norm _dispersion_TSS_-[500|1000|2000]_[0|25|50|75]%: percentiles as specified (0|25|50|75%) of normalized ChIP over input enrichment metagene profile values within the interval TSS +/- (500bp|1Kb|2Kb), as specified

Scaled whole gene metaprofiles

chip_hotSpots_twopoints_[-2000|0|500|2500|3000|4000]: ChIP-signal at the specified coordinate position in the scaled whole gene metagene: i.e. respectively (TSS-2Kb | TSS | TSS+500bp | TES-500bp | TES | TES+1Kb).

chip_localMax_twopoint_1_[x|y]: metagene (x|y) coordinate of maximum ChIP-signal in interval [-2Kb, TSS]

chip_localMax_twopoint_2_[x|y]: metagene (x|y) coordinate of maximum ChIP-signal in interval [TSS, TSS+500bp]

chip_localMax_twopoint_3_[x|y]: metagene (x|y) coordinate of maximum ChIP-signal in interval [TSS+500bp, TES-500bp]

chip_localMax_twopoint_4_[x|y]: metagene (x|y) coordinate of maximum ChIP-signal in interval [TES-500bp, TES]

chip_localMax_twopoint_5_[x|y]: metagene (x|y) coordinate of maximum ChIP-signal in interval [TES, TES+1Kb]

chip_auc_twopoint_1: ChIP -signal AUC in interval [-2Kb, TSS]

chip_auc_twopoint_2: ChIP -signal AUC in interval TSS, TSS+500bp]

chip_auc_twopoint_3: ChIP -signal AUC in interval [TSS+500bp, TES-500bp]

chip_auc_twopoint_4: ChIP -signal AUC in interval [TES-500bp, TES]

chip_auc_twopoint_5: ChIP -signal AUC in interval [TES, TES+1Kb]

norm_hotSpots_twopoints_[-2000|0|500|2500|3000|4000]: nomralized ChIP over input enrichment at the specified coordinate position in the scaled whole gene metagene: i.e. respectively (TSS-2Kb | TSS | TSS+500bp | TES-500bp | TES | TES+1Kb).

norm_localMax_twopoint_1_[x|y]: metagene (x|y) coordinate of maximum ChIP enrichment in interval [-2Kb, TSS]

norm_localMax_twopoint_2_[x|y]: metagene (x|y) coordinate of maximum ChIP enrichment in interval [TSS, TSS+500bp]

norm_localMax_twopoint_3_[x|y]: metagene (x|y) coordinate of maximum ChIP enrichment in interval [TSS+500bp, TES-500bp]

norm_localMax_twopoint_4_[x|y]: metagene (x|y) coordinate of maximum ChIP enrichment in interval [TES-500bp, TES]

norm_localMax_twopoint_5_[x|y]: metagene (x|y) coordinate of maximum ChIP enrichment in interval [TES, TES+1Kb]

norm_auc_twopoint_1: ChIP enrichment AUC in interval [-2Kb, TSS]

norm_auc_twopoint_2: ChIP enrichment AUC in interval TSS, TSS+500bp]

norm_auc_twopoint_3: ChIP enrichment AUC in interval [TSS+500bp, TES-500bp]

norm_auc_twopoint_4: ChIP enrichment AUC in interval [TES-500bp, TES]

norm_auc_twopoint_5: ChIP enrichment AUC in interval [TES, TES+1Kb]