Supplemental Table 1: Genetic variants in *Hp1bp3* across the BXDs.

All sequence polymorphisms and structural variants (insertions/deletions) between the reference sequence (B6) and parental strain D2 according to the Sanger Insititute's Mouse Genomes Project. Those variants predicted to have 'moderate' impact on transcript structure, splicing, and/or protein function according to the Ensembl Variant Effect Predictor are highlighted in red.

| Chr | Position | Gene | dbSNP | Ref | DBA_2J | Consequence | Predicted Impact |
|---|---|---|---|---|---|---|---|
| 4 | 138216326 | Hp1bp3 | rs260379634 | C | G* | 5_prime_utr_variant upstream_gene_variant downstr | MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138216606 | Hp1bp3 | rs249561826 | T | C* | 5_prime_utr_variant upstream_gene_variant downstr | MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138216882 | Hp1bp3 | rs264114702 | G | A* | intron_variant upstream_gene_variant downstream_g | MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138216964 | Hp1bp3 | rs249512381 | T | C* | intron_variant upstream_gene_variant downstream_g | MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138217113 | Hp1bp3 | rs228537698 | T | C* | intron_variant upstream_gene_variant downstream_g | MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138217421 | Hp1bp3 | rs258034730 | A | G* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138217890 | Hp1bp3 | rs27561944 | G | A* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138217988 | Hp1bp3 | rs27561943 | G | A* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138218390 | Hp1bp3 | rs32579151 | G | T* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138218488 | Hp1bp3 | rs27561942 | T | C* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138218495 | Hp1bp3 | rs27561941 | G | C* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138218530 | Hp1bp3 | rs27561940 | G | A* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138218653 | Hp1bp3 | rs27561939 | T | C* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138218842 | Hp1bp3 | rs32813154 | T | C* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138218871 | Hp1bp3 | rs27561938 | C | T* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138218989 | Hp1bp3 | rs27561937 | G | A* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138219328 | Hp1bp3 | rs27561936 | G | A* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138219372 | Hp1bp3 | rs27561935 | T | C* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138219440 | Hp1bp3 | rs32156789 | G | T* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138219586 | Hp1bp3 | rs27561934 | A | G* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138219753 | Hp1bp3 | rs50804257 | T | C* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138219764 | Hp1bp3 | rs46494031 | C | A* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138219802 | Hp1bp3 | rs32543755 | G | A* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138220057 | Hp1bp3 | rs27561933 | C | T* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138220297 | Hp1bp3 | rs27561932 | C | T* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138221216 | Hp1bp3 | rs27561931 | G | T* | intron_variant _ | LOW |
| 4 | 138221304 | Hp1bp3 | rs31894288 | C | T* | intron_variant _ | LOW |
| 4 | 138221306 | Hp1bp3 | rs27561930 | T | C* | intron_variant _ | LOW |
| 4 | 138221340 | Hp1bp3 | rs27561929 | G | A* | intron_variant _ | LOW |
| 4 | 138221478 | Hp1bp3 | rs27561928 | T | C* | intron_variant _ | LOW |
| 4 | 138221496 | Hp1bp3 | rs51709295 | T | C* | intron_variant _ | LOW |
| 4 | 138221507 | Hp1bp3 | rs27561927 | C | A* | intron_variant _ | LOW |
| 4 | 138221639 | Hp1bp3 | rs13460658 | T | C* | synonymous_variant intron_variant _ | LOW |
| 4 | 138221935 | Hp1bp3 | rs50541458 | T | A* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138221995 | Hp1bp3 | rs3714652 | A | T* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138222006 | Hp1bp3 | rs3714683 | T | C* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138222265 | Hp1bp3 | rs27561926 | T | C* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138222317 | Hp1bp3 | rs27561925 | A | G* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138222368 | Hp1bp3 | rs27561924 | A | T* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138222386 | Hp1bp3 | rs31777655 | T | A* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138222700 | Hp1bp3 | rs27561921 | C | G* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138223180 | Hp1bp3 | rs32709312 | C | T* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138223239 | Hp1bp3 | rs27561920 | A | G* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138223345 | Hp1bp3 | rs27561919 | A | G* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138223483 | Hp1bp3 | rs27561918 | A | G* | splice_region_variant intron_variant downstream_ger | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138223622 | Hp1bp3 | rs27561917 | A | G* | missense_variant upstream_gene_variant downstrea | MODERATE |
| 4 | 138223678 | Hp1bp3 | rs31891751 | T | G* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138223718 | Hp1bp3 | rs47358365 | G | C* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138223774 | Hp1bp3 | rs51940989 | T | C* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138223930 | Hp1bp3 | rs51522878 | A | G* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138223932 | Hp1bp3 | rs46819709 | T | A* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138223974 | Hp1bp3 | rs27561916 | C | G* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138224013 | Hp1bp3 | rs47607176 | C | A* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138224071 | Hp1bp3 | rs255773552 | C | A* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138224131 | Hp1bp3 | rs229582955 | A | T* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138224157 | Hp1bp3 | rs215445878 | A | g* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138224168 | Hp1bp3 | - | G | g/c* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138224177 | Hp1bp3 | rs213746275 | T | t/c* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138224183 | Hp1bp3 | - | C | c/a* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138224331 | Hp1bp3 | rs46382517 | C | G* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138224350 | Hp1bp3 | rs46481928 | T | C* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138224651 | Hp1bp3 | rs50744670 | A | T* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138225001 | Hp1bp3 | rs247357327 | C | c/a* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138225300 | Hp1bp3 | rs32826042 | G | A* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138225487 | Hp1bp3 | rs27561915 | T | C* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138225550 | Hp1bp3 | rs32836020 | C | T* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138225699 | Hp1bp3 | rs32219941 | G | T* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138225729 | Hp1bp3 | rs32895752 | T | C* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138225824 | Hp1bp3 | rs27561913 | G | A* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138225855 | Hp1bp3 | rs27561912 | T | G* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138226164 | Hp1bp3 | rs27561911 | C | G* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138226374 | Hp1bp3 | rs52311263 | G | C* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138226603 | Hp1bp3 | rs27561909 | A | T* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138226727 | Hp1bp3 | rs32054202 | T | C* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138226775 | Hp1bp3 | rs32011533 | G | A* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138226861 | Hp1bp3 | rs32683801 | T | G* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138226876 | Hp1bp3 | rs31904113 | G | A* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138227064 | Hp1bp3 | rs27561908 | G | A* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138227190 | Hp1bp3 | rs27561907 | G | A* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138227223 | Hp1bp3 | rs27561906 | G | A* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138227251 | Hp1bp3 | rs46997968 | G | A* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138227442 | Hp1bp3 | rs49365344 | A | G* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138227700 | Hp1bp3 | rs27561905 | A | G* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138227781 | Hp1bp3 | rs32564962 | C | G* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138227928 | Hp1bp3 | rs52228715 | G | C* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138228393 | Hp1bp3 | rs27561903 | C | A* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138228470 | Hp1bp3 | rs46938168 | T | A* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138228633 | Hp1bp3 | rs27561901 | G | A* | missense_variant intron_variant upstream_gene_vari | MODERATE |
| 4 | 138228709 | Hp1bp3 | rs48140976 | G | T* | synonymous_variant upstream_gene_variant downstı | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138228717 | Hp1bp3 | rs49484233 | G | A* | missense_variant upstream_gene_variant downstrea | MODERATE |
| 4 | 138228739 | Hp1bp3 | rs49645824 | G | C* | synonymous_variant upstream_gene_variant downstı | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138228742 | Hp1bp3 | rs47783718 | C | T* | synonymous_variant upstream_gene_variant downstı | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138228751 | Hp1bp3 | rs46245848 | G | A* | synonymous_variant upstream_gene_variant downstı | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138228783 | Hp1bp3 | rs48651274 | G | A* | missense_variant upstream_gene_variant downstrea | MODERATE |
| 4 | 138228794 | Hp1bp3 | rs49785036 | C | G* | splice_region_variant intron_variant upstream_gene | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138228803 | Hp1bp3 | rs48379430 | G | A* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |

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|---|---|---|---|---|---|---|---|
| 4 | 138228818 | Hp1bp3 | - | C | t* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138228856 | Hp1bp3 | rs27561900 | C | G* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138228883 | Hp1bp3 | rs27561899 | G | A* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138228924 | Hp1bp3 | rs27561898 | C | T* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138229092 | Hp1bp3 | rs50526110 | A | G* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138229194 | Hp1bp3 | rs27561897 | G | A* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138229213 | Hp1bp3 | rs47160765 | G | A* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138229365 | Hp1bp3 | rs27561895 | C | T* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138229515 | Hp1bp3 | rs32939611 | T | C* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138229565 | Hp1bp3 | rs27561894 | T | C* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138229608 | Hp1bp3 | rs27561893 | C | T* | intron_variant upstream_gene_variant downstream_g | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138229859 | Hp1bp3 | rs31758148 | C | T* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138229948 | Hp1bp3 | rs27561891 | C | G* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138230132 | Hp1bp3 | rs27561890 | A | G* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138230230 | Hp1bp3 | rs52146751 | A | G* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138230290 | Hp1bp3 | rs27561889 | C | T* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138230321 | Hp1bp3 | rs27561888 | C | T* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138230355 | Hp1bp3 | rs27561887 | G | A* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138230648 | Hp1bp3 | rs45929530 | T | A* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138231048 | Hp1bp3 | rs107825535 | A | G* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138231109 | Hp1bp3 | - | G | g/a* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138231176 | Hp1bp3 | - | A | g* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138231217 | Hp1bp3 | rs586398641 | A | a/g* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138231294 | Hp1bp3 | - | A | G* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138231352 | Hp1bp3 | rs27561882 | A | T* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138231448 | Hp1bp3 | rs27561881 | T | C* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138231724 | Hp1bp3 | rs32898813 | T | C* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138231762 | Hp1bp3 | rs32529955 | G | A* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138231914 | Hp1bp3 | rs27561880 | C | T* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138231941 | Hp1bp3 | rs32851338 | C | T* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138231944 | Hp1bp3 | rs32895179 | G | A* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138232083 | Hp1bp3 | rs27561878 | T | G* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138232106 | Hp1bp3 | rs27561877 | C | T* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138232256 | Hp1bp3 | rs27561876 | T | C* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138232284 | Hp1bp3 | rs27561875 | G | A* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138232313 | Hp1bp3 | rs27561874 | T | C* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138232432 | Hp1bp3 | rs27561872 | A | G* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138232499 | Hp1bp3 | rs27561870 | G | A* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138232549 | Hp1bp3 | rs27561869 | T | C* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138232755 | Hp1bp3 | rs27561868 | A | C* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138232817 | Hp1bp3 | rs27561866 | C | T* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138232823 | Hp1bp3 | rs27561865 | T | C* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138232877 | Hp1bp3 | rs27561863 | A | G* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138232950 | Hp1bp3 | rs46358525 | G | A* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138233066 | Hp1bp3 | rs49442108 | T | A* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138233067 | Hp1bp3 | rs47188322 | T | C* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138233110 | Hp1bp3 | rs27561862 | G | A* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138233460 | Hp1bp3 | rs51099382 | A | G* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138233515 | Hp1bp3 | rs27561861 | T | C* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138233831 | Hp1bp3 | rs52038410 | A | T* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138234499 | Hp1bp3 | rs27561858 | T | C* | intron_variant downstream_gene_variant _ | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138234878 | Hp1bp3 | rs32057335 | A | G* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138234884 | Hp1bp3 | rs27561857 | G | C* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138235537 | Hp1bp3 | rs27561855 | T | C* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138235820 | Hp1bp3 | rs27561854 | C | T* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138235910 | Hp1bp3 | rs27561853 | T | C* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138236092 | Hp1bp3 | rs31833434 | A | T* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138236243 | Hp1bp3 | rs27561852 | A | G* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138236257 | Hp1bp3 | rs27561851 | T | C* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138236278 | Hp1bp3 | rs27561850 | T | C* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138236355 | Hp1bp3 | rs27561849 | A | G* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138236873 | Hp1bp3 | rs27561848 | T | A* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138237172 | Hp1bp3 | rs32855308 | C | T* | synonymous_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138237329 | Hp1bp3 | rs27561846 | T | C* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138237348 | Hp1bp3 | rs27561845 | A | G* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138237433 | Hp1bp3 | rs27561843 | G | A* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138237655 | Hp1bp3 | rs46975598 | C | T* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138237839 | Hp1bp3 | rs27561842 | A | G* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138238537 | Hp1bp3 | rs235030201 | A | G* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138238552 | Hp1bp3 | rs47425034 | T | C* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138238560 | Hp1bp3 | rs32857872 | T | G* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138238571 | Hp1bp3 | rs47447018 | A | C* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138238572 | Hp1bp3 | rs47802811 | A | G* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138238589 | Hp1bp3 | rs52464059 | A | G* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138238600 | Hp1bp3 | rs52467386 | A | G* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138238639 | Hp1bp3 | rs27561840 | T | G* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138238703 | Hp1bp3 | rs211907094 | C | T* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138238873 | Hp1bp3 | rs51969587 | C | T* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138238918 | Hp1bp3 | rs50836126 | T | G* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138239121 | Hp1bp3 | rs27561839 | A | G* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138239681 | Hp1bp3 | rs27561838 | C | T | intron_variant | LOW |
| 4 | 138239861 | Hp1bp3 | rs27561837 | G | A | intron_variant | LOW |
| 4 | 138240106 | Hp1bp3 | rs27561836 | G | T | intron_variant | LOW |
| 4 | 138240122 | Hp1bp3 | rs27561835 | T | C | intron_variant | LOW |
| 4 | 138240432 | Hp1bp3 | rs50474080 | A | C | intron_variant | LOW |
| 4 | 138240441 | Hp1bp3 | rs32859446 | T | C | intron_variant | LOW |
| 4 | 138240663 | Hp1bp3 | rs13460661 | C | T | synonymous_variant | LOW |
| 4 | 138240675 | Hp1bp3 | rs13460659 | A | C | missense_variant | MODERATE |
| 4 | 138241056 | Hp1bp3 | rs31901529 | C | G* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138241061 | Hp1bp3 | rs32685251 | T | C* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138241171 | Hp1bp3 | rs31824005 | T | G* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138241255 | Hp1bp3 | rs33029512 | G | C* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138241384 | Hp1bp3 | rs27561830 | A | C* | intron_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138241575 | Hp1bp3 | rs13460660 | A | G* | synonymous_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138241784 | Hp1bp3 | rs27561829 | C | T* | 3_prime_utr_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138242037 | Hp1bp3 | rs27561828 | A | G* | 3_prime_utr_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138242068 | Hp1bp3 | rs27561827 | C | T* | 3_prime_utr_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138242553 | Hp1bp3 | rs13460655 | T | G* | 3_prime_utr_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138243313 | Hp1bp3 | - | A | C* | 3_prime_utr_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138243314 | Hp1bp3 | rs32758310 | G | A* | 3_prime_utr_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138243551 | Hp1bp3 | rs50718000 | G | A* | 3_prime_utr_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |

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|---|---|---|---|---|---|---|---|
| 4 | 138243679 | Hp1bp3 | rs49258114 | G | A* | 3_prime_utr_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138243981 | Hp1bp3 | rs27561826 | T | A* | 3_prime_utr_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138244059 | Hp1bp3 | rs27561825 | G | A* | 3_prime_utr_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138244063 | Hp1bp3 | rs48595395 | C | T* | 3_prime_utr_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138244156 | Hp1bp3 | rs27561824 | A | G* | 3_prime_utr_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138244163 | Hp1bp3 | rs27561823 | A | C* | 3_prime_utr_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138244213 | Hp1bp3 | rs50571538 | A | G* | 3_prime_utr_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138244215 | Hp1bp3 | rs49412085 | G | A* | 3_prime_utr_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138244535 | Hp1bp3 | rs27561822 | G | T* | 3_prime_utr_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138244544 | Hp1bp3 | rs48108757 | A | G* | 3_prime_utr_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138244588 | Hp1bp3 | rs46058661 | G | A* | 3_prime_utr_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |
| 4 | 138244667 | Hp1bp3 | rs27561820 | T | C* | 3_prime_utr_variant downstream_gene_variant | LOW/MODIFIER (non-coding variant, difficult prediction or no evidence of impact) |

INSERTIONS/DELETIONS

| | | | | | | |
|---|---|---|---|---|---|---|
| 4 | 138217250 | Hp1bp3 | rs261417297 | T | TCCGCCC | 5_prime_utr_variant intron_variant upstream_gene_variant downstream_gene_variant _ |
| 4 | 138217334 | Hp1bp3 | rs259647506 | T | TCGCCGC | 5_prime_utr_variant intron_variant downstream_gene_variant _ |
| 4 | 138218392 | Hp1bp3 | rs236249025 | A | AACT* | intron_variant downstream_gene_variant _ |
| 4 | 138219564 | Hp1bp3 | rs263338746 | C | CGTGTGT | intron_variant downstream_gene_variant _ |
| 4 | 138220819 | Hp1bp3 | rs243008536 | T | TAAGAA* | intron_variant downstream_gene_variant _ |
| 4 | 138221944 | Hp1bp3 | rs245866351 | A | AAAAAAC | intron_variant downstream_gene_variant _ |
| 4 | 138222068 | Hp1bp3 | rs260386774 | ATCTTT | AT* | intron_variant downstream_gene_variant _ |
| 4 | 138222872 | Hp1bp3 | rs256314394 | TGGCC | T* | intron_variant downstream_gene_variant _ |
| 4 | 138223845 | Hp1bp3 | rs218528109 | T | TC* | intron_variant upstream_gene_variant downstream_gene_variant _ |
| 4 | 138224114 | Hp1bp3 | rs262596616 | TTGA | T* | intron_variant upstream_gene_variant downstream_gene_variant _ |
| 4 | 138224191 | Hp1bp3 | rs246831585 | TC | t* | intron_variant upstream_gene_variant downstream_gene_variant _ |
| 4 | 138224518 | Hp1bp3 | rs256008323 | T | TTTATTC | intron_variant upstream_gene_variant downstream_gene_variant _ |
| 4 | 138224616 | Hp1bp3 | rs243668013 | G | GA* | intron_variant upstream_gene_variant downstream_gene_variant _ |
| 4 | 138224999 | Hp1bp3 | - | AGC | A* | intron_variant upstream_gene_variant downstream_gene_variant _ |
| 4 | 138225108 | Hp1bp3 | rs260534159 | A | AG* | intron_variant upstream_gene_variant downstream_gene_variant _ |
| 4 | 138226343 | Hp1bp3 | - | GT | G* | intron_variant upstream_gene_variant downstream_gene_variant _ |
| 4 | 138226830 | Hp1bp3 | - | ATAT | A* | intron_variant upstream_gene_variant downstream_gene_variant _ |
| 4 | 138227192 | Hp1bp3 | rs220831465 | G | GA* | intron_variant upstream_gene_variant downstream_gene_variant _ |
| 4 | 138227324 | Hp1bp3 | - | TATTTA | T* | intron_variant upstream_gene_variant downstream_gene_variant _ |
| 4 | 138228526 | Hp1bp3 | rs243700773 | G | GT* | intron_variant upstream_gene_variant downstream_gene_variant _ |
| 4 | 138228816 | Hp1bp3 | rs214296438 | A | AC* | intron_variant upstream_gene_variant downstream_gene_variant _ |
| 4 | 138228939 | Hp1bp3 | - | CTTTTT | ctttt/cttt* | intron_variant upstream_gene_variant downstream_gene_variant _ |
| 4 | 138229822 | Hp1bp3 | rs257597561 | AG | A* | intron_variant downstream_gene_variant _ |
| 4 | 138229845 | Hp1bp3 | rs253279359 | T | TG* | intron_variant downstream_gene_variant _ |
| 4 | 138230614 | Hp1bp3 | rs241155294 | G | GT* | intron_variant downstream_gene_variant _ |
| 4 | 138230655 | Hp1bp3 | rs262482259 | C | CG* | intron_variant downstream_gene_variant _ |
| 4 | 138231958 | Hp1bp3 | rs229217050 | AG | A* | intron_variant downstream_gene_variant _ |
| 4 | 138232026 | Hp1bp3 | rs262378565 | AAT | A* | intron_variant downstream_gene_variant _ |
| 4 | 138232325 | Hp1bp3 | rs222348322 | AACCTC | A* | intron_variant downstream_gene_variant _ |
| 4 | 138232373 | Hp1bp3 | rs216236080 | C | CCT* | intron_variant downstream_gene_variant _ |
| 4 | 138232615 | Hp1bp3 | rs252595698; | CACAG/ | CACAGAC | intron_variant downstream_gene_variant _ |
| 4 | 138236713 | Hp1bp3 | rs228130645 | TTCTGC | T* | intron_variant downstream_gene_variant |
| 4 | 138237075 | Hp1bp3 | rs245026168 | GC | G* | intron_variant downstream_gene_variant |
| 4 | 138238838 | Hp1bp3 | rs254261317 | CTTTT | C* | intron_variant downstream_gene_variant |
| 4 | 138238877 | Hp1bp3 | rs237588707 | CTG | C* | intron_variant downstream_gene_variant |
| 4 | 138239310 | Hp1bp3 | rs264666330 | TG | T* | intron_variant downstream_gene_variant |
| 4 | 138239524 | Hp1bp3 | rs229817259 | A | AT* | intron_variant downstream_gene_variant |
| 4 | 138240191 | Hp1bp3 | rs248640828 | C | CG | intron_variant |
| 4 | 138240440 | Hp1bp3 | rs255522189 | A | ACGGG | intron_variant |
| 4 | 138241148 | Hp1bp3 | rs223201062 | AT | A* | intron_variant downstream_gene_variant |
| 4 | 138241175 | Hp1bp3 | rs223166740 | A | AT* | intron_variant downstream_gene_variant |
| 4 | 138241342 | Hp1bp3 | rs227541260 | CAT | C* | intron_variant downstream_gene_variant |
| 4 | 138241910 | Hp1bp3 | rs263029223 | T | TTC* | 3_prime_utr_variant downstream_gene_variant |
| 4 | 138242379 | Hp1bp3 | rs216332941 | GCAC | G* | 3_prime_utr_variant downstream_gene_variant |
| 4 | 138242611 | Hp1bp3 | rs235605724 | GC | G* | 3_prime_utr_variant downstream_gene_variant |
| 4 | 138243790 | Hp1bp3 | rs251988415 | GA | G* | 3_prime_utr_variant downstream_gene_variant |
| 4 | 138244200 | Hp1bp3 | rs233852353 | A | AT* | 3_prime_utr_variant downstream_gene_variant |