**HS.totals Term Reference List**

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| Chr | Chromosome number |
| Start | Feature start position (bp), from hotspot template. |
| End | Feature end position (bp), from hotspot template. |
| Length | Feature length (bp), from hotspot template (End-Start) |
| Midpoint | Feature mean point position (bp). |
| WatsonHpM | Sum of the hits on the Watson strand within this feature as a proportion of total combined reads for the library, where this total is normalised to be to 1million |
| CrickHpM | Sum of the hits on the Crick strand within this feature as a proportion of total combined reads for the library, where this total is normalised to be 1million |
| TotalHpM | Combined sum of the hits on both the Watson & Crick strands within this feature as a proportion of total combined reads for the library, where this total is normalised to be 1million |
| BGHpM | Presumed background signal within this feature:  determined by multiplying this feature’s length with a presumed average background value (i.e., the average value per base pair within the 50 longest gene regions of presumed Spo11 inactivity, as normalised to the total for the library, where this total is normalised to be 1 million) |
| TotalBGHpM | The total presumed *non-backgroun­d* signal within this feature as a proportion of total library: TotalHpM (combined sum within this feature as proportion of total library) minus the BGHpM value (presumed background with this feature as a proportion of total library). |
| WatsonHpM300, CrickHpM300, TotalHpM300  BGHpM300, TotalBGHpM300 | Same as WatsonHpM, CrickHpM, TotalHpM, BGHpM and TotalBGHpM except that the length of the feature to be considered has been extended 300 bp. |
| NormHpM | The total presumed *non-backgroun­d* signal within this feature as a proportion of the summed feature table (ignores reads outside features): TotalBGHpM (i.e. the total presumed *non-backgroun­d* signal within this feature) as a proportion of the total combined reads that are only within the features defined in the hotspot template where this total is normalised to be 1million. |
| NormHpM300 | Same as NormHpM except that the length of the feature to be considered has been extended 300 bp. |
| NormHpChr | Same as NormHpM but only considering hits on each chromosome. |