

S1 Table. Top ten most significant common SNPs identified based on the univariable analyses and the subsequent multivariable analyses under the additive genetic models.

| SNP ID | Univariable | | Multivariable* | |
|-------------------------------|---------------------|----------|---------------------|----------|
| | OR (95% CI) | P-value | OR (95% CI) | P-value |
| rs11159673 (AG + 2*AA vs. GG) | 3.096 (1.879-5.073) | 7.11E-06 | 3.016 (1.766-5.138) | 4.53E-05 |
| rs7314811 (CT + 2*CC vs. TT) | 2.387 (1.611-3.567) | 1.67E-05 | 2.129 (1.409-3.242) | 3.59E-04 |
| rs4843335 (AG + 2*AA vs. GG) | 3.818 (2.040-7.037) | 1.97E-05 | 4.160 (2.130-8.107) | 2.64E-05 |
| rs10511330 (CT + 2*CC vs. TT) | 3.013 (1.788-5.031) | 2.59E-05 | 3.908 (2.211-6.945) | 2.65E-06 |
| rs12915222 (CT + 2*TT vs. CC) | 2.476 (1.623-3.801) | 2.76E-05 | 2.664 (1.685-4.260) | 3.19E-05 |
| rs12956191 (GA + 2*GG vs. AA) | 2.364 (1.580-3.549) | 2.86E-05 | 2.397 (1.555-3.726) | 8.18E-05 |
| rs11648965 (GA + 2*GG vs. AA) | 3.033 (1.786-5.104) | 3.04E-05 | 3.250 (1.867-5.671) | 2.82E-05 |
| rs16822593 (AG + 2*AA vs. GG) | 2.977 (1.767-4.968) | 3.11E-05 | 3.899 (2.205-6.930) | 2.78E-06 |
| rs205536 (CT + 2*CC vs. TT) | 2.494 (1.636-3.885) | 3.28E-05 | 2.681 (1.717-4.294) | 2.34E-05 |
| rs2384298 (CT + 2*CC vs. TT) | 2.332 (1.563-3.489) | 3.42E-05 | 2.406 (1.576-3.702) | 5.14E-05 |

CI: confidence interval, OR: odds ratio.

OR is the ratio of the odds of having mucinous tumors for one minor allele increase.

*Multivariable logistic regression model adjusting for the selected baseline characteristics listed in S5 Table.

S2 Table. Top ten most significant common SNPs identified based on the univariable analyses and the subsequent multivariable analysis under the dominant genetic models.

| SNP ID (a vs. b) | Univariable | | Multivariable* | |
|-----------------------------|------------------|----------|------------------|----------|
| | OR (95% CI) | P-value | OR (95% CI) | P-value |
| rs716897 (CC + CT vs. TT) | 0.27 (0.15-0.47) | 5.33E-06 | 0.26 (0.14-0.47) | 1.12E-05 |
| rs10511330 (CC + CT vs. TT) | 3.77 (2.06-6.81) | 1.24E-05 | 4.85 (2.54-9.23) | 1.40E-06 |
| rs11968293 (CC + CA vs. AA) | 0.28 (0.16-0.50) | 1.27E-05 | 0.26 (0.14-0.48) | 1.48E-05 |
| rs17712784 (AA + AG vs. GG) | 3.47 (1.97-6.12) | 1.54E-05 | 3.30 (1.80-6.06) | 1.12E-04 |
| rs13019215 (TT + TC vs. CC) | 0.27 (0.14-0.48) | 1.56E-05 | 0.23 (0.12-0.43) | 8.20E-06 |
| rs16822593 (AA + AG vs. GG) | 3.70 (2.02-6.68) | 1.59E-05 | 4.83 (2.53-9.20) | 1.50E-06 |
| rs12471607 (TT + TC vs. CC) | 0.27 (0.14-0.48) | 1.65E-05 | 0.23 (0.12-0.43) | 8.42E-06 |
| rs4843335 (AA + AG vs. GG) | 4.11 (2.11-7.79) | 2.06E-05 | 4.67 (2.30-9.34) | 1.48E-05 |
| rs11216624 (AA + AG vs. GG) | 3.56 (1.93-6.46) | 3.34E-05 | 3.07 (1.60-5.79) | 5.67E-04 |
| rs9809129 (AA + AG vs. GG) | 0.23 (0.11-0.45) | 4.78E-05 | 0.23 (0.10-0.45) | 6.52E-05 |

CI: confidence interval, OR: odds ratio.

OR compares the odds of having mucinous tumors in subgroup a to the odds of having mucinous tumors in subgroup b.

*Multivariable logistic regression model adjusting for the selected baseline characteristics listed in S5 Table.

S3 Table. Top ten most significant common SNPs identified based on the univariable analyses and the subsequent multivariable analyses under the recessive genetic models.

| SNP ID (a vs. b) | Univariable | | Multivariable* | |
|------------------------------|----------------------|----------|----------------------|----------|
| | OR (95% CI) | P-value | OR (95% CI) | P-value |
| rs9481067 (GG vs. AG + AA) | 4.171 (2.332-7.431) | 1.24E-06 | 4.747 (2.527-8.948) | 1.24E-06 |
| rs4837345 (TT vs. TC + CC) | 4.721 (2.403-9.052) | 4.00E-06 | 4.563 (2.242-9.107) | 1.97E-05 |
| kgp10457679 (CC vs. CT + TT) | 4.721 (2.403-9.052) | 4.00E-06 | 4.563 (2.242-9.107) | 1.97E-05 |
| kgp4136779 (TT vs. TC + CC) | 4.721 (2.403-9.052) | 4.00E-06 | 4.563 (2.242-9.107) | 1.97E-05 |
| rs1075650 (GG vs. AG + AA) | 4.721 (2.403-9.052) | 4.00E-06 | 4.563 (2.242-9.107) | 1.97E-05 |
| rs7314811 (CC vs. CT + TT) | 4.586 (2.338-8.772) | 5.66E-06 | 3.654 (1.746-7.425) | 4.15E-04 |
| rs6596805 (GG vs. AG + AA) | 3.862 (2.139-6.908) | 5.72E-06 | 3.683 (1.957-6.887) | 4.51E-05 |
| rs11047047 (GG vs. AG + AA) | 3.734 (2.104-6.613) | 5.92E-06 | 3.505 (1.908-6.426) | 4.79E-05 |
| rs1661281 (TT vs. TC + CC) | 5.284 (2.518-10.764) | 6.12E-06 | 5.403 (2.442-11.704) | 2.17E-05 |
| rs919001 (AA vs. AG + GG) | 3.913 (2.134-7.077) | 7.46E-06 | 3.151 (1.636-5.953) | 4.66E-04 |

CI: confidence interval, OR: odds ratio.

OR compares the odds of having mucinous tumors in subgroup a to the odds of having mucinous tumors in subgroup b.

*Multivariable logistic regression model adjusting for the selected baseline characteristics listed in S5 Table.

S4 Table. Top ten most significant common SNPs identified under the univariable analyses and the subsequent multivariable analyses under the co-dominant genetic models.

| SNP ID (a vs. b) | Univariable | | Multivariable* | |
|------------------------|----------------------|----------|----------------------|----------|
| | OR (95% CI) | P-value | OR (95% CI) | P-value |
| rs7314811 (CC vs. TT) | 5.974 (2.803-12.805) | 3.48E-06 | 4.788 (2.109-10.853) | 1.63E-04 |
| rs16907305 (AA vs. GG) | 5.550 (2.611-11.857) | 7.91E-06 | 4.505 (1.994-10.162) | 2.66E-04 |
| rs11216624 (AG vs. GG) | 3.872 (2.092-7.050) | 1.15E-05 | 3.326 (1.727-6.302) | 2.57E-04 |
| rs17712784 (AG vs. GG) | 3.520 (1.988-6.243) | 1.50E-05 | 3.304 (1.788-6.106) | 1.28E-04 |
| rs6573132 (AG vs. GG) | 4.814 (2.308-9.722) | 1.62E-05 | 5.183 (2.382-11.030) | 2.27E-05 |
| rs8019850 (TC vs. CC) | 4.802 (2.302-9.699) | 1.67E-05 | 5.011 (2.310-10.619) | 3.07E-05 |
| rs17093005 (TG vs. GG) | 4.802 (2.302-9.699) | 1.67E-05 | 5.098 (2.345-10.828) | 2.66E-05 |
| rs11656626 (GG vs. AA) | 7.194 (2.866-17.642) | 1.72E-05 | 7.156 (2.675-18.933) | 6.94E-05 |
| rs1189903 (AC vs. CC) | 4.759 (2.284-9.589) | 1.78E-05 | 4.952 (2.283-10.488) | 3.47E-05 |
| rs4779810 (TT vs. CC) | 5.965 (2.608-13.499) | 1.79E-05 | 4.286 (1.731-10.343) | 1.30E-03 |

CI: confidence interval, OR: odds ratio.

OR compares the odds of having mucinous tumors in subgroup a to the odds of having mucinous tumors in subgroup b.

*Multivariable logistic regression model adjusting for the selected baseline characteristics listed in S5 Table.

S5 Table. Baseline characteristics selected through a stepwise variable selection method under the multivariable model.

| Characteristics | | OR (95% CI) | P-value |
|-----------------|-----------------------|-------------------|---------|
| Age | ≤60 | | |
| | 60-65 | 2.29 (1.08-4.81) | 0.018 |
| | >65 | 1.19 (0.60-2.37) | 0.611 |
| Sex | Female | | |
| | Male | 0.58 (0.32-1.04) | 0.067 |
| Location | Colon | | |
| | Rectum | 0.45 (0.21-0.90) | 0.031 |
| Stage | I | | |
| | II | 4.41 (1.48-18.98) | 0.018 |
| | III | 3.65 (1.18-16.02) | 0.044 |
| | IV | 4.57 (1.18-22.43) | 0.036 |
| Grade | Well/moderately diff. | | |
| | Poorly diff. | 1.90 (0.70-4.54) | 0.169 |

CI: confidence interval, diff.: differentiated.

OR: odds ratio (compares the odds of having mucinous tumors with the corresponding factor level to the odds of having mucinous tumors with the reference factor level).

S6 Table. AIC estimates under the multivariable models of common SNPs identified in the univariable analysis.

| SNP ID | Initial Model | AIC | | | | Plausible Model | P-value** |
|----------------------|---------------|-------|-------|-------|-------|-----------------|-----------|
| | | A* | D* | R* | C* | | |
| rs9481067 | Recessive | 322.4 | 336.5 | 318.4 | 320.2 | Recessive | 1.24E-06 |
| rs10511330 | Dominant | 320.1 | 319.2 | 338.6 | 321.0 | Dominant | 1.40E-06 |
| rs16822593 | Dominant | 320.2 | 319.3 | 338.6 | 321.1 | Dominant | 1.50E-06 |
| rs13019215 | Dominant | 319.0 | 318.6 | 336.5 | 320.2 | Dominant | 8.20E-06 |
| rs12471607 | Dominant | 318.9 | 318.6 | 336.4 | 320.1 | Dominant | 8.42E-06 |
| rs716897 | Dominant | 323.4 | 321.2 | 337.0 | 323.0 | Dominant | 1.12E-05 |
| rs4843335 | Dominant | 324.5 | 324.1 | 339.9 | 326.0 | Dominant | 1.48E-05 |
| rs11968293 | Dominant | 327.2 | 322.4 | 338.9 | 324.4 | Dominant | 1.48E-05 |
| rs4837345 | Recessive | 333.9 | 340.5 | 324.6 | 325.7 | Recessive | 1.97E-05 |
| kgp10457679 | Recessive | 333.9 | 340.5 | 324.6 | 325.7 | Recessive | 1.97E-05 |
| kgp4136779 | Recessive | 333.9 | 340.5 | 324.6 | 325.7 | Recessive | 1.97E-05 |
| rs1075650 | Recessive | 334.1 | 340.6 | 324.6 | 325.6 | Recessive | 1.97E-05 |
| rs1661281 | Recessive | 338.2 | 340.8 | 324.9 | 322.7 | Recessive | 2.17E-05 |
| rs6573132[1] | Co-Dominant | 334.3 | 328.9 | 339.0 | 325.0 | Co-Dominant | 2.27E-05 |
| rs205536 | Additive | 321.3 | 330.3 | 326.0 | 323.3 | Additive | 2.34E-05 |
| rs17093005[1] | Co-Dominant | 334.2 | 328.9 | 338.8 | 325.1 | Co-Dominant | 2.66E-05 |
| rs11648965 | Additive | 324.4 | 325.2 | 336.7 | 326.3 | Additive | 2.82E-05 |
| rs8019850[1] | Co-Dominant | 334.4 | 329.2 | 338.9 | 325.4 | Co-Dominant | 3.07E-05 |
| rs12915222 | Additive | 323.5 | 327.9 | 331.9 | 325.5 | Additive | 3.19E-05 |
| rs1189903[1] | Co-Dominant | 328.0 | 323.4 | 334.2 | 320.9 | Co-Dominant | 3.47E-05 |
| rs6596805 | Recessive | 331.2 | 339.6 | 325.3 | 327.1 | Recessive | 4.51E-05 |
| rs11159673 | Additive | 325.5 | 329.4 | 331.1 | 326.8 | Additive | 4.53E-05 |
| rs11047047 | Recessive | 328.4 | 338.3 | 325.2 | 327.1 | Recessive | 4.79E-05 |
| rs2384298 | Additive | 323.3 | 324.0 | 333.6 | 324.5 | Additive | 5.14E-05 |
| rs9809129 | Dominant | 319.6 | 321.4 | 335.0 | 321.0 | Additive | 6.52E-05 |
| rs11656626[2] | Co-Dominant | 331.5 | 337.6 | 326.6 | 328.3 | Recessive | 6.94E-05 |
| rs12956191 | Additive | 325.5 | 330.0 | 331.2 | 327.4 | Additive | 8.18E-05 |
| rs17712784 | Dominant | 327.6 | 326.5 | 340.7 | 328.5 | Dominant | 1.12E-04 |
| rs7314811[2] | Co-Dominant | 328.2 | 334.1 | 329.8 | 329.4 | Additive | 1.63E-04 |
| rs16907305[2] | Co-Dominant | 329.1 | 334.8 | 330.3 | 330.3 | Additive | 2.66E-04 |
| rs919001 | Recessive | 330.4 | 337.4 | 329.7 | 331.0 | Recessive | 4.66E-04 |
| rs11216624 | Dominant | 332.7 | 330.0 | 339.9 | 329.5 | Co-Dominant | 5.67E-04 |
| rs4779810[2] | Co-Dominant | 330.5 | 333.7 | 334.5 | 332.5 | Additive | 1.30E-03 |

*A: Additive, D: Dominant, R: Recessive, C: Co-dominant.

**p-value under the multivariable model based on the initial genetic model.

[1]: heterozygous genotype/major allele homozygous genotype.

[2]: minor allele homozygous genotype/major allele homozygous genotype.

The SNPs in bold were identified under their plausible genetic model.

S7 Table. Haploreg results for the top 10 SNPs in the common variant analysis.

| SNP ID | chr | r2 | D' | rs ID | GENCODE_name |
|-------------------|-----|------|-------|-------------|---------------|
| rs10819474 | 9 | 0.92 | 0.96 | rs4837345 | PPP2R4 |
| | 9 | 0.91 | 0.96 | rs192983 | IER5L |
| | 9 | 0.9 | -0.97 | rs944072 | IER5L |
| | 9 | 0.86 | -0.99 | rs10819473 | IER5L |
| | 9 | 0.94 | -0.99 | rs1966223 | IER5L |
| | 9 | 0.94 | -0.99 | rs1966222 | IER5L |
| | 9 | 0.99 | 1 | rs12057089 | IER5L |
| | 9 | 1 | 1 | rs10819474 | IER5L |
| | 9 | 1 | 1 | rs10819475 | IER5L |
| | 9 | 1 | 1 | rs419636 | IER5L |
| | 9 | 0.96 | -1 | rs12237274 | IER5L |
| | 9 | 0.9 | -0.99 | rs10739743 | IER5L |
| | 9 | 0.88 | -0.99 | rs4837346 | IER5L |
| | 9 | 0.94 | -0.99 | rs1556147 | IER5L |
| | 9 | 0.97 | 0.99 | rs141780496 | IER5L |
| | 9 | 0.97 | 0.99 | rs1075650 | IER5L |
| | 9 | 0.97 | 0.99 | rs184457 | IER5L |
| | 9 | 0.93 | 0.97 | rs882616 | RP11-247A12.2 |
| | 9 | 0.93 | -0.99 | rs7034195 | RP11-247A12.2 |
| | 9 | 0.91 | -0.99 | rs2005078 | RP11-247A12.2 |
| | 9 | 0.83 | -0.93 | rs967497 | RP11-247A12.2 |
| | 9 | 0.85 | 0.95 | rs913264 | RP11-247A12.2 |
| | 9 | 0.83 | -0.93 | rs4837347 | RP11-247A12.2 |
| | 9 | 0.82 | -0.92 | rs7871824 | RP11-247A12.2 |
| rs716897 | 5 | 1 | 1 | rs716897 | RASGRF2 |
| rs4843335 | 16 | 0.96 | 0.98 | rs7500355 | RP11-805I24.1 |
| | 16 | 1 | 1 | rs4843335 | RP11-805I24.1 |
| rs4837345 | 9 | 0.8 | 0.94 | rs9408986 | PPP2R4 |
| | 9 | 0.8 | 0.94 | rs71497442 | PPP2R4 |
| | 9 | 0.8 | 0.94 | rs4836641 | PPP2R4 |
| | 9 | 0.8 | 0.94 | rs1107329 | PPP2R4 |
| | 9 | 1 | 1 | rs4837345 | PPP2R4 |
| | 9 | 0.97 | 1 | rs192983 | IER5L |
| | 9 | 0.95 | -1 | rs944072 | IER5L |
| | 9 | 0.82 | -0.97 | rs10819473 | IER5L |
| | 9 | 0.9 | -0.97 | rs1966223 | IER5L |
| | 9 | 0.9 | -0.97 | rs1966222 | IER5L |
| | 9 | 0.91 | 0.95 | rs12057089 | IER5L |
| | 9 | 0.92 | 0.96 | rs10819474 | IER5L |
| | 9 | 0.92 | 0.96 | rs10819475 | IER5L |
| | 9 | 0.92 | 0.96 | rs419636 | IER5L |
| | 9 | 0.89 | -0.97 | rs12237274 | IER5L |
| | 9 | 0.83 | -0.95 | rs10739743 | IER5L |
| | 9 | 0.81 | -0.95 | rs4837346 | IER5L |
| | 9 | 0.87 | -0.95 | rs1556147 | IER5L |

| | | | | | |
|-------------------|---|------|-------|-------------|---------------|
| | 9 | 0.89 | 0.95 | rs141780496 | IER5L |
| | 9 | 0.89 | 0.95 | rs1075650 | IER5L |
| | 9 | 0.89 | 0.95 | rs184457 | IER5L |
| | 9 | 0.86 | 0.93 | rs882616 | RP11-247A12.2 |
| | 9 | 0.87 | -0.95 | rs7034195 | RP11-247A12.2 |
| | 9 | 0.84 | -0.95 | rs2005078 | RP11-247A12.2 |
| rs9481067 | 6 | 1 | 1 | rs9481067 | SLC22A16 |
| | 6 | 0.99 | 1 | rs910399 | SLC22A16 |
| rs13019215 | 6 | 1 | 1 | rs761589 | SLC22A16 |
| | 2 | 1 | 1 | rs13019215 | CCDC141 |
| | 2 | 0.94 | 1 | rs11680978 | CCDC141 |
| | 2 | 0.93 | 1 | rs150840830 | CCDC141 |
| rs12471607 | 2 | 0.93 | 1 | rs10930850 | CCDC141 |
| | 2 | 0.92 | 0.99 | rs12471607 | CCDC141 |
| | 2 | 0.92 | 0.99 | rs13019215 | CCDC141 |
| | 2 | 0.98 | 0.99 | rs11680978 | CCDC141 |
| | 2 | 0.98 | 0.99 | rs150840830 | CCDC141 |
| | 2 | 0.98 | 0.99 | rs10930850 | CCDC141 |
| rs10511330 | 2 | 1 | 1 | rs12471607 | CCDC141 |
| | 3 | 0.92 | 0.96 | rs16822588 | ZBTB20 |
| | 3 | 0.95 | 0.99 | rs16822593 | ZBTB20 |
| | 3 | 0.97 | 0.99 | rs73857113 | ZBTB20 |
| | 3 | 1 | 1 | rs6763403 | ZBTB20 |
| | 3 | 1 | 1 | rs10511330 | ZBTB20 |
| rs16822593 | 3 | 0.94 | 0.97 | rs73860251 | ZBTB20 |
| | 3 | 0.91 | 0.97 | rs16822606 | ZBTB20 |
| | 3 | 0.91 | 0.97 | rs7428451 | ZBTB20 |
| | 3 | 0.9 | 0.96 | rs6778079 | ZBTB20 |
| | 3 | 0.9 | 0.96 | rs6792964 | ZBTB20 |
| | 3 | 0.9 | 0.96 | rs6793257 | ZBTB20 |
| | 3 | 0.9 | 0.96 | rs57864250 | ZBTB20 |
| | 3 | 0.9 | 0.96 | rs73857603 | ZBTB20 |
| | 3 | 0.9 | 0.96 | rs6785090 | ZBTB20 |
| | 3 | 0.9 | 0.96 | rs73857605 | ZBTB20 |
| | 3 | 0.9 | 0.96 | rs2067756 | ZBTB20 |
| | 3 | 0.97 | 1 | rs16822588 | ZBTB20 |
| | 3 | 1 | 1 | rs16822593 | ZBTB20 |
| | 3 | 0.97 | 1 | rs73857113 | ZBTB20 |
| | 3 | 0.95 | 0.99 | rs6763403 | ZBTB20 |
| | 3 | 0.95 | 0.99 | rs10511330 | ZBTB20 |
| | 3 | 0.88 | 0.95 | rs73860251 | ZBTB20 |
| | 3 | 0.86 | 0.93 | rs16822606 | ZBTB20 |
| | 3 | 0.86 | 0.93 | rs7428451 | ZBTB20 |
| | 3 | 0.85 | 0.92 | rs6778079 | ZBTB20 |
| | 3 | 0.85 | 0.92 | rs6792964 | ZBTB20 |
| | 3 | 0.85 | 0.92 | rs6793257 | ZBTB20 |
| | 3 | 0.85 | 0.92 | rs57864250 | ZBTB20 |
| | 3 | 0.85 | 0.92 | rs73857603 | ZBTB20 |

| | | | | | |
|-------------------|---|------|------|------------|--------------------|
| rs11968293 | 3 | 0.85 | 0.92 | rs6785090 | ZBTB20 |
| | 3 | 0.85 | 0.92 | rs73857605 | ZBTB20 |
| | 3 | 0.85 | 0.92 | rs2067756 | ZBTB20 |
| | 6 | 0.9 | 0.98 | rs10708664 | SLC35F1 |
| | 6 | 0.88 | 0.99 | rs6940985 | SLC35F1 |
| | 6 | 1 | 1 | rs11968293 | SLC35F1 |
| | 6 | 1 | 1 | rs1572226 | SLC35F1 |
| | 6 | 0.85 | 0.97 | rs72967533 | 16kb 3' of SLC35F1 |
| | 6 | 0.82 | 0.93 | rs11153730 | 29kb 3' of SLC35F1 |

To retrieve the data, we used the default conditions and selected the CEU (Caucasian) as the population.

Chr: chromosome, r²: correlation coefficient,

D': ratio of given and min/max coefficient of linkage disequilibrium depending on allele frequencies.

S8 Table. Proteins which have reported evidence of binding to the genomic region in which kgp10457679 resides (extracted from RegulomeDB).

| Location | Bound Protein |
|--------------------------|---------------|
| chr9:131930083-131930707 | PHF8 |
| chr9:131930124-131930734 | POLR2A |
| chr9:131930177-131930837 | SMARCB1 |
| chr9:131930235-131930775 | EP300 |
| chr9:131930398-131930728 | EP300 |
| chr9:131930394-131930710 | EP300 |
| chr9:131930310-131930710 | FOS |
| chr9:131930295-131930751 | GTF2F1 |
| chr9:131930295-131930751 | JUND |
| chr9:131930321-131930661 | JUN |
| chr9:131930369-131930709 | JUN |
| chr9:131930291-131930687 | MAX |
| chr9:131930308-131930772 | POLR2A |
| chr9:131930314-131930520 | POLR2A |
| chr9:131930373-131930729 | RCOR1 |
| chr9:131930379-131930709 | RFX5 |
| chr9:131930359-131930715 | TAF1 |
| chr9:131930275-131930711 | UBTF |
| chr9:131930369-131930679 | IRF1 |
| chr9:131930380-131930700 | JUND |
| chr9:131930343-131930699 | MAX |
| chr9:131930332-131930702 | MAZ |
| chr9:131930374-131930684 | MYC |
| chr9:131930403-131930699 | RCOR1 |
| chr9:131930351-131930667 | YY1 |
| chr9:131930381-131930677 | JUN |
| chr9:131930388-131930672 | FOS |
| chr9:131930392-131930656 | CEBPB |
| chr9:131930395-131930671 | JUND |
| chr9:131930405-131930655 | FOS |
| chr9:131930406-131930666 | FOSL2 |
| chr9:131930420-131930656 | BACH1 |
| chr9:131930423-131930659 | ATF3 |
| chr9:131930419-131930649 | JUN |
| chr9:131930417-131930627 | MAFF |
| chr9:131930376-131930666 | USF2 |
| chr9:131930451-131930567 | MAFK |
| chr9:131930484-131930584 | FOS |
| chr9:131930489-131930574 | FOS |
| chr9:131930462-131930577 | NFE2 |
| chr9:131930433-131930605 | FOSL2 |
| chr9:131930433-131930610 | MAFF |
| chr9:131930436-131930602 | MAFK |

| | |
|--------------------------|--------|
| chr9:131930442-131930598 | MAFK |
| chr9:131930432-131930604 | MAFK |
| chr9:131930210-131930654 | POLR2A |
| chr9:131930433-131930663 | FOSL1 |
| chr9:131930443-131930622 | BACH1 |
| chr9:131930438-131930615 | MAFK |
