Flow of the project

CP design	Download bin-mapped ESTs from the wEST database into the ConservedPrimers 2.0 pipeline. (6,045 ESTs downloaded)
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	Design primers with the pipeline and manually. (Primer pairs for 2111 unigenes designed)
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GSP design	PCR amplify and sequence *T. urartu, Ae. tauschii,* and *Ae. speltoides* amplicons and at lest 12 clones of each 'Langdon' durum amplicon.
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	Align sequences, allocate them to the A, B, and D genomes and find divergent nucleotides.
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	Use a divergent nucleotide to design a genome-specific primer and pair it with one of the CP primers (11,764 GSPs designed and tested)
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GSP validation	Perform PCR using GSPs with relevant wheat nullisomic-tetrasomic lines and validate primer genome specificity (GSPs for 2114 loci belonging to 1,102 unigenes validated)
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SNP discovery	Amplify gene targets using GSPs in the panel of 32 wheat lines. (2,114 genes amplified)
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	Align sequences and search for SNPs (5,471 SNPs discovered at 1,791 gene loci)
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Data base construction	Submit the alignments with SNPs to the project database (http://probes.pw.usda.gov:8080/snpworld/Search)