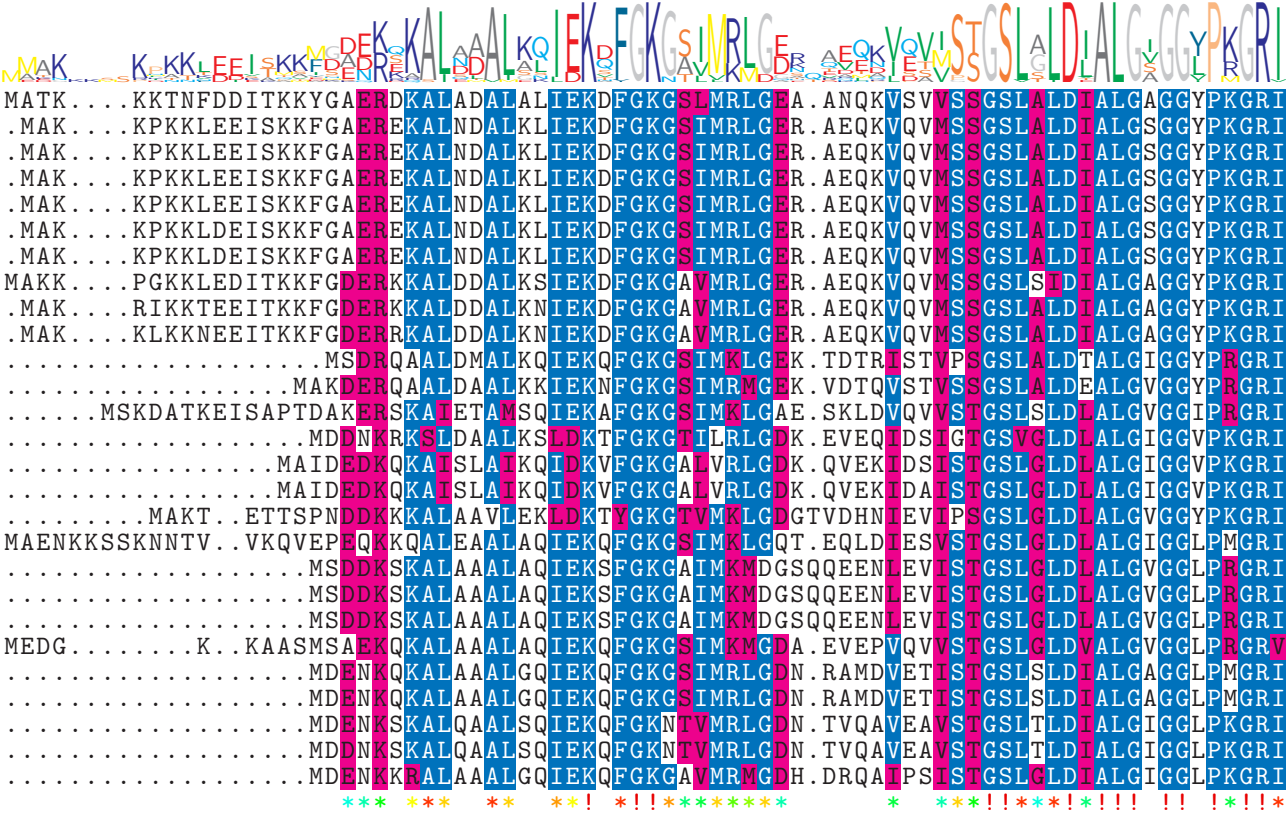


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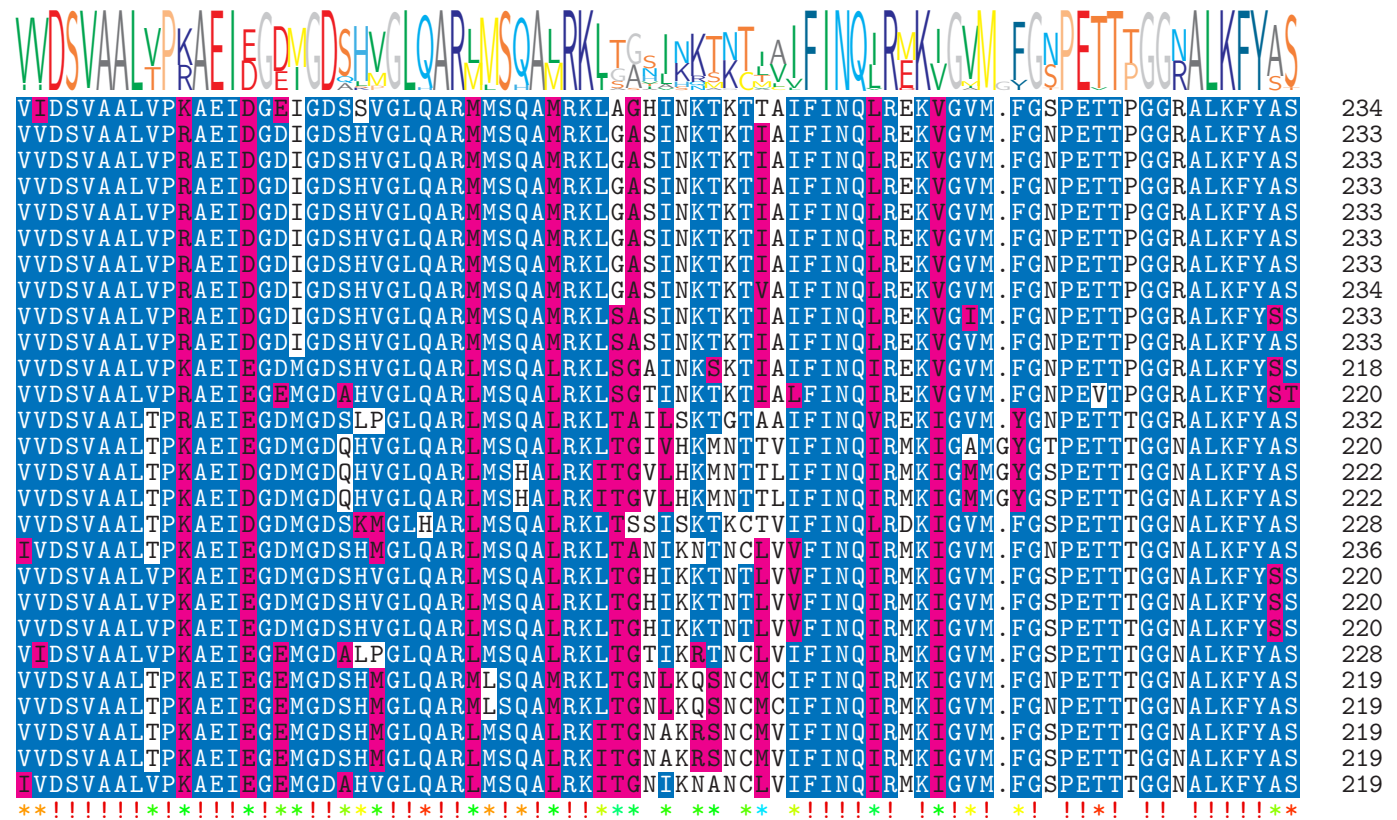
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NTDB id 194 SPR RS08825 WP 001085462.1	IEIYGPESSGKTTVALHAVA	AQAQKEGGIAAFIDAHAELDPAYAAALGVNIDELL	LSQPDSEGGGLEIAGKLIDSGAVDLV	154
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NTDB id 527 SMSK321 RS11065 WP 001085454.1	IEIYGPESSGKTTVALHAVA	AQAQKEGGIAAFIDAHAELDPAYAAALGVNIDELL	LSQPDSEGGGLEIAGKLIDSGAVDLV	154
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consensus

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Sequence logo for the 1000bp upstream region of the H19 gene. The x-axis represents the distance from the transcription start site (TSS) in base pairs, ranging from -1000 to 0. The y-axis represents the information content in bits. The sequence is color-coded: A (green), C (blue), G (red), and T (yellow). The logo shows a strong conservation of the sequence 5'-GAGTGG-3' around the TSS, which is the binding site for the H19 promoter.

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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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Sequence	Score
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EKIGQGS ¹ E ² N ³ A ⁴ K ⁵ K ⁶ Y ⁷ LA ⁸ EH ⁹ PE ¹⁰ IF ¹¹ DE ¹² ID ¹³ K ¹⁴ Q ¹⁵ V ¹⁶ R ¹⁷ SK ¹⁸ FG ¹⁹ L ²⁰ ID ²¹ GEEV ²² SEQD ²³ T... ²⁴ EN ²⁵ KK ²⁶ DE ²⁷ ... ²⁸ KK ²⁹ EEA ³⁰ .. ³¹ VNEEV ³² PLD ³³ LGDE ³⁴ .	381
EKIGQGS ¹ E ² N ³ A ⁴ K ⁵ K ⁶ Y ⁷ LA ⁸ EH ⁹ PE ¹⁰ IF ¹¹ DE ¹² ID ¹³ K ¹⁴ Q ¹⁵ V ¹⁶ R ¹⁷ SK ¹⁸ FG ¹⁹ L ²⁰ ID ²¹ GEEV ²² SEQD ²³ T... ²⁴ EN ²⁵ KK ²⁶ DE ²⁷ ... ²⁸ KK ²⁹ EEA ³⁰ .. ³¹ VNEEV ³² PLD ³³ LGDE ³⁴ .	381
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EKIGQGS ¹ E ² N ³ A ⁴ K ⁵ K ⁶ Y ⁷ LA ⁸ EH ⁹ PE ¹⁰ IF ¹¹ DE ¹² ID ¹³ K ¹⁴ Q ¹⁵ V ¹⁶ R ¹⁷ SK ¹⁸ FG ¹⁹ L ²⁰ ID ²¹ GEEV ²² SEQD ²³ T... ²⁴ EN ²⁵ KK ²⁶ DE ²⁷ ... ²⁸ KK ²⁹ EEA ³⁰ .. ³¹ VNEEV ³² PLD ³³ LGDE ³⁴ .	381
EKIGQGS ¹ E ² N ³ A ⁴ K ⁵ K ⁶ Y ⁷ LA ⁸ DN ⁹ PE ¹⁰ IF ¹¹ DE ¹² ID ¹³ H ¹⁴ Q ¹⁵ V ¹⁶ R ¹⁷ V ¹⁸ Q ¹⁹ FL ²⁰ ID ²¹ GEE ²² IA ²³ ES... ²⁴ .. ²⁵ KK ²⁶ DEA ²⁷ ... ²⁸ AQ ²⁹ VDS ³⁰ .. ³¹ VNEEV ³² TLD ³³ LGDE ³⁴ .	377
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EKIGQGS ¹ E ² N ³ A ⁴ K ⁵ K ⁶ FLA ⁷ DN ⁸ PA ⁹ IF ¹⁰ DE ¹¹ ID ¹² R ¹³ K ¹⁴ IR ¹⁵ V ¹⁶ HY ¹⁷ GL ¹⁸ EA ¹⁹ DG ²⁰ VEEV ²¹ AT... ²² .. ²³ EEA ²⁴ . ²⁵ PVV... ²⁶ .. ²⁷ AE... ²⁸ EIQD ²⁹ VILD ³⁰ LDGG ³¹ .	378
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ERLGGG ¹ RE ² NA ³ K ⁴ Q ⁵ FL ⁶ KN ⁷ KD ⁸ I ⁹ ML ¹⁰ MI ¹¹ Q ¹² EQ ¹³ LE ¹⁴ IRE ¹⁵ HY ¹⁶ GL ¹⁷ DN ¹⁸ NG ¹⁹ V ²⁰ V ²¹ QQ ²² QAE... ²³ .. ²⁴ ET ²⁵ QEE ²⁶ LEFE ²⁷ .E... ²⁸ ..	348
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ERIGGG ¹ KE ² K ³ TI ⁴ AY ⁵ IA ⁶ ER ⁷ PE ⁸ ME ⁹ QE ¹⁰ IR ¹¹ DR ¹² VM ¹³ AA ¹⁴ IR ¹⁵ AG ¹⁶ NAGE ¹⁷ AP ¹⁸ AL ¹⁹ AP ²⁰ AA ²¹ PE ²² AAEA... ²³ ..	363
KKLGGG ¹ RE ² NS ³ KA ⁴ FL ⁵ KN ⁶ PE ⁷ IA ⁸ DE ⁹ IT ¹⁰ KA ¹¹ I ¹² Q ¹³ NS ¹⁴	

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NTDB id 1211 C694 RS00795 WP 000963128.1		347
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NTDB id 1334 RAOC RS04870 WP 004918236.1		343
NTDB id 1389 A4U84 RS07560 WP 021112712.1		372
NTDB id 1130 NGFG RS03960 WP 003688695.1		348
NTDB id 1124 NGFG RS03960 WP 003688695.1		348
NTDB id 1123 OK783 RS03845 WP 003688695.1		348
NTDB id 1427 RS RS02760 WP 011000510.1		352
NTDB id 1165 A1552VC RS01565 WP 000344154.1		354
NTDB id 1142 GTF74 RS11550 WP 000344154.1		354
NTDB id 1074 ABD1 RS10195 WP 000344167.1		349
NTDB id 1022 ACIAD RS06390 WP 004925639.1		349
NTDB id 1205 PSJM300 05545 AFN77183.1		347
consensus		

-  non conserved
-  similar
-  ≥ 50% conserved