Exact position where reads come from

Hi,

I have sequenced many RNA paired-end reads, and mapped to genome reference sequence, and now I want to know whether the read is mapped correctly. And from the read identifier, for example: `chr1:4847775-4887990W:NM_001159750:1:2668:917:1137:S/2, I know this read is come from the range [4847775,4887990],and the segment range is [917,1137], but I am still not clear how to get the exact genomic start position of the read? Is it possible to get it from the read identifier? If not, is there a way to get the exact genomic start position of a read? Thank you very much.`