**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). |
| **Franklin | WatsonHpM** | Sum of the hits on the Franklin | Watson strand within this feature as a proportion of total combined reads for the library, where this total is normalised to be to 1 million |
| **Rosalind | CrickHpM** | Sum of the hits on the Rosalind | Crick strand within this feature as a proportion of total combined reads for the library, where this total is normalised to be 1 million |
| **TotalHpM** | Combined sum of the hits on both the Franklin | Watson & Rosalind | Crick strands within this feature as a proportion of total combined reads for the library, where this total is normalised to be 1 million |
| **BGHpM** | Estimated background signal within this feature: determined by multiplying this feature’s length with an estimated average background value (the average value per base pair within the central area of the 50 longest gene regions [presumed Spo11 inactivity] as normalised to the total for the library, where this total is normalised to be 1 million) |
| **TotalBGHpM** | The total estimated *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). |
| **Franklin | WatsonHpM300, Rosalind | CrickHpM300, TotalHpM300, BGHpM300, TotalBGHpM300** | Same as Franklin | WatsonHpM, Rosalind | CrickHpM, TotalHpM, BGHpM and TotalBGHpM except that the length of the feature to be considered has been extended 300 bp. |
| **NormHpM** | The total estimated *non-backgroun­d* signal within this feature as a proportion of the summed feature table (ignores reads outside features): Specifically, it is the TotalBGHpM (i.e. the total estimated *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 1 million. |
| **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. |