865a | 1 | .352 |  |  |
| Continuity Correctionb | .317 | 1 | .573 |  |  |
| Likelihood Ratio | .806 | 1 | .369 |  |  |
| Fisher's Exact Test |  |  |  | .462 | .276 |
| Linear-by-Linear Association | .860 | 1 | .354 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is 2.73. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Crosstab** | | | | | |
|  | | | [150-159] height group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 79 | 30 | 109 |
| % within mild+/ stage2 - 3 | 72.5% | 27.5% | 100.0% |
| Yes | Count | 26 | 15 | 41 |
| % within mild+/ stage2 - 3 | 63.4% | 36.6% | 100.0% |
| Total | | Count | 105 | 45 | 150 |
| % within mild+/ stage2 - 3 | 70.0% | 30.0% | 100.0% |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 1.165a | 1 | .280 |  |  |
| Continuity Correctionb | .774 | 1 | .379 |  |  |
| Likelihood Ratio | 1.140 | 1 | .286 |  |  |
| Fisher's Exact Test |  |  |  | .320 | .189 |
| Linear-by-Linear Association | 1.157 | 1 | .282 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 12.30. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Crosstab** | | | | | |
|  | | | [160-169] height group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 52 | 57 | 109 |
| % within mild+/ stage2 - 3 | 47.7% | 52.3% | 100.0% |
| Yes | Count | 17 | 24 | 41 |
| % within mild+/ stage2 - 3 | 41.5% | 58.5% | 100.0% |
| Total | | Count | 69 | 81 | 150 |
| % within mild+/ stage2 - 3 | 46.0% | 54.0% | 100.0% |

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| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | .467a | 1 | .494 |  |  |
| Continuity Correctionb | .250 | 1 | .617 |  |  |
| Likelihood Ratio | .469 | 1 | .493 |  |  |
| Fisher's Exact Test |  |  |  | .582 | .309 |
| Linear-by-Linear Association | .464 | 1 | .496 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 18.86. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

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| **Crosstab** | | | | | |
|  | | | [170-179] height group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 87 | 22 | 109 |
| % within mild+/ stage2 - 3 | 79.8% | 20.2% | 100.0% |
| Yes | Count | 39 | 2 | 41 |
| % within mild+/ stage2 - 3 | 95.1% | 4.9% | 100.0% |
| Total | | Count | 126 | 24 | 150 |
| % within mild+/ stage2 - 3 | 84.0% | 16.0% | 100.0% |

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| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | .358a | 1 | .550 |  |  |
| Continuity Correctionb | .017 | 1 | .896 |  |  |
| Likelihood Ratio | .395 | 1 | .530 |  |  |
| Fisher's Exact Test |  |  |  | 1.000 | .477 |
| Linear-by-Linear Association | .356 | 1 | .551 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.64. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

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| **Crosstab** | | | | | |
|  | | | [18.5-24.9] BMI group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 77 | 32 | 109 |
| % within mild+/ stage2 - 3 | 70.6% | 29.4% | 100.0% |
| Yes | Count | 28 | 13 | 41 |
| % within mild+/ stage2 - 3 | 68.3% | 31.7% | 100.0% |
| Total | | Count | 105 | 45 | 150 |
| % within mild+/ stage2 - 3 | 70.0% | 30.0% | 100.0% |

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| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | .078a | 1 | .780 |  |  | |
| Continuity Correctionb | .006 | 1 | .936 |  |  | |
| Likelihood Ratio | .078 | 1 | .780 |  |  | |
| Fisher's Exact Test |  |  |  | .842 | .463 | |
| Linear-by-Linear Association | .078 | 1 | .780 |  |  | |
| N of Valid Cases | 150 |  |  |  |  | |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 12.30. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

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| **Crosstab** | | | | | |
|  | | | [25-29.9] BMI group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 67 | 42 | 109 |
| % within mild+/ stage2 - 3 | 61.5% | 38.5% | 100.0% |
| Yes | Count | 22 | 19 | 41 |
| % within mild+/ stage2 - 3 | 53.7% | 46.3% | 100.0% |
| Total | | Count | 89 | 61 | 150 |
| % within mild+/ stage2 - 3 | 59.3% | 40.7% | 100.0% |

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| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | .753a | 1 | .386 |  |  |
| Continuity Correctionb | .464 | 1 | .496 |  |  |
| Likelihood Ratio | .748 | 1 | .387 |  |  |
| Fisher's Exact Test |  |  |  | .457 | .247 |
| Linear-by-Linear Association | .748 | 1 | .387 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 16.67. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

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| **Crosstab** | | | | | |
|  | | | [30-34.9] BMI group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 87 | 22 | 109 |
| % within mild+/ stage2 - 3 | 79.8% | 20.2% | 100.0% |
| Yes | Count | 35 | 6 | 41 |
| % within mild+/ stage2 - 3 | 85.4% | 14.6% | 100.0% |
| Total | | Count | 122 | 28 | 150 |
| % within mild+/ stage2 - 3 | 81.3% | 18.7% | 100.0% |

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| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | .604a | 1 | .437 |  |  |
| Continuity Correctionb | .294 | 1 | .588 |  |  |
| Likelihood Ratio | .629 | 1 | .428 |  |  |
| Fisher's Exact Test |  |  |  | .491 | .300 |
| Linear-by-Linear Association | .600 | 1 | .438 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 7.65. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

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| **Crosstab** | | | | | |
|  | | | BMI ≥ 35 | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 101 | 8 | 109 |
| % within mild+/ stage2 - 3 | 92.7% | 7.3% | 100.0% |
| Yes | Count | 39 | 2 | 41 |
| % within mild+/ stage2 - 3 | 95.1% | 4.9% | 100.0% |
| Total | | Count | 140 | 10 | 150 |
| % within mild+/ stage2 - 3 | 93.3% | 6.7% | 100.0% |

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| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | .290a | 1 | .590 |  |  |
| Continuity Correctionb | .029 | 1 | .864 |  |  |
| Likelihood Ratio | .308 | 1 | .579 |  |  |
| Fisher's Exact Test |  |  |  | .728 | .452 |
| Linear-by-Linear Association | .288 | 1 | .591 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 1 cells (25.0%) have expected count less than 5. The minimum expected count is 2.73. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

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| **Crosstab** | | | | | |
|  | | | [40-50] age group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 77 | 32 | 109 |
| % within mild+/ stage2 - 3 | 70.6% | 29.4% | 100.0% |
| Yes | Count | 33 | 8 | 41 |
| % within mild+/ stage2 - 3 | 80.5% | 19.5% | 100.0% |
| Total | | Count | 110 | 40 | 150 |
| % within mild+/ stage2 - 3 | 73.3% | 26.7% | 100.0% |

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| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 1.477a | 1 | .224 |  |  |
| Continuity Correctionb | 1.016 | 1 | .313 |  |  |
| Likelihood Ratio | 1.542 | 1 | .214 |  |  |
| Fisher's Exact Test |  |  |  | .301 | .157 |
| Linear-by-Linear Association | 1.467 | 1 | .226 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 10.93. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

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| **Crosstab** | | | | | |
|  | | | ]50-60] age group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 67 | 42 | 109 |
| % within mild+/ stage2 - 3 | 61.5% | 38.5% | 100.0% |
| Yes | Count | 23 | 18 | 41 |
| % within mild+/ stage2 - 3 | 56.1% | 43.9% | 100.0% |
| Total | | Count | 90 | 60 | 150 |
| % within mild+/ stage2 - 3 | 60.0% | 40.0% | 100.0% |

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| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | .358a | 1 | .550 |  |  |
| Continuity Correctionb | .169 | 1 | .681 |  |  |
| Likelihood Ratio | .356 | 1 | .551 |  |  |
| Fisher's Exact Test |  |  |  | .579 | .339 |
| Linear-by-Linear Association | .356 | 1 | .551 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 16.40. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

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| **Crosstab** | | | | | |
|  | | | ]60-70] age group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 92 | 17 | 109 |
| % within mild+/ stage2 - 3 | 84.4% | 15.6% | 100.0% |
| Yes | Count | 27 | 14 | 41 |
| % within mild+/ stage2 - 3 | 65.9% | 34.1% | 100.0% |
| Total | | Count | 119 | 31 | 150 |
| % within mild+/ stage2 - 3 | 79.3% | 20.7% | 100.0% |

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| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 6.253a | 1 | .012 |  |  |
| Continuity Correctionb | 5.173 | 1 | .023 |  |  |
| Likelihood Ratio | 5.832 | 1 | .016 |  |  |
| Fisher's Exact Test |  |  |  | .022 | .013 |
| Linear-by-Linear Association | 6.211 | 1 | .013 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 8.47. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

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| **Crosstab** | | | | | |
|  | | | ]70-80] age group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 91 | 18 | 109 |
| % within mild+/ stage2 - 3 | 83.5% | 16.5% | 100.0% |
| Yes | Count | 40 | 1 | 41 |
| % within mild+/ stage2 - 3 | 97.6% | 2.4% | 100.0% |
| Total | | Count | 131 | 19 | 150 |
| % within mild+/ stage2 - 3 | 87.3% | 12.7% | 100.0% |

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| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 5.335a | 1 | .021 |  |  |
| Continuity Correctionb | 4.139 | 1 | .042 |  |  |
| Likelihood Ratio | 6.914 | 1 | .009 |  |  |
| Fisher's Exact Test |  |  |  | .025 | .014 |
| Linear-by-Linear Association | 5.300 | 1 | .021 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 5.19. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

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| **Crosstab** | | | | | |
|  | | | {11] first of Menstrual period group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 95 | 14 | 109 |
| % within mild+/ stage2 - 3 | 87.2% | 12.8% | 100.0% |
| Yes | Count | 31 | 10 | 41 |
| % within mild+/ stage2 - 3 | 75.6% | 24.4% | 100.0% |
| Total | | Count | 126 | 24 | 150 |
| % within mild+/ stage2 - 3 | 84.0% | 16.0% | 100.0% |

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| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 2.955a | 1 | .086 |  |  |
| Continuity Correctionb | 2.159 | 1 | .142 |  |  |
| Likelihood Ratio | 2.763 | 1 | .096 |  |  |
| Fisher's Exact Test |  |  |  | .131 | .074 |
| Linear-by-Linear Association | 2.936 | 1 | .087 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 6.56. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

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| **Crosstab** | | | | | |
|  | | | [12] first of Menstrual period group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 79 | 30 | 109 |
| % within mild+/ stage2 - 3 | 72.5% | 27.5% | 100.0% |
| Yes | Count | 35 | 6 | 41 |
| % within mild+/ stage2 - 3 | 85.4% | 14.6% | 100.0% |
| Total | | Count | 114 | 36 | 150 |
| % within mild+/ stage2 - 3 | 76.0% | 24.0% | 100.0% |

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| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 2.713a | 1 | .100 |  |  |
| Continuity Correctionb | 2.053 | 1 | .152 |  |  |
| Likelihood Ratio | 2.917 | 1 | .088 |  |  |
| Fisher's Exact Test |  |  |  | .133 | .073 |
| Linear-by-Linear Association | 2.695 | 1 | .101 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 9.84. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

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| **Crosstab** | | | | | |
|  | | | [13] first of Menstrual period group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 87 | 22 | 109 |
| % within mild+/ stage2 - 3 | 79.8% | 20.2% | 100.0% |
| Yes | Count | 28 | 13 | 41 |
| % within mild+/ stage2 - 3 | 68.3% | 31.7% | 100.0% |
| Total | | Count | 115 | 35 | 150 |
| % within mild+/ stage2 - 3 | 76.7% | 23.3% | 100.0% |

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| --- | --- | --- | --- | --- | --- |
| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 2.212a | 1 | .137 |  |  |
| Continuity Correctionb | 1.614 | 1 | .204 |  |  |
| Likelihood Ratio | 2.121 | 1 | .145 |  |  |
| Fisher's Exact Test |  |  |  | .193 | .103 |
| Linear-by-Linear Association | 2.197 | 1 | .138 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 9.57. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

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| **Crosstab** | | | | | |
|  | | | [14] first of Menstrual period group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 84 | 25 | 109 |
| % within mild+/ stage2 - 3 | 77.1% | 22.9% | 100.0% |
| Yes | Count | 32 | 9 | 41 |
| % within mild+/ stage2 - 3 | 78.0% | 22.0% | 100.0% |
| Total | | Count | 116 | 34 | 150 |
| % within mild+/ stage2 - 3 | 77.3% | 22.7% | 100.0% |

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| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | .016a | 1 | .898 |  |  |
| Continuity Correctionb | .000 | 1 | 1.000 |  |  |
| Likelihood Ratio | .017 | 1 | .898 |  |  |
| Fisher's Exact Test |  |  |  | 1.000 | .543 |
| Linear-by-Linear Association | .016 | 1 | .898 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 9.29. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

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| **Crosstab** | | | | | |
|  | | | [15] first of Menstrual period group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 91 | 18 | 109 |
| % within mild+/ stage2 - 3 | 83.5% | 16.5% | 100.0% |
| Yes | Count | 38 | 3 | 41 |
| % within mild+/ stage2 - 3 | 92.7% | 7.3% | 100.0% |
| Total | | Count | 129 | 21 | 150 |
| % within mild+/ stage2 - 3 | 86.0% | 14.0% | 100.0% |

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| --- | --- | --- | --- | --- | --- |
| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 2.093a | 1 | .148 |  |  |
| Continuity Correctionb | 1.399 | 1 | .237 |  |  |
| Likelihood Ratio | 2.340 | 1 | .126 |  |  |
| Fisher's Exact Test |  |  |  | .191 | .115 |
| Linear-by-Linear Association | 2.079 | 1 | .149 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 5.74. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

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| **Crosstab** | | | | | | | | | |
|  | | | | [40-42] end and pre- end of Menstrual period group | | | | Total | |
| No | | Yes | |
| mild+/ stage2 - 3 | | No | Count | | 92 | | 17 | | 109 | |
| % within mild+/ stage2 - 3 | | 84.4% | | 15.6% | | 100.0% | |
| Yes | Count | | 33 | | 8 | | 41 | |
| % within mild+/ stage2 - 3 | | 80.5% | | 19.5% | | 100.0% | |
| Total | Count | | | 125 | | 25 | | 150 | |
| % within mild+/ stage2 - 3 | | | 83.3% | | 16.7% | | 100.0% | |

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| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | .329a | 1 | .566 |  |  |
| Continuity Correctionb | .107 | 1 | .743 |  |  |
| Likelihood Ratio | .321 | 1 | .571 |  |  |
| Fisher's Exact Test |  |  |  | .625 | .363 |
| Linear-by-Linear Association | .327 | 1 | .568 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 6.83. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

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| **Crosstab** | | | | | |
|  | | | [43-45] end and pre- end of Menstrual period group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 90 | 19 | 109 |
| % within mild+/ stage2 - 3 | 82.6% | 17.4% | 100.0% |
| Yes | Count | 32 | 9 | 41 |
| % within mild+/ stage2 - 3 | 78.0% | 22.0% | 100.0% |
| Total | | Count | 122 | 28 | 150 |
| % within mild+/ stage2 - 3 | 81.3% | 18.7% | 100.0% |

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| --- | --- | --- | --- | --- | --- |
| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | .401a | 1 | .527 |  |  |
| Continuity Correctionb | .158 | 1 | .691 |  |  |
| Likelihood Ratio | .391 | 1 | .532 |  |  |
| Fisher's Exact Test |  |  |  | .638 | .339 |
| Linear-by-Linear Association | .398 | 1 | .528 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 7.65. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

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| **Crosstab** | | | | | |
|  | | | [46-48] end and pre- end of Menstrual period group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 93 | 16 | 109 |
| % within mild+/ stage2 - 3 | 85.3% | 14.7% | 100.0% |
| Yes | Count | 31 | 10 | 41 |
| % within mild+/ stage2 - 3 | 75.6% | 24.4% | 100.0% |
| Total | | Count | 124 | 26 | 150 |
| % within mild+/ stage2 - 3 | 82.7% | 17.3% | 100.0% |

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| --- | --- | --- | --- | --- | --- |
| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 1.961a | 1 | .161 |  |  |
| Continuity Correctionb | 1.342 | 1 | .247 |  |  |
| Likelihood Ratio | 1.858 | 1 | .173 |  |  |
| Fisher's Exact Test |  |  |  | .225 | .125 |
| Linear-by-Linear Association | 1.948 | 1 | .163 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 7.11. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Crosstab** | | | | | |
|  | | | [49-51] end and pre- end of Menstrual period group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 78 | 31 | 109 |
| % within mild+/ stage2 - 3 | 71.6% | 28.4% | 100.0% |
| Yes | Count | 34 | 7 | 41 |
| % within mild+/ stage2 - 3 | 82.9% | 17.1% | 100.0% |
| Total | | Count | 112 | 38 | 150 |
| % within mild+/ stage2 - 3 | 74.7% | 25.3% | 100.0% |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | 2.035a | 1 | .154 |  |  |
| Continuity Correctionb | 1.479 | 1 | .224 |  |  |
| Likelihood Ratio | 2.153 | 1 | .142 |  |  |
| Fisher's Exact Test |  |  |  | .207 | .110 |
| Linear-by-Linear Association | 2.022 | 1 | .155 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 10.39. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Crosstab** | | | | | |
|  | | | [52-54] end and pre- end of Menstrual period group | | Total |
| No | Yes |
| mild+/ stage2 - 3 | No | Count | 83 | 26 | 109 |
| % within mild+/ stage2 - 3 | 76.1% | 23.9% | 100.0% |
| Yes | Count | 34 | 7 | 41 |
| % within mild+/ stage2 - 3 | 82.9% | 17.1% | 100.0% |
| Total | | Count | 117 | 33 | 150 |
| % within mild+/ stage2 - 3 | 78.0% | 22.0% | 100.0% |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Chi-Square Tests** | | | | | |
|  | Value | df | Asymptotic Significance (2-sided) | Exact Sig. (2-sided) | Exact Sig. (1-sided) |
| Pearson Chi-Square | .798a | 1 | .372 |  |  |
| Continuity Correctionb | .452 | 1 | .501 |  |  |
| Likelihood Ratio | .829 | 1 | .362 |  |  |
| Fisher's Exact Test |  |  |  | .508 | .254 |
| Linear-by-Linear Association | .793 | 1 | .373 |  |  |
| N of Valid Cases | 150 |  |  |  |  |
| a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 9.02. | | | | | |
| b. Computed only for a 2x2 table | | | | | |

Table26: Mild OI+/ low BMD(osteopenia =stage2, osteoporosis= stage3) \* parameters groups